**Additional File 2.** Peptide identification from BALF of heaves-affected and control horses. The fold change and p-value results are from the comparison of the peak relative concentration between heaves-affected and control horses after exposure to hay. A p-value of ≤ 0.01 was considered significant. A positive fold change indicates over-expression in control horses after exposure to hay and a negative fold change indicates over-expression in heaves-affected horses. Bold text indicates proteins that were previously identified in healthy horses.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **RefSeq or GenBank #** | **Fold Change** | **P-Value** | **Species** | **Peptide Sequence** | **Gene Name** |
| AAB88212.1 | 1.0 | 0.9470 | Equus caballus | (R)GYSFTTTAER(E) | **actin, beta** |
| AAB88212.1 | 1.5 | 0.4458 | Equus caballus | (K)AGFAGDDAPR(A) | **actin, beta** |
| AAC78364.1 | -1.4 | 0.6674 | Equus caballus | (K)LLCPDGTR(K) | **transferrin** |
| AAC78370.1 | -2.9 | 0.5270 | Equus caballus | (K)APNHAVVSR(K) | **transferrin** |
| AAC78388.1 | -2.1 | 0.2401 | Equus caballus | (R)NPDDWAK(D) | **transferrin** |
| AAC78388.1 | -1.5 | 0.0764 | Equus caballus | (R)NPDDWAK(D) | **transferrin** |
| AAC83412.1 | 2.9 | 0.4556 | Equus caballus | (K)LSISGTYDLTSILPELGITK(V) | **alpha-1-antitrypsin** |
| AAF05481.1 | 1.3 | 0.4092 | Equus caballus | (R)TAGWNIPMGLLYSEIK(H) | **transferrin** |
| AAF05500.1 | 1.7 | 0.0600 | Equus caballus | (R)WCTVSNHEVSK(C) | **transferrin** |
| AAF05516.1 | -1.6 | 0.7695 | Equus caballus | (R)SAGWNIPIGLLYWQLPEPR(E) | **transferrin** |
| AAF05516.1 | 1.5 | 0.4210 | Equus caballus | (K)NSNFQLNQLQGK(K) | **transferrin** |
| AAF08280.1 | -1.4 | 0.5457 | Equus caballus | (R)IPPAMDTWLYLGYEYVTAIR(N) | **transferrin** |
| AAF08280.1 | 1.6 | 0.4497 | Equus caballus | (R)EDIRPEVPKDECK(K) | **transferrin** |
| AAF08280.1 | 13.0 | 0.0994 | Equus caballus | (K)DSALGFLR(I) | **transferrin** |
| AAF60301.1 | 2.5 | 0.5934 | Capra hircus | (R)WSSESGRPVAGGDR(E) | RLF |
| AAG01010.1 | 3.5 | 0.4117 | Equus caballus | (K)VNDAVTTDGVQTTR(S) | immunoglobulin G light chain |
| AAG01010.1 | 1.7 | 0.5674 | Equus caballus | (R)VSGVPDR(F) | immunoglobulin G light chain |
| AAG01011.1 | 2.5 | 0.0993 | Equus caballus | (K)APDVFPLSICGNTPDPK(V) | immunoglobulin G heavy chain |
| AAG40944.1 | -2.1 | 0.4967 | Equus caballus | (R)NECFLTHK(D) | albumin |
| AAG40944.1 | -1.1 | 0.9178 | Equus caballus | (K)DDHPNLPK(L) | albumin |
| AAH60513.1 | 1.3 | 0.6530 | Homo sapiens | (K)LSSPADITDK(V) | **plasminogen** |
| AAH89302.1 | 4.9 | 0.0028 | Mus musculus | (K)SITHSTVGAKGEK(A) | euchromatic histone methyltransferase 1 |
| AAP78708.1 | 1.2 | 0.5803 | Equus caballus | (R)QIFNGTFVKLNKASVNmLR(I) | ribosomal protein L7 |
| AAP80145.1 | -1.4 | 0.3885 | Equus caballus | (R)GDVFSCMVGHEALPLSFTQK(S) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | -1.4 | 0.3445 | Equus caballus | (K)EVLVLWLQGHEK(L) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | 1.9 | 0.7657 | Equus caballus | (K)YLVFKPLR(E) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | 10.0 | 0.0097 | Equus caballus | (K)EPLFQPQVHVLPPPSEELALNELVTLTCLVR(G) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | 3.2 | 0.2989 | Equus caballus | (R)KADSGDPVVIACLIK(G) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | 1.3 | 0.4487 | Equus caballus | (K)GFFPLGFPEPVK(V) | immunoglobulin alpha constant heavy chain |
| AAP80145.1 | 2.9 | 0.0962 | Equus caballus | (K)KETFSCTAK(H) | immunoglobulin alpha constant heavy chain |
| AAS18415.1 | 1.1 | 0.9204 | Equus caballus | (R)EPQVYVLAPHRDELSK(N) | immunoglobulin gamma 4 heavy chain |
| AAS18415.1 | -1.3 | 0.8772 | Equus caballus | (R)EPQVYVLAPHRDELSK(N) | immunoglobulin gamma 4 heavy chain |
| AAU09792.1 | -1.4 | 0.4279 | Rattus norvegicus | (-)mPNVTK(I) | **olfactory receptor 24** |
| AAW69159.1 | -1.1 | 0.8462 | Equus caballus | (R)LVCQATGFSPK(E) | immunoglobulin light chain variable region |
| AAW69159.1 | 9.7 | 0.0113 | Homo sapiens | (R)LLIYGASGRATGIPDR(F) | immunoglobulin light chain variable region |
| AAW83218.1 | -1.5 | 0.6936 | Equus caballus | (K)AAATQLK(T) | secretoglobin, family 1A, member 1 (uteroglobin) |
| AAW83220.1 | 4.4 | 0.1595 | Equus caballus | (K)DSILK(L) | secretoglobin, family 1A, member 1 (uteroglobin) |
| AAW83220.1 | -1.0 | 0.9843 | Equus caballus | (K)DSILK(L) | secretoglobin, family 1A, member 1 (uteroglobin) |
| AAW83220.1 | -1.9 | 0.5160 | Equus caballus | (K)SPLCA(-) | secretoglobin, family 1A, member 1 (uteroglobin) |
| AAW83220.1 | 3.5 | 0.6556 | Equus caballus | (K)TLVDFLPK(N) | secretoglobin, family 1A, member 1 (uteroglobin) |
| AAZ43326.1 | -2.4 | 0.2408 | Equus caballus | (K)ESGPGLVK(I) | immunoglobulin heavy chain variable region |
| ABB02691.1 | 4.2 | 0.0044 | Equus caballus | (-)MGPRIGPVSEGPQmPDK(D) | solute carrier organic anion transporter family, member 2B1 |
| ABG91734.1 | 5.5 | 0.1080 | Homo sapiens | (R)EGAGSPYEQYFGPGTRLTVTGK(-) | T cell receptor beta |
| BAA09637.1 | 1.5 | 0.4601 | Homo sapiens | (-)IPKAPPTACYAGAAPAPSQVKSK(A) | CCAAT/enhancer binding protein (C/EBP), beta |
| BAA20757.1 | -2.7 | 0.2209 | Homo sapiens | (R)AVKVDCPYPLSQITAR(N) | tectonin beta-propeller repeat containing 2 |
