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BRUNO AUGUSTO ALVES MARTINS

**ESTUDO PROTEÔMICO PARA PROSPECÇÃO DE POTENCIAIS BIOMARCADORES
PLASMÁTICOS E URINÁRIOS EM PACIENTES COM ADENOCARCINOMA COLORRETAL:
ANÁLISE POR ESPECTROMETRIA DE MASSAS**

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Dissertação apresentada ao Programa de Pós-graduação em Ciências Médicas da Faculdade de Medicina da Universidade de Brasília como requisito parcial à obtenção do grau de Mestre.

Área de Concentração: Medicina

Orientador: Prof. Dr. Paulo Gonçalves de Oliveira

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“Ouça conselhos e aceite instruções, e acabará sendo sábio.”

Provérbios 19:20.

RESUMO

O câncer colorretal (CCR) representa um dos tipos mais comuns de câncer no Brasil e no mundo. Grande parte dos pacientes ainda são diagnosticados em fases avançadas da doença, o que reduz drasticamente as taxas de sobrevivência. O principal método de rastreamento do CCR é a colonoscopia, entretanto, o exame apresenta baixa aceitação e complicações importantes. Sendo assim, a prospecção de biomarcadores que possam auxiliar não só no diagnóstico, mas também na estratificação prognóstica e na predição de tratamento, ainda é necessária no manejo de pacientes com CCR. A proteômica surge como ferramenta poderosa na descoberta de biomarcadores, sendo a espectrometria de massas o método mais empregado. O objetivo deste estudo foi avaliar e comparar o perfil proteômico sérico e urinário de pacientes portadores de adenocarcinoma colorretal e pacientes sem neoplasia e avaliar o proteoma tecidual tumoral de pacientes com adenocarcinoma colorretal, visando a identificação de potenciais proteínas biomarcadoras. Foram coletadas amostras de tecido tumoral, plasma e urina de 9 pacientes portadores de adenocarcinoma colorretal e amostras de plasma e urina de 9 pacientes sem a doença. O material foi analisado através de espectrometria de massas sob abordagem *label-free* LC-MS/MS, sendo identificadas 26 proteínas com regulação diferenciada entre os cenários analisados, apresentando assim potencial para uso como biomarcadores. Estudos subsequentes são necessários para verificação e validação do papel dessas moléculas na abordagem do CCR.

Descritores: câncer colorretal, espectrometria de massas, proteômica, biomarcadores.

ABSTRACT

Colorectal cancer is one of the most common types of cancer in Brazil and worldwide. Most patients are still diagnosed in advanced stages of the disease, which dramatically reduces survival rates. The main method of screening for colorectal cancer is colonoscopy, however, the test has low acceptance and major complications. Thus, the prospection of biomarkers that may help not only in diagnosis, but also in prognostic stratification and prediction of treatment, is still necessary in the management of patients with colorectal cancer. Proteomics appears as a powerful tool in the discovery of biomarkers, with mass spectrometry being the most used method. The objective of this study was to evaluate and compare the plasmatic and urinary proteomic profile of patients with colorectal adenocarcinoma and patients without neoplasia and to evaluate the tumor tissue proteome of patients with colorectal adenocarcinoma, aiming the identification of potential protein biomarkers. Samples of tumor tissue, plasma and urine were collected from 9 patients with colorectal adenocarcinoma and plasma and urine samples were collected from 9 patients without the disease. The material was analyzed by mass spectrometry under a label-free LC-MS/MS approach. Twenty-six proteins with differential regulation were identified among the analyzed scenarios, thus presenting potential for use as biomarkers. Subsequent studies are required to verify and validate the role of these molecules in the approach of patients with colorectal cancer.

Key words: colorectal cancer, mass spectrometry, proteomic, biomarkers.

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LISTA DE ABREVIATURAS E SIGLAS

ACTBL-2: Actina beta *2-like*

Alb: Albumina

ANOVA: *Analysis of Variance*

B2M: Beta-2-microglobulina

CEA: Antígeno carcinoembrionário

CCR: Câncer colorretal

CDC5L: Proteína 5 do ciclo de divisão celular

COL1A1: Colágeno tipo-1-alfa-1

COL1A2: Colágeno tipo-1-alfa-2

DPEP1: Dipeptidase 1

DTT: Ditioneitol

EFEMP2: Proteína da matriz celular 2 semelhante a fibulina contendo EGF

EFEMP1: Proteína da matriz celular 1 semelhante a fibulina contendo EGF

EGF: Fator de crescimento epidérmico

EGFR: Receptor do fator de crescimento epidérmico

ELISA: Ensaio de imunoabsorção enzimática

ESI: *Electrospray*

FDR: *False Discovery Rate*

FPLC: *Fast Protein Liquid Chromatography*

FT-ICR: *Fourier-transform ion cyclotron resonance*

GP: *Gene Ontology*

IAA: Iodoacetoamida

IgG: Imunoglobulina G

IGJ: Cadeia da imunoglobulina J

HCD: *Higher Energy Collisional Dissociation*

iTRAQ: Quantificação com marcadores isobáricos e absolutos

KRT18: Queratina 18

KNG1: Cininogênio-1

LC-MS/MS: Espectrometria de massas em tandem

LRG1: Alfa-2-glicoproteína 1 rica em leucina

LTQ: *Linear Trap Quadrupole*

MALDI: *Matrix-Assisted Laser Desorption Ionization*

MeOH: Metanol

MRC1: Proteína receptora 1 de manose do macrófago

MS: Espectrometria de massas

mTOR: Proteína alvo de rapamicina em mamíferos

m/z: Razão massa-carga

OLFM4: Olfactomedina-4

PCA: *Principal Component Analysis*

PI3K: Fosfatidilinositol-3-quinase

Sec24C: Proteína de transporte Sec24C

SERPINA1: Alfa-1-antitripsina

SERPINA3: Alfa-1antiquimotripsina

SERPINC1: Antitrombina-3

SOF: Sangue oculto nas fezes

STK4 ou MST1: Proteína serina/treonina quinase 4

S100A9: Proteína ligante de cálcio S100 A9

TEAB: Bicarbonato de trietilamônio

TFA: Ácido trifluoroacético

TfR1: Receptor de transferrina tipo 1

TOF: *Time-of-flight*

TUBB5: Cadeia beta-5 da tubulina

UHPLC: *Ultra high-performance liquid chromatography*

v/v: Volume/Volume

1. INTRODUÇÃO

O câncer colorretal (CCR) representa o terceiro tipo mais comum de câncer diagnosticado entre adultos e a terceira causa mais comum de óbitos relacionados ao câncer nos Estados Unidos.(1) No Brasil, o CCR figura como o terceiro tipo de câncer mais comum entre homens e o segundo entre as mulheres, sendo estimados 17.380 casos novos em homens e 18.980 em mulheres para cada ano do biênio 2018-2019.(2) A maioria dos cânceres colorretais ocorre de maneira esporádica, sendo caracterizados por um processo de carcinogênese sequenciado que envolve acúmulo progressivo de mutações em um período que dura em média 10 a 15 anos.(3-6) Esse longo intervalo de evolução permite o emprego de métodos de rastreamento, detecção precoce do câncer e remoção das lesões pré-malignas (adenomas), levando à redução das taxas de incidência e mortalidade do adenocarcinoma colorretal.(6-9) Apesar da oportunidade de diagnóstico precoce, aproximadamente 45% dos casos de CCR são diagnosticados no estadio IV, quando os pacientes já apresentam metástases à distância e sobrevida em 5 anos menor que 10%. Em contraste com a baixa sobrevida dos pacientes com doença avançada, a taxa de sobrevida em 5 anos de pacientes com doença localizada, quando a ressecção cirúrgica é a primeira linha de tratamento, alcança os 90%.(10)

A colonoscopia é o exame padrão-ouro no rastreamento de CCR. Trata-se do único teste que possui a capacidade de identificar e remover os pólipos adenomatosos, que configuram as lesões pré-malignas, resultando assim em redução da mortalidade pelo CCR.(11,12) As diretrizes atuais recomendam que adultos acima de 45 anos, sem fatores de risco para o desenvolvimento de CCR, iniciem o rastreamento por esse método.(9) Entretanto, a colonoscopia tem baixa aceitação pelos pacientes. O procedimento tem custo elevado, é invasivo, operador-dependente e apresenta complicações importantes, como perfuração, sangramento e complicações cardiorrespiratórias. Outras razões para a adesão limitada dos pacientes ao exame incluem questões relacionadas ao pudor e vergonha pela instrumentação da região anal, desconforto, necessidade de sedação e obrigatoriedade do preparo de cólon.(13,14)

Exames diagnósticos não-invasivos como a pesquisa de sangue oculto nas fezes (SOF) pelo teste de guaiaco ou por imunistoquímica e a pesquisa de DNA fecal podem ser usados em programas de rastreamento, porém, testes positivos devem ser seguidos pela realização da colonoscopia.(9) A pesquisa de sangue oculto nas fezes é o método não invasivo mais utilizado e mais bem aceito pelos participantes nos programas de rastreamento populacionais, entretanto, apesar de ser um exame simples e de baixo custo, apresenta taxas relativamente baixas de sensibilidade e especificidade, resultando em número elevado de testes falso-positivos, falso-negativos e baixas taxas de detecção de pólipos colônicos.(5,6,15-17)

Sendo assim, métodos de rastreamento não-invasivos, tais como os biomarcadores moleculares, que agreguem custo-efetividade, altas taxas de acurácia e facilidade de aferição ainda são necessários no contexto diagnóstico do CCR. Entretanto, as possíveis aplicações clínicas de biomarcadores no CCR vão além da detecção precoce da doença, sendo também de suma importância na estratificação de prognóstico, vigilância e determinação de tratamento personalizado.(18-20)

O biomarcador de maior aplicação no CCR é o antígeno carcinoembrionário (CEA), uma glicoproteína de alto peso molecular encontrada em tecidos embrionários e neoplasias colorretais, que foi descoberta em 1965. Níveis elevados de CEA são associados com a progressão neoplásica e podem indicar recorrência da doença após o tratamento cirúrgico. Entretanto, altos valores de CEA não são específicos para o CCR e também podem ser encontrados em outras malignidades e em condições inflamatórias, como doenças inflamatórias intestinais, doenças hepáticas e pancreatite.(21) Recentemente, outros parâmetros têm sido usados na determinação do prognóstico. Marcadores genéticos como a instabilidade de microssatélites e a mutação do gene BRAF tiveram seus papéis elucidados e já têm uso difundido na abordagem do CCR (22).

No campo do tratamento do CCR, o crescente aumento no número de quimioterápicos, abordagens neoadjuvantes e a recente descoberta da aplicação da imunoterapia no tratamento de pacientes com CCR resultaram na necessidade de implementação de biomarcadores preditivos que possam guiar o processo de decisão

terapêutica.(23,24) Um exemplo da importância dos marcadores preditivos é a quimioterapia com drogas antagonistas do receptor do fator de crescimento epidérmico (EGFR) em pacientes com tumores KRAS selvagem. A descoberta desta estratégia de terapia-alvo transformou a determinação do *status* mutacional da família RAS em um passo mandatório na adequação do esquema quimioterápico em pacientes com CCR metastático.(25)

Na constante busca por ferramentas que possam auxiliar na abordagem dos pacientes portadores de CCR, recentes progressos em genômica, transcriptômica, proteômica e metabolômica têm contribuído para a descoberta e aumento no número de candidatos à biomarcadores, maior entendimento da progressão da doença e identificação de perfis moleculares associados ao CCR.(10,22,26–30) Dentre essas áreas de expansão, a proteômica representa extensa variedade de abordagens utilizadas para identificação, aferição, caracterização e análise de proteínas em ampla escala.(31) Os tecidos neoplásicos e displásicos regulam a expressão de proteínas e produzem perfis proteicos que podem estar associados com a progressão dessas lesões em diferentes e intercambiáveis vias de sinalização.(32) A pesquisa proteômica translacional prioriza a aplicação dos conceitos gerais da proteômica para determinar a expressão de perfis proteicos relacionados à variações fenotípicas patológicas, contribuindo assim para a aplicação na prática clínica.(25)

A maioria dos estudos para prospecção de biomarcadores emprega técnicas baseadas em espectrometria de massas (MS) para identificação e validação de proteínas com expressão alterada.(31) A MS consiste em uma técnica que permite a determinação da razão entre a massa e a carga (m/z) de espécies ionizadas em uma fase gasosa. De modo geral, todo espectrômetro de massas apresenta três componentes principais: uma fonte de íons; um analisador de massas; e um detector. As fontes de ionização mais empregadas em MS são o *Electrospray* (ESI) e a MALDI (*Matrix-Assisted Laser Desorption Ionization*), e elas têm a função de converter as moléculas a serem analisadas em espécies ionizadas em fase gasosa. O analisador de massas irá separar os íons conforme a m/z . Os principais analisadores de massa, que podem ser utilizados de maneira individual ou acoplados, são os quadrupolos, *ion-traps* tridimensionais ou lineares, *time-of-flight* (TOF), *Fourier-*

transform ion cyclotron resonance (FT-ICR) e o orbitrap. Por último, o detector irá gravar o sinal de separação dos íons, amplificando e armazenando eletronicamente.(33,34)

A MS permite a identificação e quantificação da expressão de proteínas de modo extremamente sensível, mesmo daquelas moléculas presentes em baixos níveis nas amostras biológicas. Além disso, esse método é eficaz na detecção de modificações pós-translacionais, funcionalidades, localização e interações das proteínas, favorecendo a compreensão das vias de sinalização celular. Essas características fazem com que a MS seja a principal técnica da proteômica translacional nas pesquisas para prospecção de biomarcadores, especialmente no campo da oncologia.(35)

2. OBJETIVO

- Avaliar e comparar o perfil proteômico sérico e urinário de pacientes portadores de adenocarcinoma colorretal e pacientes sem neoplasia, visando a identificação de proteínas biomarcadoras com potencial diagnóstico.
- Avaliar o proteoma tecidual tumoral e comparar com os proteomas plasmático e urinário de pacientes com adenocarcinoma colorretal.

3. MÉTODOS

3.1. Protocolo de estudo

O presente trabalho obedeceu à resolução 196/96 das Diretrizes e Normas Regulamentadoras de Pesquisas Envolvendo Seres Humanos do Conselho Nacional de Saúde, tendo sido submetido previamente a aprovação do Comitê Nacional de Ética em Pesquisa através da submissão na Plataforma Brasil, parecer CAAE número 83200917.9.0000.5558. Todos os participantes foram informados a respeito dos detalhes do estudo e assinaram Termo de Consentimento Livre e Esclarecido.

3.1.1. Critérios de inclusão

Pacientes encaminhados ao Serviço de Coloproctologia do Hospital Universitário de Brasília para realização de colonoscopia ou para realização de tratamento cirúrgico de adenocarcinomas colorretais foram convidados a participar do estudo. Dados referentes ao quadro clínico, história familiar, antecedentes patológicos e hábitos de vida foram coletados por meio de entrevista ou pesquisa de prontuário.

3.1.2. Critérios de exclusão

Foram excluídos: indivíduos com doença inflamatória intestinal; pacientes com critérios clínicos para diagnóstico de polipose adenomatosa familiar, câncer colorretal hereditário não polipose ou outras síndromes de câncer colorretal hereditário; pacientes que realizaram quimioterapia e/ou radioterapia neoadjuvante; e aqueles com tumores colônicos sincrônicos e metacrônicos.

3.1.3. Casuística

Foram coletadas e avaliadas amostras de plasma e urina de dois grupos de pacientes: um grupo de indivíduos submetidos a colonoscopia que não apresentavam neoplasias colorretais (grupo Controle) e um grupo submetido a colonoscopia ou tratamento cirúrgico que apresentava adenocarcinoma colorretal (grupo CCR).

As amostras de sangue foram coletadas no momento da punção venosa periférica para realização da sedação ou anestesia, em tubos EDTA, sendo o plasma separado por centrifugação (3500g, 8 min, em temperatura ambiente) e armazenado a -80°C em tubos criogênicos até a subsequente análise. As amostras de urina foram coletadas em tubos tipo Falcon, a partir de jato médio ou sonda vesical, sendo armazenadas a -80°C em tubos criogênicos para posterior análise.

No grupo CCR foram coletadas ainda amostras de tecido tumoral por meio de biópsia endoscópica ou biópsia direta de peça cirúrgica ressecada. Os fragmentos tissulares tumorais foram armazenados em tubos criogênicos à -80°C para posterior análise. Quinze indivíduos foram submetidos à coleta de material, entretanto, 6 foram excluídos da análise: quatro devido amostras insuficientes ou inadequadas para avaliação; um por se tratar de paciente com antecedente de quimiorradioterapia; e um por ter apresentado quantificação de proteínas insuficiente após processamento da amostra.

No grupo controle foram efetuadas coletas de 14 pacientes, entretanto, cinco foram excluídos da análise devido amostras insuficientes ou inadequadas para avaliação.

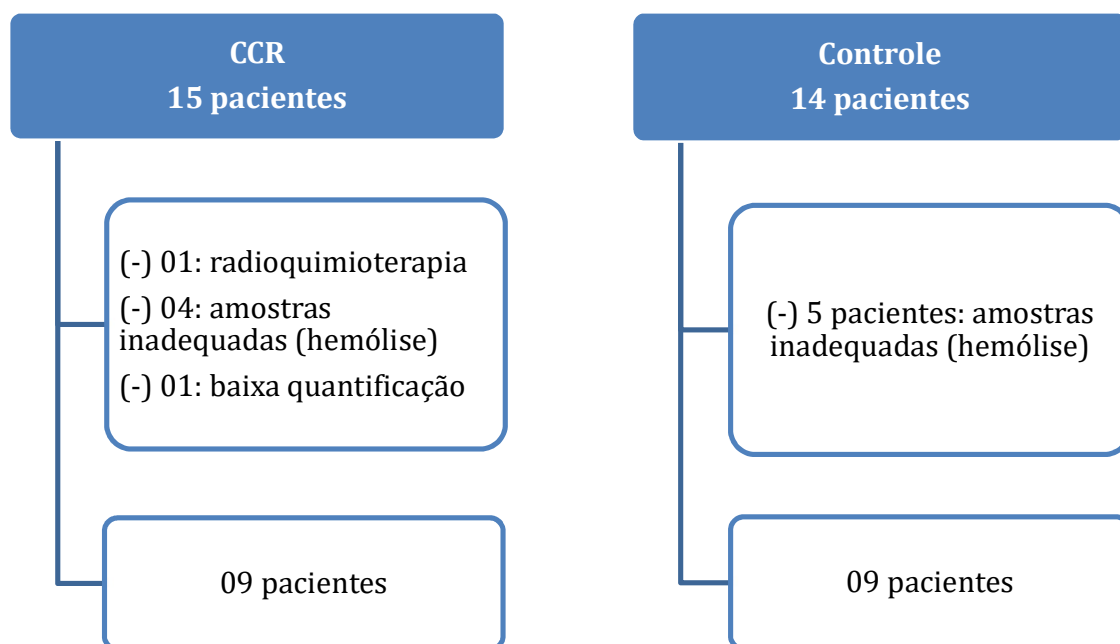


Figura 1. Fluxograma da formação da casuística

Tabela 1- Características clínico-patológicas dos participantes do estudo

	Grupo CCR (n=9)	Grupo controle (n=9)
Sexo		
Masculino	3 (33,3%)	3 (33,3%)
Feminino	6 (66,7%)	6 (66,7%)
Idade (anos, mediana [variação])	62 [43-85]	63 [38-76]
IMC (kg/m ² , mediana [variação])	23,7 [17,5-30,1]	27,04 [22,9-35,9]
Estadiamento		
I	1(11,1%)	-
II	3 (33,3%)	-
III	3 (33,3%)	-
IV	2 (22,2%)	-
Localização do tumor		
Cólon direito	3 (33,3%)	-
Cólon esquerdo	2 (22,2%)	-
Reto	4 (44,4%)	-
CEA (mediana [ng/mL] /variação)	2,78 [1,17-180]	-

3.2. Descrição da preparação de amostras e análise proteômica

Todo processo de preparo e análise do material coletado foi realizado no Instituto de Ciências Biológicas da Universidade de Brasília.

As principais etapas do processo de preparação e análise proteômica encontram-se descritas na Figura 2.

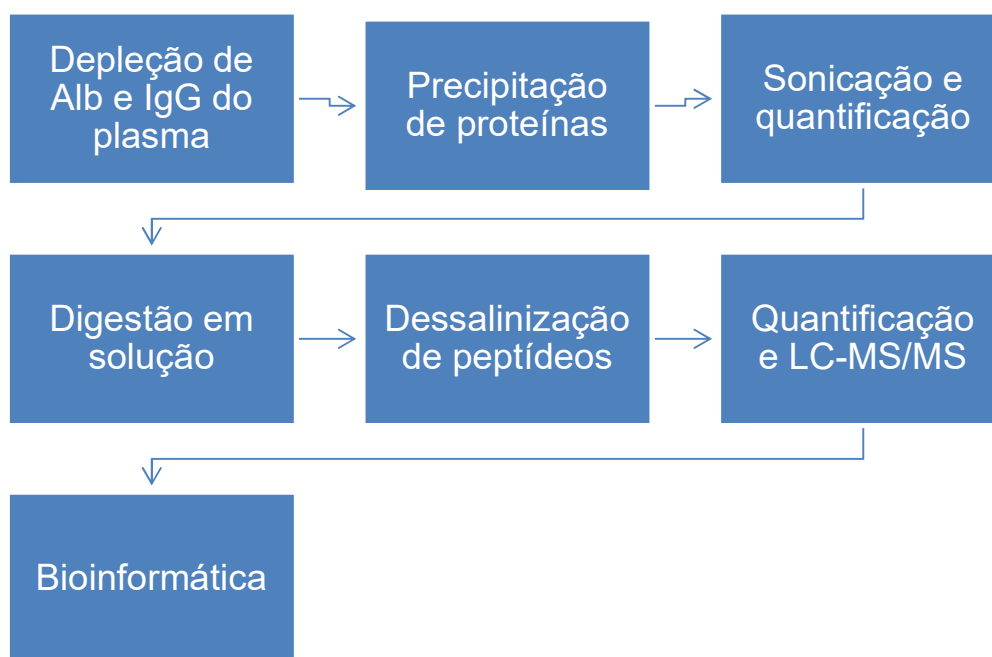


Figura 2. Fluxograma de passos da análise proteômica

- **Depleção de proteínas abundantes do plasma, sonicação e precipitação de proteínas**

As amostras de plasmas foram submetidas inicialmente à depleção de proteínas abundantes como albumina (Alb) e imunoglobulina G (IgG). As amostras de urina e tecido não passaram por processo de depleção, sendo abordadas já no passo seguinte de precipitação e sonicação.

A partir de uma alíquota não diluída de 100µL de plasma foi realizada a depleção de Alb e IgG. Em sistema *Fast Protein Liquid Chromatography* (FPLC) (Amersham Biosciences ÄKTA Explorer 10), a coluna de afinidade pré-empacotada (Hitrap Collum GE)

foi previamente lavada e reequilibrada com tampão de ativação fosfato de sódio 20mM, NaCl 0.15M (pH 7.4). As amostras foram injetadas separadamente após centrifugação a 2500g e 4°C por 5 min. A fração de proteínas depletada foi eluída pelo tampão de ativação enquanto Alb e IgG permaneciam ligadas à resina. Posteriormente as proteínas abundantes foram eluídas em tampão de eluição Glicina-HCl 0.1M (pH 2.7).

Ao final das corridas, as frações eluídas foram estocadas a -80°C para futuras análises e as frações proteicas depletadas foram submetidas a precipitação *overnight* a -20°C com acetona 100% e NaCl em concentração final de 0.1M. As frações precipitadas foram ressuspensas em solução de TEAB 0.02M e submetidas à sonicação em Tip Sonicador Q125 (QSonica) com intensidade a 40% do potencial em 3 ciclos de 10 seg cada.

- **Quantificação de proteínas**

A quantificação da concentração de proteínas das amostras foi realizada a partir da detecção de fluorescência pela técnica de Qubit™ (Invitrogen). Primeiramente, preparou-se o reagente fluorescente a partir da junção entre soluções de fluoróforo e tampão na proporção de 1:200. Em seguida, alíquotas de 5µl de amostra diluídas em água Milli-Q® (1:3) foram adicionadas ao reagente para atingir volume final de 200µl. As misturas foram incubadas por 15 min cada, de forma sequencial, e então analisadas no equipamento portátil Qubit™. Após a leitura de cada amostra, a concentração final foi obtida multiplicando o valor da leitura pelo fator de diluição escolhido.

- **Digestão em solução de tripsina**

Foram aliqüotadas 30µg de proteína em tubos Eppendorf de baixa adsorção para proteínas e peptídeos (LoBind) para o processo de digestão. Liofilizados em concentrador rotatório SpeedVac™ SC100 (Savant™), os extratos proteicos foram inicialmente ressuspensos em solução de TEAB 20mM, ureia 8M e DTT 50mM (pH 7,9) e incubados por 25 min a 55°C e 400rpm. Sob abrigo de luz e após resfriamento, foi adicionada solução de IAA suficiente para atingir concentração final de 14mM e incubou-se novamente por 40 min a 21°C e 400rpm. Posteriormente foi adicionada solução de DTT na concentração final de 5mM para parada da reação de alquilação.

As amostras foram então diluídas na razão 1:5 com solução de TEAB 20mM (pH 7,9), devido a intolerância da enzima tripsina a altas concentrações de ureia, considerando a adição de solução de CaCl₂ suficiente para atingir concentração final de 1mM e a adição de tripsina (Promega) na razão 1:50. Em seguida, as amostras foram incubadas por 13 horas a 37°C e 300rpm, e após o período de digestão, foi adicionado TFA na concentração final de 1% para evitar clivagens inespecíficas e cessar a reação. Os digestos proteicos foram dessalinizados imediatamente.

- **Dessalinização**

Os peptídios trípticos foram dessalinizados em microcolunas *home-made* de fase reversa. Construídas a partir de discos Empore™ SPE (Sigma-Aldrich, USA), com partículas C18 de característica hidrofóbica. As microcolunas permitem a purificação e enriquecimento dos peptídeos a partir da retirada de sal e subsequente eluição dos mesmos.

Para o preparo das microcolunas, construídas em ponteiras P200, foram realizadas sequências de centrifugação a 1000g por 3 min com 100µL de MeOH 100%, seguido de 100µL de solução de acetonitrila 80% (v/v) e ácido acético 0,5% (v/v), e por fim 100µL de solução de ácido acético 0,5% (v/v).

Finalmente, os digestos proteicos foram adicionados às colunas, centrifugados a 900g durante 4 min e dessalinizados duas vezes com 100µL de solução de ácido acético 0,5% (v/v) a 1000g por 3 min.

A eluição dos peptídeos foi realizada com concentrações crescentes de acetonitrila (25%, 50%, 80% e 100%), mantendo a concentração de ácido acético a 0,5% nas soluções, e centrifugações lentas de 600g durante 3 min. As frações, de 20µL (v/v) cada, foram coletadas em tubos Eppendorf LoBind.

Os peptídeos eluídos foram liofilizados em concentrador rotatório SpeedVac™ SC100 (Savant™) e armazenados a -80°C até a quantificação, também realizada segundo a plataforma Qubit™.

- **Análise por LC-MS/MS e bioinformática**

As amostras foram analisadas com um sistema UHPLC-nano (Dionex) acoplado *online* com um espectrômetro de massas LTQ-Orbitrap Elite (ThermoScientific). Precisamente 6 µg de proteína total extraída a partir do volume inicial de amostra foram carregadas em uma coluna PepSwift Monolithic Trap Column de 5 cm (diâmetro interno de 200 µm, Dionex-nanoViper) e separadas em uma coluna analítica de alta resolução PepSwift Monolithic Nano Column de 25 cm (diâmetro interno de 100 µm, Dionex-nanoViper) e eluídas usando um gradiente de 100% fase A (0.1% ác. fórmico) até 26% fase B (0.1% ác. fórmico, 95% acetonitrila) por 180 min, 26% até 100% fase B por 5 min e 100% fase B por 8 min (um total de 193 min a 200 nL/min). Após cada corrida, a coluna foi lavada com 90% fase B e reequilibrada com fase A.

Os espectros de massas foram adquiridos no modo positivo aplicando-se *data-dependent automatic survey MS scan* e aquisição de espectros de massas em tandem (MS/MS). Cada MS no Orbitrap (amplitude de massa: m/z 350-1800 e resolução: 120000) foi seguida por MS/MS dos quinze íons mais intensos no LTQ. A fragmentação no LTQ ocorreu por dissociação de alta energia induzida por colisão (HCD) e as sequências de íons selecionados foram excluídas dinamicamente por 15 segundos.

O processamento dos dados foi feito com ProteomeDiscoverer v.1.3 beta (ThermoScientific). A busca e identificação das proteínas também foi realizada com o programa ProteomeDiscoverer e o *software* Peaks, com algoritmo Mascot v.2.3 contra um banco de dados de *Homo sapiens* instalado no servidor do laboratório, usando a ferramenta Database on Demand (Reisinger & Martens 2009) contendo as proteínas encontradas no UniProt/SWISS-PROT e UniProt/TrEMBL. Proteínas contaminantes (diversos tipos de albumina, queratinas humanas, BSA e tripsina porcina) foram adicionadas ao banco de dados e removidas manualmente das listas de identificações. As buscas foram feitas com os seguintes parâmetros: precisão no MS de 10 ppm, no MS/MS de 0.05 Da, até 2 sítios de clivagem perdidos, carbamidometilação de cisteínas como modificação e oxidação da metionina e acetilação N-terminal da proteína como modificações variáveis. O número de proteínas, grupo de proteínas e número de peptídeos

foram filtrados com uma taxa de detecção de falsos positivos (FDR) menor que 1% e peptídeos com rank 1 e mínimo de 2 peptídeos por proteínas foram aceitos para identificação com ProteomeDiscoverer.

O *software* Progenesis QI (<http://www.nonlinear.com/progenesis/qi>) (Nonlinear Dynamics©) foi utilizado para processamento dos espectros, análise e interpretação dos dados relativos à comparação dos cenários biológicos propostos. Foram aplicados filtros de ANOVA ($p \leq 0,05$) e *Fold Change* (≥ 2) para determinação de significância estatística. As análises multivariadas de *Principal Component Analysis* (PCA) finalizaram o refinamento de dados baseado no desenho experimental.

Para identificação de peptídeos, foi utilizada a plataforma Peaks® Studio 7.0 (<http://www.bioinfor.com/peaks-studio>) (Bioinformatics Solutions, Inc.).

Para avaliação das anotações funcionais (função molecular, componente celular e processo biológico), a partir da categorização por *Gene Ontology* (GO), foi utilizado o *software* Strap (<http://www.bumc.bu.edu/cardiovascularproteomics/cpctools>).

4. RESULTADOS

A formulação dos resultados foi realizada por meio da construção de três padrões de análises comparativas:

- 1- Comparação dos perfis proteicos expressos nas amostras urinárias e plasmáticas dos pacientes portadores de adenocarcinoma colorretal, utilizando como espelho o perfil expresso no tecido tumoral.
- 2- Comparação dos perfis expressos no plasma de pacientes portadores e não portadores de adenocarcinoma colorretal.
- 3- Comparação dos perfis expressos na urina de pacientes portadores e não portadores de adenocarcinoma colorretal.

4.1 Resultados da análise 1

Neste cenário, foram avaliados os perfis proteicos expressos nas amostras dos pacientes portadores de adenocarcinoma (plasma, urina e tecido tumoral). Para essa abordagem, o tecido tumoral foi determinado como referência para a comparação, visto que, se determinada proteína é expressa no tecido tumoral e também é detectada na urina ou no sangue, esta proteína pode ser um possível biomarcador de um fenótipo patológico.

A estimativa da amostra ideal calculada pelo *software* Progenesis QI evidenciou que o número de replicatas que refletiria em poder estatístico suficiente para o desenho de estudo seria de 9 (figura 3).

Neste cenário de comparação, foram identificadas 16 proteínas com expressão apresentando significância estatística (ANOVA $p \leq 0,05$).

Tabela 2. Proteínas reguladas no cenário de comparação de amostras de pacientes portadores de CCR (valor de $p \leq 0,05$)

Entrada UniprotKB	Proteína	Fold	Maior abundância relativa
V9HWA9	Proteína ligante 62p secretora do espermatozoide do epidídimo	58,96	Plasma
I6L965	Queratina 18 (KRT 18)- fragmento	20,31	Tecido
P68871	Subunidade beta da hemoglobina	371,57	Tecido
P01876	Imunoglobulina constante pesada alfa 1	65,85	Plasma
B4E1B2	Proteína altamente similar à serotransferrina	99,15	Plasma
A0A0K2BM D8	Cadeia globina alfa 2 da hemoglobina mutante	57,05	Tecido

P02671	Cadeia alfa do fibrinogênio	218,69	Plasma
Q9BS19	Hemopexina (HPX)	769,13	Plasma
P62805	Histona H4	192,92	Tecido
Q7Z7J6	Actina alfa 1, músculo esquelética	151,53	Tecido
A0A140TA32	Complemento C4-A	27,24	Plasma
G3V3A0	Alfa-1-antiquimotripsina	331,96	Plasma
B4E368	Proteína altamente similar à cadeia leve 1 da miosina	34,81	Tecido
E5RII2	Anidrase carbônica 1	213,22	Tecido
Q7Z7M7	Superóxido dismutase	383,11	Tecido
B4DSH1	Proteína altamente similar à proteína 5 do ciclo de divisão celular	14,06	Plasma

Os dados em termos GO, quanto à composição celular, revelaram que as proteínas reguladas estão prioritariamente representadas por moléculas presentes no meio extracelular (28%), em complexos macromoleculares (14%) e no citoplasma (10%).

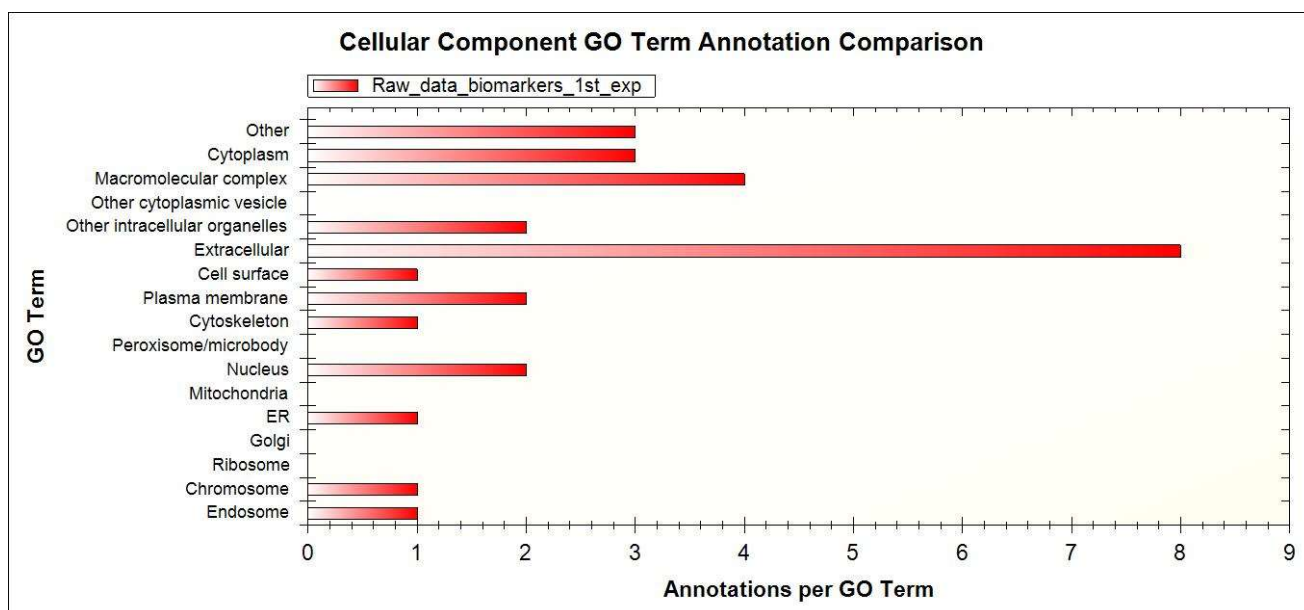


Figura 5. Anotações GO quanto ao componente celular para proteínas reguladas nas amostras de pacientes com CCR (software Strap).

Já, quando foram avaliados os processos biológicos, a proteínas reguladas demonstram-se majoritariamente ligadas à regulação (24%), processos celulares (18%) e resposta à estímulos (15%).

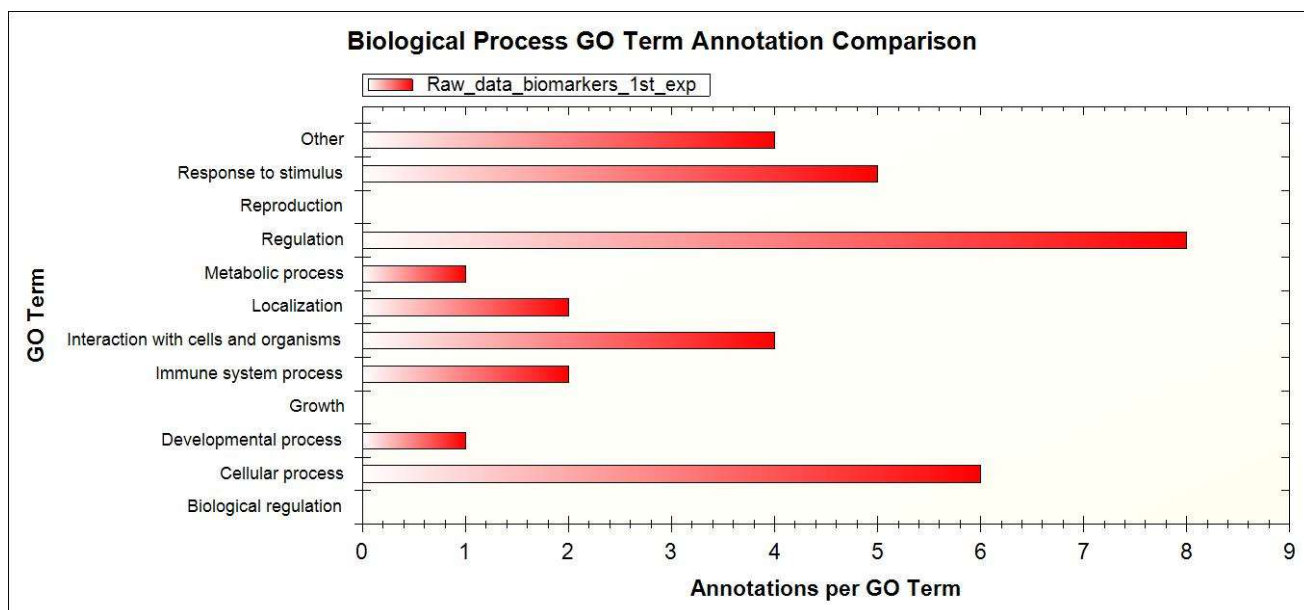


Figura 6. Anotações GO quanto aos processos biológicos para proteínas reguladas nas amostras de pacientes com CCR (software Strap)

Em relação às funções moleculares das proteínas reguladas, os dados em termos GO revelaram que 60% estão relacionadas à função de ligação.

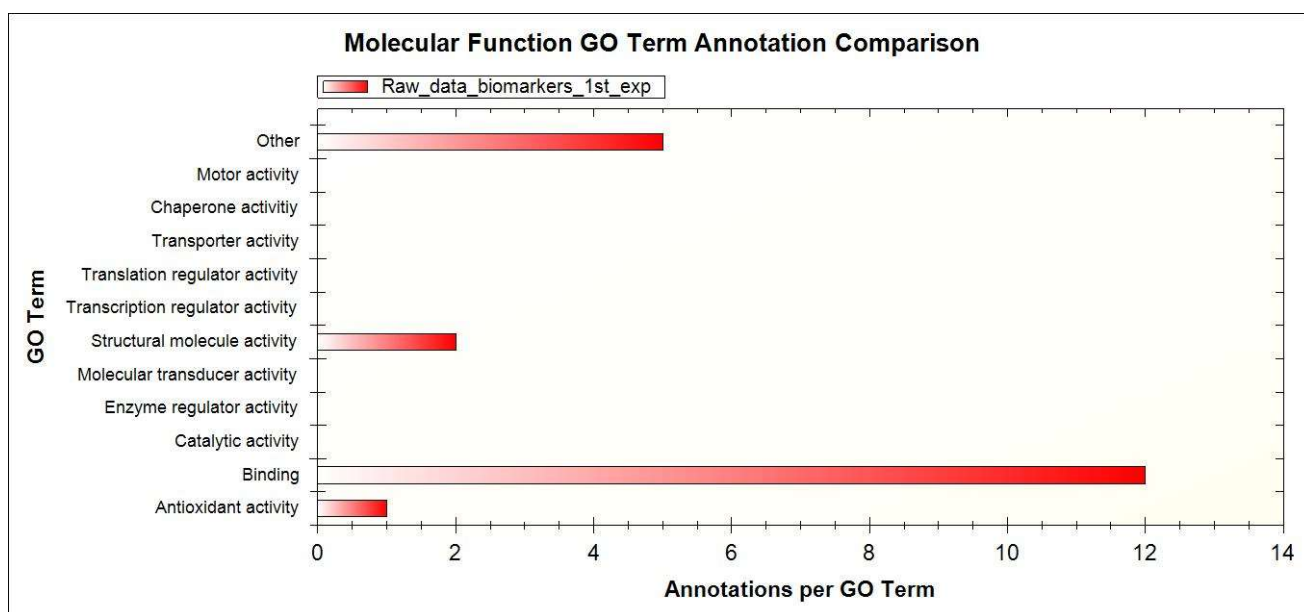


Figura 7. Anotações GO quanto à função molecular para proteínas reguladas nas amostras de pacientes com CCR (software Strap)

4.2. Resultados da análise 2

Neste cenário, foram comparados os perfis proteômicos plasmáticos entre pacientes portadores de adenocarcinoma colorretal e pacientes sem a doença.

A estimativa da amostra ideal calculada pelo *software* Progenesis Q1 evidenciou que o número de replicatas que refletiria em poder estatístico suficiente para o desenho de estudo seria de 259 (figura 8).

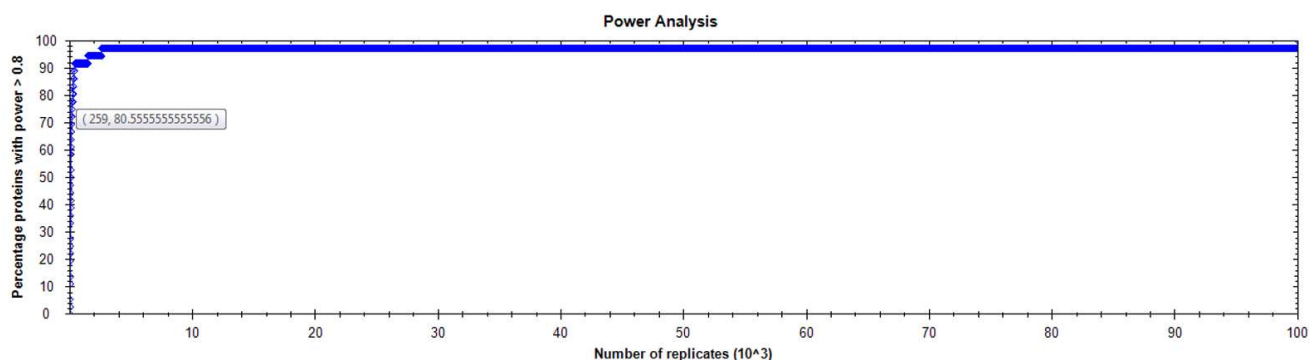


Figura 8. Potência estatística de dados proteômicos do segundo modelo de análise.

A Figura 9 apresenta o resultado da análise multivariada PCA adquirido no *software* Progenesis Q1 a partir do perfil global de proteínas reguladas nas amostras plasmáticas de pacientes do grupo controle e grupo experimental.

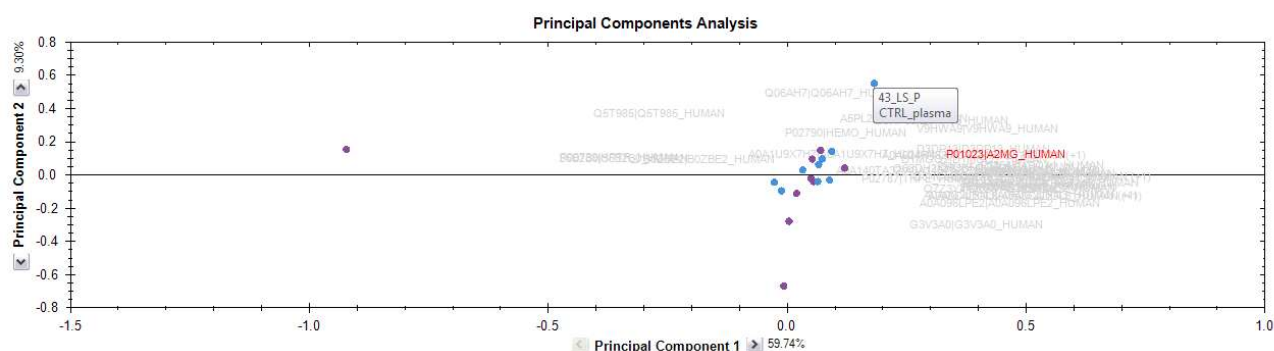


Figura 9. Análise PCA apresentando os scores plot das proteínas reguladas em amostras plasmáticas de pacientes portadores de neoplasia colorretal e grupo controle pelo *software* Progenesis Q1. Grupo controle: cor azul. Grupo CCR: cor roxa.

Foram identificadas 36 proteínas com expressão plasmática discriminante entre pacientes do grupo experimental e do grupo controle. Entretanto, apenas uma proteína (variante da subunidade beta da hemoglobina) apresentou significância estatística com $p \leq 0,05$ e *Fold Change* ≥ 2 .

Tabela 3. Proteínas reguladas nas amostras plasmáticas. (* $p \leq 0,05$)

Entrada UniprotKB	Proteína	Fold	Maior abundância relativa
Q9UK54	Variante da subunidade beta da hemoglobina*	5,21	Controle
Q06AH7	Transferrina	1,35	Controle
V9HWA	Proteína ligante 62p secretora do espermatozoide do epidídimo	1,16	Controle
P02671	Cadeia alfa do fibrinogênio	1,16	Controle
P02671	Proteína altamente similar à cadeia C da imunoglobina alfa-1	1,46	Controle
A0A140VJJ6	Proteína Li 70 do tecido testicular	1,19	Controle
P01023	Alfa-2-macroglobulina	1,50	Controle
D3DP13	Isoforma CRA_e da cadeia beta do fibrinogênio	1,12	Controle

A0A0C4DGL8	Haptoglobina	1,20	CCR
P02647	Apolipoproteína A-I	1,27	Controle
A0A140TA32	Complemento C4-A	1,23	CCR
A0A0G2JRN3	Alfa-1-antitripsina	1,11	CCR
E1A689	Apolipoproteína B mutante	1,24	CCR
P02790	Hemopexina	1,17	Controle
Q68DH2	Proteína não caracterizada DKFZp686G21125	1,04	Controle
P0DOX6	Cadeia pesada de imunoglobulina 1	1,47	Controle
A0A096LPE2	Proteína SAA2-SAA4 readthrough	1,10	CCR
Q7Z3Y4	Proteína não caracterizada	1,15	Controle
V9HWD8	Proteína ligante 163pA secretora do esperma do epidídimo	1,27	Controle
A0A024R962	Isoforma CRA_b da proteína HCG40889	1,18	Controle

D6RF35	Proteína ligante da vitamina D	1,21	Controle
Q5T985	Cadeia pesada H2 do inibidor da inter-alfa-tripsina	1,19	CCR
P05090	Apolipoproteína D	1,01	CCR
S6B2B0	Cadeia L da IgG	1,38	CCR
G3V3A0	Alfa-1-antiquimotripsina	1,22	CCR
A0A1U9X7H7	Fator complemento B	1,70	Controle
F8WAS2	Cadeia pesada H1 do inibidor da inter-alfa-tripsina	1,03	Controle
A0A024R462	Isoforma CRA_n da fibronectina-1	15,47	Controle
B4DPP8	Proteína altamente similar ao cininogênio-1	1,39	Controle
K7ERI9	Fragmento da apolipoproteína C-I	1,65	Controle
D1MGQ2	Cadeia globina alfa-2	20,78	Controle
A5PL27	Ceruloplasmina	16,41	Controle

F8WCZ6	Subcomponente do complemento C1s	1,43	Controle
B0ZBE2	Angiotensinogênio	1,34	CCR
P00739	Proteína relacionada à haptoglobina	1,51	CCR
P02787	Serotransferrina	1,15	CCR

As anotações do termo GO quanto aos componentes celulares, evidenciaram que as proteínas reguladas apresentam localização predominante em meio extracelular (39%).

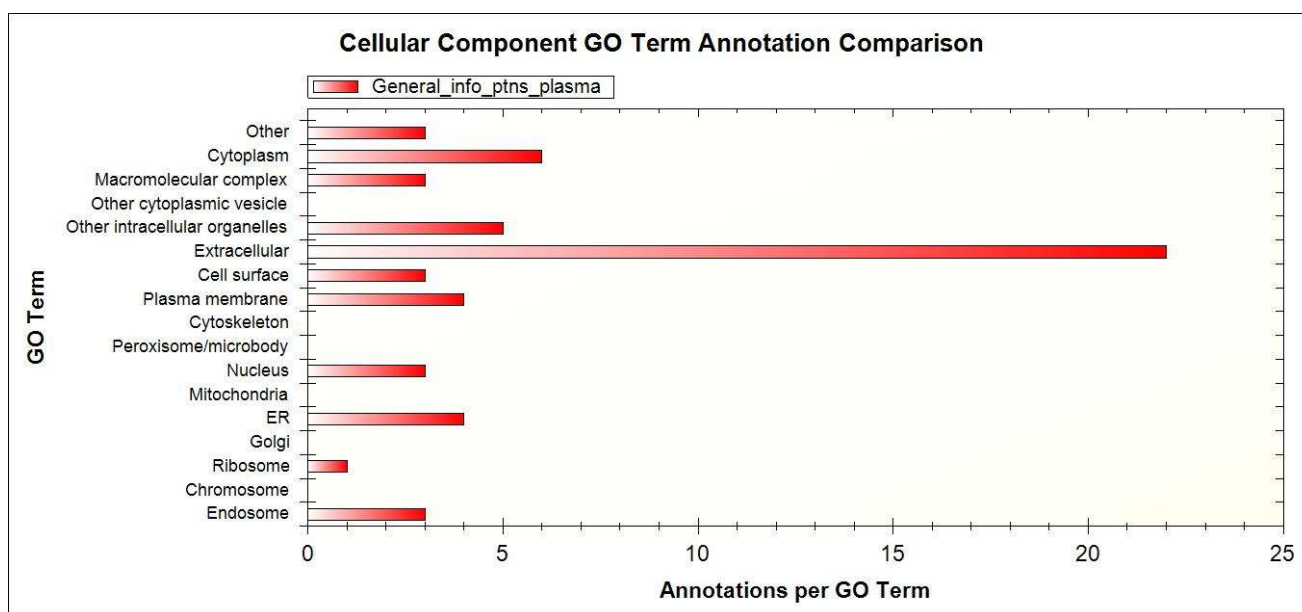


Figura 10. Anotações em termo GO quanto ao componente celular para proteínas reguladas no plasma.

Quanto aos processos biológicos em que as proteínas reguladas estão envolvidas, as anotações em termo GO revelaram prevalência em regulação (27%), processos celulares (12%) e resposta à estímulos (12%).

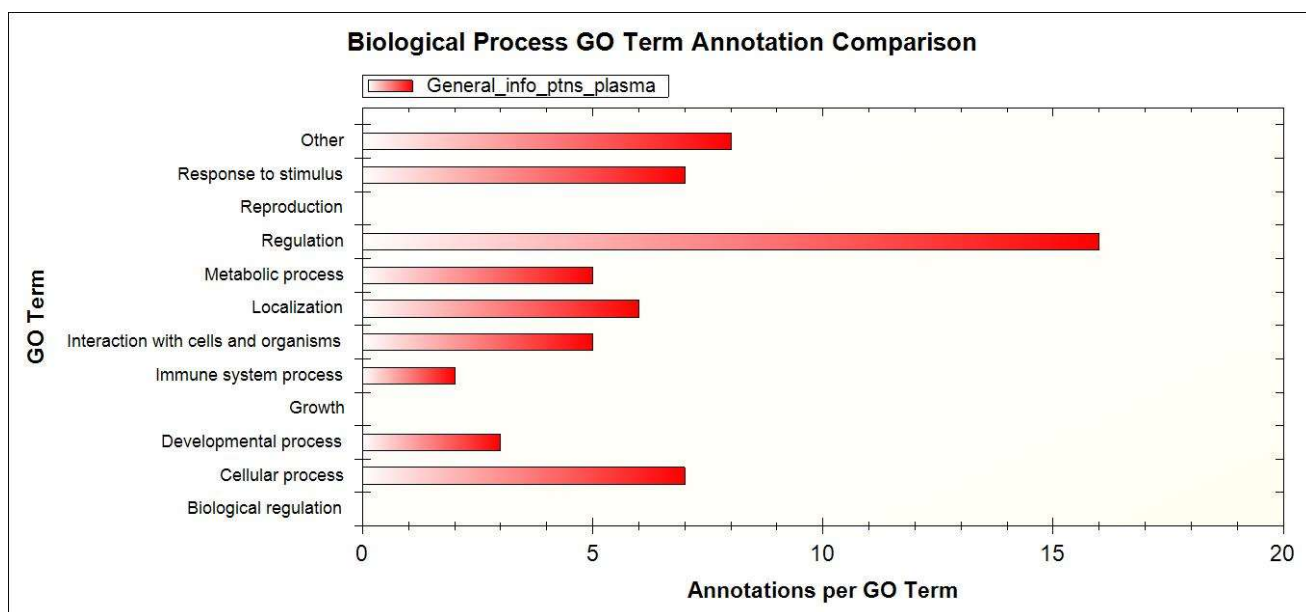


Figura 11. Anotações em termo GO quanto aos processos biológicos para proteínas reguladas no plasma.

Em relação às funções moleculares, evidenciou-se envolvimento majoritário com ligação (45%) e atividade catalítica (13%).

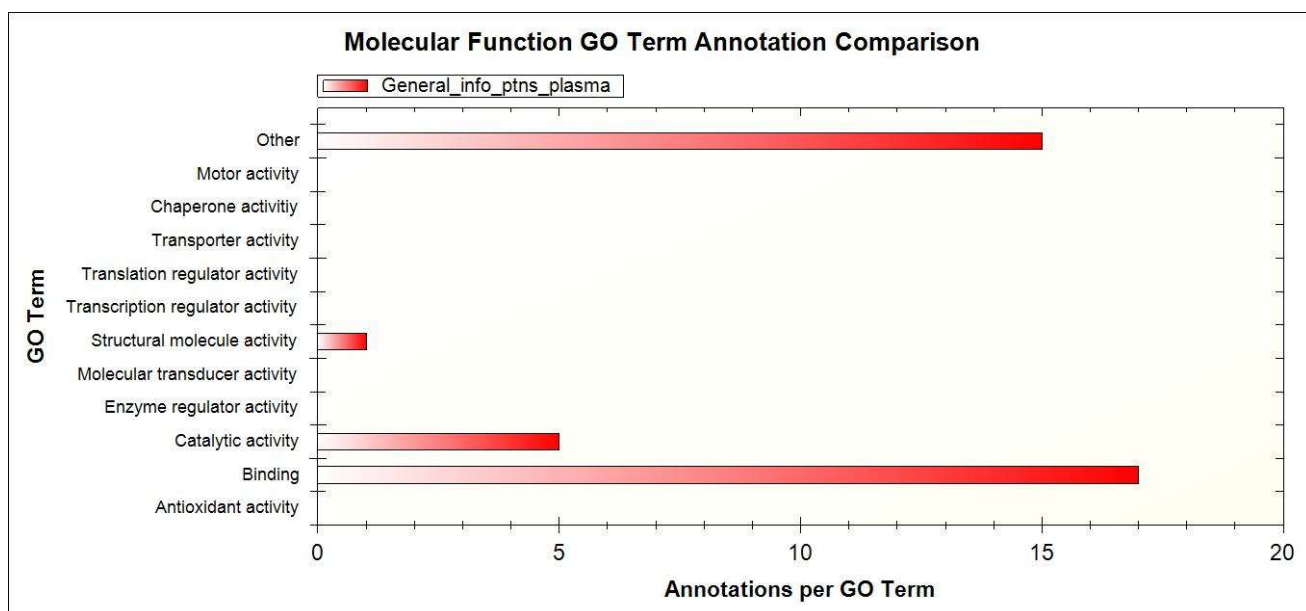


Figura 12. Anotações em termo GO quanto à função molecular para proteínas reguladas no plasma.

4.3. Resultados da análise 3

Neste cenário, foram comparados os perfis proteômicos urinários entre pacientes portadores de adenocarcinoma colorretal e pacientes sem a doença.

A estimativa da amostra ideal calculada pelo software Progenesis QI evidenciou que o número de replicatas que refletiria em poder estatístico suficiente para o desenho de estudo seria de 18 (figura 13).

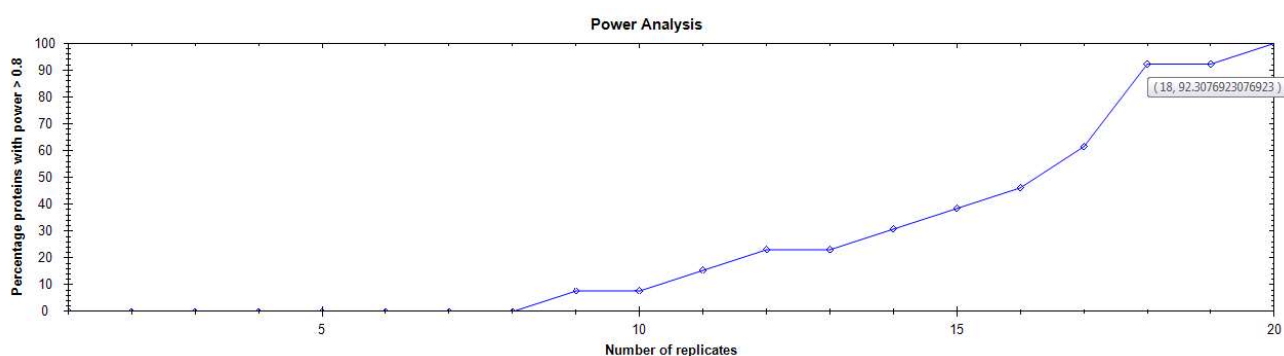


Figura 13. Potência estatística de dados proteômicos no terceiro modelo de análise.

A Figura 14 apresenta o resultado da análise multivariada PCA adquirido no software Progenesis QI a partir do perfil global de proteínas reguladas nas amostras urinárias de pacientes do grupo controle e grupo experimental.

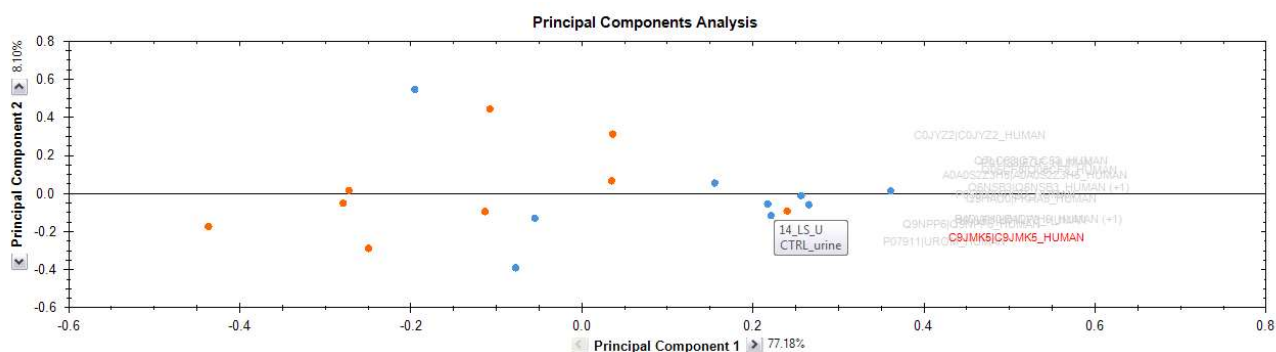


Figura 14. Análise PCA apresentando os scores plot das proteínas reguladas em amostras de urina de pacientes portadores de neoplasia colorretal e grupo controle pelo software Progenesis QI. Grupo controle: cor azul. Grupo CCR: cor laranja.

Foram identificadas 10 proteínas com regulação diferenciada entre pacientes do grupo experimental e do grupo controle, apresentando significância estatística com valor de $p \leq 0,05$.

