

4	HR	Accession	Score	Mass	LH	SD(geo)	#													
4	10	QX002		52	49484		0													
4	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications										
4	1	z	GFSSGSAVSSGSSR	X	24.51	0.2319	0.5799	0.9925	122.9											
4	11	P0078920		43	10594		0													
4	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications										
5	1	P00307259		911	377426		13													
5	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications										
5	1	z	ELVGFVFR	X	0.9775	0.02854	0.8545	0.996	302.3											
5	2	z	DSLALSLDGVFR	X	0.9785	0.02224	0.9019	0.9958	209.2											
5	3	z	GGQTEFLTPFR	X	0.9388	0.02432	0.892	0.8301	555.4											
5	4	z	FAPQAVVLR	X	1.02	0.01183	0.9306	0.9931	287.5											
5	5	z	VLALTELCVLR	X	2.865	0.999	0.1614	0.6617	260.6											
5	6	z	SLQGEQVNELCR	X	1.055	0.03614	0.9759	0.9914	416.1											
5	7	z	LLGQLELDSPATK	X	1.046	0.01907	0.9779	0.9927	611.8											
5	8	z	LLLEEDNEESGSKR	X	1.046	0.02106	0.8264	0.9965	399.8											
5	9	z	3LGGVLAEEQATEPNTFR	X	2.573	0.2231	0.3517	0.8422	88.22											
5	10	z	2LGGVLAEEQATEPNTFR	X	1.067	0.01411	0.9683	0.9941	168.8											
5	11	z	3LGMVLDLDFCNSTPQVFR	X	1.076	0.02789	0.9144	0.9895	344.9 (Oxidation(M))											
5	12	z	3KPVLEVTGPGGDQNPATFR	X	1.085	0.01701	0.9932	0.9924	646.2											
5	13	z	4FNKNSGSAHWYDGLFSEKVEK	X	1.134	0.06872	0.8248	0.8626	457.6											
5	14	z	3ESPLPAATELAFHVCNLSAIEELR	X	0.7274	0.1113	0.389	0.7653	86.78											
5	15	z	4ESPLPAATELAFHVCNLSAIEELR	X	1.038	0.05207	0.823	0.9546	427											
5	16	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	17	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	18	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	19	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	20	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	21	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	22	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	23	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	24	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	25	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	26	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	27	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	28	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	29	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	30	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	31	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	32	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	33	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	34	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	35	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	36	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	37	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	38	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	39	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	40	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	41	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	42	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	43	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	44	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	45	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	46	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	47	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	48	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	49	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	50	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	51	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	52	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	53	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	54	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	55	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	56	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	57	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	58	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	59	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	60	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	61	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	62	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	63	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	64	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	65	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											
5	66	z	2EGTQESQVSSSTR	X	0.892	0.01499	0.9819	0.995	374.7 (Oxidation(M))											
5	67	z	2LQVWVTSLQOEYK	X	0.902	0.02238	0.8612	0.9886	139.8											
5	68	z	2LAFETATQYK	X	0.923	0.01707	0.9176	0.9939	326.5											

HR	Accession	Score	Mass	LH	SD(geo)	#	HR	Accession	Score	Mass	LH	SD(geo)	#		
8	16 Q4F2U2	49	5555			0	9	17 P0028135	72	19814			1		
8	Keatn1, type I cytoskeletal 6A OS=Rattus norvegicus GN/KR6A PE=1 SV=1						9	Gene_Symbol=HCG_21078 hypothetical protein LOC389435 hg=148 # SNP[153.p,118.P]SNP[165.a,133.A]							
8	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
8	1	2 SLDLDSAEVVK		6.297	6.457	0.7503	0.9957	100.2			1.034	0.01163	0.9004	0.9952	716.8
8	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
8	17 P04264	47	65149			0	9	18 P0003358	68	22440			1.036		1
8	Keatn1, type I cytoskeletal 1 OS=Homo sapiens GN/KR1 PE=1 SV=5						9	Gene_Symbol=EEF1E1 Eukaryotic translation elongation factor 1 epsilon-1 hg=174 # SNP[181.v,142.V]#							
8	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
8	1	2 SLDLDSAEVVK		6.297	6.457	0.7503	0.9957	100.2			1.036	0.02249	0.7607	0.9757	163.8
8	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
8	18 P00290460	46	66566			0	9	19 P00644408	65	107031					0
8	Gene_Symbol=EF3EG Eukaryotic translation initiation factor 3 subunit G hg=320 # SNP[336.a,118.A]SNP[38.1]						9	Gene_Symbol=EPH2 Ephrin receptor hg=946							
8	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
8	1	2 SLDLDSAEVVK		6.297	6.457	0.7503	0.9957	100.2			0.4039	0.2354	0.9288	0.9226	486.7