| BAB13938.1 | -1.0 | 0.9592 | Homo sapiens | (K)QSPPIVK(I) | solute carrier family 41, member 3 |
| BAB67795.1 | 8.5 | 0.0089 | Homo sapiens | (R)AADmGNAGSMDSQQTDFR(A) | formin-like 2 |
| BAC97986.1 | 10.1 | 0.0088 | Mus musculus | (-)PAPPTPVDRPSSRVSADQR(A) | Rho GTPase activating protein 26 |
| BAE24836.1 | -1.9 | 0.1580 | Mus musculus | (R)VILWGGK(K) | DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed |
| BAE27147.1 | 8.1 | 0.0124 | Mus musculus | (R)EQHQVFER(Q) | TatD DNase domain containing 2 |
| BAE40457.1 | -1.9 | 0.4061 | Mus musculus | (K)TQVNRISDVKYSCK(T) | RAD1 homolog (S. pombe) |
| BAG06725.1 | -2.7 | 0.0384 | Homo sapiens | (K)RHAImPKLQQLMAAALAELEGLLAK(A) | dynein heavy chain domain 1 |
| CAA46170 | 10.4 | 0.0101 | Rattus norvegicus | (R)GQAPRVTFPGR(G) | **integrin, alpha 7** |
| CAC44624.1 | 1.2 | 0.5311 | Equus caballus | (R)SQEPQVYVLAPHPDELSK(S) | immunogobulin gamma 1 heavy chain constant region |
| CAC44624.1 | 10.0 | 0.0083 | Equus caballus | (K)CPAPELLGGPSVFIFPPNPK(D) | immunogobulin gamma 1 heavy chain constant region |
| CAC44624.1 | 2.3 | 0.1597 | Equus caballus | (K)NVSKNPGK(-) | immunogobulin gamma 1 heavy chain constant region |
| CAC44761.1 | 1.2 | 0.7040 | Equus caballus | (K)DALMISR(T) | immunoglobulin gamma 2 heavy chain constant region |
| CAC44761.1 | 3.5 | 0.1288 | Equus caballus | (K)DFYPPDISVEWQSNR(W) | immunoglobulin gamma 2 heavy chain constant region |
| CAC44761.1 | -2.9 | 0.4597 | Equus caballus | (R)VPQVYVLPPHPDELAK(S) | immunoglobulin gamma 2 heavy chain constant region |
| CAC44761.1 | 2.2 | 0.2929 | Equus caballus | (K)DALMISR(T) | immunoglobulin gamma 2 heavy chain constant region |
| CAC44762.1 | -1.1 | 0.9402 | Equus caballus | (R)VVSVLPIQHK(D) | immunoglobulin gamma 4 heavy chain constant region |
| CAC44763.1 | -1.3 | 0.4782 | Equus caballus | (K)YSTTPAQLDSDGSYFLYSK(L) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 1.5 | 0.5150 | Equus caballus | (K)DFYPTDIDIEWK(S) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 1.7 | 0.6886 | Equus caballus | (K)DWLSGK(E) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | -1.4 | 0.7991 | Equus caballus | (R)EPQVYVLAPHR(A) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | -2.3 | 0.1617 | Equus caballus | (R)VVSILAIQHK(D) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 3.1 | 0.3669 | Equus caballus | (R)EPQVYVLAPHR(A) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 1.5 | 0.4039 | Equus caballus | (K)DVLmISR(T) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | -1.8 | 0.4709 | Equus caballus | (K)LTVETNR(W) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 1.2 | 0.8646 | Equus caballus | (K)DVLMISR(T) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | 1.3 | 0.7492 | Equus caballus | (K)DVLMISR(T) | immunoglobulin gamma 7 heavy chain constant region |
| CAC44763.1 | -4.0 | 0.0642 | Equus caballus | (K)LTVETNR(W) | immunoglobulin gamma 7 heavy chain constant region |
| CAC86339.1 | 7.2 | 0.0359 | Equus caballus | (K)VSVTCLVK(D) | immunoglobulin gamma 3 heavy chain constant region |
| CAC86340.1 | 1.4 | 0.5912 | Equus caballus | (K)CPAPELPGGPSVFIFPPKPK(D) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86340.1 | -1.8 | 0.3171 | Equus caballus | (R)VPQVYVLAPHPDELAK(N) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86340.1 | -1.4 | 0.7374 | Equus caballus | (K)CPAPELPGGPSVFIFPPKPK(D) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86340.1 | -1.1 | 0.8442 | Equus caballus | (K)CPAPELPGGPSVFIFPPKPK(D) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86340.1 | -2.9 | 0.3809 | Equus caballus | (R)VPQVYVLAPHPDELAK(N) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86340.1 | -15.6 | 0.0022 | Equus caballus | (K)LSVETSR(W) | immunoglobulin gamma 5 heavy chain constant region |
| CAC86341.1 | 1.2 | 0.4836 | Equus caballus | (R)TPEVTCVVVDVSQENPDVK(F) | immunoglobulin gamma 6 heavy chain constant region |
| CAC86341.1 | -2.5 | 0.3761 | Equus caballus | (K)SQTYICNVAHPASSTK(V) | immunoglobulin gamma 6 heavy chain constant region |
| CAC86341.1 | 1.7 | 0.2572 | Equus caballus | (R)VVSVLPIQHQDWR(R) | immunoglobulin gamma 6 heavy chain constant region |
| CAD19940.1 | 1.2 | 0.7979 | Homo sapiens | (K)APKLLIYDASTLQSGVPSR(F) | immunoglobulin kappa light chain variable region |
| CAD39127.1 | 1.3 | 0.8804 | Homo sapiens | (R)SLKGKLmNSK(K) | retinoic acid induced 1 |
| CAD91892.1 | 2.6 | 0.6136 | Homo sapiens | (R)GGSGGGYGSGCGGGGGSYGGSGRSGR(G) | keratin 77 |
| EAW82096.1 | 2.8 | 0.0441 | Homo sapiens | (K)GNLNRCIADVVSVRPSPQGTWLGEPR(L) | vacuolar protein sorting 28 homolog (S. cerevisiae) |
| EAW93342.1 | 1.3 | 0.7972 | Homo sapiens | (K)CLVPMYFSSGFRK(G) | hCG1985824 |
| EAX10298.1 | 1.2 | 0.8677 | Homo sapiens | (K)TIPAPKIVTR(A) | hCG2045837 |
| EDL02646.1 | -10.0 | 0.0110 | Mus musculus | (K)GGGHTTGAGAVSHSAKmWAR(H) | mCG145719 |
| EDL02646.1 | -1.9 | 0.7337 | Mus musculus | (K)GGGHTTGAGAVSHSAKmWAR(H) | mCG145719 |
| EDL11309.1 | 1.3 | 0.6665 | Mus musculus | (R)GKLRSATGPGALLQGCGR(I) | RIKEN cDNA E130303B06 gene |
| EDL14543.1 | 1.8 | 0.6883 | Mus musculus | (K)IKVILHSYKISLR(S) | EDL14543 |