Tabela 4. Proteínas reguladas nas amostras de urina (valor de $p \leq 0,05$)

Entrada UniprotKB	Proteína	Fold	Maior abundância relativa
A0A0S2Z3H5	Fragmento da isoforma 1 do colágeno tipo 1, alfa-2	6,81	Controle
P05090	Apolipoproteína D	7,34	Controle
P07911	Uromodulina	4,34	Controle
Q05CF8	Cininogênio 1	10,60	Controle
H0YLF3	Fragmento de beta-2-microglobulina	2,62	CCR
B4DWH0	Altamente similar à proteína da matriz extracelular 1 semelhante a fibulina contendo EGF	10,71	Controle
Q6NSB3	Fragmento alfa-amilase	37,68	Controle

C9JMK5	Fragmento da proteína 1 de interação com a fosfatidilinositol-3-quinase	6,57	Controle
C0JYZ2	Titina	2,71	Controle
Q9HAU0	Domínios de homologia à plectrina contendo membro 5 da família A	5,78	Controle

As anotações do termo GO quanto aos componentes celulares evidenciaram que as proteínas reguladas apresentam localização predominante no meio extracelular (23%) e na membrana plasmática (14%).

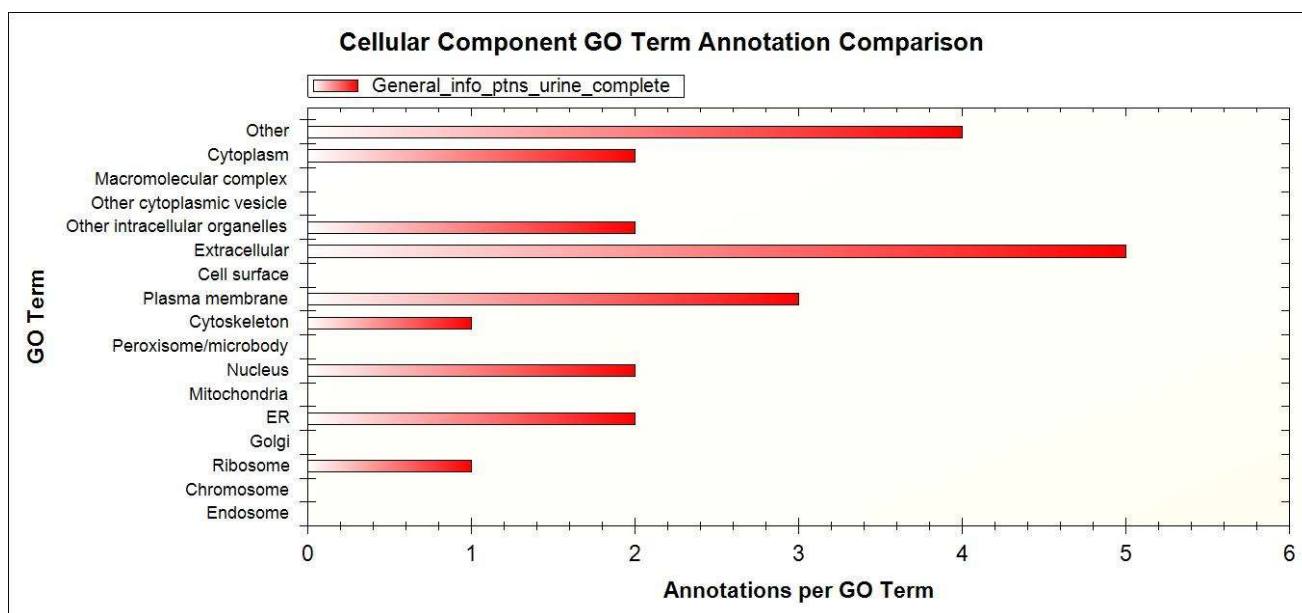


Figura 15. Anotações em termo GO quanto ao componente celular para proteínas reguladas na urina.

Quanto aos processos biológicos em que as proteínas reguladas estão envolvidas, as anotações em termo GO revelaram prevalência em desenvolvimento (23%), processos celulares (14%), processos metabólicos (14%) e regulação (14%).

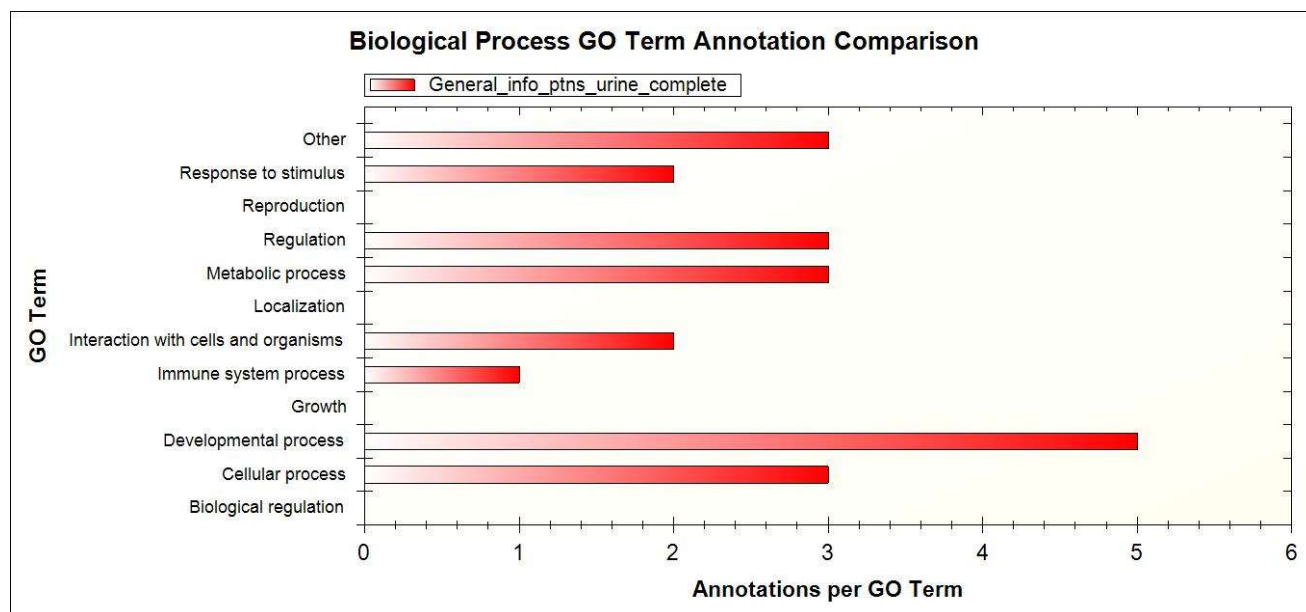


Figura 16. Anotações em termo GO quanto aos processos biológicos para proteínas reguladas na urina.

Em relação às funções moleculares, evidenciou-se envolvimento majoritário com ligação (53%) e atividade catalítica (24%).

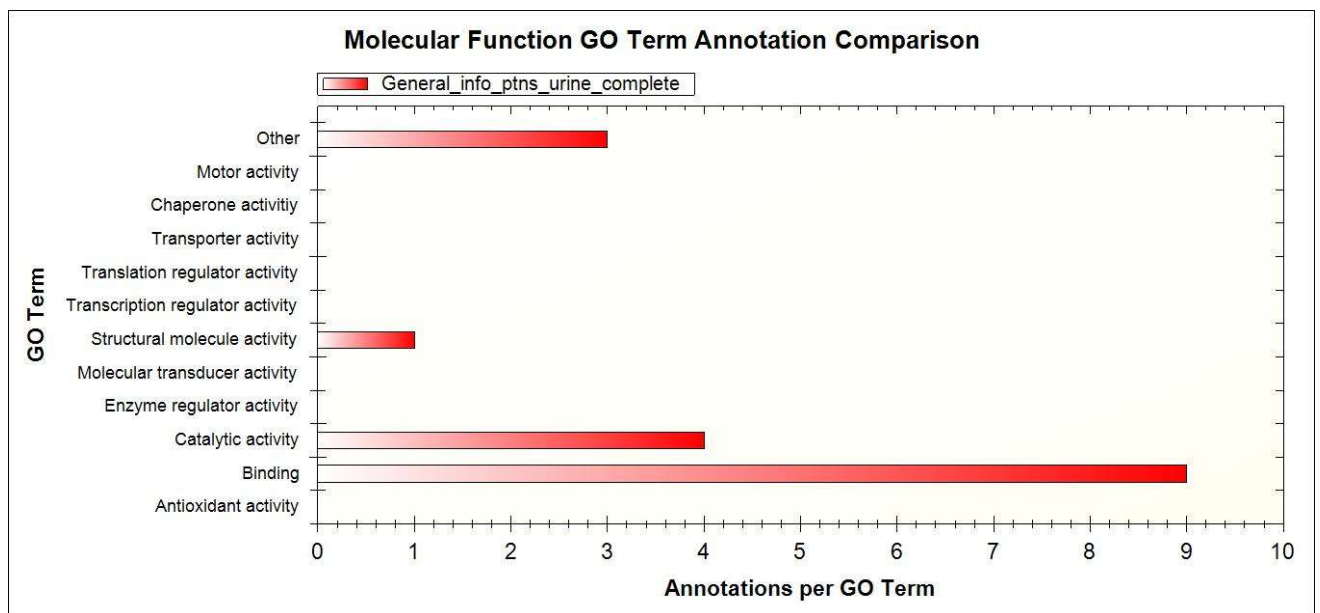


Figura 17. Anotações em termo GO quanto à função molecular para proteínas reguladas na urina.

DISCUSSÃO

Os estudos proteômicos para prospecção de biomarcadores diagnósticos englobam uma ampla variedade de abordagens e tipos de matrizes. As principais matrizes utilizadas são as amostras baseadas em sangue (soro e plasma), amostras de tecido tumoral, amostras de urina, fezes e amostras provenientes de modelos de neoplasia colorretal (modelos animais ou culturas organóides).(31) No presente trabalho, foi optada pela análise de amostras de plasma, tecido e urina.

Levando em consideração estudos proteômicos baseados em análises de tecidos tumorais, Ghazanfar e cols (2017) utilizaram a espectrometria de massas e gel-eletroforese bidimensional para avaliar o perfil de proteínas proveniente de amostras de peças frescas de 12 pacientes portadores de tumores colorretais. Além das amostras de tecido tumoral, foram coletadas amostras de tecido adjacente não-tumoral para controle. A comparação dos perfis expressos nos dois tipos de amostras identificou diferenças na abundância de 6 proteínas (tropomiosina B, ativador da subunidade 1 do proteossoma, actina beta *2-like*, anexina 2, miosina de cadeia leve 9 e proibitina), entretanto, com destaque para a regulação positiva da actina beta *2-like* (ACTBL-2) no tecido tumoral.(36) Hao e cols (2017) utilizaram a espectrometria de massas de alta resolução por transformada de Fourier para avaliar espécimes frescos de tecido neoplásico e tecido adjacente sadio coletados de 22 pacientes. Essa análise evidenciou que a proteína que apresentou maior grau de superexpressão no tecido tumoral em comparação com o tecido normal foi a dipeptidase 1 (DPEP1).(37) A DPEP1 é uma metaloproteinase dependente de zinco que já foi associada a outros eventos na carcinogênese colorretal, sendo um fator de mau prognóstico e um marcador de transição de displasia de baixo grau para displasia de alto grau nas neoplasias intraepiteliais.(38)

Os tecidos fixados em formol e incluídos em parafina também podem ser utilizados nas análises proteômicas, permitindo acesso a bancos de amostras, estudos em coortes mais numerosas e com dados mais robustos, além de facilitar a obtenção de dados de seguimento dos pacientes.(18) Entretanto, existe a possibilidade de haver maior perda de proteínas em relação às análises realizadas em espécimes frescos, pois, o processo de

fixação em formaldeído modifica significativamente o conjunto de proteínas por meio de eventos de ligação-cruzada e exposição à aquecimento e solventes orgânicos. Sendo assim, para o uso desse grupo de amostras, é necessária a realização de técnicas de reversão das ligações cruzadas induzidas pelo formaldeído.(39,40)

Quesada-Calvo e cols (2017) analisaram 76 espécimes de tecidos colorretais, fixados em formol e incluídos em parafina, originados de tumores precoces (pT1N0M0 e pT2N0M0) e de mucosas normais ou inflamadas. Por meio de uma abordagem proteômica *label-free*, foram evidenciados níveis de expressão diferentes nas amostras de CCR da olfactomedina-4 (OLFM4), cininogênio-1 (KNG1) e da proteína de transporte Sec24C (Sec24C). Embora o experimento tenha sido realizado com uma técnica de alta performance, a cromatografia líquida acoplada à espectrometria de massas em tandem (LC-MS/MS), os marcadores também foram validados através de imunistoquímica.(32) Yamamoto and cols (2016) também realizaram abordagem semelhante com LC-MS/MS em peças fixadas em formaldeído e incluídas em parafina, revelando diferentes níveis de expressão de ciclofilina A, anexina A2 e aldolase A em tecidos tumorais, quando comparados à tecidos colônicos sem câncer.(41)

As amostras derivadas do sangue são as melhores matrizes em potencial para diagnóstico precoce e vigilância no CCR, visto que, os espécimes podem ser obtidos facilmente, de maneira pouco invasiva, com riscos baixos e custos reduzidos.(31,42) Yu e cols (2017) utilizaram *magnetic beads e Matrix-Assisted-Laser-Desorption/Ionization-Time-Of-Flight* (MALDI-TOF) para analisar 127 amostras séricas de pacientes portadores de CCR e 90 amostras de pacientes-controle saudáveis. A proteína serina/treonina quinase 4 (STK4 ou MST1) foi identificada por MS/MS e validada através de *Western Blotting* e ensaio de imunoabsorção enzimática (ELISA). Foi evidenciada regulação negativa de MST1 em pacientes com CCR, com sensibilidade de 92,3% e especificidade de 100% no diagnóstico de CCR quando combinado com a dosagem de CEA e pesquisa de sangue oculto nas fezes. Também foi inferido o papel potencial da MST1 como preditora de metástases à distância, visto que foi evidenciada abundância menor da proteína no estadio IV, em comparação com os outros estadios de CCR.(43)

Fan e cols (2016) também conduziram um estudo com amostras séricas que foram analisadas por uma combinação de cromatografia líquida e espectrometria de massas de alta performance, com posterior validação dos resultados por *Western Blotting*. Foi verificada regulação positiva nos pacientes portadores de CCR da proteína receptora 1 de manose do macrófago (MRC1) e da proteína ligante de cálcio S100 A9 (S100A9).(44)

Os membros da superfamília de proteínas serpina também parecem ser candidatos promissores à biomarcadores diagnósticos de prospecção no sangue. Proteínas como a SERPINA1 (alfa-1-antitripsina, A1AT), SERPINA3 (alfa-1-antiquimotripsina, AACT), SERPINC1 (antitrombina-3, AT-III), têm sido descritas como potenciais marcadores de pólipos adenomatosos e carcinomas colorretais, por meio de análises de amostras séricas por quantificação com marcadores isobáricos e absolutos (iTRAQ).(45) A alfa-1-antiquimotripsina foi uma das proteínas que demonstraram significância estatística na análise realizada no primeiro cenário deste trabalho, corroborando o exposto acima.

A urina também é uma fonte promissora para prospecção de biomarcadores, visto que é uma matriz de fácil obtenção.(31) Um exemplo de biomarcador identificado na urina é o metabólito da prostaglandina PGE-M. Essa molécula é o principal metabólito urinário da prostaglandina E2 e apresenta papel importante na mediação de efeitos da ciclooxigenase-2 na carcinogênese colorretal. Níveis elevados da PGE-M parecem estar associados com adenomas avançados e risco aumentado de CCR.(46–50) Os peptídeos derivados do colágeno também são exemplos de moléculas encontradas na urina e que podem estar relacionadas à detecção de metástases colorretais.(51,52)

Os modelos animais também têm seu papel na pesquisa de possíveis biomarcadores. Liu e cols (2018), por meio de abordagem proteômica com iTRAQ acoplado com LC-MS/MS, avaliaram tecidos colônicos de vinte e cinco camundongos BALB/c tratados com N,N-dimetil-hidrazina, uma substância que induz câncer colônico com características histopatológicas similares às observadas nos tumores de cólon esporádicos do ser humano. Nesse estudo, foram identificados diferentes níveis de expressão da beta-catenina, decorina, septina-7, e S100A10 nos tecidos cancerígenos dos camundongos.(53) Em outro estudo com modelo animal, foi utilizada abordagem por

iTRAQ para avaliar tecido colônico de camundongos AOM-DSS. Neste modelo animal, a sequência adenoma-carcinoma é induzida por meio da infusão intraperitoneal de baixas doses de azoximetano seguida de administração oral de sulfato sódico de dextrana. Neste experimento foi identificada regulação positiva da alfa-2-glicoproteína 1 rica em leucina (LRG1), da cadeia beta-5 da tubulina (TUBB5) e da cadeia da imunoglobulina J (IGJ) em camundongos portadores de CCR.(54)

Referências às proteínas descritas no presente estudo

Nesta seção, foram incluídas para discussão apenas as proteínas que demonstraram nível de expressão discriminante entre os cenários e com significância estatística ($p \leq 0,05$).

1-Proteínas expressas no primeiro modelo de análise comparativa (tecido tumoral x plasma x urina de paciente portadores de CCR)

A tabela 5 demonstra as proteínas que apresentaram potencial como biomarcadores na primeira análise comparativa e o cenário correspondente em que foi identificada maior abundância relativa.

Tabela 5. Proteínas com potencial a biomarcadores e cenário de maior abundância relativa na primeira análise comparativa

Proteínas	Maior abundância relativa
Proteína ligante 62p do espermatozoide do epidídimo	Plasma
KRT 18 (fragmento)	Tecido tumoral
Subunidade beta da hemoglobina	Tecido tumoral
Imunoglobulina constante pesada alfa 1	Plasma
Serotransferrina	Plasma
Cadeia globina alfa 2 da Hb mutante	Tecido tumoral
Cadeia alfa do fibrinogênio	Plasma
Hemopexina	Plasma
Histona H4	Tecido tumoral
Actina alfa 1 músculo-esquelética	Tecido tumoral

Complemento C4a	Plasma
Alfa-1-antiquimotripsina	Plasma
Cadeia leve 1 da miosina	Tecido tumoral
Anidrase carbônica 1	Tecido tumoral
Superóxido dismutase	Tecido tumoral
Proteína 5 do ciclo de divisão celular	Plasma

- Proteína ligante 62p secretora do espermatozoide do epidídimo

As proteínas ligadoras do espermatozóide são produzidas nas vesículas seminais e se ligam aos espermatozoides durante a ejaculação, por meio da interação com os fosfolípidos da membrana dos espermatozoides. A assinatura molecular dessa família de proteínas é a presença de domínios de duas fibronectinas tipo II. Elas estão presentes em quantidades variáveis no fluido seminal e têm a função principal de promover a capacitação do espermatozóide no sítio de fertilização.(55,56)

Não foram encontrados relatos de participação dessas proteínas no processo de carcinogênese. No presente estudo, foi encontrada maior abundância relativa dessa proteína no plasma de pacientes com CCR, em relação ao tecido tumoral e a urina.

- Queratina 18 (fragmento)

Os fragmentos da queratina 18 têm sido reportados como marcadores em diversos tipos de câncer, como o de mama, endométrio, próstata e pulmão. Eles possibilitam a discriminação entre pacientes portadores de câncer e pacientes saudáveis, além de apresentarem aplicação na avaliação do prognóstico e no monitoramento do tratamento. No câncer colorretal, os níveis de citoqueratina 18 estão relacionados principalmente ao prognóstico, sendo os seus fragmentos M30 e M65, as principais formas para aferição no plasma.(57) O fragmento M65 da queratina 18 apresenta níveis séricos elevados tanto nos

estágios precoces, quanto nos avançados, com marcada ascensão nos casos de doença sistêmica.(58) Também já foi demonstrado que o fragmento M30 apresenta uso potencial na vigilância pós-resssecção cirúrgica, sendo que, níveis elevados no pós-operatório podem representar tumoração residual e estão relacionados à recorrência da doença (59). Além disso, a alta expressão de fosforilação da queratina 18 estimula a autofagia de células neoplásicas in vitro e aumenta a sensibilidade à oxaliplatina. (60)

No presente estudo, foi encontrada abundância relativa elevada dessa proteína no tecido tumoral.

- Subunidade beta da hemoglobina

A subunidade beta da hemoglobina já foi apontada em outro estudo como um possível marcador de progressão na sequência adenoma-carcinoma. Choi e cols (2013) realizaram análise de plasma de pacientes portadores de adenomas e adenocarcinomas, por meio de eletroforese bidimensional e espectrometria de massas. Esta análise proteômica propiciou o achado de 11 proteínas com regulação positiva e 13 com regulação negativa, demonstrando padrão com potencial de predição de progressão adenoma-carcinoma. A subunidade beta da hemoglobina apresentou regulação positiva neste contexto.(61) As subunidades alfa e beta da hemoglobina também já foram relatadas como potenciais biomarcadores séricos de câncer de ovário.(62)

No presente estudo, não foi encontrada regulação positiva da subunidade beta da hemoglobina no plasma de pacientes com CCR, entretanto, foi identificada uma abundância relativa elevada dessa proteína no tecido tumoral.

- Imunoglobulina constante pesada alfa 1

Não foram identificados relatos da associação direta entre a imunoglobulina alfa 1 e o CCR, entretanto, é conhecido que alguns tipos de neoplasias epiteliais expressam essa proteína, que parece estar relacionada com o estímulo de crescimento e proliferação das células cancerígenas, por meio da promoção da fase S da mitose.(63)

Na análise realizada, foi encontrada abundância relativa elevada da imunoglobulina constante pesada alfa 1 no plasma de pacientes com CCR, em relação ao tecido tumoral e a urina.

- Proteína altamente similar à serotransferrina

O metabolismo do ferro parece estar envolvido no processo de desenvolvimento de vários tipos de cânceres epiteliais, incluindo os de mama, fígado e colorretais.(64-66)

A serotransferrina tem o papel de captar o ferro absorvido pelo intestino e armazenado em reservas tissulares, e, transportá-lo para células que expressam os receptores de transferrina. O receptor de transferrina tipo 1 (TfR1) é o receptor predominante para captação de ferro pelas células, sendo expresso em quase todos os tipos de células.(67,68) Os TfR1 são expressos pelos colonócitos, havendo regulação positiva desses receptores no CCR, o que infere a participação do metabolismo do ferro na carcinogênese.(66) Além disso, sabe-se que a saturação elevada da transferrina está associada ao risco aumentado para desenvolvimento de câncer.(69)

Ward e cols (2006) realizaram análise proteômica por espectrometria de massas de amostras de sangue de 62 pacientes portadores de CCR e 31 pacientes sem câncer. Foram identificadas 3 proteínas com potencial diagnóstico, sendo elas: transferrina, alfa-1-antitripsina e complemento C3a.(70)

Na presente análise, entre as amostras estudadas de pacientes com CCR, foi identificada uma abundância relativa elevada da transferrina no plasma.

Além da detecção na matriz sanguínea, alguns estudos sugerem que a determinação da transferrina nas fezes em conjunto com a pesquisa de sangue oculto seria uma ferramenta para diagnóstico precoce do CCR, entretanto, os resultados da literatura são conflituosos à respeito da superioridade dessa medida em relação ao rastreamento convencional utilizando apenas o SOF.(71,72)

- Cadeia globina alfa 2 da hemoglobina mutante

Como já citado anteriormente, as subunidades alfa e beta da hemoglobina são relacionadas como possíveis biomarcadores de neoplasias, sendo a de ovário um exemplo.(62) Ang e cols (2010) realizaram estudo proteômico de matriz fecal de modelos murinos por meio de espectrometria de massas, identificando várias proteínas com potencial diagnóstico, entre elas, a subunidade alfa da hemoglobina.(73) Rho e cols (2008) realizaram análise de tecidos tumorais e tecidos normais por meio de espectrometria de massas, identificando uma regulação negativa da subunidade alfa da hemoglobina no CCR. Essa regulação negativa da subunidade alfa foi justificada pela relativa redução de volume sanguíneo no tecido tumoral quando comparado à mucosa normal. Embora os carcinomas colônicos apresentem típico aumento de densidade vascular, eles também apresentam componente sólido epitelial elevado, o que faz com que a razão de hemoglobina por unidade de volume de massa seja menor que no tecido colônico normal.(74)

- Cadeia alfa do fibrinogênio

O fibrinogênio é uma proteína produzida pelos hepatócitos, estando relacionado a diversos processos fisiopatológicos no corpo humano, como a trombogênese, inflamação e aterogênese.(75) Vários estudos colocam a hiperfibrinogenemia como fator preditor de mau prognóstico no câncer colorretal, marcando potencial de recorrência, doença metastática e refratariedade ao tratamento.(76–79)

No presente estudo, entre os tipos de amostras analisadas nos pacientes com CCR, foi encontrada abundância relativa elevada da cadeia alfa do fibrinogênio no plasma.

Wang e cols (2017) realizaram estudo do perfil do peptidoma sérico de pacientes portadores de CCR em duas coortes independentes de prospecção e validação. Foram identificadas cinco proteínas com potencial diagnóstico, sendo eles: cadeia alfa do fibrinogênio, complemento C4, complemento C3, e, os peptídeos relacionados aos picos de m/z 2080.7 e 2656.8. O painel diagnóstico formado por essas proteínas conseguiu diferenciar os pacientes portadores de CCR dos pacientes saudáveis na coorte de

validação, apresentando acurácia de 91,8%, sensibilidade de 95,6% e especificidade de 87,9%.(80)

A cadeia alfa do fibrinogênio também é relatada como preditor de metástases hepáticas metacrônicas. Zhu e colaboradores (2013) realizaram análise de amostras séricas, por meio de espectrometria de massas acoplada com fracionamento por *bead-magnético*, de 64 pacientes com metástases hepáticas e 64 pacientes sem recorrência da doença após 3 anos da ressecção do tumor primário. Foram identificadas 8 proteínas com potencial promissor para predição de metástases, sendo a cadeia alfa do fibrinogênio uma delas.(81) Outra proteína identificada nessa análise foi o complemento C4-A, uma das proteínas que também demonstrou significância estatística no presente estudo.

- Hemopexina

A hemopexina é uma glicoproteína plasmática, expressa principalmente no fígado, que faz parte do grupo das proteínas de fase aguda e apresenta alta afinidade pelo grupamento heme. Sua produção é determinada pelas interleucinas 1 e 6, e apresenta como principal função a prevenção do estresse oxidativo determinado pelo heme.(82)

A hemopexina é associada à vários tipos de cânceres, como o meningioma, o câncer de mama e o câncer de ovário.(83–86) Em trabalho já citado anteriormente nesta discussão, Ang e cols (2010), por meio de análise proteômica de fezes de modelos murinos, demonstraram que a hemopexina apresenta potencial diagnóstico também para o CCR.(73) Níveis elevados de hemopexina também já foram evidenciados em análises de plasma de modelos murinos de CCR.(87)

Na presente análise, dentre as matrizes verificadas, foi observada maior abundância relativa da hemopexina no plasma de pacientes com CCR.

- Histona H4

As histonas são os componentes proteicos primários da cromatina e apresentam a função de regular a compactação do DNA e a expressão gênica. São octâmeros que consistem de duas cópias de quatro proteínas nucleares- H2A, H2B, H3 e H4. Essas

proteínas nucleares têm caudas específicas que são passíveis de modificações como acetilação, metilação, ubiquitinação, fosforilação e sumoilação. Essas modificações alteram a estrutura tridimensional do nucleossomo e afetam o controle transcricional dos genes associados. Vários estudos têm demonstrado que a desregulação das modificações das histonas ocorre nos processos neoplásicos, inclusive no CCR.(88,89)

Sendo assim, os mecanismos epigenéticos relacionados às modificações pós-traducionais das histonas têm sido o principal foco nas pesquisas para prospecção de biomarcadores relacionadas a essas proteínas. Sabe-se que a dimetilação da H3K4 é um fator prognóstico independente em pacientes portadores de CCR, sendo associada à presença de metástases hepáticas metacrônicas.(90) Já a expressão nuclear combinada da trimetilação de histonas em H3K4 (baixa expressão), H3K9 (alta expressão) and H4K20 (alta expressão) é associada com melhor prognóstico em pacientes com tumores precoces, sendo fator preditor de maior tempo de sobrevivência e menor taxa de recorrência.(91) Leszinski e cols (2012) e Gezer e cols (2015) demonstraram que a expressão de H4K20me3 and H3K27me3 é reduzida nos nucleossomos circulantes de pacientes portadores de CCR, sendo esse perfil um potencial marcador diagnóstico.(92,93)

- Actina alfa 1 músculo-esquelética

A actina é uma proteína abundante que tem papel essencial no funcionamento da célula, participando de muitos processos fisiológicos que incluem mobilidade celular, transdução de sinais, manutenção da estrutura celular, divisão celular, adesão, transcrição e contração muscular. O vertebrados apresentam seis isoformas da actina: beta e gama não-musculares, alfa esquelética, alfa cardíaca, e alfa e gama de músculo liso.(94-96)

Por estarem associadas à regulação do citoesqueleto, motilidade celular e ao processo de transição epitélio-mesenquimal, as actinas apresentam papel central na invasão neoplásica, sendo também relacionadas com o mecanismo de metástases.(97) Suspeita-se que a polimerização da actina seja um dos passos iniciais no ciclo de motilidade da célula cancerígena, gerando formação de protrusões celulares e determinando a direção da migração.(98) Zeng e cols (2018) descreveram o papel da expressão da proteína *actina-like 6A* na promoção de invasão neoplásica, gênese de

metástases e transição epitélio-mesenquimal no câncer de cólon (99). A expressão dessa proteína também é descrita como preditor de mau prognóstico no carcinoma hepatocelular e no osteossarcoma.(100,101)

As isoformas da actina também podem apresentar função na predição de resposta à quimioterapia, sendo os altos níveis de expressão de actina alfa de musculatura lisa associados com resistência ao uso de oxaliplatina e 5-fluoracil em primeira linha.(102) Sabe-se ainda que tumores que apresentam alta quantidade de miofibroblastos com expressão de actina alfa de musculatura lisa estão associados a um pior prognóstico.(103,104)

Na presente análise, dentre as matrizes verificadas, foi observada maior abundância relativa da actina alfa 1 músculo-esquelética no tecido tumoral de pacientes com CCR.

- Complemento C4-A

O sistema complemento consiste em uma série de proteínas que, em sua maioria, são produzidas no fígado e estão presentes no plasma e na superfície celular como precursores inativos. O complemento faz parte do sistema imune inato e tem a função de mediar a resposta aos gatilhos inflamatórios por meio de uma cascata enzimática coordenada que desencadeia a depuração de patógenos por meio de processo de reconhecimento, opsonização e lise.(105)

O complemento C4-A é fator-chave na via de ativação clássica do sistema complemento. Os produtos proteolíticos do C4-A têm sido relacionados a vários tipos de câncer, como o de mama, esôfago, ovário, hepatocarcinoma, carcinoma espinocelular de pênis.(106–110) No contexto do câncer colorretal, o complemento C4-A é descrito como marcador de progressão, sendo também relacionado como fator preditor de metástases hepáticas metacrônicas.(81,111)

No presente estudo, dentre as matrizes verificadas, foi observada maior abundância relativa do complemento C4-A no plasma de pacientes com CCR.

- Alfa-1-antiquimotripsina

A alfa-1-antiquimotripsina é uma glicoproteína alfa globulina que pertence à família dos inibidores de serino-proteases (SERPINS). Trata-se de um grupo de proteínas com estrutura altamente conservada, sendo os inibidores de protease mais abundantes no ser humano. Essas proteínas apresentam função importante na homeostase celular e papel essencial em vias proteolíticas como a coagulação sanguínea, remodelamento tecidual, angiogênese, inflamação, apoptose e metástases. A alfa-1-antiquimotripsina (SERPINA3) é produzida no fígado e é considerada uma proteína de fase aguda, sendo associada aos mecanismos de inflamação.(45,61)

O papel da SERPINA3 no desenvolvimento do CCR ainda é pouco compreendido. Dimberg e cols (2011) evidenciaram níveis menores de alfa-1-antiquimotripsina no tecido tumoral em relação aos tecidos saudáveis, entretanto, com aumento desses níveis nos estágios disseminados em relação às doenças localizadas. Nesse estudo, a determinação plasmática da SERPINA3 não mostrou poder diagnóstico no CCR.(112) Entretanto, Peltier e cols (2016), em análise proteômica quantitativa seguida por validação por ELISA em plasma de pacientes portadores de CCR e pacientes saudáveis, evidenciaram níveis 1,3 vezes maiores de SERPINA3 no CCR, com sensibilidade de 95% e especificidade de 55% no diagnóstico.(45)

Estudo recente de Cao e cols (2018) reforça a possibilidade do uso da SERPINA3 não só como marcador diagnóstico, mas também, como possível alvo terapêutico em pacientes metastáticos. Abordagem imunistoquímica foi realizada em tecidos tumorais e tecidos saudáveis adjacentes provenientes de 131 pacientes, sendo demonstrada expressão elevada da SERPINA3 no CCR. A análise foi complementada com estudo em linhagens celulares e em modelos animais, sendo identificado que o silenciamento da SERPINA3 implicou em diminuição do potencial de migração e invasão celular *in vitro*, e redução de metástases hepáticas e expressão de metaloproteinases no tecido tumoral metastático dos camundongos.(113)

No presente estudo, dentre as matrizes verificadas, foi observada maior abundância relativa da SERPINA3 no plasma de pacientes com CCR.

- Proteína altamente similar à cadeia leve 1 da miosina

A miosina é o principal componente dos elementos contráteis da musculatura lisa, sendo composta por duas cadeias pesadas similares e duas cadeias leves de 20 e 17kDa. A cadeia leve de 20kDa é chamada de cadeia leve reguladora e tem papel central na regulação da musculatura lisa.(114)

A cadeia leve da miosina parece estar envolvida no mecanismo de carcinogênese devido sua participação nas vias de apoptose. A fosforilação da cadeia leve da miosina pelas proteínas serina-treonina quinases leva ao aumento da contratilidade celular e consequente formação de bolhas na membrana. Esse processo encontra-se ainda, aparentemente ligado com a regulação da morfologia, migração celular e invasão neoplásica.(115–117) Análises em linhagens celulares de CCR confirmam a regulação positiva da fosforilação da cadeia leve da miosina, sendo esta via um possível alvo terapêutico. Sua inibição pode resultar em atenuação do processo de transição epitélio-mesenquimal e do potencial metastático.(118,119)

Na presente análise, dentre as matrizes avaliadas, foi identificada abundância relativa elevada da proteína altamente similar à cadeia leve 1 da miosina no tecido tumoral.

- Anidrase carbônica 1

O grupo das anidrases carbônicas é formado por metaloenzimas de zinco que têm como principal função a catálise da hidratação reversível do dióxido de carbono em bicarbonato, sendo essa reação crucial para a manutenção do equilíbrio do pH do corpo. Esse mecanismo químico possibilita a ocorrência de outros processos fisiológicos, tais como a reabsorção óssea, visão, produção de saliva, bile, suco pancreático e suco gástrico.(120)

As isoenzimas da anidrase carbônica têm sido descritas como possíveis marcadores de vários tipos de câncer, como o de cólon, hepatobiliar, esôfago, estômago, pâncreas, sistema nervoso e mama.(120–122) A contribuição da anidrase carbônica nas vias de carcinogênese reside no mecanismo de adaptação das células tumorais ao

ambiente de hipóxia, que estimula o aumento da expressão e da funcionalidade dessa enzima, permitindo a regulação do pH intracelular e extracelular.(123)

Além de biomarcador diagnóstico, a anidrase carbônica ganhou foco nas pesquisas de desenvolvimento de terapias-alvo. Existem evidências que demonstram que a inibição da anidrase carbônica IX aumenta a sensibilidade das células cancerígenas à quimioterapia convencional nos casos de câncer de mama, adenocarcinoma de cólon e melanoma.(123-126)

Na presente análise, dentre as matrizes avaliadas, foi identificada abundância relativa elevada da anidrase carbônica no tecido tumoral.

- Superóxido dismutase

A superóxido dismutase trata-se de uma enzima responsável por converter o superóxido em peróxido de hidrogênio, protegendo a célula das espécies reativas de oxigênio.(127) Essa enzima apresenta duas formas no ser humano: a superóxido dismutase dependente de cobre/zinco, presente no citoplasma, e a superóxido dismutase dependente de manganês, que se localiza na matriz mitocondrial. Outra enzima que apresenta papel fundamental no controle do dano oxidativo é a catalase, que tem por função, a conversão do peróxido de hidrogênio em H₂O e O.₂.(128)

As alterações que atingem essas enzimas responsáveis pelo controle antioxidativo intrínseco celular são conectadas com as vias de carcinogênese.(129,130) As células neoplásicas apresentam expressão elevada da superóxido dismutase mitocondrial e redução dos níveis de catalase, o que leva a desajuste nos níveis de peróxido de hidrogênio e desencadeamento de processos de resistência a apoptose, proliferação celular desordenada e surgimento de condições permissivas para desenvolvimento da doença metastática.(131)

Expressões elevadas da superóxido dismutase são encontradas em diversos tipos de câncer, tais como, câncer gástrico, esofágico, mama, tireóide e sistema nervoso central.(130) No câncer colorretal, também são evidenciados altos níveis desta enzima, sendo também correlacionada com a presença de invasão linfovascular,

comprometimento linfonodal e graus G2/G3 de diferenciação. Além disso, existe ainda regulação positiva da superóxido dismutase nos pólipos adenomatosos em relação à mucosa normal.(131) O desajuste do controle oxidativo no CCR parece afetar até mesmo a resposta à quimioterapia com oxilaplatina, visto que, a citotoxicidade decorrente do uso desta droga é dependente da produção de peróxido de hidrogênio.(132)

No presente estudo, dentre as matrizes avaliadas, foi identificada abundância relativa elevada da superóxido dismutase no tecido tumoral.

- Proteína altamente similar à proteína 5 do ciclo de divisão celular

A proteína 5 do ciclo de divisão celular (CDC5L) tem função essencial na progressão da fase G2 do ciclo celular e na entrada do processo de mitose, apresentando ainda papel na regulação da transcrição. Expressão elevada da CDC5L é associada a encurtamento da fase G2 e redução do tamanho da célula. Já a redução na expressão dessa proteína leva a desalinhamentos cromossômicos e danos ao processo mitótico. A CDC5L tem sido associada ao processo de carcinogênese dos gliomas, hepatocarcinomas, osteossarcomas e tumores cervicais.(133,134)

No CCR é encontrada elevada expressão da proteína 5 do ciclo celular, sendo os níveis correlacionados com doença avançada e taxas reduzidas de sobrevida. Foi evidenciado que a CDCL5 apresenta relação íntima com a expressão da transcriptase reversa da telomerase humana, proteína esta associada ao processo de gênese tumoral, migração e invasão neoplásica.(135)

No presente estudo, dentre as matrizes avaliadas, foi identificada abundância relativa elevada da CDC5L no plasma de pacientes com CCR.

2- Proteínas expressas no segundo modelo de análise (amostras plasmáticas-grupo CCR x grupo controle)

Nesse cenário de estudo, apenas a subunidade beta da hemoglobina apresentou significância estatística (proteína já discutida na seção anterior). A baixa diferenciação

entre os cenários pode ser explicada pelo número insuficiente utilizado no trabalho e evidenciado pelo cálculo da amostra ideal. Entretanto, dentre os elementos identificados, mesmo que sem significância estatística, nota-se congruência de algumas proteínas que também foram encontradas nos outros cenários de análise. Entre elas, é possível citar: transferrina, cadeia alfa do fibrinogênio, hemopexina, apolipoproteína D, complemento C4A.

3- Proteínas expressas no terceiro modelo de análise (amostras urinárias-grupo CCR x grupo controle)

Neste cenário de análise comparativa, foram identificadas 10 proteínas expressas na urina com potencial para biomarcadores. A tabela 6 demonstra as proteínas encontradas e o cenário correspondente de maior abundância relativa.

Tabela 6. Proteínas com potencial a biomarcadores urinários e cenário de maior abundância relativa

Proteínas	Maior abundância relativa
Isoforma 1 do colágeno tipo1 alfa 2	Controle
Apolipoproteína D	Controle
Uromodulina	Controle
Cininogênio 1	Controle
Beta-2-microglobulina	CCR
EFEMP1	Controle
Alfa-amilase	Controle
Fragmento da proteína 1 de interação com a PI3K	Controle

Titina	Controle
Domínios de homologia à plecstrina contendo membro 5 da família A	Controle

- Isoforma 1 do colágeno tipo 1 alfa 2

Durante a progressão neoplásica, o equilíbrio entre a formação e a degradação da matriz extracelular é afetado, com excessivo remodelamento do colágeno pelas metaloproteinases. Como consequência, pequenos fragmentos proteicos dos colágenos degradados são liberados na circulação, fazendo desses, potenciais marcadores da carcinogênese.(136)

A família dos colágenos é formada por 28 diferentes tipos de colágeno, sendo o tipo I o mais abundante no corpo humano e na matriz extracelular.(137) Trata-se de uma proteína heterotrimérica formada por duas cadeias alfa-1(COL1A1) e uma cadeia alfa-2 (COL1A2). (138)

Apesar de a maioria dos estudos evidenciarem expressão aumentada das proteínas do colágeno no CCR, inclusive como preditor de metástases hepáticas, o papel específico do COL1A2 é desconhecido. Aparentemente, o COL1A2 apresenta regulação negativa no CCR devido hipermetilação de seu gene codificador. Foi demonstrado *in vitro* que a hiperexpressão do COL1A2 inibe a proliferação, invasão e migração das células cancerígenas, sendo possível a utilização do mesmo como biomarcador prognóstico no CCR. (52,137-139)

No presente estudo, foi encontrada abundância relativa inferior do COL1A2 na urina de pacientes portadores de CCR em relação ao grupo controle.

- Apolipoproteína D

A apolipoproteína D é um membro da família da lipocalinas que está primariamente associada com lipoproteínas de alta densidade no plasma. Essa proteína

parece ter um papel multifuncional, estando associada ao ciclo e proliferação celular. Encontra-se altamente expressa nas adrenais, rins, baço, placenta, pâncreas, pulmões, ovários, testículos e sistema nervoso. Evidencia-se acúmulo dessa proteína em doenças neurodegenerativas, como o mal de Alzheimer.(140)

Em relação às condições neoplásicas, ocorre baixa expressão da apolipoproteína D no ambiente peritumoral, sendo evidenciada regulação negativa em vários tipos de câncer, como mama, próstata, ovário, esôfago, fígado e colorretal. Suspeita-se que a apolipoproteína D possa ter papel na promoção de apoptose de células.(141)

Na análise realizada nas amostras de urina no presente estudo, observou-se regulação negativa da apolipoproteínas nos pacientes portadores de CCR, fato esse, que está em concordância com o explicitado acima.

- Uromodulina

A uromodulina, também conhecida como proteína de Tamm-Horsfall, é uma glicoproteína codificada pelo gene UMOD, produzida exclusivamente nos rins, correspondendo a proteína mais abundante na urina. Ela participa de processos de transporte de íons, reduz a agregação de cristais de cálcio e apresenta função imunomoduladora no trato urinário.(142)

Essa proteína é considerada um biomarcador de doenças renais agudas e crônicas, sendo evidenciada regulação negativa da mesma em casos de neoplasias renais. (143,144) De modo semelhante, o presente estudo encontrou regulação negativa da uromodulina na urina de pacientes portadores de neoplasia colorretal em relação aos pacientes controle. Não foram encontrados outros relatos na literatura da expressão da uromodulina no câncer colorretal.

- Cininogênio 1

Os cininogênios são proteínas tiol-proteases, precursoras do sistema calicreína-kinina, apresentando papel importante na ativação da via intrínseca da cascata de

coagulação. Estão presentes em maior abundância no plasma, sendo produzidas no fígado.(145)

O cininogênio 1 é relatado como um potencial marcador sérico de adenomas colorretais em pacientes com história familiar de neoplasia.(146) Também é evidenciada regulação positiva dessa proteína nas amostras teciduais de adenocarcinomas colorretais precoces.(32)

- Beta-2-microglobulina

A beta-2-microglobulina (B2M) é uma pequena proteína que está presente na superfície das células nucleares e em quase todos os fluidos corporais, sendo componente-chave do complexo de histocompatibilidade.(147) Níveis elevados de B2M são associados com variadas condições patológicas, como doenças renais, imunodeficiências, doenças autoimunes, tumores sólidos e neoplasias hematológicas. Em relação ao CCR, nota-se relação robusta da regulação positiva dessa proteína com o risco de desenvolvimento da doença.(148) Mutações do gene B2M apresentam ainda valor na determinação de prognóstico no CCR.(149,150) A B2M parece estar envolvida no processo de crescimento, apoptose e metástases das células neoplásicas, sendo um possível foco para as terapias-alvo.(151)

No presente estudo, notou-se abundância relativa elevada da proteína na urina dos pacientes portadores de CCR. Devido a eliminação renal da B2M, a prospecção desse potencial marcador na urina parece ser uma abordagem interessante.

- Proteína da matriz extracelular 1 semelhante a fibulina contendo EGF

A família das fibulinas consiste de glicoproteínas com diferentes características do domínio C terminal e módulos semelhantes ao fator de crescimento epidérmico (EGF). Essas proteínas têm papel fundamental em vários processos biológicos, como desenvolvimento embrionário, organogênese, homeostase, coagulação e cicatrização. Além disso, essas proteínas estão envolvidas no controle da morfologia, crescimento, adesão e motilidade celular. No contexto do câncer colorretal, estudos relatam papel da

proteína da matriz celular 2 semelhante a fibulina contendo EGF (EFEMP2) como marcador de detecção precoce, recorrência e prognóstico do CCR.(152,153)

Já em relação à proteína da matriz extracelular 1 semelhante a fibulina contendo EGF (EFEMP1), também conhecida como fibulina 3, cujo gene codificador está relacionado à distrofia retiniana em favo de mel de Doyme, estudos evidenciam que a regulação negativa da mesma encontra-se associada com tumores avançados de cólon, sendo preditor de pior prognóstico e metástases linfonodais.(154,155)

No corrente estudo, também foi encontrada abundância relativa menor da fibulina 3 no grupo de pacientes portadores de CCR.

- Alfa-amilase

As alfa-amilases são uma família de hidrolases de glicosídeos produzidas principalmente pelas glândulas salivares e pelo pâncreas. Essas proteínas são utilizadas como marcadores de processos inflamatórios como a pancreatite, sendo também identificadas em tumores de mama, pulmão, tireoide, ovário e plasmocitomas.(156,157)

Não foram identificadas associações da alfa-amilase com a carcinogênese colorretal.

- Fragmento da proteína 1 de interação com a fosfatidilinositol-3-quinase

A sinalização do fosfatidilinositol-3-quinase (PI3K) é um dos eventos mais frequentes nos processos de carcinogênese, sendo também descrito para o câncer colorretal. O PI3K configura uma família de quinases lipídicas que têm por função a ativação da cascata de sinalização intracelular da proteína quinase específica de serina/treonina Akt. Por sua vez, a Akt exerce controle do crescimento e da proliferação celular.(158)

A Akt é conhecida como um dos principais fatores de ativação da proteína alvo de rapamicina em mamíferos (mTOR), sendo esta, importante na regulação da translação de proteínas e no crescimento celular. A ativação aberrante da via de sinalização PI3k/Akt/mTOR constitui um dos mecanismos primários para sustentação da

proliferação tumoral e gênese de metástases. Esse fato faz com que essa via seja foco de pesquisas para introdução de terapias-alvo. (159,160)

- Proteína titina

A titina é uma proteína que participa ativamente da formação das miofibrinas durante a miogênese, determina a elasticidade muscular e atua como mecanossensor para desencadear vias de sinalização.(161) Alterações dessa proteína são relacionadas ao desenvolvimento de desordens neuromusculares e cardiopatias, sendo um potencial marcador urinário dessas doenças.(162,163) A mutação do gene TTN é encontrada em vários tipos de tumores sólidos, entretanto, não se conhece ainda o papel exato da titina no processo de carcinogênese.(164)

- Domínios de homologia à plecstrina contendo membro 5 da família A

Os domínios de homologia à plecstrina estão ligados aos processos de carcinogênese por fazerem parte da via de sinalização da PI3k/Akt, que participa do controle do crescimento e proliferação celular. A ativação da Akt ocorre por meio de recrutamento direto na membrana plasmática pela ligação dos produtos do PI3K, fosfatidilinositol-3,4,5-trifosfato e fosfatidilinositol-3,4-bisfosfato aos domínios de homologia à plecstrina, o que resulta na fosforilação dos aminoácidos reguladores serina 473 e treonina 308. Mutações somáticas nesses domínios são identificadas em tumores de mama, cólon, ovário, pulmão, endométrio e melanomas.(165–167)

Limitações do estudo

Uma das limitações do estudo foi o número reduzido da amostra, evidenciado pelo cálculo da amostra ideal, principalmente no cenário de comparação das amostras de plasma.

Também não foi realizada coleta de tecido colônico de pacientes sem neoplasia para comparação com o tecido tumoral. Esse fato justifica-se pela questão ética para realização de biópsias em paciente sem doença. Muitos estudos utilizam como controle a

avaliação de peças em parafina de pacientes submetidos à ressecções colônicas por doenças não-neoplásicas (doença diverticular, por exemplo) ou os produtos de biópsias no tecido sadio contralateral ao tumor, entretanto, esses tipos de abordagens não foram realizadas neste estudo.

Outro ponto a ser considerado foi a inclusão de pacientes com estágios avançados de neoplasia. Cinco dos nove pacientes no grupo CCR apresentavam doença em estágio avançado (3 indivíduos com estágio III e 2 indivíduos com estágio IV). Levando-se em consideração a importância do diagnóstico precoce, teria sido interessante um estudo comparativo entre os diferentes estadios ou mesmo a adição de um grupo de pacientes portadores de pólipos adenomatosos.

6. CONCLUSÃO

A análise proteômica por espectrometria de massas das amostras de tecido tumoral, plasma e urina dos pacientes portadores de adenocarcinoma colorretal e a comparação com o perfil proteômico expresso nas amostras plasmáticas e urinárias de pacientes sem a doença permitiu a identificação de vinte e seis proteínas com potencial discriminativo. Futuras análises com validação em coortes maiores são necessárias para confirmar o papel diagnóstico desses potenciais biomarcadores no manejo do câncer colorretal.

Apesar da evolução da técnica da espectrometria de massas e do grande número de estudo proteômicos no CCR, ainda não se percebe translação desses conhecimentos para a prática clínica. Talvez o caminho para personalizar a abordagem aos pacientes portadores de CCR passe pela integração da proteômica com outras áreas como a genômica, a transcriptômica e a metabolômica, gerando condições para a gênese de um painel de biomarcadores que permita melhora de acurácia diagnóstica, estratificação de risco e predição de terapias individualizadas.

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8.1. ANEXO I- Termo de consentimento livre e esclarecido

TERMO DE CONSENTIMENTO LIVRE E ESCLARECIDO

Você está sendo convidado(a) a participar do estudo “Avaliação proteômica sérica, urinária e fecal na predição de adenomas e adenocarcinomas colorretais”. O(a) senhor(a) receberá todos os esclarecimentos necessários antes e no decorrer da pesquisa e lhe asseguramos que seu nome não aparecerá sendo mantido o mais rigoroso sigilo através da omissão total de quaisquer informações que permitam identificá-lo(a). Os avanços na área da saúde ocorrem através de estudos como este, por isso a sua participação é importante. O objetivo deste estudo é avaliar amostras de sangue, fezes e urina, visando identificação de marcadores que possam ajudar no diagnóstico e tratamento do câncer de intestino.

Para tal, solicitamos o seu consentimento para a coleta de amostras de sangue, urina e fezes durante a realização do seu exame de colonoscopia no setor de endoscopia do Hospital Universitário de Brasília. Não será feito nenhum procedimento além daqueles que você já iria realizar, caso não estivesse participando deste estudo. Informamos que o(a) Senhor(a) pode se recusar a responder (ou participar de qualquer procedimento) qualquer questão que lhe traga constrangimento, podendo desistir de participar da pesquisa em qualquer momento sem nenhum prejuízo para o(a) senhor(a). Sua participação é voluntária, isto é, não há pagamento por sua colaboração.

Os resultados da pesquisa serão divulgados na Instituição Faculdade de Medicina da Universidade de Brasília, podendo ser publicados posteriormente. Os dados e materiais utilizados na pesquisa ficarão sob a guarda do pesquisador por um período de no mínimo cinco anos, após isso serão destruídos ou mantidos na instituição.

Se o(a) Senhor(a) tiver qualquer dúvida em relação à pesquisa, por favor telefone para: Dr Bruno Augusto Alves Martins, na instituição FM/UnB, telefone: (61) 98188-3862, no horário de 08:00-11:00.

Este projeto foi Aprovado pelo Comitê de Ética em Pesquisa da Faculdade de Medicina da Universidade de Brasília. As dúvidas com relação à assinatura do TCLE ou os direitos do sujeito da pesquisa podem ser obtidos através do telefone: (61) 3107-1918 ou do e-mail cepfm@unb.br. Você também pode entrar em contato com o Comitê de Ética em Pesquisa do Hospital Universitário de Brasília, pelos telefones (61) 2028-5522/5533.

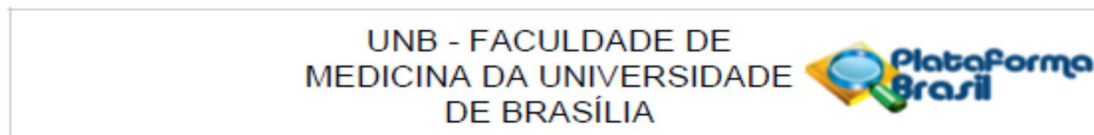
Este documento foi elaborado em duas vias, uma ficará com o pesquisador responsável e a outra com o sujeito da pesquisa.

Nome / assinatura

Pesquisador Responsável

Bruno Augusto Alves Martins

8.2. ANEXO II- Parecer consubstanciado do CEP

**PARECER CONSUBSTANCIADO DO CEP****DADOS DO PROJETO DE PESQUISA**

Título da Pesquisa: Avaliação proteômica sérica, urinária e fecal na predição de adenomas e adenocarcinomas colorretais

Pesquisador: Bruno Augusto Alves Martins

Área Temática:

Versão: 1

CAAE: 83200917.9.0000.5558

Instituição Proponente: Faculdade de Medicina da Universidade de Brasília - UNB

Patrocinador Principal: Financiamento Próprio

DADOS DO PARECER

Número do Parecer: 2.523.200

Apresentação do Projeto:

Projeto de pesquisa clínica envolvendo amostras de seres humanos intitulado Avaliação proteômica sérica, urinária e fecal na predição de adenomas e adenocarcinomas colorretais.

Apresenta como referencial teórico: O câncer colorretal é o terceiro câncer mais comum no mundo. A colonoscopia é o método padrão-ouro para rastreamento do câncer colorretal, porém, tem baixa aceitação entre os pacientes, custo elevado e riscos inerentes ao procedimento. O método não invasivo mais utilizado é o teste de sangue oculto nas fezes, entretanto, apesar de ser simples e barato, apresenta sensibilidade e especificidade contestáveis. Recentes avanços na genômica, proteômica e metabolômica têm aumentado o número de biomarcadores e contribuído para o entendimento da progressão do câncer colorretal. A descoberta de perfis proteicos ou biomarcadores associados à presença de um adenoma ou progressão para o adenocarcinoma representaria um grande avanço no diagnóstico e tratamento do câncer colorretal. Metodologia: Os pacientes encaminhados ao Serviço de Coloproctologia do Hospital Universitário de Brasília para realização de colonoscopia serão convidados a participar do estudo. Serão avaliadas amostras de plasma, urina e fezes de 3 grupos de pacientes: um grupo de pacientes submetidos a colonoscopia que não apresentam neoplasias colorretais (grupo controle do experimento); um grupo de pacientes submetidos a colonoscopia que apresentam pólipos adenomatosos colorretais; um grupo de pacientes submetidos a colonoscopia que apresentam adenocarcinomas colorretais. Cada um dos grupos terá um número amostral de 10 pacientes. Os

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Telefone: (61)3107-1918	E-mail: cepfm@unb.br

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Continuação do Parecer: 2.523.200

materiais biológicos serão processados e armazenados, sendo posteriormente analisados através de espectrômetro de massas LTQ- Orbitrap Elite (ThermoScientific). Será analisado e interpretado o perfil proteômico de cada cenário proposto, em busca da identificação possíveis perfis ou biomarcadores de progressão adenoma-adenocarcinoma.

Critério de Inclusão:

Pacientes encaminhados ao Serviço de Coloproctologia do Hospital Universitário de Brasília para realização de colonoscopia serão convidados a participar do estudo. Todos serão informados à respeito dos detalhes do estudo, sendo solicitada a assinatura do termo de consentimento livre e esclarecido. Dados referentes ao quadro clínico, história familiar, antecedentes patológicos e hábitos de vida serão coletados. Serão coletadas amostras de sangue e urina dos pacientes e amostras do aspirado colônico resultante da colonoscopia. Serão avaliados plasma, urina e amostras do aspirado colônico resultante da colonoscopia de 3 grupos de pacientes: um grupo de pacientes submetidos a colonoscopia que não apresenta nenhuma alteração colônica (grupo controle do experimento); um grupo de pacientes submetidos a colonoscopia que apresentam pólipos adenomatosos na região do cólon; um grupo de pacientes submetidos a colonoscopia que apresentam adenocarcinomas na região do cólon. Cada um dos grupos terá um número amostral de 10 pacientes.

Critério de Exclusão:

Serão excluídos pacientes portadores de doença inflamatória intestinal, polipose adenomatosa familiar, câncer colorretal hereditário não polipose ou outras síndromes de câncer colorretal hereditário; pacientes que realizaram quimioterapia e/ou radioterapia neoadjuvante; pacientes com tumores metacrônicos.

Objetivo da Pesquisa:

Objetivo Primário:

O objetivo do presente estudo é avaliar o perfil proteômico sérico, urinário e fecal de pacientes portadores de adenoma e adenocarcinoma, visando maior entendimento dos mecanismos moleculares envolvidos na carcinogênese e identificação de perfis proteicos associados à progressão displásica.

Objetivo Secundário:

Identificação de perfis proteicos associados à progressão displásica.

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Continuação do Parecer: 2.523.200

Avaliação dos Riscos e Benefícios:

Riscos:

Os pacientes que aceitarem participar do estudo serão expostos aos riscos inerentes aos processos de coleta de material biológico (sangue, urina e fezes).

Benefícios:

Possibilidade de identificação de perfis proteômicos compatíveis com a progressão adenoma-carcinoma, auxiliando no diagnóstico e tratamento precoce de pacientes portadores de neoplasias colorretais.

Comentários e Considerações sobre a Pesquisa:

A pesquisa está adequada aos critérios éticos estabelecidos pela CONEP.

Considerações sobre os Termos de apresentação obrigatória:

O pesquisador apresentou todos os documentos necessários, incluindo TCLE e projeto na íntegra.

Recomendações:

Atualizar no Projeto de Pesquisa na íntegra o número da resolução CONEP e incluir no projeto os riscos e benefícios apresentados.

Conclusões ou Pendências e Lista de Inadequações:

Aprovado.

Considerações Finais a critério do CEP:

Projeto apreciado na 2ª Reunião Ordinária do CEP-FM-UnB-2018. Após apresentação do parecer do (a) Relator (a), aberta a discussão para os membros do Colegiado. O projeto foi Aprovado.

De acordo com a Resolução 466/2012-CONEP/CNS, itens X.1.- 3.b. e XI.-2.d, este Comitê chama a atenção da obrigatoriedade de envio do relatório parcial semestral e final do projeto de pesquisa para o CEP-FM, através de Notificações submetidas pela Plataforma Brasil, contados a partir da data de aprovação do protocolo de pesquisa.

Este parecer foi elaborado baseado nos documentos abaixo relacionados:

Tipo Documento	Arquivo	Postagem	Autor	Situação
Informações Básicas do Projeto	PB_INFORMAÇÕES_BÁSICAS_DO_PROJETO_959432.pdf	24/01/2018 21:56:39		Aceito
Folha de Rosto	Folha_de_rosto_CEP2.pdf	24/01/2018 21:54:30	Bruno Augusto Alves Martins	Aceito

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Continuação do Parecer: 2.523.200

Projeto Detalhado / Brochura Investigador	Projeto_de_pesquisa.docx	17/12/2017 12:59:37	Bruno Augusto Alves Martins	Aceito
Outros	Curriculo_Marcos_Nogueira_Eberlin.pdf	17/12/2017 12:53:12	Bruno Augusto Alves Martins	Aceito
Outros	Curriculo_Aline_Maria_Araujo_Martins.pdf	17/12/2017 12:52:22	Bruno Augusto Alves Martins	Aceito
Outros	Curriculo_Paulo_Goncalves_de_Oliveira.pdf	17/12/2017 12:51:48	Bruno Augusto Alves Martins	Aceito
Outros	Curriculo_Bruno_Augusto_Alves_Martins.pdf	17/12/2017 12:51:21	Bruno Augusto Alves Martins	Aceito
Outros	Carta_encaminhamento.pdf	17/12/2017 12:46:08	Bruno Augusto Alves Martins	Aceito
Declaração de Pesquisadores	Decalacao_responsabilidade_CEPFM.pdf	17/12/2017 12:45:13	Bruno Augusto Alves Martins	Aceito
TCLE / Termos de Assentimento / Justificativa de Ausência	TERMO_DE_ESCLARECIMENTO.docx	17/12/2017 12:44:36	Bruno Augusto Alves Martins	Aceito
Orçamento	Planilha_orcamentaria.docx	17/12/2017 12:44:02	Bruno Augusto Alves Martins	Aceito
Outros	termo_ciencia_instituicao_coparticipante.pdf	05/10/2017 15:17:44	Bruno Augusto Alves Martins	Aceito
Outros	declaracao_isencao_onus_financieiro.pdf	05/10/2017 15:15:54	Bruno Augusto Alves Martins	Aceito
Declaração de Pesquisadores	declaracao_pesquisador.pdf	05/10/2017 15:13:16	Bruno Augusto Alves Martins	Aceito
Declaração de Instituição e Infraestrutura	termo_de_concordancia_institucional.pdf	05/10/2017 15:11:26	Bruno Augusto Alves Martins	Aceito
Cronograma	cronograma_do_projeto.docx	05/10/2017 15:06:57	Bruno Augusto Alves Martins	Aceito

Situação do Parecer:

Aprovado

Necessita Apreciação da CONEP:

Não

BRASILIA, 02 de Março de 2018

Assinado por:
Florêncio Figueiredo Cavalcanti Neto
(Coordenador)

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8.3. ANEXO III- Comprovante de submissão de artigo.

