OpenCustomDB: Integration of unannotated open reading frames and genetic variants to generate more comprehensive customised protein databases

Supporting information

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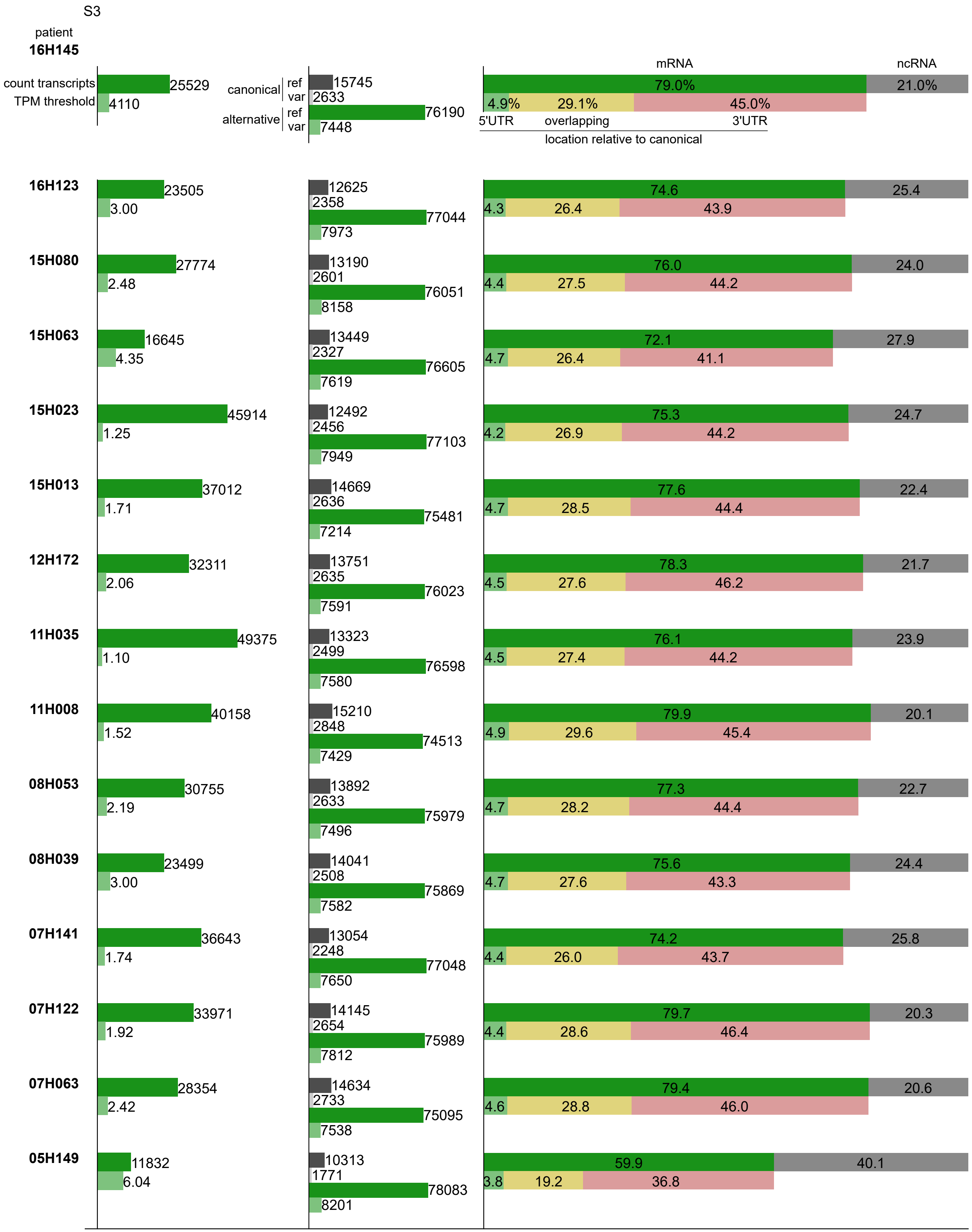
Supplementary figure 1: Customised protein sequence databases that integrate reference and variant proteins. For each patient, both the composition (left) and the localisation of predicted coding sequences (right) are shown. OpenCustomDB was run with (green bars) or without (grey bars) integration of altProts and novel isoforms. The size of the databases with altProts and novel isoforms was limited to a total of 100,000 entries by imposing the corresponding TPM threshold.

Supplementary Figure 2: Number of genes coding for proteins identified with OpenCustomDB libraries with and without alternative proteins. For each patient, the number of genes identified using customised protein sequence databases integrating reference and variant proteins with alternative proteins (green) and without (canonical library only, grey). Despite the difference in size between the two databases for each patient, there is a notable overlap in identified genes.

Supplementary Figure 3: Examples of MS2 spectra assigned to a reference protein with a canonical protein database and reassigned to an alternative protein with a database containing canonical proteins, altProts, and novel isoforms. MS/MS spectrum confidently mapped to either a peptide unique to the reference protein P46100 (A) or Q96QH2 (B) using a database containing canonical proteins only (bottom spectrum), or to a peptide unique to the novel isoform II_726022 (A) or IP_643011 (B) using a database containing canonical proteins, altProts, and novel isoforms (top spectrum). Peaks are represented by their mass over charge ratios (m/z) and their intensity relative to the highest (relative intensity). The y ions are colored in red, the b ions in blue and the unannotated peaks appear in grey.

Supplementary Table 1: list of variant peptides in canonical and alternative proteins.