| EDL17868.1 | 1.7 | 0.2073 | Mus musculus | (R)NQDTLGHAHGPCVK(S) | mCG132992 |
| EDM09673.1 | 2.5 | 0.0516 | Rattus norvegicus | (R)EmGSESKRHLADGSGR(L) | similar to eEF1A2 binding protein (predicted) |
| NP\_001012302.2 | -1.0 | 0.9920 | Homo sapiens | (R)FPLHKGEGR(L) | anoctamin 9 |
| NP\_001013969.1 | 2.6 | 0.5320 | Rattus norvegicus | (K)KDIAQNLTTEDLRSK(V) | solute carrier family 22 (organic cation transporter), member 22 |
| NP\_001014042.1 | 1.4 | 0.6593 | Rattus norvegicus | (R)NFTEVLSPNMYNSK(L) | **threonyl-tRNA synthetase-like 2** |
| NP\_001069.1 | 9.3 | 0.0114 | Homo sapiens | (K)mVVILGASNILWImFAASQAFK(I) | vascular cell adhesion molecule 1 |
| NP\_001074407.1 | -11.4 | 0.0009 | Rattus norvegicus | (R)EDRDPSTKAHR(N) | taste receptor, type 2, member 124 |
| NP\_001075415.1 | -3.2 | 0.0094 | Equus caballus | (K)TEPQTHYYAVAVVK(K) | **transferrin** |
| NP\_001075415.1 | 11.3 | 0.0324 | Equus caballus | (K)HQTVEQNTDGR(N) | **transferrin** |
| NP\_001075972.1 | -1.5 | 0.5639 | Equus caballus | (K)ECCHGDLLECADDR(A) | **albumin** |
| NP\_001075972.1 | 7.1 | 0.0112 | Equus caballus | (K)EACFAEEGPK(L) | **albumin** |
| NP\_001075972.1 | 11.5 | 0.0073 | Equus caballus | (K)ADFAEVSK(I) | **albumin** |
| NP\_001075972.1 | 2.7 | 0.2789 | Equus caballus | (K)DVFLGTFLYEYSR(R) | **albumin** |
| NP\_001075972.1 | -2.0 | 0.6270 | Equus caballus | (K)ADFTECCPADDK(L) | **albumin** |
| NP\_001075972.1 | 1.1 | 0.8200 | Equus caballus | (K)LVNEVTEFAK(K) | **albumin** |
| NP\_001075972.1 | -2.1 | 0.5461 | Equus caballus | (K)ECCHGDLLECADDR(A) | **albumin** |
| NP\_001075972.1 | -1.0 | 0.8519 | Equus caballus | (R)RPCFSALELDEGYVPK(E) | **albumin** |
| NP\_001075972.1 | 1.1 | 0.9256 | Equus caballus | (K)GLVLVAFSQYLQQCPFEDHVK(L) | **albumin** |
| NP\_001075972.1 | 3.3 | 0.5757 | Equus caballus | (K)KAPQVSTPTLVEIGR(T) | **albumin** |
| NP\_001075972.1 | 9.1 | 0.0093 | Equus caballus | (K)YICEHQDSISGK(L) | **albumin** |
| NP\_001075972.1 | 11.6 | 0.0084 | Equus caballus | (R)RPCFSALELDEGYVPK(E) | **albumin** |
| NP\_001075972.1 | 7.9 | 0.2963 | Equus caballus | (K)ACCDKPLLQK(S) | **albumin** |
| NP\_001075972.1 | 2.3 | 0.6517 | Equus caballus | (K)TYEATLEK(C) | **albumin** |
| NP\_001075972.1 | -1.8 | 0.3941 | Equus caballus | (R)TVFDQFTPLVEEPK(S) | **albumin** |
| NP\_001075972.1 | 1.8 | 0.4991 | Equus caballus | (K)ECCHGDLLECADDRADLAK(Y) | **albumin** |
| NP\_001075972.1 | 3.3 | 0.3862 | Equus caballus | (K)LVNEVTEFAK(K) | **albumin** |
| NP\_001075972.1 | 1.9 | 0.4917 | Equus caballus | (K)LDALK(E) | **albumin** |
| NP\_001075972.1 | 1.7 | 0.0922 | Equus caballus | (K)CCTDSLAER(R) | **albumin** |
| NP\_001075972.1 | 4.5 | 0.1306 | Equus caballus | (K)KAPQVSTPTLVEIGR(T) | **albumin** |
| NP\_001075972.1 | -3.3 | 0.4123 | Equus caballus | (K)YICEHQDSISGK(L) | **albumin** |
| NP\_001075972.1 | -2.0 | 0.6676 | Equus caballus | (K)YLYEVAR(R) | **albumin** |
| NP\_001075972.1 | 1.6 | 0.0567 | Equus caballus | (R)LCVLHEK(T) | **albumin** |
| NP\_001075972.1 | -1.3 | 0.8407 | Equus caballus | (R)LCVLHEK(T) | **albumin** |
| NP\_001075972.1 | -1.9 | 0.4945 | Equus caballus | (K)ACCDKPLLQK(S) | **albumin** |
| NP\_001075972.1 | 1.5 | 0.7483 | Equus caballus | (K)LPESER(L) | **albumin** |
| NP\_001075972.1 | -1.3 | 0.4951 | Equus caballus | (K)SEIAHR(F) | **albumin** |
| NP\_001077435.1 | -4.1 | 0.0401 | Rattus norvegicus | (K)GRDSSVTFTKESTYSmK(Y) | REV3-like, catalytic subunit of DNA polymerase zeta (yeast) |
| NP\_001093793.1 | -1.8 | 0.5509 | Bos taurus | (K)NTEVEVEPR(M) | DSN1, MIND kinetochore complex component, homolog (S. cerevisiae) |
| NP\_001156744.1 | 2.2 | 0.3694 | Equus caballus | (R)NGELLWKNAIR(H) | forkhead box P3 |
| NP\_001157081.1 | 3.3 | 0.1140 | Mus musculus | (K)ALLEVVQSGGKNIELAIIR(R) | **proteasome (prosome, macropain) subunit, alpha type, 8** |
| NP\_001157490.1 | 1.7 | 0.3650 | Equus caballus | (K)VLHSFGEGVHHLDNLK(G) | **hemoglobin, beta** |
| NP\_001178038.1 | 1.3 | 0.6920 | Rattus norvegicus | (K)SDVVETACEEECRAPGAGAHTAV(-) | neuregulin 4 |
| NP\_001182454.1 | 1.7 | 0.1127 | Equus caballus | (R)DYAAQTSPAPKAGAATGR(I) | **ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide** |
| NP\_001182477.1 | 2.4 | 0.0118 | Equus caballus | (R)GTGRGGGGGGGGGAPR(G) | serine/arginine-rich splicing factor 1 |
| NP\_001182565.1 | 1.1 | 0.9359 | Equus caballus | (R)LYARAGHALEDMLLDCRYR(G) | **amiloride-sensitive cation channel 3** |
| NP\_001185992.1 | 8.5 | 0.0099 | Bos taurus | (R)LDKmPGMFLSANPK(E) | regulator of G-protein signaling 1 |
| NP\_001192555.1 | 1.0 | 0.9557 | Bos taurus | (K)ANAmEWK(S) | hCG1641896-like |
| NP\_001229459.1 | -1.7 | 0.1793 | Equus caballus | (K)GDRGEQGDPGLPGVCKCGSIVLK(S) | C1q and tumor necrosis factor related protein 7 |
| NP\_001229474.1 | -1.1 | 0.8794 | Equus caballus | (R)AGVILNRGFSILEADEENR(A) | centromere protein J |
| NP\_001229495.1 | -2.0 | 0.4716 | Equus caballus | (R)mPGDIHVVPIGVGPHADVQELER(I) | **von Willebrand factor** |
| NP\_004032.2 | 1.6 | 0.1626 | Homo sapiens | (K)GmKDDKEEEEDGTGSPQLNNR(-) | arrestin, beta 1 |
| NP\_008835.5 | 2.6 | 0.0399 | Homo sapiens | (K)mLKALKLNSNEAR(L) | protein kinase, DNA-activated, catalytic polypeptide |