The screenshot displays the Frontiers review forum interface. At the top, the browser address bar shows the URL review.frontiersin.org/review/476229/16/748705/#tab/History. The navigation menu includes HOME, ABOUT, SUBMIT, JOURNALS, and RESEARCH TOPICS. The main header identifies the user as the Corresponding Author and provides a link for help or contact. A progress bar at the top indicates the current stage: 1. Initial Validation, with other stages including Editorial Assignment, Independent Review, Interactive Review, Review Finalized, Final Validation, and Final Decision.

The main content area features the title **BIOMARKERS IN COLORECTAL CANCER: THE ROLE OF TRANSLATIONAL PROTEOMICS RESEARCH**. The authors listed are Bruno Augusto Alves Martins*, Gabriel Fonseca De Bulhões, Igor Norat Cavalcanti, Mickaella Michelson Martins, Paulo Gonçalves de Oliveira, and Aline Maria Araujo Martins. The manuscript is for review in *Front. Oncol. - Gastrointestinal Cancers*. It was submitted on 02 Jun 2019 and has no associate editor assigned. The manuscript ID is 476229. The keywords are colorectal cancer, biomarkers, Translational research, Proteomics, and Mass Spectrometry.

On the right side, there are three utility links: [Download latest manuscript](#), [View submitted files history](#), and [View invoice](#).

A prominent message states: **NO ACTION IS REQUIRED FROM YOU**. Below this, it explains: "Your manuscript has been submitted successfully and is being verified by the editorial office as part of the initial manuscript validation."

8.4. ANEXO IV- Relatório do Progenesis do primeiro modelo de análise.

22/06/2019

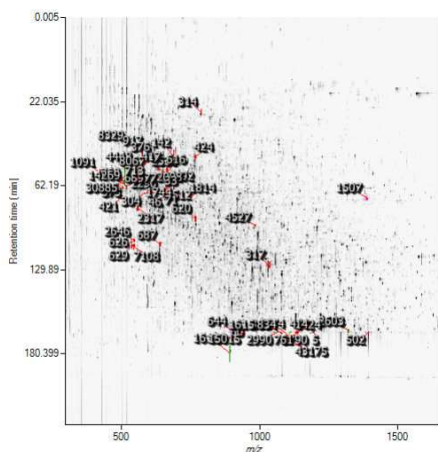
Biomarkers_CCR_1stexp

Biomarkers_CCR_1stexp

Experiment: Biomarkers_CCR_1stexp

Report created: 10/4/2018 9:10:27 PM

Overview image



Data Processing Methods

Peak processing method Profile data
 Feature detection method High resolution

Experiment Design

Condition	CCR	Plasma	Urine
Replicates	9	9	9

Proteins

Protein building options

Protein grouping Group similar proteins

Protein quantitation Using only features with no protein conflicts

Accession	Peptides	Score	Anova (p) ^a	Fold	Tags	Description	Average Normalised Abundances		
							CCR	Plasma	Urine
V9HWA9 V9HWA9_HUMAN	6	334.53	8.43e-012	58.96	●	Epikidymis secretory sperm binding protein LI 62p OS=Homo sapiens GN=HEL-5-62p PE-2 SV-1	3024.90	1.65e+005	2803.84
I6L965 I6L965_HUMAN	4	282.10	0.04	20.31	●	KRT18 protein (Fragment) OS=Homo sapiens GN=KRT18 PE-2 SV-1	7306.17	540.36	359.75
P68871 HBB_HUMAN	5	269.97	1.17e-004	371.57	●	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE-1 SV-2	2.11e+006	1.31e+005	5665.84
P01876 IGHA1_HUMAN	2	236.41	7.74e-006	65.85	●	Immunoglobulin heavy constant alpha 1 OS=Homo sapiens GN=IGHA1 PE-1 SV-2	1.56e+004	1.02e+006	1.85e+004
B4F1B2 B4F1B2_HUMAN	5	190.74	1.45e-006	99.15	●	cDNA FLJ53691, highly similar to Sero transferrin OS=Homo sapiens PE-2 SV-1	5322.49	5.28e+005	1.90e+005
A0A0K2BMD8 A0A0K2BMD8_HUMAN	3	184.84	6.49e-003	57.05	●	Mutant hemoglobin alpha 2 globin chain OS=Homo sapiens GN=HBA2 PE-3 SV-1	5.11e+005	1.14e+004	8954.68
P02671 FIBA_HUMAN	3	143.48	3.01e-008	218.69	●	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE-1 SV-2	1.50e+004	5.16e+005	2361.40
Q9BS19 Q9BS19_HUMAN	2	134.16	1.55e-006	769.13	●	HPX protein OS=Homo sapiens GN=HPX PE-1 SV-1	435.48	4.90e+004	63.73
P62805 H4_HUMAN	3	123.76	1.61e-003	192.92	●	Histone H4 OS=Homo sapiens GN=HIST1H4A PE-1 SV-2	1.00e+005	518.12	6510.08
Q77746 Q77746_HUMAN	2	83.30	1.91e-003	151.53	●	Actin alpha 1 skeletal muscle protein OS=Homo sapiens GN=ACTA1 PE-2 SV-1	2.49e+004	164.06	494.68

22/06/2019

Biomarkers_CCR_1stexp

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							CCR	Plasma	Urine
AQA140TA32 AQA140TA32_HUMAN	2	72.59	5.50e-004	27.24	●	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	1599.90	4.36e+004	2427.72
G3V3A0 G3V3A0_HUMAN	1	53.86	5.05e-003	331.96	●	Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=1	163.47	5.43e+004	6068.20
B4E36R B4E36R_HUMAN	1	48.81	0.01	34.81	●	cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform OS=Homo sapiens PE=2 SV=1	2081.74	59.80	1170.41
ESRI2 ESRI2_HUMAN	1	46.02	0.04	213.22	●	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=1	3446.34	16.16	1538.65
Q7Z7A7 Q7Z7A7_HUMAN	1	29.67	2.62e-003	383.11	●	Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1	118.19	0.31	46.26
B4DSH1 B4DSH1_HUMAN	1	23.59	5.12e-003	14.06	●	cDNA FLJ51295, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1	64.83	911.63	70.71

Tags	
●	Anova p-value ≤ 0.05

V9HWA9 | V9HWA9_HUMAN

Epididymis secretory sperm binding protein Li 62p OS=Homo sapiens GN=HEL-5-62p PE=2 SV=1
6 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
GQGTLSVVTMYHAK	1814	44.93	1	1490.7550	2		0		yes	1500.31	3.32e+004	618.61
QLYVVEATSYALLALLQLK	3834	56.99	1	2150.1973	2		0		yes	293.08	2.07e+004	1206.87
QVREPGQDLVPLSLITDFIP5FR	1615	90.72	2	2826.5290	3		0		yes	282.92	1.55e+004	45.89
QVREPGQDLVPLSLITDFIP5FR	15015	57.34	1	2826.5292	3		0		yes	155.69	977.30	67.32
VLLDGVQNPFR	713	45.79	1	1109.6191	2		0		yes	92.43	3.62e+004	590.75
VQLSNDFDEYMAAEQTIK	43175	53.25	1	2256.0987	2		0		yes	143.66	395.15	49.69
VQLSNDFDEYMAAEQTIK	1424	62.91	1	2256.0983	2		0		yes	323.77	2.44e+004	216.20
VVLVAVDK	1091	33.19	1	841.5262	2		0		yes	233.04	3.40e+004	8.50

Tags

I6L965 | I6L965_HUMAN

KRT18 protein (Fragment) OS=Homo sapiens GN=KRT18 PE=2 SV=1
4 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
AQIFANTVDNAR	2512	83.50	1	1318.6636	2		0		yes	3592.69	219.25	263.00
ASLENSLR	4448	35.53	1	888.4667	2		0		yes	1068.10	53.77	50.16
VIDDTNITR	8329	34.57	1	1045.5421	2		0		yes	705.36	256.27	43.18
YALQAEQLNGILLHLESELAQTR	16126	128.50	1	2669.3850	3		0		yes	1940.04	11.07	3.41

Tags

P68871 | HBB_HUMAN

Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2
5 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
FFESFGDLSTPDVAVAGNPK	317	68.68	1	2057.9399	2		0		yes	1.43e+006	1.05e+005	4465.68
LLVYYPWTQR	687	41.87	1	1273.7177	2		0		yes	1.05e+005	125.29	54.64

22/06/2019

Biomarkers_CCR_1stexp

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
VNVDEVGGEALGR	33	82.35	1	1313.6569	2		0		yes	2.82e+005	721.96	357.29
VNVDEVGGEALGR	46	58.39	1	1313.6570	2		0		yes	1.22e+005	2.43e+004	41.79
VNVDEVGGEALGR	71	81.68	1	1313.6571	2		0		yes	6.48e+004	89.58	489.16
VVAGVANALAH	14269	21.49	1	1020.5718	2		0		yes	420.97	1.63	116.47
VVAGVANALAHK	417	55.58	1	1148.6661	2		0		yes	3.74e+004	211.18	70.18
VVAGVANALAHK	376	49.88	1	1148.6666	2		0		yes	6.36e+004	4.60	70.63

Tags

P01876 | IGHA1_HUMAN

Immunoglobulin heavy constant alpha 1 OS=Homo sapiens GN=IGHA1 PE=1 SV=2
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
SGNTFRPEVHLLPPPSEELALNELVTLTCLAR	439	65.32	1	3572.8663	3		0	[29] C(+57.02)	yes	783.46	5.02e+004	4.88
SGNTFRPEVHLLPPPSEELALNELVTLTCLAR	644	78.80	5	3572.8675	4		0	[29] C(+57.02)	yes	1039.59	2.43e+004	80.09
SGNTFRPEVHLLPPPSEELALNELVTLTCLAR	5	112.54	1	3572.8658	3		0	[29] C(+57.02)	yes	3315.05	2.95e+005	1881.07
SGNTFRPEVHLLPPPSEELALNELVTLTCLAR	60	33.83	1	3572.8683	4		0	[29] C(+57.02)	yes	2418.19	1.56e+005	1795.39
TFTCTAAYPEK	142	45.07	1	1374.6123	2		0	[4] C(+57.02)	yes	7994.51	4.98e+005	1.47e+004

Tags

B4E1B2 | B4E1B2_HUMAN

cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1
5 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CCR	Plasma
AIAANEADAVTL DAGLVYDAYLAPNNLKPVAEFYGSK	2603	58.56	2	3953.0099	3		0		yes	1425.69	1.59e+004
AIAANEADAVTL DAGLVYDAYLAPNNLKPVAEFYGSKEDPQTFYVAIVVK	502	35.80	1	5563.8097	4		0		yes	486.32	1.55e+004
ASYLDCTIR	421	31.70	1	996.4696	2		0	[6] C(+57.02)	yes	732.15	8.77e+003
CTSSLLLEACTFR	620	30.76	1	1530.6806	2		0	[1] C(+57.02) [10] C(+57.02)	yes	2426.13	2.04e+004
LKCDSEWNSVGVK	768	33.92	1	1520.7296	3		0	[3] C(+57.02)	yes	252.19	6.56e+003

Tags

AOA0K2BMD8 | AOA0K2BMD8_HUMAN

Mutant hemoglobin alpha 2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
MFLSFPTTK	629	56.14	1	1070.5463	2		0		yes	5.73e+004	507.33	465.96
MFLSFPTTK	626	37.81	1	1070.5468	2		0		yes	5034.04	4257.85	49.77
MFLSFPTTK	2646	39.36	1	1086.5399	2		0	[1] M(+15.99)	yes	5.78e+004	310.49	5064.98
MFLSFPTTK	7108	26.27	1	1086.5400	2		0	[1] M(+15.99)	yes	4287.07	2734.39	1156.12
VGAHAGEYGAEALER	424	58.98	1	1528.7266	2		0		yes	2.50e+005	239.15	1223.74
VGAHAGEYGAEALER	573	30.36	1	1528.7271	3		0		yes	1.37e+005	3351.23	994.11

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Biomarkers_CCR_1stexp

Tags

P02671 | FIBA_HUMAN

Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances
GGSTSYGTGSETESPR	314	34.61	1	1571.6693	2		0		yes	3
NPGSSGTGGTATWKPSSGPGSTGSWNSGSSGTGSTGNQNGSPRPGSTGTWNPSSER	1507	18.52	1	5533.4458	4		0		yes	1.00
TFPGFFSPMLGEFVSETESR	761	90.35	1	2264.0443	2		0		yes	-
TFPGFFSPMLGEFVSETESR	2790	89.93	3	2264.0449	2		0		yes	-

Tags

Q9BS19 | Q9BS19_HUMAN

HPX protein OS=Homo sapiens GN=HPX PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CCR	Plasma
GE ⁺ QAEGLVFFQGDREWFWDLATGTAK	2990	115.50	1	3177.4334	3		0	[3] C(+57.02)	yes	204.06	2.25e+004
LLQDEFFGIPSPDAAYE ⁺ CHRG ⁺ EQAEGLVFFQGDREWFWDLATGTAK	5574	18.66	1	5522.5821	5		0	[19] C(+57.02) [24] C(+57.02)	yes	231.42	2.65e+004

Tags

P62805 | H4_HUMAN

Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
DNIQGITKPAIR	2531	41.36	1	1324.7464	2		0		yes	2.95e+004	56.86	977.38
DNIQGITKPAIR	616	32.04	1	1324.7462	2		0		yes	5.52e+004	215.53	2825.81
IQGITKPAIR	8067	18.94	1	1095.6765	2		0		yes	2068.24	28.53	828.81
ISGLIYEETR	1744	63.46	1	1179.6135	2		0		yes	1.32e+004	217.20	1878.07

Tags

Q7Z7J6 | Q7Z7J6_HUMAN

Actin alpha 1 skeletal muscle protein OS=Homo sapiens GN=ACTA1 PE=2 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
EITALAPSTAK	304	53.49	1	1160.6109	2		0		yes	7604.93	35.64	95.13
YPIEHGII ⁺ TNWDMEK	4527	29.81	1	1959.9039	2		0		yes	1.73e+004	128.42	399.56

Tags

A0A140TA32 | A0A140TA32_HUMAN

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Biomarkers_CCR_1stexp

Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
EMSGSPASGIPVK	2098	45.58	1	1258.6219	2		0		yes	1343.83	2.22e+004	1745.49
VGDTLNLNLR	2317	27.01	1	1113.6130	2		0		yes	256.06	2.13e+004	682.22

Tags

G3V3A0 | G3V3A0_HUMAN

Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
NLAVSQVVK	917	53.86	1	1093.6240	2		0		yes	163.47	5.43e+004	6068.20

Tags

B4E368 | B4E368_HUMAN

cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform OS=Homo sapiens PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
ILYSQCGDVWR	7092	48.81	1	1340.6225	2		0	[6] C(+57.02)	yes	2081.74	59.80	1170.41

Tags

E5RII2 | E5RII2_HUMAN

Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
HDTSLRPIVSYNPATAK	2290	46.02	1	1928.0007	3		0		yes	3446.34	16.16	1538.65

Tags

Q7Z7M7 | Q7Z7M7_HUMAN

Superoxide dismutase (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CCR	Plasma	Urine
GELLEAIKR	68977	29.67	1	1027.6026	2		0		yes	118.19	0.31	46.26

Tags

B4DSH1 | B4DSH1_HUMAN

cDNA FLJ51295, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances
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Biomarkers_CCR_1stexp

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average	Classified Abundance	Abundances
										CCR	Plasma	Urine
ILLGGYQSR	30885	23.59	1	1005.5612	2		0		yes	64.83	911.63	70.71

Tags

Accession V9HWA9 | V9HWA9_HUMAN

Description Epididymis secretory sperm binding protein L1 62p 05=Homo sapiens GN=HEL-S-62p PE=2 SV=1

Peptides 6

Score 334.53

Anova 8.43e-012

Fold 58.96

Anova p-value ≤ 0.05



Accession P02671 | FIBA_HUMAN

Description Fibrinogen alpha chain 05=Homo sapiens GN=FGA PE=1 SV=2

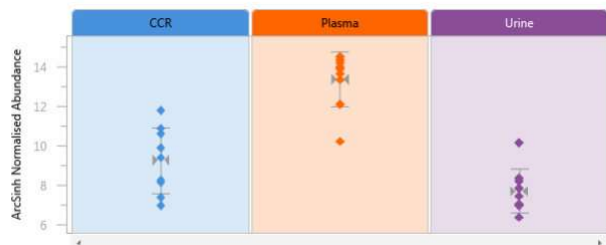
Peptides 3

Score 143.48

Anova 3.01e-008

Fold 218.69

Anova p-value ≤ 0.05



Accession B4E1B2 | B4E1B2_HUMAN

Description cDNA FLJ53691, highly similar to Serotransferrin 05=Homo sapiens PE=2 SV=1

Peptides 5

Score 190.74

Anova 1.45e-006

Fold 99.15

Anova p-value ≤ 0.05



Accession Q9BS19 | Q9BS19_HUMAN

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Biomarkers_CCR_1stexp

Description HPX protein OS=Homo sapiens GN=HPX PE=1 SV=1

Peptides 2

Score 134.16

Anova 1.55e-006

Fold 769.13

● Anova p-value \leq 0.05



Accession P01876 | IGHA1_HUMAN

Description Immunoglobulin heavy constant alpha 1 OS=Homo sapiens GN=IGHA1 PE=1 SV=2

Peptides 2

Score 236.41

Anova 7.74e-006

Fold 65.85

● Anova p-value \leq 0.05



Accession P68871 | HBB_HUMAN

Description Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

Peptides 5

Score 269.97

Anova 1.17e-004

Fold 371.57

● Anova p-value \leq 0.05



Accession A0A140TA32 | A0A140TA32_HUMAN

Description Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1

Peptides 2

Score 72.59

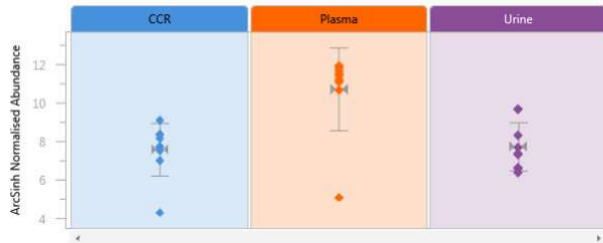
Anova 5.50e-004

Fold 27.24

● Anova p-value \leq 0.05

22/06/2019

Biomarkers_CCR_1stexp



Accession P62805 | H4_HUMAN

Description Histone H4 O5=Homo sapiens GN=HIST1H4A PE=1 SV=2

Peptides 3

Score 123.76

Anova 1.61e-003

Fold 192.92

● Anova p-value ≤ 0.05



Accession Q7Z7J6 | Q7Z7J6_HUMAN

Description Actin alpha 1 skeletal muscle protein O5=Homo sapiens GN=ACTA1 PE=2 SV=1

Peptides 2

Score 83.30

Anova 1.91e-003

Fold 151.53

● Anova p-value ≤ 0.05



Accession Q7Z7M7 | Q7Z7M7_HUMAN

Description Superoxide dismutase (Fragment) O5=Homo sapiens GN=SOD2 PE=2 SV=1

Peptides 1

Score 29.67

Anova 2.62e-003

Fold 383.11

● Anova p-value ≤ 0.05

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Biomarkers_CCR_1stexp



Accession G3V3A0 | G3V3A0_HUMAN

Description Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=1

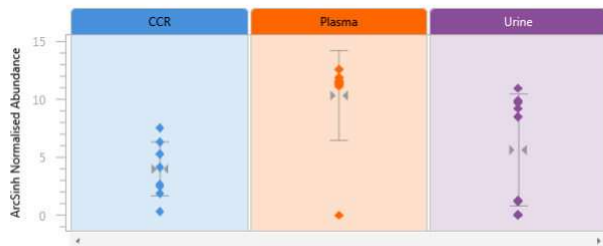
Peptides 1

Score 53.86

Anova 5.05e-003

Fold 331.96

Anova p-value ≤ 0.05



Accession B4DSH1 | B4DSH1_HUMAN

Description cDNA FLJ51295, highly similar to Cell division cycle 5-like protein OS=Homo sapiens PE=2 SV=1

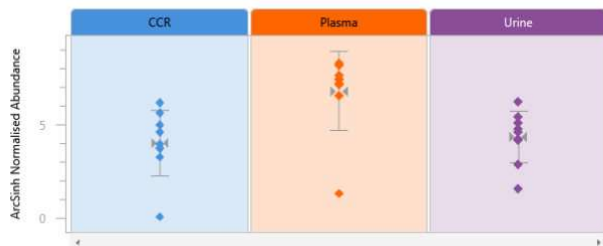
Peptides 1

Score 23.59

Anova 5.12e-003

Fold 14.06

Anova p-value ≤ 0.05



Accession A0A0K2BMD8 | A0A0K2BMD8_HUMAN

Description Mutant hemoglobin alpha 2 globin chain OS=Homo sapiens GN=HBAZ PE=3 SV=1

Peptides 3

Score 184.84

Anova 6.49e-003

Fold 57.05

Anova p-value ≤ 0.05

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Biomarkers_CCR_1stexp



Accession B4E368 | B4E368_HUMAN

Description cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform OS=Homo sapiens PE=2 SV=1

Peptides 1

Score 48.81

Anova 0.01

Fold 34.81

● Anova p-value ≤ 0.05



Accession I6L965 | I6L965_HUMAN

Description KRT18 protein (Fragment) OS=Homo sapiens GN=KRT18 PE=2 SV=1

Peptides 4

Score 282.10

Anova 0.04

Fold 20.31

● Anova p-value ≤ 0.05



Accession E5R112 | E5R112_HUMAN

Description Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=1

Peptides 1

Score 46.02

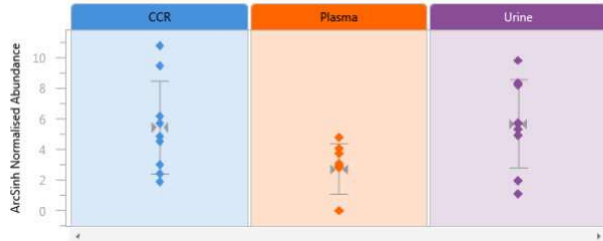
Anova 0.04

Fold 213.22

● Anova p-value ≤ 0.05

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Biomarkers_CCR_1stexp



Features

#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances		
								CCR	Plasma	Urine
713	6.071e-006	392.0	2	555.8168	58.6			92.428	3.623e+004	590.753
1091	6.100e-006	4002.6	2	421.7704	53.7			233.040	3.404e+004	8.504
1424	2.234e-005	112.6	2	1129.0564	171.2			323.769	2.435e+004	216.200
43175	9.485e-005	8.0	2	1129.0566	177.4			143.660	395.150	49.688
1615	7.630e-006	337.1	3	943.1836	170.8			282.922	1.547e+004	45.889
15015	0.140	14.5	3	943.1837	170.1			155.889	977.303	67.325
1814	4.268e-004	53.6	2	746.3848	70.7			1500.309	3.319e+004	618.608
3834	6.488e-005	70.5	2	1076.1059	172.0			293.085	2.066e+004	1206.870
314	1.658e-006	2340.4	2	786.8419	25.8			3670.464	3.242e+005	138.535
761	1.961e-006	282.6	2	1133.0294	171.3			483.212	4.075e+004	144.190
2790	0.007	54.0	2	1133.0297	170.6			834.020	6603.495	122.231
1507	5.873e-006	74.0	4	1384.3687	72.8			1.001e+004	1.448e+005	1956.448
421	5.099e-005	119.8	2	499.2421	71.1			732.153	8.769e+004	4099.157
502	4.025e-006	524.6	4	1391.9597	170.6			486.322	1.545e+005	294.564
620	0.002	84.1	2	766.3476	90.6			2426.134	2.040e+005	1.840e+005
768	3.503e-005	260.1	3	507.9171	59.8			252.188	6.559e+004	298.672
2603	0.010	13.5	3	1318.6773	169.7			1425.693	1.593e+004	1178.491
2990	3.429e-006	557.7	3	1060.1518	170.7			204.057	2.249e+004	40.326
5574	2.645e-007	1133.5	5	1105.5237	170.6			231.419	2.652e+004	23.400
5	1.876e-005	157.1	3	1191.9625	170.5			3315.049	2.955e+005	1881.067
60	4.280e-005	86.7	4	894.2243	170.5			2418.191	1.556e+005	1795.386
439	0.009	1.0e+004	3	1191.9627	169.7			783.465	5.023e+004	4.880
644	0.003	303.5	4	894.2242	169.7			1039.592	2.430e+004	80.092
142	0.001	62.3	2	688.3134	49.2			7994.509	4.984e+005	1.470e+004
33	0.039	788.1	2	657.8357	65.1			2.816e+005	721.955	357.289
46	1.327e-004	2923.1	2	657.8358	69.3			1.222e+005	2.433e+004	41.795
71	0.106	722.9	2	657.8358	67.8			6.476e+004	89.579	489.160
317	4.440e-004	320.4	2	1029.9772	126.0			1.431e+006	1.054e+005	4465.681
376	1.048e-004	1.4e+004	2	575.3406	44.9			6.359e+004	4.601	70.629
417	1.939e-004	533.6	2	575.3403	50.4			3.744e+004	211.180	70.177
687	0.120	1915.0	2	637.8661	110.5			1.046e+005	125.288	54.643
14269	0.046	259.0	2	511.2932	60.8			420.972	1.626	116.472
2098	0.040	16.6	2	630.3182	51.9			1343.834	2.225e+004	1745.492
2317	3.868e-005	83.3	2	557.8138	82.7			256.064	2.133e+004	682.223
616	0.046	256.2	2	663.3804	54.1			5.523e+004	215.532	2825.806
2531	0.086	518.4	2	663.3805	47.9			2.948e+004	56.860	977.384
1744	0.500	60.7	2	590.8140	67.6			1.318e+004	217.200	1878.072
8067	0.668	72.5	2	548.8455	54.3			2068.240	28.528	828.814
304	0.439	213.4	2	581.3127	68.0			7604.931	35.643	95.126
4527	0.059	134.4	2	980.9592	94.5			1.726e+004	128.420	399.556
68977	0.003	383.1	2	514.8086	62.5			118.190	0.309	46.264
917	0.005	332.0	2	547.8193	42.3			163.466	5.426e+004	6068.202
30885	0.005	14.1	2	503.7879	64.2			64.828	911.629	70.707
424	0.008	1044.7	2	765.3706	45.8			2.498e+005	239.146	1223.741
573	0.035	137.4	3	510.5830	50.8			1.366e+005	3351.234	994.107
626	0.110	101.1	2	536.2807	109.2			5034.038	4257.851	49.773
629	0.508	122.9	2	536.2804	110.9			5.728e+004	507.335	465.956

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Biomarkers_CCR_1stexp

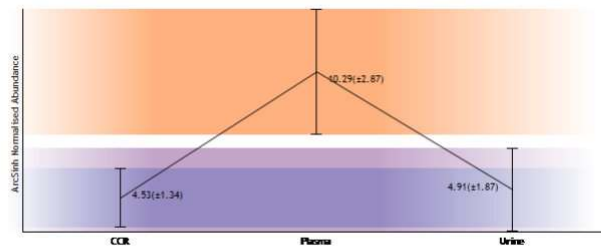
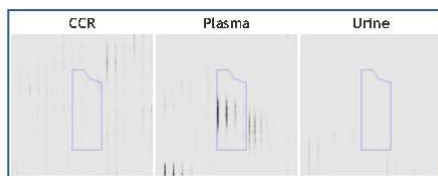
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								CCR	Plasma	Urine
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7108	0.098	3.7	2	544.2773	110.7			4287.071	2734.386	1156.117
7092	0.014	34.8	2	671.3185	61.7			2081.742	59.800	1170.409
2512	0.561	16.4	2	660.3391	62.8			3592.687	219.248	263.002
4448	0.608	21.3	2	445.2406	45.9			1068.095	53.768	50.165
8329	0.114	16.3	2	523.7783	38.3			705.355	256.271	43.176
16126	0.003	568.8	3	890.8023	179.4			1940.037	11.074	3.411
2290	0.042	213.2	3	643.6742	55.6			3446.340	16.163	1538.648

Tags

Feature number 713

Charge 2
m/z 555.8168
Retention Time 58.6
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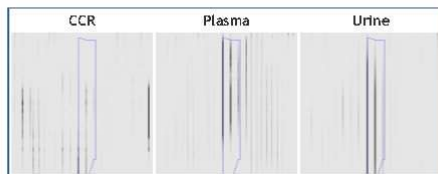
Score	Protein	Description
45.79	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein LI 62p OS-Homo sapiens GN-HEL-5-62p PE-2 SV-1



Feature number 1091

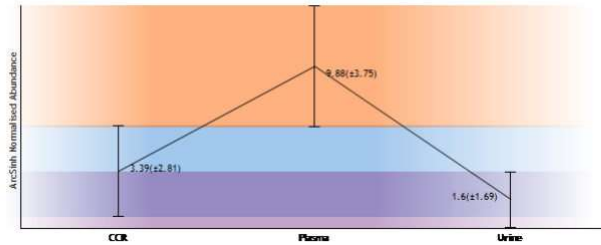
Charge 2
m/z 421.7704
Retention Time 53.7
Notes

Score	Protein	Description
33.19	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein LI 62p OS-Homo sapiens GN-HEL-5-62p PE-2 SV-1



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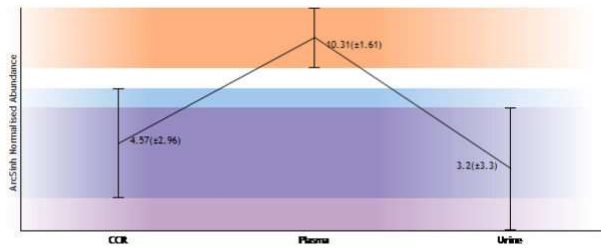
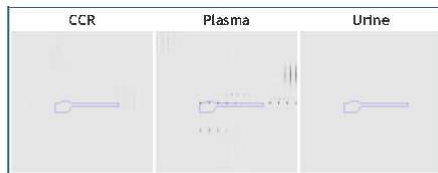


Feature number 1424

Charge 2
m/z 1129.0564

Retention Time 171.2
Notes

Score	Protein	Description
62.91	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1

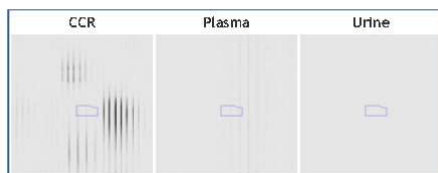


Feature number 43175

Charge 2
m/z 1129.0566

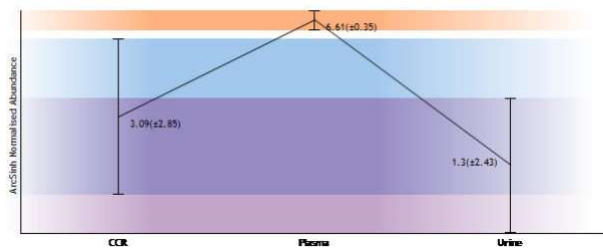
Retention Time 177.4
Notes

Score	Protein	Description
53.25	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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Feature number 1615

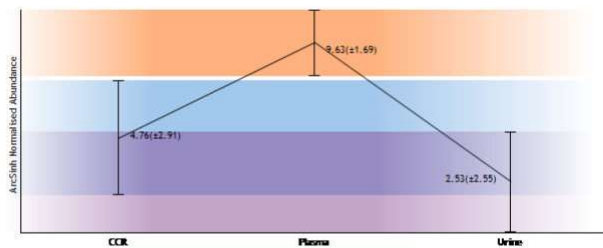
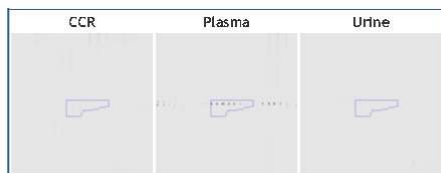
Charge 3

m/z 943.1836

Retention Time 170.8

Notes

Score	Protein	Description
90.72	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



Feature number 15015

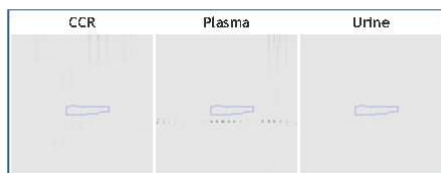
Charge 3

m/z 943.1837

Retention Time 170.1

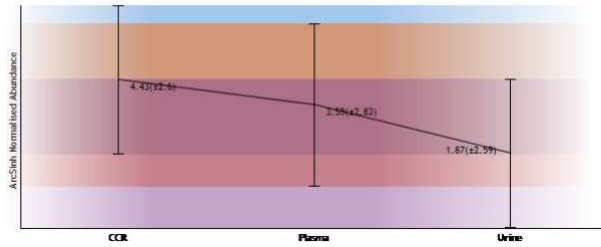
Notes

Score	Protein	Description
57.34	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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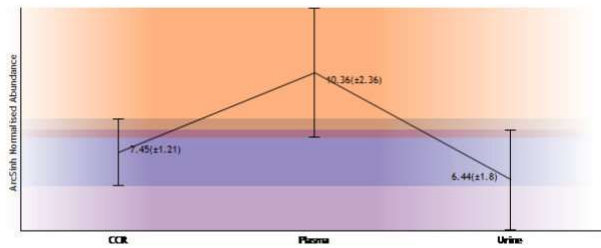
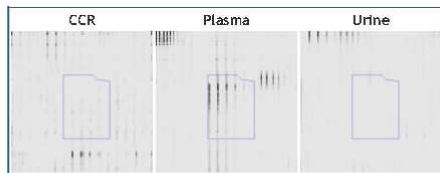
Feature number 1814

Charge 2
m/z 746.3848

Retention Time 70.7

Notes

Score	Protein	Description
44.93	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein LI 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



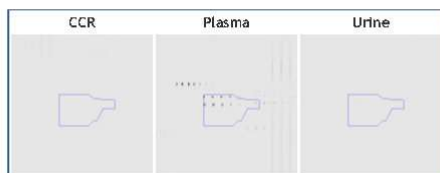
Feature number 3834

Charge 2
m/z 1076.1059

Retention Time 172.0

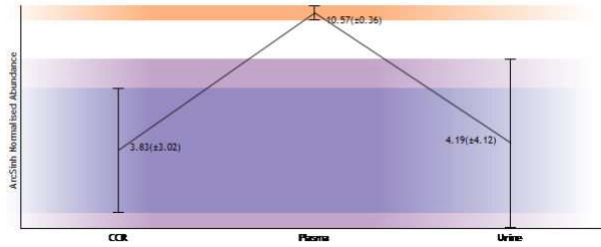
Notes

Score	Protein	Description
56.99	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein LI 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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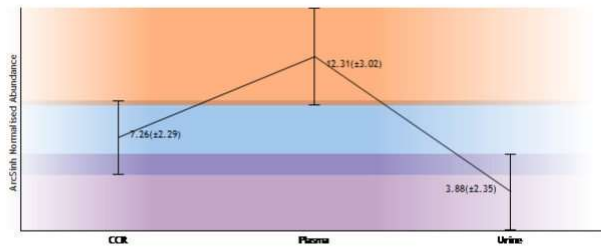
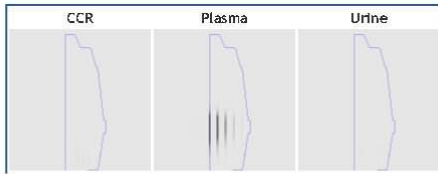
Feature number 314

Charge 2
m/z 786.8419

Retention Time 25.8

Notes

Score	Protein	Description
34.61	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



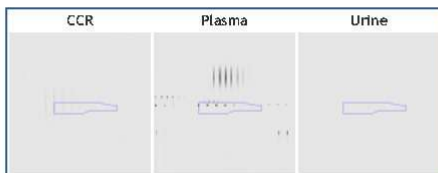
Feature number 761

Charge 2
m/z 1133.0294

Retention Time 171.3

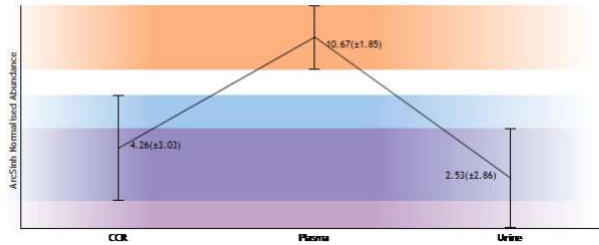
Notes

Score	Protein	Description
90.35	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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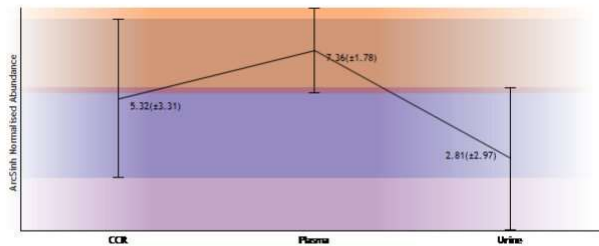
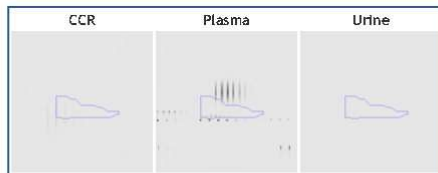


Feature number 2790

Charge 2
m/z 1133.0297

Retention Time 170.6
Notes

Score	Protein	Description
89.93	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2

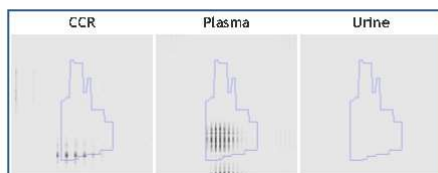


Feature number 1507

Charge 4
m/z 1384.3687

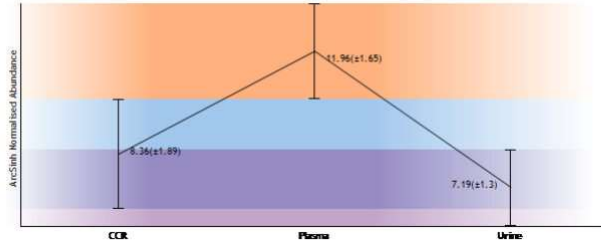
Retention Time 72.8
Notes

Score	Protein	Description
18.52	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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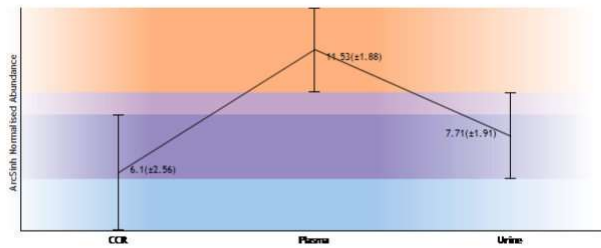
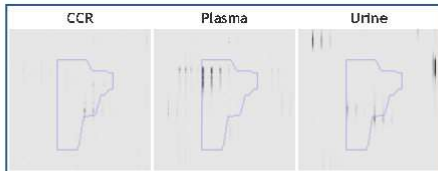


Feature number 421

Charge 2
m/z 499.2421

Retention Time 71.1
Notes

Score	Protein	Description
31.70	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1

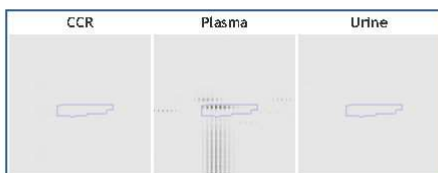


Feature number 502

Charge 4
m/z 1391.9597

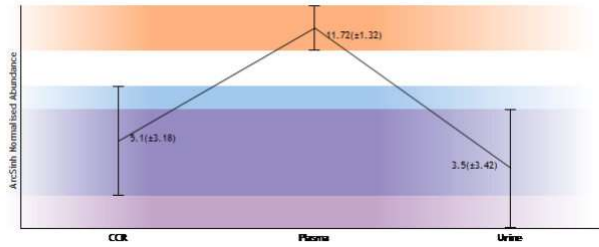
Retention Time 170.6
Notes

Score	Protein	Description
35.80	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



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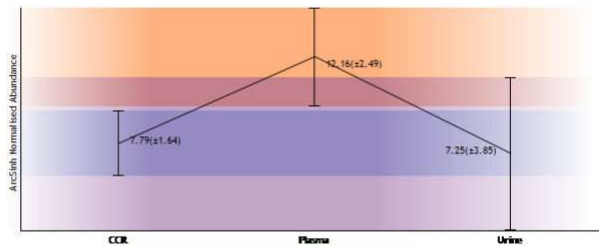
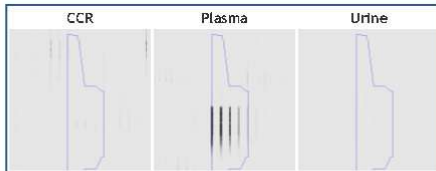


Feature number 620

Charge 2
m/z 766.3476

Retention Time 90.6
Notes

Score	Protein	Description
30.76	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1

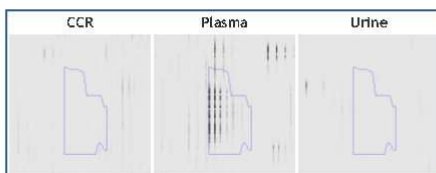


Feature number 768

Charge 3
m/z 507.9171

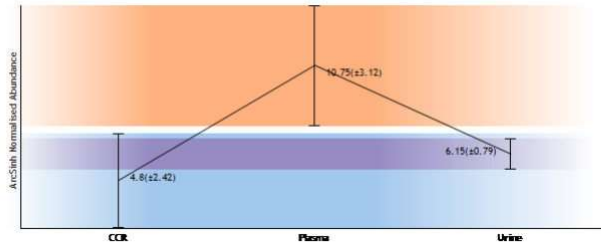
Retention Time 59.8
Notes

Score	Protein	Description
33.92	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



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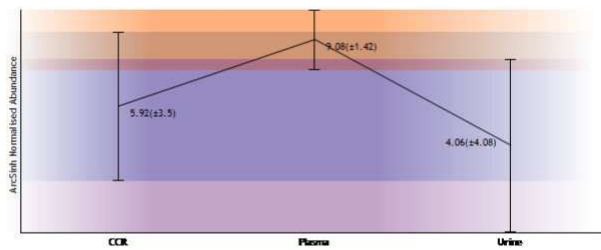
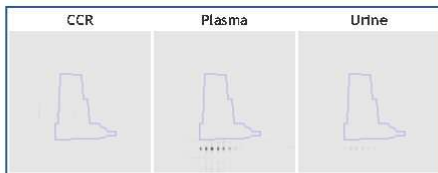
Feature number 2603

Charge 3
m/z 1318.6773

Retention Time 169.7

Notes

Score	Protein	Description
58.56	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



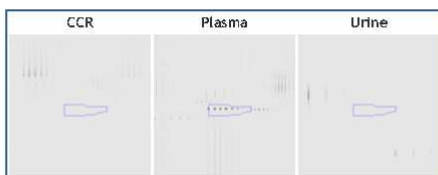
Feature number 2990

Charge 3
m/z 1060.1518

Retention Time 170.7

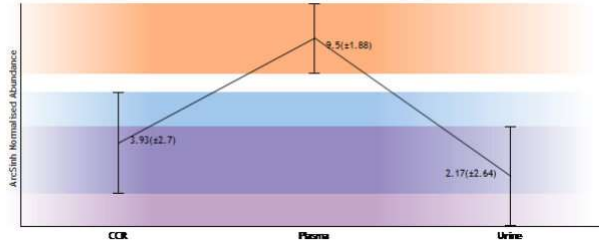
Notes

Score	Protein	Description
115.50	Q9B519 Q9B519_HUMAN	HPX protein OS-Homo sapiens GN-HPX PE-1 SV-1



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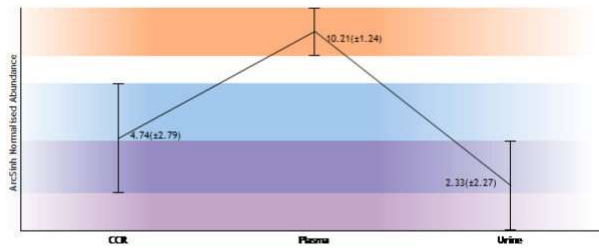
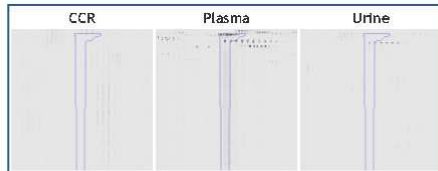
Feature number 5574

Charge 5
m/z 1105.5237

Retention Time 170.6

Notes

Score	Protein	Description
18.66	Q9BS19 Q9BS19_HUMAN	HPX protein OS=Homo sapiens GN=HPX PE=1 SV=1



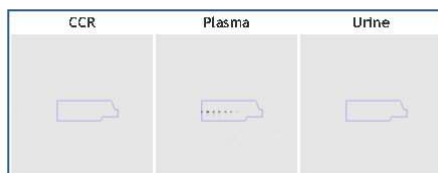
Feature number 5

Charge 3
m/z 1191.9625

Retention Time 170.5

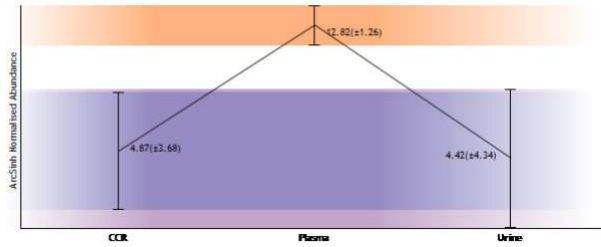
Notes

Score	Protein	Description
112.54	P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 OS=Homo sapiens GN=IGHA1 PE=1 SV=2



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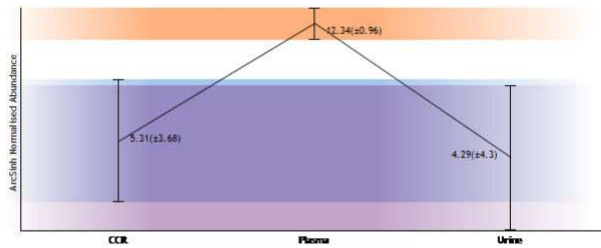
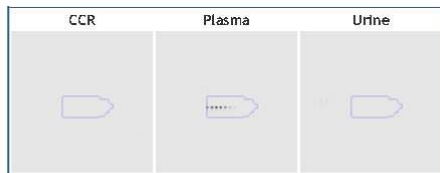


Feature number 60

Charge 4
m/z 894.2243

Retention Time 170.5
Notes

Score	Protein	Description
33.83	P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 D5-Homo sapiens GN-IGHA1 PE-1 SV-2

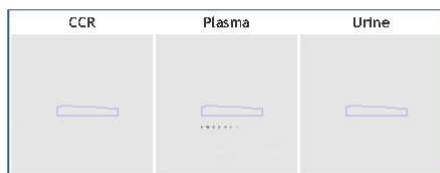


Feature number 439

Charge 3
m/z 1191.9627

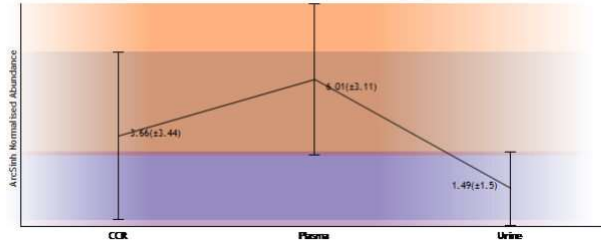
Retention Time 169.7
Notes

Score	Protein	Description
65.32	P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 D5-Homo sapiens GN-IGHA1 PE-1 SV-2



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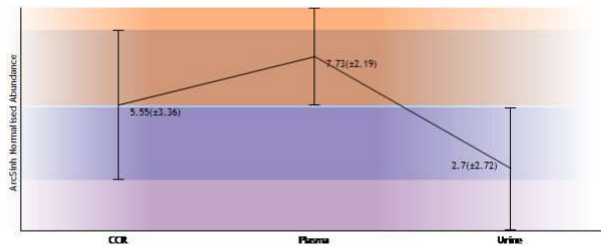
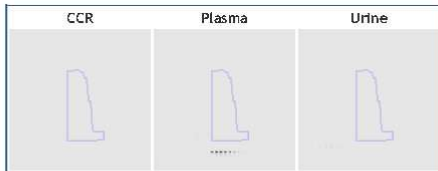
Feature number 644

Charge 4
m/z 894.2242

Retention Time 169.7

Notes

Score	Protein	Description
78.80	P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 D5-Homo sapiens GN-IGHA1 PE-1 SV-2



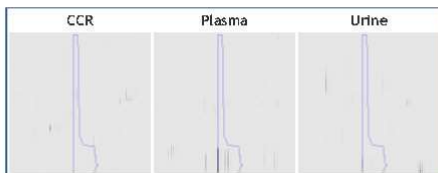
Feature number 142

Charge 2
m/z 688.3134

Retention Time 49.2

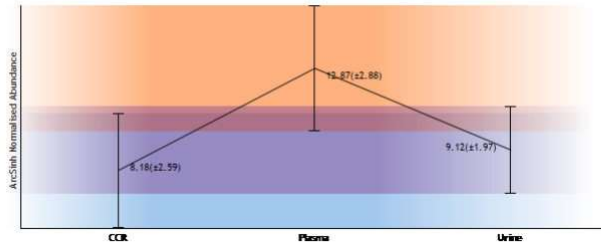
Notes

Score	Protein	Description
45.07	P01876 IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 D5-Homo sapiens GN-IGHA1 PE-1 SV-2



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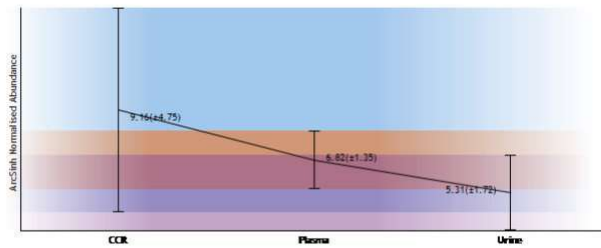
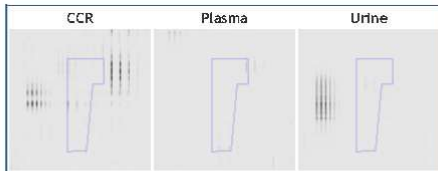


Feature number 33

Charge 2
m/z 657.8357

Retention Time 65.1
Notes

Score	Protein	Description
82.35	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2

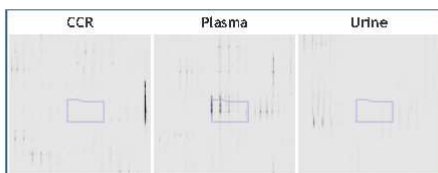


Feature number 46

Charge 2
m/z 657.8358

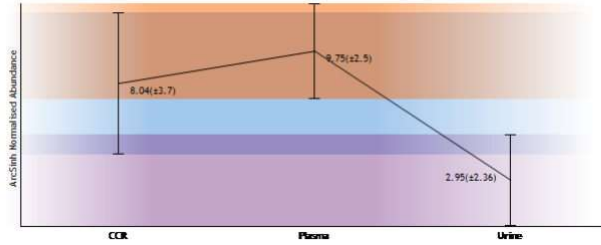
Retention Time 69.3
Notes

Score	Protein	Description
58.39	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



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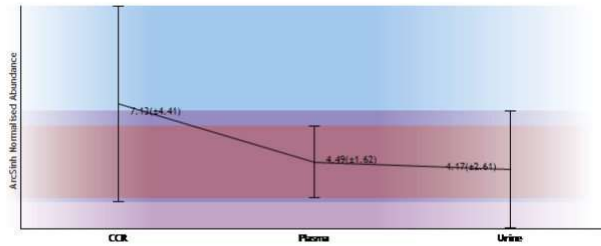
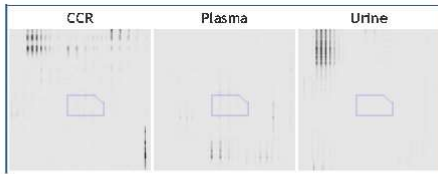
Feature number 71

Charge 2
m/z 657.8358

Retention Time 67.8

Notes

Score	Protein	Description
81.68	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



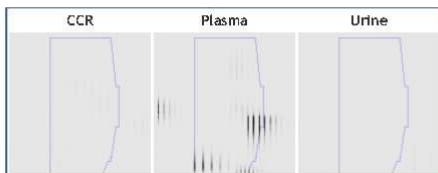
Feature number 317

Charge 2
m/z 1029.9772

Retention Time 126.0

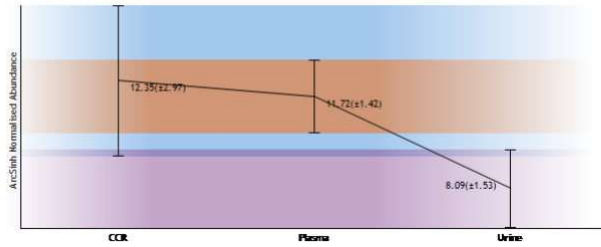
Notes

Score	Protein	Description
68.68	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



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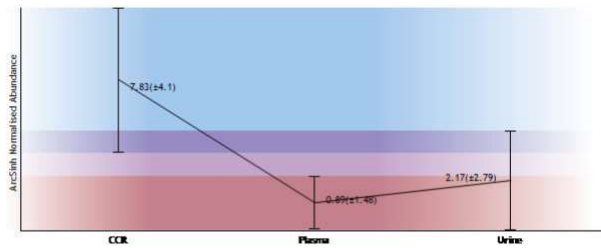
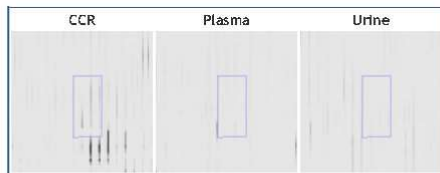


Feature number 376

Charge 2
m/z 575.3406

Retention Time 44.9
Notes

Score	Protein	Description
49.88	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2

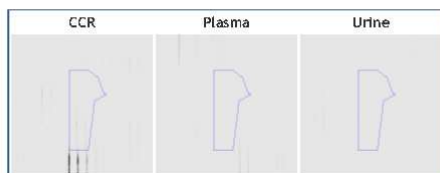


Feature number 417

Charge 2
m/z 575.3403

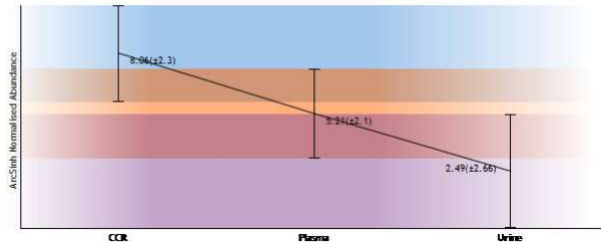
Retention Time 50.4
Notes

Score	Protein	Description
55.58	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



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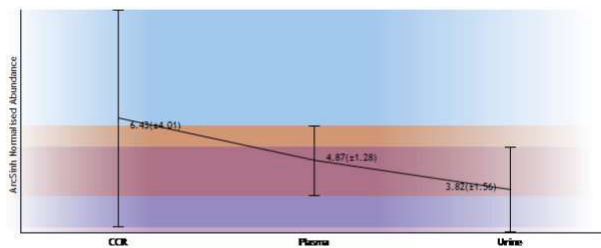
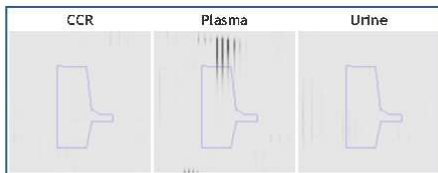
Feature number 687

Charge 2
m/z 637.8661

Retention Time 110.5

Notes

Score	Protein	Description
41.87	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



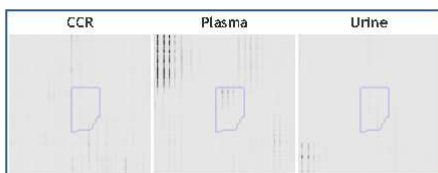
Feature number 14269

Charge 2
m/z 511.2932

Retention Time 60.8

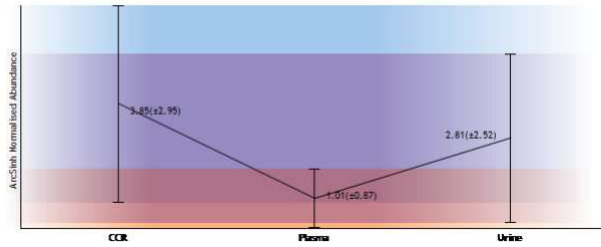
Notes

Score	Protein	Description
21.49	P68871 HBB_HUMAN	Hemoglobin subunit beta OS-Homo sapiens GN-HBB PE-1 SV-2



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Biomarkers_CCR_1stexp



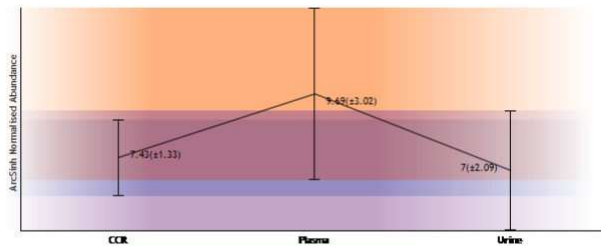
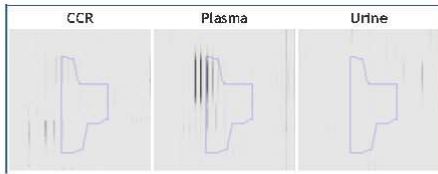
Feature number 2098

Charge 2
m/z 630.3182

Retention Time 51.9

Notes

Score	Protein	Description
45.58	ADA140TA32 ADA140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



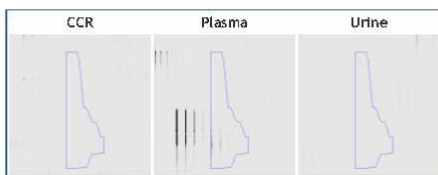
Feature number 2317

Charge 2
m/z 557.8138

Retention Time 82.7

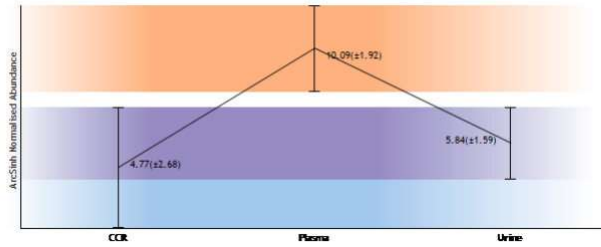
Notes

Score	Protein	Description
27.01	ADA140TA32 ADA140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



22/06/2019

Biomarkers_CCR_1stexp



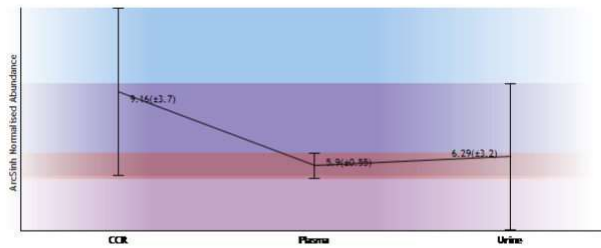
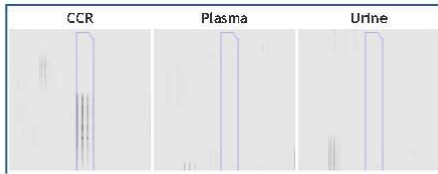
Feature number 616

Charge 2
m/z 663.3804

Retention Time 54.1

Notes

Score	Protein	Description
32.04	P62805 H4_HUMAN	Histone H4 OS-Homo sapiens GN-HIST1H4A PE-1 SV-2



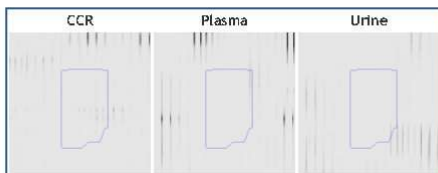
Feature number 2531

Charge 2
m/z 663.3805

Retention Time 47.9

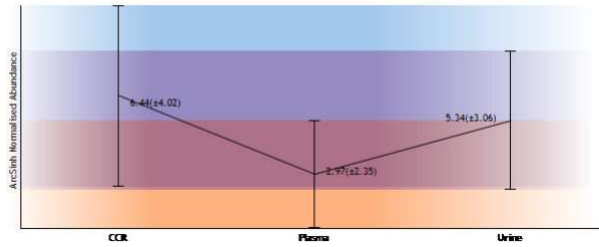
Notes

Score	Protein	Description
41.36	P62805 H4_HUMAN	Histone H4 OS-Homo sapiens GN-HIST1H4A PE-1 SV-2