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	1 P00044282	451	65979			7	9	20 P00002366	58	150109			1.011		1
9	Gene_Symbol=NCL cDNA FLJ45706 fs, clone FEBRA202457, highly similar to Nucleolin hg=603						9	Gene_Symbol=HSPA4 Heat shock 70 kDa protein 4 hg=840 # SNP[847.a,159.A]SNP[880.159.A]SNP[934.1]							
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 TGSDFVAFK	X	1.019	0.01205	0.8995	0.9993	519.9			0.5519	0.1161	0.4238	0.6068	71.11
9	2	2 NDIAVVDVR	X	1.023	0.04087	0.7794	0.9976	444.4			1.011	0.04827	0.6696	0.9143	111.9
9	3	2 EYFDEAER	X	1.008	0.02712	0.815	0.9935	315.9							
9	4	2 TEADAKTFEEK	X	0.7461	1.388	0.5485	0.9518	64.02							
9	5	3 TEADAKTFEEK	X	0.983	0.02119	0.7778	0.9974	77.27							
9	6	2 GFGVDFMSDEDAK	X	1.08	0.01044	0.9396	0.9915	1245							
9	7	3 VTGDELKVFDAER	X	1.146	0.01347	0.84	0.9891	755.4							
9	8	3 CLSEDTTEELTKESFDGSR	X	1.243	0.1812	0.8363	0.9549	1071							
9	9	5 EAMGEGDGKRVLDVAKPK	X	-1.842	0.1837	0.8218	0.959	794 (3) Oxidation (M)							
9	10	4 EAMGEGDGKRVLDVAKPK	X	1.435	0.07966	0.7416	0.9751	185.9 (8) Oxidation (M)							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	2 P00013286	273	32845			3	9	21 P00021570	68	37232			0.7814		1
9	Gene_Symbol=RPS18LOC10013553 40S ribosomal protein S18 hg=152 # SNP[159.m,44.V]SNP[169.v,4.1]						9	Gene_Symbol=RPS19 40S ribosomal protein S19 hg=145 # SNP[166.v,12.V]SNP[167.1,123.V]SNP[188.a,1.1]							
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 VLNINDGR	X	0.9882	0.02108	0.9414	0.9582	668.9							
9	2	2 AGELTDEVER	X	0.9976	0.02398	0.9725	0.9166	911.4							
9	3	2 YSGVLANGLDNK	X	1.045	0.04596	0.5871	0.9767	468.9 (7) Deamidated (N)							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	3 P0064224	229	87548			3	9	23 P000221093	54	33481					0
9	Gene_Symbol=HDDPU cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U hg=7						9	Gene_Symbol=RPS17 40S ribosomal protein S17 hg=135 # SNP[152.1,119.V]SNP[169.1,126.V]SNP[209.2.1]							
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 VNLGNTMIDK	X	0.917	0.01553	0.9415	0.9945	402.4 (10) Oxidation (M)							
9	2	2 NFLDQTNVSAQAQR	X	1.016	0.01233	0.9634	0.9927	602.1							
9	3	2 SSGPTSLFAVYVPPGAR	X	1.015	0.01836	0.9812	0.9913	1035							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	4 P00761	202	25078			0	9	Gene_Symbol=Similar to 60S ribosomal protein L31 hg=48							
9	Trypsin OS=Sus scrofa PE=1 SV=1						9	1	2 SANEVVTNR	X	0.758	0.09282	0.684	0.9626	153.7
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	1 VATVSLPR		#####	22.45	0.9572	0.9936	6174							
9	2	2 VATVSLPR		-65.07	0.06034	0.8014	0.9535	4875							
9	3	2 LSSPATLNSR		-576	0.1952	0.8996	0.9812	5015							
9	4	3 LGEHNDVLEGNQFNAAK		-510.2	0.168	0.8535	0.9571	5688							
9	5	3 ITHVFNKGLTINDMLK		3.959	27.18	0.8467	0.9931	768.9 (8) Deamidated (N)							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	5 P00026271	156	13933			1.042	1.238	4.4							
9	Gene_Symbol=RPS14 40S ribosomal protein S14 hg=151 # SNP[155.a,10.X]SNP[204.x,10.X]SNP[258.a,1.1]														
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 EDVPPDSDTR	X	1.067	0.009896	0.9732	0.9925	1444							
9	2	3 EDVPPDSDTR	X	0.9921	0.01676	0.8257	0.9948	462.8							
9	3	3 ADREDSPPAMLAAGDVAQR	X	1.073	0.10102	0.8517	0.9904	213.5							
9	4	3 ADREDSPPAMLAAGDVAQR	X	1.038	0.01168	0.8963	0.9947	366.8 (12) Oxidation (M)							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	6 P0047455	139	19396			1.056	1.056	1							
9	Gene_Symbol=H2BFS Histone H2B type F-3 hg=126														
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 AMGMNSYVDFEER	X	1.056	0.02013	0.9263	0.9888	669.4 (2) Oxidation (M)							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	7 P00554834	133	103463			1.012	2	9	27 P00910438	43	100301				0
9	Gene_Symbol=EML4 EML4 protein hg=923							9	Gene_Symbol=SDH1 cDNA FLJ54574, highly similar to Staphylococcal nuclease domain-containing protein 1						
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 ADGFLVGTGR	X	1.101	0.03683	0.838	0.9938	226.3							
9	2	2 LSLPQNEVADTTLTK	X	1.082	0.03251	0.9682	0.9931	227							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	8 P00550247	125	18089			1.053	1.049	2	9	25 P00056342	47	93625			0
9	Gene_Symbol=RPL35 11 kDa protein hg=96							9	Gene_Symbol=HEDD9 neural precursor cell expressed, developmentally down-regulated 9 isoform 3 hg=634						
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 VLVNQTQK	X	1.063	0.03185	0.9116	0.996	1194							
9	2	3 OLDDLVKVELSLQR	X	1.018	0.01358	0.8006	0.9968	637.6							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	9 P00412607	124	23419			1.053	1.819	2							
9	Gene_Symbol=RPL35 60S ribosomal protein L35 hg=123 # SNP[128.1,109.R]SNP[136.1,109.R]SNP[143.1,1.1]														
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 VLVNQTQK	X	1.063	0.03185	0.9116	0.996	1194							
9	2	3 OLDDLVKVELSLQR	X	1.018	0.01358	0.8006	0.9968	637.6							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	10 P00641339	124	95638			1.016	1	9	26 P00016994	107	81899			1.008	1
9	Gene_Symbol=BCAR1 cDNA FLJ55515, highly similar to Breast cancer anti-estrogen resistance protein 1 hg=1							9	Gene_Symbol=GIT2 Isoform 5 of ARF GTPase-activating protein (GEF) hg=729						
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	3 GGSAGTEDLDLRLVACSR	X	1.016	0.02623	0.6187	0.9751	332.7							
9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td> <td>9</td> <td>HR</td> <td>Accession</td> <td>Score</td> <td>Mass</td> <td>LH</td> <td>SD(geo) <td>#</td> </td>	#	9	HR	Accession	Score	Mass	LH	SD(geo) <td>#</td>	#
9	11 P00021267	121	112476			1.014	1.002	2							
9	Gene_Symbol=EPHA2 Ephrin type A receptor 2 hg=976 # SP[976.A,24.A]#														
9	z	Sequence	Incl	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications						
9	1	2 VQAGFEVEYK	X	1.012											

HR	Accession	Score	Mass	LH	SD(geo)	#			
16	6 P00761		133	25078		0			
16	Tyrosin OS-Sus scrofa PE=1 SV=1								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 VAVTSLR	X	1099	0.2626	0.955	0.9971	2206	