| NP\_033055.2 | -1.3 | 0.7013 | Mus musculus | (K)VYRLAYLRLNTLCAR(L) | retinoblastoma 1 |
| NP\_054828.2 | 1.8 | 0.3813 | Homo sapiens | (K)KKAVLQALEVLPVAPPPEPR(S) | ATPase family, AAA domain containing 2 |
| NP\_055368.1 | -1.1 | 0.8740 | Homo sapiens | (R)ASPTQLNAVEFLWDPAK(R) | transcription factor CP2-like 1 |
| NP\_056534.2 | 9.2 | 0.0096 | Homo sapiens | (K)NKEIWTSSPPPDSAENQTSTDIPK(T) | collagen, type V, alpha 3 |
| NP\_060252.3 | -1.5 | 0.7275 | Homo sapiens | (K)ASMPHmVQSK(K) | chromosome 10 open reading frame 18 |
| NP\_062290.2 | 2.4 | 0.2497 | Mus musculus | (R)NRDCRVDLGSEVYR(M) | PDZ and LIM domain 4 |
| NP\_443198.1 | 9.7 | 0.0091 | Homo sapiens | (K)TEAAIKNFSPYYSR(Q) | family with sequence similarity 129, member A |
| NP\_444402.2 | -1.3 | 0.2681 | Mus musculus | (R)NITQPVK(S) | matrix extracellular phosphoglycoprotein with ASARM motif (bone) |
| NP\_542414.1 | -1.1 | 0.9044 | Homo sapiens | (R)DPLREIALETAMTQR(K) | **protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)** |
| NP\_612411.4 | -10.0 | 0.0078 | Homo sapiens | (R)ELITNKMFEDSEDSCR(N) | SP140 nuclear body protein-like |
| NP\_653247.1 | 1.0 | 0.9904 | Homo sapiens | (R)FVYHLSDLCK(K) | immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides |
| NP\_659415.1 | -1.6 | 0.6082 | Homo sapiens | (R)LKGSSHAVHEmKSLK(Q) | coiled-coil domain containing 138 |
| NP\_780763.3 | 1.6 | 0.3747 | Mus musculus | (K)DSSKPQVRR(R) | claspin homolog (Xenopus laevis) |
| O77811.1 | 9.2 | 0.0117 | Equus caballus | (K)SCHTGLGR(S) | **lactotransferrin** |
| Q2QLA9.1 | -1.7 | 0.2144 | Equus caballus | (K)TKAFFmLDGIHSK(Y) | met proto-oncogene (hepatocyte growth factor receptor) |
| Q2V905.1 | 8.9 | 0.0101 | Equus caballus | (K)TDSSCR(L) | transferrin receptor (p90, CD71) |
| S17598 | 2.0 | 0.5014 | Equus caballus | (-)ATVVCLISDFSPSGLEVIWK(V) | **Ig lambda chain** |
| XP\_001074232.1 | -1.2 | 0.9205 | Rattus norvegicus | (R)MmAmQMMTNTISDDMERYK(E) | PREDICTED: hypothetical protein |
| XP\_001084939.2 | 2.2 | 0.2255 | Macaca mulatta | (R)VRRGEGNAWSR(R) | hypothetical LOC696295 |
| XP\_001086486.1 | 8.7 | 0.0131 | Macaca mulatta | (K)AALGEPSKATVSINDSVSDLPK(M) | FRAS1 related extracellular matrix protein 2 |
| XP\_001095294.2 | -1.4 | 0.2323 | Macaca mulatta | (K)TLVDTQR(G) | DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked |
| XP\_001098957.2 | 3.5 | 0.0847 | Macaca mulatta | (R)ALPRALARPPGAGDSR(A) | metal transporter CNNM3-like |
| XP\_001101291.1 | 1.3 | 0.3614 | Macaca mulatta | (K)KRDNED(-) | nucleolar protein 58-like |
| XP\_001103771.1 | 2.6 | 0.0872 | Macaca mulatta | (R)SNIYGKALTLGKNR(I) | PREDICTED: similar to zinc finger protein 382 |
| XP\_001115980.1 | 10.0 | 0.0090 | Macaca mulatta | (K)RKNSCSDLSPDESPVSVYLR(D) | nesca protein |
| XP\_001135843.1 | 9.7 | 0.0087 | Pan troglodytes | (K)VVNLYWEKPSRTVL(-) | PREDICTED: hypothetical protein |
| XP\_001146302.1 | 10.3 | 0.0115 | Pan troglodytes | (R)VFPEIDKTmRYAQmLEK(A) | tRNA-dihydrouridine synthase 1-like |
| XP\_001174699.1 | 1.4 | 0.7231 | Pan troglodytes | (R)HGmEWNGMESTRME(-) | hypothetical protein LOC750570 |
| XP\_001487909.1 | -3.0 | 0.1309 | Equus caballus | (R)STIADYLNHLIDLGVAGFR(L) | **alpha-amylase 2B-like** |
| XP\_001488384.1 | 8.5 | 0.0094 | Equus caballus | (-)MRSLGALLLLLTACLAVR(A) | protein AMBP-like |
| XP\_001488557.2 | -10.0 | 0.0103 | Equus caballus | (R)RFGTMSSmSGADDTVYMEYHSSR(S) | TFIIH basal transcription factor complex helicase XPB subunit-like |
| XP\_001488660.1 | 1.8 | 0.5382 | Equus caballus | (R)ILLAVKEFGYHRYK(F) | tctex1 domain-containing protein 3-like |
| XP\_001488679.1 | 1.0 | 0.9817 | Equus caballus | (K)mILFAFGNALAQARLLYGNDTK(V) | 39S ribosomal protein L37, mitochondrial-like |
| XP\_001488759.1 | 2.2 | 0.0974 | Equus caballus | (R)MEETKELLTEK(M) | uncharacterized protein C18orf19 homolog |
| XP\_001489045.1 | -2.1 | 0.1007 | Equus caballus | (K)NKSQmSGVKAAASDPSEK(V) | FK506 binding protein 15, 133kDa |
| XP\_001489246.1 | 10.2 | 0.0100 | Equus caballus | (R)EETNAEmLRQELDRER(Q) | GRAM domain containing 4 |
| XP\_001489301.2 | 1.3 | 0.6575 | Equus caballus | (K)mPKLGSEIIDSSTR(R) | dual serine/threonine and tyrosine protein kinase |
| XP\_001489384.3 | 1.1 | 0.6359 | Equus caballus | (K)HHQPQKRYSSR(K) | regulator of G-protein signaling like 1 |
| XP\_001489400.1 | 1.7 | 0.0608 | Equus caballus | (K)VPTADLEDVLPLAEDITTILSK(C) | **vitamin D-binding protein-like** |
| XP\_001489514.2 | 5.3 | 0.0871 | Equus caballus | (K)NGKVLYSIRLTLTLSCPMDLK(N) | glycine receptor, alpha 2 |
| XP\_001489645.2 | -1.5 | 0.8543 | Equus caballus | (R)ImNHSSILR(K) | nicotinamide mononucleotide adenylyltransferase 2-like |
| XP\_001489659.2 | 1.9 | 0.0490 | Equus caballus | (K)INRAVFSMDTLDRGAGLAK(G) | cat eye syndrome critical region protein 5-like |
| XP\_001490072.3 | 1.6 | 0.4158 | Equus caballus | (K)SGQDRPASAPQGLVLEEGPGR(L) | 5-azacytidine induced 1 |
| XP\_001490256.3 | 2.7 | 0.1127 | Equus caballus | (R)QTFENYEMNSFEILmYK(K) | potassium voltage-gated channel, subfamily H (eag-related), member 1 |
| XP\_001490256.3 | 11.0 | 0.0102 | Equus caballus | (R)RSSQSPQELFEISRPQSPESERDIFGAS(-) | potassium voltage-gated channel, subfamily H (eag-related), member 1 |