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Biomarkers_CCR_1stexp



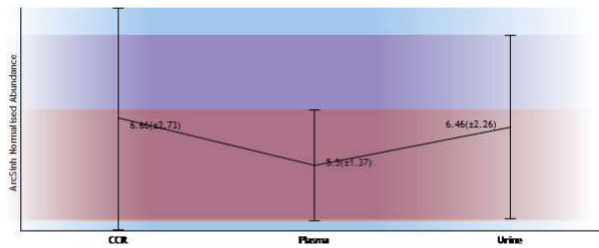
Feature number 1744

Charge 2
m/z 590.8140

Retention Time 67.6

Notes

Score	Protein	Description
63.46	P62805 H4_HUMAN	Histone H4 OS-Homo sapiens GN-HIST1H4A PE-1 SV-2



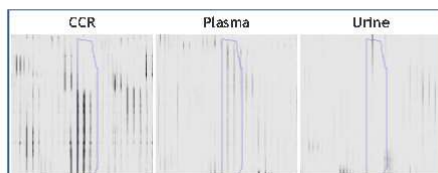
Feature number 8067

Charge 2
m/z 548.8455

Retention Time 54.3

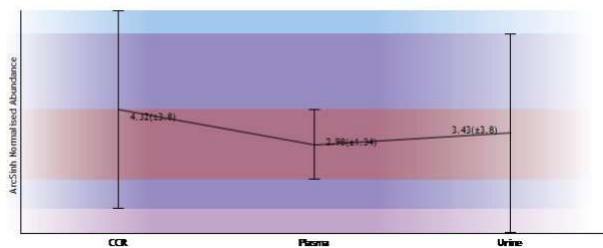
Notes

Score	Protein	Description
18.94	P62805 H4_HUMAN	Histone H4 OS-Homo sapiens GN-HIST1H4A PE-1 SV-2



22/06/2019

Biomarkers_CCR_1stexp



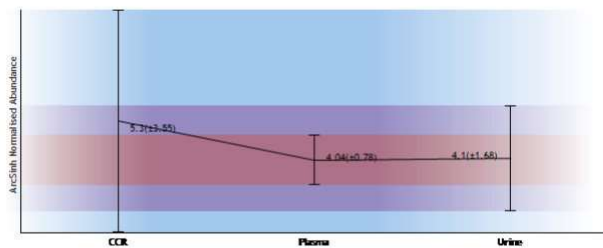
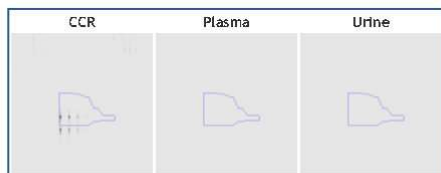
Feature number 304

Charge 2
m/z 581.3127

Retention Time 68.0

Notes

Score	Protein	Description
53.49	Q7Z7J6 Q7Z7J6_HUMAN	Actin alpha 1 skeletal muscle protein OS-Homo sapiens GN=ACTA1 PE=2 SV=1



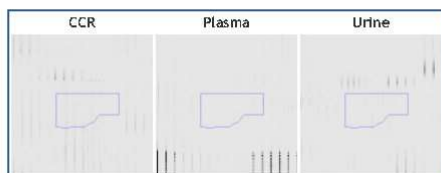
Feature number 4527

Charge 2
m/z 980.9592

Retention Time 94.5

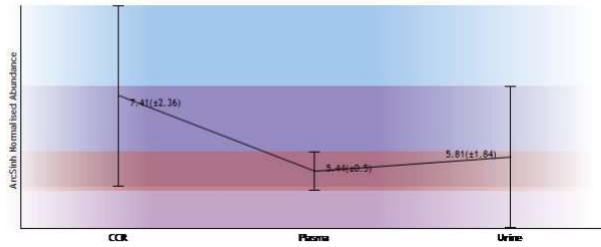
Notes

Score	Protein	Description
29.81	Q7Z7J6 Q7Z7J6_HUMAN	Actin alpha 1 skeletal muscle protein OS-Homo sapiens GN=ACTA1 PE=2 SV=1



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Biomarkers_CCR_1stexp

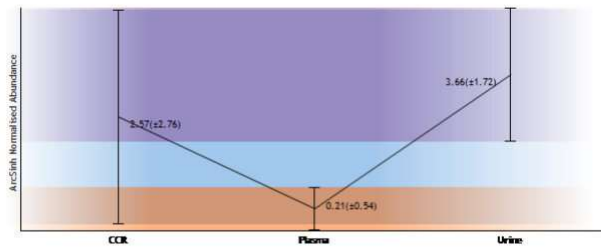
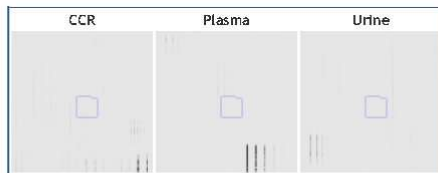


Feature number 68977

Charge 2
m/z 514.8086

Retention Time 62.5
Notes

Score	Protein	Description
29.67	Q7Z7A7 Q7Z7A7_HUMAN	Superoxide dismutase (Fragment) OS-Homo sapiens GN-SOD2 PE-2 SV-1

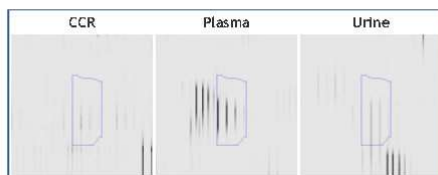


Feature number 917

Charge 2
m/z 547.8193

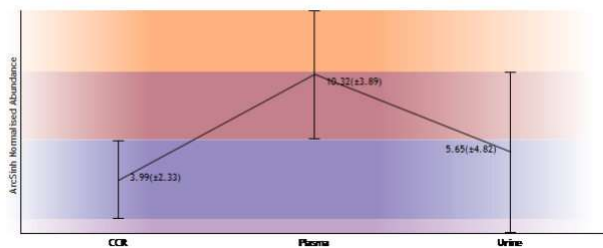
Retention Time 42.3
Notes

Score	Protein	Description
53.86	G3V3A0 G3V3A0_HUMAN	Alpha-1-antichymotrypsin OS-Homo sapiens GN-SERPINA3 PE-1 SV-1



22/06/2019

Biomarkers_CCR_1stexp



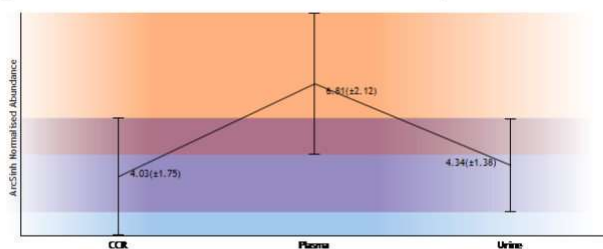
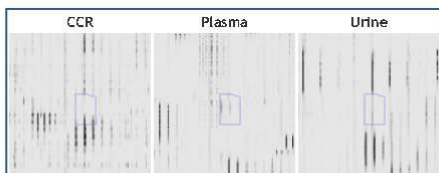
Feature number 30885

Charge 2
m/z 503.7879

Retention Time 64.2

Notes

Score	Protein	Description
23.59	B4DSH1 B4DSH1_HUMAN	cDNA FLJ51295, highly similar to Cell division cycle 5-like protein OS-Homo sapiens PE-2 SV-1



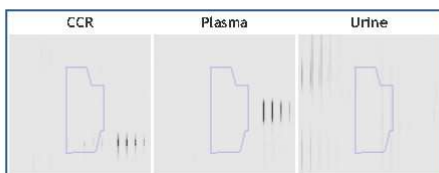
Feature number 424

Charge 2
m/z 765.3706

Retention Time 45.8

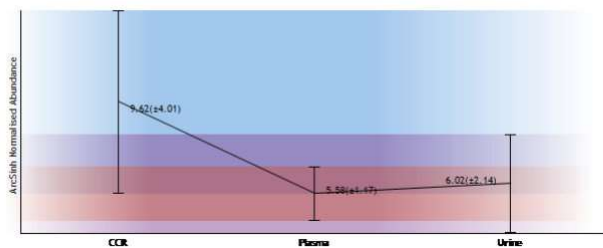
Notes

Score	Protein	Description
58.98	A0A0K2BWD8 A0A0K2BWD8_HUMAN	Mutant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1



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Biomarkers_CCR_1stexp



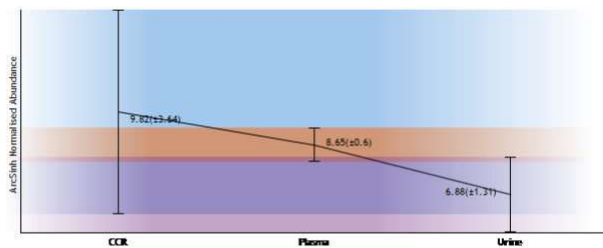
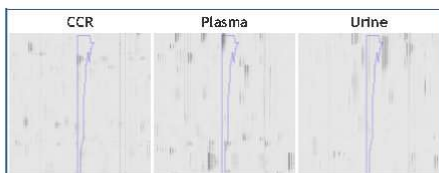
Feature number 573

Charge 3
m/z 510.5830

Retention Time 50.8

Notes

Score	Protein	Description
30.36	A0A0K2BMD8 A0A0K2BMD8_HUMAN	Alutant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBAZ PE-3 SV-1



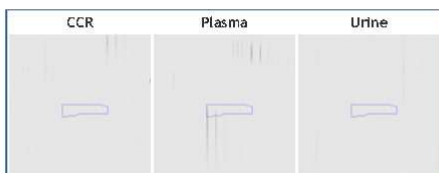
Feature number 626

Charge 2
m/z 536.2807

Retention Time 109.2

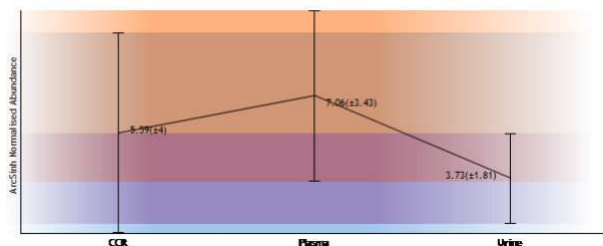
Notes

Score	Protein	Description
37.81	A0A0K2BMD8 A0A0K2BMD8_HUMAN	Alutant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBAZ PE-3 SV-1



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Biomarkers_CCR_1stexp



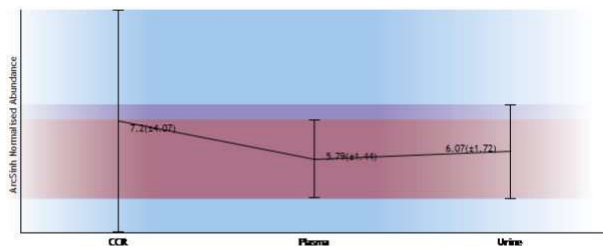
Feature number 629

Charge 2
m/z 536.2804

Retention Time 110.9

Notes

Score	Protein	Description
56.14	A0A0K2BMD8 A0A0K2BMD8_HUMAN	Autant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1



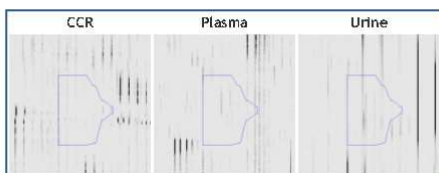
Feature number 2646

Charge 2
m/z 544.2772

Retention Time 107.3

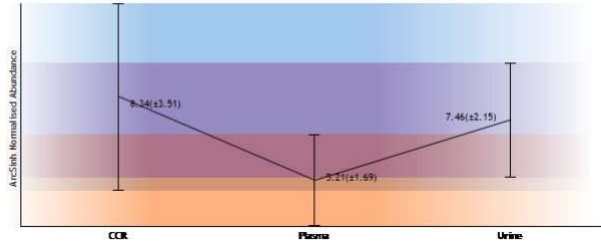
Notes

Score	Protein	Description
39.36	A0A0K2BMD8 A0A0K2BMD8_HUMAN	Autant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1



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Biomarkers_CCR_1stexp



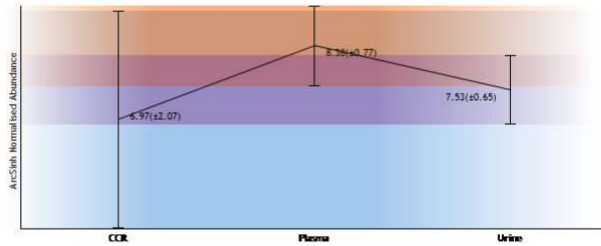
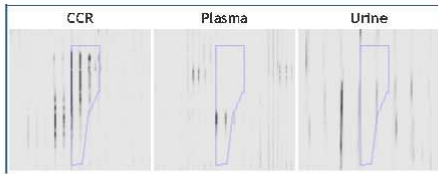
Feature number 7108

Charge 2
m/z 544.2773

Retention Time 110.7

Notes

Score	Protein	Description
26.27	A0A0K2BMD8 A0A0K2BMD8_HUMAN	Alutant hemoglobin alpha 2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1



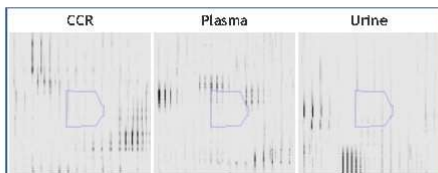
Feature number 7092

Charge 2
m/z 671.3185

Retention Time 61.7

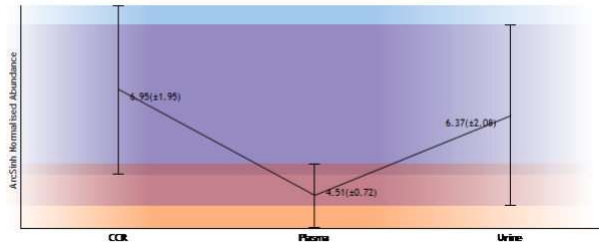
Notes

Score	Protein	Description
48.81	B4E368 B4E368_HUMAN	cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform OS-Homo sapiens PE-2 SV-1



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Biomarkers_CCR_1stexp



Feature number 2512

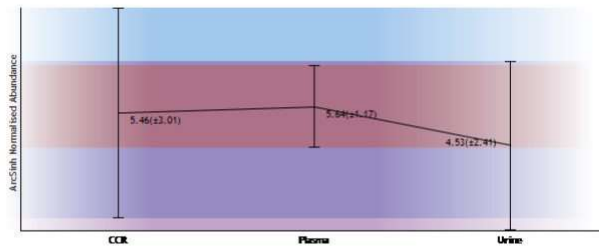
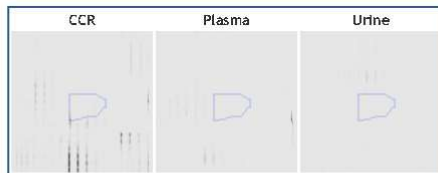
Charge 2

m/z 660.3391

Retention Time 62.8

Notes

Score	Protein	Description
83.50	I6L965 I6L965_HUMAN	KRT18 protein (Fragment) OS-Homo sapiens GN-KRT18 PE-2 SV-1



Feature number 4448

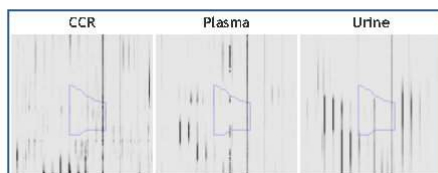
Charge 2

m/z 445.2406

Retention Time 45.9

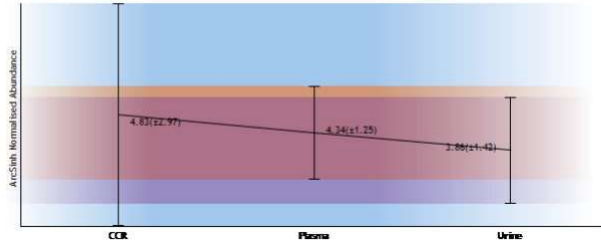
Notes

Score	Protein	Description
35.53	I6L965 I6L965_HUMAN	KRT18 protein (Fragment) OS-Homo sapiens GN-KRT18 PE-2 SV-1



22/06/2019

Biomarkers_CCR_1stexp



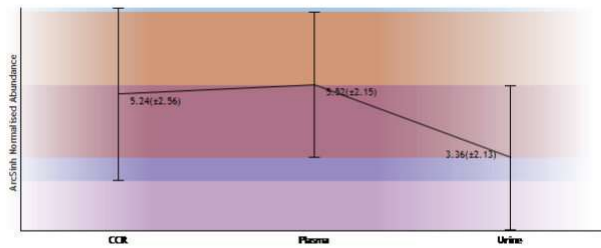
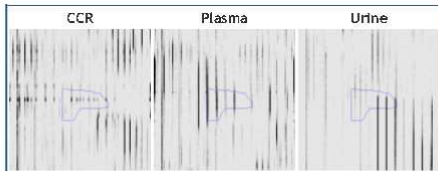
Feature number 8329

Charge 2
m/z 523.7783

Retention Time 38.3

Notes

Score	Protein	Description
34.57	I6L965 I6L965_HUMAN	KRT18 protein (Fragment) OS-Homo sapiens GN-KRT18 PE-2 SV-1



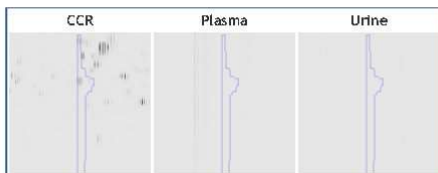
Feature number 16126

Charge 3
m/z 890.8023

Retention Time 179.4

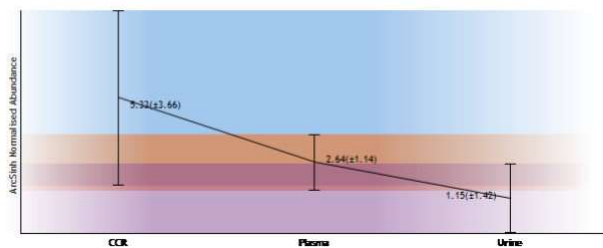
Notes

Score	Protein	Description
128.50	I6L965 I6L965_HUMAN	KRT18 protein (Fragment) OS-Homo sapiens GN-KRT18 PE-2 SV-1



22/06/2019

Biomarkers_CCR_1stexp



Feature number 2290

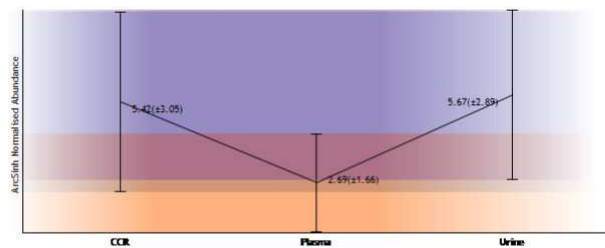
Charge 3

m/z 643.6742

Retention Time 55.6

Notes

Score	Protein	Description
46.02	ESRII2 ESRII2_HUMAN	Carbonic anhydrase 1 OS-Homo sapiens GN-CA1 PE-1 SV-1



8.5. ANEXO V. Relatório do Progenesis do segundo modelo de análise

23/06/2019

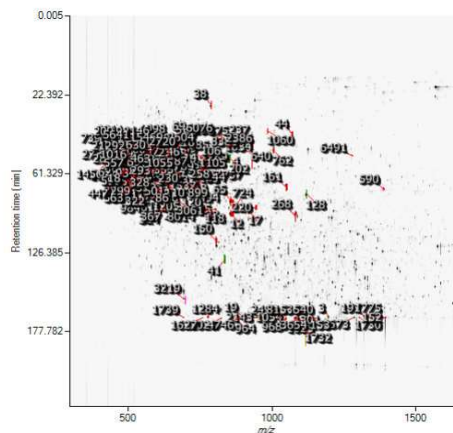
biomarkers_ccr_plasma_dez2018

biomarkers_ccr_plasma_dez2018

Experiment: biomarkers_ccr_plasma_dez2018

Report created: 12/15/2018 3:56:00 PM

Overview image



Data Processing Methods

Peak processing method **Profile data**

Feature detection method **High resolution**

Experiment Design

Condition	CTRL_plasma	CRC_plasma
Replicates	9	9

Proteins

Protein building options

Protein grouping **Group similar proteins**

Protein quantitation **Using only features with no protein conflicts**

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTRL_plasma	CRC_plasma
DQ6AH7 DQ6AH7_HUMAN	15	1100.41	0.08	1.35		Transferrin OS-Homo sapiens GN-TF PE-2 SV-1	4.46e+006	3.31e+006
V9HWA9 V9HWA9_HUMAN	15	992.72	0.32	1.16		Epitidymis secretory sperm binding protein LI 62p OS-Homo sapiens GN-HEL-S-62p PE-2 SV-1	7.36e+005	6.36e+005
PDZ671 FIBA_HUMAN	15	978.17	0.28	1.16		Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2	1.98e+006	1.71e+006
Q8NCL6 Q8NCL6_HUMAN	11	669.24	0.32	1.46		CDNA FLJ90170 fis, clone MAMWA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1	3.35e+006	2.29e+006
ADA140V LI6 ADA140V.LI6_HUMAN	9	461.52	0.30	1.19		Tesicular tissue protein LI 70 OS-Homo sapiens PE-2 SV-1	1.09e+006	9.16e+005
P01023 AZMG_HUMAN	8	398.22	0.09	1.50		Alpha-2-macroglobulin OS-Homo sapiens GN-AZM PE-1 SV-3	8.71e+005	5.82e+005
D3DP13 D3DP13_HUMAN	8	378.87	0.27	1.12		Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1	7.65e+005	6.82e+005
ADA0C4DGLR ADA0C4DGLR_HUMAN	7	343.43	0.63	1.20		Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1	2.44e+006	2.91e+006
PDZ647 APOA1_HUMAN	7	303.28	0.33	1.27		Apolipoprotein A-1 OS-Homo sapiens GN-APOA1 PE-1 SV-1	8.72e+005	6.89e+005
ADA140TA32 ADA140TA32_HUMAN	6	286.97	0.27	1.23		Complement C4-A OS-Homo sapiens GN-C4A PE-1 SV-1	1.24e+005	1.53e+005
ADA0G2JRN3 ADA0G2JRN3_HUMAN	6	239.45	0.83	1.11		Alpha-1-antitrypsin OS-Homo sapiens GN-SERPINA1 PE-1 SV-1	1.16e+006	1.28e+006

23/06/2019

biomarkers_ccr_plasma_dez2018

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTRL_plasma	CRC_plasma
E1A689 E1A689_HUMAN	4	188.23	0.67	1.24		Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1	2.65e+004	3.30e+004
P02790 HEMO_HUMAN	3	158.67	0.18	1.17		Hemopexin OS-Homo sapiens GN-HPX PE-1 SV-2	1.14e+006	9.78e+005
Q68DH2 Q68DH2_HUMAN	2	141.47	0.50	1.04		Uncharacterized protein DKFZp686G21125 (Fragment) OS-Homo sapiens GN-DKFZp686G21125 PE-2 SV-1	3.83e+004	3.69e+004
P0DQX6 IGM_HUMAN	3	124.93	0.15	1.47		Immunoglobulin mu heavy chain OS-Homo sapiens PE-1 SV-1	5.32e+005	3.62e+005
A0A096LPE2 A0A096LPE2_HUMAN	2	123.30	0.64	1.10		5AA2-5AA4 readthrough OS-Homo sapiens GN-5AA2-5AA4 PE-4 SV-1	2.19e+004	2.40e+004
Q7Z3Y4 Q7Z3Y4_HUMAN	2	116.39	0.32	1.15		Uncharacterized protein OS-Homo sapiens PE-1 SV-1	8.02e+005	6.99e+005
V9HWDB V9HWDB_HUMAN	1	111.41	0.12	1.27		Epididymis secretory sperm binding protein Li 163pA OS-Homo sapiens GN-HEL-5-163pA PE-2 SV-1	4.21e+004	3.32e+004
A0A024R962 A0A024R962_HUMAN	3	110.43	0.30	1.18		HCG40889, isoform CRA_b OS-Homo sapiens GN-hCG_40889 PE-4 SV-1	9.09e+004	7.71e+004
D6RF35 D6RF35_HUMAN	3	109.01	0.21	1.21		Vitamin D-binding protein OS-Homo sapiens GN-GC PE-1 SV-1	3.29e+005	2.72e+005
Q5T9B5 Q5T9B5_HUMAN	2	100.62	0.45	1.19		Inter-alpha-trypsin inhibitor heavy chain H2 OS-Homo sapiens GN-ITH2 PE-1 SV-1	2.10e+004	2.50e+004
P05090 APOD_HUMAN	2	96.45	0.51	1.01		Apolipoprotein D OS-Homo sapiens GN-APOD PE-1 SV-1	7.41e+004	7.49e+004
S6B2B0 S6B2B0_HUMAN	1	83.45	0.99	1.38		IgG L chain OS-Homo sapiens PE-2 SV-1	1.71e+004	2.36e+004
Q9UKS4 Q9UKS4_HUMAN	2	83.39	0.02	5.21	●	Hemoglobin beta subunit variant (Fragment) OS-Homo sapiens GN-HSB PE-2 SV-1	4.02e+004	7707.60
G3V3A0 G3V3A0_HUMAN	2	81.67	0.87	1.22		Alpha-1-antichymotrypsin OS-Homo sapiens GN-5ERPINA3 PE-1 SV-1	7.36e+004	8.96e+004
A0A1U9X7H7 A0A1U9X7H7_HUMAN	2	75.43	0.15	1.70		CFB OS-Homo sapiens PE-3 SV-1	5166.60	3034.26
FWAS2 FWAS2_HUMAN	1	64.95	0.42	1.03		Inter-alpha-trypsin inhibitor heavy chain H1 OS-Homo sapiens GN-ITH1 PE-1 SV-1	1.54e+004	1.49e+004
A0A024R462 A0A024R462_HUMAN	1	57.64	0.09	15.47		Fibronectin 1, isoform CRA_n OS-Homo sapiens GN-FN1 PE-4 SV-1	1655.90	107.06
B4DPPR B4DPPR_HUMAN	1	41.30	0.36	1.39		cDNA FLJ53075, highly similar to Kininogen-1 OS-Homo sapiens PE-2 SV-1	4.60e+004	3.31e+004
KZER19 KZER19_HUMAN	1	40.66	0.23	1.65		Apolipoprotein C-1 (Fragment) OS-Homo sapiens GN-APOC1 PE-1 SV-1	1.75e+004	1.06e+004
D1MGG2 D1MGG2_HUMAN	1	39.68	0.45	20.78		Alpha-2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1	3866.80	186.05
ASPL27 ASPL27_HUMAN	1	34.30	0.19	16.41		CP protein OS-Homo sapiens GN-CP PE-2 SV-1	8846.51	539.05
FRWC76 FRWC76_HUMAN	1	33.96	0.23	1.43		Complement C1s subcomponent OS-Homo sapiens GN-C1S PE-1 SV-1	2433.68	1700.89
R07BE2 R07BE2_HUMAN	1	26.87	0.61	1.34		Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS-Homo sapiens GN-AGT PE-2 SV-1	4424.95	5929.30
P00739 HPTP_HUMAN	1	21.34	0.60	1.51		Haptoglobin-related protein OS-Homo sapiens GN-HPR PE-2 SV-2	5263.13	7936.51
P02787 TRF_HUMAN	1	16.13	0.48	1.15		Serotransferrin OS-Homo sapiens GN-TF PE-1 SV-3	2.09e+004	2.40e+004

Tags	
●	Anova p-value ≤ 0.05
●	Anova p-value ≤ 0.05

Q06AH7|Q06AH7_HUMAN


Transferrin OS-Homo sapiens GN=TF PE=2 SV=1
15 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalized Abundances	
										CTRL_plasma	CI
ADRDQYELLCLDNTR		220	40.40	1	1880.8670	2	●	0	C(+57.02)	yes	5.33e+005
ADRDQYELLCLDNTR		367	22.21	1	1880.8694	3	●	0	C(+57.02)	yes	1.81e+005
AIAANEADAVTL DAGLVYDAYLAPNNLKPVAEFYGSK		197	61.53	2	3953.0110	3		0		yes	1.13e+005
AIAANEADAVTL DAGLVYDAYLAPNNLKPVAEFYGSKEDPQTFY YAVAVVK		152	39.45	1	5563.8107	4		0		yes	7.12e+004
AIAANEADAVTL DAGLVYDAYLAPNNLKPVAEFYGSKEDPQTFY YAVAVVK		1732	36.96	1	5563.8056	5		0		yes	2.86e+004
ASYLDQIR		63	51.40	2	996.4700	2	●	0	[6] C(+57.02)	yes	1.66e+005
CTSSLLLEACTFR		118	40.81	1	1530.6807	2		0	[1] C(+57.02) [10] C(+57.02)	yes	2.89e+005
DGAGDVAFYK		18	66.06	2	977.4818	2		0		yes	1.84e+005

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biomarkers_ccr_plasma_dez2018


Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CI
DSGFQANQLR	86	85.85	2	1194.5454	2		0		yes	2.14e+005	
EDUWELLNQAQEHFGK	2492	87.98	1	2069.0218	2		0		yes	6049.23	
EDUWELLNQAQEHFGK	1739	53.13	3	2069.0228	3		0		yes	4322.84	
IECVSAETTEDCIAK	4	59.29	1	1724.7594	2		0	[3] C(+57.02) [12] C(+57.02)	yes	9.82e+005	
KPVDEYKDCHLAQVPSHTVVAR	202	20.07	1	2548.2855	3		0	[9] C(+57.02)	yes	2.67e+005	
KPVDEYKDCHLAQVPSHTVVAR	104	35.24	1	2548.2857	4		0	[9] C(+57.02)	yes	2.85e+005	
KPVDEYKDCHLAQVPSHTVVAR	6491	59.54	1	2548.2868	2		0	[9] C(+57.02)	yes	4433.65	
KPVDEYKDCHLAQVPSHTVVAR	463	41.78	3	2548.2851	5		0	[9] C(+57.02)	yes	7.03e+004	
LCAGSGLNLCEPNNK	65	60.43	2	1705.7578	2		0	[2] C(+57.02) [10] C(+57.02)	yes	7.20e+005	
LKCEDEWSVNSVGK	328	34.29	2	1520.7293	3		0	[3] C(+57.02)	yes	8.82e+004	
SASDLTWDNLK	28	62.81	6	1248.5989	2		0		yes	1.58e+005	
SETKDLLFRDDTVCLAK	3061	25.62	1	2010.0081	3		0	[14] C(+57.02)	yes	1.11e+004	
SKEFQLFSSPHGK	557	60.89	1	1490.7521	3		0		yes	4.29e+004	
SKEFQLFSSPHGK	1105	54.67	1	1490.7520	2		0		yes	4.32e+004	

Tags
 Anova p-value ≤ 0.08

V9HWA9 | V9HWA9_HUMAN

Epididymis secretory sperm binding protein Li 62p OS=Homo sapiens GN=HEL-5-62p PE=2 SV=1
15 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AAVYHFISDGVR	3045	66.70	1	1470.7387	3		0		yes	2629.50	509.90
AKDQLTQNKFDLK	8383	35.09	1	1579.8020	2		0	[7] C(+57.02)	yes	1075.00	11.78
FISLGEACK	325	30.16	1	1023.5064	2		0	[8] C(+57.02)	yes	2.52e+004	2.14e+004
GQGTLSVVTMYHAK	520	61.35	1	1490.7559	3		0		yes	1.96e+004	2.39e+004
GQGTLSVVTMYHAK	494	47.16	1	1490.7550	2		0		yes	3.85e+004	4.18e+004
GYTQLAFR	544	52.84	1	1082.5505	2		0		yes	4.71e+004	4.36e+004
KVLLDGVQNPFR	500	60.24	1	1237.7142	2		0		yes	1.25e+004	24.54
LDKACPEGVYDYK	717	29.95	1	1655.7867	3		0	[3] K+57.02	yes	1.41e+004	3.31e+004
QLYVVEATSYALLALLQLK	1301	63.09	1	2150.1971	2		0		yes	1.91e+004	1.94e+004
QVREPGQDLVPLSLITTDIIPSPFR	1054	96.69	5	2826.5284	3		0		yes	6698.88	1.79e+004
SEETKENEGFTVTAEGK	640	51.36	1	1854.8478	2		0		yes	1.52e+005	8.02e+004
SEETKENEGFTVTAEGK	387	43.04	2	1854.8486	3		0		yes	1.00e+005	6.56e+004
SGQSEDRQPVPGQQMTLK	254	64.60	1	2000.9581	3		0	[15] M(+15.99)	yes	9.27e+004	1.10e+005
SGQSEDRQPVPGQQMTLK	762	42.76	1	2000.9580	2		0	[15] M(+15.99)	yes	7.04e+004	6.79e+004
TGLQEVEVK	1161	48.74	1	1001.5396	2		0		yes	5158.26	588.66
VLLDGVQNPFR	169	54.04	1	1109.6193	2		0		yes	3.48e+004	3.93e+004
VQLSNDFDEYMAIEQTIK	302	106.32	4	2256.0985	2		0		yes	3.73e+004	3.44e+004
VVLVAVDK	277	38.59	3	841.5267	2		0		yes	5.70e+004	3.66e+004

Tags
 Anova p-value ≤ 0.08


P02671 | FIBA_HUMAN

Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2
15 peptides

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biomarkers_ccr_plasma_dez2018


Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Ave Abi
ADSGEGDFLAEGGGVR	120	33.13	1	1535.6848	2		0		yes	
ALTDMPQAR	3299	26.87	1	1043.4904	2		0	[4] D(-18.01)	yes	
ALTDMPQAR	3299	29.03	2	1043.4904	2		0	[4] D(-18.01)	yes	
ALTDMPQAR	934	47.19	2	1077.4945	2		0	[5] M(+15.99)	yes	
ESSSHHPGIAEFPSPR	575	43.55	1	1636.7580	2		0		yes	
ESSSHHPGIAEFPSPR	146	52.18	2	1636.7595	3		0		yes	
EVDLKDYEDQK	106	60.17	1	1508.6987	2		0		yes	
EVDLKDYEDQK	472	18.14	1	1508.6998	3		0		yes	
GGSTSYGTGSETESPR	38	37.70	1	1571.6698	2		0		yes	
GSESGIFTNTK	327	56.30	1	1139.5461	2		0		yes	
GSESGIFTNTK	1277	68.78	1	1139.5463	2		0		yes	
HRHPDEAAFFDTASTGK	183	82.71	4	1885.8716	3		0		yes	
HRHPDEAAFFDTASTGK	1034	71.34	1	1885.8698	2		0		yes	
AELEKRPGGNEITR	59	35.18	1	1500.7350	2		0		yes	
AELEKRPGGNEITR	519	25.70	1	1500.7357	3		0		yes	
AELEKRPGGNEITR	671	33.72	1	1516.7300	3		0	[1] M(+15.99)	yes	
NPGSSGTGGTATWKPQSGSGSTGSWNSGSSGTGSTGNQNPQSPRPGSTGTWNPQSSER	590	17.38	1	5533.4451	4		0		yes	
NPSAGSWSNSGSSGPGSTGNR	1060	82.13	1	1962.8417	2		0		yes	
QLEQVIK	209	29.74	1	927.5389	2		0		yes	
TFPGFFSPMLGEFVSETESR	1627	84.71	1	2264.0474	3		0		yes	
TFPGFFSPMLGEFVSETESR	153	100.32	6	2264.0446	2		0		yes	
VQHIQLLQKNVR	6233	25.37	1	1517.8792	3		0	[9] K+43.01	yes	

Tags
 Anova p-value ≤ 0.08

Q8NCL6 | Q8NCL6_HUMAN

cDNA FLJ90170 fis, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS=Homo sapiens PE=2 SV=1
11 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AEDTAVYYCAR	2622	77.83	1	1317.5669	2		0	[9] C(+57.02)	yes	3916.13	614.02
AEDTAVYYCAR	789	68.71	1	1317.5667	2		0	[9] C(+57.02)	yes	3.24e+004	2.85e+004
DASGVYFTWTPSSGK	33	58.60	2	1539.7202	2		0		yes	6.45e+005	4.46e+005
SGNTFRPEVHLLPPPSEELALNELVTLTLCLAR	19	77.50	8	3572.8679	4		0	[29] C(+57.02)	yes	4.54e+005	1.99e+005
SGNTFRPEVHLLPPPSEELALNELVTLTLCLAR	3	109.93	5	3572.8653	3		0	[29] C(+57.02)	yes	8.63e+005	3.79e+005
TFTCTAAYPEK	10	47.18	4	1374.6122	2		0	[4] C(+57.02)	yes	4.96e+005	5.49e+005
TFTCTAAYPEK	9085	51.96	1	1356.6034	2		0	[3] T(-18.01) [4] C(+57.02)	yes	2364.61	2949.40
TPLTATLSK	31	71.02	2	930.5384	2		0		yes	1.36e+005	1.58e+005
VAAEDWKK	6355	25.87	1	988.4980	2		0	[7] K+43.01	yes	869.93	327.85
WLQGSQELPR	886	18.23	1	1212.6589	2		0		yes	2.96e+004	2.99e+004
WLQGSQELPR	21	52.90	4	1212.6255	2		0		yes	6.05e+005	4.14e+005
WLQGSQELPREK	1193	30.62	1	1450.7198	2		0		yes	8059.27	1373.73
YLTWASR	102	47.60	3	895.4548	2		0		yes	7.92e+004	8.22e+004

Tags
 Anova p-value ≤ 0.08

AOA140VJJ6 | AOA140VJJ6_HUMAN

Testicular tissue protein Li 70 OS=Homo sapiens PE=2 SV=1
9 peptides

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biomarkers_ccr_plasma_dez2018

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
C H AGHL N GVYYQGGTYSK	232	50.61	1	1993.8730	3		0	[1] C(+57.02)[7] N-17.03	yes	5.28e+004	7.66e+004
DN C ILDER	24	57.00	1	1193.4807	2		0	[3] C(+57.02)[4] C(+57.02)	yes	1.54e+005	1.47e+005
D N CCILDER	3507	20.43	2	1209.4757	2		0	[1] D+15.99[3] C(+57.02)[4] C(+57.02)	yes	3121.81	3014.27
Q SGLYFIKPLK	8014	32.18	1	1275.7225	2		0	[1] Q-17.03	yes	1949.81	1690.17
RLDGSVDFK	298	20.17	1	1035.5304	2		0		yes	1.89e+004	6427.20
TSTADYAMFK	111	57.99	1	1133.5063	2		0		yes	1.10e+005	1.08e+005
TSTADY A MFK	836	29.35	1	1149.5009	2		0	[8] M(+15.99)	yes	3.29e+004	1.76e+004
YEASILTDSSIR	218	64.22	4	1490.7360	2		0		yes	2.49e+005	1.53e+005
YEASILTDSSIR	522	50.60	1	1490.7373	3		0		yes	6.75e+004	4.94e+004
YLQEIYNSNNQK	23	78.97	10	1512.7201	2		0		yes	3.97e+005	3.54e+005

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

P01023 | A2MG_HUMAN

Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3
8 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AFQPPFVELTAPYSVIR	815	111.53	7	2044.0484	2		0		yes	2.12e+004	1.66e+004
AIGYLN T GYQR	110	39.46	1	1254.6358	2		0		yes	8.77e+004	6.81e+004
IAQWQSFQLEGG L K	150	38.52	1	1603.8358	2		0		yes	2.16e+005	1.75e+005
LPPN V VEESAR	230	54.98	1	1209.6355	2		0		yes	1.30e+005	8.35e+004
LPPN V VEESAR	276	57.79	1	1209.6355	2		0		yes	6.91e+004	3.49e+004
Q T VS W AVTPK	501	36.57	1	1115.5975	2		0		yes	3.61e+004	2.74e+004
SGSLL N NAIK	293	35.60	1	1102.5981	2		0		yes	2.98e+004	2.58e+004
VSNQ T LSLFF T VLQ D VPV R	3654	45.69	1	2162.1723	2		0		yes	4681.91	4329.55
V T AA P Q S V C ALR	46	33.06	1	1271.6658	2		0	[9] C(+57.02)	yes	2.76e+005	1.46e+005

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

D3DP13 | D3DP13_HUMAN

Fibrinogen beta chain, isoform CRA_e OS=Homo sapiens GN=FGB PE=4 SV=1
8 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AH Y GGFTVQNEANK	15469	45.90	1	1516.7070	3		0	[3] Y-18.01	yes	574.32	64.05
AH Y GG F T V QNEANK	21292	33.49	1	1517.6924	3		0	[7] T-18.01 [9] Q+0.98	yes	630.87	37.69
EDGGG W WY N R	324	43.87	1	1238.5098	2		0		yes	6.80e+004	5.84e+004
GS W YS M R	447	46.09	1	885.3806	2		0		yes	1.41e+004	1.56e+004
K W DPYK Q SFG N W A T N T D G K	899	29.65	1	2125.0247	3		0		yes	2.13e+004	3.92e+004
Q G F G N V A T N T D G K	69	53.67	1	1307.6093	2		0		yes	1.21e+005	1.07e+005
Q G F G N W A T N T D G K	1537	72.05	2	1290.5838	2		0	[1] Q-17.03	yes	1.95e+004	2.26e+004
V Y C D A N T E N G W T V I Q N R	268	54.15	1	2155.9402	2		0	[3] C(+57.02)	yes	5.20e+005	4.39e+005

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

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biomarkers_ccr_plasma_dez2018

AOA0C4DGL8 | AOA0C4DGL8_HUMAN

Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1
7 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AVGDKLPECEAVCGKPK	237	48.75	1	1856.9110	2			[9] C(+57.02) [13] C(+57.02)	yes	2.59e+005	2.62e+005
TEGDGYTLNDK	92	59.03	1	1310.5982	2				yes	1.26e+005	1.15e+005
VDSGNDVTDIADDGCKPKPEIAHGYVEHSVR	128	32.35	1	3348.5310	3			[15] C(+57.02)	yes	5.87e+005	7.34e+005
VGYSVWGR	11	61.44	3	979.4876	2				yes	1.42e+005	1.93e+005
VGYSVWGR	1935	22.42	2	1011.4756	2			[7] W+31.99	yes	1.05e+004	7655.70
YVWLPVADQDCIR	12	59.84	2	1706.8117	2			[12] C(+57.02)	yes	1.19e+006	1.42e+006
YVWLPVADQDCIR	724	59.60	1	1722.8040	2			[3] M(+15.99) [12] C(+57.02)	yes	1.21e+005	1.79e+005

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

P02647 | APOA1_HUMAN

Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1
7 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
ATEHLSTLSEK	359	37.51	2	1257.6192	2			[1] A+43.01	yes	3.21e+004	3.82e+004
DEPPQSPWDR	29	52.22	2	1225.5365	2				yes	5.64e+005	4.67e+005
LEALKENGGAR	1742	34.20	1	1200.6097	2			[1] L+43.01 [7] N+0.98	yes	2.32e+004	1.76e+004
LSPLGEEMR	215	53.42	2	1046.5059	2			[8] M(+15.99)	yes	7.41e+004	4.68e+004
QEASKDLEEVK	2811	23.48	1	1334.6388	3	<input checked="" type="checkbox"/>			yes	2588.21	1259.58
THLAPYSDELK	139	56.61	5	1300.6410	3				yes	1.51e+005	1.01e+005
THLAPYSDELK	1456	45.84	1	1282.6308	3			[7] S-18.01	yes	2.44e+004	1.67e+004
THLAPYSDELK	1456	16.90	1	1282.6308	3			[8] D-18.01	yes	2.44e+004	1.67e+004

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

AOA140TA32 | AOA140TA32_HUMAN

Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1
6 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
EMSGSPASGIPVK	355	52.47	1	1258.6226	2				yes	2.40e+004	2.34e+004
EMSGSPASGIPVK	987	35.99	1	1274.6183	2			[2] M(+15.99)	yes	1.15e+004	2.52e+004
RAICYPR	593	51.95	1	975.4278	2			[3] C(+57.02)	yes	1.00e+004	1.46e+004
LHLETDSLALVALGALDTALYAAGSK	964	53.90	2	2612.4058	3				yes	1.28e+004	1.53e+004
VGDTLNLNLR	984	27.52	1	1113.6129	2				yes	2.07e+004	2.31e+004
VLSLAQEQVGGSEPK	244	65.14	1	1540.8093	2				yes	4.53e+004	5.13e+004

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

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biomarkers_ccr_plasma_dez2018

AOA0G2JRN3 | AOA0G2JRN3_HUMAN

Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1
6 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
ELDRDVTVALVNYIFFK	968	46.58	3	2089.0877	2		0		yes	1.99e+004	2.81e+004
LGAFNIQHCK	103	42.18	5	1246.5952	2		0	[9] C(+57.02)	yes	9.25e+004	1.17e+005
LGAFNIQHCK	1344	37.73	3	1262.5896	2		0	[3] M(+15.99) [9] C(+57.02)	yes	1.72e+004	1.67e+004
LGAFNIQHCKK	6155	21.79	1	1374.6891	2		0	[9] C(+57.02)	yes	650.25	193.89
RLGAFNIQHCK	701	41.48	1	1402.6965	3		0	[10] C(+57.02)	yes	1.58e+004	3.76e+004
VFSNGADLSGVTEEAPLK	17	49.69	2	1832.9148	2		0		yes	1.01e+006	1.08e+006

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

E1A689 | E1A689_HUMAN

Mutant Apo B 100 OS=Homo sapiens PE=2 SV=1
4 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
IGQDGISSATTNLK	997	68.54	3	1504.7733	2		0		yes	1.30e+004	2.16e+004
KLTISEQNIQR	3588	19.91	1	1328.7413	2		0		yes	1382.17	0.10
KLTISEQNIQR	7396	41.79	1	1328.7420	3		0		yes	368.21	0.68
QIDIDIVR	2858	39.05	1	972.4871	2		0		yes	3437.92	3499.39
VSALLTPAEQTGTWK	2035	18.94	1	1600.8438	2		0		yes	8275.93	7863.57

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

P02790 | HEMO_HUMAN

Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
EVGTPHGIILDSVDAAFICPGSSR	41	24.06	1	2497.2281	3		0	[19] C(+57.02)	yes	1.03e+006	8.90e+005
GGYTLVSGYPK	339	67.70	1	1140.5816	2		0		yes	1.08e+005	8.81e+004
VDGALDAEK	1016	66.91	1	1021.4570	2	<input checked="" type="checkbox"/>	0	[6] C(+57.02)	yes	7107.73	522.55

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

Q68DH2 | Q68DH2_HUMAN

Uncharacterized protein DKFZp686G21125 (Fragment) OS=Homo sapiens GN=DKFZp686G21125 PE=2 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
GPOVLTATVSGK	869	73.95	3	1143.6135	2		0		yes	1.97e+004	1.89e+0
RIHEDSDSALQLQDFYQEVANPLLTAVTFEYPSNAVEEVTQNNFR	1730	67.52	2	5197.4930	4		0		yes	1.85e+004	1.81e+0

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

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PODOX6 | IGM_HUMAN

Immunoglobulin mu heavy chain OS=Homo sapiens PE=1 SV=1
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
FTCTVYHTDLP5PLK	322	33.59	1	1715.8551	3		0	[3] C(+57.02)	yes	5.70e+004	3.23e+004
QVGSQVTTDQVQAEAK	133	20.60	1	1616.8000	2		0		yes	2.26e+005	1.32e+005
YVTSAPMPEPQAPGR	137	70.74	2	1599.7717	2		0		yes	2.49e+005	1.98e+005

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

AOA096LPE2 | AOA096LPE2_HUMAN

SAA2-SAA4 readthrough OS=Homo sapiens GN=SAA2-SAA4 PE=4 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
EALQGVGDAMGR	1090	56.05	1	1131.5343	2		0		yes	1.86e+004	1.75e+004
SFFSFLGEAFDGR	1284	67.25	1	1549.7206	2		0		yes	3272.02	6590.92

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

Q7Z3Y4 | Q7Z3Y4_HUMAN

Uncharacterized protein OS=Homo sapiens PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
VDNALQSGNSQESVTEQDSK	485	16.67	1	2134.9616	3		0		yes	6.16e+004	4.86e+004
VDNALQSGNSQESVTEQDSK	44	65.06	1	2134.9603	2		0		yes	5.43e+005	4.05e+005
VYAEVTHQGLSSPYTK	62	34.66	1	1874.9197	3		0	[4] C(+57.02)	yes	1.98e+005	2.45e+005

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

V9HWD8 | V9HWD8_HUMAN

Epididymis secretory sperm binding protein Li 163pA OS=Homo sapiens GN=HEL-5-163pA PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
SLPAPWLSMAPVSWITPGLK	540	111.41	6	2150.1594	2		0		yes	4.21e+004	3.32e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

AOA024R962 | AOA024R962_HUMAN

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HCG40889, isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE=4 SV=1
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
SPDVINGSPISQK	314	54.58	2	1340.6930	2		0		yes	2.98e+004	2.92e+004
TGESVEFVCK	962	38.97	2	1154.5281	2		0	[9] C(+57.02)	yes	3.88e+004	2.15e+004
TKEEYGHSEVVEYYCNPR	1289	16.88	1	2258.9904	3		0	[15] C(+57.02)	yes	2.22e+004	2.64e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

D6RF35 | D6RF35_HUMAN

Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
SCESNSPPFVHPGTAECCTK	258	24.16	1	2263.9295	3		0	[2] C(+57.02) [17] C(+57.02) [18] C(+57.02)	yes	2.55e+004	1.12e+004
SLGECEDVEDSTTCFNAK	161	56.66	1	2091.8173	2		0	[5] C(+57.02) [6] C(+57.02) [14] C(+57.02)	yes	2.75e+005	2.34e+005
THLPEVFLSK	1205	28.19	2	1169.6442	2		0		yes	2.78e+004	2.70e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

Q5T985 | Q5T985_HUMAN

Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AGELEVFNGYFVHFFAPDNLPIPK	2143	47.02	2	2835.3901	3		0		yes	6755.79	1.36e+004
TEVNVLPGAK	848	53.60	1	1026.5710	2		0		yes	1.43e+004	1.14e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

P05090 | APOD_HUMAN

Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
CPNPPVQENFDVINK	757	27.61	1	1656.7568	2		0	[1] C(+57.02)	yes	6.55e+004	6.55e+004
MTYTDQVNEPK	1998	68.84	2	1291.5913	2		0	[9] C(+57.02)	yes	8586.64	9435.06

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

S6B2B0 | S6B2B0_HUMAN

IgG L chain OS=Homo sapiens PE=2 SV=1
1 peptide

file:///C:/Users/bruno/Documents/Bruno/Mestrado/Colorectal proteomic/Tese/Estatistica/CTRLxCRC_plasma.htm

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Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
ATLVCLISDFYPGAVTVAWK	1025	83.45	1	2210.1431	2		0	[5] C(+57.02)	yes	1.71e+004	2.36e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

Q9UK54 | Q9UK54_HUMAN

Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
LHVDPENFR	1055	24.27	1	1125.5563	2		0		yes	9892.70	2037.36
VVAGVANALAHK	630	59.12	1	1148.6662	2		0		yes	2.72e+004	5666.08
VVAGVANALAHK	2720	39.42	1	1148.6664	2		0		yes	3034.09	4.16

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

G3V3A0 | G3V3A0_HUMAN

Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
FNRPFLMIIVPTDTQNIFFASK	1775	21.04	1	2658.3686	2		0		yes	2.47e+004	3.03e+004
NLAVSQVYHK	171	60.63	5	1093.6240	2		0		yes	4.90e+004	5.93e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

AOA1U9X7H7 | AOA1U9X7H7_HUMAN

CFB OS=Homo sapiens PE=3 SV=1
2 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
DFHINLFQVLPWLK	4746	48.88	1	1768.9661	2		0		yes	3132.87	2715.73
QLNEINYEDHK	6076	26.55	1	1401.6523	2	<input checked="" type="checkbox"/>	0		yes	2033.73	318.53

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

F8WAS2 | F8WAS2_HUMAN

Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITI1 PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
AAISGENAGLVR	850	64.95	3	1156.6194	2		0		yes	1.54e+004	1.49e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

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A0A024R462 | A0A024R462_HUMAN

Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
TYHVGEQWQK	2604	57.64	1	1274.6041	2		0		yes	1655.90	107.06

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

B4DPP8 | B4DPP8_HUMAN

cDNA FLJ53075, highly similar to Kininogen-1 OS=Homo sapiens PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
TVGSDTFYSFK	611	41.30	5	1250.5842	2		0		yes	4.60e+004	3.31e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

K7ER19 | K7ER19_HUMAN

Apolipoprotein C-I (Fragment) OS=Homo sapiens GN=APOC1 PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
TPDVSSALDK	604	40.66	2	1031.5136	2		0		yes	1.75e+004	1.06e+004

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

D1MGQ2 | D1MGQ2_HUMAN

Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
VGAHAGEYGAEALER	2515	39.68	1	1528.7271	3		0		yes	3866.80	186.05

Tags
<input checked="" type="checkbox"/> Anova p-value \leq 0.08

A5PL27 | A5PL27_HUMAN

CP protein OS=Homo sapiens GN=CP PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_plasma	CRC_plasma
TYSDHPEKVNKDEEFIESNK	2386	34.30	1	2523.1401	3		0		yes	8846.51	539.05

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Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

F8WCZ6 | F8WCZ6_HUMAN

Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CTRL_plasma	CRC_plasma	
CYPVCGVPR		56.41	33.96	1	1042.5050	2		0	[1] C(+57.02) [5] C(+57.02)	yes	2433.68	1700.89

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

BOZBE2 | BOZBE2_HUMAN

Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS=Homo sapiens GN=AGT PE=2 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CTRL_plasma	CRC_plasma	
ADSQAQLLLSTVVGFTAPGLHLK		2026	26.87	1	2464.3693	3		0		yes	4424.95	5929.30

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

P00739 | HPTTR_HUMAN

Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CTRL_plasma	CRC_plasma	
YQEDTCTGDAGSAFAVHOLEEDTWYAAGILSFDK		3673	21.34	1	3843.6518	3		0	[6] C(+57.02)	yes	5263.13	7936.51

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

P02787 | TRFE_HUMAN

Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										CTRL_plasma	CRC_plasma	
SMGGKEDLIWELLNQAQEHFGKDK		3219	16.13	1	2788.3471	4		0	[2] M(+15.99)	yes	2.09e+004	2.40e+004

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

Accession Q9UK54 | Q9UK54_HUMAN (+1)

Description Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1

Peptides 2

Score 83.39

Anova 0.02

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Accession Q06AH7|Q06AH7_HUMAN (+1)

Description Transferrin OS=Homo sapiens GN=TF PE=2 SV=1

Peptides 15

Score 1100.41

Anova 0.08

Fold 1.35

● Anova p-value ≤ 0.08



Accession P01023|A2MG_HUMAN

Description Alpha-2-macroglobulin OS=Homo sapiens GN=AZM PE=1 SV=3

Peptides 8

Score 398.22

Anova 0.09

Fold 1.50



Accession A0A024R462|A0A024R462_HUMAN (+1)

Description Fibronectin 1, isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1

Peptides 1

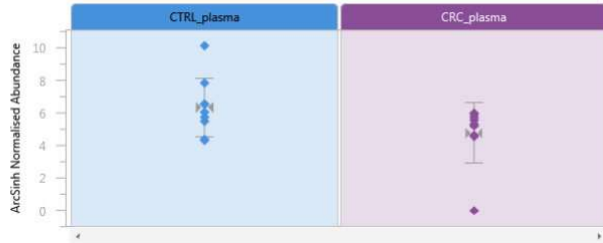
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Anova 0.09

Fold 15.47

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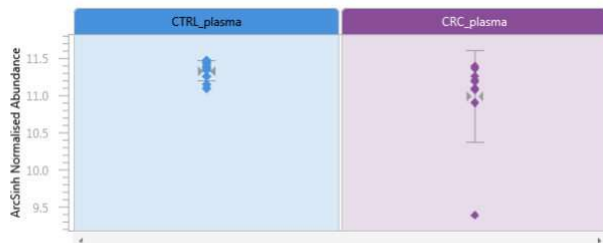
biomarkers_ccr_plasma_dez2018



Accession V9HWD8 | V9HWD8_HUMAN

Description Epididymis secretory sperm binding protein L1 163pA O5=Homo sapiens GN=HEL-5-163pA PE=2 SV=1

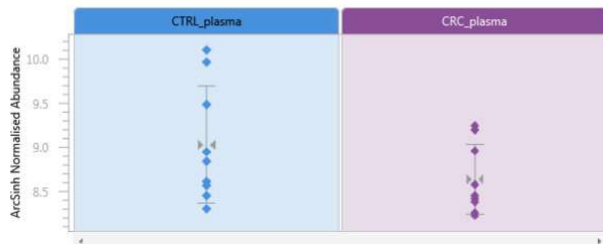
Peptides 1
Score 111.41
Anova 0.12
Fold 1.27



Accession A0A1U9X7H7 | A0A1U9X7H7_HUMAN (+1)

Description CFB O5=Homo sapiens PE=3 SV=1

Peptides 2
Score 75.43
Anova 0.15
Fold 1.70



Accession P0DOX6 | IGM_HUMAN

Description Immunoglobulin mu heavy chain O5=Homo sapiens PE=1 SV=1

Peptides 3
Score 124.93
Anova 0.15
Fold 1.47



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Accession P0279D|HEMO_HUMAN

Description Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

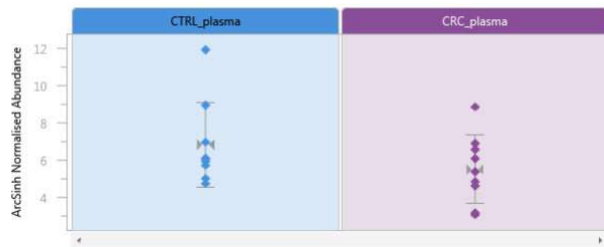
Peptides 3
 Score 158.67
 Anova 0.18
 Fold 1.17



Accession A5PL27|A5PL27_HUMAN

Description CP protein OS=Homo sapiens GN=CP PE=2 SV=1

Peptides 1
 Score 34.30
 Anova 0.19
 Fold 16.41



Accession D6RF35|D6RF35_HUMAN

Description Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1

Peptides 3
 Score 109.01
 Anova 0.21
 Fold 1.21



Accession K7ER19|K7ER19_HUMAN

Description Apolipoprotein C-I (Fragment) OS=Homo sapiens GN=APOC1 PE=1 SV=1

Peptides 1
 Score 40.66
 Anova 0.23
 Fold 1.65

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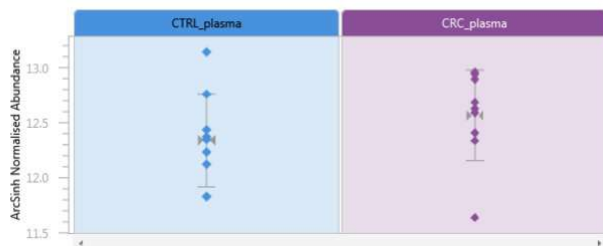
Accession F8WCZ6 | F8WCZ6_HUMAN

Description Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1
Peptides 1
Score 33.96
Anova 0.23
Fold 1.43



Accession ADA140TA32 | ADA140TA32_HUMAN (+1)

Description Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1
Peptides 6
Score 286.97
Anova 0.27
Fold 1.23



Accession D3DP13 | D3DP13_HUMAN

Description Fibrinogen beta chain, isoform CRA_e OS=Homo sapiens GN=FGB PE=4 SV=1
Peptides 8
Score 378.87
Anova 0.27
Fold 1.12



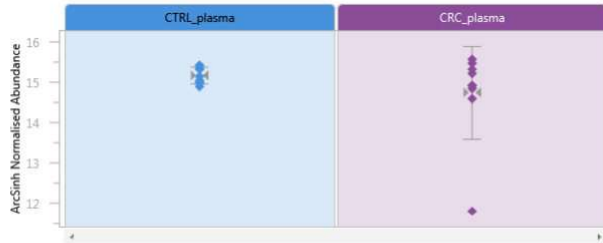
23/06/2019

biomarkers_ccr_plasma_dez2018

Accession P02671 | FIBA_HUMAN (+1)

Description Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

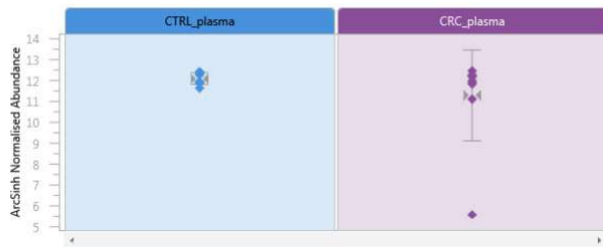
Peptides 15
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 Anova 0.28
 Fold 1.16



Accession A0A024R962 | A0A024R962_HUMAN (+1)

Description HCG40889, isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE=4 SV=1

Peptides 3
 Score 110.43
 Anova 0.30
 Fold 1.18



Accession ADA140VJJ6 | ADA140VJJ6_HUMAN

Description Testicular tissue protein LI 70 OS=Homo sapiens PE=2 SV=1

Peptides 9
 Score 461.52
 Anova 0.30
 Fold 1.19



Accession V9HWA9 | V9HWA9_HUMAN

Description Epididymis secretory sperm binding protein LI 62p OS=Homo sapiens GN=HEL-5-62p PE=2 SV=1