16	2	2 VAVTSLR	X	54.74	0.2821	0.7524	0.9556	1955	
16	3	3 LGEHNDVLEGEQFNAAK	X	45.65	0.2109	0.7396	0.9621	3187	
16	4	4 LGEHNDVLEGEQFNAAK	X	261.7	1.226	0.9499	0.9682	4068	
16	5	5 ITHFNKGLDMLDK	X	2.955	7.588	0.1764	0.8252	2055	(8) Deamidated (N)
16	6	6 ITHFNKGLDMLDK	X	9.683	1.724	0.8558	0.9664	9851	(8) Deamidated (N)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	7 P0025447		119	48181	1.049		1	
16	Gene_Symbol:EEF1A1 Elongation factor 1-alpha hq=41								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 IGGTVFVGR	X	1.049	0.0526	0.8788	0.8018	5405	
16	2	2 IGGTVFVGR	X	1.055	0.1849	0.8376	0.7831	1228	
16	3	3 SGGAMDMVPGKACVSEFSDYFPLGR	X	0.6139	0.1168	0.4583	0.5091	1769	(9) Oxidation (M)
16	4	4 SGGAMDMVPGKACVSEFSDYFPLGR	X	0.7058	0.2154	0.7543	0.9465	1604	(9) Oxidation (M)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	8 Q8EGZ7		78	59932			0	
16	Gene_Symbol:EEF1A1 Elongation factor 1-alpha hq=41								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 AQVEDANR	X	1.091	0.5749	0.8905	0.9851	8855	
16	2	2 SLDLSAEVK	X	56.41	3.132	0.56	0.9961	2009	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	9 P00220556		56	0	1.035		1	
16	Tyrosin OS-Sus scrofa PE=1 SV=1								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 GDFPFLSLAK	X	1.035	0.02704	0.8154	0.9784	363.1	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	10 P00472610		56	0			0	
16	Tyrosin OS-Sus scrofa PE=1 SV=1								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 SRWQQGWFSCSMVEALHNYHTOK	X	62.22	1.089	0.8608	0.9356	2330	(4) Deamidated (N)
16	2	2 SRWQQGWFSCSMVEALHNYHTOK	X	107.2	2.398	0.6738	0.9488	2665	(4) Deamidated (N)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	11 Q7ZT54		55	48601	1.024		1	
16	Gene_Symbol:EEF1A1 Elongation factor 1-alpha hq=41								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 LVLODIAR	X	1.024	0.05047	0.6655	0.9215	1642	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	12 P00747497		52	50326	0.985		1	
16	Gene_Symbol:EEF1A1 Elongation factor 1-alpha hq=41								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 WFLTGNQFGR	X	0.985	0.04666	0.8258	0.9334	826.9	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	13 P00008765		52	138871	0.985		1	
16	Gene_Symbol:EEF1A1 Elongation factor 1-alpha hq=41								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 WFLTGNQFGR	X	0.985	0.04666	0.8258	0.9334	826.9	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	14 P00029225		52	60011	0.723		1	
16	Gene_Symbol:CTG8 59 kDa protein hq=547								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 FAEFAEAPR	X	0.723	0.06277	0.5338	0.9395	385.3	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	15 P00011253		377	96665	0.8444	1.033	5	
16	Gene_Symbol:RPS3 40S ribosomal protein S3 hq=243 # SNP127.6.103.EJ[SNP]276.6.103.EJ[SNP]286.1.11								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 TEILAR	X	0.9439	0.0176	0.6888	0.9983	715.8	
16	2	2 GLCAQAQSLR	X	0.8962	0.02809	0.8955	0.9937	808.9	
16	3	3 ELAEDGCVNLR	X	0.9432	0.02326	0.9093	0.9948	843	
16	4	4 FGGPEVSELYAEK	X	0.9753	0.01904	0.9344	0.9943	653.2	
16	5	5 FVDGLMHSDGPPVYDVAIR	X	0.9655	0.01038	0.9431	0.9924	567.6	(6) Oxidation (M)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	16 P00761		216	25078			0	
16	Tyrosin OS-Sus scrofa PE=1 SV=1								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 VAVTSLR	X	2.946	27.87	0.9586	0.9897	4494	
16	2	2 VAVTSLR	X	29.36	1.587	0.9603	0.9617	8016	
16	3	3 LSSPATLNSR	X	-72.26	0.2293	0.9646	0.9916	3738	
16	4	4 LGEHNDVLEGEQFNAAK	X	17.03	55.94	0.6989	0.8893	4616	
16	5	5 LGEHNDVLEGEQFNAAK	X	57.59	4.757	0.9785	0.99	325.4	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	17 P00472171		174	30476	1.038	1.995	5	
16	Gene_Symbol:RPL7 30 kDa protein hq=259								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 VLQLLR	X	0.7354	0.161	0.3601	0.9602	20.77	
16	2	2 VLQLLR	X	0.9079	0.03438	0.4947	0.9965	101.2	
16	3	3 EVPAVETIK	X	1.147	0.01156	0.8814	0.9966	696.1	
16	4	4 ALTDNALNR	X	1.074	0.01526	0.9577	0.9971	1598	
16	5	5 THFVGGDAGNREDDNR	X	0.994	0.02638	0.7384	0.9912	70.85	
16	6	6 THFVGGDAGNREDDNR	X	1.084	0.01213	0.7645	0.9975	239.7	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	18 P0178440		168	90228	1.133	1.034	3	
16	Gene_Symbol:EEF1B2 Elongation factor 1-beta hq=225 # SNP124.6.161.GJ[SNP]277.187.TJ[SNP]320.187								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 SIADGCVLWSSK	X	1.118	0.01825	0.7999	0.9814	910.3	
16	2	2 SPAGLVNDVLDK	X	1.106	0.02136	0.9068	0.987	588	
16	3	3 SLLLDVLPVDEIDMAK	X	1.177	0.03723	0.7286	0.9824	193.5	(16) Oxidation (M)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	19 P00217030		150	89468	1.07	1.061	4	
16	Gene_Symbol:RPS4X 40S ribosomal protein S4, X isoform hq=263 # SNP1275.1105.TJ[SNP]290.4.119A[SNP]								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 LSNFVFK	X	0.9932	0.02068	0.9198	0.9936	1456	
16	2	2 FDTGNLCMVTGGANLGR	X	1.058	0.04698	0.5848	0.9286	218.1	(8) Oxidation (M)
16	3	3 FDTGNLCMVTGGANLGR	X	1.091	0.01283	0.9862	0.9922	728.7	(8) Oxidation (M)
16	4	3 VMDTDLQETKIDFK	X	1.144	0.05653	0.825	0.9947	507.1	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	20 P00465361		104	84652	0.9509	1.122	2	
16	Gene_Symbol:RPL13 60S ribosomal protein L13 hq=211 # SNP1322.1.112A[SNP]237.112A[SNP]249.1								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 GFSLELR	X	0.8766	0.02705	0.799	0.9972	353.7	
16	2	2 STESLQANVR	X	1.031	0.08128	0.97	0.997	400.6	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	21 P00318470		91	8402	1.074		4	
16	Gene_Symbol:8 kDa protein hq=78								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 FNTGNLCMVTGGANLGR	X	1.058	0.04698	0.5848	0.9286	218.1	(5) Deamidated (N)
16	2	2 FNTGNLCMVTGGANLGR	X	1.091	0.01283	0.9862	0.9922	728.7	(5) Deamidated (N)
16	3	3 FNTGNLCMVTGGANLGR	X	1.058	0.04698	0.5848	0.9286	218.1	(2) Deamidated (N)
16	4	2 FNTGNLCMVTGGANLGR	X	1.091	0.01283	0.9862	0.9922	728.7	(2) Deamidated (N)
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	22 P00011334		72	63992	1.002		1	
