

Table S1. Genetic characteristics of cell lines

HGNC Gene Symbol	MMR- Cell Lines						MMR+ Cell Lines			
	HCT116	LS174T	RKO	HCT15*	DLD1*	LOVO	CACO2	COLO205	HT29	SW480
MLH1	S252*	T117M	methyalted methyalted	WT	WT	WT	WT	WT	WT	WT
MSH2	WT	WT	WT	WT	WT	ΔEx3-8	WT	WT	WT	WT
MSH6	WT	WT	WT	L290fs D1171fs	L290fs D1171fs	WT	WT	WT	WT	WT
KRAS	G13D WT	G12D WT	WT	G13D WT	G13D WT	G13D WT	WT	WT	WT	G12V
APC	WT	WT	WT	I1417fs* R2166*	I1417fs R2166*	M1430fs* R1114*	Q1367*	T1556fs*	E853* T1556fs	Q1338*
TP53	WT	WT	WT	S241F Intronic Sub	S241F WT	WT	E204*	Y103-L111>L	R273H	R273H
CTNNB1	ΔS45 WT	S45F	WT	WT	WT	WT	G245A	N287S	WT	WT
PIK3CA	H1047R WT	H1047R WT	H1047R WT	E545K D549N	E545K D549N	WT	WT	WT	P449T WT	WT
BRAF	WT	WT	V600E WT	WT	WT	WT	WT	V600E WT	V600E WT	WT

Table S1. Summary of mutations in cancer related genes in colorectal cancer cell lines. Source: Catalogue Of Somatic Mutations In Cancer - (COSMIC), v50)
 *HCT15 and DLD1 were derived from tumor cells obtained from different sites in the same patient

S2 STANDARD SEARCH

Group/Source/Spectrum	Distinct Peptides	Distinct Matches	Filtered Spectra	Distinct Analyses	Distinct Charges	Protein Groups
	55922	71889	732057	2	3	6094
pepXML-ENS	55922	71889	732057	2	3	6094
CaCo2	25763	31032	76996	1	3	5463
Rep3	12457	14117	22150	1	3	4182
Rep1	17984	20602	31756	1	3	4771
Rep2	15701	18802	23090	1	3	4460
COLO205	22668	27380	71648	1	3	5435
Rep3	15013	17725	22553	1	3	4477
Rep1	13698	15469	21778	1	3	4667
Rep2	12897	14751	27317	1	3	4312
RKO	24979	31126	79453	1	3	5315
Rep3	16269	19717	23740	1	3	4544
Rep1	14186	16257	24723	1	3	4391
Rep2	16273	19469	30990	1	3	4423
HCT15	26553	32294	80879	1	3	5614
Rep3	16938	19861	24628	1	3	4605
Rep1	16169	18610	26265	1	3	4953
Rep2	15714	18256	29986	1	3	4673
LS174T	25678	31263	84816	1	3	5472
Rep3	14968	17644	22128	1	3	4294
Rep1	14949	17767	29443	1	3	4636
Rep2	18057	20891	33245	1	3	4704
HCT116	23796	28814	74880	2	3	5415
Rep3	16074	18780	24212	1	3	4534
Rep1	13522	15632	22324	1	3	4252
Rep2	14098	16518	28344	1	3	4505
LoVo	23952	29080	73033	1	3	5342
Rep3	14480	17600	21296	1	3	4179
Rep1	11963	13509	20903	1	3	4042
Rep2	16416	18883	30834	1	3	4629
HT29	24590	29391	66924	1	3	5429
Rep3	14939	17782	22057	1	3	4273
Rep1	16243	18417	26106	1	3	4828
Rep2	10655	11341	18761	1	3	3957
SW480	21232	25794	61442	1	3	4974
Rep3	11920	13957	17864	1	3	3897
Rep1	8192	9231	13606	1	3	3183
Rep2	14950	17849	29972	1	3	4203
DLD1	23101	27603	61986	1	3	5322
Rep3	15656	18382	22702	1	3	4512
Rep1	13463	15061	20752	1	3	4311
Rep2	10075	11305	18532	1	3	3781