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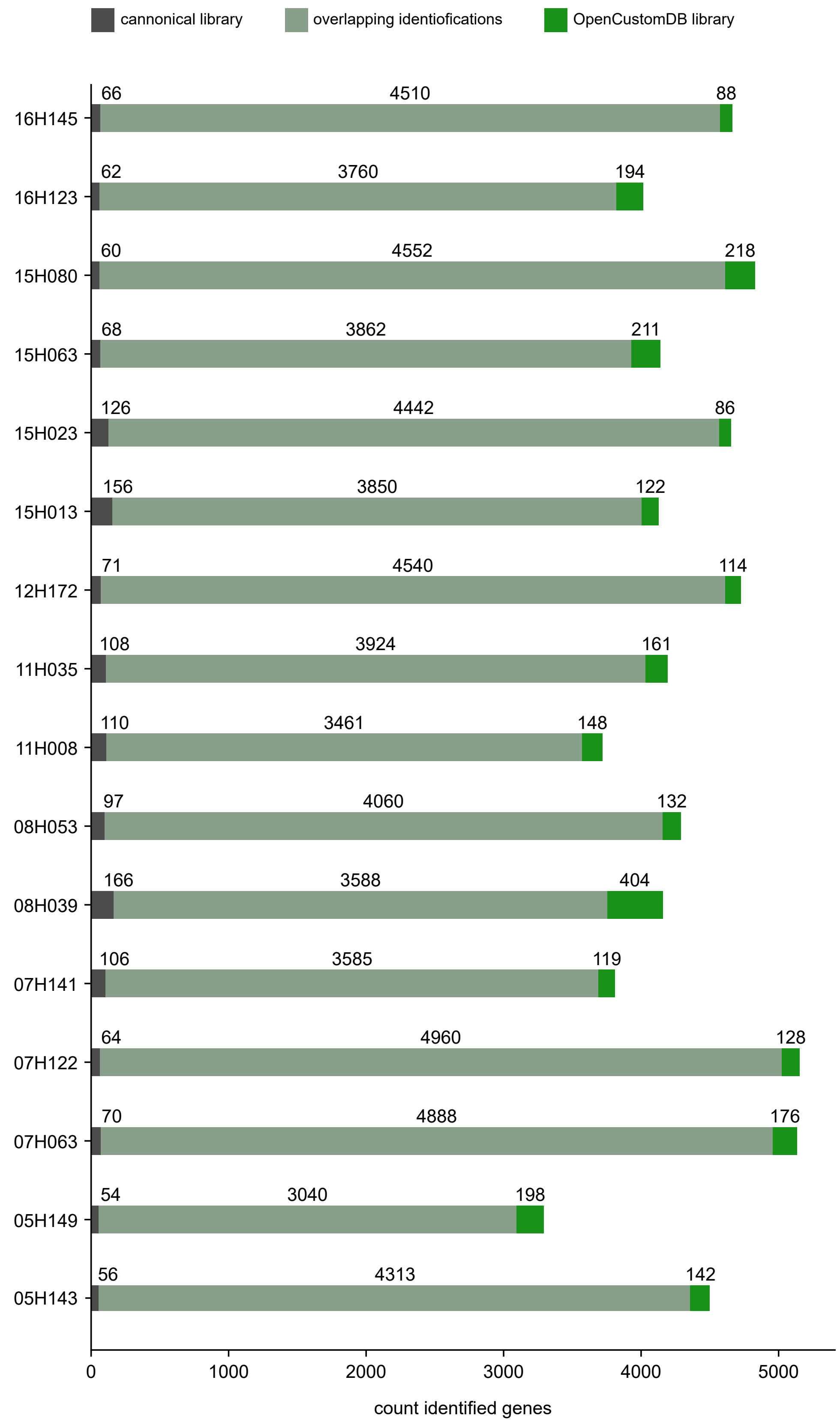
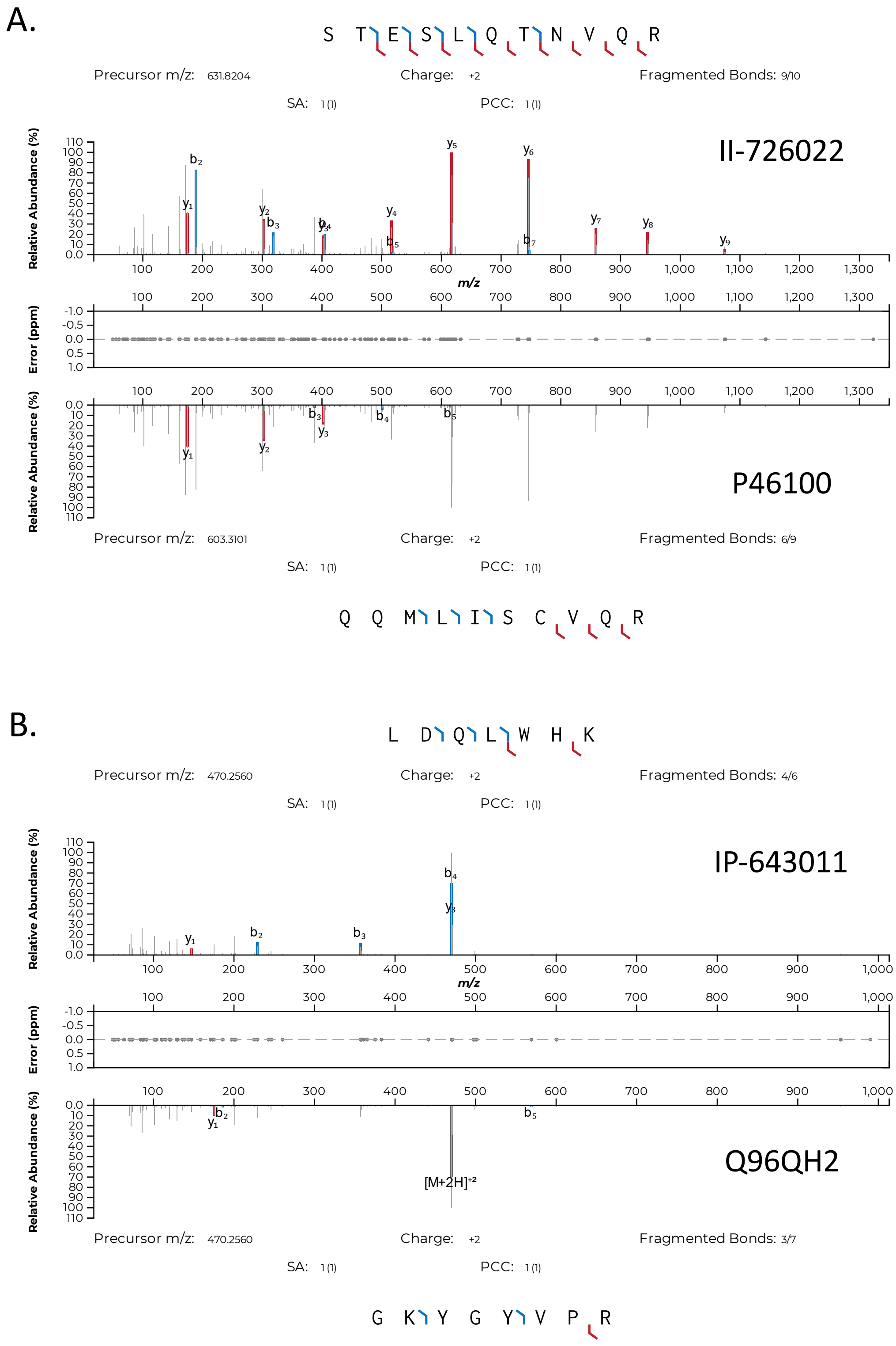


Supplementary figure 2: Number of genes coding for proteins identified with OpenCustomDB libraries with and without alternative proteins. For each patient the number of genes identified using customized protein sequence databases integrating reference and variant proteins with alternative proteins (green) and without (canonical only library, gray). Despite the difference in size between the two databases for each patient, there is a remarkable overlap in identified genes.



Supplementary Figure 3: Examples of MS2 spectra assigned to a reference protein with a canonical protein database and reassigned to an alternative protein with a database containing canonical proteins, altProts, and novel isoforms. MS/MS spectrum confidently mapped to either a peptide unique to the reference protein P46100 (A) or Q96QH2 (B) using a database containing canonical proteins only (bottom spectrum), or to a peptide unique to the novel isoform II_726022 (A) or IP_643011 (B) using a database containing canonical proteins, altProts, and novel isoforms (top spectrum). Peaks are represented by their mass over charge ratios (m/z) and their intensity relative to the highest (relative intensity). The y ions are colored in red, the b ions in blue and the unannotated peaks appear in grey.

Supplementary Table 1

variant_canonical: variants in canonical proteins. The Ensembl accession ID is indicated in the first co

variant_non-canonical: variants in altProts (accession ID: IP_XXXXXX) and novel isoforms (accession

Variant	**Numer of patient**
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ENSP00000216605.12@Lys134ArgArg653Gln	11
ENSP00000323889.8@Pro358Leu	11
ENSP00000272163.8@Ser154Asn[Pro87ProVal39Val]	9
ENSP00000345445.4@Asp110GlyIle345Val[Gly137GlyHis260HisLeu339LeuGly	9
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ENSP00000342139.10@Phe19TyrArg36CysMet56ValArg184Ser[Pro24ProLeu1	8
ENSP00000267884.10@Pro124Ala[Leu94LeuLys43Lys]	8
ENSP00000366934.5@Ser58AlaTrp50ArgArg10Trp[Asp476Asp]	7
ENSP00000236959.13@Thr116Ser	7
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ENSP00000216714.7@Ile64ValAsp148Glu	6
ENSP00000483501.4@Pro85Thr	5
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ENSP00000366927.3@Arg107LeuVal253Met[Ile65Ile]	5
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ENSP00000246747.8@Val141Ala	5
ENSP00000362463.4@Glu111Ala	5
ENSP00000419475.5@Ile113Leu[Asn189AsnLeu165Leu]	5
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ENSP00000005587.6@Ala202Ser	4
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ENSP00000355990.5@Gln109Glu	4
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Gene	Identified Peptides
ECHS1	IFEEDPAVGAIVLTGGDK
NAT10	TLHEVSLQESIR
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TRIM25	LQELTPSSGDPGEHDPASTHK
LBR	FNLSQESSYIATQYSLRPR
SAMM50	FYLGGPTSVR
FAM241A	EAAGTEWDPGASPR
LGALS8	SGTPQLSLPFAAR
SRP14	AAAAAAAAAPAAAATAATTAATTAATAAQ
NOL9	LLQAQAAGVDWR
ATIC	TVASPGVSVEEAVEQIDIGGVTLLR
CPPED1	LADKFIHAGVR
LHPP	GLRPYLLIHDGVR
APEX1	VSYGIGEEEHDQEGR
SLC4A1AP	SLQEEQSRPTTAVSSPGGPAR
TRAPPC5,AC0C	VFSVAELQAR
ALDH1B1	LLNLLADLVER
SCFD1	FGQDIISPLLSVR
ARL2	EALELDSIR
GLO1	ATLELTHNWGTEDDATQSYHNGNSDPR KATLELTHNWGTEDDATQSYHNGNSDPR
COMMD2	TLLSELAPSLPSYHNLEWR
TMEM43	EIGHNNPSAMAVESFTATAPFVQIGR
FBP1	IYSLNEGYAK
PLIN3	AQEALLQLSQALSLMETVK
TAPBPL	NEVLWHPTLNLPLSPQGTVR
NDUFA6	QVTSTASTFVKPIFSR
SKAP2	IYQFTASSPK
BCL2L13	ESDTEVITVEK
PML	VVIQPEALFSIYSK
TOR1AIP1	LQQQHSEQPPLQPSPVTTR SVLSSGYQK
THEMIS2	WLDLTVVEAK
SGPL1	AFEPYLEILELYSTK
PCYOX1	YGFQFLR
AIP	EQPGSPEWIQLDK
ALDH5A1	VYGDIIYTPAK
PNPT1	EVGTSDKEILTSR
TRAF3IP3	FLENEHQELQAK
MCM7	FELYFQGPSSSKPR RFELYFQGPSSSKPR
MAN2B1	LIQLVNAQQAK
BDH2	QIDQFASEVER
PLIN3	AQEALLQLSQALSLMETVK ESYPHVKTVCDAAEK
GSTO1	SQNKEDYDGLKEEFR EDYDGLKEEFRK
CPPED1	LADKFIHAGVR FIHAGVRVVFSGHYHR
PECAM1	TTAEYQLLVEGVPSPR
GLO1	KATLELTHNWGTEDDATQSYHNGNSDPR
CMPK1	KNPDSHYGELIEK