16	Gene_Symbol:Phb Phorbol hq=272 # SNP1291.6.111.GJ[SNP]322.6.111.GJ[SNP]365.4.113.DJ[SNP]394.4								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 QVSDDLTER	X	7.657	2.45	0.7808	0.7367	135.8	
16	2	2 FTSGEDYDER	X	1.002	0.02559	0.8886	0.9954	252.8	
16	HR	Accession	Score	Mass	LH	SD(geo)	#		
16	16	23 P00002821		72	23389	1.063		1	
16	Gene_Symbol:RPL14 60S ribosomal protein L14 hq=213								
16	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
16	1	1 LVAVDVDNRR	X	1.063	0.02415	0.8268	0.9948	690.1	

HR	Accession	Score	Mass	LH	SD(geo)	#			
13	20 P00141318		52	88089	1.175	1			
13	Gene_Symbol:CKAP4 isoform 1 of Cytoskeleton-associated protein 4 hq=602 # SNP1011.111.1J[SNP]650.4								
13	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
13	1	1 VQEQVHTLLSDQQAQAR	X	0.3477	0.3841	0.5039	0.5109	64.93	
13	2	2 VQEQVHTLLSDQQAQAR	X	1.175	0.05778	0.8626	0.9806	78.81	
13	HR	Accession	Score	Mass	LH	SD(geo)	#		
13	13	21 P00480103		47	114533			0	
13	Gene_Symbol:FAM33D hypothetical protein LOC181610 hq=15 # SNP1624.164.HJ[SNP]648.164.HJ[SNP]								
13	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
13	1	1 TITGNVYAR	X	2.004	0.4594	0.783	0.9161	122.3	
13	HR	Accession	Score	Mass	LH	SD(geo)	#		
13	13	22 P00045219		47	134218	1.315		1	
13	Gene_Symbol:SNX18 isoform 1 of Sorting nexin-18 hq=628 # SNP1639.204.GJ[SNP]685.282.DJ[SNP]697								
13	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications
13	1	1 AEPFGAGDGGGAPAR	X	1.315	0.034	0.9083	0.9971	82.76	

27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	7	P0019330		82	2788	0.9671	1											
27	Gene_Symbol	LBC_RPS27A	LBC ubiquitin and ribosomal protein S27A precursor	156	SNP[162,d,106]													
27	1	z	3	CCLTYCFKFKEDK	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
27								0.9671	0.02449	0.954	205.3							
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	8	P00451413		58	5950	0.8589	1											
27	Gene_Symbol	HST1H4A	HST1H4F,HST1H4C,HST1H4I,HST1H4J,HST1H4K,HST1H4L,HST1H4M,HST1H4N,HST1H4O,HST1H4P,HST1H4Q,HST1H4R,HST1H4S,HST1H4T,HST1H4U,HST1H4V,HST1H4W,HST1H4X,HST1H4Y,HST1H4Z															
27	1	z	2	IGLVYEIETR	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
27								0.8589	0.03238	0.9745	110.6							
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	9	P00472610		58	5740		0											
27	Gene_Symbol	GHM	GHM protein	478	SP[460,E,20,E]													
27	1	z																
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	10	P00017664		56	15299	1.023	1											
27	Gene_Symbol	SNRPD3	Small nuclear ribonucleoprotein Sm D3	126	SNP[131,a,101,A]													
27	1	z	2	VAQLEQVYR	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
27								1.023	0.04646	0.7541	128.8							
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	11	P00974		54	11352		0											
27	Gene_Symbol	PHF5A	PHF5A PDZ finger-like domain-containing protein 5A	110														
27	1	z	2	AGLCQTFVGGCR														
27								2355	5.902	0.9062	997.8	275.1						
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	12	P00221091		52	27703	0.9733	1											
27	Gene_Symbol	RPS15A	40S ribosomal protein S15a	130	SNP[139,F,9,F]SNP[157,a,79,F]SNP[175,L]													
27	1	z	2	NVNLGTR	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
27								0.9733	0.01139	0.9425	998.8	764.9						
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	13	P00005511		51	13138	0.6632	1											
27	Gene_Symbol	PHF5A	PHF5A PDZ finger-like domain-containing protein 5A	110														
27	1	z																
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	14	P00216237		45	23115		0											
27	Gene_Symbol	RPL36	60S ribosomal protein L36	105	SNP[111,a,67,K]SNP[121,L,67,K]SNP[134,L]													
27	1	z																
27	HR	Accession	Score	Mass	LH	SD(geo)	#											
27	15	P00332157		42	33026	0.9126	1											
27	Gene_Symbol	MRPL54	39S ribosomal protein L54, mitochondrial	138	SNP[145,L,129,H]SNP[157,a,1]													
27	1	z	2	TLEELDPESR	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
27								0.9126	0.05022	0.6941	984.5	58.07						
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	1	AS40M5		192	426621		0											
28	Gene_Symbol	KRT1	keratin, type I cytoskeletal 1	OS=Pan troglodytes GN-KRT1 PE=2 SV=1														
28	1	z	2	LALDEIATYR														
28								41.41	1.613	0.7759	0.9672	108						
28	2	2	2	SLDLSIAEVK														
28								32.09	0.7766	0.9981	253.5							
28	3	2	2	FLEQQKVLQTK														
28								1111	1.576	0.9227	0.9981	218.9						
28	4	3	3	SLNNQFASFDKVR														
28								6.242	5.984	0.7777	0.9828	106.9						
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	2	P00203327		192	426606		0											
28	Gene_Symbol	KRT1	keratin, type I cytoskeletal 1	192	SNP[66,g,133,G]SNP[81,d,155,V]SNP[910,v]													
28	1	z	2	LALDEIATYR														
28								41.41	1.613	0.7759	0.9672	108						
28	2	2	2	SLDLSIAEVK														
28								32.09	0.7766	0.9981	253.5							
28	3	2	2	FLEQQKVLQTK														
28								358.7	0.7163	0.8511	0.9982	220.8						
28	4	3	3	SLNNQFASFDKVR														
28								6.242	5.984	0.7777	0.9828	106.9						
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	3	P00761		112	25078		0											
28	Gene_Symbol	OS-Sus	scrofa PE=1 SV=1															
28	1	z	1	VATVSLPR														
28								0.6769	0.9689	0.9914	7062							
28	2	2	2	VATVSLPR														
28								65.31	0.8799	0.9662	4020							
28	3	2	2	LSSPATLNLR														
28								47.26	0.3192	0.9923	4020							
28	4	3	3	LGEHNDVLEQNEGFNAAK														
28								15.15	0.6824	0.9826	4349							
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	4	P13645		102	59703		0											
28	Gene_Symbol	KRT10	keratin, type I cytoskeletal 10	OS=Homo sapiens GN-KRT10 PE=1 SV=4														
28	1	z	2	VTMQNLNDR														
28								4.104	8.696	0.5735	0.9953	53.87						
28	2	2	2	ALEESNVELEK														
28								4.125	1.708	0.7177	0.9976	123.4						