Peptides 15
 Score 992.72
 Anova 0.32
 Fold 1.16

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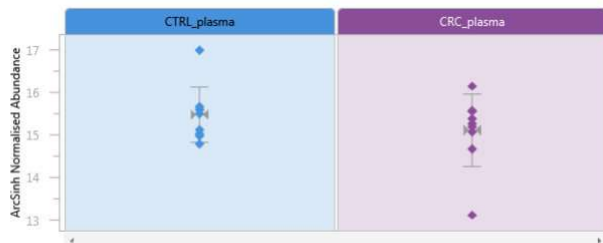
biomarkers_ccr_plasma_dez2018



Accession Q8NCL6 | Q8NCL6_HUMAN (+1)

Description cDNA FLJ90170 fis, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region O5=Homo sapiens PE=2 SV=1

Peptides 11
 Score 669.24
 Anova 0.32
 Fold 1.46



Accession Q7Z3Y4 | Q7Z3Y4_HUMAN

Description Uncharacterized protein O5=Homo sapiens PE=1 SV=1

Peptides 2
 Score 116.39
 Anova 0.32
 Fold 1.15



Accession P02647 | APOA1_HUMAN

Description Apolipoprotein A-I O5=Homo sapiens GN=APOA1 PE=1 SV=1

Peptides 7
 Score 303.28
 Anova 0.33
 Fold 1.27



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Accession B4DPP8 | B4DPP8_HUMAN

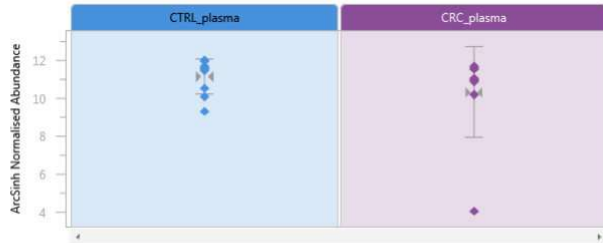
Description cDNA FLJ53075, highly similar to Kininogen-1 OS=Homo sapiens PE=2 SV=1

Peptides 1

Score 41.30

Anova 0.36

Fold 1.39



Accession F8WAS2 | F8WAS2_HUMAN

Description Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=1

Peptides 1

Score 64.95

Anova 0.42

Fold 1.03



Accession Q5T985 | Q5T985_HUMAN

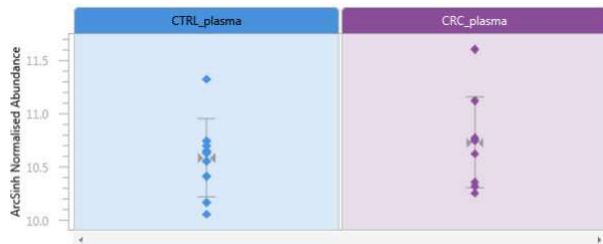
Description Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=1

Peptides 2

Score 100.62

Anova 0.45

Fold 1.19



Accession D1MGQ2 | D1MGQ2_HUMAN

Description Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1

Peptides 1

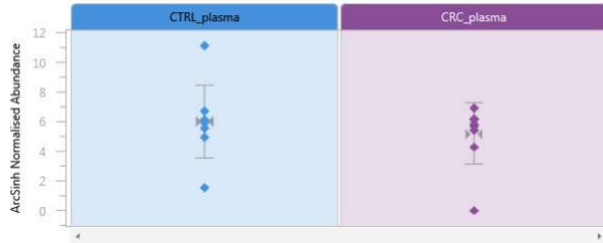
Score 39.68

Anova 0.45

Fold 20.78

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Accession P02787 | TRFE_HUMAN

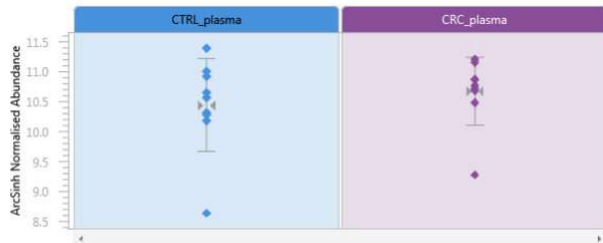
Description Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

Peptides 1

Score 16.13

Anova 0.48

Fold 1.15



Accession Q68DH2 | Q68DH2_HUMAN (+1)

Description Uncharacterized protein DKFZp686G21125 (Fragment) OS=Homo sapiens GN=DKFZp686G21125 PE=2 SV=1

Peptides 2

Score 141.47

Anova 0.50

Fold 1.04



Accession P05090 | APOD_HUMAN

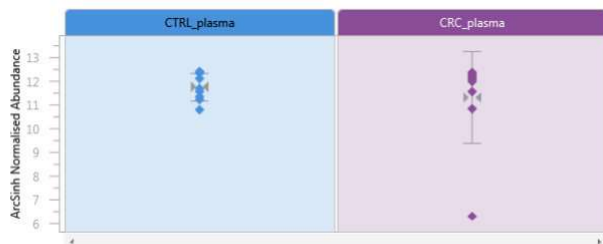
Description Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1

Peptides 2

Score 96.45

Anova 0.51

Fold 1.01



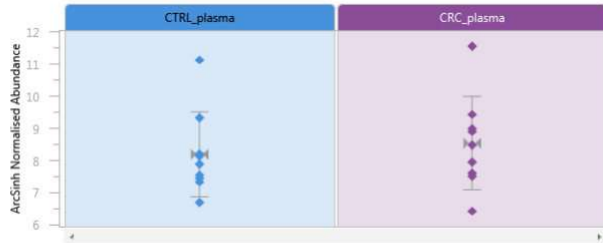
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Accession P00739|HPTR_HUMAN

Description Haptoglobin-related protein O5=Homo sapiens GN=HPR PE=2 SV=2

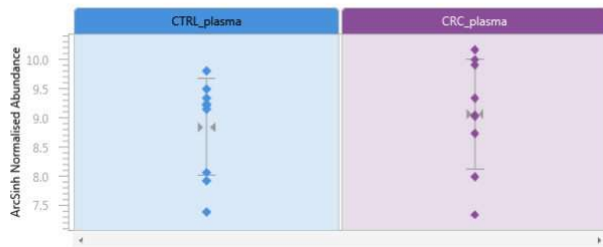
Peptides 1
 Score 21.34
 Anova 0.60
 Fold 1.51



Accession B0ZBE2|B0ZBE2_HUMAN

Description Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) O5=Homo sapiens GN=AGT PE=2 SV=1

Peptides 1
 Score 26.87
 Anova 0.61
 Fold 1.34



Accession A0ADC4DGL8|A0ADC4DGL8_HUMAN (+1)

Description Haptoglobin O5=Homo sapiens GN=HP PE=1 SV=1

Peptides 7
 Score 343.43
 Anova 0.63
 Fold 1.20



Accession A0A096LPE2|A0A096LPE2_HUMAN

Description SAA2-SAA4 readthrough O5=Homo sapiens GN=SAA2-SAA4 PE=4 SV=1

Peptides 2
 Score 123.30
 Anova 0.64
 Fold 1.10

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Accession E1A689 | E1A689_HUMAN (+1)

Description Mutant Apo B 100 O5=Homo sapiens PE=2 SV=1
Peptides 4
Score 188.23
Anova 0.67
Fold 1.24



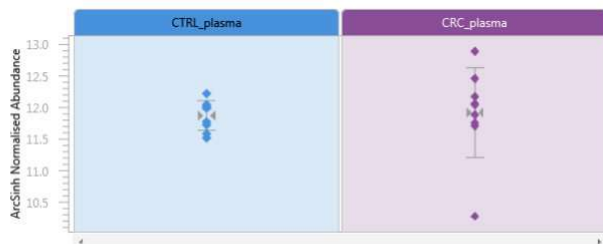
Accession A0A0G2JRN3 | A0A0G2JRN3_HUMAN (+1)

Description Alpha-1-antitrypsin O5=Homo sapiens GN=SERPINA1 PE=1 SV=1
Peptides 6
Score 239.45
Anova 0.83
Fold 1.11



Accession G3V3A0 | G3V3A0_HUMAN

Description Alpha-1-antichymotrypsin O5=Homo sapiens GN=SERPINA3 PE=1 SV=1
Peptides 2
Score 81.67
Anova 0.87
Fold 1.22



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Accession S6B2BD|S6B2BD_HUMAN

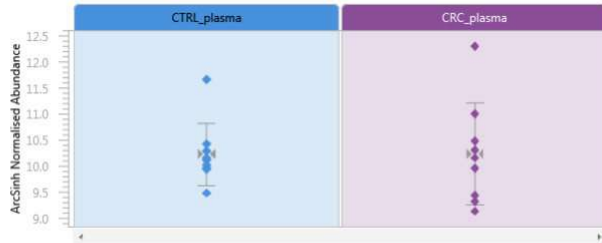
Description Ig L chain O5=Homo sapiens PE=2 SV=1

Peptides 1

Score 83.45

Anova 0.99

Fold 1.38



Features

#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_plasma	CRC_plasma
630	0.106	4.8	2	575.3404	49.8			2.724e+004	5666.082
2720	0.264	729.7	2	575.3405	47.7			3034.092	4.158
1055	0.147	4.9	2	563.7854	59.6			9892.697	2037.358
4	0.188	1.4	2	863.3870	59.9			9.820e+005	7.192e+005
18	0.104	1.7	2	489.7482	58.1			1.845e+005	1.075e+005
28	0.267	1.3	2	625.3067	88.8			1.579e+005	1.246e+005
63	0.066	1.7	2	499.2423	72.2	■		1.662e+005	9.519e+004
65	0.110	1.5	2	853.8862	84.4			7.198e+005	4.802e+005
86	0.966	1.0	2	598.2800	73.9			2.140e+005	2.085e+005
104	0.235	1.4	4	638.0787	51.5			2.848e+005	2.023e+005
202	0.130	1.7	3	850.4358	51.5			2.667e+005	1.557e+005
463	0.229	1.3	5	510.6643	51.5			7.033e+004	5.262e+004
6491	0.163	29.3	2	1275.1507	50.3			4433.648	151.223
118	0.218	1.3	2	766.3477	91.6			2.893e+005	2.211e+005
152	0.517	3.2	4	1391.9600	170.5			7.122e+004	2.247e+005
1732	0.294	4.3	5	1113.7684	170.5			2.859e+004	1.229e+005
197	0.987	1.5	3	1318.6776	170.5			1.132e+005	1.648e+005
220	0.045	2.3	2	941.4408	89.6	■		5.326e+005	2.355e+005
367	0.069	1.8	3	627.9638	89.6	■		1.815e+005	1.033e+005
328	0.311	1.3	3	507.9170	59.9			8.816e+004	6.831e+004
557	0.137	263.8	3	497.9246	59.7			4.290e+004	162.605
1105	0.164	105.1	2	746.3833	59.7			4.321e+004	411.164
1739	0.250	1.7	3	690.6815	171.2			4322.841	2523.991
2492	0.129	2.1	2	1035.5182	171.2			6049.232	2917.676
3061	0.844	1.7	3	671.0100	85.4			1.107e+004	1.891e+004
46	0.102	1.9	2	636.8402	54.0			2.758e+005	1.456e+005
110	0.336	1.3	2	628.3252	68.8			8.774e+004	6.811e+004
150	0.278	1.2	2	802.9252	115.8			2.158e+005	1.753e+005
230	0.167	1.6	2	605.8250	55.4			1.304e+005	8.350e+004
276	0.157	2.0	2	605.8250	54.0			6.910e+004	3.489e+004
293	0.376	1.2	2	552.3063	64.9			2.979e+004	2.577e+004
501	0.353	1.3	2	558.8060	67.6			3.613e+004	2.736e+004
815	0.365	1.3	2	1023.0315	171.5			2.119e+004	1.660e+004
3654	0.755	1.1	2	1082.0934	171.8			4681.905	4329.554
2604	0.088	15.5	2	638.3093	45.0			1655.896	107.062
540	0.125	1.3	2	1076.0870	171.4			4.208e+004	3.322e+004
4746	0.489	1.2	2	885.4903	171.9			3132.873	2715.730
6076	0.044	6.4	2	701.8334	41.0	■		2033.730	318.533
133	0.082	1.7	2	809.4073	41.5			2.256e+005	1.323e+005
137	0.269	1.3	2	800.8931	62.1			2.489e+005	1.977e+005
322	0.104	1.8	3	572.9590	78.1			5.702e+004	3.234e+004

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#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_plasma	CRC_plasma
41	0.216	1.2	3	833.4166	129.2			1.028e+006	8.897e+005
339	0.268	1.2	2	571.2981	73.2			1.077e+005	8.808e+004
1016	0.028	13.6	2	511.7358	44.8			7107.731	522.551
2386	0.193	16.4	3	842.0540	45.6			8846.510	539.055
161	0.212	1.2	2	1046.9159	70.0			2.754e+005	2.342e+005
258	0.987	2.3	3	755.6504	56.7			2.547e+004	1.123e+004
1205	0.392	1.0	2	585.8294	80.7			2.783e+004	2.699e+004
604	0.230	1.7	2	516.7641	47.5			1.752e+004	1.060e+004
5641	0.233	1.4	2	522.2598	45.3			2433.680	1700.889
244	0.509	1.1	2	771.4119	64.4			4.528e+004	5.126e+004
355	0.667	1.0	2	630.3186	53.2			2.398e+004	2.338e+004
593	0.729	1.5	2	488.7212	59.6			1.002e+004	1.464e+004
964	0.887	1.2	3	871.8092	172.6			1.279e+004	1.526e+004
984	0.538	1.1	2	557.8137	83.5			2.071e+004	2.310e+004
987	0.758	2.2	2	638.3164	53.2			1.151e+004	2.520e+004
69	0.284	1.1	2	654.8119	41.4			1.215e+005	1.069e+005
268	0.187	1.2	2	1078.9774	94.6			5.199e+005	4.393e+005
324	0.239	1.2	2	620.2622	91.5			6.803e+004	5.840e+004
447	0.376	1.1	2	443.6976	71.6			1.411e+004	1.563e+004
899	0.959	1.8	3	709.3488	69.1			2.127e+004	3.917e+004
1537	0.498	1.2	2	646.2992	62.1			1.948e+004	2.263e+004
15469	0.183	9.0	3	506.5763	45.5			574.315	64.052
21292	0.185	16.7	3	506.9047	45.5			630.872	37.688
38	0.594	1.1	2	786.8422	26.0			3.198e+005	3.550e+005
59	0.305	1.2	2	751.3748	51.5			1.526e+005	1.296e+005
519	0.072	12.1	3	501.2525	49.9			2.052e+004	1692.619
106	0.092	2.0	2	755.3566	53.2			2.757e+005	1.397e+005
472	0.172	1.6	3	503.9072	53.2			5.251e+004	3.258e+004
120	0.374	1.1	2	768.8497	76.4			2.236e+005	2.102e+005
146	0.201	1.5	3	546.5938	42.1			1.006e+005	6.896e+004
575	0.214	1.4	2	819.3863	42.1			7.281e+004	5.229e+004
153	0.010	1.6	2	1133.0296	171.3			8.351e+004	5.121e+004
1627	0.034	1.4	3	755.6898	171.3			6773.246	4674.964
183	0.705	1.4	3	629.6311	51.5			1.805e+005	2.440e+005
1034	0.550	1.0	2	943.9422	51.3			8.010e+004	7.629e+004
209	0.183	1.7	2	464.7767	42.8			4.776e+004	2.796e+004
327	0.615	1.2	2	570.7803	48.0			5.776e+004	6.732e+004
1277	0.558	21.1	2	570.7804	46.4			8255.350	390.542
590	0.999	1.1	4	1384.3686	73.8			1.675e+005	1.530e+005
671	0.565	1.2	3	506.5839	51.7			2.656e+004	3.189e+004
934	0.189	1.4	2	539.7545	68.0			2.342e+004	1.620e+004
1060	0.074	1.8	2	982.4281	37.4			6.935e+004	3.811e+004
3299	0.392	1.1	2	522.7525	67.4			4973.210	4389.808
6233	0.155	1.8	3	506.9670	66.4			777.722	1421.069
314	0.375	1.0	2	671.3538	56.7			2.985e+004	2.916e+004
962	0.096	1.8	2	578.2713	54.5			3.878e+004	2.148e+004
1289	0.529	1.2	3	754.0041	57.3			2.223e+004	2.643e+004
23	0.333	1.1	2	757.3673	58.0			3.971e+005	3.536e+005
24	0.506	1.1	2	597.7476	57.7			1.544e+005	1.470e+005
111	0.399	1.0	2	567.7604	72.3			1.096e+005	1.077e+005
218	0.135	1.6	2	746.3753	64.9			2.490e+005	1.528e+005
522	0.217	1.4	3	497.9197	65.5			6.750e+004	4.939e+004
232	0.732	1.4	3	665.6316	59.2			5.282e+004	7.658e+004
298	0.105	2.9	2	518.7725	45.2			1.894e+004	6427.196
836	0.116	1.9	2	575.7577	72.1			3.295e+004	1.757e+004
3507	0.452	1.0	2	605.7451	57.4			3121.808	3014.268
8014	0.779	1.2	2	638.8685	91.2			1949.811	1690.172
169	0.609	1.1	2	555.8169	59.6			3.481e+004	3.935e+004
254	0.558	1.2	3	667.9933	47.6			9.273e+004	1.096e+005
762	0.404	1.0	2	1001.4863	47.6			7.043e+004	6.786e+004

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#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_plasma	CRC_plasma
277	0.206	1.6	2	421.7706	54.8			5.701e+004	3.663e+004
302	0.628	1.1	2	1129.0565	171.5			3.727e+004	3.438e+004
325	0.347	1.2	2	512.7605	67.8			2.520e+004	2.139e+004
387	0.072	1.5	3	619.2901	44.5			1.005e+005	6.560e+004
640	0.010	1.9	2	928.4312	44.5			1.515e+005	8.025e+004
494	0.784	1.1	2	746.3848	71.9			3.846e+004	4.179e+004
520	0.693	1.2	3	497.9259	71.9			1.963e+004	2.394e+004
500	0.193	508.4	2	619.8644	45.6			1.248e+004	24.544
544	0.378	1.1	2	542.2825	69.9			4.712e+004	4.359e+004
717	0.710	2.3	3	552.9362	61.5			1.411e+004	3.307e+004
1054	0.090	2.7	3	943.1834	171.0			6698.876	1.786e+004
1161	0.488	8.8	2	501.7771	48.0			5158.260	588.657
1301	0.592	1.0	2	1076.1058	172.0			1.914e+004	1.935e+004
3045	0.395	5.2	3	491.2535	47.7			2629.496	509.897
8383	0.826	91.2	2	790.9083	47.4			1075.003	11.783
3	0.339	2.3	3	1191.9624	170.6			8.626e+005	3.794e+005
19	0.546	2.3	4	894.2243	170.6			4.539e+005	1.992e+005
10	0.523	1.1	2	688.3134	50.2			4.955e+005	5.490e+005
21	0.185	1.5	2	607.3200	72.4			6.046e+005	4.141e+005
31	0.424	1.2	2	466.2765	52.8			1.355e+005	1.576e+005
33	0.183	1.4	2	770.8674	95.2			6.454e+005	4.463e+005
102	0.446	1.0	2	448.7347	70.2			7.917e+004	8.222e+004
789	0.381	1.1	2	659.7906	50.2			3.244e+004	2.845e+004
2622	0.981	6.4	2	659.7907	49.0			3916.135	614.024
886	0.390	1.0	2	607.3367	73.3			2.959e+004	2.988e+004
1193	0.938	5.9	2	726.3672	58.9			8059.274	1373.733
6355	0.123	2.7	2	495.2563	45.0			869.925	327.854
9085	0.585	1.2	2	679.3090	50.2			2364.609	2949.397
44	0.150	1.3	2	1068.4874	39.3			5.431e+005	4.050e+005
485	0.225	1.3	3	712.6612	39.3			6.160e+004	4.863e+004
62	0.948	1.2	3	625.9805	57.3			1.975e+005	2.450e+005
29	0.422	1.2	2	613.7755	59.6			5.642e+005	4.672e+005
139	0.150	1.5	3	434.5543	54.0			1.512e+005	1.013e+005
215	0.115	1.6	2	524.2602	65.0			7.409e+004	4.683e+004
359	0.566	1.2	2	629.8169	57.1			3.212e+004	3.817e+004
1456	0.163	1.5	3	428.5509	54.0			2.441e+004	1.667e+004
1742	0.263	1.3	2	601.3121	64.8			2.315e+004	1.756e+004
2811	0.053	2.1	3	445.8869	41.9			2588.208	1259.577
611	0.361	1.4	2	626.2994	89.3			4.598e+004	3.309e+004
850	0.418	1.0	2	579.3170	49.0			1.537e+004	1.489e+004
848	0.369	1.2	2	514.2928	53.4			1.426e+004	1.143e+004
2143	0.244	2.0	3	946.1373	170.9			6755.792	1.357e+004
2515	0.451	20.8	3	510.5830	47.7			3866.800	186.052
3219	0.483	1.1	4	698.0940	156.5			2.092e+004	2.398e+004
869	0.340	1.0	2	572.8140	63.1			1.974e+004	1.886e+004
1730	0.524	1.0	4	1300.3805	171.1			1.853e+004	1.807e+004
757	0.501	1.0	2	829.3857	62.1			6.553e+004	6.546e+004
1998	0.543	1.1	2	646.8029	41.4			8586.639	9435.058
3673	0.602	1.5	3	1282.2245	170.8			5263.134	7936.510
2026	0.608	1.3	3	822.4637	171.7			4424.947	5929.299
11	0.631	1.4	2	490.7511	69.3			1.420e+005	1.925e+005
12	0.524	1.2	2	854.4131	94.7			1.190e+006	1.422e+006
92	0.195	1.1	2	656.3064	51.8			1.257e+005	1.153e+005
128	0.802	1.3	3	1117.1843	78.6			5.871e+005	7.343e+005
237	0.428	1.0	2	929.4628	42.1			2.585e+005	2.616e+005
724	0.858	1.5	2	862.4093	94.4			1.213e+005	1.792e+005
1935	0.254	1.4	2	506.7451	69.3			1.046e+004	7655.699
1090	0.339	1.1	2	566.7744	55.4			1.862e+004	1.745e+004
1284	0.437	2.0	2	775.8676	171.1			3272.017	6590.920
997	0.940	1.7	2	753.3939	56.7			1.301e+004	2.160e+004

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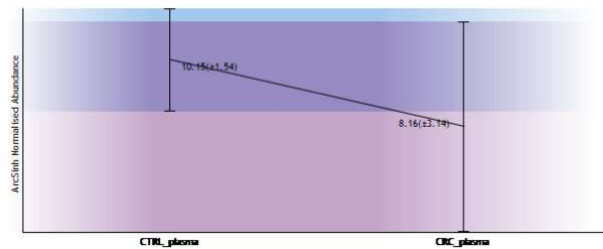
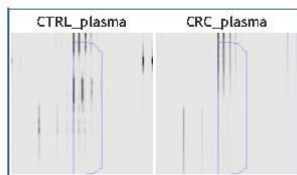
#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_plasma	CRC_plasma
2035	0.346	1.1	2	801.4292	91.2			8275.929	7863.574
2858	0.426	1.0	2	487.2508	52.8			3437.917	3499.390
3588	0.143	1.4e+004	2	665.3779	45.1			1382.170	0.096
7396	0.501	542.1	3	443.9213	45.1			368.214	0.679
17	0.681	1.1	2	917.4647	92.5			1.011e+006	1.084e+006
103	0.619	1.3	2	624.3049	69.1			9.249e+004	1.166e+005
701	0.980	2.4	3	468.5728	57.5			1.579e+004	3.765e+004
968	0.198	1.4	2	1045.5511	172.1			1.991e+004	2.810e+004
1344	0.703	1.0	2	632.3021	69.1			1.724e+004	1.673e+004
6155	0.117	3.4	2	688.3518	53.2			650.250	193.895
171	0.430	1.2	2	547.8193	42.8			4.899e+004	5.929e+004
1775	0.357	1.2	2	1330.1916	170.6			2.465e+004	3.029e+004
1025	0.992	1.4	2	1106.0788	171.6			1.709e+004	2.361e+004

Tags
<input checked="" type="checkbox"/> Anova p-value ≤ 0.08

Feature number 630

Charge 2
m/z 575.3404
Retention Time 49.8
Notes

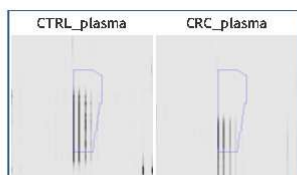
Score	Protein	Description
59.12	Q9UK54 Q9UK54_HUMAN	Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1



Feature number 2720

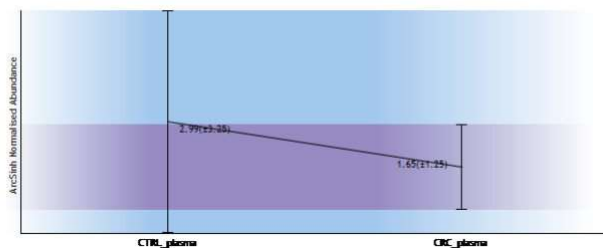
Charge 2
m/z 575.3405
Retention Time 47.7
Notes

Score	Protein	Description
39.42	Q9UK54 Q9UK54_HUMAN	Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
36.24	Q6VFRQ5 Q6VFRQ5_HUMAN	Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1



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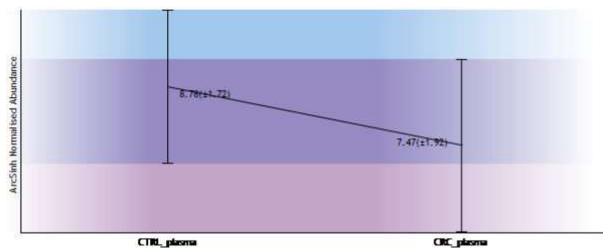
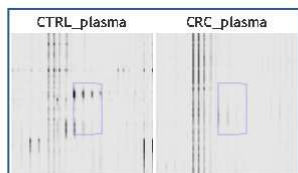
Feature number 1055

Charge 2
m/z 563.7854

Retention Time 59.6

Notes

Score	Protein	Description
24.27	Q9UK54 Q9UK54_HUMAN	Hemoglobin beta subunit variant (Fragment) OS-Homo sapiens GN+HBB PE-2 SV-1



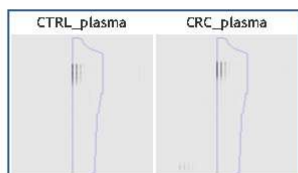
Feature number 4

Charge 2
m/z 863.3870

Retention Time 59.9

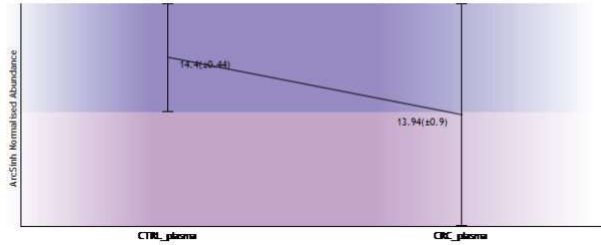
Notes

Score	Protein	Description
59.29	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN+TF PE-2 SV-1



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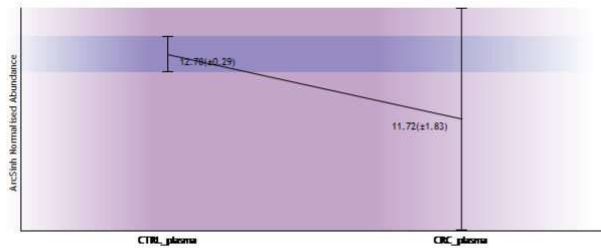
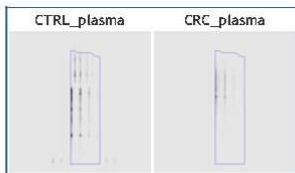
Feature number 18

Charge 2
m/z 489.7482

Retention Time 58.1

Notes

Score	Protein	Description
75.25	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1
66.06	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



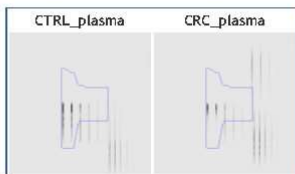
Feature number 28

Charge 2
m/z 625.3067

Retention Time 88.8

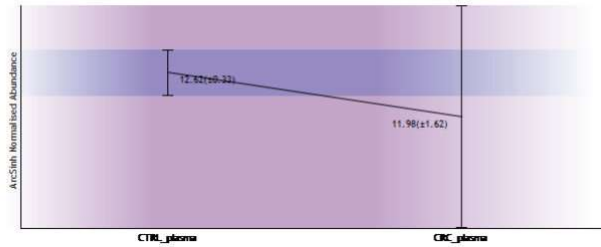
Notes

Score	Protein	Description
62.81	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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Feature number 63

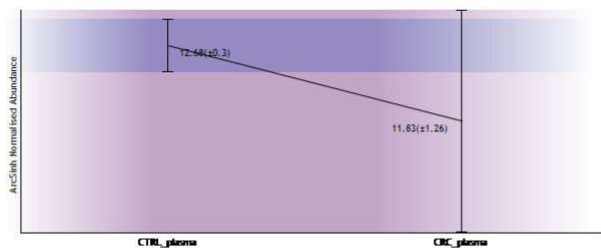
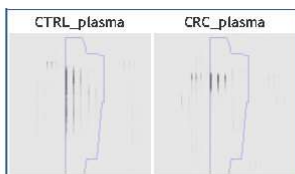
Charge 2
m/z 499.2423

Retention Time 72.2

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
51.40	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



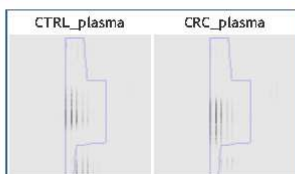
Feature number 65

Charge 2
m/z 853.8862

Retention Time 84.4

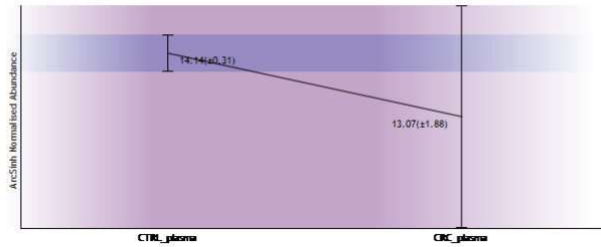
Notes

Score	Protein	Description
60.43	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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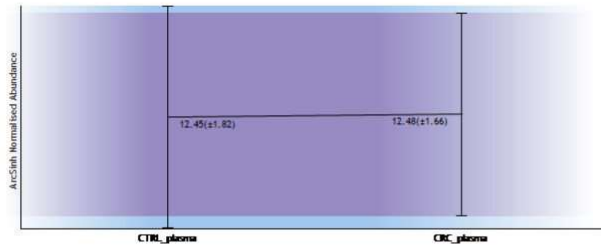
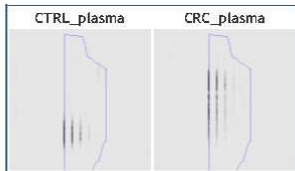


Feature number 86

Charge 2
m/z 598.2800

Retention Time 73.9
Notes

Score	Protein	Description
85.85	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1

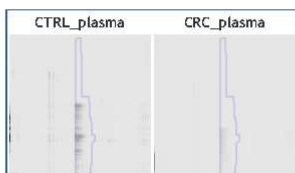


Feature number 104

Charge 4
m/z 638.0787

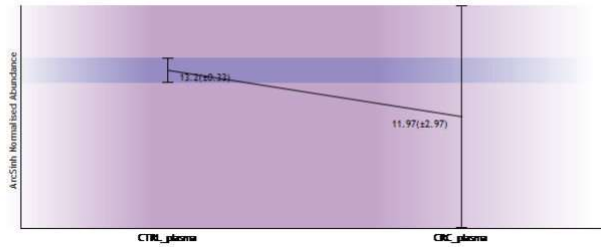
Retention Time 51.5
Notes

Score	Protein	Description
35.24	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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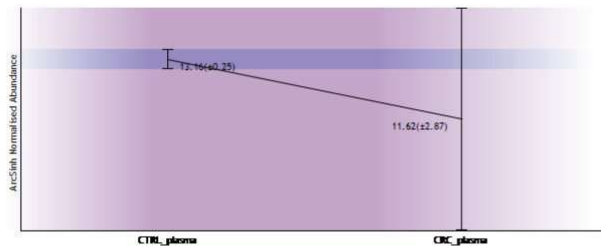
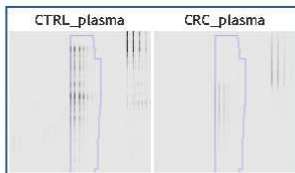


Feature number 202

Charge 3
m/z 850.4358

Retention Time 51.5
Notes

Score	Protein	Description
20.07	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1

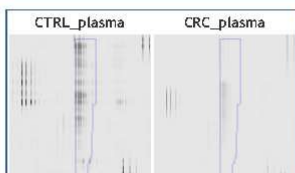


Feature number 463

Charge 5
m/z 510.6643

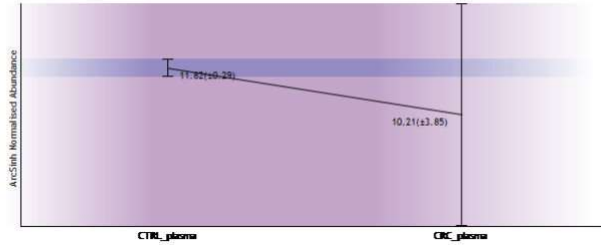
Retention Time 51.5
Notes

Score	Protein	Description
41.78	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1
40.69	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



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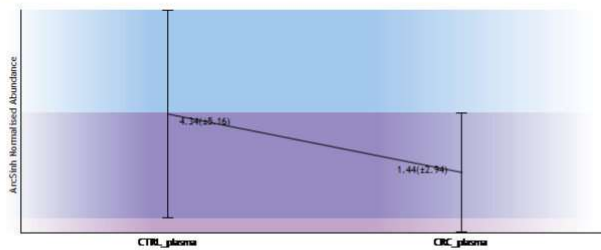
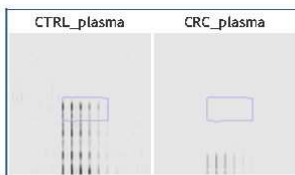
Feature number 6491

Charge 2
m/z 1275.1507

Retention Time 50.3

Notes

Score	Protein	Description
59.54	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1
51.93	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



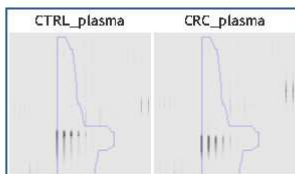
Feature number 118

Charge 2
m/z 766.3477

Retention Time 91.6

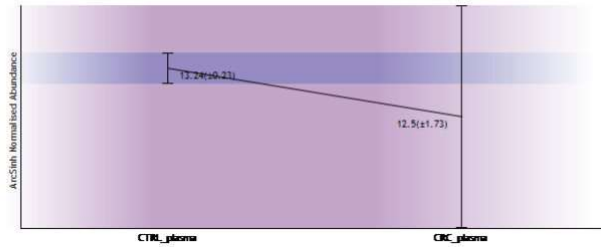
Notes

Score	Protein	Description
40.81	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1
38.64	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



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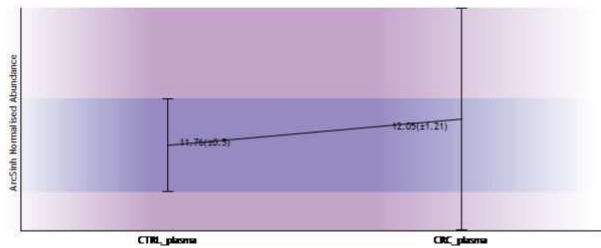
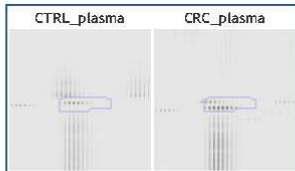
Feature number 152

Charge 4
m/z 1391.9600

Retention Time 170.5

Notes

Score	Protein	Description
39.45	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



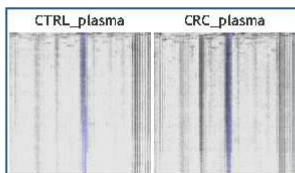
Feature number 1732

Charge 5
m/z 1113.7684

Retention Time 170.5

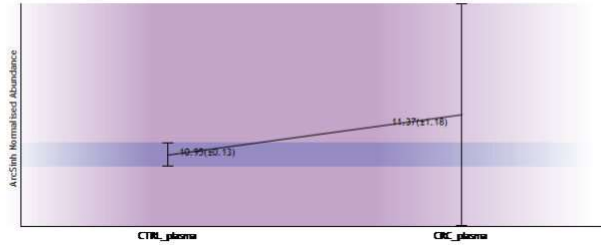
Notes

Score	Protein	Description
36.96	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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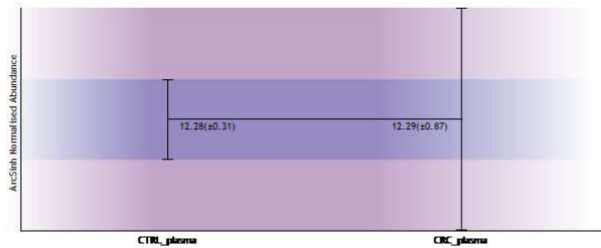
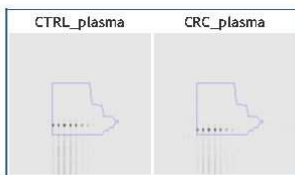


Feature number 197

Charge 3
m/z 1318.6776

Retention Time 170.5
Notes

Score	Protein	Description
61.53	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1
36.77	B4E1B2 B4E1B2_HUMAN	cDNA FLJ53691, highly similar to Serotransferrin OS-Homo sapiens PE-2 SV-1



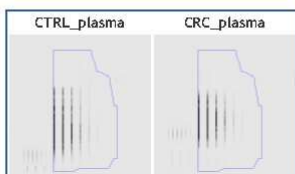
Feature number 220

Charge 2
m/z 941.4408

Retention Time 89.6
Notes

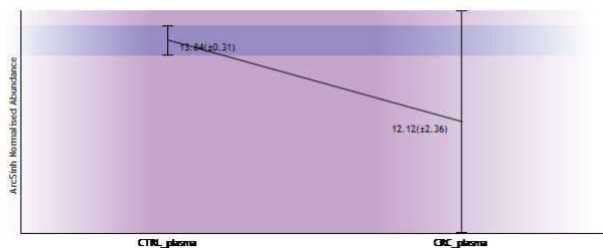
Anova p-value ≤ 0.08

Score	Protein	Description
40.40	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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Feature number 367

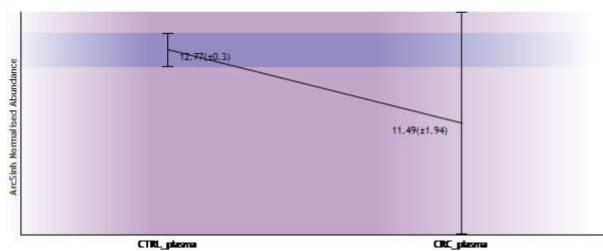
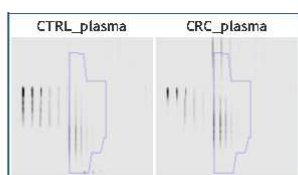
Charge 3
m/z 627.9638

Retention Time 89.6

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
22.21	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



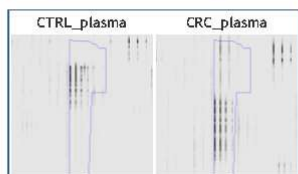
Feature number 328

Charge 3
m/z 507.9170

Retention Time 59.9

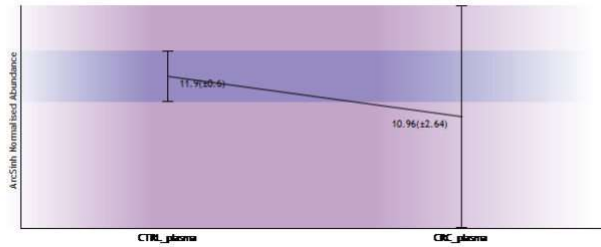
Notes

Score	Protein	Description
34.29	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



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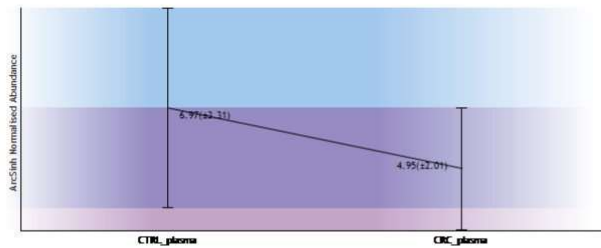
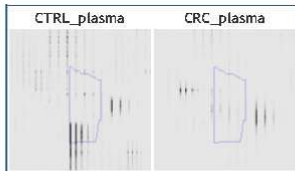
Feature number 557

Charge 3
m/z 497.9246

Retention Time 59.7

Notes

Score	Protein	Description
60.89	Q06AH7 Q06AH7_HUMAN	Transferrin OS=Homo sapiens GN=TF PE=2 SV=1



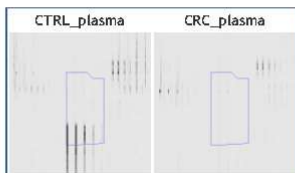
Feature number 1105

Charge 2
m/z 746.3833

Retention Time 59.7

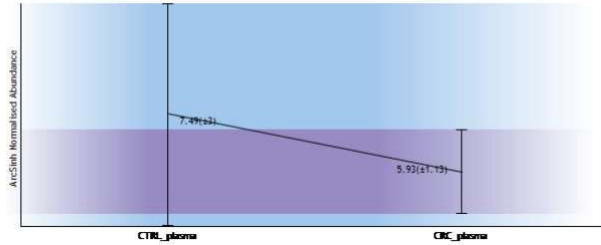
Notes

Score	Protein	Description
54.67	Q06AH7 Q06AH7_HUMAN	Transferrin OS=Homo sapiens GN=TF PE=2 SV=1



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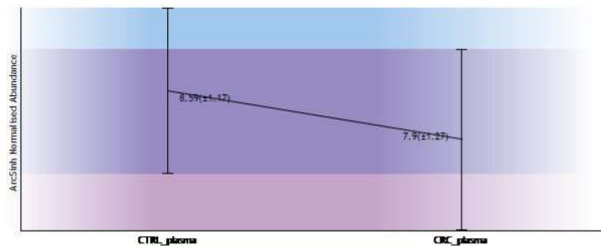
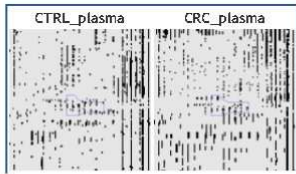
Feature number 1739

Charge 3
m/z 690.6815

Retention Time 171.2

Notes

Score	Protein	Description
53.13	Q06AH7 Q06AH7_HUMAN	Transferrin OS=Homo sapiens GN-TF PE-2 SV-1



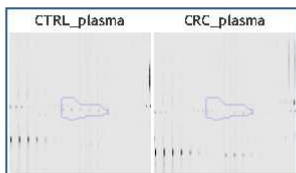
Feature number 2492

Charge 2
m/z 1035.5182

Retention Time 171.2

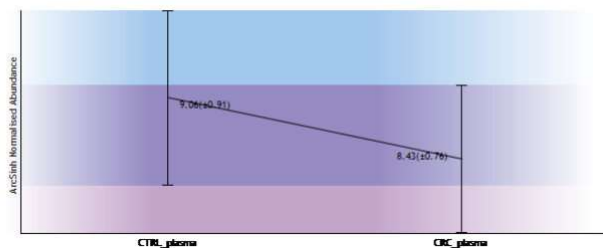
Notes

Score	Protein	Description
87.98	Q06AH7 Q06AH7_HUMAN	Transferrin OS=Homo sapiens GN-TF PE-2 SV-1



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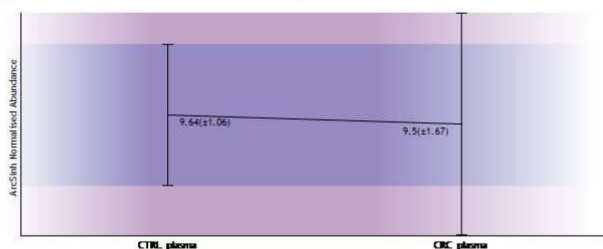
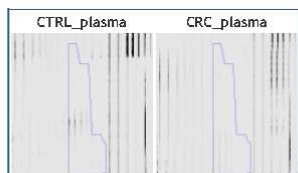
Feature number 3061

Charge 3
m/z 671.0100

Retention Time 85.4

Notes

Score	Protein	Description
25.62	Q06AH7 Q06AH7_HUMAN	Transferrin OS-Homo sapiens GN-TF PE-2 SV-1



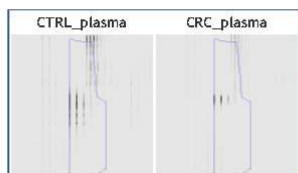
Feature number 46

Charge 2
m/z 636.8402

Retention Time 54.0

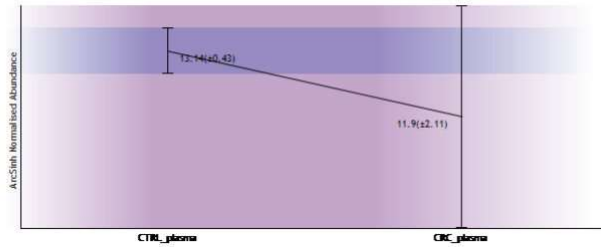
Notes

Score	Protein	Description
33.06	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS-Homo sapiens GN-A2M PE-1 SV-3



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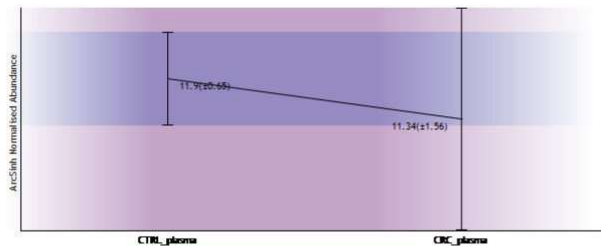
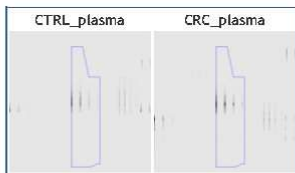
Feature number 110

Charge 2
m/z 628.3252

Retention Time 68.8

Notes

Score	Protein	Description
39.46	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3



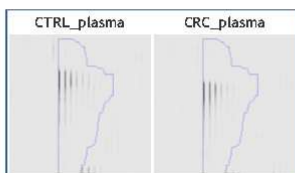
Feature number 150

Charge 2
m/z 802.9252

Retention Time 115.8

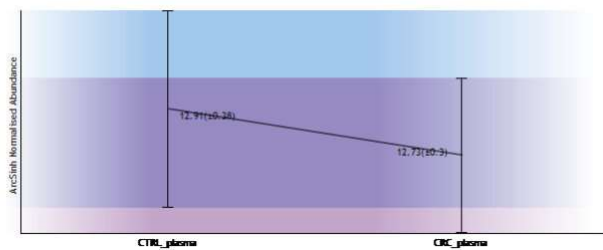
Notes

Score	Protein	Description
38.52	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3



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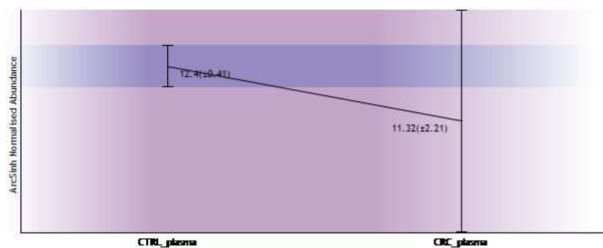
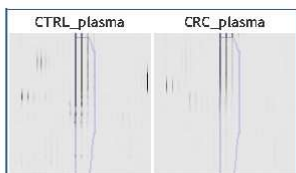
Feature number 230

Charge 2
m/z 605.8250

Retention Time 55.4

Notes

Score	Protein	Description
54.98	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN-A2M PE-1 SV-3



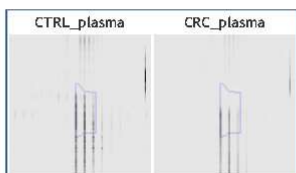
Feature number 276

Charge 2
m/z 605.8250

Retention Time 54.0

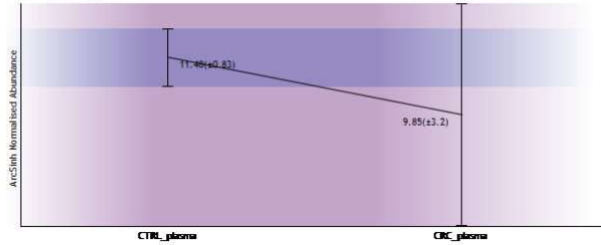
Notes

Score	Protein	Description
57.79	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN-A2M PE-1 SV-3



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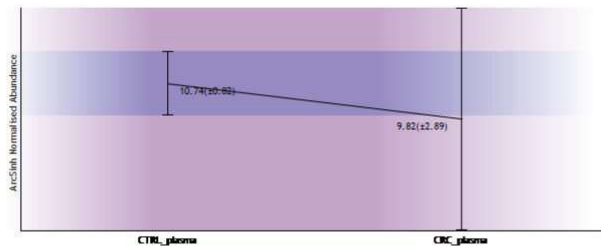
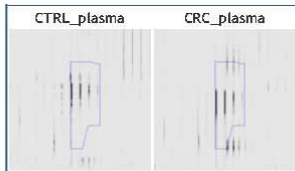
Feature number 293

Charge 2
m/z 552.3063

Retention Time 64.9

Notes

Score	Protein	Description
35.60	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3



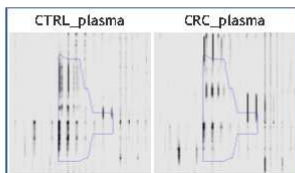
Feature number 501

Charge 2
m/z 558.8060

Retention Time 67.6

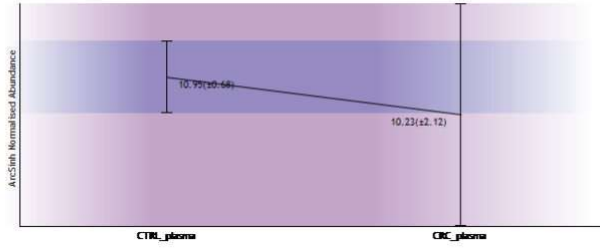
Notes

Score	Protein	Description
36.57	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3



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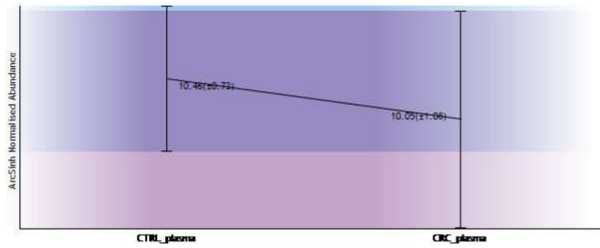
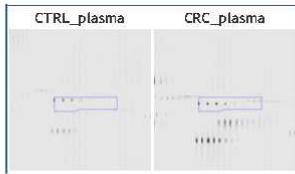


Feature number 815

Charge 2
m/z 1023.0315

Retention Time 171.5
Notes

Score	Protein	Description
111.53	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS-Homo sapiens GN-A2M PE-1 SV-3

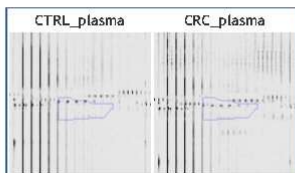


Feature number 3654

Charge 2
m/z 1082.0934

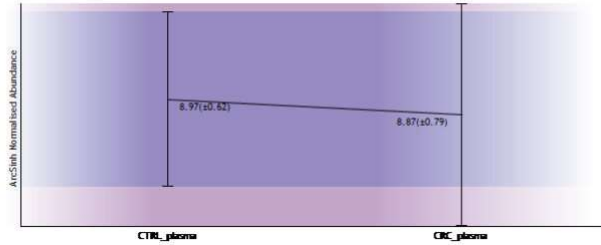
Retention Time 171.8
Notes

Score	Protein	Description
45.69	P01023 A2M_HUMAN	Alpha-2-macroglobulin OS-Homo sapiens GN-A2M PE-1 SV-3



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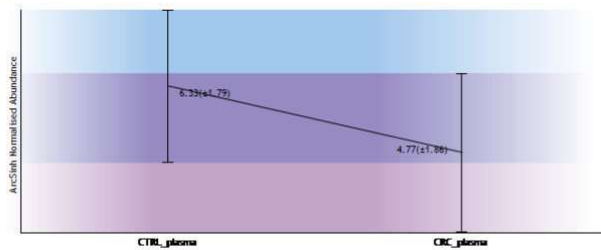
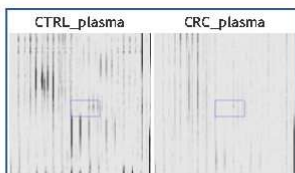
Feature number 2604

Charge 2
m/z 638.3093

Retention Time 45.0

Notes

Score	Protein	Description
61.76	Q53527 Q53527_HUMAN	Uncharacterized protein FN1 (Fragment) OS=Homo sapiens GN-FN1 PE-4 SV-1
57.64	A0A024R462 A0A024R462_HUMAN	Fibronectin 1, isoform CRA_n OS=Homo sapiens GN-FN1 PE-4 SV-1



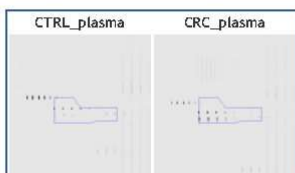
Feature number 540

Charge 2
m/z 1076.0870

Retention Time 171.4

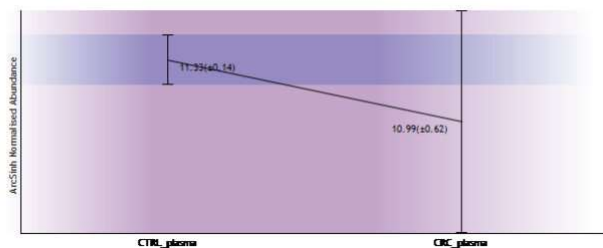
Notes

Score	Protein	Description
111.41	V9HWD8 V9HWD8_HUMAN	Epididymis secretory sperm binding protein LI 163pA OS=Homo sapiens GN-HEL-5-163pA PE-2 SV-1



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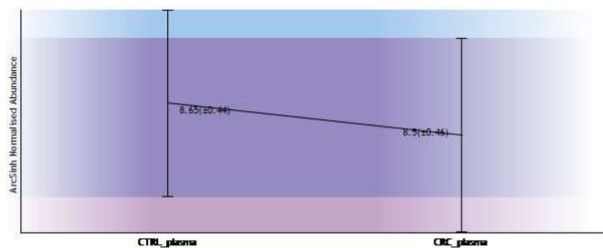
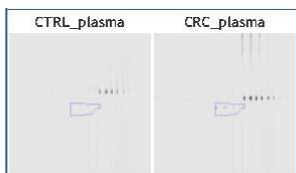
Feature number 4746

Charge 2
m/z 885.4903

Retention Time 171.9

Notes

Score	Protein	Description
48.88	ADA1U9X7H7 ADA1U9X7H7_HUMAN	CFB OS-Homo sapiens PE-3 SV-1



Feature number 6076

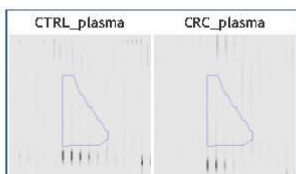
Charge 2
m/z 701.8334

Retention Time 41.0

Notes

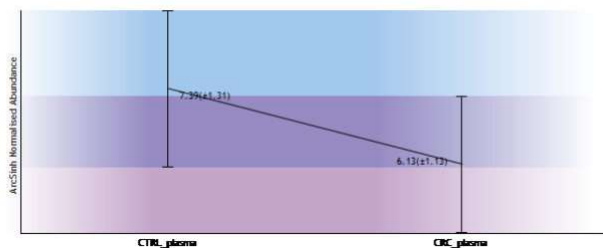
Anova p-value ≤ 0.08

Score	Protein	Description
29.06	ADA1U9X7I0 ADA1U9X7I0_HUMAN	CFB OS-Homo sapiens PE-3 SV-1
26.55	ADA1U9X7H7 ADA1U9X7H7_HUMAN	CFB OS-Homo sapiens PE-3 SV-1



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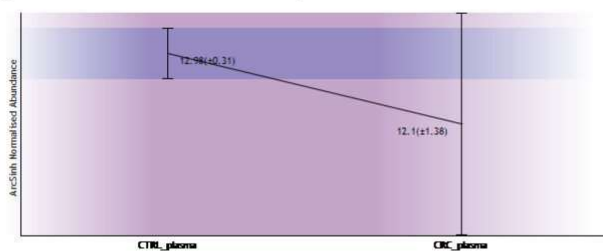
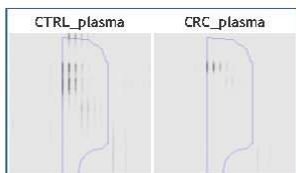
Feature number 133

Charge 2
m/z 809.4073

Retention Time 41.5

Notes

Score	Protein	Description
20.60	P0DOX6 IGM_HUMAN	Immunoglobulin mu heavy chain OS-Homo sapiens PE-1 SV-1



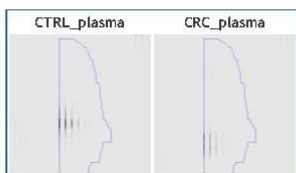
Feature number 137

Charge 2
m/z 800.8931

Retention Time 62.1

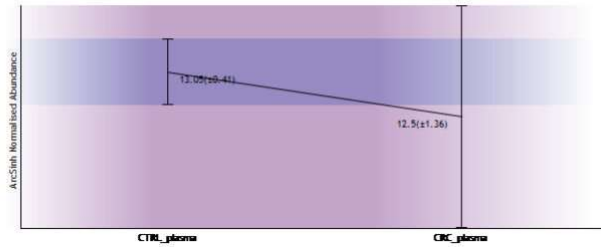
Notes

Score	Protein	Description
70.74	P0DOX6 IGM_HUMAN	Immunoglobulin mu heavy chain OS-Homo sapiens PE-1 SV-1



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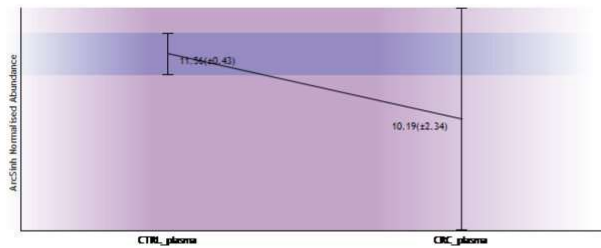
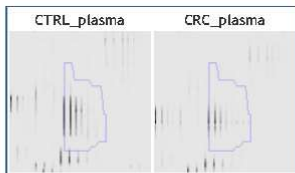


Feature number 322

Charge 3
m/z 572.9590

Retention Time 78.1
Notes

Score	Protein	Description
33.59	P0DOX6 IGM_HUMAN	Immunoglobulin mu heavy chain OS-Homo sapiens PE-1 SV-1

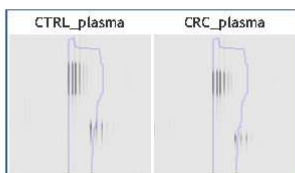


Feature number 41

Charge 3
m/z 833.4166

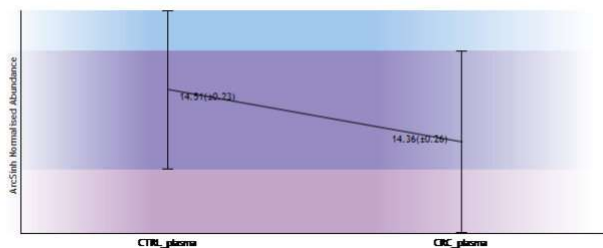
Retention Time 129.2
Notes

Score	Protein	Description
24.06	P02790 HEMO_HUMAN	Hemopexin OS-Homo sapiens GN-HPX PE-1 SV-2



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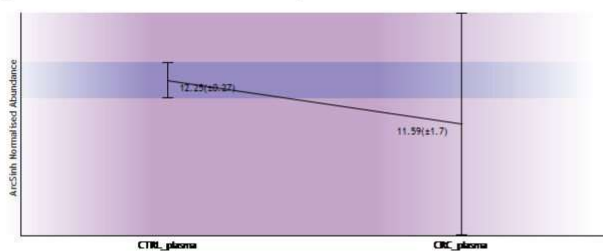
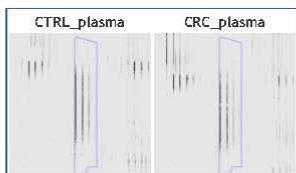
Feature number 339

Charge 2
m/z 571.2981

Retention Time 73.2

Notes

Score	Protein	Description
67.70	P02790 HEMO_HUMAN	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2



Feature number 1016

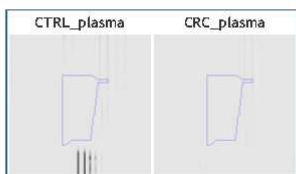
Charge 2
m/z 511.7358

Retention Time 44.8

Notes

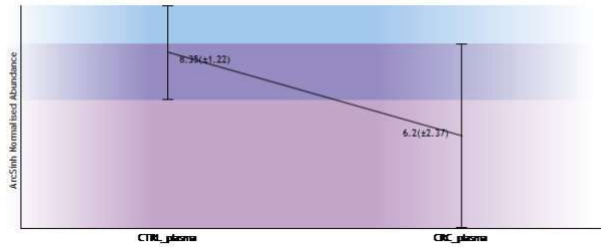
Anova p-value ≤ 0.08

Score	Protein	Description
66.91	P02790 HEMO_HUMAN	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2