NMI	EHLPDEFIKDEQNK
CYBA	KKPSEEEAAAAAGGPPGGPQVNPIPVTDEVV
HMGA1	KQPPKEPSEVPTPK
SLC16A1	AAESPDQKDTEGGPKEEESPV
SDR39U1	RTLATGYQYSFPELGAALK
GBE1	LFAYSSWEVLR
SYTL4	DTVNPLYDETLR
GFM1	GIIDLIEER
DHX16	FSTFFDGAPVFR
NOL9	LLQAQAAGVDWR
MRPL37	VFHFLVFQLNTTDLDSNEGVK
DYNC1LI1	YGAALIYTSVK
GSTO1	SQNKEDYDGLKEEFR
HEXB	PGPALWPLPLSVK GILVDTSR
MYH9	DLEAHVDSANK DLEAHVDSANKNRDEAIK
NCF2	LYEPVVIPVGR
DUS3L	FAGAHLGPEGQNLVQEELAAR
HEXB	PGPALWPLPLSVK
GBP1	VQLPTESLQELLDLHR
TAPBPL	NEVLWHPTLNLPLSPQGTVR AVDVVLDCFLVK
IDH1	VTYLVHNFEEGGGIAMGMYNQDK
HAT1	LMQGFNEDMAIEAQQK
DDRGK1	VSIAELAQASNSLITWGR
NLE1	AAAVADEAVAR TGKSYLASLR
DIDO1	LAAETGEGEGEPLSR
ALDH1B1	LLNLLADLVER EVFRLGSPWRR
CEBPZ	ASLIEEDEPAEKENSSK
FKBP15	FGAAVLGNHTTR
PRKDC	KEEENASVTDSAELQAYPALVVEK EEENASVTDSAELQAYPALVVEK
NUP210	NPLLDLAAYDQEGR NPLLDLAAYDQEGRR
PDLIM1	TAASGVEASSRPLDHAQPPSSLVIDKESEVYK TAASGVEASSRPLDHAQPPSSLVIDK
LRRC8C	SNTIQSGPEGSLVNSQSLK
AIP	EQPGSPEWIQLDK QITPLLLNYCQCK
HEXB	PGPALWPLPLSVK GILVDTSR GILVDTSRHYLPVKIILK
RPA1	NIYLMDASGK
MYH9	DLEAHVDSANK
RNASEH2A	LQDSDTEYGSGYPNDPK
MYO1G	DKDGFGAVLFSSHVR IFLQTLDTHHR
RETREG2	DLGEGEEGELAPPEDLLGHPQALSR
CPVL	QVGDFHQVIIR
BCL2L13	LQEQHLSSPQGVQLDR ASQSLDQEILLK
SCRN2	SVFKPFIFGVGVAQAPQVLSPTFGAQDPVR
HLA-DPA1	ETVWHLEEFGR
HDHD3	RLEGILEGLGLR LEGILEGLGLR
PECAM1	TTAEYQLLVEGVPSPR
RETREG2	DLGEGEEGELAPPEDLLGHPQALSR
GART	GIQQHKEEAWVIGSVVAR

QPRT	YGLLVGGAVSHR
LACTB	YAMAWGVVEK
CTSG	NVSPVALPR
PDLIM1	TAASGVEASSRPLDHAQPPSSLVIDKESEVYK
WDR55	AHGAPINSLLLVDENVLATGDDTGGIR
CBR4	EHDVQNTFEEMEK
DIDO1	LAAETGEGEGEPLSR RLAAETGEGEGEPLSR
MCM3	DSKEPFSSVEIQAALSK EPFSSVEIQAALSK
NUDCD1	SFTFVQAGQDLEENMDEDVSEK
APEX1	VSYGIGEEEHDQEGR VCSWNVDGLRAWIKK
WDR55	AHGAPINSLLLVDENVLATGDDTGGIR
LRCH1	VLPQELVDLPLVK
SCLY	VSGQTEVDDILAAVRPTTR
MYO1G	IFLQTLDTHHR DKDGFGAVLFSSHVR
SUCLA2	SFQGPVLIGSSHGGVNIEDVAAETPEAIIK SFQGPVLIGSSHGGVNIEDVAAETPEAIIKEPIDIEEGIKK
USE1	QSAAELDLVLQR
LMAN1	NSLSETVR
MIA2	NLQTQQASLQSENTHFENENQK
NCAPD2	SIDPGLKEDTLEFLIK
PNPT1	EVGTSDKEILTSR REVGTSDKEILTSR
SDR39U1	RTLATGYQYSFPELGAALK WNETFQKEVLGSR
ERCC2	ETDAHLANPVLPNEVLQEAVPGSIR
NUP210	NPLLDLAAYDQEGR
ZNF22	SFGQSSTLFQHQK
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SRP14	AAAAAAAAAPAAAATAATTAATTAATAAQ
NOL9	LLQAQAAGVDWR
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PRKDC	KEEENASVTDSAELQAYPALVVEK EEENASVTDSAELQAYPALVVEKMLK
NUP133	SSFYSLTSSNVSK
TMX4	SEANDQGPPREDGVTR
PML	VVIQPEALFSIYSK
HEXB	PGPALWPLPLSVK GILVDTSR RYHGYIFGFYKWHHEPAEFQAR
DPP3	LIVQPNTHLEGSDVQLLEYEASAAGLIR KLIVQPNTHLEGSDVQLLEYEASAAGLIR
TOR1A	ITHVALDFWR
HOMER3	AAQLLDVR LFELSELR
ALDH5A1	VYGDIIYTPAK RVYGDIIYTPAK
TOR1AIP1	LQQQHSEQPPLQPSPVTTR
ARFGAP3	YFDEPVELR YFDEPVELRSSSFSSWDDSSDSYWKK
HEXB	PGPALWPLPLSVK
DIDO1	LAAETGEGEGEPLSR
DMAC1	PATPATPGAPTSPAEHR LSQPFESYITAPPGTAAAPAKPATPATPGAPTSPAEHR
TRAP1	DVGEWQHEEFYR
GFM1	AIYFDGDFGQIVR
HLA-A	APWIEQEGPEYWDGETRK APWIEQEGPEYWDGETR KGGSYSQAASSDSAQGSDVSLTACKV KGGSY
DGKZ	RPSSVGLPTGK
TRAF3IP3	FLENEHQELQAK

DIS3	SQWVAPSSVVLHDEGQNEEDVEKEEERER EEERERMLK
LMNB1	CQSLTEDLEFHK
COMT	MVDFAGMK
THRAP3	DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK PSQAAGDNQGDEVKEQTFSGGTSQDTK
MRPL9	LPAEPITR
SAMM50	FYLGGPTSVR QVDVLIDTCQGDGALPNGLDVTFEVTELR
CEBPZ	ASLIEEDEPAEKENSSK ASLIEEDEPAEKENSSKK
RPA1	NIYLMDASGK RNIYLMDASGK
HLA-F	DYIALNEDLSSWTAADTAAQITQR
CPT2	DGSTAIHFEHSWGDGVAVLR ALEDVFDALEGK
DYNC1LI1	YGAALIYTSVK
NNT	QLTVGVPR
ITGA4	GIVQFLSK
MAN2B1	LIQLVNAQQAK
NDUFA6	QVTSTASTFVKPIFSR MAGSGVRQVTSTASTFVKPIFSR QVTSTASTFVK
ZMYM3	TGSPGPDLLFHEGQQK
EIF2A	NTVLATWQPYSTSK
NUP210	NPLLDLAAYDQEGR NPLLDLAAYDQEGRR
GFM1	AIYFDGDFGQIVR LEFSDETFGSNIPKQFVPAVEKVNF
AHNAK	VDIDVPDVGVQGPDWHLK VEGDLKGPEVDIRGPK IEGEMQFPDVDIRGPKVDIK
WASHC4	KLGITPEGQSYLDQFR LGITPEGQSYLDQFR
DPP3	LIVQPNTHLEGSDVQLLEYEASAAGLIR
SRP14	MAYSNLLR AYSNLLR
TFRC	LSEKLDSTDFTSTIK LDSTDFTSTIK
HLA-DPA1	ETVWHLEEFGR
DIDO1	LAAETGEGEGEPLSR
PITRM1	DPSWIIR
ATP5PO	SLNDITAR SLNDITARER
GEMIN4	ALFREPDLVLR DLAIHILELLCETVSANAETFSPDVWIK
MRPL50	DVFDFYNVPIQDR VRDVFDFYNVPIQDR
NQO2	VLIVYAHQEPR NVAVDELSRQGCTVTVSDLYAMNFEPR
WDFY4	ATSEDTLNLR ATSEDTLNLRR
IRF2BP2	DILLQQQQQQLGHGGPEAAPR SPPGAAAPAAAKPPPLSAK
EIF3B	TLLSQEQIK
WDR3	LITGVSDSELR
PARP14	SEDVQSIEVQVK
CYBA	KKPSEEEAAAAAGGPPGGPQVNPIPVTDEVV
ACIN1	EFKEEGEEMPR NLKTEEEEEEEEEEEDDEEEEGDDEGQK
TRAP1	GVVDSEEIPLNLSR DVGEWQHEEFYR ELRALLLWGCRLR
HLA-DPB1	HNYELDEAVTLQR ATPENYVYQLR DLLEEER
PITRM1	LSVFSTIDAPVAPSDK DPSWIIR
SNRNP200	VDTDLETMDLDQGGEALAPR
NAT10	TLHEVSLQESIR AGPNTSIISLK
FKBP4	FEIGEGEKLDLPYGLER LDLPYGLER FEIGEGEK
FAM241A	EAAGTEWDPGASPR LRGGDGGER
WDFY4	ATSEDTLNLR EVKIEDVTPLWEETMLK
PLBD1	HWDFNIIDKDTSSSR