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	5	P35908		99	66111		0											
28	Gene_Symbol	KRT2	keratin, type I cytoskeletal 2	epidermal OS=Homo sapiens GN-KRT2 PE=1 SV=1														
28	1	z																
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	1	AS40M5		192	426606		0											
28	2	2	2	FLEQQKVLQTK														
28								1111	1.576	0.9227	0.9981	218.9						
28	HR	Accession	Score	Mass	LH	SD(geo)	#											
28	6	P00215790		93	61055	0.9518	1											
28	Gene_Symbol	RPL38	60S ribosomal protein L38	170	SNP[77,d,10,D]SNP[91,y,10,D]SNP[106,L,11,F]S													
28	1	z	3	EEDKLLTAR	X	LH	Std.Err.	Fraction	Correlator	Intensity	Modifications							
28								0.9518	0.02413	0.6781	0.9932	272.7						

表3 システイン酸化プロテオーム解析結果

Fraction	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications	
1	1	P00769134	237	26024	1.281	1.064	3	z									
1	1	Gene_Symbol=	Glyceraldehyde 3-phosphate dehydrogenase	hg206													
1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications							
1	1	1	2 VPTANVSVLDTLGR	X	1.246	0.02847	0.905	0.955	1095								
1	1	2	ISNASCITNKLAPLAK	X	1.375	0.009136	0.9872	0.9938	1675								
1	1	3	3 VPTANVSVLDTLGR	X	1.227	0.02916	0.8302	0.957	426.4								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	2	P00847889	207	50436	1.348	1.032	3	z								
1	1	1	Gene_Symbol=	cDNA FLJ53368, highly similar to Pyruvate kinase isozymes M1/M2	hg457												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 CCSGAVLTK	X	1.39	0.04611	0.8697	0.9553	417.8								
1	1	2	HTGKTFGASR	X	1.351	0.02477	0.9972	0.9346	1431								
1	1	3	2 CDELNLVLDK	X	1.306	0.01493	0.8525	0.998	215.5								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	3	P00387144	183	22926	1.217	1.034	4	z								
1	1	1	Gene_Symbol=	TUBA1B Tubulin alpha-1B chain	hg451												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 SQFVVDVCPGFK	X	1.264	0.02616	0.948	0.9566	322.2								
1	1	2	2 RQFVDVCPGFK	X	0.5581	0.3836	0.6294	0.8213	42.68								
1	1	3	3 RQFVDVCPGFK	X	1.173	0.01546	0.8029	0.9949	161.9								
1	1	4	3 AVCLMSNTAAEAWAR	X	1.197	0.05816	0.6917	0.9528	28.18								
1	1	5	2 AVCLMSNTAAEAWAR	X	1.237	0.0317	0.9014	0.9556	89.82								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	4	P00759506	169	0	1.349	1.119	1	z								
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 VNGQSVTEIQLACK	X	1.349	0.01138	0.9551	0.9933	111.9								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	5	P00031420	150	84517	1.193	1.033	2	z								
1	1	1	Gene_Symbol=	UGDH UDP-glucose 6-dehydrogenase	hg194												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 ASVFGGSCFK	X	1.221	0.02826	0.9343	0.9564	965.7								
1	1	2	3 AVGALCAVYEHVPR	X	1.167	0.03908	0.8523	0.9974	106.3								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	6	P00472718	142	18337	1.265	1.055	2	z								
1	1	1	Gene_Symbol=	Peptidyl-prolyl cis-trans isomerase	hg164												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 KITADACGLE	X	1.237	0.01071	0.9512	0.9561	154.1								
1	1	2	2 IFGFGCGGDFTR	X	1.335	0.00716	0.9327	0.994	107.6								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	7	P00185290	136	18523	1.172	1.028	3	z								
1	1	1	Gene_Symbol=	EEF2 Elongation factor 2	hg858												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 STLTDLSVCK	X	1.155	0.01037	0.94	0.9949	764.7								
1	1	2	2 EGALCEENMR	X	1.152	0.02338	0.8596	0.9984	137								
1	1	3	2 CLYASVLTAGPR	X	1.212	0.0181	0.8559	0.9974	315.7								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	8	P00796333	135	22711	1.296	1.105	2	z								
1	1	1	Gene_Symbol=	TPH 22 kDa protein	hg210												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 IVAAGCNCK	X	1.208	0.01809	0.9479	0.9569	125.7								
1	1	2	2 VGGSVTGTACK	X	1.391	0.1182	0.9341	0.994	209.6								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	9	P00148661	126	54300	1.284	1.1	1	z								
1	1	1	Gene_Symbol=	LDHA L-lactate dehydrogenase A-like 6A	hg332												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 VGGGCDLSAR	X	1.284	0.01271	0.9562	0.9962	745.4								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	10	P00220301	120	49676	1.264	1.092	2	z								
1	1	1	Gene_Symbol=	PRDX6 Peroxisome oxidoreductin-6	hg224												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 DTFPVTCTELGR	X	1.263	0.01445	0.931	0.9961	570.6								
1	1	2	2 DNAVYCEETEK	X	1.266	0.04849	0.9436	0.997	127.5								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	11	P00641950	116	38378	1.284	1.105	0	z								
1	1	1	Gene_Symbol=	GNBL1 Guanine nucleotide-binding protein subunit beta-1	hg347												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 VAAAGCNCK	X	1.208	0.01809	0.9479	0.9569	125.7								
1	1	2	2 VGGSVTGTACK	X	1.391	0.1182	0.9341	0.994	209.6								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	12	P00016610	116	116651	1.331	1.02	2	z								
1	1	1	Gene_Symbol=	PCBP2 Poly(rC)-binding protein 2	hg356												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 NSEGNCFPER	X	1.313	0.01368	0.9435	0.9973	365.8								
1	1	2	2 AITAGVPSVTECVK	X	1.349	0.013	0.9339	0.9887	333								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	13	P00026781	109	77235	1.221	1.071	2	z								
1	1	1	Gene_Symbol=	FASN Fatty acid synthase	hg2511												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 LGLMSPGTCCK	X	1.164	0.02683	0.8262	0.998	145								
1	1	2	2 SPYGLTFLGR	X	1.282	0.02156	0.8855	0.993	242.8								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	14	P00040897	103	28612	1.324	1.105	1	z								
1	1	1	Gene_Symbol=	LOC119358 similar to hCG040270	hg117												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 NITQVLLNCR	X	1.324	0.02855	0.9704	0.9548	351								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	15	P00012066	102	58555	1.313	1.02	1	z								
1	1	1	Gene_Symbol=	PCBP2 poly(rC) binding protein 2	hg356												
1	1	1	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications						