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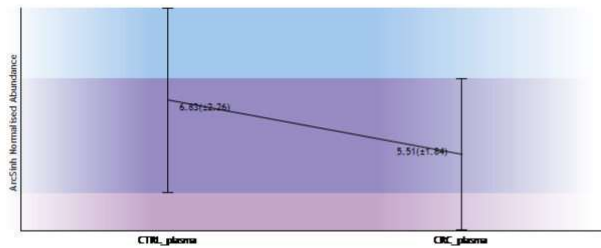
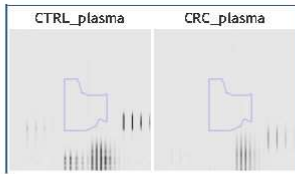


Feature number 2386

Charge 3
m/z 842.0540

Retention Time 45.6
Notes

Score	Protein	Description
34.30	ASPL27 ASPL27_HUMAN	CP protein OS-Homo sapiens GN-CP PE-2 SV-1

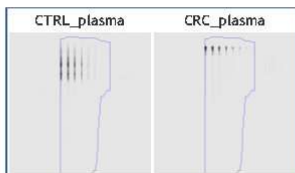


Feature number 161

Charge 2
m/z 1046.9159

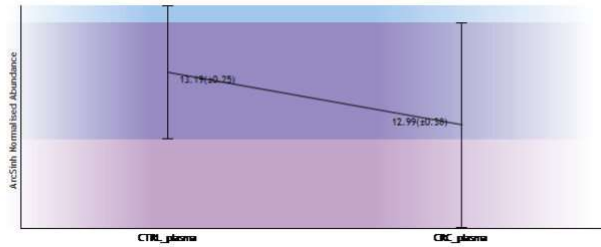
Retention Time 70.0
Notes

Score	Protein	Description
56.66	D6RF35 D6RF35_HUMAN	Vitamin D-binding protein OS-Homo sapiens GN-GC PE-1 SV-1



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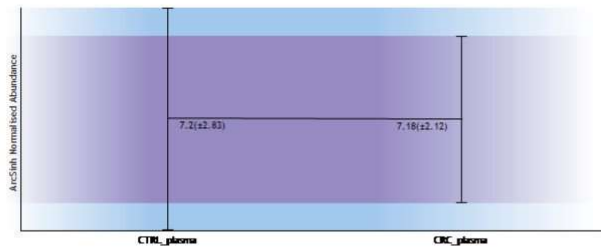
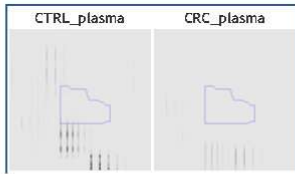
Feature number 258

Charge 3
m/z 755.6504

Retention Time 56.7

Notes

Score	Protein	Description
24.16	D6RF35 D6RF35_HUMAN	Vitamin D-binding protein OS-Homo sapiens GN-GC PE-1 SV-1



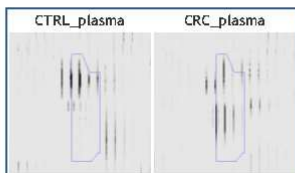
Feature number 1205

Charge 2
m/z 585.8294

Retention Time 80.7

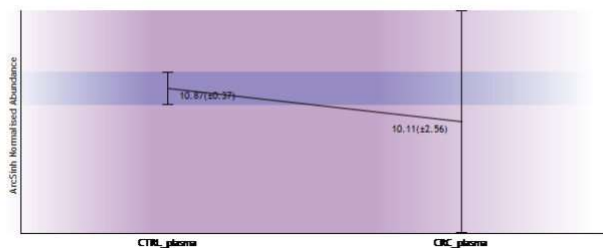
Notes

Score	Protein	Description
28.19	D6RF35 D6RF35_HUMAN	Vitamin D-binding protein OS-Homo sapiens GN-GC PE-1 SV-1



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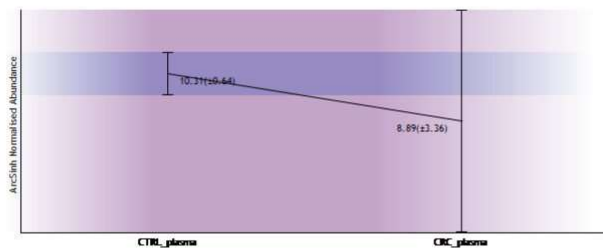
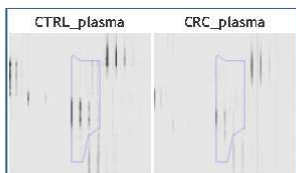
Feature number 604

Charge 2
m/z 516.7641

Retention Time 47.5

Notes

Score	Protein	Description
40.66	K7ER19 K7ER19_HUMAN	Apolipoprotein C-I (Fragment) OS-Homo sapiens GN-APOC1 PE-1 SV-1



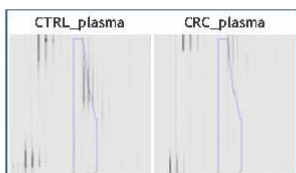
Feature number 5641

Charge 2
m/z 522.2598

Retention Time 45.3

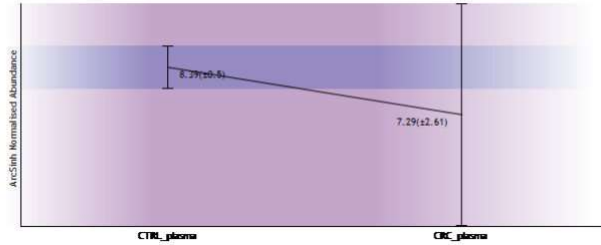
Notes

Score	Protein	Description
33.96	F8WCZ6 F8WCZ6_HUMAN	Complement C1s subcomponent OS-Homo sapiens GN-C15 PE-1 SV-1



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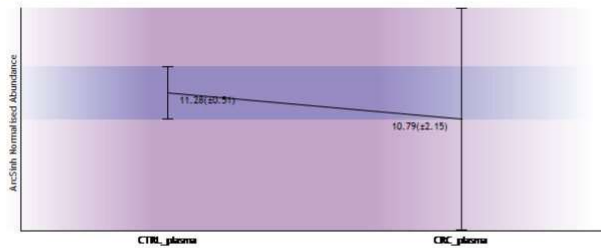
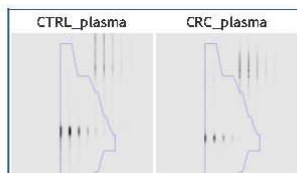


Feature number 244

Charge 2
m/z 771.4119

Retention Time 64.4
Notes

Score	Protein	Description
69.19	F5GX50 F5GX50_HUMAN	Complement C4-B 05-Homo sapiens GN-C4B PE-1 SV-1
65.14	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1

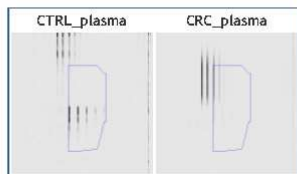


Feature number 355

Charge 2
m/z 630.3186

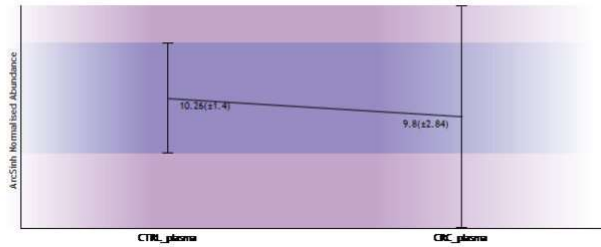
Retention Time 53.2
Notes

Score	Protein	Description
52.47	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1
49.34	F5GX50 F5GX50_HUMAN	Complement C4-B 05-Homo sapiens GN-C4B PE-1 SV-1



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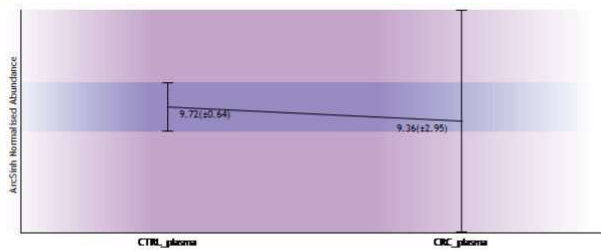
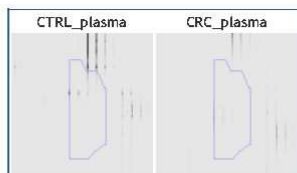
Feature number 593

Charge 2
m/z 488.7212

Retention Time 59.6

Notes

Score	Protein	Description
64.91	F5GX50 F5GX50_HUMAN	Complement C4-B 05-Homo sapiens GN-C4B PE-1 SV-1
51.95	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



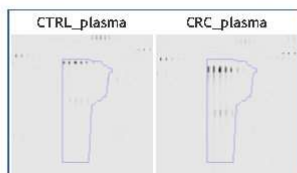
Feature number 964

Charge 3
m/z 871.8092

Retention Time 172.6

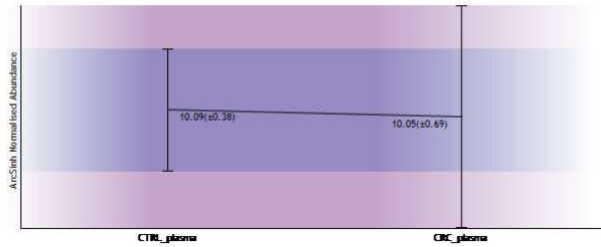
Notes

Score	Protein	Description
53.90	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



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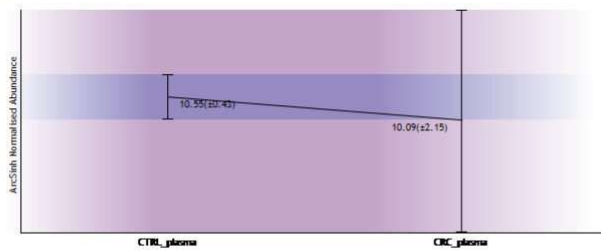
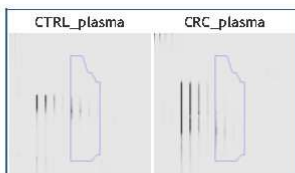
Feature number 984

Charge 2
m/z 557.8137

Retention Time 83.5

Notes

Score	Protein	Description
41.74	F5GX50 F5GX50_HUMAN	Complement C4-B 05-Homo sapiens GN-C4B PE-1 SV-1
27.52	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



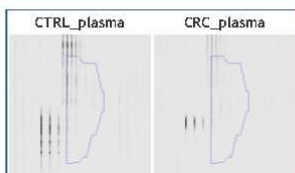
Feature number 987

Charge 2
m/z 638.3164

Retention Time 53.2

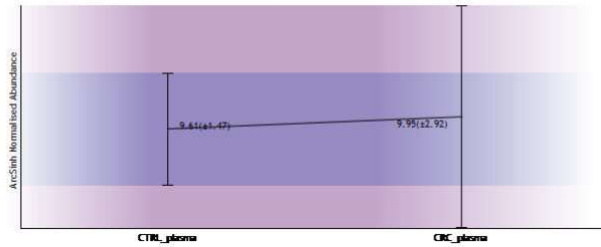
Notes

Score	Protein	Description
35.99	A0A140TA32 A0A140TA32_HUMAN	Complement C4-A 05-Homo sapiens GN-C4A PE-1 SV-1



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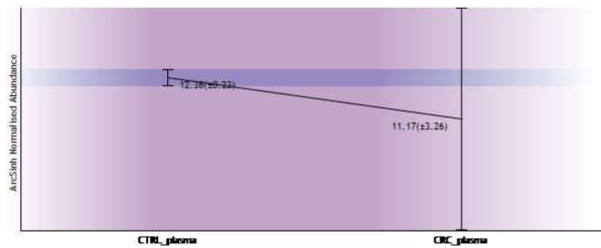
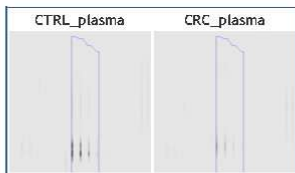


Feature number 69

Charge 2
m/z 654.8119

Retention Time 41.4
Notes

Score	Protein	Description
53.67	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1

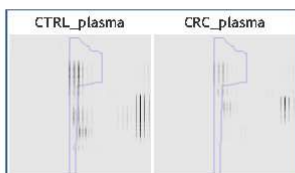


Feature number 268

Charge 2
m/z 1078.9774

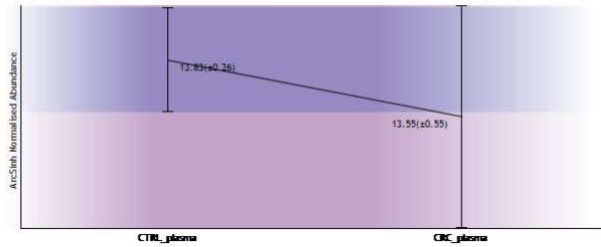
Retention Time 94.6
Notes

Score	Protein	Description
54.15	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



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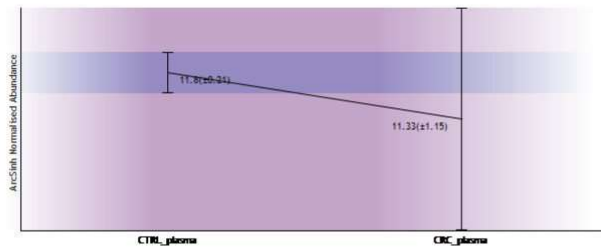
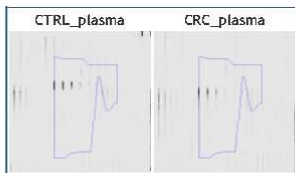
Feature number 324

Charge 2
m/z 620.2622

Retention Time 91.5

Notes

Score	Protein	Description
43.87	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



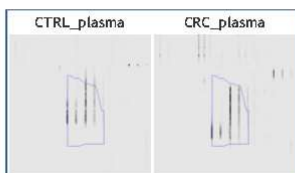
Feature number 447

Charge 2
m/z 443.6976

Retention Time 71.6

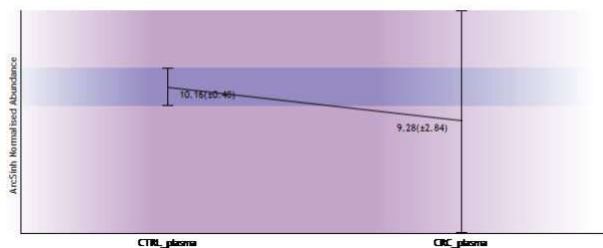
Notes

Score	Protein	Description
46.09	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



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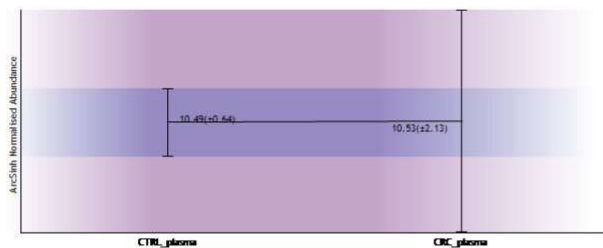
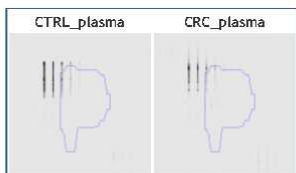
Feature number 899

Charge 3
m/z 709.3488

Retention Time 69.1

Notes

Score	Protein	Description
29.65	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



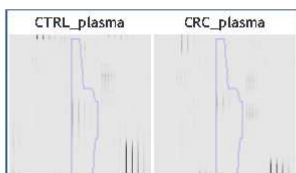
Feature number 1537

Charge 2
m/z 646.2992

Retention Time 62.1

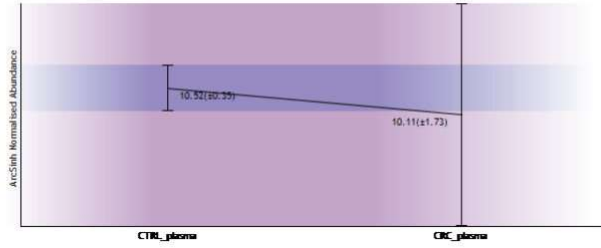
Notes

Score	Protein	Description
72.05	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



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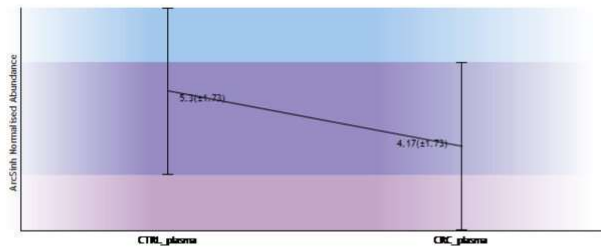
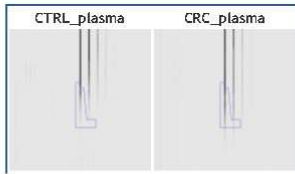
Feature number 15469

Charge 3
m/z 506.5763

Retention Time 45.5

Notes

Score	Protein	Description
45.90	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



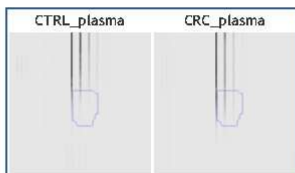
Feature number 21292

Charge 3
m/z 506.9047

Retention Time 45.5

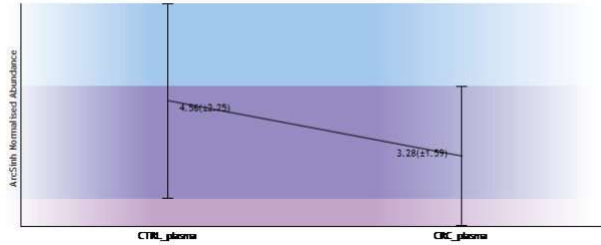
Notes

Score	Protein	Description
33.49	D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_e OS-Homo sapiens GN-FGB PE-4 SV-1



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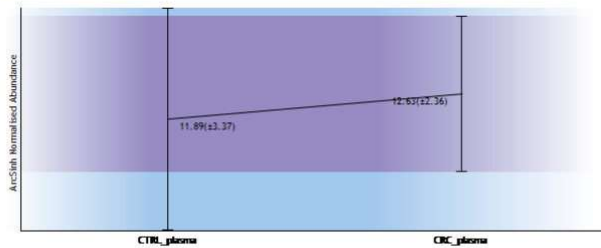
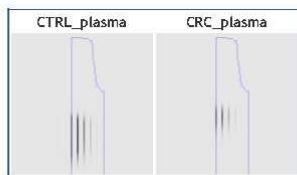
Feature number 38

Charge 2
m/z 786.8422

Retention Time 26.0

Notes

Score	Protein	Description
47.80	A0A0S2Z3E8 A0A0S2Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1
37.70	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



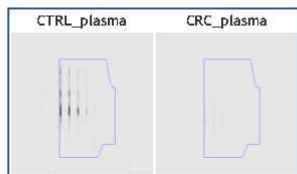
Feature number 59

Charge 2
m/z 751.3748

Retention Time 51.5

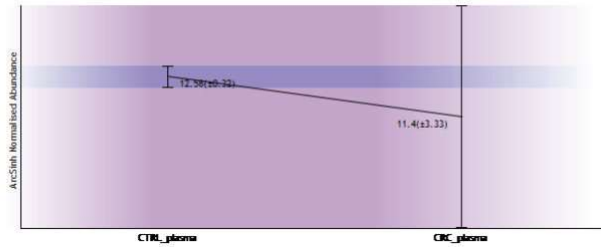
Notes

Score	Protein	Description
35.18	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2
34.64	A0A0S2Z3E8 A0A0S2Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1



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Feature number 519

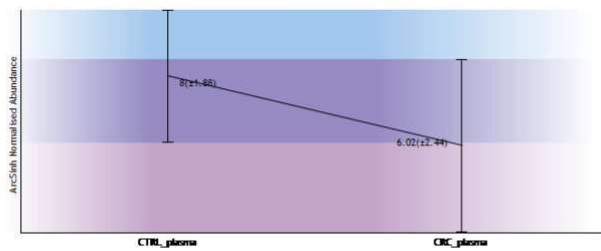
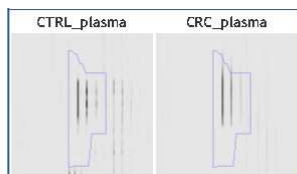
Charge 3
m/z 501.2525

Retention Time 49.9

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
25.70	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



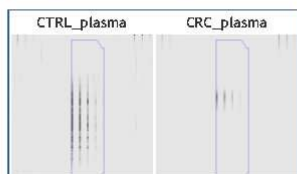
Feature number 106

Charge 2
m/z 755.3566

Retention Time 53.2

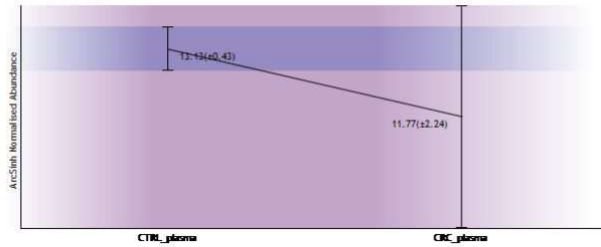
Notes

Score	Protein	Description
60.17	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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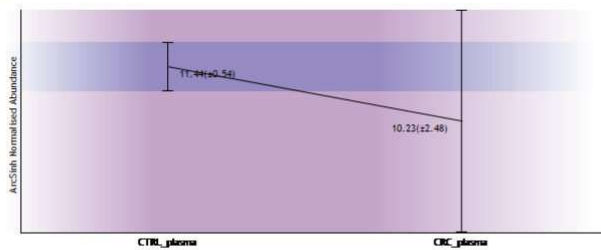
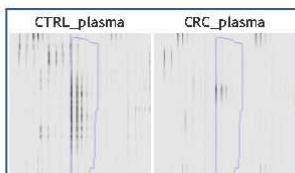


Feature number 472.

Charge 3
m/z 503.9072

Retention Time 53.2
Notes

Score	Protein	Description
18.14	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2
16.45	A0A0S2Z3E8 A0A0S2Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1

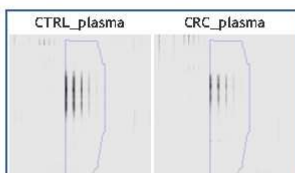


Feature number 120

Charge 2
m/z 768.8497

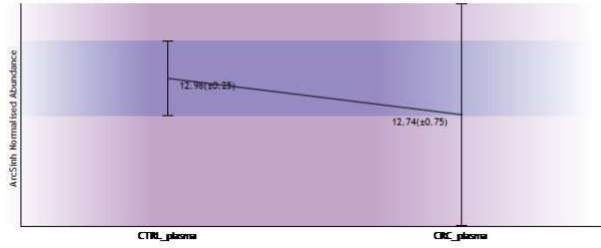
Retention Time 76.4
Notes

Score	Protein	Description
33.13	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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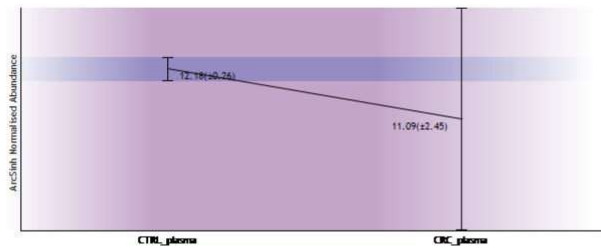
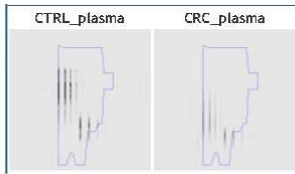
Feature number 146

Charge 3
m/z 546.5938

Retention Time 42.1

Notes

Score	Protein	Description
52.18	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



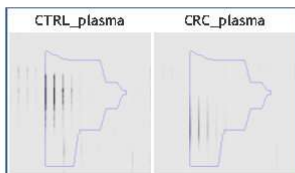
Feature number 575

Charge 2
m/z 819.3863

Retention Time 42.1

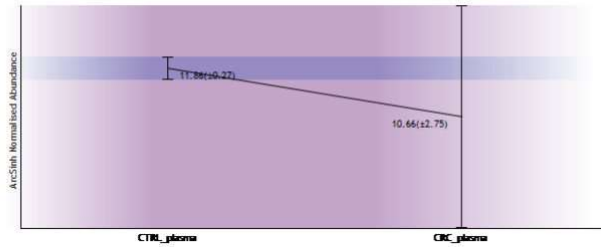
Notes

Score	Protein	Description
43.55	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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Feature number 153

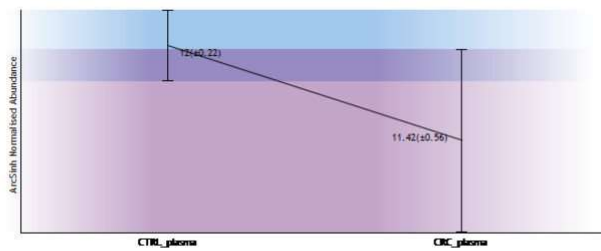
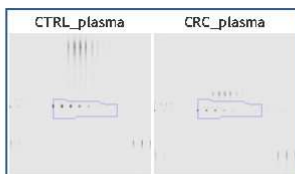
Charge 2
m/z 1133.0296

Retention Time 171.3

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
100.32	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



Feature number 1627

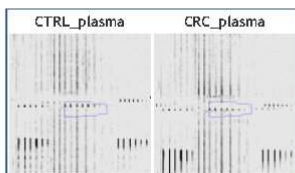
Charge 3
m/z 755.6898

Retention Time 171.3

Notes

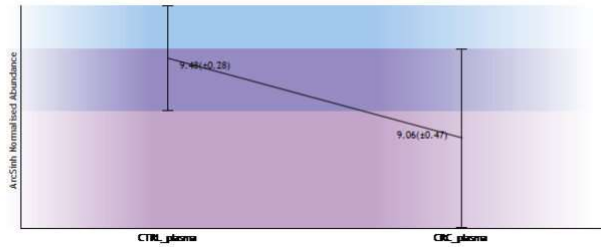
Anova p-value ≤ 0.08

Score	Protein	Description
84.71	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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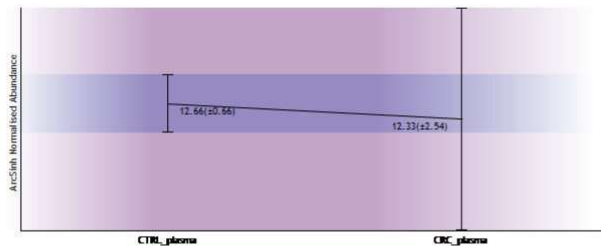
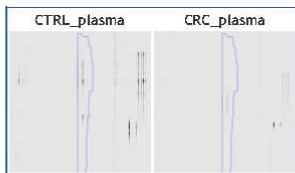


Feature number 183

Charge 3
m/z 629.6311

Retention Time 51.5
Notes

Score	Protein	Description
82.71	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2

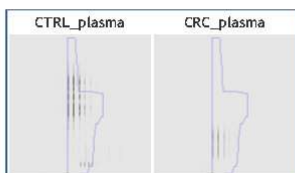


Feature number 1034

Charge 2
m/z 943.9422

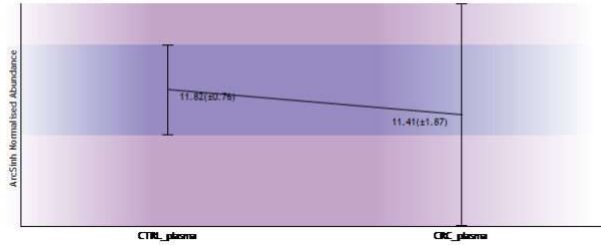
Retention Time 51.3
Notes

Score	Protein	Description
71.34	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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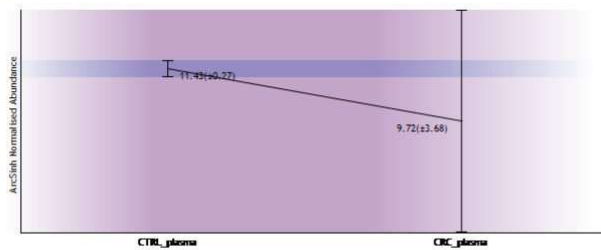
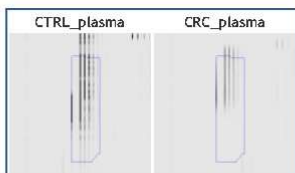
Feature number 209

Charge 2
m/z 464.7767

Retention Time 42.8

Notes

Score	Protein	Description
45.55	A0A0S2Z3E8 A0A0S2Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1
29.74	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



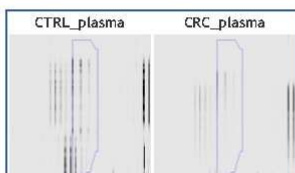
Feature number 327

Charge 2
m/z 570.7803

Retention Time 48.0

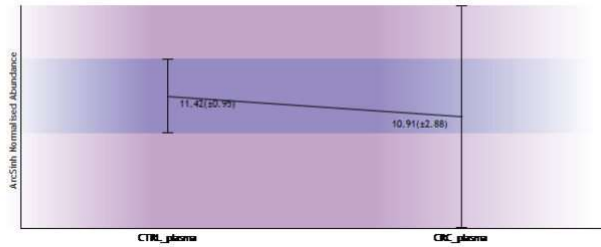
Notes

Score	Protein	Description
56.30	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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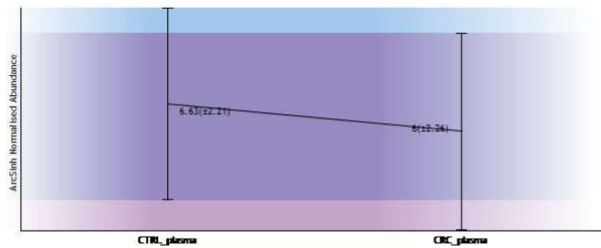
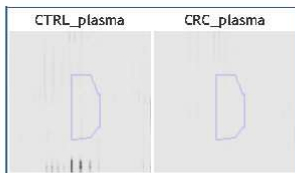
Feature number 1277

Charge 2
m/z 570.7804

Retention Time 46.4

Notes

Score	Protein	Description
68.78	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



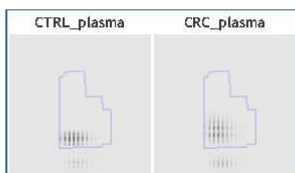
Feature number 590

Charge 4
m/z 1384.3686

Retention Time 73.8

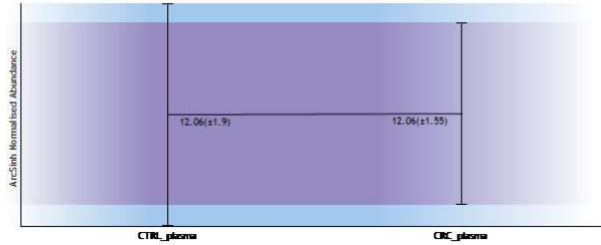
Notes

Score	Protein	Description
17.38	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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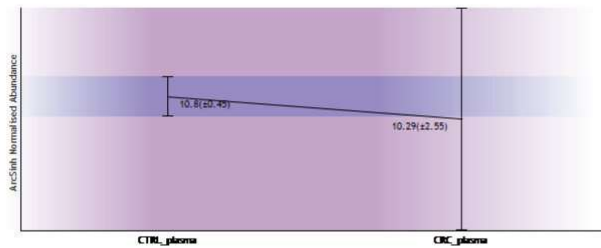
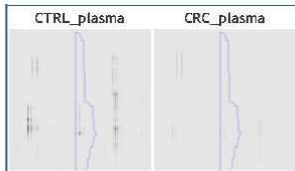


Feature number 671

Charge 3
m/z 506.5839

Retention Time 51.7
Notes

Score	Protein	Description
33.72	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2

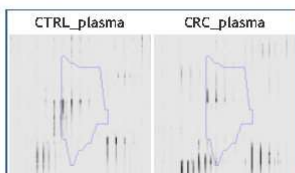


Feature number 934

Charge 2
m/z 539.7545

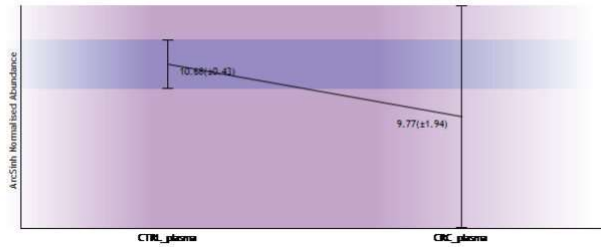
Retention Time 68.0
Notes

Score	Protein	Description
63.83	A0A0S2Z3E8 A0A0S2Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1
47.19	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



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Feature number 1060

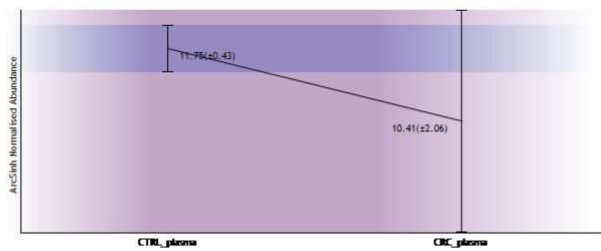
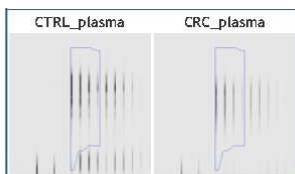
Charge 2
m/z 982.4281

Retention Time 37.4

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
82.13	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2



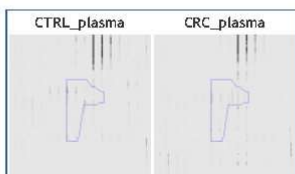
Feature number 3299

Charge 2
m/z 522.7525

Retention Time 67.4

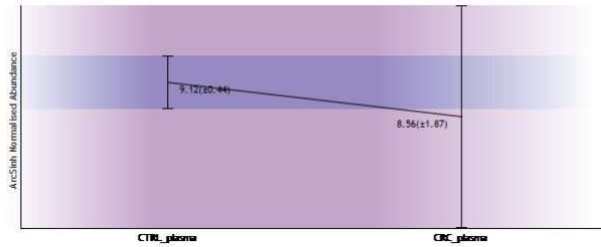
Notes

Score	Protein	Description
29.03	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2
26.87	A0A052Z3E8 A0A052Z3E8_HUMAN	Fibrinogen alpha chain isoform 2 (Fragment) OS-Homo sapiens GN-FGA PE-2 SV-1



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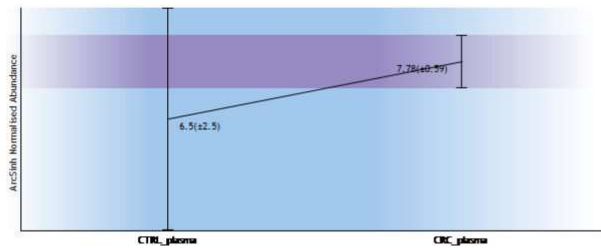
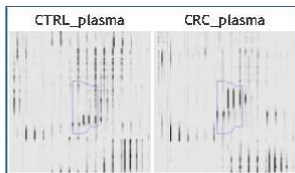


Feature number 6233

Charge 3
m/z 506.9670

Retention Time 66.4
Notes

Score	Protein	Description
25.37	P02671 FIBA_HUMAN	Fibrinogen alpha chain OS-Homo sapiens GN-FGA PE-1 SV-2

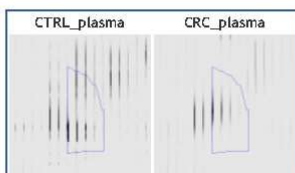


Feature number 314

Charge 2
m/z 671.3538

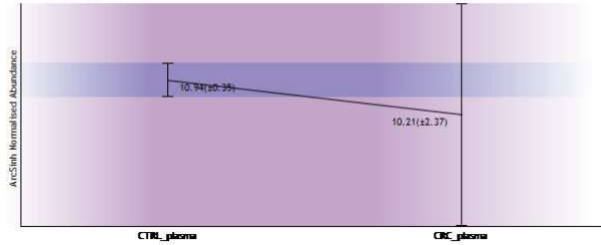
Retention Time 56.7
Notes

Score	Protein	Description
67.49	A0A024R984 A0A024R984_HUMAN	HCG-40889, isoform CRA_a OS-Homo sapiens GN-hCG_40889 PE-4 SV-1
54.58	A0A024R962 A0A024R962_HUMAN	HCG-40889, isoform CRA_b OS-Homo sapiens GN-hCG_40889 PE-4 SV-1



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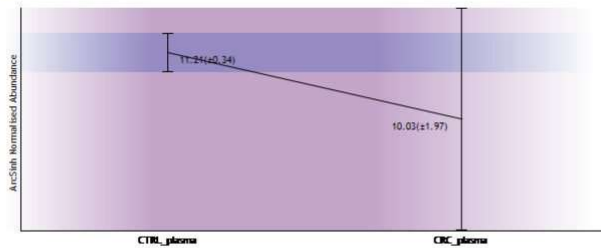
Feature number 962

Charge 2
m/z 578.2713

Retention Time 54.5

Notes

Score	Protein	Description
50.32	ADA024R984 ADA024R984_HUMAN	HCG40889, isoform CRA_a OS-Homo sapiens GN-hCG_40889 PE-4 SV-1
38.97	ADA024R962 ADA024R962_HUMAN	HCG40889, isoform CRA_b OS-Homo sapiens GN-hCG_40889 PE-4 SV-1



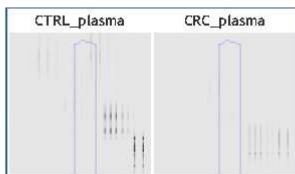
Feature number 1289

Charge 3
m/z 754.0041

Retention Time 57.3

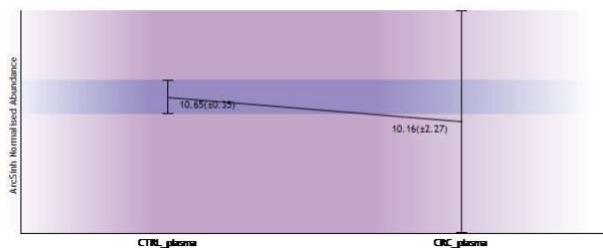
Notes

Score	Protein	Description
27.92	ADA024R984 ADA024R984_HUMAN	HCG40889, isoform CRA_a OS-Homo sapiens GN-hCG_40889 PE-4 SV-1
16.88	ADA024R962 ADA024R962_HUMAN	HCG40889, isoform CRA_b OS-Homo sapiens GN-hCG_40889 PE-4 SV-1



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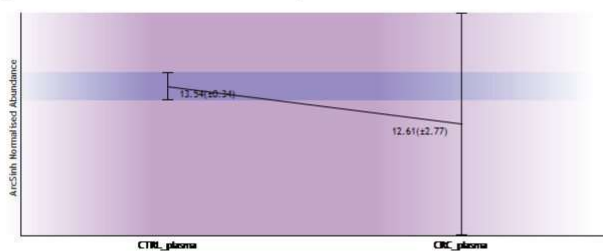
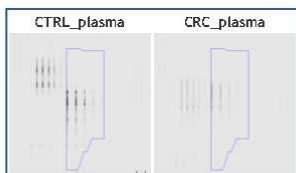
Feature number 23

Charge 2
m/z 757.3673

Retention Time 58.0

Notes

Score	Protein	Description
78.97	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein LI 70 O5-Homo sapiens PE-2 SV-1



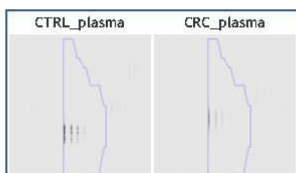
Feature number 24

Charge 2
m/z 597.7476

Retention Time 57.7

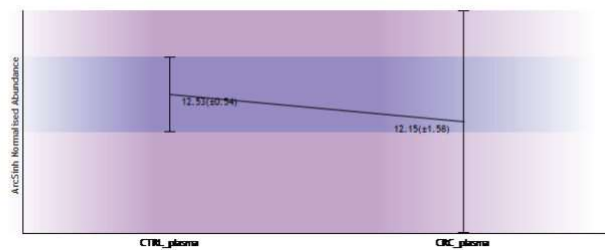
Notes

Score	Protein	Description
57.00	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein LI 70 O5-Homo sapiens PE-2 SV-1



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Feature number 111

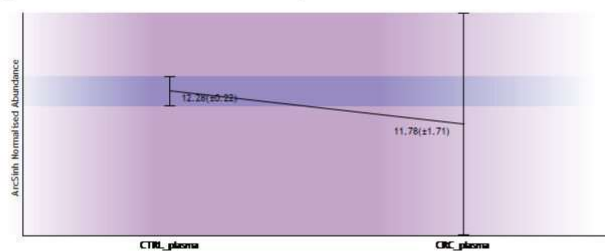
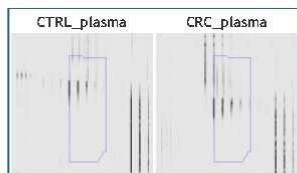
Charge 2

m/z 567.7604

Retention Time 72.3

Notes

Score	Protein	Description
57.99	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



Feature number 218

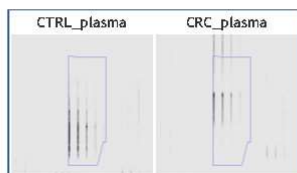
Charge 2

m/z 746.3753

Retention Time 64.9

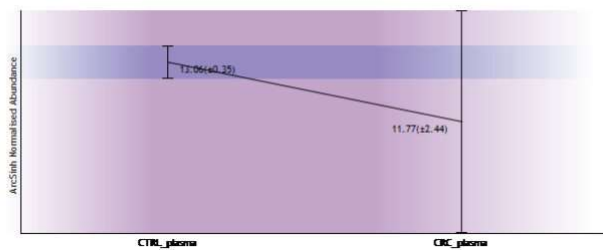
Notes

Score	Protein	Description
64.22	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



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Feature number 522.

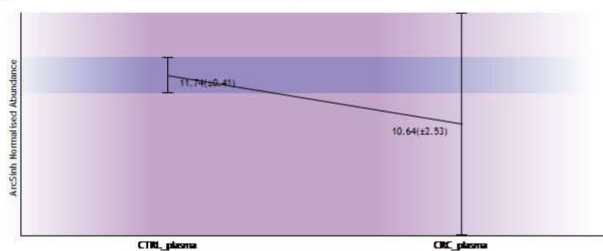
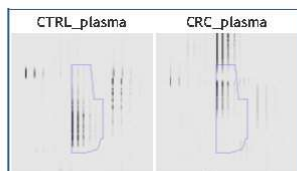
Charge 3

m/z 497.9197

Retention Time 65.5

Notes

Score	Protein	Description
50.60	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



Feature number 232.

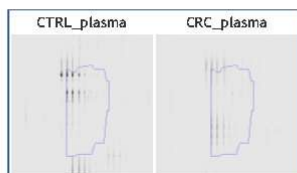
Charge 3

m/z 665.6316

Retention Time 59.2

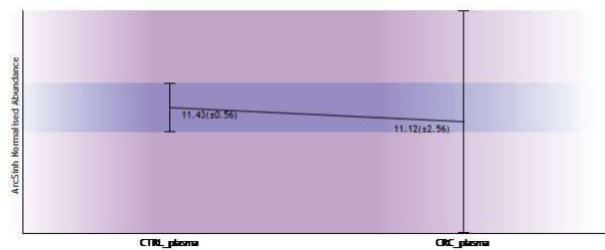
Notes

Score	Protein	Description
50.61	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



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Feature number 298

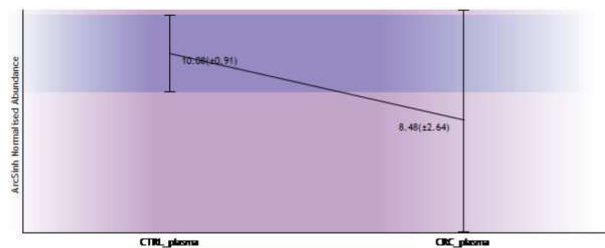
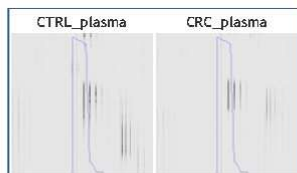
Charge 2

m/z 518.7725

Retention Time 45.2

Notes

Score	Protein	Description
20.17	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



Feature number 836

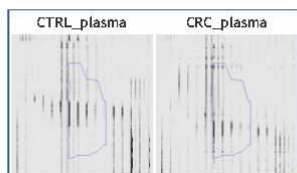
Charge 2

m/z 575.7577

Retention Time 72.1

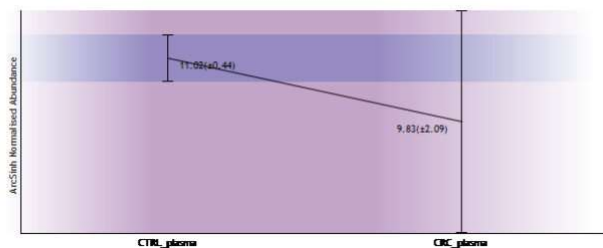
Notes

Score	Protein	Description
29.35	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



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Feature number 3507

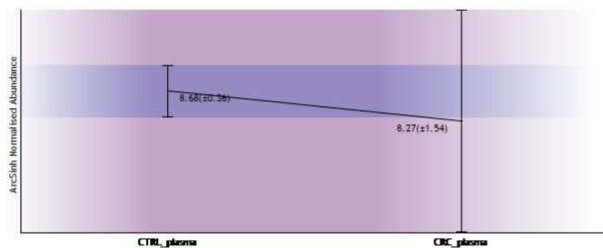
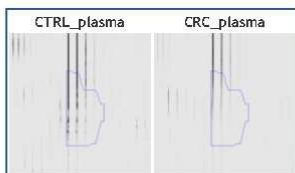
Charge 2

m/z 605.7451

Retention Time 57.4

Notes

Score	Protein	Description
20.43	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



Feature number 8014

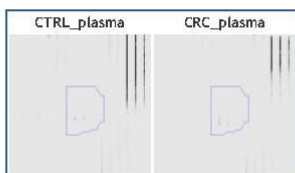
Charge 2

m/z 638.8685

Retention Time 91.2

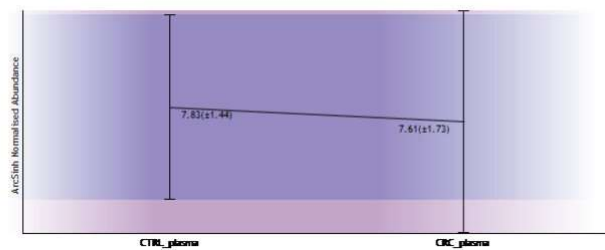
Notes

Score	Protein	Description
32.18	AQA140VJJ6 AQA140VJJ6_HUMAN	Testicular tissue protein Li 70 O5-Homo sapiens PE-2 SV-1



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Feature number 169

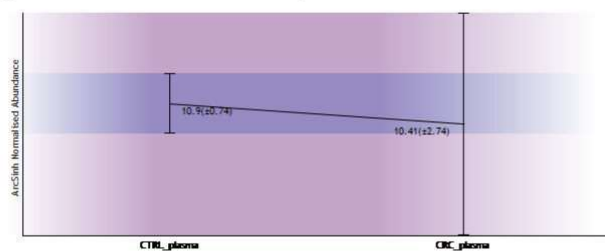
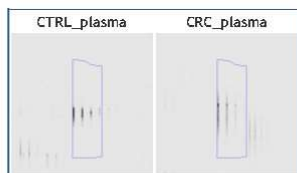
Charge 2

m/z 555.8169

Retention Time 59.6

Notes

Score	Protein	Description
54.04	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



Feature number 254

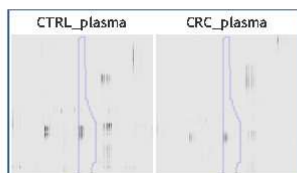
Charge 3

m/z 667.9933

Retention Time 47.6

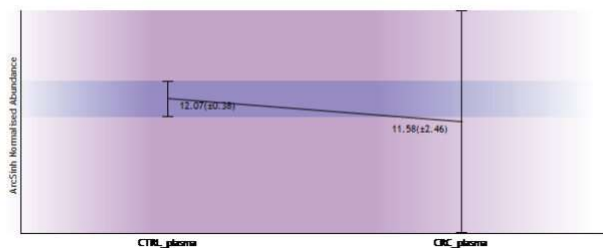
Notes

Score	Protein	Description
64.60	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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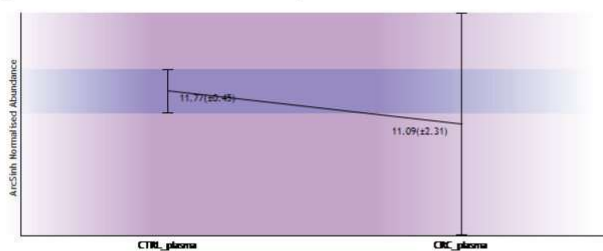
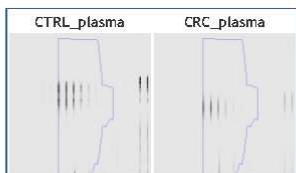
Feature number 762

Charge 2
m/z 1001.4863

Retention Time 47.6

Notes

Score	Protein	Description
42.76	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



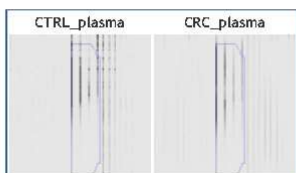
Feature number 277

Charge 2
m/z 421.7706

Retention Time 54.8

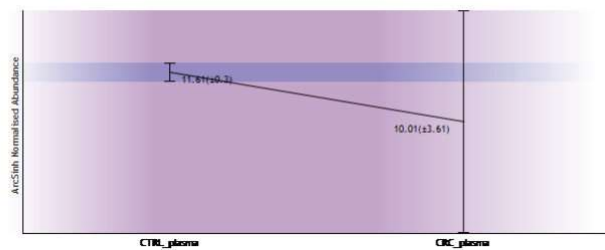
Notes

Score	Protein	Description
38.59	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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Feature number 302

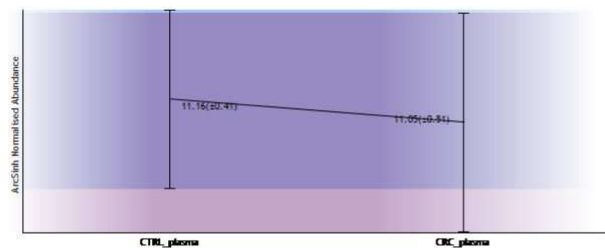
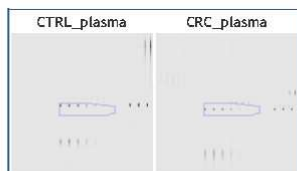
Charge 2

m/z 1129.0565

Retention Time 171.5

Notes

Score	Protein	Description
106.32	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p 05-Homo sapiens GN-HEL-5-62p PE-2 SV-1



Feature number 325

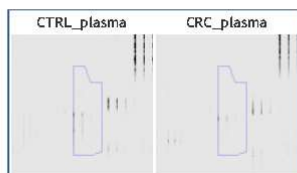
Charge 2

m/z 512.7605

Retention Time 67.8

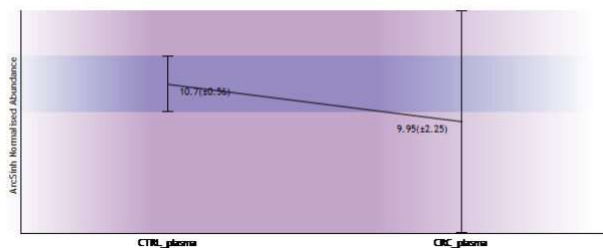
Notes

Score	Protein	Description
30.16	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p 05-Homo sapiens GN-HEL-5-62p PE-2 SV-1



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Feature number 387

Charge 3

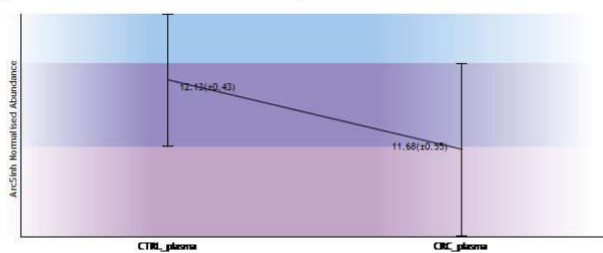
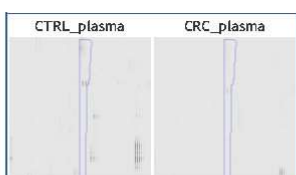
m/z 619.2901

Retention Time 44.5

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
43.04	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 SV-1



Feature number 640

Charge 2

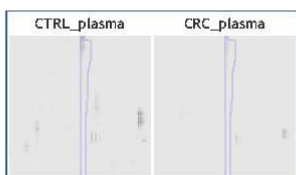
m/z 928.4312

Retention Time 44.5

Notes

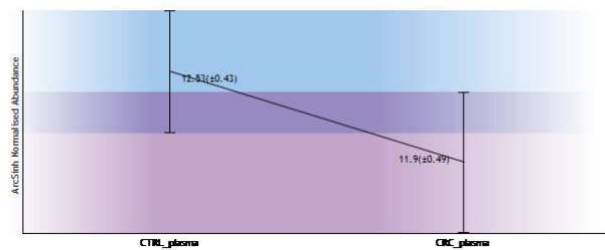
Anova p-value ≤ 0.08

Score	Protein	Description
51.36	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 SV-1



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Feature number 494

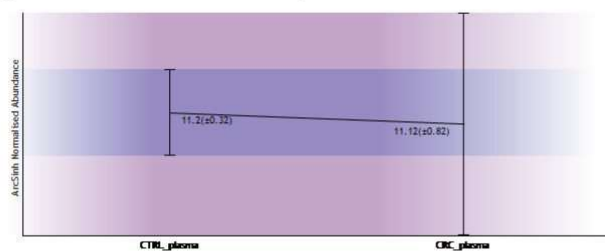
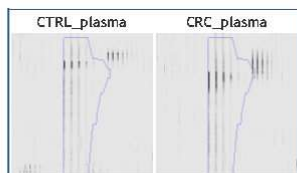
Charge 2

m/z 746.3848

Retention Time 71.9

Notes

Score	Protein	Description
47.16	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



Feature number 520

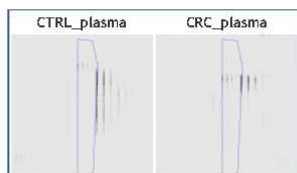
Charge 3

m/z 497.9259

Retention Time 71.9

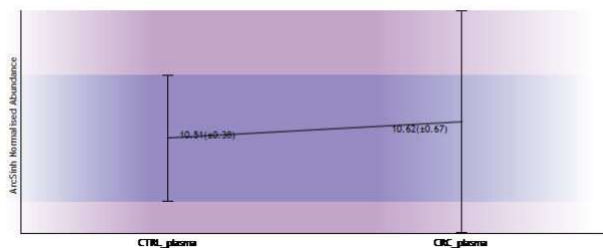
Notes

Score	Protein	Description
61.35	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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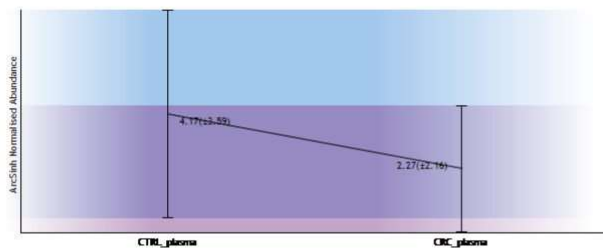
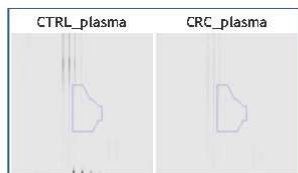
Feature number 500

Charge 2
m/z 619.8644

Retention Time 45.6

Notes

Score	Protein	Description
60.24	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



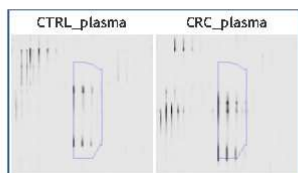
Feature number 544

Charge 2
m/z 542.2825

Retention Time 69.9

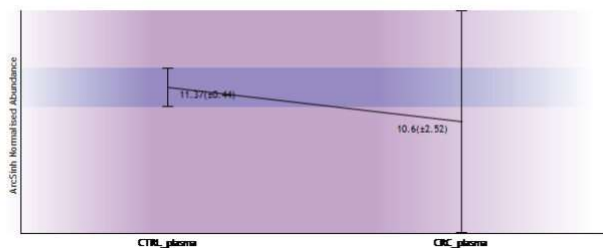
Notes

Score	Protein	Description
52.84	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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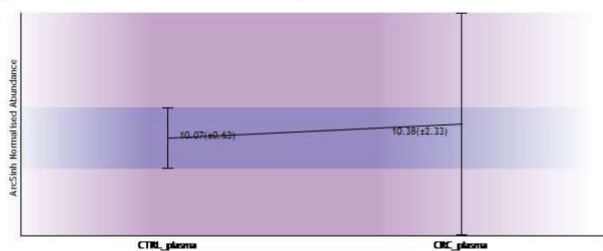
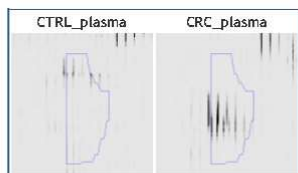
Feature number 717

Charge 3
m/z 552.9362

Retention Time 61.5

Notes

Score	Protein	Description
29.95	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



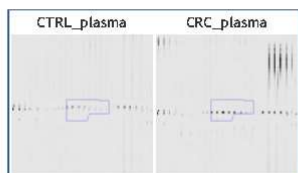
Feature number 1054

Charge 3
m/z 943.1834

Retention Time 171.0

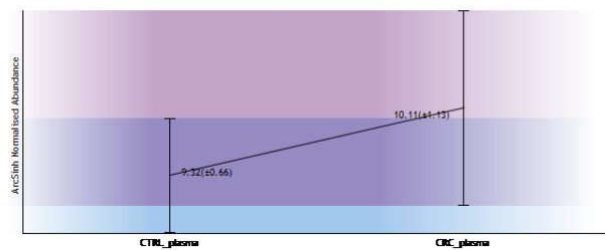
Notes

Score	Protein	Description
96.69	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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Feature number 1161

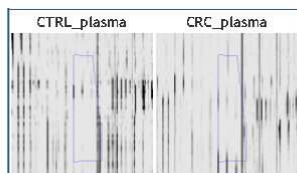
Charge 2

m/z 501.7771

Retention Time 48.0

Notes

Score	Protein	Description
48.74	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



Feature number 1301

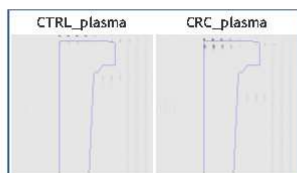
Charge 2

m/z 1076.1058

Retention Time 172.0

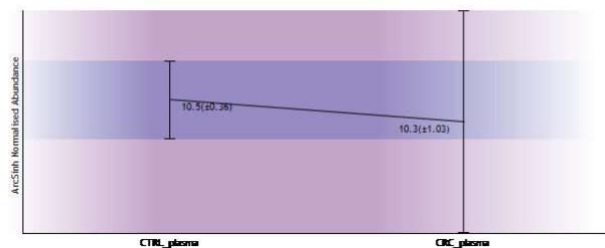
Notes

Score	Protein	Description
63.09	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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Feature number 3045

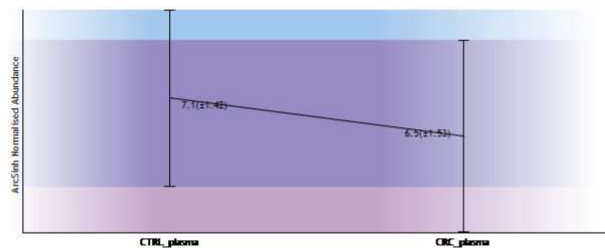
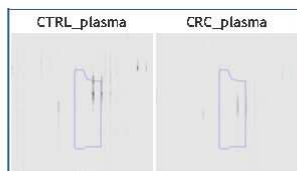
Charge 3

m/z 491.2535

Retention Time 47.7

Notes

Score	Protein	Description
66.70	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



Feature number 8383

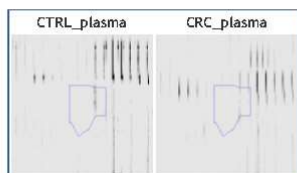
Charge 2

m/z 790.9083

Retention Time 47.4

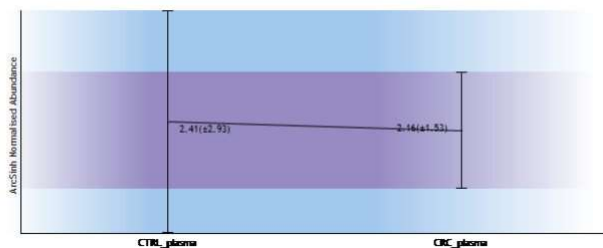
Notes

Score	Protein	Description
35.09	V9HWA9 V9HWA9_HUMAN	Epididymis secretory sperm binding protein Li 62p O5-Homo sapiens GN-HEL-5-62p PE-2 5V-1