GLRX3	HASSGSFLSSANEHLKEDLNLR HASSGSFLSSANEHLK
HEATR1	NFGAENPDPFVPVLSTAVK
WASHC4	LGITPEGQSYLDQFR
LY75	LHLAGFSSVR
TAP2	LAQLQEGQDLYSR LVQQRLMD
PSMB4	FQTATVTEK
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ALYREF	QQLSVEELDAQLDAYNAR QQLSVEELDAQLDAYNARMDTS
SARS	KLDLEAWFPGSEAFR LDLEAWFPGSEAFR
MSH6	AAAAPEASPSPGGDAAWSEAGPGPRPLAR
NCAPD2	SIDPGLKEDTLEFLIK
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GAA	APSPLYSVEFSEEPFGVIVHR YEVPLETPR
CORO7	VAVPLLSSGGQVAVLELQKPGR QLQIFDPR
CPPED1	LADKFIHAGVR FIHAGVR
ATP5PO	SLNDITAR
PSMD2	EWQELDDTEK
LRRFIP1	KALDSNSLENDDLSAPGREPGDFNPESR ALDSNSLENDDLSAPGREPGDFNPESR
PSMB3	FGIQAQLVTTDFQK
F13A1	AVPPNNSNAAEDDLPTVELQGLVPR RAVPPNNSNAAEDDLPTVELQGLVPR
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SUPV3L1	LLNLEGFLSGSQSR
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IDH2	SPNGTIQNILGGTVFR
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RUNX1	APDGQDLAVGQAR QAWPGWAPRAAAFASGR RQAWPGWAPRAAAFASGR
GSTO1	SQNKEDYDGLKEEFR EDYDGLKEEFRK
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LYRM4	AQVLALYR
IBA57	LLTQDEGPALVPGSR LLTQDEGPALVPGSRLGDLWDYHQHR
XRCC1	LPAPTHTPATAPVPAR RPKLPAPTHTPATAPVPAR
HEXA	DFYVVEPLAFEGTPEQK ISYGPDWKDFYVVEPLAFEGTPEQK
CPT2	DGSTAIHFEHSWGDGVAVLR
NDUFA6	QVTSTASTFVKPIFSR
TRAP1	DVGEWQHEEFYR
THRAP3	DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK
ECHS1	IFEEDPAVGAIVLTGGDK VLLSCARGPLRPPVR
LBR	FNLSQESSYIATQYSLRPR NDAPHKNTQEKFNLSQESSYIATQYSLR

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PLEC	YSELTTLTSQYIK EQLQQEQALLEEIER AGVAAPATQVVQVTLQSVQR QEQIQAMPLADSQAVREQLQ
HSP90B1	TETVEEPVEEEEAAK TETVEEPVEEEEAAKEEKEESDDEAAVEEEEEEK
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NOL9	LLQAQAAGVDWR
PITRM1	DPSWIIR EAYFSVGLQGIVEKDIETVR
CBR4	EHDVQNTFEEMEK
HEXB	PGPALWPLPLSVK GILVDTSR
CPPED1	LADKFIHAGVR TLDAFPAEKESEWKGPFYFILGADPQFGLIK TLDAFPAEKESEWK
GPX1	LAAAAAQSVYAFSAR LAAAAAQSVYAFSARPLAGGEPVSLGSLR
NCF2	LYEPVVIPVGR LYEPVVIPVGRLFRPNER
PCYOX1	YGFQFLR YGFQFLRMHMWVEDVLDK
TRAF3IP3	FLENEHQELQAK
SDHA	KHTLSFVDVGTGK HTLSFVDVGTGK
MRPS28	TPAGGFASALER TPAGGFASALERHSELLQKVEPLQK
CYBRD1	SDSELNNEVAAR
ICAM1	EVTVNVLSPR
ARHGDIA	SIQEIQELDKYDESLRK SIQEIQELDKYDESLR
GSTO1	SQNKEDYDGLKEEFR EDYDGLKEEFRK EDYDGLKEEFR
HEXB	PGPALWPLPLSVK WHHEPAEFQAR
NOL9	LLQAQAAGVDWR MADSGLLLKWGSCR
CCDC93	TALLAGLSATEK TALLAGLSATEKADAHEEDELR
AHNAK	AEDPEVDVNLPK EADVNLPK VDIDVPDVGVQGPDWHLK VSVGATDLSLEASEGSIK GPSLQGDLAVS
IMPA2	LQVSGETDLSK
SLC12A7	DGTSHLIQSAGLGGLK
GLRX3	LVGAHAPELTK LVGAHAPELTKKVQR
GLO1	ATLELTHNWGTEDDATQSYHNGNSDPR
DIS3	SQWVAPSSVVLHDEGQNEEDVEKEEERER
PLEC	AGVAAPATQVVQVTLQSVQR YSELTTLTSQYIK EQLQQEQALLEEIER WQEYRELVLLLLQWMQHHT
NDUFS3	TYTDELTPIESAVSLFK
AHCY	DRPLNMILDDGGDLTNLIHTK
SORL1	TNVYISSSAGTR EENTCLRNQYR
HLA-DPB1	ATPENYVYQLR YIYNREELVR FLERYIYNREELVR
PSMD2	EWQELDDTEK EWQELDDTEKVQR
WDFY4	ATSEDTLNLR IPTIIGILACQLRGHFSTQDLLR
RRBP1	EHTLHLEAELEK QKLTAEFEEAQTSACLLQEELEK
NCF2	LYEPVVIPVGR
MACF1	AALLDQALSNAR KAALLDQALSNAR QHADHLALNEEIVNR ALEEDIENHATDVHQAVK IGQSLSSLTSI
XRCC1	LPAPTHTPATAPVPAR LPSRRYLMAGPGSSSEEDEASHSGGSGDEAPK
GLRX3	HASSGSFLSSANEHLK HASSGSFLSSANEHLKEDLNLR
SVIL	LFVLSSSSGDFAATEFVYPAR
FLII	LAGASPATVAAAAAGSGPK
IDH1	LVSGWVKPIIIGHHAYGDQYR PIIIGHHAYGDQYR NIPRLVSGWVKPIIIGHHAYGDQYR
THEMIS2	WLDLTVVEAK
GSTM1	IFEPNCLDAFPNLK IFEPNCLDAFPNLKDFISR
PLEC	YSELTTLTSQYIK EQLQQEQALLEEIER AGVAAPATQVVQVTLQSVQR VPVDVAYRHGYFDEEMNR
SPOUT1	TEEAILISLAALQPGLTQAGAR

ARHGAP1	NPEQEPIPIVFR
CORO7	QLQIFDPR
TOR1AIP1	TPQEWAPHTAR TTRSSSQYIESFWQSSQSQNFTAHDKQR
DGUOK	NLFENGSLSDIEWHIYR YIFAKNLFENGSLSDIEWHIYRDWHSFLLWEFASR
PITRM1	EAYFSVGLQGIVEKDIETVR EAYFSVGLQGIVEK GLCVLRRLSGGHAHHR
PDPR	LYHQLEQETGIQTGYTR NSASAAEARSMALPTQAQVVICGGGITGTSVAYHLSK
ASMTL	HDPIPAADTFEDLSDVEGGGSEPTQR HDPIPAADTFEDLSDVEGGGSEPTQRDAGSR
CYB5R1	RPQVTLLDPSEK SRRPQVTLLDPSEK PQVTLLDPSEKYLLR
APPL1	LIAASSRPNQASSEGQFVVLSSSQSEESDLGGGGK
NRAS	LVVVGADGVGK
LY75	TPDWYNPER
HLA-DRB5	AVTELGRPVAESWNSQK PVAESWNSQK
PNPT1	EVGTSDKEILTSR EVGTSDK
TAP2	LAQLQEGQDLYSR LVQQRLMD
AHNAK	VDIDVPDVGVQGPDWHLK VEGDLKGPEVDIRGPK GPKVDIDVPDVGVQGPDWHLK IEGEMQFPDV
WASHC4	KLGITPEGQSYLDQFR LGITPEGQSYLDQFR
TOR1A	ITHVALDFWR
ESD	AFSEYLGTDQSK KAFSEYLGTDQSK
MUT	YQLEKEDTVEVLAIDNTSVR EVAQQAVDADVHAVGVSTLAAGHK EDTVEVLAIDNTSVR EVAQQAVD
MAN2B1	LIQLVNAQQAK
MYO1C	NVLDTSWPTPPPALR
POLE4	EEEVPAGEAAASQPQAPTSVPGAR AAAAAAGSGTPREEEVPAGEAAASQPQAPTSVPGARLSR
HOMER3	AAQLLDVR LFELSELR AEVGRAAQLLDVR
DDX11	DFASIVLLDQR
SLC37A2	ELLGGVDNAFLVAYAIGMFISGVFGER
GINS1	WEYGSILPNALR
MYH9	DLEAHVDSANK DLGEELEALKTELEDTLDSTAAQQELRAK LEMDLKDLEAHVDSANK
RRBP1	EHTLHLEAELEK LTAEFEEAQTSACLLQEELEKLR
TRMT10C	NESTRPSEELELDKWK
GMPPB	INAGMYILSPAVLR
PITRM1	LSVFSTIDAPVAPSDK DPSWIIR GLCVLRRLSGGHAHHR
CKAP4	LTLQALTEK
MCM4	FDLIFLMLDPQDEAYDRR
CYP20A1	LTPVSAQFQDIEGK QHINPNKTLDPFETMLKSLLR
RARS	IYDALDISLIER IYDALDISLIERGESFYQDRMNDIVK
PKM	IENHEGVWR
LRPAP1	SLNVILAK
WDFY4	ATSEDTLNLR
VPS11	DLHDQFQHQLR RDLHDQFQHQLR RDLHDQFQHQLRCSNDSFSVIADYFGR
TFRC	LDSTDFTSTIK LSEKLDSTDFTSTIK KLSEKLDSTDFTSTIK
GEMIN4	FLGQILTAFPALR ALFREPDLVLR
TOR1A	ITHVALDFWR ITHVALDFWRSGKQR
SWAP70	EQALQEAMEQLEELELER EQALQEAMEQLEELELERK
HEXB	PGPALWPLPLSVK GILVDTSR FSHRGILVDTSR
EHD4	SISIIDSPGILSGEK SISIIDSPGILSGEKQRISR
SORBS3	SPADPTDLGGQTSPR
HLA-A	APWIEQERPEYWDQETR