S4 CUSTOMIZED SEARCH

Group/Source/Spectrum	Distinct Peptides	Distinct Matches	Filtered Spectra	Protein Groups
	59803	76023	734278	6513
pepXML	59803	76023	734278	6513
CACO2	26377	31640	77581	5798
Rep1	18290	20915	32138	5073
Rep2	12543	14196	22193	4447
Rep3	15842	18934	23250	4729
COLO205	23126	27818	71872	5750
Rep1	13838	15601	21927	4939
Rep2	13030	14867	27268	4589
Rep3	15132	17843	22677	4728
DLD1	23399	27904	61952	5659
Rep1	13512	15105	20695	4589
Rep2	10095	11323	18504	4022
Rep3	15756	18463	22753	4806
HCT116	24207	29209	75218	5765
Rep1	13693	15804	22521	4587
Rep2	14118	16499	28262	4763
Rep3	16244	18970	24435	4844
HCT15	27409	33205	81972	5991
Rep1	16583	19048	26720	5238
Rep2	16019	18567	30352	4986
Rep3	17146	20094	24900	4879
HT29	24956	29754	66851	5762
Rep1	16355	18540	26119	5106
Rep2	10605	11285	18621	4182
Rep3	15026	17863	22111	4572
LOVO	24325	29425	72901	5683
Rep1	16487	18932	30739	4928
Rep2	12070	13592	20897	4333
Rep3	14542	17636	21265	4448
LS174T	26109	31713	85095	5814
Rep1	18087	20915	33238	4977
Rep2	15087	17883	29507	4957
Rep3	15117	17821	22350	4543
RKO	25601	31819	80515	5637
Rep1	16527	19712	31358	4745
Rep2	14310	16412	24968	4634
Rep3	16533	20078	24189	4819
SW480	21272	25723	60321	5310
Rep1	14932	17766	29483	4505
Rep2	8013	9008	13246	3363
Rep3	11849	13824	17592	4179

S6 SelTarBase genes

ABCC2
ABCF1
ACVR2A
AIM2
ANGPT2
APAF1
APC
ASTE1
ASTE
ATM
ATR
AXIN2
B2M
BAT2D1
BAT3
BAX
BCL10
BLM
BRCA1
BRCA2
C14orf106
Corf106
Corf6
C6orf80
CANX
CASP1
CASP5
CCKBR
CDC25C
CDH1
CDK2AP1
CDKL2
CDX2
CEBPZ
CEP164
CEP290
CEP57
CHD
CHEK1
COBLL1
COIL
CREBBP
CRSP3
CYSLTR1
CYSLTR
DSTN
EDD1
ELAVL3
EP300
EPHB2
ERCC5
F8
FAS
FBX046
FGFBP1
FILIP1L
FLCN
FLT3LG

FXR1
GART
GBP3
GCC2
GPRK2L
GRB14
HDAC2
HMMR
ICA1
IGF2R
INPPL1
JARID1A
KIAA0355
KIAA1333
KIF22
LARP7
LIG3
LIMK2
MAP1S
MARCKS
MBD4
MKI67
MLH3
MNS1
MSH3
MSH6
MYBL1
MYH11
MYO10
NDUFC2
NF1
NIPBL
NKTR
NRIP1
P4HB
PA2G4
PARP14
PHF14
PLXNA3
POLD3
PPRC1
PRCC
PRDM2
PRKCI
PRKDC
PRRG1
PSMB8
PTEN
PTHLH
PTPN21
PTPN23
PTPN5
PTPRA
PTPRE
PTPRS
RAD50
RBBP8
RBM35A
RECQL
REV1
REV3L
REV2L

