

Gene	PacBio accession	Peptide sequence	CPM	Raw mass spectrum	Manual spectrum annotation validation notes	Passed Manual Annotation	Raw file name	Scan Number	Annotation of the novelty event	Event of the novel event on the protein isoform sequence	Maps to a single isoform	Link to corresponding UCSC browser track	Isoform track image	Zoom in of image
FXR1	PB.3060.6	GYATDESTVS SVQGSR	6.014723		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 44% (rough minimum is 20%)	Yes	210827_HUVEC5.6_tryp_HCDorbi_4hr_F r4	58931	Intron retention event	Insertion	No (PB.3060.6, PB.3060.8)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed&nonVirtPosition=chr3%3A449674383%2D49874573&position=multi%3A58605299%2D58605489&hgslid=13238013734Vn42a7GvdrAaCReEnrBP6l		
APEH	PB.2610.6	AGPDGQVSPAQVLLSEPEEAALYR	5.638803		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 24% (rough minimum is 20%); y9 ends in proline and is most abundant as expected	Yes	210827_HUVEC5.6_tryp_HCDorbi_4hr_F r11	220913	Intron retention event	Insertion	No (PB.2610.6, PB.2610.7)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed&nonVirtPosition=chr3%3A449674383%2D49874573&position=multi%3A58605299%2D58605489&hgslid=13238013734Vn42a7GvdrAaCReEnrBP6l		
TUBA1A	PB.8359.9	AVFVDLEPTVIGKEDANNYYR	2.631441		MS2 TIC only 13%, too many missing fragment ions and unassigned peaks, 1 missed cleavage	No	210827_HUVEC5.6_tryp_HCDorbi_4hr_F r11	148203						
NASP	PB.473.10	ATLVESSTSGFTPGGGSS VSMR	1.879601		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 48% (rough minimum is 20%); y11 ending in proline is most abundant as expected	Yes	210827_HUVEC5.6_tryp_HCDorbi_4hr_F r12	113107	Exon skipping event	Deletion	Yes (PB.473.10)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed&nonVirtPosition=chr3%3A449674383%2D49874573&position=multi%3A58605299%2D58605489&hgslid=13238013734Vn42a7GvdrAaCReEnrBP6l		
NASP	PB.473.10	ATLVESSTSGFTPGGGSS VSMR	1.879601	same sequence as above			210827_HUVEC5.6_tryp_HCDorbi_4hr_F r7	83077						
MAP4	PB.2568.9	KKPQSETSQIEGSPTEFLEEK	3.007362		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 27% (rough minimum is 20%); y8 ending in proline is most abundant as expected	Yes	210827_HUVEC5.6_tryp_HCDorbi_4hr_F r8	86426	Exon skipping event	Deletion	Yes (PB.2568.9)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed&nonVirtPosition=chr3%3A449674383%2D49874573&position=multi%3A58605299%2D58605489&hgslid=13238013734Vn42a7GvdrAaCReEnrBP6l		