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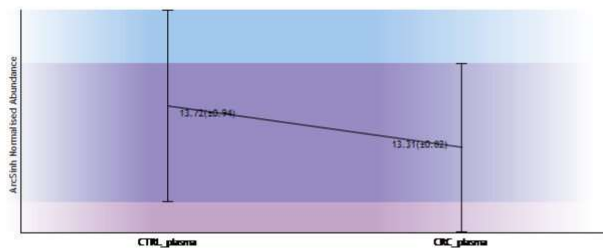
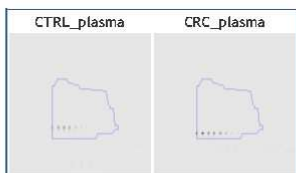
Feature number 3

Charge 3
m/z 1191.9624

Retention Time 170.6

Notes

Score	Protein	Description
109.93	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 fs, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



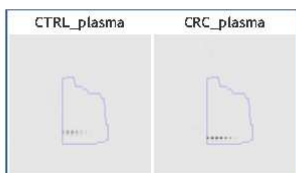
Feature number 19

Charge 4
m/z 894.2243

Retention Time 170.6

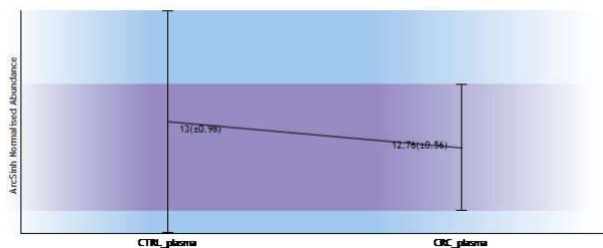
Notes

Score	Protein	Description
77.50	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 fs, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



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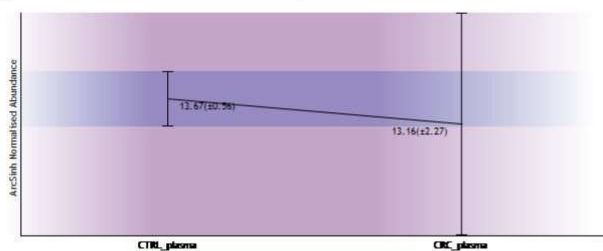
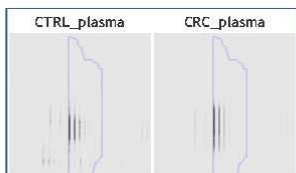
Feature number 10

Charge 2
m/z 688.3134

Retention Time 50.2

Notes

Score	Protein	Description
47.18	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



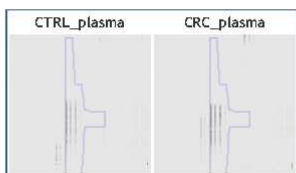
Feature number 21

Charge 2
m/z 607.3200

Retention Time 72.4

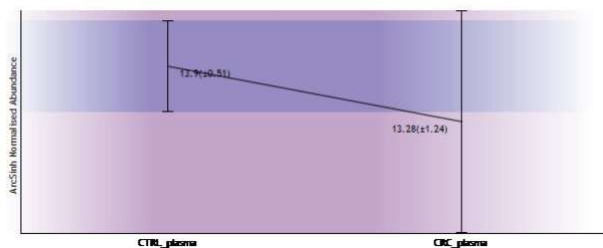
Notes

Score	Protein	Description
52.90	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



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Feature number 31

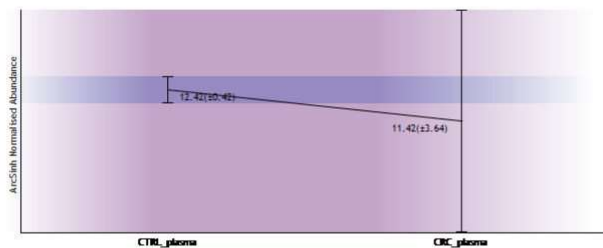
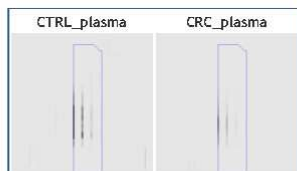
Charge 2

m/z 466.2765

Retention Time 52.8

Notes

Score	Protein	Description
71.02	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



Feature number 33

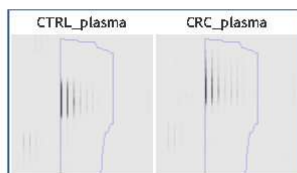
Charge 2

m/z 770.8674

Retention Time 95.2

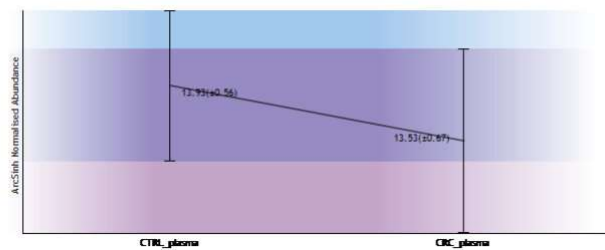
Notes

Score	Protein	Description
58.60	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



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Feature number 102

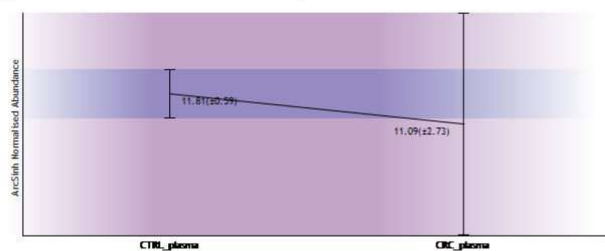
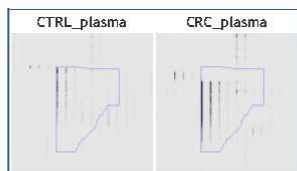
Charge 2

m/z 448.7347

Retention Time 70.2

Notes

Score	Protein	Description
47.60	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



Feature number 789

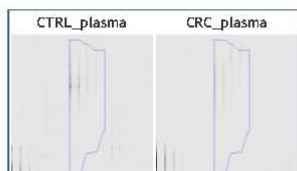
Charge 2

m/z 659.7906

Retention Time 50.2

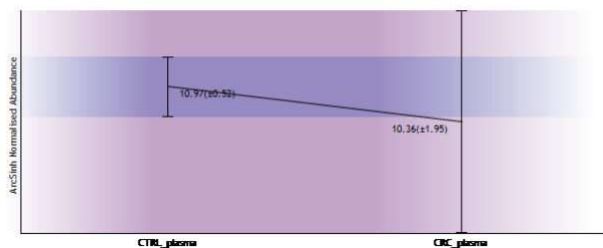
Notes

Score	Protein	Description
68.71	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1
67.36	Q0ZC16 Q0ZC16_HUMAN	Immunoglobulin heavy chain variable region (Fragment) OS-Homo sapiens PE-4 SV-1



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Feature number 2622

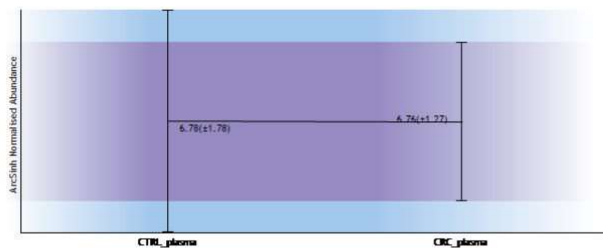
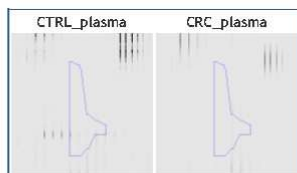
Charge 2

m/z 659.7907

Retention Time 49.0

Notes

Score	Protein	Description
77.83	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



Feature number 886

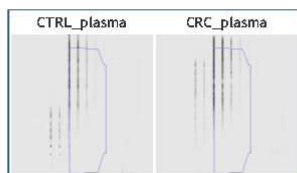
Charge 2

m/z 607.3367

Retention Time 73.3

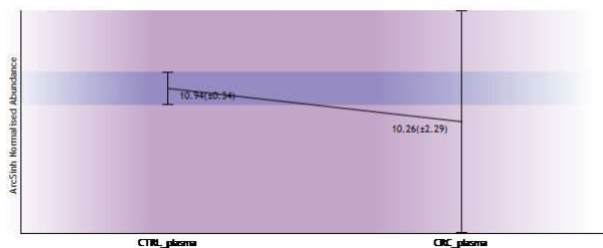
Notes

Score	Protein	Description
18.23	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



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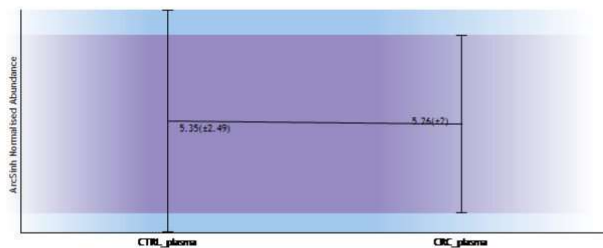
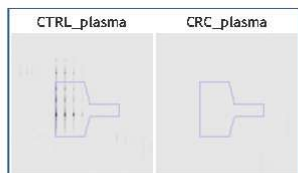
Feature number 1193

Charge 2
m/z 726.3672

Retention Time 58.9

Notes

Score	Protein	Description
30.62	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



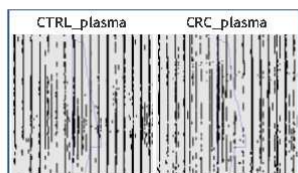
Feature number 6355

Charge 2
m/z 495.2563

Retention Time 45.0

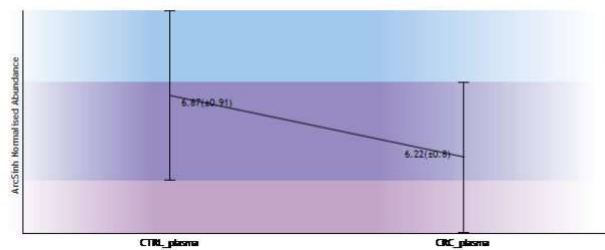
Notes

Score	Protein	Description
25.87	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



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Feature number 9085

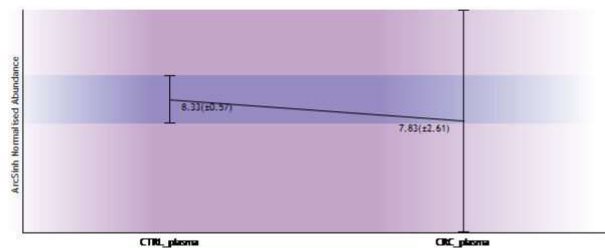
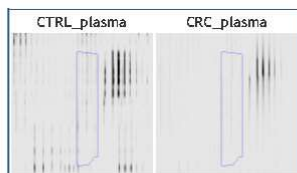
Charge 2

m/z 679.3090

Retention Time 50.2

Notes

Score	Protein	Description
51.96	Q8NCL6 Q8NCL6_HUMAN	cDNA FLJ90170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region OS-Homo sapiens PE-2 SV-1



Feature number 44

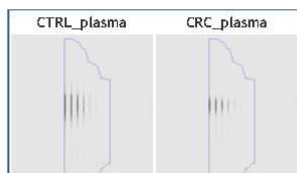
Charge 2

m/z 1068.4874

Retention Time 39.3

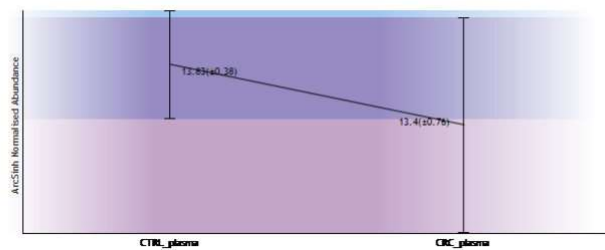
Notes

Score	Protein	Description
65.06	Q7Z3Y4 Q7Z3Y4_HUMAN	Uncharacterized protein OS-Homo sapiens PE-1 SV-1



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Feature number 485

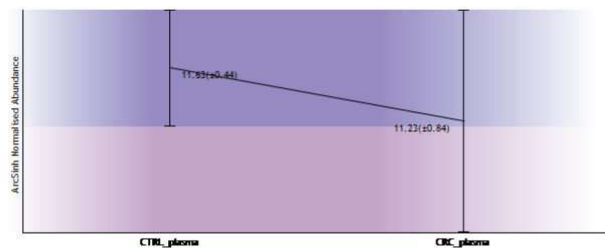
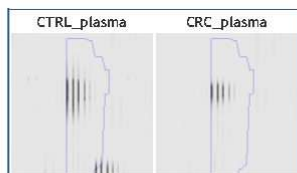
Charge 3

m/z 712.6612

Retention Time 39.3

Notes

Score	Protein	Description
16.67	Q7Z3Y4 Q7Z3Y4_HUMAN	Uncharacterized protein O5-Homo sapiens PE-1 SV-1



Feature number 62

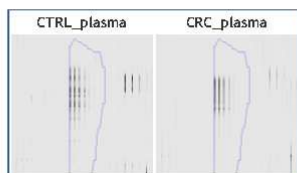
Charge 3

m/z 625.9805

Retention Time 57.3

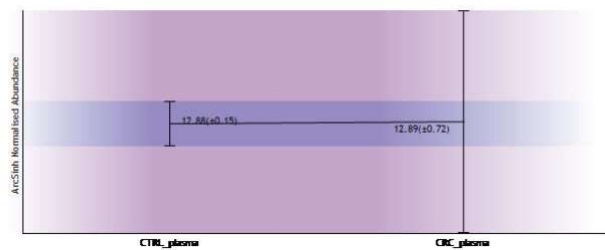
Notes

Score	Protein	Description
34.66	Q7Z3Y4 Q7Z3Y4_HUMAN	Uncharacterized protein O5-Homo sapiens PE-1 SV-1



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Feature number 29

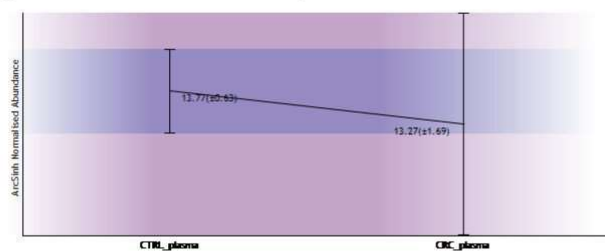
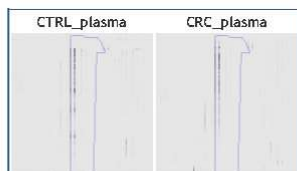
Charge 2

m/z 613.7755

Retention Time 59.6

Notes

Score	Protein	Description
52.22	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



Feature number 139

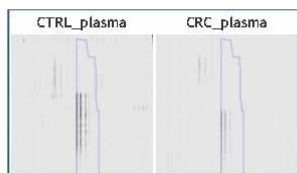
Charge 3

m/z 434.5543

Retention Time 54.0

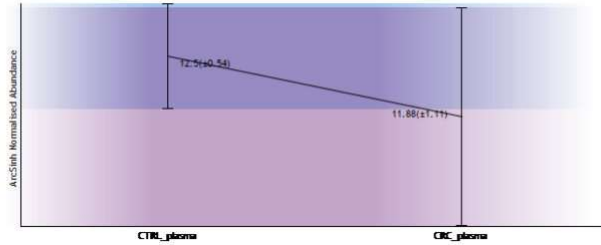
Notes

Score	Protein	Description
56.61	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



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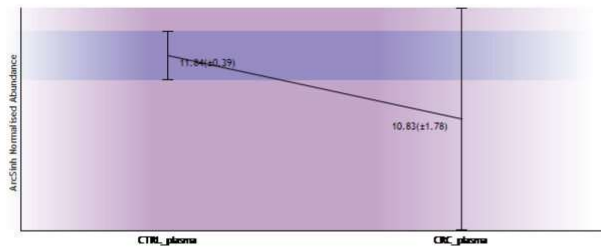
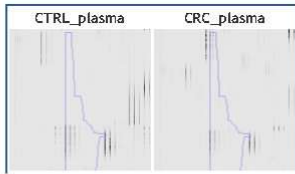
Feature number 215

Charge 2
m/z 524.2602

Retention Time 65.0

Notes

Score	Protein	Description
53.42	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



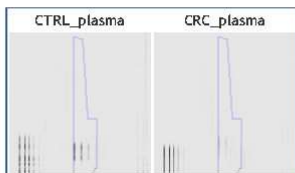
Feature number 359

Charge 2
m/z 629.8169

Retention Time 57.1

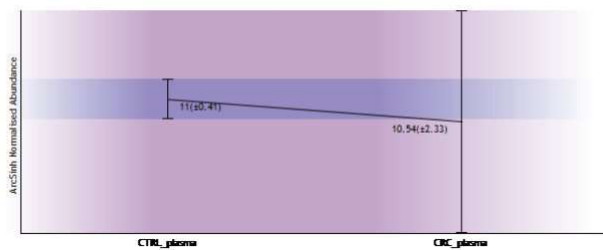
Notes

Score	Protein	Description
37.51	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



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Feature number 1456

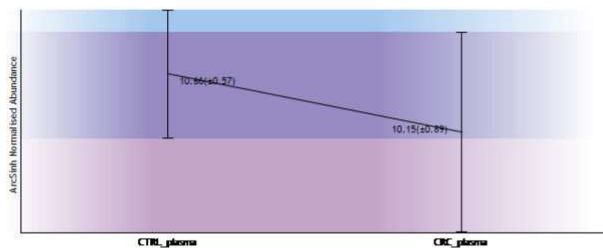
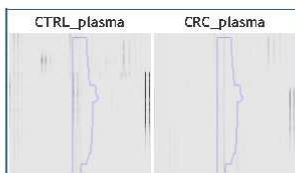
Charge 3

m/z 428.5509

Retention Time 54.0

Notes

Score	Protein	Description
45.84	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



Feature number 1742

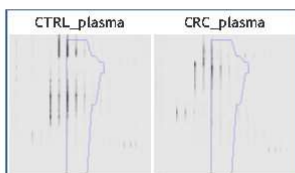
Charge 2

m/z 601.3121

Retention Time 64.8

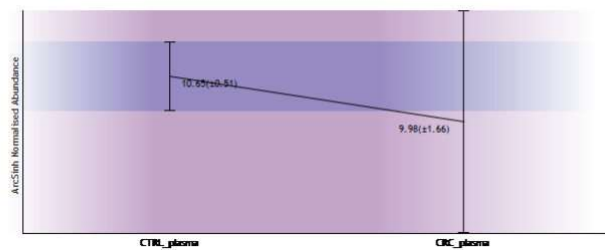
Notes

Score	Protein	Description
34.20	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



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Feature number 2811

Charge 3

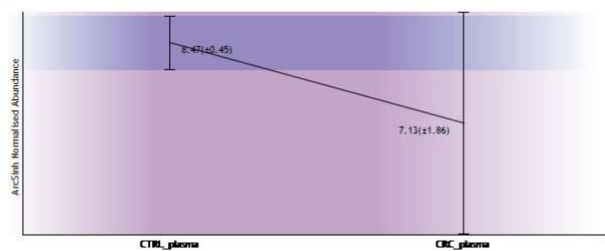
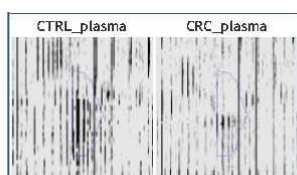
m/z 445.8869

Retention Time 41.9

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
23.48	P02647 APOA1_HUMAN	Apolipoprotein A-I OS-Homo sapiens GN-APOA1 PE-1 SV-1



Feature number 611

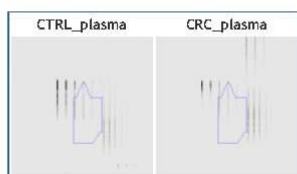
Charge 2

m/z 626.2994

Retention Time 89.3

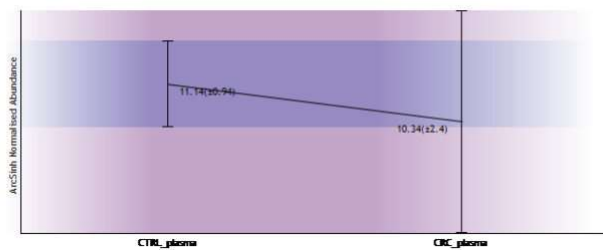
Notes

Score	Protein	Description
41.30	B4DPP8 B4DPP8_HUMAN	cDNA FLJ53075, highly similar to Kininogen-1 OS-Homo sapiens PE-2 SV-1



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Feature number 850

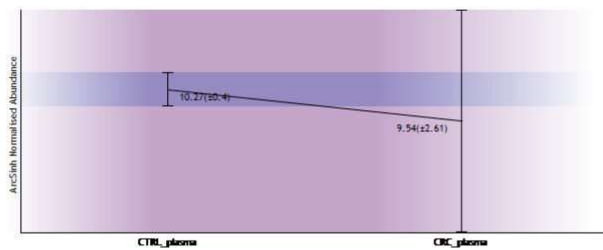
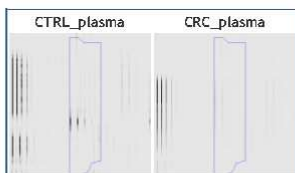
Charge 2

m/z 579.3170

Retention Time 49.0

Notes

Score	Protein	Description
64.95	F8WAS2 F8WAS2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1 OS-Homo sapiens GN-ITIH1 PE-1 SV-1



Feature number 848

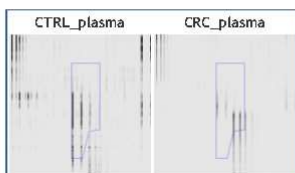
Charge 2

m/z 514.2928

Retention Time 53.4

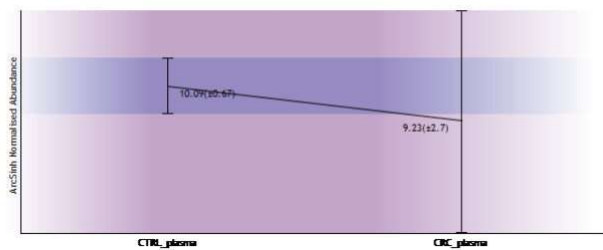
Notes

Score	Protein	Description
53.60	Q5T985 Q5T985_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 OS-Homo sapiens GN-ITIH2 PE-1 SV-1



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Feature number 2143

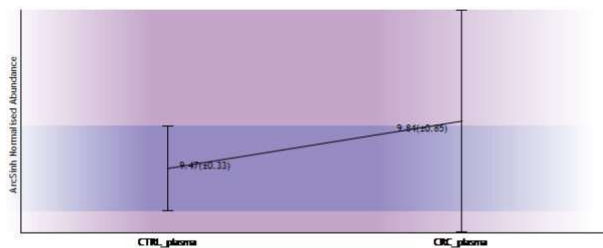
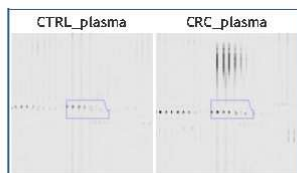
Charge 3

m/z 946.1373

Retention Time 170.9

Notes

Score	Protein	Description
47.02	Q5T985 Q5T985_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 OS-Homo sapiens GN-ITIH2 PE-1 SV-1



Feature number 2515

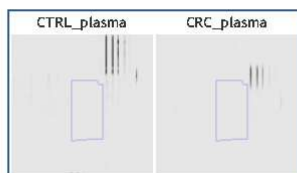
Charge 3

m/z 510.5830

Retention Time 47.7

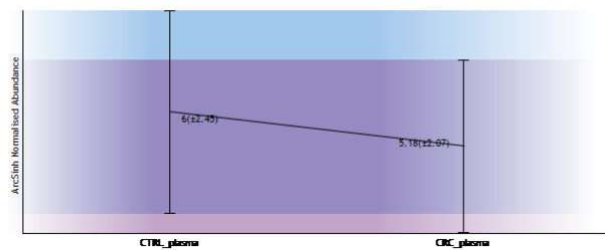
Notes

Score	Protein	Description
39.68	D1MGQ2 D1MGQ2_HUMAN	Alpha-2 globin chain OS-Homo sapiens GN-HBA2 PE-3 SV-1



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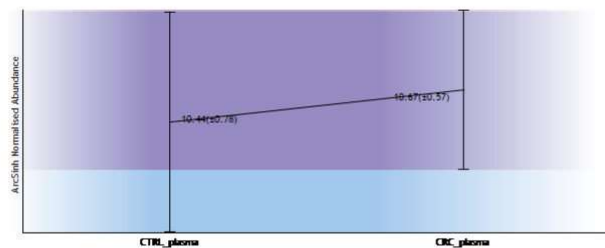
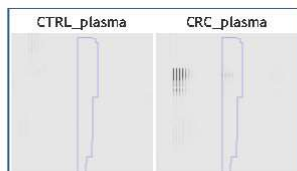
Feature number 3219

Charge 4
m/z 698.0940

Retention Time 156.5

Notes

Score	Protein	Description
16.13	P02787 TRFE_HUMAN	Serotransferrin OS=Homo sapiens GN=TF PE-1 SV-3



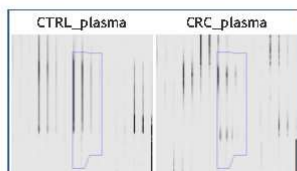
Feature number 869

Charge 2
m/z 572.8140

Retention Time 63.1

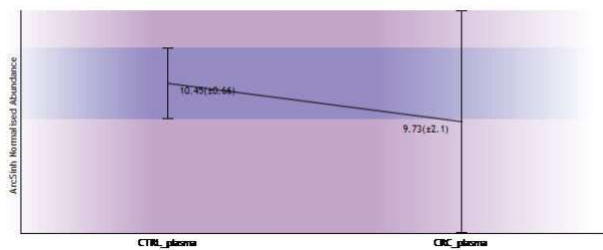
Notes

Score	Protein	Description
73.95	Q68DH2 Q68DH2_HUMAN	Uncharacterized protein DKFZp686G21125 (Fragment) OS=Homo sapiens GN=DKFZp686G21125 PE-2 SV-1
56.81	B7ZKJB B7ZKJB_HUMAN	ITIH4 protein OS=Homo sapiens GN=ITIH4 PE-1 SV-1



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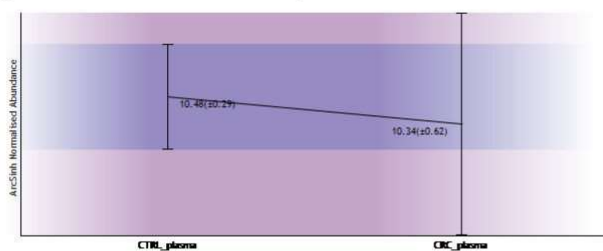
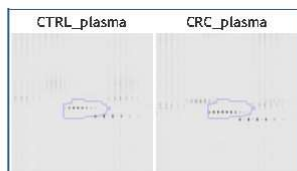
Feature number 1730

Charge 4
m/z 1300.3805

Retention Time 171.1

Notes

Score	Protein	Description
67.52	Q68DH2 Q68DH2_HUMAN	Uncharacterized protein DKFZp686G21125 (Fragment) OS=Homo sapiens GN=DKFZp686G21125 PE=2 SV=1



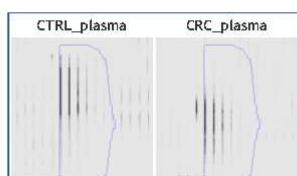
Feature number 757

Charge 2
m/z 829.3857

Retention Time 62.1

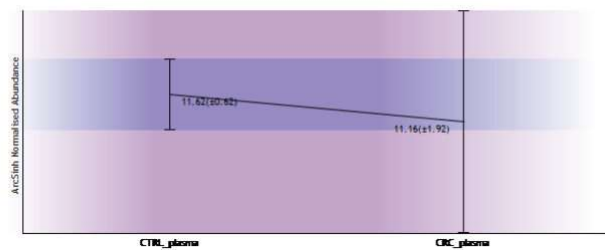
Notes

Score	Protein	Description
27.61	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



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Feature number 1998

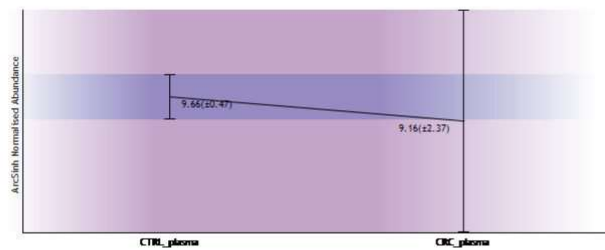
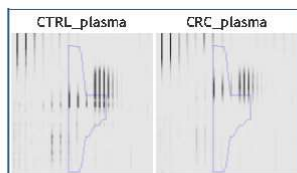
Charge 2

m/z 646.8029

Retention Time 41.4

Notes

Score	Protein	Description
68.84	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



Feature number 3673

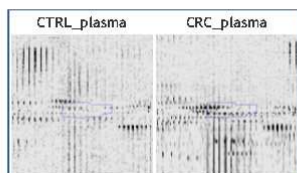
Charge 3

m/z 1282.2245

Retention Time 170.8

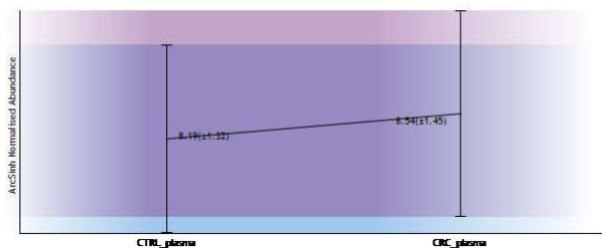
Notes

Score	Protein	Description
21.34	P00739 HPTR_HUMAN	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2



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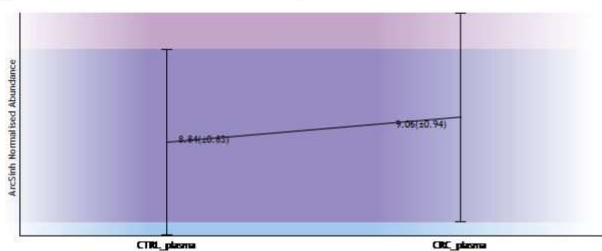
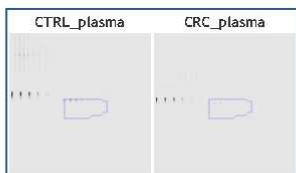
Feature number 2026

Charge 3
m/z 822.4637

Retention Time 171.7

Notes

Score	Protein	Description
26.87	B0ZBEZ B0ZBEZ_HUMAN	Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS-Homo sapiens GN-AGT PE-2 SV-1



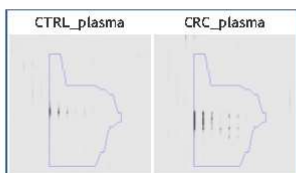
Feature number 11

Charge 2
m/z 490.7511

Retention Time 69.3

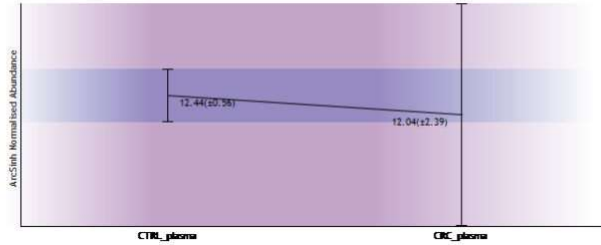
Notes

Score	Protein	Description
61.44	ADA0C4DGL8 ADA0C4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



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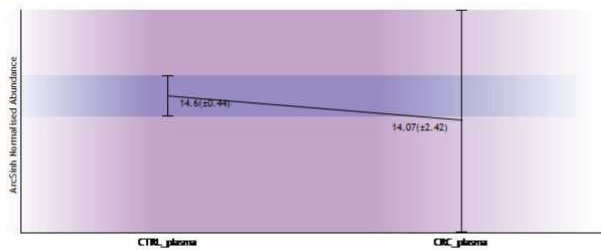
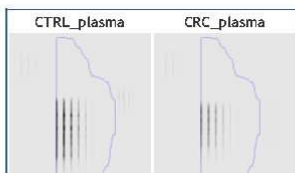


Feature number 12

Charge 2
m/z 854.4131

Retention Time 94.7
Notes

Score	Protein	Description
59.84	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1
47.54	Q6PEJ8 Q6PEJ8_HUMAN	HP protein OS-Homo sapiens GN-HP PE-2 SV-1

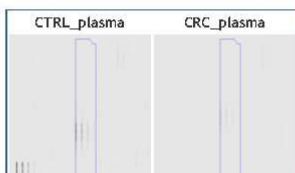


Feature number 92

Charge 2
m/z 656.3064

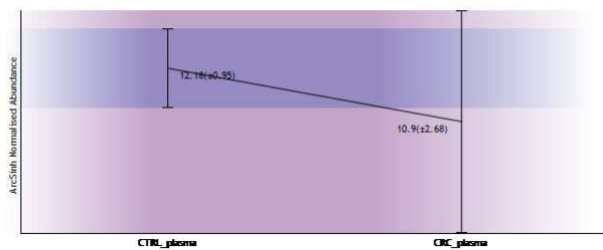
Retention Time 51.8
Notes

Score	Protein	Description
59.03	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



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Feature number 128

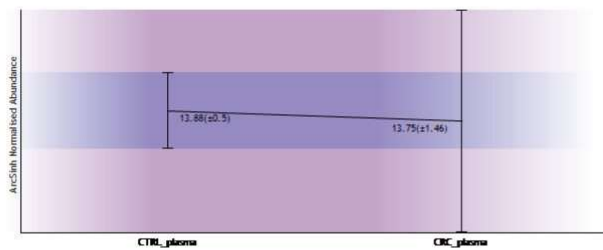
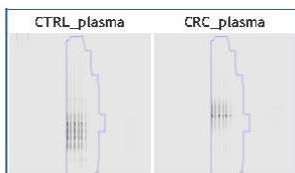
Charge 3

m/z 1117.1843

Retention Time 78.6

Notes

Score	Protein	Description
32.35	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



Feature number 237

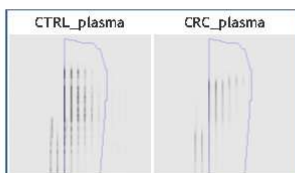
Charge 2

m/z 929.4628

Retention Time 42.1

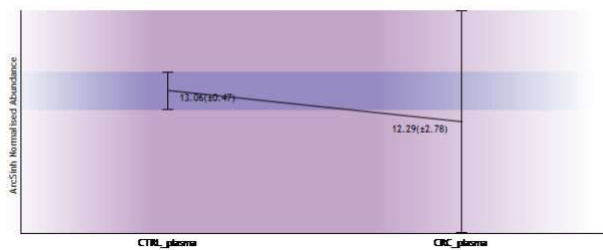
Notes

Score	Protein	Description
48.75	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



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Feature number 724

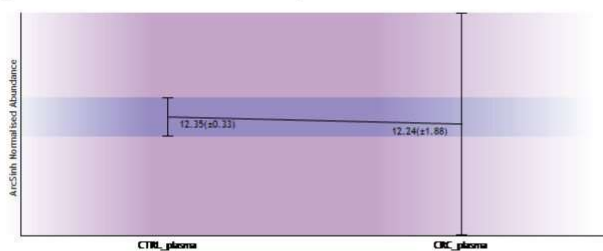
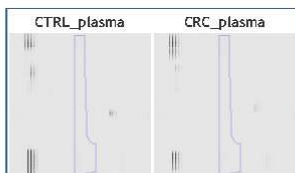
Charge 2

m/z 862.4093

Retention Time 94.4

Notes

Score	Protein	Description
59.60	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



Feature number 1935

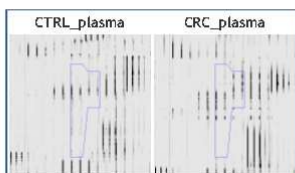
Charge 2

m/z 506.7451

Retention Time 69.3

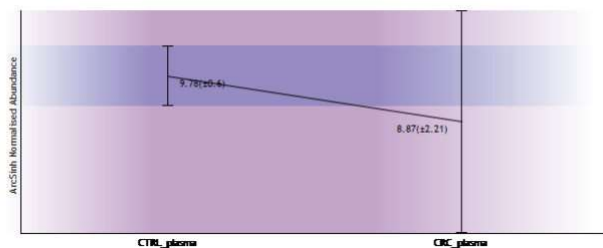
Notes

Score	Protein	Description
22.42	ADAOC4DGL8 ADAOC4DGL8_HUMAN	Haptoglobin OS-Homo sapiens GN-HP PE-1 SV-1



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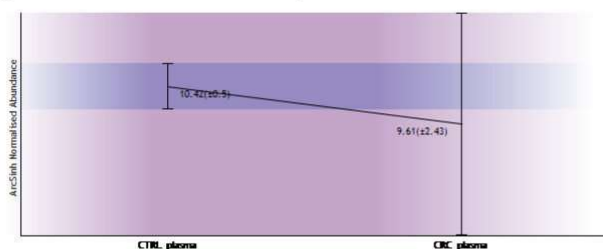
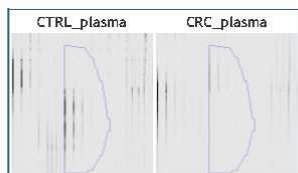
Feature number 1090

Charge 2
m/z 566.7744

Retention Time 55.4

Notes

Score	Protein	Description
56.05	A0A096LPE2 A0A096LPE2_HUMAN	SAA2-SAA4 readthrough OS-Homo sapiens GN-SAA2-SAA4 PE-4 SV-1



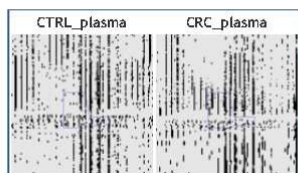
Feature number 1284

Charge 2
m/z 775.8676

Retention Time 171.1

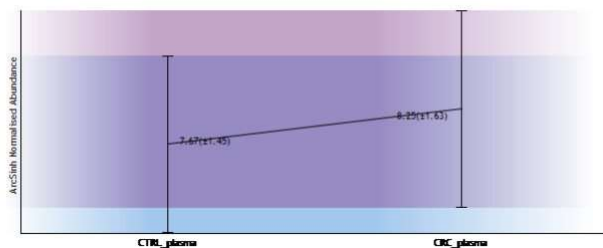
Notes

Score	Protein	Description
67.25	A0A096LPE2 A0A096LPE2_HUMAN	SAA2-SAA4 readthrough OS-Homo sapiens GN-SAA2-SAA4 PE-4 SV-1



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Feature number 997

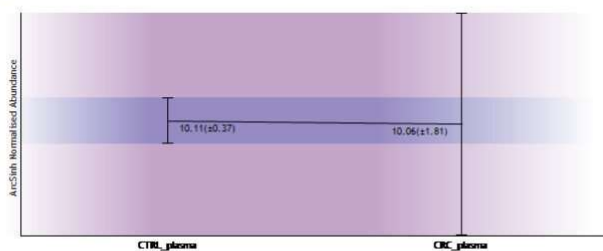
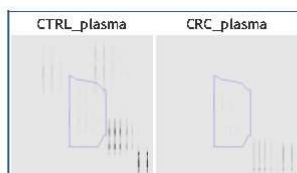
Charge 2

m/z 753.3939

Retention Time 56.7

Notes

Score	Protein	Description
68.54	E1A689 E1A689_HUMAN	Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1
46.26	C0JYY2 C0JYY2_HUMAN	Apolipoprotein B (Including Ag(X) antigen) OS-Homo sapiens GN-APQB PE-4 SV-1



Feature number 2035

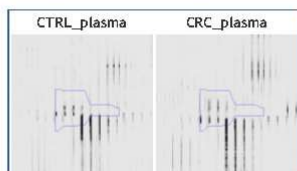
Charge 2

m/z 801.4292

Retention Time 91.2

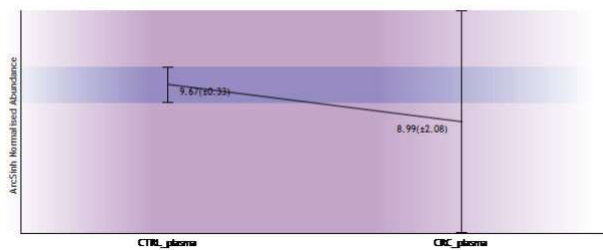
Notes

Score	Protein	Description
18.94	E1A689 E1A689_HUMAN	Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1



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Feature number 2858

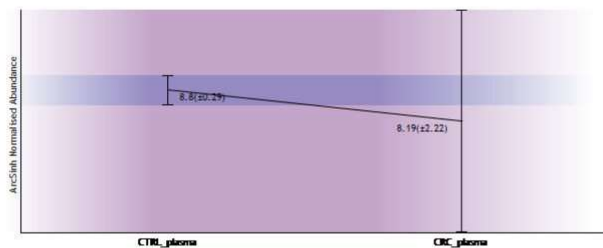
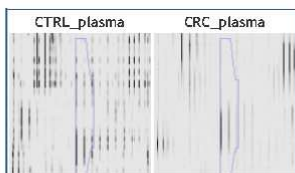
Charge 2

m/z 487.2508

Retention Time 52.8

Notes

Score	Protein	Description
39.05	E1A689 E1A689_HUMAN	Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1



Feature number 3588

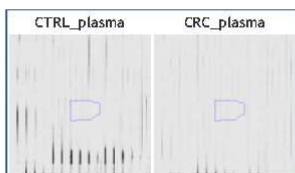
Charge 2

m/z 665.3779

Retention Time 45.1

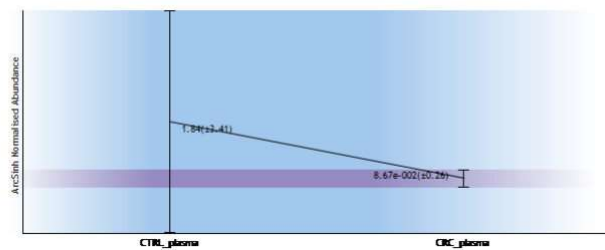
Notes

Score	Protein	Description
19.91	E1A689 E1A689_HUMAN	Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1



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Feature number 7396

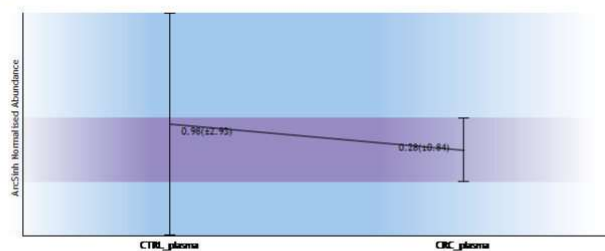
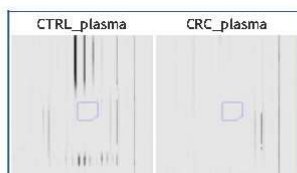
Charge 3

m/z 443.9213

Retention Time 45.1

Notes

Score	Protein	Description
41.79	E1A689 E1A689_HUMAN	Mutant Apo B 100 OS-Homo sapiens PE-2 SV-1
37.87	C0JYY2 C0JYY2_HUMAN	Apolipoprotein B (Including Ag(X) antigen) OS-Homo sapiens GN-APQB PE-4 SV-1



Feature number 17

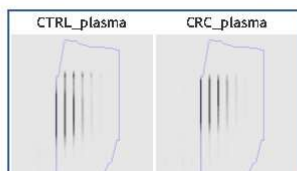
Charge 2

m/z 917.4647

Retention Time 92.5

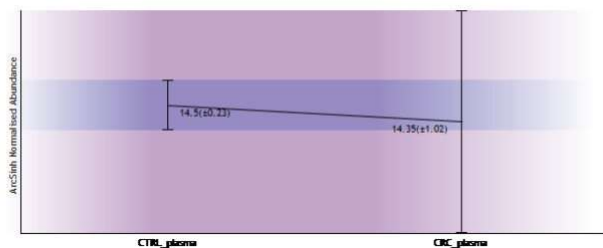
Notes

Score	Protein	Description
49.69	A0A0G2JRN3 A0A0G2JRN3_HUMAN	Alpha-1-antitrypsin OS-Homo sapiens GN-SERPINA1 PE-1 SV-1



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Feature number 103

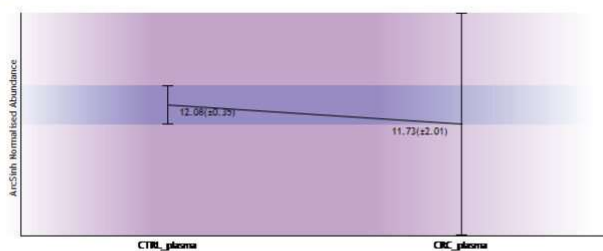
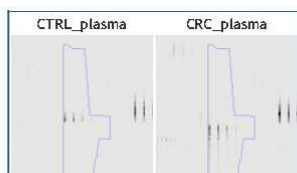
Charge 2

m/z 624.3049

Retention Time 69.1

Notes

Score	Protein	Description
42.18	A0A0G2JRN3 A0A0G2JRN3_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1
39.38	A0A0Z4R6I7 A0A0Z4R6I7_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1



Feature number 701

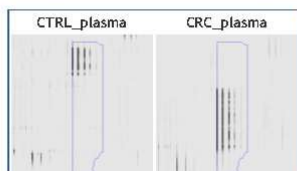
Charge 3

m/z 468.5728

Retention Time 57.5

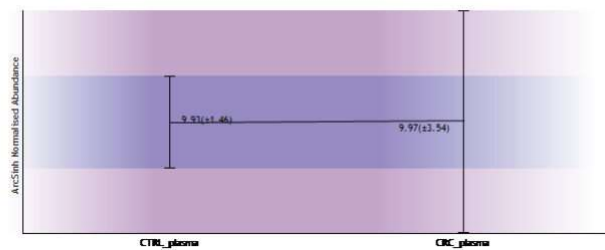
Notes

Score	Protein	Description
41.48	A0A0G2JRN3 A0A0G2JRN3_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1



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Feature number 968

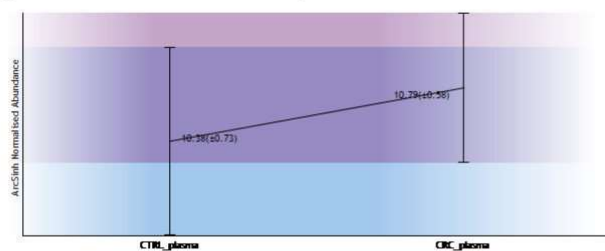
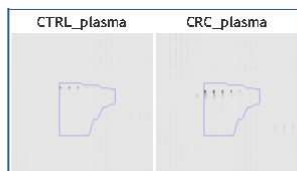
Charge 2

m/z 1045.5511

Retention Time 172.1

Notes

Score	Protein	Description
46.58	ADA0G2.JRN3 ADA0G2.JRN3_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1



Feature number 1344

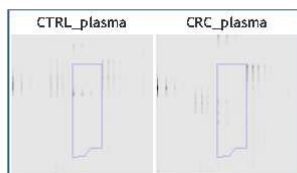
Charge 2

m/z 632.3021

Retention Time 69.1

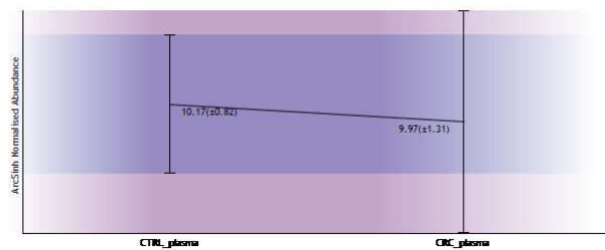
Notes

Score	Protein	Description
37.73	ADA0G2.JRN3 ADA0G2.JRN3_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=1



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Feature number 6155

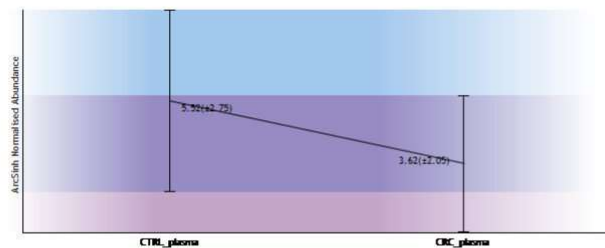
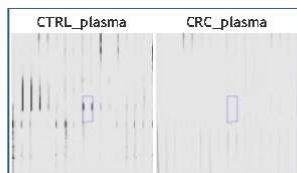
Charge 2

m/z 688.3518

Retention Time 53.2

Notes

Score	Protein	Description
21.79	A0A0G2JRN3 A0A0G2JRN3_HUMAN	Alpha-1-antitrypsin OS-Homo sapiens GN-SERPINA1 PE-1 SV-1



Feature number 171

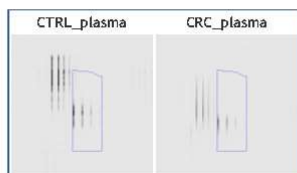
Charge 2

m/z 547.8193

Retention Time 42.8

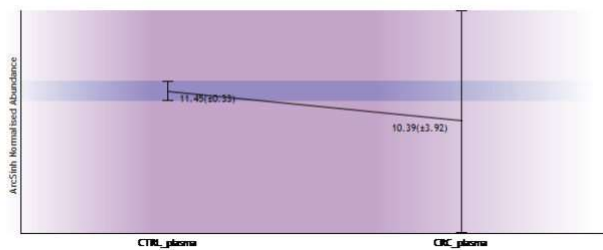
Notes

Score	Protein	Description
60.63	G3V3A0 G3V3A0_HUMAN	Alpha-1-antichymotrypsin OS-Homo sapiens GN-SERPINA3 PE-1 SV-1



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Feature number 1775

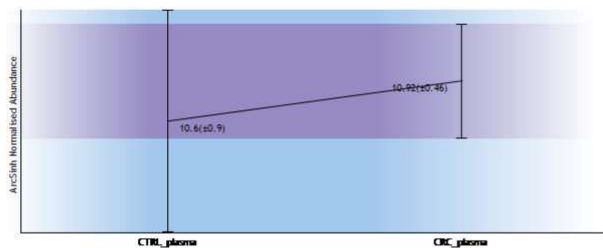
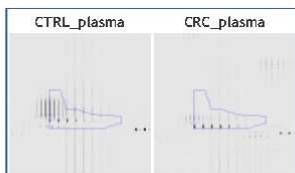
Charge 2

m/z 1330.1916

Retention Time 170.6

Notes

Score	Protein	Description
21.04	G3V3A0 G3V3A0_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA3 PE=1 SV=1



Feature number 1025

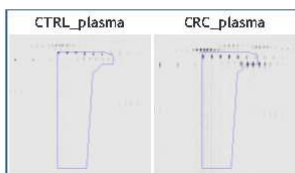
Charge 2

m/z 1106.0788

Retention Time 171.6

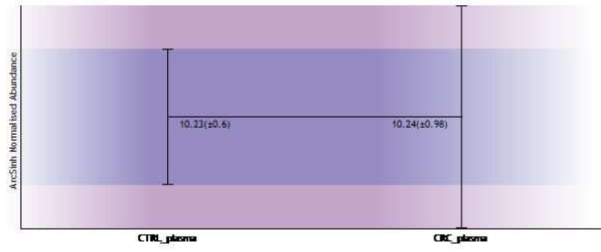
Notes

Score	Protein	Description
83.45	S6B2B0 S6B2B0_HUMAN	IgG L chain OS=Homo sapiens PE=2 SV=1



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8.6. ANEXO VI. Relatório do Progenesis do terceiro modelo de análise

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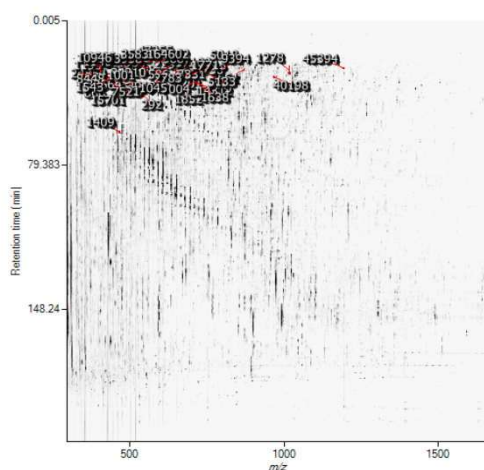
biomarker_CCR_urina_dez2018

biomarker_CCR_urina_dez2018

Experiment: biomarker_CCR_urina_dez2018

Report created: 12/15/2018 4:14:07 PM

Overview image



Data Processing Methods

Peak processing method Profile data

Feature detection method High resolution

Experiment Design

Condition	CTRL_urine	CRC_urine
Replicates	9	9

Proteins

Protein building options

Protein grouping Group similar proteins

Protein quantitation Using only features with no protein conflicts

Accession	Peptides	Score	Anova (p) [†]	Fold	Tags	Description	Average Normalised Abundances	
							CTRL_urine	CRC_urine
A0A05Z73H5 A0A05Z73H5 HUMAN	7	402.36	0.03	6.81	●	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1	6.60e+004	9694.46
P05090 AFOD HUMAN	5	293.01	0.04	7.34	●	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	1.05e+005	1.43e+004
P07911 UROM HUMAN	6	259.60	0.03	4.34	●	Uromodulin OS=Homo sapiens GN=UROM PE=1 SV=1	2.75e+005	6.33e+004
Q7LCS3 Q7LCS3 HUMAN	6	238.66	0.06	6.18	●	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CLUBN PE=4 SV=1	9.18e+004	1.49e+004
P01133 EGF HUMAN	3	196.42	0.07	14.81	●	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2	2350.68	158.69
Q05CF8 Q05CF8 HUMAN	5	180.22	0.02	10.60	●	KNG1 protein OS=Homo sapiens GN=KNG1 PE=2 SV=1	1.63e+004	1535.96

file://C:/Users/bruno/Documents/Bruno/Mestrado/Colorectal proteomic/Tese/Estadística/CTRLxCRC_urine.htm

1/35

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Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances	
							CTRL_urine	CRC_urine
H0YLE3 H0YLE3_HUMAN	1	133.46	0.05	2.62		Beta-2-microglobulin (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1	2.03e+004	5.33e+004
B4DWHO B4DWHO_HUMAN	3	131.51	0.05	10.71		cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens PE=2 SV=1	2680.12	250.26
Q6NSB3 Q6NSB3_HUMAN	3	105.90	7.47e-003	37.68		Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1	8774.93	232.90
C9JMK5 C9JMK5_HUMAN	1	67.16	0.01	6.57		Phosphoinositide-3-kinase-interacting protein 1 (Fragment) OS=Homo sapiens GN=PIK3IP1 PE=1 SV=8	2.51e+004	3814.07
Q9NPP6 Q9NPP6_HUMAN	1	55.14	0.06	5.72		Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1	1671.74	292.37
C0JYZZ C0JYZZ_HUMAN	1	31.57	0.05	2.71		Titin OS=Homo sapiens GN=TTN PE=4 SV=1	1089.29	402.62
Q9HAU0 PKHA5_HUMAN	1	31.42	0.05	5.78		Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens GN=PLEKHA5 PE=1 SV=1	832.50	144.00

Tags	
	Anova p-value ≤ 0.05
	Anova p-value ≤ 0.08

AOA0S2Z3H5 | AOA0S2Z3H5_HUMAN

Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1
7 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
ATGDRGEAGAAGPAGPAGPR	2783	54.60	1	1734.8409	3		0		yes	7470.55	1244.11
ATGDRGEAGAAGPAGPAGPR	4461	70.97	1	1734.8382	2		0		yes	6627.01	821.43
GESGNKGEFGSAGPQPPGSGEEGK	45394	57.44	1	2379.0542	2		0	[9] P+15.99	yes	692.00	89.78
GHHGDQGAFGSVGPAGPR	12997	41.75	1	1668.7719	3		0	[9] P+15.99	yes	999.82	49.20
HHGDQGAFGSVGPAGPR	35830	32.98	1	1611.7501	3		0	[8] P+15.99	yes	354.60	78.83
NGEAGSAGPPGPPGLR	1638	34.32	1	1464.6952	2		0	[12] P+31.99	yes	4.27e+004	6826.99
SKGESGNKGEFGSAGPQPPGSGEEGK	5018	66.14	1	2594.1841	3		0	[11] P+15.99	yes	6756.36	535.83
TGDRGEAGAAGPAGPAGPR	43958	44.16	1	1663.8035	3		0		yes	401.09	48.28

Tags	
	Anova p-value ≤ 0.08

P05090 | APOD_HUMAN

Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
5 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
KMTVTDQVNC ^R PK	7004	50.48	1	1419.6846	2		0	[10] C(+57.02)	yes	1.37e+004	2247.65
KMTVTDQVNC ^R PK	14312	47.07	1	1435.6799	2		0	[2] M(+15.99) [10] C(+57.02)	yes	1479.68	135.87

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Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
KMTVTDQVNC PK	4895	32.73	1	1435.6801	3		0	M(+15.99) [2] C(+57.02) [10]	yes	2262.93	97.91
MTVTDQVNC PK	1852	32.38	1	1291.5904	2	<input checked="" type="checkbox"/>	0	[11] K+57.02	yes	4.00e+004	9067.12
MTVTDQVNC PK	3331	84.06	1	1307.5850	2		0	M(+15.99) [1] C(+57.02) [9]	yes	5195.23	709.71
VLNQELR	866	46.29	2	870.4929	2	<input checked="" type="checkbox"/>	0		yes	4.22e+004	2013.30

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

P07911 | UROM_HUMAN

Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1
6 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
C KPTCSGTRF	566	32.76	1	1212.5378	2		0	[1] C(+57.02) [5] C(+57.02)	yes	4.14e+004	3071.77
C KPTCSGTRF	1140	33.09	1	1212.5377	3		0	[1] C(+57.02) [5] C(+57.02)	yes	9030.11	184.53
C VCPAGYR	33564	27.94	1	981.4164	2		0	[1] C(+57.02) [3] C(+57.02)	yes	204.84	205.65
DGP C GTVLTR	292	48.21	1	1074.5126	2	<input checked="" type="checkbox"/>	0	[4] C(+57.02)	yes	2.16e+005	5.81e+004
FSVQ M FR	1409	36.24	1	929.4425	2		0	[5] M(+15.99)	yes	3006.11	1727.80
LE C GAND M K	47255	45.48	1	1052.4271	2		0	[3] C(+57.02) [8] M(+15.99)	yes	76.42	2.01
WH C Q C K	1001	35.88	1	960.3697	2		0	[1] W+43.01 [3] C(+57.02) [5] C(+57.02)	yes	4837.02	6.72

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

Q7LC53 | Q7LC53_HUMAN

Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1
6 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
FHADYAR	24854	30.04	1	878.4035	2		0		yes	439.73	20.09
GSPESPIIQY C GN S NP R	1278	29.42	1	2025.8661	2		0	[12] C(+57.02) [15] S+79.97 [18] R+14.02	yes	8.93e+004	1.42e+004
IAQL C TQR	29132	46.94	1	988.5123	2		0	[5] C(+57.02)	yes	163.64	51.62
S C GGYLHADR	121984	62.66	1	1134.4877	2		0	[2] C(+57.02)	yes	404.26	180.22
SSSTENHGFM A K	37103	29.98	1	1294.5615	2		0		yes	493.13	287.49
YSIAQ C GGR	24210	39.62	1	1010.4608	2		0	[6] C(+57.02)	yes	1003.35	121.57

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

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P01133 | EGF_HUMAN

Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2
3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
CHQLVSCPR	22971	43.63	1	1155.5292	2		0	[1] C(+57.02) [7] C(+57.02)	yes	846.97	91.63
GIAVHPMAK	27832	39.63	1	922.5058	2		0		yes	225.64	12.71
VVHPLAQPK	7408	63.73	1	987.5868	2		0		yes	852.09	53.44
VVHPLAQPK	8448	49.43	1	987.5865	3		0		yes	425.99	0.92

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

Q05CF8 | Q05CF8_HUMAN

KNG1 protein OS=Homo sapiens GN=KNG1 PE=2 SV=1
5 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
ETTCSKESNEELTESCETK	5133	55.59	1	2260.9328	3	<input checked="" type="checkbox"/>	0	[4] C(+57.02) [16] C(+57.02)	yes	3117.04	38.10
ETTCSKESNEELTESCETKK	9394	34.22	1	2389.0265	3	<input checked="" type="checkbox"/>	0	[4] C(+57.02) [16] C(+57.02)	yes	4182.84	277.97
GEIKEETTSHLR	17715	29.02	1	1398.7098	2		0		yes	1979.55	3.52
GRPPKAGAEPASEREVS	64602	30.91	1	1736.8807	3		0		yes	182.49	2.44
ICVGCPR	1543	30.48	1	860.3997	2		0	[2] C(+57.02) [5] C(+57.02)	yes	6817.84	1213.93

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

HOYLF3 | HOYLF3_HUMAN

Beta-2-microglobulin (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
VNHVTLSPK	1190	57.12	1	1121.6191	3		0		yes	2932.77	1.08e+004
VNHVTLSPK	586	76.34	1	1121.6194	2	<input checked="" type="checkbox"/>	0		yes	1.74e+004	4.24e+004

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

B4DWHO | B4DWHO_HUMAN

cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellularmatrix protein 1 OS=Homo sapiens PE=2 SV=1

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3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
C V C PPVSN A M C R	10201	51.14	1	1368.5408	2		0	[1] C(+57.02) [3] C(+57.02) [9] M(+15.99) [10] C(+57.02)	yes	1677.02	144.29
DPQRIPSNPSHR	63585	30.48	1	1402.7066	3		0		yes	70.11	1.98
T C QDINE C ETTNE C R	40198	49.89	1	1928.7308	2		0	[2] C(+57.02) [8] C(+57.02) [14] C(+57.02)	yes	932.99	103.99

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

Q6NSB3|Q6NSB3_HUMAN

Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1

3 peptides

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
LGTVIRK	10946	33.07	1	785.5123	2		0		yes	275.71	0.00
SSDYFGNGR	15701	42.35	1	1001.4207	2	<input checked="" type="checkbox"/>	0		yes	4306.17	195.83
YQPVS Y K	7521	30.48	1	883.4437	2	<input checked="" type="checkbox"/>	0		yes	4193.05	37.07