1	1	1	2 NSEGNCFPER	X	1.313	0.01368	0.9435	0.9973	365.8								
1	1	HR	Accession	Score	Mass	LH	SD(geo)	#	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
1	1	16	P0055645	95	27589	1.148	1.1	1	z				</				

HR	Accession	Score	Mass	LH	SD(geo)	#												
1	41	P0005433	65	50363	1.155	1												
1	Gene_Symbol	RP55 40S ribosomal protein S5	hg=204 # SNP[236,125,5]SNP[273,125,5]SNP[287,125,5]															
1	z	VNQAWLCTGAR	X	1.155	0.04138	0.9485	0.9563	330.6										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	42	P00217592	63	79555	1.055	1												
1	Gene_Symbol	GFP11 Isoform 1 of Glucosaminyl-fructose-6-phosphate aminotransferase [isomerizing]																
1	z	CQNALQVAVR	X	1.055	0.04059	0.8766	0.9814	210										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	43	P00024933	63	20890	1.203	1												
1	Gene_Symbol	RPL12 Isoform 1 of 60S ribosomal protein L12	hg=165 # SNP[169,5,120,5]SNP[183,112,120,5]															
1	z	CTGEGVATSLAFK	X	1.203	0.02163	0.95	0.9972	299.6										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	44	P00290566	62	88423	1.333	1												
1	Gene_Symbol	TCP1 T-complex protein 1 subunit alpha	hg=558 # SNP[374,1,143,1]SNP[594,1,194,1]SNP[611,1,194,1]															
1	z	IACLDLFLSK	X	1.333	0.06852	0.8091	0.9976	145.5										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	45	P00642816	61	58214	1.359	1												
1	Gene_Symbol	SRP94 Hsp90 signal recognition particle 9 kDa protein	hg=86 # SNP[93,3,36,3]SNP[100,3,36,3]															
1	z	VTDDLVLVYK	X	1.359	0.03459	0.7584	0.978	165.1										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	46	P00285334	61	482211	1.194	0												
1	Gene_Symbol	FLNB Isoform 1 of Filamin B	hg=2602 # SNP[2616,10,108,10]SNP[2656,10,108,10]SNP[2677,10,108,10]															
1	z	IACLDLFLSK	X	1.194	0.02553	0.8879	0.9846	91.42										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	47	P00562559	60	126352	1.194	1												
1	Gene_Symbol	PABPC1L Polyadenylate-binding protein 1-like	hg=614 # SNP[641,2,212,2]SNP[677,2,212,2]															
1	z	GFQVCFSSPEATK	X	1.194	0.02553	0.8879	0.9846	91.42										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	48	P00785970	60	60434	1.146	1												
1	Gene_Symbol	SHMT2 Serine hydroxymethyltransferase (Fragment)	hg=504 # M506,Q27,QJ															
1	z	AAEALGSLNNK	X	1.146	0.04623	0.7804	0.9842	161.8										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	49	P00064607	60	63839	1.397	1												
1	Gene_Symbol	HSP90AA1 Hsp90 alpha delta-N	hg=539															
1	z	IKFEMLCK	X	1.397	0.0494	0.8848	0.9831	123.1										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	50	P00306332	59	30710	1.234	1												
1	Gene_Symbol	RPL24 60S ribosomal protein L24	hg=157 # SNP[167,9,150,9]SNP[183,9,150,9]SNP[191,9,150,9]															
1	z	VELCSFGWK	X	1.234	0.0365	0.8858	0.9568	512.8										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	51	P00786051	59	12264	1.144	1												
1	Gene_Symbol	HGST1 12 kDa protein	hg=106															
1	z	VFANFEDCVAFGK	X	1.144	0.03137	0.9159	0.9937	285.5										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	52	P00027223	58	109473	1.227	1												
1	Gene_Symbol	DH1 Isoform 1 of Nicotinamide dehydrogenase [NAD(P)] cytoplasmic	hg=14 # SNP[427,9,105,9]SNP[461,9,105,9]															
1	z	SEGGFWACK	X	1.227	0.01875	0.9155	0.9976	548.2										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	53	P00216308	57	34885	1.267	1												
1	Gene_Symbol	HVAC1 Voltage-dependent anion-selective channel protein 1	hg=283 # CCN291,L225,Y															
1	z	YQDPDAFSAK	X	1.267	0.02028	0.9345	0.9885	214										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	54	P00792538	55	17122	1.094	1												
1	Gene_Symbol	APEX1 Protein	hg=150															
1	z	CSWNVVGLR	X	1.094	0.05311	0.8288	0.9549	214.5										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	55	P00184838	54	24970	1.152	0												
1	Gene_Symbol	25 kDa protein	hg=224															
1	z	ALVDGPGTQVR	X	1.152	0.01207	0.8937	0.9958	215.1										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	56	P00002821	54	23389	1.167	1												
1	Gene_Symbol	RPL14 60S ribosomal protein L14	hg=213															
1	z	AGLCOIFVYGGCR	X	1.167	0.047	0.9139	0.9955	190.9										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	57	P00974	51	11352	1.152	0												
1	Gene_Symbol	Pancreatic trypsin inhibitor OS-Bos taurus PE-1	SV=2															
1	z	TGPLNFVTCMR	X	1.152	0.03707	0.8166	0.989	456.3										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	58	P00072044	51	42451	1.155	0												
1	Gene_Symbol	CE11orf54 Isoform 1 of Ester hydrolase C11orf54	hg=315 # CCN323,L184,FJCN336,G															
1	z	MAGCSLSFR	X	1.155	0.03707	0.8166	0.989	456.3										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	60	P00786333	48	45688	1.757	0												
1	Gene_Symbol	ALDOA cDNA FLJ56890, highly similar to Fructose-bisphosphate aldolase A	hg=18															
1	z	PNWVTPGACTCK	X	1.757	0.1102	0.5465	0.8433	86.85										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	61	P00847774	48	18333	1.276	1												
1	Gene_Symbol	RPL18A cDNA FLJ15101, highly similar to 60S ribosomal protein L18a	hg=154															
1	z	DLTTAGVTCYR	X	1.276	0.03392	0.8263	0.9924	101										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	62	P0084475	48	0	0	0	0	0										
1	z	LLKDSLGNCR	X	2.077	0.4613	0.9712	0.9127											

HR	Accession	Score	Mass	LH	SD(geo)	#												
1	63	P00915384	47	33313	1.274	0												
1	Gene_Symbol	cDNA FLJ52880, highly similar to Malate dehydrogenase, mitochondrial	hg=266 # M291															
1	z	GSDFDCELR	X	1.274	0.0456	0.7879	0.9991	318.1										
1	HR	Accession	Score	Mass	LH	SD(geo)	#											
1	64	P00514561	47	47756	1.274	1												
1	Gene_Symbol	HNRNPK Heterogeneous nuclear ribonucleoprotein K	hg=428															
1	z	GSDFDCELR	X	1.274	0.04													

HR	Accession	Score	Mass	LH	SD(geo)	#			