| XP\_001490356.1 | 8.8 | 0.0091 | Equus caballus | (K)EGGKDACKGDSGGPLVCK(H) | kallikrein B, plasma (Fletcher factor) 1 |
| XP\_001490396.1 | -3.5 | 0.3831 | Equus caballus | (R)LPQLK(R) | protein SCO2 homolog, mitochondrial-like |
| XP\_001490399.1 | 3.6 | 0.0718 | Equus caballus | (-)mELmNRLRAVLQASPCK(S) | carbonic anhydrase 5B, mitochondrial-like |
| XP\_001490688.1 | -10.0 | 0.0113 | Equus caballus | (K)AVVHGIVLGVPVPFPIPEPDGCK(S) | **epididymal secretory protein E1-like** |
| XP\_001491008.1 | 9.7 | 0.0085 | Equus caballus | (K)HEFGWILPTVMGFPLSEGK(L) | **PREDICTED: similar to carboxylesterase D1** |
| XP\_001491008.1 | 2.3 | 0.3003 | Equus caballus | (K)HEFGWILPTVMGFPLSEGK(L) | **PREDICTED: similar to carboxylesterase D1** |
| XP\_001491027.1 | 1.4 | 0.2019 | Equus caballus | (K)HRVSmEVAASKGLPALK(Y) | 1-acylglycerol-3-phosphate O-acyltransferase 3 |
| XP\_001491079.1 | -1.2 | 0.8234 | Equus caballus | (R)VQQQVSRCLAAYAPRGSR(G) | testis-specific protein 10-interacting protein-like |
| XP\_001491081.3 | 3.3 | 0.0159 | Equus caballus | (R)QDVDTESQKR(N) | hypothetical protein LOC100050744 |
| XP\_001491191.1 | -10.0 | 0.0102 | Equus caballus | (R)GCCFDSSIPR(V) | trefoil factor 3-like |
| XP\_001491333.3 | 2.1 | 0.4718 | Equus caballus | (K)AELLAEFANYFHYGYHECmK(N) | hairy and enhancer of split-related protein HELT-like |
| XP\_001491603.2 | 1.9 | 0.1125 | Equus caballus | (R)GLSLPAERKQALSTWK(D) | uncharacterized protein KIAA1211-like |
| XP\_001491645.1 | 10.1 | 0.0093 | Equus caballus | (K)KVLENKVIEmLPGLQR(V) | histidine protein methyltransferase 1 homolog |
| XP\_001491647.2 | -1.2 | 0.7303 | Equus caballus | (R)RVLKNANSTFEELER(L) | ATP-binding cassette, sub-family A (ABC1), member 4 |
| XP\_001491761.1 | 1.8 | 0.5574 | Equus caballus | (R)IVGVLQKPQmGER(Y) | uncharacterized protein C1orf51-like |
| XP\_001492099.2 | -1.3 | 0.6119 | Equus caballus | (R)QRPGKMTWPNNIVKTmSK(E) | ash2 (absent, small, or homeotic)-like (Drosophila) |
| XP\_001492292.3 | 2.4 | 0.2956 | Equus caballus | (K)ATLNAEEMADFYKEFLSK(N) | UPF0671 protein C14orf153-like |
| XP\_001492320.3 | 1.5 | 0.4754 | Equus caballus | (K)ESKPSGNTSmVPETSR(H) | lysine (K)-specific demethylase 6A |
| XP\_001492348.2 | -1.2 | 0.8902 | Equus caballus | (K)VSISCPFTSANLPNVK(S) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | 1.3 | 0.3764 | Equus caballus | (K)VSISCPFTSANLPNVK(S) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | 1.2 | 0.3642 | Equus caballus | (R)ILSQNNNGVFSVDVTNLR(K) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | -1.2 | 0.8515 | Equus caballus | (R)FDCALGPEVVNVAK(F) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | 1.3 | 0.7338 | Equus caballus | (K)CYYPPTSVNR(H) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | 1.2 | 0.7664 | Equus caballus | (K)IVEGQPNLK(V) | **polymeric immunoglobulin receptor** |
| XP\_001492348.2 | -1.5 | 0.2785 | Equus caballus | (K)GTGSGALSSVR(A) | **polymeric immunoglobulin receptor** |
| XP\_001492351.2 | 1.2 | 0.5254 | Equus caballus | (K)GLETGSREVVSHVIKQGK(I) | 4-hydroxyphenylpyruvate dioxygenase-like |
| XP\_001492354.2 | -1.5 | 0.0578 | Equus caballus | (K)WHSISVTRFGNVGSLSVR(E) | **laminin, alpha 1** |
| XP\_001492414.1 | 1.3 | 0.4821 | Equus caballus | (R)RIGFDVVTLSGmR(G) | vancer-related nucleoside-triphosphatase-like |
| XP\_001492506.1 | 9.0 | 0.0107 | Equus caballus | (R)NQFMHLTNYSVNK(K) | **tubulin tyrosine ligase-like family, member 10** |
| XP\_001492602.1 | 10.1 | 0.0107 | Equus caballus | (R)DFHINLFQVLPWLK(E) | **complement factor B** |
| XP\_001492692.1 | 2.0 | 0.4736 | Equus caballus | (K)QQQAAVSKKVADLILEK(Q) | coiled-coil domain containing 132 |
| XP\_001492768.1 | -3.3 | 0.5140 | Equus caballus | (K)IQDEPENKSmLCK(I) | coiled-coil domain containing 62 |
| XP\_001492787.2 | 1.5 | 0.4578 | Equus caballus | (K)WGQEDFEDNR(H) | DEP domain containing 1B |
| XP\_001492795.2 | 1.9 | 0.2339 | Equus caballus | (K)YAASSYLTR(T) | **similar to lambda-immunoglobulin** |
| XP\_001492795.2 | -1.6 | 0.7482 | Equus caballus | (K)KLSPSECP(-) | **similar to lambda-immunoglobulin** |
| XP\_001492872.2 | 9.8 | 0.0104 | Equus caballus | (K)ATVVCLISDFSPSDLTVSWK(V) | **PREDICTED: similar to IGL@ protein** |
| XP\_001492872.2 | -1.4 | 0.7888 | Equus caballus | (K)ATVVCLISDFSPSDLTVSWK(V) | **PREDICTED: similar to IGL@ protein** |
| XP\_001492872.2 | -1.6 | 0.4234 | Equus caballus | (K)YAASSYLTLTPAQWK(S) | **PREDICTED: similar to IGL@ protein** |
| XP\_001492872.2 | 4.3 | 0.1126 | Equus caballus | (K)ATVVCLISDFSPSDLTVSWK(V) | **PREDICTED: similar to IGL@ protein** |
| XP\_001492872.2 | -2.2 | 0.2480 | Equus caballus | (K)LSPSECS(-) | **PREDICTED: similar to IGL@ protein** |
| XP\_001493144.2 | -2.0 | 0.3980 | Equus caballus | (K)KLAVTEDEKFAK(D) | regulator of G-protein signaling 22 |
| XP\_001493325.1 | 1.5 | 0.2476 | Equus caballus | (R)HPEIK(V) | zinc finger protein 462-like |
| XP\_001493758.2 | -10.0 | 0.0090 | Equus caballus | (K)KmNHILQWLHPGTKGK(S) | **protein FAM75D1-like** |
| XP\_001493830.2 | -1.3 | 0.6391 | Equus caballus | (R)STQFKVIIHEVQK(E) | FYVE, RhoGEF and PH domain-containing protein 1-like |
| XP\_001493930.2 | 9.6 | 0.0103 | Equus caballus | (K)DLMSEVCKmIALSATDLK(I) | **myomesin 1, 185kDa** |