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

C9JMK5|C9JMK5_HUMAN

Phosphoinositide-3-kinase-interacting protein 1 (Fragment) OS=Homo sapiens GN=PIK3IP1 PE=1 SV=8

1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
EDQTS P APGLR	1045	67.16	1	1169.5678	2	<input checked="" type="checkbox"/>	0		yes	2.51e+004	3814.07

Tags	
<input checked="" type="checkbox"/>	Anova p-value ≤ 0.08

Q9NPP6|Q9NPP6_HUMAN

Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1

1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
GTTVTVSSASPTSPK	15514	55.14	1	1418.7246	2	<input checked="" type="checkbox"/>	0		yes	1671.74	292.37

Tags	
<input type="checkbox"/>	Anova p-value ≤ 0.08

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 Anova p-value \leq 0.08

C0JYZ2 | C0JYZ2_HUMAN

Titin OS=Homo sapiens GN=TTN PE=4 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
WDVPENDGGAPVK	28730	31.57	1	1382.6441	2	<input checked="" type="checkbox"/>	0		yes	1089.29	402.62

Tags
 Anova p-value \leq 0.08

Q9HAU0 | PKHA5_HUMAN

Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens GN=PLEKHA5 PE=1 SV=1
1 peptide

Sequence	Feature	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances	
										CTRL_urine	CRC_urine
SEVSSPIQR	27857	31.42	1	1001.5144	2	<input checked="" type="checkbox"/>	0		yes	832.50	144.00

Tags
 Anova p-value \leq 0.08

Accession Q6NSB3 | Q6NSB3_HUMAN (+1)

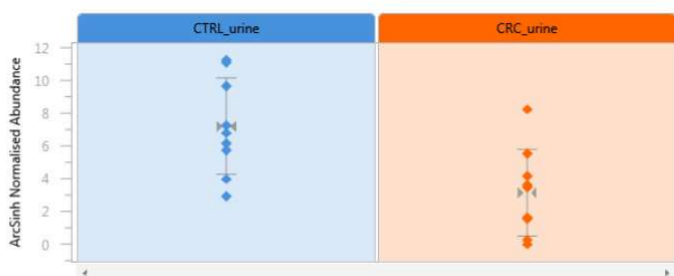
Description Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1

Peptides 3

Score 105.90

Anova 7.47e-003

Fold 37.68

 Anova p-value \leq 0.08


Accession C9JMK5 | C9JMK5_HUMAN

Description Phosphoinositide-3-kinase-interacting protein 1 (Fragment) OS=Homo sapiens GN=PIK3IP1 PE=1 SV=8

Peptides 1

Score 67.16

Anova 0.01

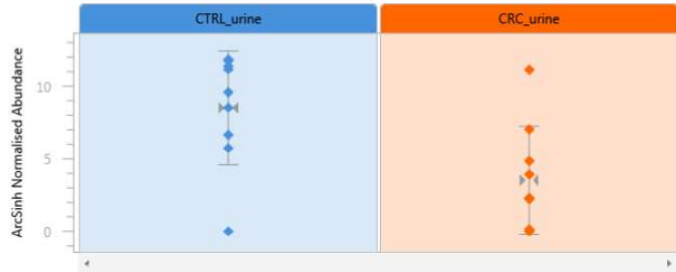
Fold 6.57

 Anova p-value \leq 0.05

 Anova p-value \leq 0.08

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Accession Q05CF8|Q05CF8_HUMAN

Description KNG1 protein OS=Homo sapiens GN=KNG1 PE=2 SV=1

Peptides 5

Score 180.22

Anova 0.02

Fold 10.60

Anova p-value ≤ 0.08



Accession A0A052Z3H5|A0A052Z3H5_HUMAN

Description Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1

Peptides 7

Score 402.36

Anova 0.03

Fold 6.81

Anova p-value ≤ 0.08



Accession P07911|UROM_HUMAN

Description Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1

Peptides 6

Score 259.60

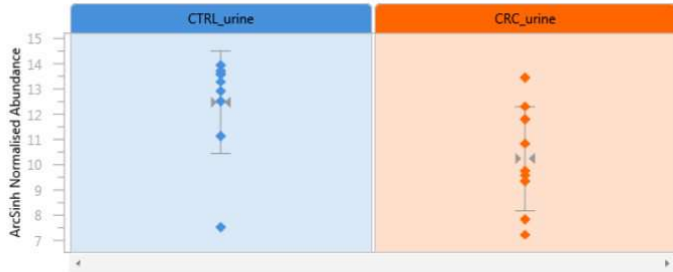
Anova 0.03

Fold 4.34

Anova p-value ≤ 0.08

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biomarker_CCR_urina_dez2018



Accession P05090|APOD_HUMAN

Description Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1

Peptides 5

Score 293.01

Anova 0.04

Fold 7.34

Anova p-value ≤ 0.08



Accession C0JYZ2|C0JYZ2_HUMAN

Description Titin OS=Homo sapiens GN=TTN PE=4 SV=1

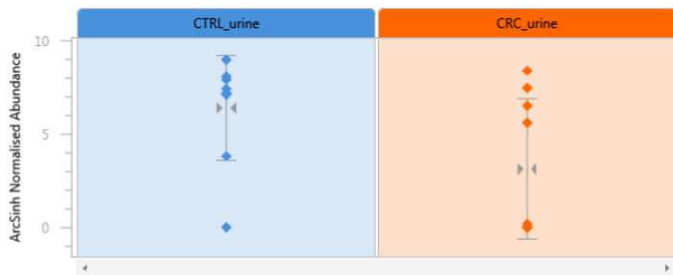
Peptides 1

Score 31.57

Anova 0.05

Fold 2.71

Anova p-value ≤ 0.08



Accession H0YLF3|H0YLF3_HUMAN

Description Beta-2-microglobulin (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1

Peptides 1

Score 133.46

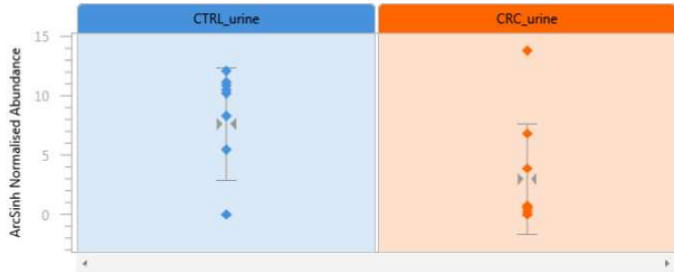
Anova 0.05

Fold 2.62

Anova p-value ≤ 0.08

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biomarker_CCR_urina_dez2018



Accession B4DWHO|B4DWHO_HUMAN (+1)

Description cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellularmatrix protein 1 OS=Homo sapiens PE=2 SV=1

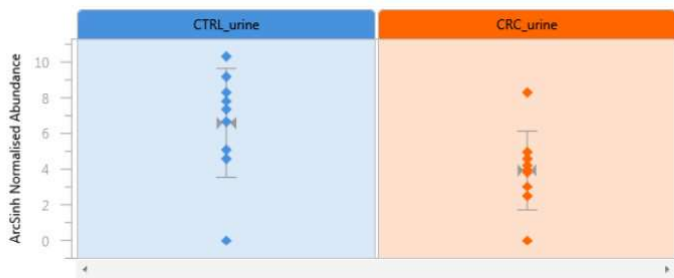
Peptides 3

Score 131.51

Anova 0.05

Fold 10.71

Anova p-value ≤ 0.08



Accession Q9HAU0|PKHA5_HUMAN

Description Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens GN=PLEKHA5 PE=1 SV=1

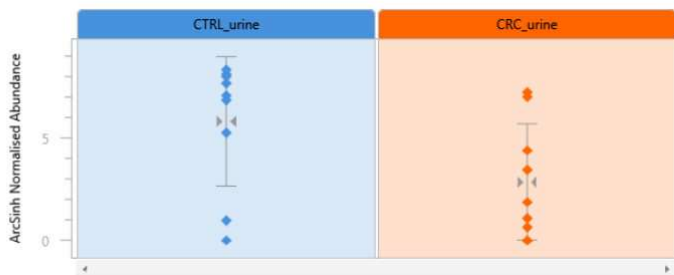
Peptides 1

Score 31.42

Anova 0.05

Fold 5.78

Anova p-value ≤ 0.08



Accession Q9NPP6|Q9NPP6_HUMAN

Description Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1

Peptides 1

Score 55.14

Anova 0.06

Fold 5.72

Anova p-value ≤ 0.08

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Accession Q7LC53 | Q7LC53_HUMAN

Description Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1

Peptides 6

Score 238.66

Anova 0.06

Fold 6.18

Anova p-value ≤ 0.08



Accession P01133 | EGF_HUMAN

Description Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2

Peptides 3

Score 196.42

Anova 0.07

Fold 14.81

Anova p-value ≤ 0.08



Features

#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_urine	CRC_urine
7521	0.072	113.1	2	442.7291	34.0			4193.048	37.069
10946	0.155	Infinity	2	393.7634	20.6			275.714	0.000
15701	0.008	22.0	2	501.7176	40.0			4306.169	195.835
1045	0.013	6.6	2	585.7912	31.1			2.507e+004	3814.072

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#	Anova (p)	Fold	Charge	m/z	Retention Time	Tags	Notes	Average Normalised Abundances	
								CTRL_urine	CRC_urine
1543	0.240	5.6	2	431.2071	29.7			6817.841	1213.933
5133	0.023	81.8	3	754.6516	26.4			3117.045	38.100
9394	0.020	15.0	3	797.3494	21.4			4182.836	277.966
17715	0.305	562.2	2	700.3622	25.7			1979.553	3.521
64602	0.456	74.8	3	579.9675	17.3			182.488	2.440
1638	0.011	6.3	2	733.3549	37.0			4.274e+004	6826.992
2783	0.245	6.0	3	579.2876	22.6			7470.551	1244.110
4461	0.644	8.1	2	868.4264	22.6			6627.012	821.432
5018	0.461	12.6	3	865.7353	18.4			6756.357	535.832
12997	0.906	20.3	3	557.2646	16.8			999.824	49.197
35830	0.904	4.5	3	538.2573	16.8			354.597	78.833
43958	0.296	8.3	3	555.6084	21.7			401.088	48.283
45394	0.216	7.7	2	1190.5344	21.4			692.003	89.777
292	0.047	3.7	2	538.2636	41.8			2.162e+005	5.814e+004
566	0.179	13.5	2	607.2762	24.7			4.137e+004	3071.770
1140	0.172	48.9	3	405.1865	24.7			9030.110	184.531
1001	0.130	720.3	2	481.1921	27.9			4837.024	6.716
1409	0.718	1.7	2	465.7285	62.9			3006.107	1727.796
33564	0.814	1.0	2	491.7155	28.7			204.845	205.652
47255	0.108	38.1	2	527.2208	15.3			76.417	2.005
866	0.032	20.9	2	436.2537	33.3			4.215e+004	2013.296
1852	0.043	4.4	2	646.8025	39.6			3.999e+004	9067.124
3331	0.105	7.3	2	654.7998	26.6			5195.229	709.707
4895	0.552	23.1	3	479.5673	20.3			2262.933	97.909
14312	0.472	10.9	2	718.8472	33.3			1479.676	135.870
7004	0.366	6.1	2	710.8496	32.1			1.373e+004	2247.652
28730	0.051	2.7	2	692.3293	23.0			1089.295	402.620
586	0.047	2.4	2	561.8170	26.1			1.741e+004	4.244e+004
1190	0.122	3.7	3	374.8803	26.1			2932.770	1.082e+004
10201	0.093	11.6	2	685.2777	27.1			1677.023	144.291
40198	0.143	9.0	2	965.3727	29.0			932.987	103.992
63585	0.873	35.4	3	468.5762	19.7			70.114	1.980
27857	0.053	5.8	2	501.7645	32.0			832.497	143.996
15514	0.056	5.7	2	710.3696	32.5			1671.744	292.374
1278	0.092	6.3	2	1013.9403	25.5			8.928e+004	1.419e+004
24210	0.110	8.3	2	506.2377	32.0			1003.354	121.567
24854	0.103	21.9	2	440.2090	26.3			439.726	20.094
29132	0.943	3.2	2	495.2634	29.5			163.636	51.617
37103	0.196	1.7	2	648.2880	24.9			493.127	287.489
121984	0.137	2.2	2	568.2511	26.1			404.258	180.218
7408	0.246	15.9	2	494.8007	23.1			852.089	53.441
8448	0.277	465.2	3	330.2028	23.1			425.990	0.916
22971	0.149	9.2	2	578.7719	25.5			846.969	91.627
27832	0.106	17.8	2	462.2602	30.4			225.636	12.709

Tags
Anova p-value ≤ 0.08

Feature number 7521

Charge 2

m/z 442.7291

Retention Time 34.0

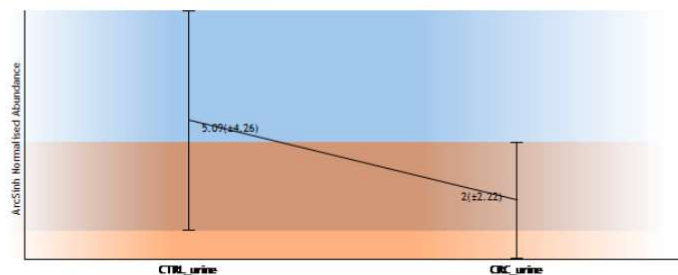
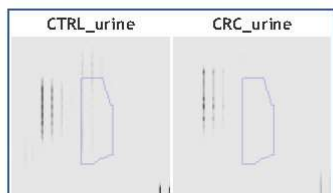
Notes

Anova p-value ≤ 0.08

23/06/2019

biomarker_CCR_urina_dez2018

Score	Protein	Description
30.48	Q6NSB3 Q6NSB3_HUMAN	Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1



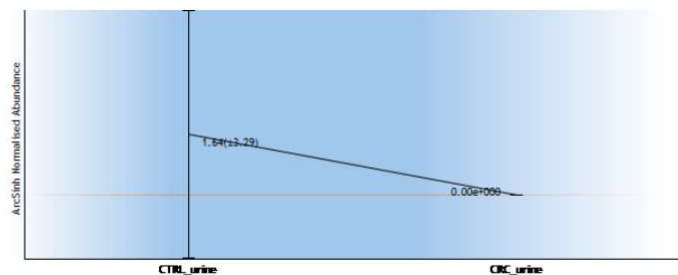
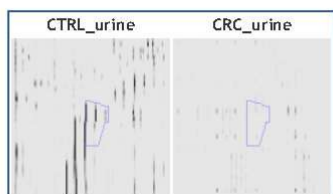
Feature number 10946

Charge 2
m/z 393.7634

Retention Time 20.6

Notes

Score	Protein	Description
33.07	Q6NSB3 Q6NSB3_HUMAN	Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1
29.62	H7BZQ8 H7BZQ8_HUMAN	Pancreatic alpha-amylase (Fragment) OS=Homo sapiens GN=AMY2A PE=1 SV=1



Feature number 15701

Charge 2
m/z 501.7176

Retention Time 40.0

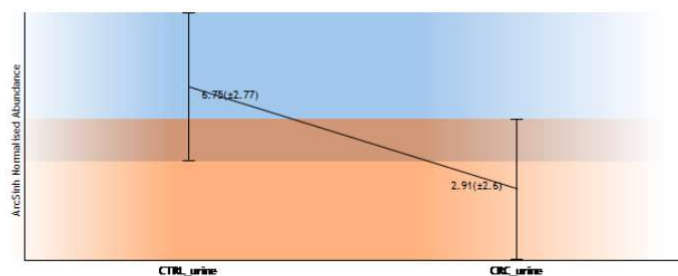
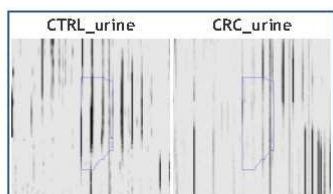
Notes

■ Anova p-value ≤ 0.08

23/06/2019

biomarker_CCR_urina_dez2018

Score	Protein	Description
43.70	H7BZQ8 H7BZQ8_HUMAN	Pancreatic alpha-amylase (Fragment) OS=Homo sapiens GN=AMY2A PE=1 SV=1
42.35	Q6NSB3 Q6NSB3_HUMAN	Alpha-amylase (Fragment) OS=Homo sapiens GN=AMY1A PE=2 SV=1



Feature number 1045

Charge 2

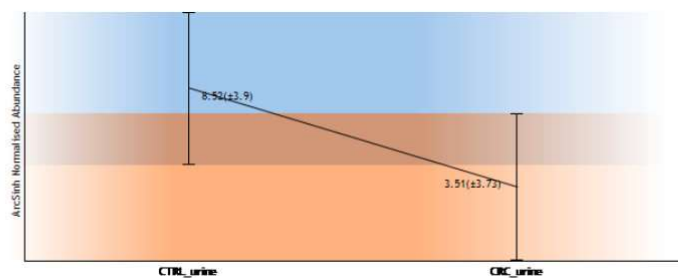
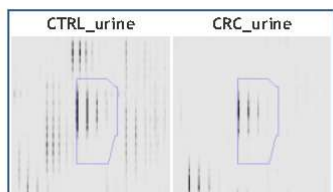
m/z 585.7912

Retention Time 31.1

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
67.16	C9JMK5 C9JMK5_HUMAN	Phosphoinositide-3-kinase-interacting protein 1 (Fragment) OS=Homo sapiens GN=PIK3IP1 PE=1 SV=8



Feature number 1543

Charge 2

m/z 431.2071

Retention Time 29.7

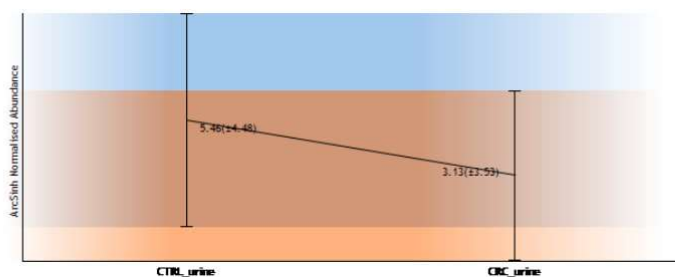
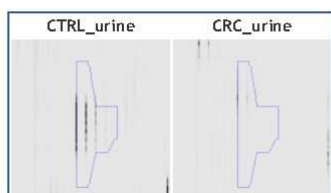
Notes

Score	Protein	Description

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biomarker_CCR_urina_dez2018

30.48 | Q05CF8|Q05CF8_HUMAN | KNG1 protein OS=Homo sapiens GN=KNG1 PE=Z SV=1



Feature number 5133

Charge 3

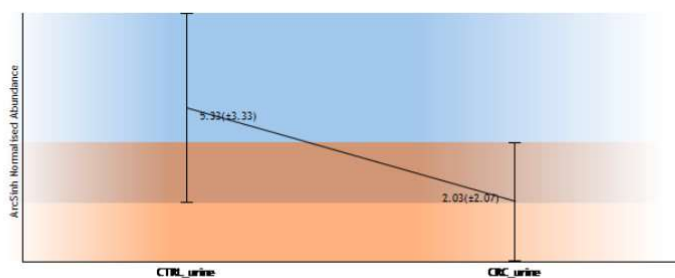
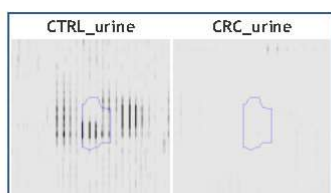
m/z 754.6516

Retention Time 26.4

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
55.59	Q05CF8 Q05CF8_HUMAN	KNG1 protein OS=Homo sapiens GN=KNG1 PE=Z SV=1



Feature number 9394

Charge 3

m/z 797.3494

Retention Time 21.4

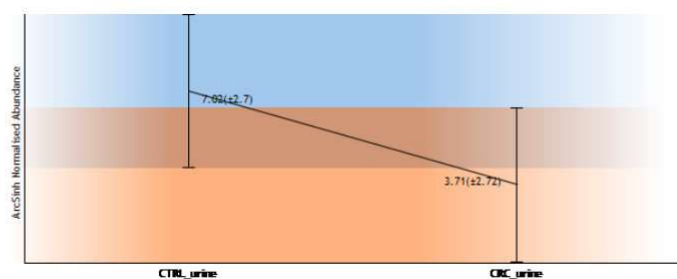
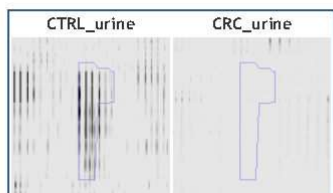
Notes

Anova p-value ≤ 0.08

Score	Protein	Description
34.22	Q05CF8 Q05CF8_HUMAN	KNG1 protein OS=Homo sapiens GN=KNG1 PE=Z SV=1

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biomarker_CCR_urina_dez2018



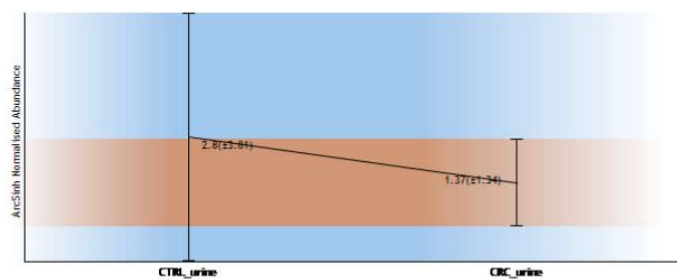
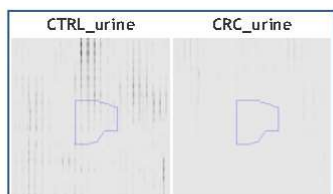
Feature number 17715

Charge 2
m/z 700.3622

Retention Time 25.7

Notes

Score	Protein	Description
29.02	Q05CF8 Q05CF8_HUMAN	KNG1 protein OS=Homo sapiens GN=KNG1 PE=2 SV=1



Feature number 64602

Charge 3
m/z 579.9675

Retention Time 17.3

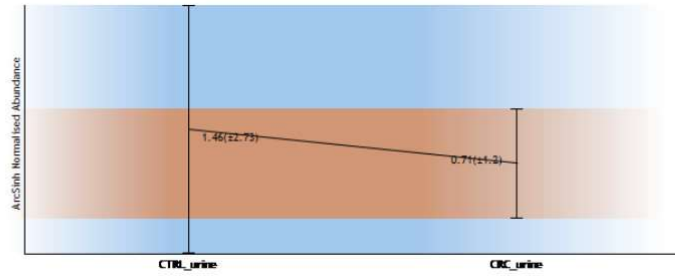
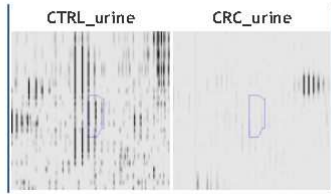
Notes

Score	Protein	Description
30.91	Q05CF8 Q05CF8_HUMAN	KNG1 protein OS=Homo sapiens GN=KNG1 PE=2 SV=1



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biomarker_CCR_urina_dez2018



Feature number 1638

Charge 2

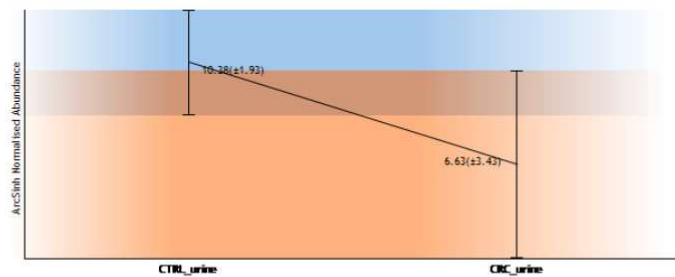
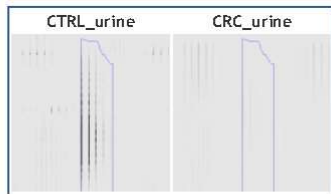
m/z 733.3549

Retention Time 37.0

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
34.32	A0A0SZZ3H5 A0A0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



Feature number 2783

Charge 3

m/z 579.2876

Retention Time 22.6

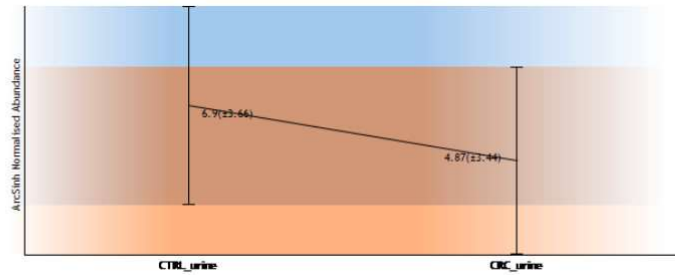
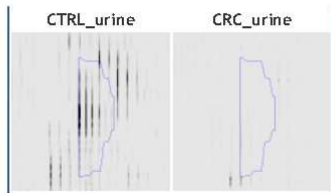
Notes

Score	Protein	Description
54.60	A0A0SZZ3H5 A0A0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



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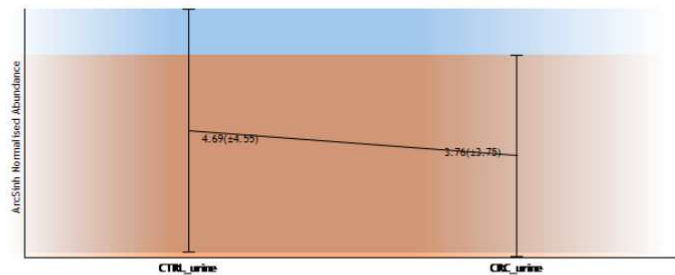
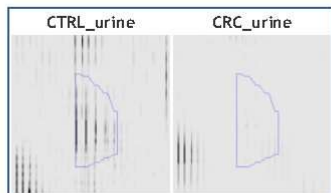
Feature number 4461

Charge 2
m/z 868.4264

Retention Time 22.6

Notes

Score	Protein	Description
70.97	A0A0SZZ3H5 A0A0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



Feature number 5018

Charge 3
m/z 865.7353

Retention Time 18.4

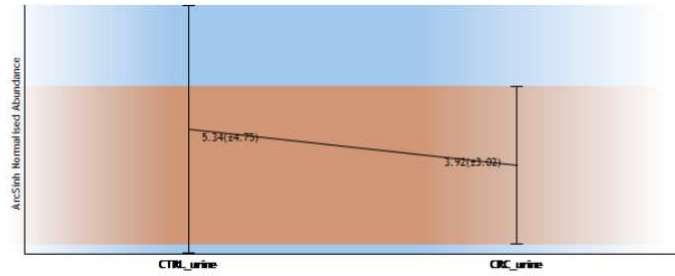
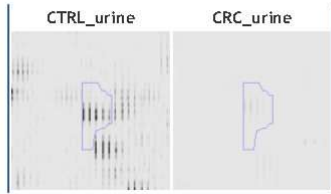
Notes

Score	Protein	Description
66.14	A0A0SZZ3H5 A0A0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



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Feature number 12997

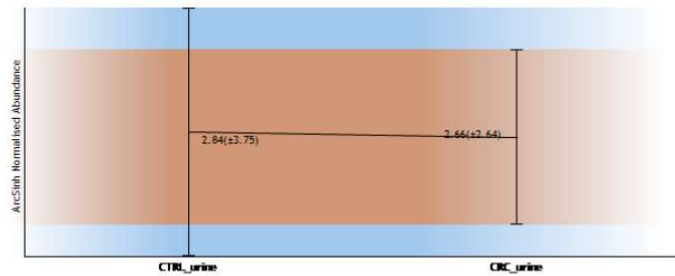
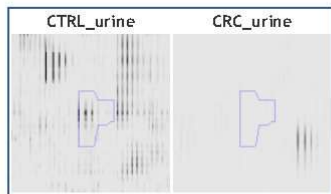
Charge 3

m/z 557.2646

Retention Time 16.8

Notes

Score	Protein	Description
41.75	A0A0S2Z3H5 A0A0S2Z3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



Feature number 35830

Charge 3

m/z 538.2573

Retention Time 16.8

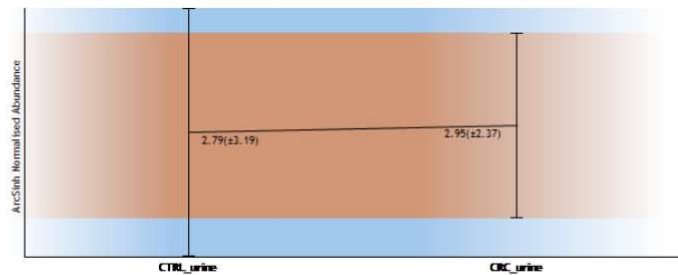
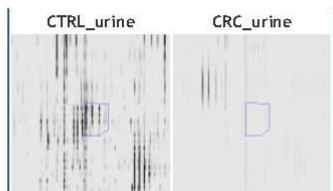
Notes

Score	Protein	Description
32.98	A0A0S2Z3H5 A0A0S2Z3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



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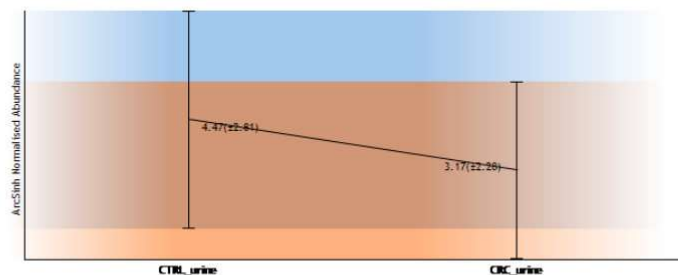
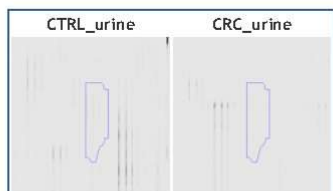
Feature number 43958

Charge 3
m/z 555.6084

Retention Time 21.7

Notes

Score	Protein	Description
44.16	AOA0SZZ3H5 AOA0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



Feature number 45394

Charge 2
m/z 1190.5344

Retention Time 21.4

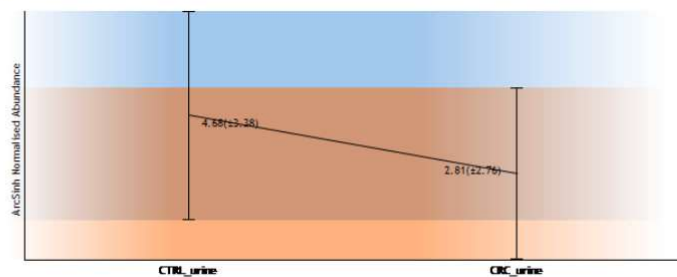
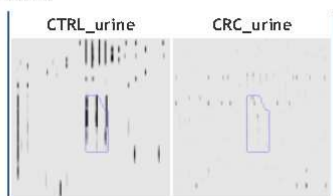
Notes

Score	Protein	Description
57.44	AOA0SZZ3H5 AOA0SZZ3H5_HUMAN	Collagen type I alpha 2 isoform 1 (Fragment) OS=Homo sapiens GN=COL1A2 PE=2 SV=1



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Feature number 292

Charge 2

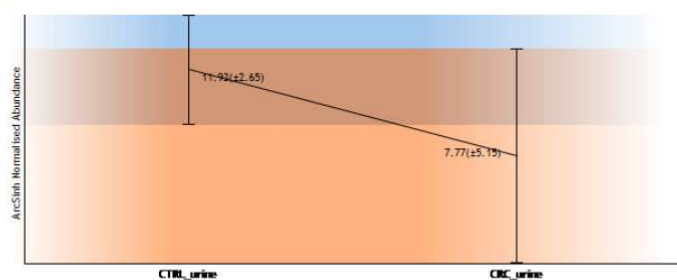
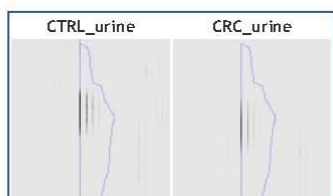
m/z 538.2636

Retention Time 41.8

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
48.21	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



Feature number 566

Charge 2

m/z 607.2762

Retention Time 24.7

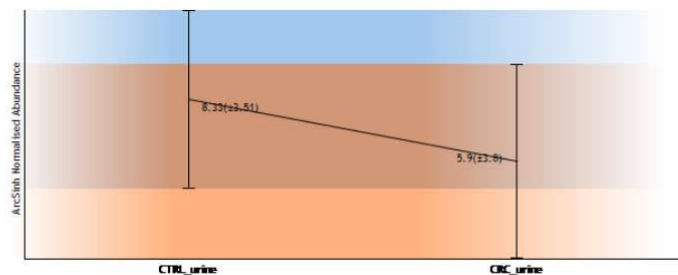
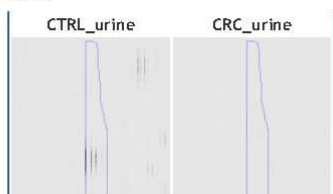
Notes

Score	Protein	Description
32.76	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



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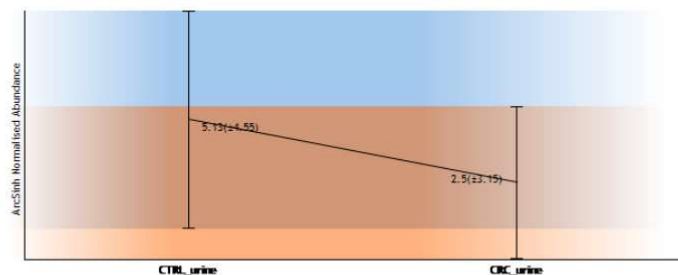
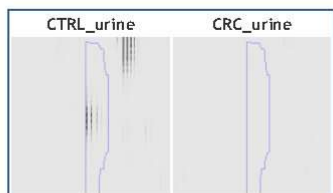
Feature number 1140

Charge 3
m/z 405.1865

Retention Time 24.7

Notes

Score	Protein	Description
33.09	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



Feature number 1001

Charge 2
m/z 481.1921

Retention Time 27.9

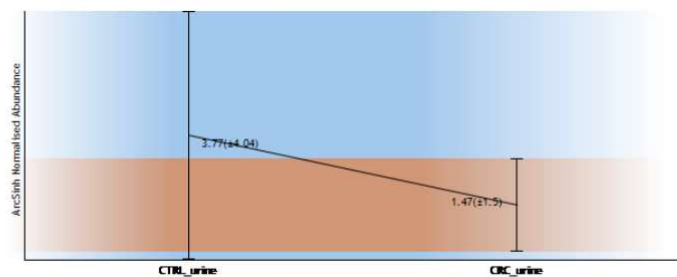
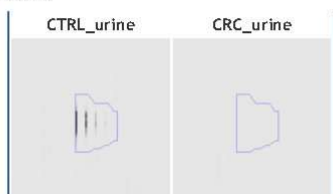
Notes

Score	Protein	Description
35.88	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



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Feature number 1409

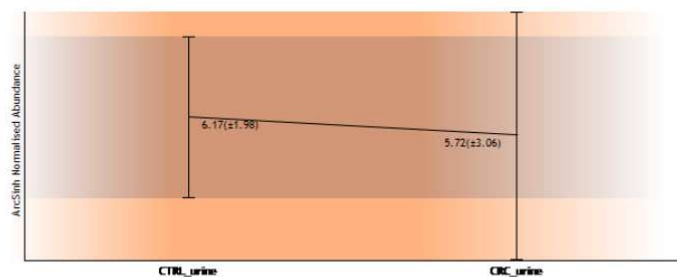
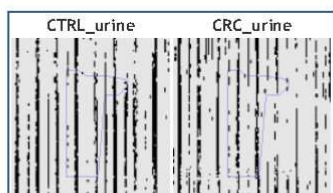
Charge 2

m/z 465.7285

Retention Time 62.9

Notes

Score	Protein	Description
36.24	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



Feature number 33564

Charge 2

m/z 491.7155

Retention Time 28.7

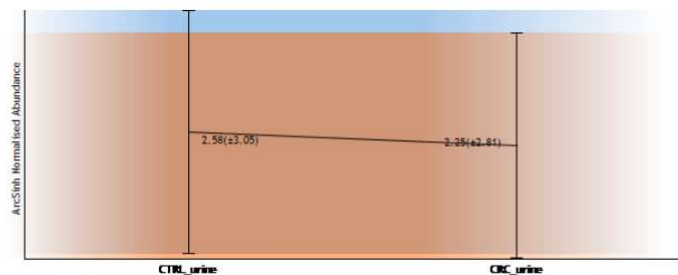
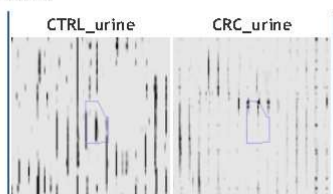
Notes

Score	Protein	Description
27.94	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UMOD PE=1 SV=1



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biomarker_CCR_urina_dez2018



Feature number 47255

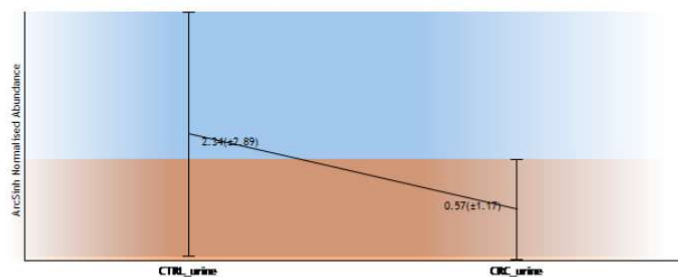
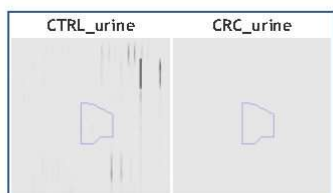
Charge 2

m/z 527.2208

Retention Time 15.3

Notes

Score	Protein	Description
45.48	P07911 UROM_HUMAN	Uromodulin OS=Homo sapiens GN=UAMOD PE=1 SV=1



Feature number 866

Charge 2

m/z 436.2537

Retention Time 33.3

Notes

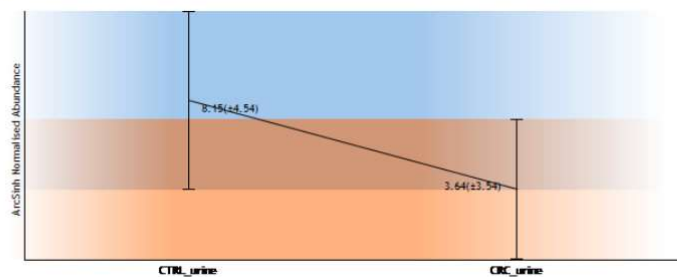
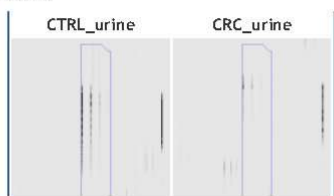
Anova p-value ≤ 0.08

Score	Protein	Description
46.29	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



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Feature number 1852

Charge 2

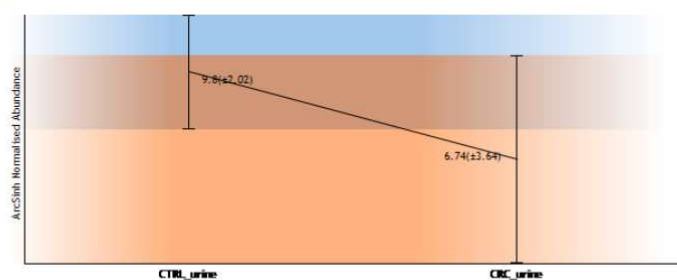
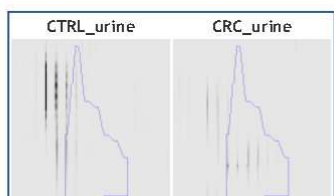
m/z 646.8025

Retention Time 39.6

Notes

Anova p-value ≤ 0.08

Score	Protein	Description
32.38	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



Feature number 3331

Charge 2

m/z 654.7998

Retention Time 26.6

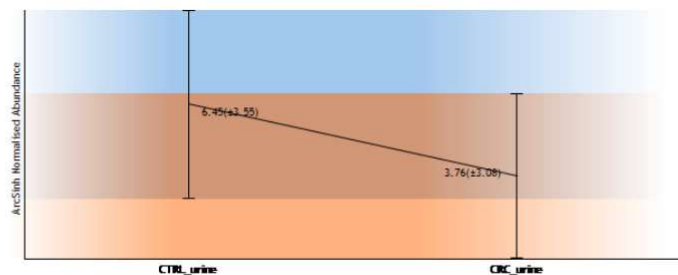
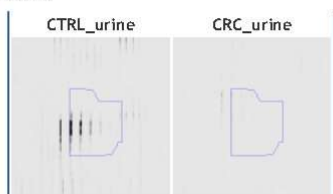
Notes

Score	Protein	Description
84.06	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



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biomarker_CCR_urina_dez2018



Feature number 4895

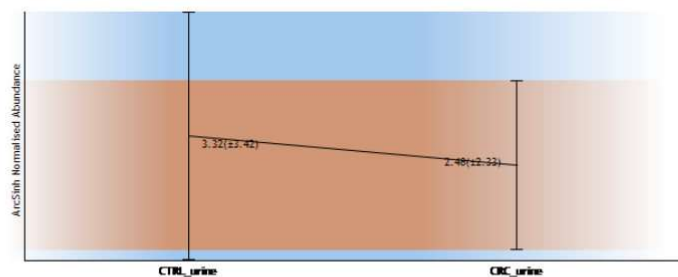
Charge 3

m/z 479.5673

Retention Time 20.3

Notes

Score	Protein	Description
32.73	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



Feature number 14312

Charge 2

m/z 718.8472

Retention Time 33.3

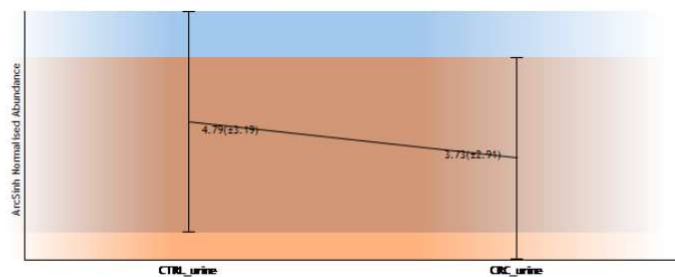
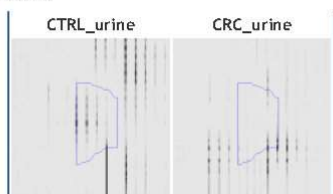
Notes

Score	Protein	Description
47.07	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



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biomarker_CCR_urina_dez2018



Feature number 7004

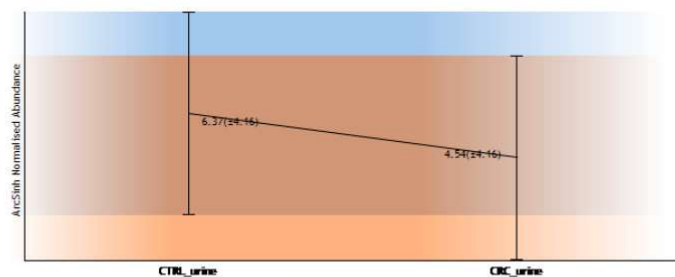
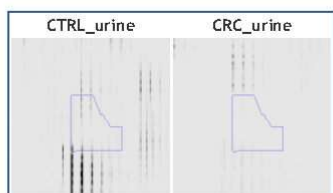
Charge 2

m/z 710.8496

Retention Time 32.1

Notes

Score	Protein	Description
50.48	P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1



Feature number 28730

Charge 2

m/z 692.3293

Retention Time 23.0

Notes

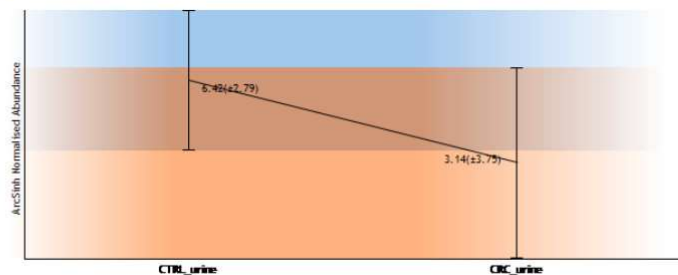
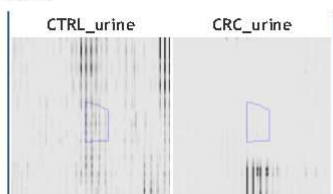
Anova p-value ≤ 0.08

Score	Protein	Description
31.57	C0JYZ2 C0JYZ2_HUMAN	Titin OS=Homo sapiens GN=TTN PE=4 SV=1



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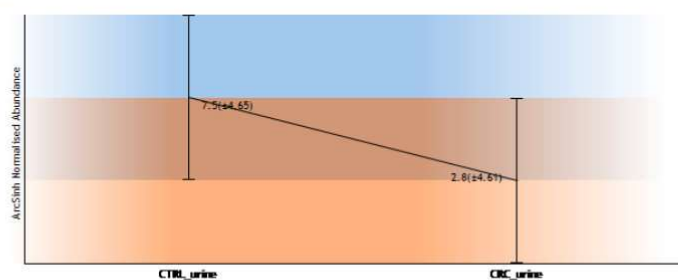
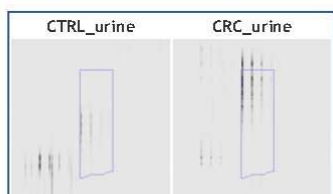
Feature number 586

Charge 2
m/z 561.8170
Retention Time 26.1

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
76.34	HOYLF3 HOYLF3_HUMAN	Beta-2-microglobulin (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1



Feature number 1190

Charge 3
m/z 374.8803
Retention Time 26.1

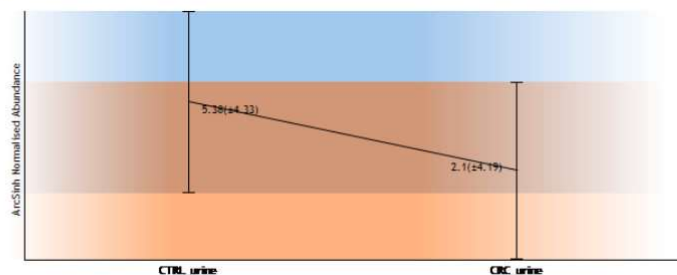
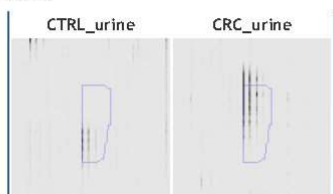
Notes

Score	Protein	Description
57.12	HOYLF3 HOYLF3_HUMAN	Beta-2-microglobulin (Fragment) OS=Homo sapiens GN=B2M PE=1 SV=1



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Feature number 10201

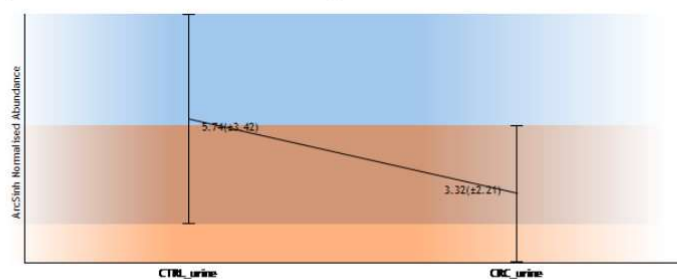
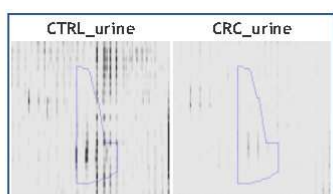
Charge 2

m/z 685.2777

Retention Time 27.1

Notes

Score	Protein	Description
51.14	B4DWH0 B4DWH0_HUMAN	cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellularmatrix protein 1 OS=Homo sapiens PE=2 SV=1
44.15	AQA05Z3V1 AQA05Z3V1_HUMAN	EGF containing fibulin-like extracellular matrix protein 1 isoform 2 (Fragment) OS=Homo sapiens GN=EFEMP1 PE=2 SV=1



Feature number 40198

Charge 2

m/z 965.3727

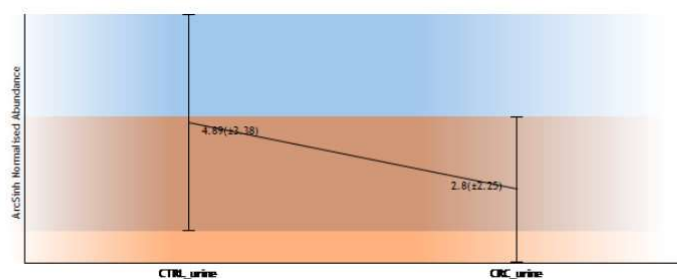
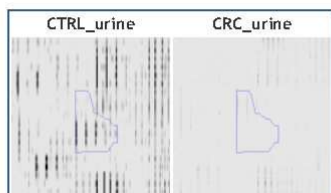
Retention Time 29.0

Notes

Score	Protein	Description
49.89	B4DWH0 B4DWH0_HUMAN	cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellularmatrix protein 1 OS=Homo sapiens PE=2 SV=1
36.00	AQA05Z3V1 AQA05Z3V1_HUMAN	EGF containing fibulin-like extracellular matrix protein 1 isoform 2 (Fragment) OS=Homo sapiens GN=EFEMP1 PE=2 SV=1

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Feature number 63585

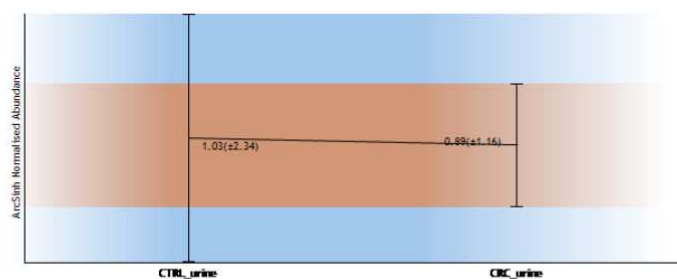
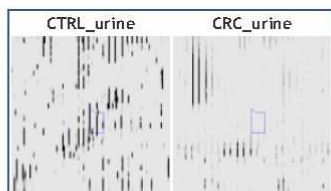
Charge 3

m/z 468.5762

Retention Time 19.7

Notes

Score	Protein	Description
30.48	B4DWHO B4DWHO_HUMAN	cDNA FLJ55670, highly similar to EGF-containing fibulin-like extracellulamatrix protein 1 OS=Homo sapiens PE=2 SV=1



Feature number 27857

Charge 2

m/z 501.7645

Retention Time 32.0

Notes

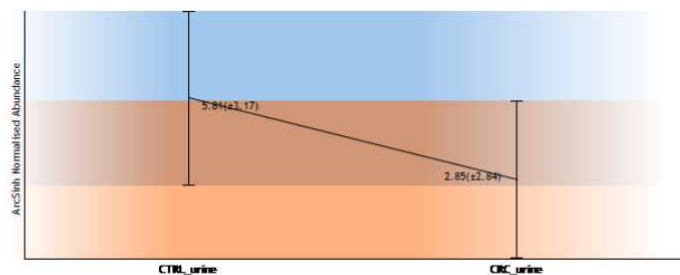
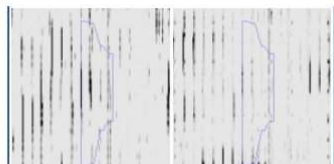
Anova p-value ≤ 0.08

Score	Protein	Description
31.42	Q9HAU0 PKHA5_HUMAN	Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens GN=PLEKHA5 PE=1 SV=1



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Feature number 15514

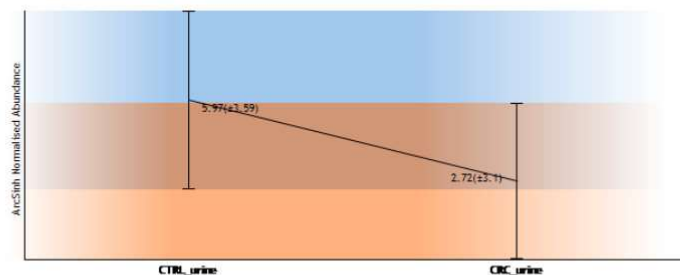
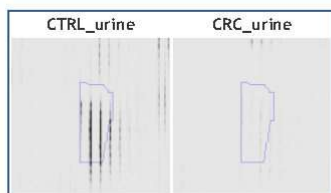
Charge 2
m/z 710.3696

Retention Time 32.5

Notes

■ Anova p-value ≤ 0.08

Score	Protein	Description
55.14	Q9NPP6 Q9NPP6_HUMAN	Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1



Feature number 1278

Charge 2
m/z 1013.9403

Retention Time 25.5

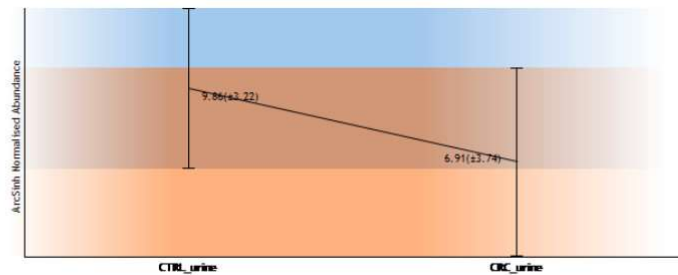
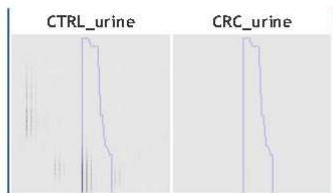
Notes

Score	Protein	Description
29.42	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



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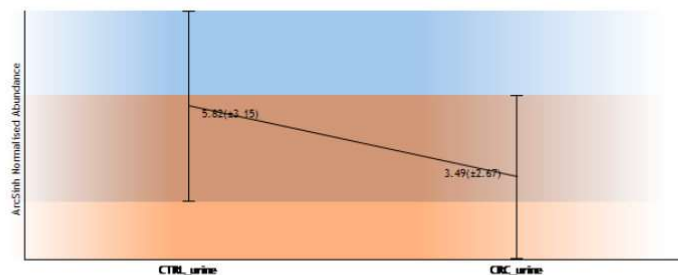
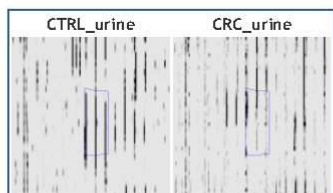
Feature number 24210

Charge 2
m/z 506.2377

Retention Time 32.0

Notes

Score	Protein	Description
39.62	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



Feature number 24854

Charge 2
m/z 440.2090

Retention Time 26.3

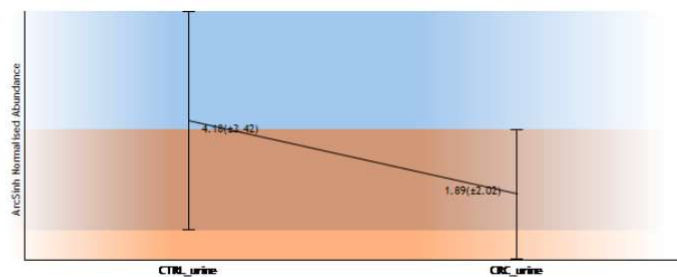
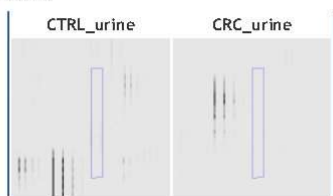
Notes

Score	Protein	Description
30.04	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



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Feature number 29132

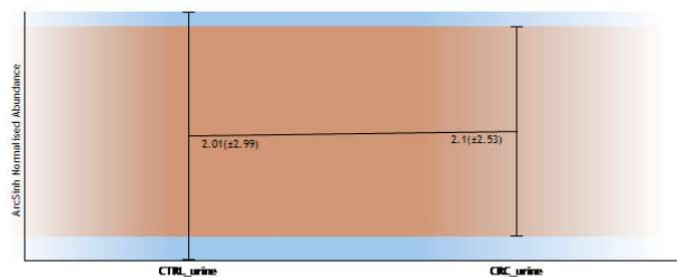
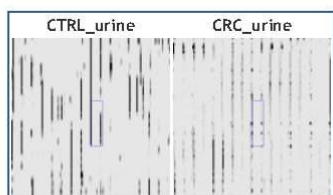
Charge 2

m/z 495.2634

Retention Time 29.5

Notes

Score	Protein	Description
46.94	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



Feature number 37103

Charge 2

m/z 648.2880

Retention Time 24.9

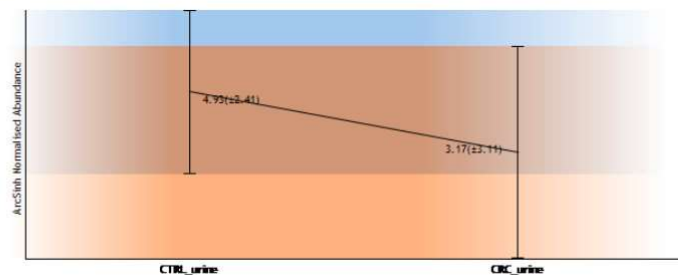
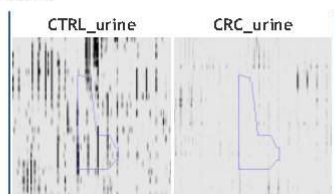
Notes

Score	Protein	Description
29.98	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



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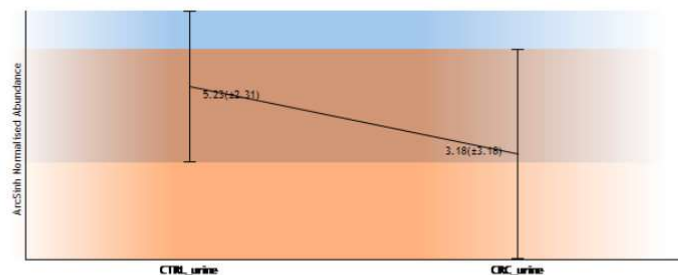
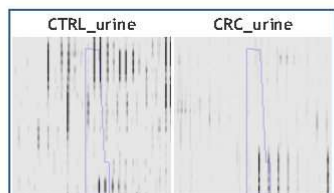
Feature number 121984

Charge 2
m/z 568.2511

Retention Time 26.1

Notes

Score	Protein	Description
62.66	Q7LC53 Q7LC53_HUMAN	Intrinsic factor-vitamin B12 receptor (Fragment) OS=Homo sapiens GN=CUBN PE=4 SV=1



Feature number 7408

Charge 2
m/z 494.8007

Retention Time 23.1

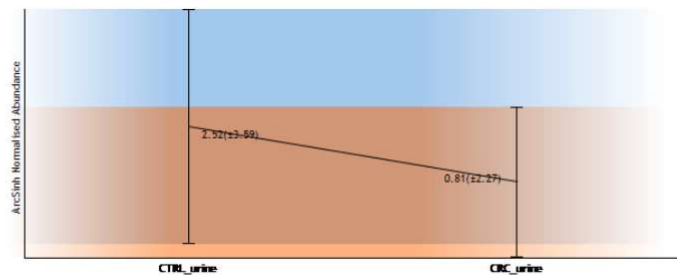
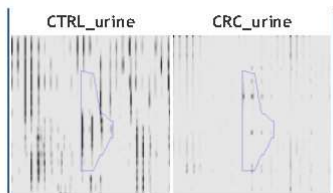
Notes

Score	Protein	Description
63.73	P01133 EGF_HUMAN	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2



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Feature number 8448

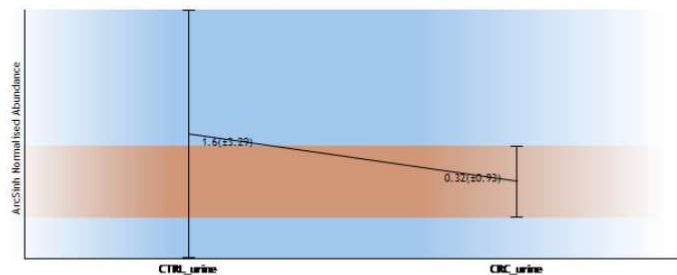
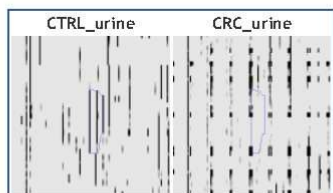
Charge 3

m/z 330.2028

Retention Time 23.1

Notes

Score	Protein	Description
49.43	P01133 EGF_HUMAN	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2



Feature number 22971

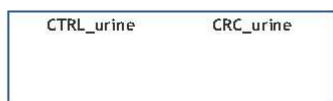
Charge 2

m/z 578.7719

Retention Time 25.5

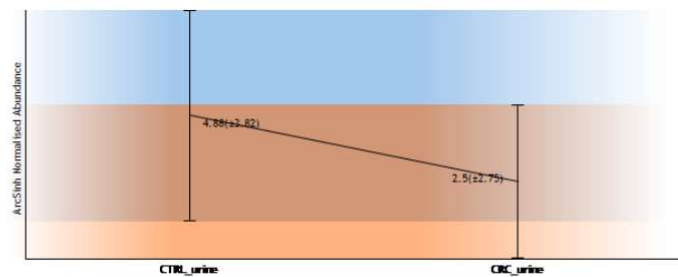
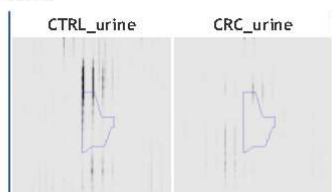
Notes

Score	Protein	Description
43.63	P01133 EGF_HUMAN	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2



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Feature number 27832

Charge 2
m/z 462.2602

Retention Time 30.4

Notes

Score	Protein	Description
39.63	P01133 EGF_HUMAN	Pro-epidermal growth factor OS=Homo sapiens GN=EGF PE=1 SV=2