2	P100291006		80	76709	1245	1017			
2	Gene_Symbol=NDH2 Malate dehydrogenase, mitochondrial								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 GCDVVVAGVPR	X	1.26	0.02341	0.9515	0.9561	604.7	
2	2	2 TIFLSGCTPK	X	1.231	0.01556	0.9639	0.9949	959.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	13	P00755288		83	21959	1325	1		
2	Gene_Symbol=PEBP1 22 kDa protein								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CDEFLSNR	X	1.325	0.0133	0.8818	0.9974	880	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	14	P00015028		83	32667	1241	1		
2	Gene_Symbol=PTGES3 Prostaglandin E synthase 3								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 LTFSCGLGSDNFK	X	1.241	0.01421	0.971	0.9563	586	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	15	P00355646		82	84411	1406	1		
2	Gene_Symbol=TXNDC5 Thioredoxin domain containing 5 isoform								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 IAEVDCTAER	X	1.406	0.08532	0.6741	0.9916	122.5	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	16	P00747432		81	27469	1349	1		
2	Gene_Symbol=PPAP19 similar to peptidylprolyl isomerase A-like								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 IFGFMCGGDFTR	X	1.349	0.0142	0.9792	0.994	1024	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	17	P00031420		74	84517	1231	1		
2	Gene_Symbol=UGDH UDP-glucose 6-dehydrogenase								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 ASVFGGSCFK	X	1.231	0.02522	0.9393	0.9963	1011	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	18	P00514561		74	47756	1338	1		
2	Gene_Symbol=HNRNPDK Heterogeneous nuclear ribonucleoprotein K								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 GSDFDCELR	X	1.336	0.06599	0.7414	0.9972	254.6	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	19	P0007752		71	143417	0	0		
2	Gene_Symbol=TUBB2C Tubulin beta-2C chain								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 NAGNCLSPAVVGLLK	X	1.23	0.03319	0.8849	0.9963	141.6	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	20	P00112000		70	121015	123	1		
2	Gene_Symbol=PHGDH D-3-phosphoglycerate dehydrogenase								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 NAGNCLSPAVVGLLK	X	1.23	0.03319	0.8849	0.9963	141.6	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	21	P00215719		70	70773	1151	1		
2	Gene_Symbol=RPL18 60S ribosomal protein L18								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 GCGTVLLSFR	X	1.224	0.03912	0.8828	0.9977	427.3	
2	2	2 GCGTVLLSFRPK	X	0.1742	0.05701	0.3933	0.2061	405.2	
2	3	2 GCGTVLLSFRPK	X	1.083	0.04847	0.5596	0.9786	114.5	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	22	P00202001		69	49678	1313	1		
2	Gene_Symbol=PRDX6 Peroxisomal protein 6								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 DFTPVCTELGR	X	1.313	0.02473	0.9465	0.9558	491.9	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	23	P00289334		67	19120	1295	1		
2	Gene_Symbol=HSP90AB1 Heat shock protein 90Da alpha (Class B) member 1								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CLEFSELAEDK	X	1.295	0.01427	0.9845	0.9948	309.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	24	P00289334		65	48221	1355	1		
2	Gene_Symbol=FLNB isoform 1 of Filamin B								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CLATGFGASTVK	X	1.355	0.03233	0.8621	0.9929	208.1	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	25	P00031804		64	51139	127	1		
2	Gene_Symbol=VDAC3 isoform 1 of Voltage-dependent anion-selective channel protein 3								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 VCNVGLTFTGK	X	1.27	0.03328	0.8733	0.9981	112	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	26	P0021678		64	190249	1195	1		
2	Gene_Symbol=HSP90AB1 Heat shock protein 90 beta								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CLEFSELAEDK	X	1.295	0.01427	0.9845	0.9948	309.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	27	P00262041		63	48224	1266	1		
2	Gene_Symbol=FRAN GTP-binding nuclear protein Ran								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 VCENFVLCGKR	X	1.286	0.01765	0.9727	0.9943	461	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	28	P00290770		63	93046	0	0		
2	Gene_Symbol=CC3 chaperonin containing TCP1, subunit 3								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 TLQKNGASTR	X	1.854	0.3668	0.6176	0.9707	724.1	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	29	P00041950		62	38378	0	0		
2	Gene_Symbol=GNB2L1 Guanine nucleotide-binding protein subunit beta 2-like 1								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 MAGCSLSFR	X	1.208	0.0634	0.7938	0.9788	573.5	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	30	P00797038		61	176589	1195	1		
2	Gene_Symbol=PK2 mitochondrial phosphoenolpyruvate carboxylase 2 isoform 1 precursor								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 VECVDDAVMKR	X	1.105	0.03118	0.8221	0.9954	68.38	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	31	P00105866		61	46420	1285	1		
2	Gene_Symbol=CLIC1 Chloride intracellular channel protein 1								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 IKNCFPSOR	X	1.285	0.01459	0.887	0.998	472	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	32	P00387144		59	224266	0	0		
2	Gene_Symbol=TUBA1B Tubulin alpha-1B chain								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 ATLDLSCNK	X	1.122	0.2051	0.8431	0.9677	422.6	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	33	P00658830		59	14914	1215	1		
2	Gene_Symbol=RP53 protein (Fragment)								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 GLCAAGAESLR	X	1.215	0.01731	0.8581	0.9964	282.1	

HR	Accession	Score	Mass	LH	SD(geo)	#			
2	P0055799		58	11851		0			
2	Gene_Symbol=HSP90AEP Heat shock protein 90A								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CLEFLTEAEDK	X	1.674	0.3058	0.7942	0.9102	81.24	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	35	P00291005		58	83735	1332	1		