| XP\_001493930.2 | 2.3 | 0.3848 | Equus caballus | (R)QKHVSGITDTEEERIK(E) | **myomesin 1, 185kDa** |
| XP\_001494473.1 | -1.1 | 0.8678 | Equus caballus | (K)VGGmQETVLTVTGKSVKEVMK(L) | supervillin |
| XP\_001495232.1 | -1.6 | 0.3644 | Equus caballus | (R)GSPAANVDVK(V) | **transthyretin-like** |
| XP\_001495344.3 | 9.4 | 0.0091 | Equus caballus | (R)RGEQELLVPMSSAYPDR(V) | **alpha-1B-glycoprotein-like** |
| XP\_001495344.3 | 3.2 | 0.2275 | Equus caballus | (R)CEGQMPDVTFELLR(V) | **alpha-1B-glycoprotein-like** |
| XP\_001495378.3 | 2.5 | 0.3219 | Equus caballus | (K)VmDELAQRSQGGGQHSR(R) | anoctamin 2 |
| XP\_001495479.3 | 2.3 | 0.0363 | Equus caballus | (R)SPGRKPPPFPQSPK(Q) | Rho GTPase activating protein 39 |
| XP\_001495600.1 | 8.1 | 0.1019 | Equus caballus | (K)QKLQDAMGQCFPIKNCSSR(H) | suppressor of cytokine signaling 6 |
| XP\_001495776.2 | 10.7 | 0.0098 | Equus caballus | (K)VEPPHSSHEDLTDDLSTR(S) | uncharacterized protein KIAA0195-like |
| XP\_001495886.2 | -2.2 | 0.1618 | Equus caballus | (R)TDNASEVPITAPGTSNHR(N) | **ankyrin repeat and sterile alpha motif domain containing 1B** |
| XP\_001495905.2 | -1.4 | 0.6871 | Equus caballus | (K)GTEAAGATIVEAIR(T) | **alpha-1-antiproteinase 2-like** |
| XP\_001495905.2 | 1.6 | 0.6134 | Equus caballus | (K)GDTHTQILEGLR(F) | **alpha-1-antiproteinase 2-like** |
| XP\_001496130.2 | -3.8 | 0.0104 | Equus caballus | (K)LRSVISEHIKKPGLLK(Q) | ADNP homeobox 2 |
| XP\_001496187.3 | 1.2 | 0.6802 | Equus caballus | (K)GAGPKALYHAGLFLWHVGHHDK(A) | tetratricopeptide repeat domain 21B |
| XP\_001496266.1 | 9.7 | 0.0102 | Equus caballus | (K)RQQLEMLVLSSDLEDSSPRNSQELSLPR(D) | caspase recruitment domain family, member 9 |
| XP\_001496378.3 | 11.5 | 0.0120 | Equus caballus | (R)ELHLTEACSSMSFCFSPGNEDQNEDTEGK(E) | uncharacterized protein C1orf228 homolog |
| XP\_001496389.2 | -2.2 | 0.5907 | Equus caballus | (K)EVDELFREANIEPNGK(V) | calmodulin-like 4 |
| XP\_001496861.1 | -2.1 | 0.4365 | Equus caballus | (R)KDAEDWFFSKTEELNR(E) | keratin, type I cytoskeletal 42-like |
| XP\_001497102.3 | 5.0 | 0.1639 | Equus caballus | (R)WVQKGmK(I) | c-C motif chemokine 25-like |
| XP\_001497214.1 | 3.6 | 0.1562 | Equus caballus | (-)mAVPAVSGLSR(Q) | **ATP synthase subunit O, mitochondrial-like** |
| XP\_001497655.2 | 11.2 | 0.0083 | Equus caballus | (R)TTSRPFLTQKETSPGGSNQEIHKSGLIPLK(A) | DEAD (Asp-Glu-Ala-Asp) box polypeptide 60 |
| XP\_001497822.2 | 2.6 | 0.3766 | Equus caballus | (K)VILFTmFLVVYLINLLGNLGMIILIR(M) | similar to olfactory receptor Olr569 |
| XP\_001497860.1 | 10.0 | 0.0111 | Equus caballus | (K)VVFHPDYQEVDIGLIK(L) | **haptoglobin-like** |
| XP\_001497860.1 | -1.6 | 0.2299 | Equus caballus | (K)VPSILDWVQK(T) | **haptoglobin-like** |
| XP\_001497860.1 | 9.0 | 0.0101 | Equus caballus | (R)IIGGLLDAK(G) | **haptoglobin-like** |
| XP\_001498046.3 | 8.8 | 0.0079 | Equus caballus | (K)DSPVLFDFFEDTELYR(Q) | **histidine-rich glycoprotein-like** |
| XP\_001498217.2 | 2.0 | 0.0336 | Equus caballus | (R)LTIFNILSGIATFLmVTImR(I) | ATP-binding cassette sub-family A member 3-like |
| XP\_001498473.2 | 4.1 | 0.0070 | Equus caballus | (R)FSLATmK(N) | PREDICTED: similar to cytochrome P450 |
| XP\_001498764.2 | -1.5 | 0.3952 | Equus caballus | (K)NALQYR(G) | ubiquitin specific peptidase 48 |
| XP\_001499311.2 | 10.7 | 0.0095 | Equus caballus | (R)QLTQHAVEGDCDVR(L) | **alpha-2-HS-glycoprotein-like** |
| XP\_001499542.1 | 2.0 | 0.4700 | Equus caballus | (K)LEQLKPR(A) | talin 2 |
| XP\_001499874.2 | -2.8 | 0.1043 | Equus caballus | (K)NIWKRALHAR(L) | WAP four-disulfide core domain protein 1-like |
| XP\_001500013.1 | -1.2 | 0.8466 | Equus caballus | (K)TGSTFKVKVGDK(E) | dynein, axonemal, heavy chain 5 |
| XP\_001500056.1 | 6.7 | 0.0993 | Equus caballus | (R)EAIEmHENGSTK(N) | HEG homolog 1 (zebrafish) |
| XP\_001500151.1 | -1.1 | 0.8910 | Equus caballus | (K)GKMWEEAISLCK(E) | dedicator of cytokinesis 2 |
| XP\_001500407.1 | 1.5 | 0.7732 | Equus caballus | (K)DCKPPVYLLVELEDK(D) | v-myb myeloblastosis viral oncogene homolog (avian)-like 2 |
| XP\_001500407.1 | 1.4 | 0.7435 | Equus caballus | (K)DCKPPVYLLVELEDK(D) | v-myb myeloblastosis viral oncogene homolog (avian)-like 2 |
| XP\_001500579.1 | 2.8 | 0.3708 | Equus caballus | (R)HDDLDGDMLGNFVSSK(R) | protein FAM188B-like |
| XP\_001500660.2 | 1.1 | 0.7888 | Equus caballus | (K)SYLLPDKQSKR(K) | synaptotagmin-like 1 |
| XP\_001500660.2 | -2.2 | 0.6877 | Equus caballus | (R)SDPYVKSYLLPDKQSK(R) | synaptotagmin-like 1 |
| XP\_001500688.2 | 2.3 | 0.1850 | Equus caballus | (R)SLPPIPSASRTGFAEFSmR(E) | coiled-coil and C2 domain containing 2A |
| XP\_001501063.2 | -10.0 | 0.0098 | Equus caballus | (R)ARAAPNVPCGVCVSAEK(V) | WD repeat-containing protein 1-like |
| XP\_001501280.2 | 1.1 | 0.8312 | Equus caballus | (K)HAMVKTRPLSQATRAAK(A) | growth inhibition and differentiation-related protein 88-like |
| XP\_001501350.1 | -3.5 | 0.0661 | Equus caballus | (R)QSmGGARAQQDLRVR(F) | tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2 |
| XP\_001501699.3 | -10.0 | 0.0101 | Equus caballus | (K)ELALFLEGEDMLRLK(K) | acyl-CoA oxidase 3, pristanoyl |
| XP\_001501823.1 | -4.5 | 0.0074 | Equus caballus | (R)EmRITTVAGTKPYMAPEMFNSRR(E) | serine/threonine kinase 32A |