MTHFD1	DVDGLTSINAGR DAIKPNLMQTLEGTPVFVHAGPFANIAHGNSSIIADQIALK
HEATR1	NFGAENPDPFVPVLSTAVK AGALMMPLVDQLENR
CYFIP1	YLTLDSFDAMFR
TAP2	LAQLQEGQDLYSR
TOR1AIP1	SIQEAPVSEDLVIR
NLE1	AAAVADEAVAR LLVSGSNDSTLKVWDVKAQK
MRPL28	LPGYYLR
WASHC4	LGITPEGQSYLDQFR KLGITPEGQSYLDQFR
RBM19	NLPAGTLAAELQETFGHFGSLGR
EIF2A	NTVLATWQPYSTSK
ARHGAP45	AEEEQAGSAPGAGGTATK ECVLHDDLLEARRPR
FDXR	DVTVPELR EAYHAVVLSYGAEDHR DVTVPELREAYHAVVLSYGAEDHR
NUP210	NPLLDLAAYDQEGR
BCL2L13	ASQSLDQEILLK LQEQHLSSPQGVQLDR ESDTEVITVEK
RANGAP1	TQVAGGQLSLK
SERPINB10	TYFGAEPQSVNFVEASDQIR TYFGAEPQSVNFVEASDQIRK DALATSINQFALELSK MDALATSINQFAI
MTRR	GQEEISGALPVASPASLR
ECH1	LTGSSAQEAASGVALGEAPDHSYESLR
KPNA3	SGILPILVR
MRPL19	GLGATFVLR
HLA-DRB5	YFYNQEEYVR
PDCD6IP	TMQGSEVVSVLK
TLN1	LLSDLLPPSTGTFQEAQSR RLLSDLLPPSTGTFQEAQSR
SLC16A1	AAESPDQKDTEGGPKEEESPV DTEGGPKEEESPV
AHNAK	VDIDVPDVGVQGPDWHLK VDIDVPDVGVQGPDWHLKMPK
TRPM2	LASLEEQVAQTAR ALHWIVRTLR KTEEPGDSYHMNAR
TBCD	LLSMTLSPDLHTR
NUDT6	FIAPAASLGFR SVLSIQQQHTNPGAFGK
ATP5MPL	NVWIPMKPYYTK
ETFA	GISFDAAATSGGSASSEK
GADD45GIP1	YGAASGVVPGSLWPSAEQLR
MIA2	EHSPYGPSPLGWPSSETR
NID1	SNGAYNIFANDRESIENLAK
ITGA4	GIVQFLSK GIVQFLSKTDK
PITRM1	DPSWIIR YHEKQAHVEATKLK
HLA-DRB5	RVHPEVTVYPAK VHPEVTVYPAK SGEVYTCQVEHPSVMSPLTVEWR DILEDRR FLWQGKYKCHFFNG
CTSC	GTDECAIESVAVAATPIPK VGTASENVYVNTAHLK RGTDECAIESVAVAATPIPK
PARP10	ELEEEGPQEQPEEEATPGHEEEEPVAPSTVAPR LQGSELSLVPHYDVLEPEELAENTSGGDHPSTQGPR
HLA-DRB1	AVTELGRPVAESWNSQKDLLEDR PVAESWNSQKDLLEDR
RRBP1	EHTLHLEAELEK QKLTAEFEEAQTSACLLQEELEK EKLHSLTQAKEESEK
MAN2B1	LIQLVNAQQAK
ARFGAP3	YFDEPVELR
PRRC2A	SSDASTAQPLESQPLPASQTPASNQPK ELPAPPAPPPASAPTPEK
COMT	MVDFAGMK
EBNA1BP2	GFSDKLDFLEGDQKPLAQHK
TRAP1	DVGEWQHEEFYR
PLPBP	IGSMIFGER IGSMIFGERDYSKK

CTSD	YSQVVPAVTEGPIPEVLK
FDXR	DVTVPELR
GZMA	LLQLTEK
ATAD3A	ATVEQEMELR
H6PD	LFGSPLSDYYAYSPVQER
HLA-DPA1	ETVWHLEEFGR KETVWHLEEFGR ALSLAFLLSLRGAGAIKADHVSTYAMFVQTHR
SULT1A1	SLPEETVDFMVQHTSFK
MRM3	VVFPSEEVVEQK
HLA-C	YTCHVQHEGLPEPLTLR THVTHHPVSDHEATLR LLRGYDQYAYDGK EAEQWRAYLEGLCVEWLR
SRPRB	LADGGGAGGTFQPYLDTLR RLADGGGAGGTFQPYLDTLR
MGMT	LGRPGLGGSSGLAGAWLK GNPVPILVPCHR
DIDO1	LAAETGEGEGEPLSR SEEKAAATAASKK
PARP14	SEDVQSIEVQVK
NMI	EHLPDEFIKDEQNK MEADKDDTQQILKEHLPDEFIK
CTSW	VAGAISPIKDQK
CDKN2AIP	ASEAEAPDKHGSSFVSLLK
SPTA1	SEQVHGVINLGNSLIER
COG3	VSDLAATAYK YTLSQQPWAQPAKVSDLAATAYKTIK
VWF	IALLLMASQEPQR IALLLMASQEPQRMSR VTGCPPFDEHKCLAER GKIMKIPGTCCDTCEEPECNDITA
CTGF	GLFCDFGSPANR
TFRC	LDSTDFTSTIK KLSEKLDSTDFTSTIK
TLN1	LLSDLLPPSTGTFQEAQSR RLLSDLLPPSTGTFQEAQSR
TUSC1	LPGEGGDGTPAEAR
TMEM106B	SAYVNYDVQK SAYVNYDVQKR YIGVKSAYVNYDVQKR
VARS2	ALQATYQLTK ALQATYQLTKAR MSKSLGNVLDPRDIISGVEMQLLQEK
FAM129A	TKPPLVPGTILYEAELSQFSEDIKK
PLEC	YSELTTLTSQYIK AGVAAPATQVVQVTLQSVQR EQLQQEQALLEEIER PKVQSGSESVIQEYVDLRTR
CEBPZ	ASLIEEDEPAEKENSSK ASLIEEDEPAEKENSSKK
DHRSX	LLAAEGSHVTANVVDPGVVNTDLYK YLYNKKETK
GLRX3	HASSGSFLSSANEHLK HASSGSFLSSANEHLKEDLNLR VQRHASSGSFLSSANEHLK
ASCC2	SIFLTFLR
LENG9	LAGVTEEALKPTAATR
GP6	AVQRPLPPLPPLPQTR
AHNAK	VDIDVPDVGVQGPDWHLK IEGEMQFPDVDIR
NOC2L	MVVVWSTGEESLR
MRPL12	REALAGAPLDNAPK EALAGAPLDNAPK
CPA3	AIFMDCGIHAR
PDPR	LYHQLEQETGIQTGYTR DAVVSSADVALALASAASQNGVQIYDR HLTIEQKMADYSNKLYHQLEQETG
HLA-DPB1	ATPENYVYQLR YIYNREELVR AVTELGRPDEGSTGTARR FLERYIYNREELVR YIYNREELVRFDSDVGE
RBM19	NLPAGTLAAELQETFGHFGSLGR
GEMIN4	ALFREPDLVLR FLGQILTAFPALR
CYP20A1	LTPVSAQFQDIEGK TLDPFETMLK
PDLIM1	TAASGVEASSRPLDHAQPPSSLVIDKESEVYK TAASGVEASSRPLDHAQPPSSLVIDK
SPEN	LGEPAGESVENQEVQSK
URB1	WVFGLLR EEVYDVVEGYIK WVFGLLRQGIRDK
GBP1	LQDEELDPEFVQK
SEC23B	GAIQFVTHYQQSSTQR GAIQFVTHYQQSSTQRRIR