2	Gene_Symbol=NDH1 Malate dehydrogenase, cytoplasmic								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 VMVGNPANTINCLTASK	X	1.332	0.01681	0.927	0.9881	449.2	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	36	P00783271		57	229397	1237	1		
2	Gene_Symbol=LRPPRC Leucine-rich PPR motif containing protein, mitochondrial								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 LASIYNVDEEGASK	X	1.237	0.04477	0.828	0.9974	88.16	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	37	P00217852		57	78555	1077	1		
2	Gene_Symbol=GFPT1 isoform 1 of Glucosamine-6-phosphate aminotransferase [isomerizing]								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CQALQGVVAR	X	1.077	0.03441	0.8713	0.9802	196.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	38	P00640929		57	10465	1375	1		
2	Gene_Symbol=PS6 Ribosomal protein S6								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 LNSFPATGCKK	X	1.375	0.0225	0.9731	0.9951	884.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	39	P00044007		57	63839	0	0		
2	Gene_Symbol=HSP90AA1 Hsp90 alpha class A								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 CLEFLTEAEDK	X	1.674	0.3058	0.7942	0.9102	81.24	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	40	P00027223		56	105473	1152	1		
2	Gene_Symbol=BDH1 isocitrate dehydrogenase [NADP] cytoplasmic								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 SEGCFWACK	X	1.152	0.0285	0.9242	0.9972	470.4	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	41	P00003897		56	28412	0	0		
2	Gene_Symbol=KCC119358 similar to hCG2040270								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 AWNEQANFSK	X	1.163	0.02276	0.9549	0.996	197.9	
2	HR	Accession	Score	Mass	LH	SD(geo)	#		
2	42	P00022774		54	104186	1163	1		
2	Gene_Symbol=TCP Translational endoplasmic reticulum ATPase								
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications
2	1	2 SCSCCPVGCCK	X	1.45	0.02263	0.9012	0.9939	10	

HR	Accession	Score	Mass	LH	SD(geo)	#					
2	57	P0078934	48	12210		0					
2	Gene_Symbol=RHMA 12 kDa protein Inq=109										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 LVVGDGAGCK	X	0.9187	0.3058	0.7521	0.9316	155.7			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	58	P00017726	48	69271		0					
2	Gene_Symbol=HSD17B10 isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2 Inq=261 # SNP[279,1,1]										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	59	P00556259	47	126352	1.212	1					
2	Gene_Symbol=PABPC1L Polyadenylate-binding protein 1-like Inq=814 # SNP[641, a, 212, S]SNP[677, a, 2]										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 GFGFVCFSSPEATK	X	1.212	0.02699	0.9248	0.9961	111.3			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	60	P00871391	47	81837	1.295	1					
2	Gene_Symbol=XRCC5 Putative uncharacterized protein XRCC5 Inq=719										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 CFSVLGFGK	X	1.295	0.02354	0.9673	0.9974	518.2			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	61	P00974	47	11352		0					
2	Gene_Symbol=Pancreatic trypsin inhibitor OS-Bos taurus PE=1 SV=2										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 AGLCQTFVVGGR	X	6.357	999	0.8327	0.9775	56.41			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	62	P00232376	46	48830	1.293	1					
2	Gene_Symbol=MF LOC284889 Macrophage migration inhibitory factor Inq=115 # SNP[133, v, 15, V]SNP[133, v, 15, V]										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 LLCGLAER	X	1.293	0.02625	0.9169	0.9975	1818			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	63	P00878470	46	0		0					
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	64	P00002459	45	88483	1.106	1					
2	Gene_Symbol=ANXA6 annexin V1 isoform 2 Inq=667 # SNP[67, y, 185, Y]SNP[730, g, 223, G]SNP[766, L, 4, V]										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 CLELASR	X	1.106	0.02951	0.8059	0.9988	140.7			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	65	P00002968	45	150109		0					
2	Gene_Symbol=HSFA4 Heat shock 70 kDa protein 4 Inq=840 # SNP[647, a, 159, A]SNP[800, L, 159, A]SNP[800, L, 159, A]										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	66	P00164441	45	259935	1.252	1					
2	Gene_Symbol=UNC13A unc-13 homolog A Inq=1791 # SNP[1797, L, 1122, L]SNP[1819, a, 1122, L]SNP[185										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 TVGLAVLQLR	X	1.252	0.02965	0.7576	0.9953	145.7			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	67	P00792207	44	54786		0					
2	Gene_Symbol=ALDH2 cDNA FLJ50888, highly similar to Aldehyde dehydrogenase, mitochondrial Inq=47										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 LLCGGGAADR	X	1.227	0.1095	0.7064	0.988	123.9			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	68	P00184402	43	25456		0					
2	Gene_Symbol=VAT1 Chromosome 17q21 mRNA clone 694.2 Inq=242										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	69	P00012493	42	24645	1.191	1					
2	Gene_Symbol=RP520 40S ribosomal protein S20 Inq=119 # SNP[134, h, 18, H]SNP[152, r, 18, H]SNP[171, j										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 VCADLR	X	1.191	0.01676	0.8602	0.999	322.4			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	70	P00815732	42	83435	1.265	1					
2	Gene_Symbol=PACS phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succi										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 SWLFGNCLVDWK	X	1.265	0.02975	0.913	0.9984	106.2			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	71	P00306332	42	30710	1.29	1					
2	Gene_Symbol=RPL24 60S ribosomal protein L24 Inq=157 # SNP[167, a, 150, A]SNP[183, d, 150, A]SNP[115										
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 VELCSFSGVK	X	1.29	0.03961	0.8711	0.997	363.2			
2	HR	Accession	Score	Mass	LH	SD(geo)	#				
2	72	P00013847	42	11608	1.268	1					
2	Gene_Symbol=UCRC1 Cytochrome b-c1 complex subunit 1, mitochondrial Inq=480 # M[482, A, 36, A]SNP[
2	z	Sequence	Incl.	LH	Std.Err.	Fraction	Correlation	Intensity	Modifications		
2	1	2 LCTSATESVAR	X	1.268	0.05741	0.7674	0.9836	95.26			