| XP\_001501849.1 | 9.5 | 0.0108 | Equus caballus | (K)ADDGCSPHKmKTVK(C) | ly6/PLAUR domain-containing protein 3-like |
| XP\_001501956.1 | 2.3 | 0.0396 | Equus caballus | (K)QEFLDKPEDVLLKHQASINELKR(T) | **erythrocyte membrane protein band 4.1-like 1** |
| XP\_001502145.2 | 1.5 | 0.5840 | Equus caballus | (K)WGSARPDK(E) | similar to 5033413D22Rik protein |
| XP\_001502226.1 | 9.9 | 0.0087 | Equus caballus | (K)HEVSVPYAmNLLNGIKLFGRPIK(I) | RNA-binding protein 7-like |
| XP\_001502242.3 | 9.1 | 0.0098 | Equus caballus | (R)AGSTFRQSDVDVNSNGGRR(R) | TBC1 domain family member 23-like |
| XP\_001502250.1 | 3.1 | 0.1772 | Equus caballus | (R)IPKPNRNILIQmDLPLVPGDK(I) | sodium channel protein type 10 subunit alpha-like |
| XP\_001502519.1 | 1.1 | 0.8918 | Equus caballus | (K)DGGGASLAEYHSK(A) | **apolipoprotein A-I-like** |
| XP\_001502657.3 | -3.5 | 0.0636 | Equus caballus | (K)ALGLSLDSPASHTQEAAGTIAAEVmPLTRK(T) | neuromedin-B-like |
| XP\_001502952.2 | 6.3 | 0.0267 | Equus caballus | (K)AmEEAVKRTR(D) | coiled-coil domain containing 91 |
| XP\_001502975.3 | 7.4 | 0.0121 | Equus caballus | (K)SEGETIVSSNMGKRTSEATK(V) | coatomer subunit delta-like |
| XP\_001503133.1 | -2.9 | 0.2605 | Equus caballus | (K)LQDKVEKCK(Q) | protein kinase C and casein kinase substrate in neurons 2 |
| XP\_001503278.1 | 2.4 | 0.1411 | Equus caballus | (R)GAMGFILmYDITNEESFNAVQDWSTQIK(T) | ras-related protein Rab-3A-like |
| XP\_001503430.1 | 3.8 | 0.0710 | Equus caballus | (R)GSNTYTLTDVR(R) | activated leukocyte cell adhesion molecule |
| XP\_001503519.1 | -2.3 | 0.5807 | Equus caballus | (K)LTVENIGYQmLMK(M) | SURP and G-patch domain-containing protein 1-like |
| XP\_001503659.1 | 9.9 | 0.0092 | Equus caballus | (K)TNKITAAMR(Q) | RUN and FYVE domain containing 2 |
| XP\_001503693.2 | -6.3 | 0.0108 | Equus caballus | (R)RISQIQQLNQMPLYPTEK(I) | aquarius homolog (mouse) |
| XP\_001503726.1 | -1.1 | 0.9519 | Equus caballus | (R)IIDKNGIHELDNISFPK(H) | proteasome subunit beta type-2-like |
| XP\_001503943.2 | -1.3 | 0.7148 | Equus caballus | (R)SISPLPGEKPLEESK(M) | cardiomyopathy associated 5 |
| XP\_001504055.1 | -1.3 | 0.3939 | Equus caballus | (K)LKVELRSAVEEVVK(E) | ring finger protein 20 |
| XP\_001504392.2 | -1.7 | 0.1017 | Equus caballus | (K)GVSHSRPNTEDTSLCYANR(S) | SET and MYND domain containing 4 |
| XP\_001504425.1 | -2.2 | 0.4382 | Equus caballus | (K)TLNDKFASFIDK(V) | keratin 7 |
| XP\_001504550.1 | -8.4 | 0.1972 | Equus caballus | (K)YEEEIKLLEEK(L) | tropomyosin beta chain-like |
| XP\_001504781.1 | 1.3 | 0.6088 | Equus caballus | (R)VEAmITKGLEAR(Q) | neuferricin-like |
| XP\_001716079.1 | 7.5 | 0.0100 | Homo sapiens | (R)GHPHPRLTDVPGTQmSRGVR(G) | |
| XP\_001718455.1 | -1.1 | 0.9110 | Homo sapiens | (R)GGALPSGKTPGSREK(V) | hypothetical protein LOC100134737 |
| XP\_001914702.1 | 2.6 | 0.4828 | Equus caballus | (K)ILLDDLmRK(A) | leucine-rich repeat serine/threonine-protein kinase 2-like |
| XP\_001914906.1 | -1.3 | 0.5911 | Equus caballus | (R)GLAVGNGTVSGIVQAVDAETGK(L) | nucleoporin 210kDa |
| XP\_001915188.2 | -3.1 | 0.0901 | Equus caballus | (K)DTVRDNSHDLSPISLSGSPSSIEVMR(C) | synaptonemal complex protein 2-like |
| XP\_001915320.1 | 10.3 | 0.0099 | Equus caballus | (R)CIIQMQGNSTSIINPKNPKEAPK(S) | kinesin family member 1B |
| XP\_001915320.1 | -1.3 | 0.6615 | Equus caballus | (R)ETSKESRCIIQMQGNSTSIINPK(N) | kinesin family member 1B |
| XP\_001915324.1 | 10.2 | 0.0106 | Equus caballus | (K)LHLLPGASKSNKLR(T) | rabphilin-3A-like |
| XP\_001915450.1 | -1.9 | 0.2851 | Equus caballus | (K)VNDAVTTDGVQTTR(S) | **similar to lambda-immunoglobulin** |
| XP\_001915450.1 | 3.5 | 0.1795 | Equus caballus | (K)VNDAVTTDGVQTTR(S) | **similar to lambda-immunoglobulin** |
| XP\_001915455.1 | -1.1 | 0.8256 | Equus caballus | (K)SYSSVSCQVK(H) | **similar to lambda-immunoglobulin** |
| XP\_001915455.1 | 1.4 | 0.5619 | Equus caballus | (K)SYSSVSCQVK(H) | **similar to lambda-immunoglobulin** |
| XP\_001915589.1 | 1.3 | 0.6026 | Equus caballus | (R)EPGQALVVLPLTITTDFIPSFR(L) | **complement C3-like** |
| XP\_001915589.1 | -1.3 | 0.4547 | Equus caballus | (K)ADIGCTPGSGR(D) | **complement C3-like** |
| XP\_001915798.1 | -10.0 | 0.0111 | Equus caballus | (K)GSRAHGHSSSGLEK(R) | DOT1-like, histone H3 methyltransferase (S. cerevisiae) |
| XP\_001915803.1 | -4.3 | 0.3122 | Equus caballus | (R)VGMPDAKAIAAEQR(G) | chromodomain helicase DNA binding protein 7 |
| XP\_001915890.2 | -1.3 | 0.8466 | Equus caballus | (K)LSLEESK(K) | nebulin |
| XP\_001916340.1 | 11.4 | 0.0093 | Equus caballus | (K)KVLHAESTKTSLLR(S) | **von Willebrand factor A domain containing 3B** |
| XP\_001916399.1 | -1.9 | 0.4064 | Equus caballus | (R)GDAWNAQEPARRPQRAAQAAGVETGVR(F) | hypothetical protein LOC100147469 |
| XP\_001916438.1 | 1.8 | 0.5021 | Equus caballus | (R)VLVARLGHFAPVDAVADQR(A) | PREDICTED: similar to chromosome 14 open reading frame 169 |
| XP\_001916535.1 | 8.5 | 0.0099 | Equus caballus | (R)RNSGATFTEGSWSPELPFDNIVGK(Q) | adenylate cyclase 8 (brain) |
| XP\_001916685.1 | 10.2 | 0.0086 | Equus caballus | (R)VSDGEQAKmSREISLSELECK(D) | **microtubule-actin crosslinking factor 1** |