SCAF1	AARPPPAASATPTAQPLPQPPAPR
PNP	LTQAQIFDYSEIPNFPR
TAP2	LAQLQEGQDLYSR LAQLQEGQDLYSRLVQQR
NUP153	KPAFNLSAFGTLSPSLGNSSVLK KCSTGYEKNMTPGQNR
PDHX	LSVNDFIIK
MYBBP1A	ALVDVLSEVSK
PRRC2C	TLSTPQEER
PDPR	LYHQLEQETGIQTGYTR
ATP5PO	SLNDITAR VKSLNDITAR
NUP210	NPLLDLAAYDQEGR NPLLDLAAYDQEGRR LPPGSEHCSGVR
GSTO1	SQNKEDYDGLKEEFR EDYDGLK
URB1	WVFGLLR
DIS3	SQWVAPSSVVLHDEGQNEEDVEKEEERER SQWVAPSSVVLHDEGQNEEDVEKEEER
TRIM22	LTGSSVEMLQDVIDVMK ENQEAEKLEDDIR ENQEAEKLEDDIRQER
CHID1	MVWDSQVSEHFFEYK DHRPRMVWDSQVSEHFFEYK
AP3B1	QLIVPNEK
SULT1A1	SLPEETVDFMVQHTSFK
IBA57	LLTQDEGPALVPGSR
H6PD	LFGSPLSDYYAYSPVQER DQNRKALDGLWNQHHVER
BDH2	QIDQFASEVER KQIDQFASEVER
DMAC1	PATPATPGAPTSPAEHR
ITGA4	GIVQFLSK
WASHC4	LGITPEGQSYLDQFR
TP53RK	DYIQSAMETEK DYIQSAMETEKTPQGLSNLAK
CA2	ILNNGHAFNVEFDDSQDEAVLK
HEATR1	NFGAENPDPFVPVLSTAVK PFADTLDQVNISK YMLPHLVVSIIHHVTGEETEGMDGQIYKR
PFAS	LSFAHPSSAEVEAIALATLHDR
NLE1	AAAVADEAVAR LLVSGSNDSTLKVWDVKAQK
XPC	KDPSLPVASSSSSSSK DPSLPVASSSSSSSKR
WDFY4	ATSEDTLNLR TYPQDPAWQAPEFLQTLAIAAFPLGAQKGVGAESTR
TMEM208	AAFSEDGALR
TLN1	LLSDLLPPSTGTFQEAQSR
HDHD3	LEGILEGLGLR
PLIN3	AQEALLQLSQALSLMETVK
GRWD1	QEPFLLSGGDDGALK
NDUFV3	LEAEGEAMEDAAAPGNDR
ALDH1B1	LLNLLADLVER EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK
RNF213	TTDNFDDILK VLQEQHQLSSR FGIVLSAVITKSWPRTTDNFDDILK
PLEC	AGVAAPATQVVQVTLQSVQR YSELTTLTSQYIK EQLQQEQALLEEIER
PDCD6IP	TMQGSEVVSVLK
NCF2	LYEPVVIPVGR LSYWPRDSNELVPLSEDSMK LEQTKLSYWPR LEQTKLSYWPRDSNELVPLSEDSMK E
CPT2	ALEDVFDALEGK DGSTAIHFEHSWGDGVAVLR EFLQCVEKALEDVFDALEGK
XRCC1	LPAPTHTPATAPVPAR RYLMAGPGSSSEEDEASHSGGSGDEAPKLPQK
TRAP1	DVGEWQHEEFYR DVGEWQHEEFYRYVAQAHDK
GLO1	ATLELTHNWGTEDDATQSYHNGNSDPR KATLELTHNWGTEDDATQSYHNGNSDPR
LBR	FNLSQESSYIATQYSLRPR
ATIC	TVASPGVSVEEAVEQIDIGGVTLLR

TFRC	LDSTDFTSTIK LDSTDFTSTIKLLNENSYVPREAGSQK
ITGAM	QNTGTWESNANVK
SDR39U1	RTLATGYQYSFPELGAALK
RBM19	NLPAGTLAAELQETFGHFGSLGR
GEMIN4	FLGQILTAFPALR ALFREPDLVLR
AHNAK	VSMPGVDLNLK VDIDTPDINIEGPEGK VDIDVPDVGVQGPDWHLK ADIDVSGPSVDTDAPDLDIEGPE
PITRM1	EAYFSVGLQGIVEKDIETVR DPSWIIR EAYFSVGLQGIVEK
STAB1	TRPGELMVGEDDAR VGVVSLGAR
APIP	IQPEDMFVYDINEK SGCDAWEGDCCSR
IQGAP2	RQTFIDNTDSVVK QTFIDNTDSVVK VLWLDEIQQAVDEANVDEDRAK
GLRX3	HASSGSFLSSANEHLK HASSGSFLSSANEHLKEDLNLR
NUP210	NPLLDLAAYDQEGR
NAT10	TLHEVSLQESIR
CPT2	ALEDVFDALEGK DGSTAIHFEHSWGDGVAVLR ALEDVFDALEGKSIK
GPX1	LAAAAAQSVYAFSAR LAAAAAQSVYAFSARPLAGGEPVSLGSLR
FKBP4	FEIGEGEKLDLPYGLER LDLPYGLER LDLPYGLERAIQRMEK
AHNAK	VDIDTPDINIEGPEGK VDIDVPDVGVQGPDWHLK VSMPGVDLNLK ADIDVSGPSVDTDAPDLDIEGPE
HSDL2	LQLQPKPHSGAVEETFR
CAPZA1	ADFDDRVSNEEK
HEXB	PGPALWPLPLSVK RYHGYIFGFYKWHHEPAEFQAR
ASCC2	SIFLTFLR
NOP58	LSELLPAEVEAEVK
BCL2L13	LQEQHLSSPQGVQLDR ASQSLDQEILLK
GEMIN4	ALFREPDLVLR
TXNRD2	TTGKEDTGTFDTVLWAIGR RLPDGQLQVTWEDR
HIST1H1C	SETAPAAPAAAPPAEKVPVK SETAPAAPAAAPPAEKVPVKK
HEATR1	NFGAENPDPFVPVLSTAVK AGALMMPLVDQLENRLGGEEK
IRF2BP2	SPPGAAAPAAAKPPPLSAK
RRBP1	EHTLHLEAELEK
NDUFA6	QVTSTASTFVKPIFSR QVTSTASTFVK
PML	VVIQPEALFSIYSK FRVVIQPEALFSIYSK
SRP14	AAAAAAAAAAPAAAATAATTAATTAATAAQ
PDPR	LYHQLEQETGIQTGYTR
PLEC	AGVAAPATQVVQVTLQSVQR EQLQQEQALLEEIER YSELTTLTSQYIK
MYO1G	IFLQTLDTHHR DKDGFGAVLFSSHVR
PRKDC	KEEENASVTDSAELQAYPALVVEK
ITGA4	GIVQFLSK
TOR1A	ITHVALDFWR AMFIFLSNAGAERITHVALDFWR
SCFD1	FGQDIISPLLSVR VLIYDRFGQDIISPLLSVRELR
TOR1AIP1	SVLSSGYQK LQQQHSEQPPLQPSPVTTR
MACF1	TLLPEDTQKLDNFLGEVR TLLPEDTQK LETMNQCWESVLQKTEER
BIN2	FEQSANNFYQQQAEGHK
PITRM1	DPSWIIR
AHNAK	VDIDVPDVGVQGPDWHLK
LHPP	GLRPYLLIHDGVR
VPS11	DLHDQFQHQLR
MYH9	DLEAHVDSANK DLEAHVDSANKNRDEAIK KLEMDLKDLEAHVDSANK