PCBP2	PB.8415.24 PB.8415.27 PB.8415.75	YSTGSDSASF PHHTTSPMCLN PDLEGPPLEL TK		There are many prolines, which might explain why there are so few b ions; meets all other criteria but PEP hovers around minimum criterion	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	185556	Exon skipping event	Deletion	No (PB.8415.24, PB.8415.27, PB.8415.75)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed&nonVirtPosition=chr12%3A53462482%2D53467240&position=multi%3A19540330%2D19540670&hgslid=1323801373_Av042a7GndrAACReEaCnRBP		
SCAMP3	PB.954.9	DGGNPFAEP SELDNPFQAS AAAAATAELLK K		MS2 TIC only 16%, PEP barely meets criterion, too many missing fragment ions and unassigned peaks	No	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r14	222797						
DAB2IP	PB.6630.12 PB.6630.3P B.6630.9	MVIENDLSGS SGVQSPAR		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 48% (rough minimum is 20%); y5 ending in proline is	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r9	87656	Alternative acceptor (3' splice site)	Deletion	No (PB.6630.3, PB.6630.9, PB.6630.12)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed&nonVirtPosition=chr12%3A53462482%2D53467240&position=multi%3A19540330%2D19540670&hgslid=1323801373_Av042a7GndrAACReEaCnRBP		
ARVCF	PB.13187.1 8 PB.13187.2 PB.13187.35 PB.13187.4 PB.13187.7	GASSAGEASE KEPLKGPSPA SCS		MS2 TIC at 20%, PEP just above minimum, significant unassigned fragment ions, 2 missed cleavages	No	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r4	42889						
PRKCSH	PB.11912.1 6	AQOQELAA DAFKELDDDM DGTLLPRPR		MS2 TIC only 13.5%, PEP just above minimum, significant unassigned fragment ions, 1 missed cleavages	No	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r10	213920						
UBAP2	PB.6339.16	SQQTLDTTSS VPAPK		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 43% (rough minimum is 20%); y4 ending in proline is among most abundant as expected	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r6	52561	Alternative acceptor (3' splice site)	Insertion	No (PB.6339.7, 6339.16)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed&nonVirtPosition=chr12%3A53462482%2D53467240&position=multi%3A19540330%2D19540670&hgslid=1323801373_Av042a7GndrAACReEaCnRBP		
FAM120A	PB.6511.1	APAAAMGVQ GFQDYIEK		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 42% (rough minimum is 20%)	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	154811	Usages of an ATG start that is further upstream than the ATG start annotated in GENCODE	Insertion	Yes (PB.6511.1)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtMode=1&multiRegionsBedUrl=%2Fuserdata%2Fsessions%2F%2F13%2Fmm5db%2F0c7b0cfc%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed&nonVirtPosition=chr12%3A53462482%2D53467240&position=multi%3A19540330%2D19540670&hgslid=1323801373_Av042a7GndrAACReEaCnRBP		
FAM120A	PB.6511.1	APAAAMGVQ GFQDYIEK	same sequence as above (oxidized methionine version of a peptide already listed earlier in the table)	Doesn't meet PEP score criterion (since this sequence is just the Mox version of the peptide above, I don't think it makes sense to track down the other spectra)		210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	126162						

MAP4	PB.2568.11	MYHDDDLADLVFPSSATADT SIFAGQNDPL KDSYVPLELA K	3.759202		Meets criteria but my only concern is that the y and b ions are not complementary and fairly sparse. This is likely because it's a z=4 ion and those don't tend to fragment very well. Would like to look at the raw data	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r13	242854	Exon skipping event	Deletion	Yes (PB.2568.11)	https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Ffr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_genome_1e56d_a22290.bed&nonVirtPosition=chr3%3A47916970%2D47928353&position=multi%3A58410401%2D58411028&hgslid=13238013734Vn42a7GvdrAAcReEnOrB96	
MAP4	PB.2568.11	MYHDDDLADLVFPSSATADT SIFAGQNDPL KDSYVPLELA K	3.759202		Too few y and b ions, PEP doesn't meet criterion, too many unassigned fragment ions	No	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r13	241977					
ACTN4	PB.12220.36	AGTQIAIAQELNELDYDISH NVNTR	2.631441		Y ion series looks very nice but the delta mass is over 300ppm, isolation of the C13 isotope	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r13	217945	Exon skipping event	Deletion	No (PB.12220.10)		
PGAM5	PB.8829.1	EGAPIEPDP VSHWKPEAV YYEDGAR	22.55521		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good y ion series; a couple of complementary peaks, extra peaks may exceed 25% above 10% relative intensity; MS2 TIC only 16% (rough minimum is 20%); fragmentation actually looks decent considering it is a z=4	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r8	126553	Alternative acceptor (3' splice site)	Deletion	Yes(PB.8829.1)		
ARRB1	PB.7883.9	TASSDDDIIVFEDFAR	0.75184		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 44% (rough minimum is 20%)	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r4	171067	Novel exon	Insertion	Yes (PB.7883.9)		
SCAMP3	PB.954.9	DGGNPFAEP SELDNPFQAS AAAAAETLLK	0.75184		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 41% (rough minimum is 20%)	Yes	210827_HUVEC5.6 tryp_HCDorbi_4hr_F r13	249752	Exon skipping event	Deletion	Yes (PB.954.9)		