| XP\_001916798.2 | 10.5 | 0.0134 | Equus caballus | (R)NIVFQSAVPKVMKVK(L) | ADP-ribosylation factor-binding protein GGA1-like |
| XP\_001916843.2 | -2.2 | 0.3740 | Equus caballus | (R)GNAYHLACFACFSCKR(Q) | LIM/homeobox protein Lhx6-like |
| XP\_001916958.2 | -1.5 | 0.6268 | Equus caballus | (K)KPEGASCSR(L) | myosin XVI |
| XP\_001917022.1 | 1.6 | 0.4591 | Equus caballus | (R)GARAAAGLGQKPGGR(A) | immunoglobulin mu binding protein 2 |
| XP\_001917072.2 | -1.4 | 0.1189 | Equus caballus | (K)LLQNRGADSNVR(D) | ankyrin repeat domain-containing protein 2-like |
| XP\_001917252.1 | -6.4 | 0.0097 | Equus caballus | (K)MGLGGNPYGPAGTGKTESVK(A) | cytoplasmic dynein 2 heavy chain 1-like |
| XP\_001917253.2 | -1.1 | 0.9196 | Equus caballus | (R)LTSTGPGLHWLSEALR(L) | prolylcarboxypeptidase (angiotensinase C) |
| XP\_001917292.1 | 1.6 | 0.5441 | Equus caballus | (R)SAGWNIPIGLLLPSDPFQEAVAK(F) | inhibitor of carbonic anhydrase-like |
| XP\_001917394.1 | 1.7 | 0.0182 | Equus caballus | (R)DLEEQIETEmGKK(T) | oiled-coil domain-containing protein 22-like |
| XP\_001917502.2 | 10.1 | 0.0121 | Equus caballus | (R)NLVYGKANDDNK(I) | **catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)** |
| XP\_001917535.2 | 4.0 | 0.0535 | Equus caballus | (R)GYRLPTSALVNLSHGSR(S) | 5'-3' exoribonuclease 1 |
| XP\_001917584.1 | 11.9 | 0.0090 | Equus caballus | (R)ImAENAAGISAPSPTSPFYK(A) | **PREDICTED: similar to titin** |
| XP\_001917584.1 | 2.3 | 0.2750 | Equus caballus | (K)GTQEITGDDKIELIKDGTK(H) | **PREDICTED: similar to titin** |
| XP\_001917633.1 | 3.9 | 0.2902 | Equus caballus | (R)AAVENGTKNGIAVDHVVGMSTGKDTETIELR(H) | biorientation of chromosomes in cell division protein 1-like |
| XP\_001917739.1 | 1.9 | 0.4244 | Equus caballus | (K)mRECHGLVDALVTYINHALDVGK(C) | plakophilin-3-like |
| XP\_001917763.2 | -1.8 | 0.3979 | Equus caballus | (R)LLLHLFR(A) | mediator complex subunit 12-like |
| XP\_001917902.1 | 10.2 | 0.0114 | Equus caballus | (-)mAAPSAVAVASTRLGSHSQGGGLR(L) | similar to WAS protein |
| XP\_001917910.1 | -2.9 | 0.1461 | Equus caballus | (R)KIDAGAmTEPLASPSGPRGAVVTTGSGK(N) | **uncharacterized protein C9orf40-like** |
| XP\_001918016.2 | 1.9 | 0.6093 | Equus caballus | (K)RGPAGTPGPEGR(Q) | collagen, type XI, alpha 2 |
| XP\_001918110.1 | 1.1 | 0.8582 | Equus caballus | (K)IDSLmSENTNLKKTMSHQHVPVK(T) | uveal autoantigen with coiled-coil domains and ankyrin repeats protein-like |
| XP\_001918231.1 | -1.1 | 0.8080 | Equus caballus | (R)VSETGKGPTLELAGTGSRGGTR(E) | additional sex combs like 2 (Drosophila) |
| XP\_001918232.2 | 9.7 | 0.0094 | Equus caballus | (R)mGPGIGAILERSIDMDRGFLTGPmGSGmR(E) | myelin expression factor 2-like |
| XP\_001918280.1 | 8.3 | 0.0104 | Equus caballus | (K)AEIAHRGVDVEAAKR(A) | protein phosphatase 1, regulatory (inhibitor) subunit 12C |
| XP\_001918366.1 | 9.4 | 0.0101 | Equus caballus | (R)EGNTQKQETTFSFK(D) | ATPase family, AAA domain containing 5 |
| XP\_001918404.1 | 5.2 | 0.2339 | Equus caballus | (K)ENASRAK(E) | protein KHNYN-like |
| XP\_001918421.1 | 1.0 | 0.9338 | Equus caballus | (R)EENGFTDVPSR(S) | F-box and WD repeat domain containing 10 |
| XP\_219988.4 | 9.8 | 0.0109 | Rattus norvegicus | (K)EEIVNLTKLIEQGSGLSmDQDSNIR(D) | coiled-coil domain containing 147 |
| XP\_512397.2 | -1.0 | 0.9570 | Pan troglodytes | (R)TRSSPSKAPR(A) | PREDICTED: similar to basic calponin isoform 4 |
| XP\_518534.2 | 8.7 | 0.0100 | Pan troglodytes | (R)NCPTVTCASHYRRVGQR(R) | polycystic kidney and hepatic disease 1 (autosomal recessive) |
| XP\_533954.2 | 2.2 | 0.1158 | Canis familiaris | (-)mGHVVRSGPR(G) | thimet oligopeptidase 1 |
| XP\_537726.2 | -3.2 | 0.1182 | Canis familiaris | (K)RPELVLAAVRTLSGmCSGHR(A) | unc-45 homolog B (C. elegans) |
| XP\_542120.2 | -1.1 | 0.9211 | Canis familiaris | (K)AEGCSIAGRGAAPPPGR(C) | hypothetical LOC485002 |
| XP\_543722.2 | 3.7 | 0.2000 | Canis familiaris | (R)SSITHLLCATK(D) | solute carrier family 38, member 2 |
| XP\_544172.2 | 1.3 | 0.5655 | Canis familiaris | (K)KGmLWSK(M) | solute carrier family 26, member 7 |
| XP\_545906.2 | 4.9 | 0.0429 | Canis familiaris | (R)GSPGSALR(S) | SH3 domain and tetratricopeptide repeats 1 |
| XP\_546536.2 | -5.1 | 0.2817 | Canis familiaris | (R)KTMAENDSTESQTSR(S) | **exophilin 5** |
| XP\_547449.2 | 2.2 | 0.1179 | Canis familiaris | (R)NTSESSTSSVK(E) | SEC16 homolog B (S. cerevisiae) |
| XP\_587457.4 | 1.8 | 0.4890 | Bos taurus | (R)AASPGHARDR(G) | ATPase, Ca++ transporting, type 2C, member 2 |
| XP\_589886.3 | -1.2 | 0.7633 | Bos taurus | (R)SQDPPDKTVDISDLATK(L) | SET domain containing 2 |
| XP\_604488.4 | 1.4 | 0.7261 | Bos taurus | (R)QCRDHEDGPLSLVMPK(K) | PREDICTED: similar to Transcription factor E2F7 |
| XP\_850769.1 | 1.1 | 0.9230 | Canis familiaris | (K)GETKMRNMmAK(Q) | similar to Hyaluronan mediated motility receptor (Intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen) |
| XP\_851577.1 | -1.3 | 0.6087 | Canis familiaris | (K)SYHMEKKSPSVYSR(S) | claudin 8 |
| XP\_852467.1 | 11.4 | 0.0102 | Canis familiaris | (R)GEGGAVPGASARGGLTAGRGR(R) | similar to homeo box D1 |
| XP\_854870.1 | 2.9 | 0.4152 | Canis familiaris | (-)MNAGPPWNKVQRSK(H) | similar to Protein C20orf177 |
| XP\_861681.1 | 9.8 | 0.0094 | Canis familiaris | (K)MGEGSLPSTSSKVR(V) | similar to exonuclease NEF-sp |