PSMD13	DVPGFLQQSQSSGPGQPAVWHR
ECH1	NQSLVNELAFTAR
HIST1H1C	SETAPAAPAAAPLAEK SETAPAAPAAAPLAEKVPVK
NUP133	SSFYSLTSSNVSK
FDXR	EAYHAVVLSYGAEDHR DVTVPELR
HLA-DRB5	YFYHQEEYVR HECHFFNGTERVRFLDR
HEXB	GILVDTSR PGPALWPLPLSVK GILVDTSRHYLPVK
LY75-CD302	TPDWYNPER
NLE1	AAAVADEAVAR MAAAVADEAVARDVQR LLVSGSNDSTLKVWDVKAQK
THRAP3	DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK DSRPSQAAGDNQGDEVK
HLA-DQA2	KETVWQLPLFR ETVWQLPLFR
MYO1G	DKDGFGAVLFSSHVR IFLQTLDTHHR
C11orf98	HQVVGAVIDQGLITR
ANP32B	SLDLFNCEVTNLNAYR
TAP2	LAQLQEGQDLYSR
LPCAT3	LVQGELTDIPGK
TLN1	LLSDLLPPSTGTFQEAQSR
MPO	NQINVLTSFVDASMVYGSEEPLAR
TRAP1	DVGEWQHEEFYR
PFAS	IGVGGGAASSVQVQGDNTSDLDYGAVQR IGVGGGAASSVQVQGDNTSDLDYGAVQRGDPEMEQK
COQ5	AQQNLSWEEITK AQQNLSWEEITKEYQNEEDSLGGSR QLRAQQNLSWEEITK
GTF2B	AVDLDLVPGR
PSMB3	FGIQAQLVTTDFQK RFGIQAQLVTTDFQK RFGIQAQLVTTDFQKIFPMGDR
AHNAK	VDIDVPDVGVQGPDWHLK VSVGATDLSLEASEGSIKLPK CPKVSVGATDLSLEASEGSIK
MRPL9	LPAEPITR
DIDO1	LAAETGEGEGEPLSR AELFQQEQQPADK
BCL2L13	ASQSLDQEILLK LQEQHLSSPQGVQLDR
LGALS8	SGTPQLSLPFAAR
NUMA1	EVACLETLVR
HEATR1	NFGAENPDPFVPVLSTAVK AGALMMPLVDQLENRLGGEEK PFADTLDQVNISK
SDR39U1	RTLATGYQYSFPELGAALK AIMLLEGQKVIPRR
MGMT	LGRPGLGGSSGLAGAWLK GNPVPILVPCHR LGRPGLGGSSGLAGAWLKGAGATSGSPPAGR
GLRX5	LGIHSTLLDEK
SCARB2	EIIEAVLK
TXNRD2	EATSVPHIYAIGDVVEGRPELTPTAIMAGR
DUSP23	LRPSSIETYEQEK
IQGAP2	QTFIDNTDSVVK VLWLDEIQQAVDEANVDEDR VLWLDEIQQAVDEANVDEDRAK IYDVEQTCYK ESS
GTF3C1	GSTESFGAANISQAAR
EHBP1L1	HAGPVPVQVPLR
TP53	VAPAPAAPTPAAPAPAPSWPLSSSVPSQK MPEAAPR
CWC22	YTSDKDVPSEQNNYSR SEKHRDQNSR
AIP	EQPGSPEWIQLDK NLQMKEQPGSPEWIQLDK
AP5B1	VGAGLGGLFTDK
NCF2	LYEPVVIPVGR
WDR81	LVAGEDDLEQATEALDSISLAGK
DBT	LGSVGQLSTTDLTGGTFTLSNIGSIGGTFAK
FKBP4	FEIGEGEKLDLPYGLER LDLPYGLER LDLPYGLERAIQR

SULT1A1	SLPEETVDFMVQHTSFK SLPEETVDFMVQHTSFKEMKK
NAT10	TLHEVSLQESIR
BIN2	AQTVFEDLNQK LLEELPILYNSR
GSTZ1	TVPINLIK IDGITIHQSLAIIEYLEETRPTPR IALALKGIDYK
PDPR	LYHQLEQETGIQTGYTR
PITRM1	DPSWIIR EAYFSVGLQGIVEKDIETVR EAYFSVGLQGIVEK PDDKYHEKQAHVEATK
PLEC	AGVAAPATQVVQVTLQSVQR YSELTTLTSQYIK LAQGHTTVDELAWR EQLQQEQALLEEIER
VPS13C	GEPLHIVNSSNVTDEPLLK
HTATIP2	GHSVPVVTVVR
SERPINB8	DGDIHQGFQSLLSEVNR MEPRFCADHPFLFFIRR
SDHA	KHTLSFVDVGTGK HTLSFVDVGTGK
TRAP1	GVVDSEEIPLNLSR DVGEWQHEEFYR
PDPR	LYHQLEQETGIQTGYTR
IQGAP2	RQTFIDNTDSVVK QTFIDNTDSVVK VLWLDEIQQAVDEANVDEDRAK VLWLDEIQQAVDEANVDED
SPTAN1	GNAMVEEGHFASEDVK
ASMTL	HDPIPAADTFEDLSDVEGGGSEPTQR
TFRC	LDSTDFTSTIK
AHNAK	VDIDVPDVGVQGPDWHLK VDVDVPDVNIK VDIDTPDINIEGPEGK ADIDVSGPSVDTDAPDLDIEGPE
DLST	LTVAPPLAEPGAGK PVSAVKLTVAPPLAEPGAGK
HLA-F	DYIALNEDLSSWTAADTAAQITQR
TRAF3IP3	FLENEHQELQAK
HLA-DRB1	AVTELGRPVAESWNSQK PVAESWNSQK AEVDTYCR WFRNGQEEK AEVDTYCRYNYGAGESFTVQR
HLA-DRB5	YFYNQEEYVR
CD200	EQLYTTASLK
TLN1	LLSDLLPPSTGTFQEAQSR
TAP1	SGAHSFISGLPQGYDTEVGEAGSQLSGGQR
GBP1	VQLPTESLQELLDLHR
ITGA4	GIVQFLSK VCALEQQKSAMQTLKGIVQFLSK
DIDO1	LAAETGEGEGEPLSR
TAP2	ALYLLIR LVQQRLMD
RANBP2	LFSTQYGK
DEPTOR	TVNNLILTGPR
PRCP	VDHFGFNAVK
APEX1	VSYGIGEEEHDQEGR EGYSGVGLLSRQCPLKVSYGIGEEEHDQEGR
SDHA	KHTLSFVDVGTGK HTLSFVDVGTGK
NLE1	AAAVADEAVAR
MAN2B1	LIQLVNAQQAK NLCWDVLCVDQPVVEDPR YYRTNHIVMTMGSDFQYENANMWFK
BCAT2	PVLIGNEPSLGVSQPR
CRYZ	VLGTAGTEEGQK AYGLKVLGTAGTEEGQKIVLQNGAHEVFNHR
PLEC	EQLQQEQALLEEIER YSELTTLTSQYIK AGVAAPATQVVQVTLQSVQR
AHNAK	VDIDVPDVGVQGPDWHLK GEGPEVDVTLPKADIDISGPSVDVDVPDVNIEGPDAK VSVGATDLSLEAS
MESD	RPSAPVDFSR
BRD3	KADTTTPTTSVITASR
DYNC1LI1	YGAALIYTSVK FCLRYGAALIYTSVK
CPT1A	KLDQEEIKPIR
HLA-A	APWIEQEGPEYWDEETGK VKAHSQTDR
CS	IYQNLYR

NUP210	NPLLDLAAYDQEGR NPLLDLAAYDQEGRR
MRM3	VVFPSEEVVEQK
ARL2	EALELDSIR
QPRT	YGLLVGGAVSHR LVEKYGLLVGGAVSHR
GSTO1	SQNKEDYDGLKEEFR EDYDGLKEEFR EDYDGLKEEFRK
HOMER3	AAQLLDVR LFELSELR
H6PD	LFGSPLSDYYAYSPVQER
TAPBPL	NEVLWHPTLNLPLSPQGTVR TAAWFMANVQVSGGGPSISLVMKTPR
TRAP1	DVGEWQHEEFYR ALLLWGCR
PDPR	LYHQLEQETGIQTGYTR MADYSNKLYHQLEQETGIQTGYTR
OPA1	ALPNSEDLVK LLLENGTR
GPX1	LAAAAAQSVYAFSAR
MCM7	RFELYFQGPSSSKPR FELYFQGPSSSKPR
MYO18A	QNPATQNVPR
TAP2	LAQLQEGQDLYSR TVLVIAHRLQAVQRAHQILVLQEGK LAQLQEGQDLYSRLVQQR
PLEC	AGVAAPATQVVQVTLQSVQR YSELTTLTSQYIK EQLQQEQALLEEIER VQSGSESVIQEYVDLRTR
NUP210	NPLLDLAAYDQEGR
AHNAK	VDIDVPDVGVQGPDWHLK VEGDLKGPEVDIRGPK
GSTO1	SQNKEDYDGLKEEFR VPSLVGSFIRSQNKEDYDGLK
GBE1	LFAYSSWEVLR
CRYZ	VLGTAGTEEGQK
NAT10	TLHEVSLQESIR
TLN1	LLSDLLPPSTGTFQEAQSR RLLSDLLPPSTGTFQEAQSR
DYNC1LI1	FSLDAISLK
PDPR	LYHQLEQETGIQTGYTR
MANBA	PVGGQVIIAIPK
HLA-A	APWIEQEGPEYWDEETGK APWIEQEGPEYWDEETGKVK
DUSP23	LRPSSIETYEQEK LAGLALPRLPAHYQFLLDVGVRHLVSLTER
NOL9	LLQAQAAGVDWR WGSCRSTWLRVR
CAVIN2	EPVSGAVEGKEELPDENK
IQGAP2	RQTFIDNTDSVVK QTFIDNTDSVVK VLWLDEIQQAVDEANVDEDRAK VLWLDEIQQAVDEANVDED
PML	VVIQPEALFSIYSK
NCF2	LYEPVVIPVGR LSYWPRDSNELVPLSEDSMK
RRBP1	EHTLHLEAELEK GELESSDQVREHTLHLEAELEKHMAAASAECQNYAK
NMI	EHLPDEFIKDEQNK
TAP2	LAQLQEGQDLYSR LAQLQEGQDLYSRLVQQRLMD
AHNAK	VDIDVPDVGVQGPDWHLK VEGDLKGPEVDIRGPK
CPVL	QVGDFHQVIIR
MACF1	TLLPEDTQK TLLPEDTQKLDNFLGEVRDK
MYO1G	DKDGFGAVLFSSHVR IFLQTLDTHHR IFLQTLDTHHRHHLHYTSR
CTSC	VGTASENVYVNTAHLK
RNASEH2A	LQDSDTDYGSGYPNDPK
DIDO1	LQQEEADVPAYPK TAPPGSTVGK SEEKAAATAASKK
GLRX3	HASSGSFLSSANEHLKEDLNLR HASSGSFLSSANEHLK
HOMER3	AAQLLDVR
TLN1	LLSDLLPPSTGTFQEAQSR
GNPAT	GVFADEFIFLPGNTLK