EDC4	PB.10482.1 0PB.10482.9	STRPAPGPFLSYGAER		Looks really good except for mass difference (>500ppm), isolation of the C13 isotope	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r15	72346	Intron retention event	Insertion	No (PB.10482.8, PB.10482.9)	<p>https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtPosition=chr16%3A67873052%2D67884499&position=multi%3A331125092%2D331196308&hsid=1331133675</p>	
RBMS1	PB.2016.3	MIFPSSSGNP GGSSNCR		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 29% (rough minimum is 20%); y14 ending in proline is most abundant	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r15	61807	Alternative first exon	Substitution	Yes (PB.2016.3)	<p>bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtPosition=chr2%3A160272151%2D160409380</p>	
RBMS1	PB.2016.3	MIFPSSSGNP GGSSNCR	same sequence as above (oxidized methionine version of a peptide already listed earlier in the table)	Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks do not exceed 25% above 10% relative intensity; MS2 TIC approx 29% (rough minimum is 20%); y8 ending in proline is most abundant	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r15	49330					
S100PBP	PB.335.4	SLVVSTSNK DVLNKDSGK		Mass difference too high (>500ppm), isolation of the C13 isotope	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r11	43051	Alternative acceptor (3' splice site)	Deletion	Yes (PB.335.4)	<p>https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtPosition=chr17%3A64319415%2D64390860&position=multi%3A37911920%2D37919452&hsid=1331133675</p>	
RPA1	PB.10683.5	IGNVPVPYNEG STVSK		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks MAY exceed 25% above 10% relative intensity; MS2 TIC approx 17% (rough minimum is 20%); y10 ending in proline is most abundant	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r8	66226	Exon skipping event	Deletion	Yes (PB.10683.5)		
PECAM1	PB.11293.4 5PB.11293.80	ELELLTSKDP PPSASQSAGI TDLGK		Mass difference too high (>300ppm), isolation of the C13 isotope	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r11	112520	Novel exon	Insertion	No (PB.11293.4 5, PB.11293.80)		
NHSL1	PB.4914.1	CAGDIFGELE GQAAALGHR		Minimum 9 amino acids, Score>5, delta mass<5ppm, PEP<0.005, good b and y ion series, extra peaks exceed 25% above 10% relative intensity; MS2 TIC approx 15% (rough minimum is 20%)	Yes	210827_HUVECS.6 tryp_HCDorbi_4hr_F r12	195591	Alternative first exon	Substitution	Yes	<p>https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg38&lastVirtModeType=customUrl&lastVirtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtModeType=customUrl&virtModeExtraState=multiRegionsBedUrl%3D%2Fuserdata%2Fsession%2Frr%2F13%2Fmm5db%2F0c7bcef%2Fhg%2FcustRgn_gnome_1e56d_a22290.bed+0&virtPosition=chr6%3A138414829%2D138503008&position=multi%3A73908187%2D73920000&hsid=1331133675</p>	

[illegible]

LRCH3	PB.3162.17	IGVPQELLK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r15	107154						
SMARCC2	PB.8453.16	EGERAGGEE VR	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r9	131372						
SPOUT1	PB.6707.6	LNOQOHPDS VTTPDCK	1.127761			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r4	32468						
ZMYND8	PB.12885.1 1	TFSMADPGSA ER	4.511042			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r7	63314						
GLA	PB.13773.3	NFEAMVAEPK	4.886963			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r8	82400						
SLC25A29	PB.9503.16	GSQVPPMQL SPGGPGR	3.759202			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r11	28193						
FTSJ1	PB.13630.7	CDSQPALTPS PCAFF	1.127761			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	210744						
SCRN1	PB.5171.16	SQAEHHAG AGEAR	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r7	34226						
PRXL2B	PB.54.12	GVSSQPWEG WGLSK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r11	137263						
UAP1L1	PB.6811.13	AVTRCAAAG GCGLPAR	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r7	145605						
ZEB1	PB.6948.22	QANPRRNNA GK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	174748						
LAMA4	PB.4847.99	TLTINAFQHO QCDGTFR	6.766564			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r13	78624						
U2SURP	PB.2954.16	LREIEEKEK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r7	54435						
RAN	PB.8811.11	RNAAMAAQG EPQVQFK	3.007362			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r6	86809						
TM9SF4	PB.12751.1 2	GLGWGGMKL DGEGR	1.127761			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r10	157495						
TM9SF4	PB.12751.1 2	GLGWGGMKL DGEGR	1.127761			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r6	121642						
TXNRD1	PB.8628.12	QLDSTIGIHPV CAEGSCHPG WSAVV	4.511042			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r12	155884						
PRKAR2A	PB.2585.28	KIWHHLQFHR ITVK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r14	45225						
MAPRE1	PB.12763.2	IVDILYATDVC V	4.135122			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r15	202173						
GSPT1	PB.10200.1 7	GPAAPPPPVG GAANNHGAG SGAGGRADA GK	0.75184			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r7	49405						
TSN	PB.1936.15	ELSQIGR	1.127761			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r11	79552						
ARHGDIA	PB.11451.3	CSOGAAQGW GFAQGCWAVI EGEVPTTGDL ESFKK	6.766564			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r14	216610						
GART	PB.13065.1	VQGILLQPP E	3.759202			210827_HUVEC5.6 tryp_HCDorbi_4hr_F r16	163319						