HLA-DPB1	HNYELDEAVTLQR ATPENYVYQLR
FAN1	LQLIHDASEESLR
CPPED1	LADKFIHAGVR
PLEC	YSELTTLTSQYIK LAQGHTTVDELAQR GANVIAGVWLEEVGQK
CTSW	VAGAISPIKDQK VAGAISPIK
CLEC3B	GGTLSTPQTGSENDALYEYLR
NSFL1C	ASSSILINESEPTTNIQIR
HOMER3	LFELSELR AAQLLDVR
SULT1A1	SLPEETVDFMVQHTSFK
SUCLG2	LEGANVQEAQK
TRAF3IP3	FLENEHQELQAK VQQLQEAAGWTT
ITGAM	DHVFQVNNYEALK QNTGTWESNANVK
GLO1	KATLELTHNWGTEDDATQSYHNGNSDPR ATLELTHNWGTEDDATQSYHNGNSDPR
SRPRB	LADGGGAGGTFQPYLDTLR
PITRM1	EAYFSVGLQGIVEKDIETVR EAYFSVGLQGIVEK
TLN1	LLSDLLPPSTGTFQEAQSR
MGMT	LGRPGLGGSSGLAGAWLK
HLA-DRB5	HNYGVGESFTVQR GIYNQEENVR GHSGLHPTGLVS VTVYPAR YECHFFNGTERVR FLHRGIYNQEEN
ARHGDIB	APNVLVTR
WASHC4	LGITPEGQSYLDQFR
MRPL10	IFPNQVLKPFLEDSK IFPNQVLK
CPVL	QVGDFHQVIIR
NUP210	NPLLDLAAYDQEGR NPLLDLAAYDQEGRR LTLVPVYTSPQLDMSCPLLQQNK QGKITELSMPSDQYEL
TKFC	ASYISSAQLEQPDPGAVAAAAILR
CPT1A	AGNTIHAILLYR
CLIC1	AEQPQVELFVK AEQPQVELFVKAGSDGAK
ZNF22	SFGQSSTLFQHQK CTECEKSFGQSSTLFQHQKIHTGK
IQGAP2	QTFIDNTDSVVK VLWLDEIQQAVDEANVDEDR VLWLDEIQQAVDEANVDEDRAK
ABCE1	AIIKPQDVDQIPK
SDR39U1	VLVGGGTGFIGTALTQLLNAR
AHNAK	VDIDVPDVGVQGPDWHLK VSVGATDLSLEASEGSIKLPK
PLIN3	AQEALLQLSQALSLMETVK QRAQEALLQLSQALSLMETVKQGVDQK
PLEC	YSELTTLTSQYIK EQLQQEQALLEEIER AGVAAPATQVVQVTLQSVQR

EGR GPTVGGGLPGTGVQGLEGNLQMPGIK VSMPGVDLNLKGPK GPEVDIDVPDVDVQGPDWHLK GPEVDIDVPD

VDVQGPDWHLKMPK

Variant	**Numer of patient**	**Gene**
II_726022@Ala112Thr	5	RPL13
II_582891@Ser583GlySer557Pro[Ser822SerAla67	2	ESYT2
IP_228485@Val37Met	1	MOAP1
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_726022@Ala112Thr	1	RPL13
IP_177302@Val25Ala	1	ASB6
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_677849@Lys89Arg	1	ADAR
II_730346@Val120Met	1	SULT1A1
II_630163@Val37Ile	1	GFM1
II_726022@Pro100Ala	1	RPL13
II_721332@Ala92Asp[Pro105Pro]	1	GLOD4
II_740517@Thr171Ile	1	ETFA
II_3437680@Val104Ala	1	ASAH1
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
IP_3428277@Glu29Val	1	GOLGA8IP
IP_160788@Val79Ala	1	LOC100506302,
IP_158738@Ala46fs[Thr35Thr]	1	GIMAP6
II_726022@Ala112Thr	1	RPL13
II_299453@Pro119Leu	1	RBM3
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_726022@Ala112Thr[Arg31Arg]	1	RPL13
II_758045@Ala342Glu	1	SPART
II_295391@Ala42Gly	1	MCAT
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_3423177@Val175AlaIle22Val	1	ASAH1
IP_213716@His22Arg	1	HAL
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
IP_261590@Pro15Leu	1	MAFG
II_299453@Pro119Leu	1	RBM3
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
II_726022@Ala112Thr	1	RPL13
IP_591885@Asn91SerPhe88Tyr[Ser36Ser]	1	GAPDHP63
IP_246386@Gln24Lys[Ala7Ala]	1	AP1G1
II_569582@Ala7Gly	1	NIPSNAP3B
IP_241298@Met25Val	1	RMI2
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H
IP_272869@Gly28SerLys20Gln[Val10Val]	1	ZNF708
II_766937@Pro697Ser[Leu693Leu]	1	CAND1
IP_213716@His22Arg	1	HAL
II_726022@Ala112Thr[Ala47Ala]	1	RPL13
II_3437162@Pro174SerAsp120Asn	1	MOGS
II_596695@Ser8ProGlu55AlaLeu59GlnAspGlyThr6	1	HLA-A
IP_280353@Thr62AlaPhe74fsArg22Gly[Val58Val]	1	ZNF587
II_597058@Ser14TrpLeu17ValThr37AlaSer50ThrG	1	HLA-H

Identified Peptides

STESLQTNVQR
FQLGNSGPNSTIK
PFVVSMPI
FDSDATSPR YFYTAMSR YFYTAMSRPGR FDSDATSPREEPR
FDSDATSPR FDSDATSPREEPR FITVGYVDDTQFVR
STESLQTNVQR LSGRPGARGQ
ASTAWRSHFIIFFFR
YFYTAMSRPGR YFYTAMSR FIAVGYVDDTQFVRFDSDDASPR GEPRFIAVGYVDDTQFVRFDSDDASPR EEPRAPV
NTNSVPETAPAAIPETR
SLPEETVDFMVQHTSFK
GIIDLIEER
TIGISVDAR
LLDDAMADDKSDEWFAK LLDDAMADDKSDEWFAKHNK
GISFDAAATSGGSASSEK
DAMWIGFLTR
GYDQYAYDGKDYIALNEDLR EGPKYWDR FITVGYVDDTQFVRFDSDDASPREEPR
TVLAGLV
ISWAWWHMHVIPATWEAEAQESLELR
PVSFTSV
STESLQTNVQR GDSSVSTRLSGR
VFGAALK VFGAALKHLIL
FITVGYVDDTQFVR LLRGYDQYAYDGKDYIALNEDLR YLENGKETLQRADPPQDTR
STESLQTNVQR
LQANWNREEEENEFQIPGR QMSDLRLQANWNREEEENEFQIPGR
KPLVSVYSNVHGHR
GYDQYAYDGKDYIALNEDLR FITVGYVDDTQFVR LLRGYDQYAYDGKDYIALNEDLR APWIEQEGPKYWDR YYNQ
DAMWIGFLTR MLKVIVNSLK
SLILLLG EPLVPVETLPR
GYDQYAYDGKDYIALNEDLR GEPHFITVGYVDDTQFVRFDSDDASPREEPR KWEAVHACVAEQR
VVLPGRVGGGPLGTALSSLSLPHSESLGGLHQCR
VFGAALK
YFSTSVSR YFSTSVSRPGR FITVGYVDDTQFVR NTQICKAHSQTYRENLR SHSMRYFSTSVSRPGR
STESLQTNVQR RNKSTESLQTNVQR
LISWYDNEYGYSNR
VRPTLLLK
PGGPGLWGDAFER
DVVSLLV
GYDQYAYDGKDYIALNEDLR EGPKYWDR APWMEREGPK YFYTAMSRPGR YYNQSEAGSHTMQVMYGCDVGP
VWMSISCTQEVTR
AVAALLTISEAEK
SLILLLG KEPLVPVETLPRSLILLLG
STESLQTNVQR
FISGHTSELGNFR LNSWFQHRPPGASPER
WASVVVPSGQEQR VAEQQRAYLEGR SWTAADMAAQITQRK AYLEGRCVEWLR
YNSFLGQSLTLSPR
FDSDATSPR TALRYYNQSEAGSHTIQR YFYTAMSRPGRGEPR

SEAGSHTMQVMYGCDVGSDWR