RFC3
RGL2
RGS12
RIF1
RNASEH2B
SEC31A
SEC63
SLC16A4
SCL16A4
SLC17A2
SLC23A2
SLC4A3
SMAP1
SPINK5
SRPK1
STK11
SYCP1
TAF1B
TAP1
TAP2
TAPBP
TCF1
TCF7L2
TEAD2
TGFBR2
TIMP3
TLOC1
TMEM97
TOP2B
TTK
USP1
UVRAG
WBP1
WISP3
WNK1
WRN
XPOT
XRCC2
XRCC6
ZFP103
ZMPSTE24
ZMYND8
ZNF365
ZNF518
ZNF609
ZNF93
ZNF297

S9 MRM PARAMETERS

HGNC Gene Symbol	Peptide	Precursor (charge state); products (m/z)
BAG3	ELLALDSVDPEGR	707 (2+); 987, 874, 573, 458
BAX	TGALLLQGFIQDR	716 (2+); 977, 863, 735, 418
CAND1	EGPAVVGQFIQDVK	744 (2+); 1034, 934, 489, 651
CARM1	YTVNFLEAK	543 (2+); 820, 721, 607, 460
CDH1	NTGVISVTTGLDR	716 (2+); 1061, 948, 761, 662
CPD	SQEGDSISVIGR	624 (2+); 1033, 903, 531, 345
DSTN	EILVGDVGVTTDPPFK	852 (2+); 1249, 978, 821, 506
EEF2	YEWVDAEAR	570 (2+); 846, 660, 545, 446
ERAP1	ILASTQFEPTAAR	703 (2+); 791, 644, 515, 590
ESRP1	GLPWQSSDQDIAR	737 (2+); 1019, 891, 804, 652
FECH	GDPYPQEVSATVQK	760 (2+); 1087, 633, 674, 544
HSP90AA1	ALLFVPR	408 (2+); 631, 518, 371, 316
HSP90AB1	HLEINPDHPIVETLR	892 (2+); 1291, 1177, 965, 827
KRT18	AQIFANTVDNAR	660 (2+); 1007, 860, 789, 475
KRT19	DAEAWFTSR	542 (2+); 767, 696, 510, 363
KRT8	YEELQSLAGK	569 (2+); 845, 716, 603, 475
LMAN1	DIDNLVQR	487 (2+); 744, 402, 303, 202
MLH1	EGLAEYIVEFLK	706 (2+); 912, 748, 635, 536
MRE11A	GNDTFVTLDEILR	747 (2+); 1106, 959, 859, 645
MSH2	LLLAVFVTPLTDLR	786 (2+); 1062, 915, 815, 714
MSH6	IIDFLSALEGFK	677 (2+); 1127, 864, 751, 664
NARS	FLTWILNR	532 (2+); 802, 701, 515, 402
PAICS	EVYELLDSPGK	625 (2+); 729, 616, 503, 388
PFAS	FGEPVLAGFAR	582 (2+); 830, 521, 450, 416
RAD50	ILELDQELIK	607 (2+); 988, 858, 745, 630
TNOP1	YSDIDIILLK	597 (2+); 1030, 943, 828, 714
TTC19	GQLENAEQLFK	639 (2+); 1092, 978, 849, 664

S10 Co-EXPRESSION MODULE ANALYSIS

Module	CACO	CACO	CACO	COLO	COLO	COLO	COLO	H2T9	H2T9	H2T9	ISW481	ISW481	ISW481	ISW481	DL.D1	DL.D1	HCT11	HCT11	HCT11	HCT11	HCT11	HCT11	LOVO	LOVO	LOVO	LOVO	LS174	LS174	LS174	RKO.R	RKO.R	RKO.R	RKO.R	m	ttest	p.value	adj.p.value
MODULE_40	-0.56	-0.59	0.56	-0.10	-0.27	-0.22	-0.16	-0.63	-0.14	-1.25	-2.55	-0.99	-0.42	-0.23	0.26	0.41	0.18	0.12	0.34	0.19	0.54	0.67	0.26	0.89	0.40	0.49	0.63	1.05	1.03	1.21	0.0869	-1.0692	-9.047	0.0000	0.0041		
MODULE_42	-0.09	-1.35	-0.41	-0.91	-0.78	-0.38	-1.19	-1.55	-1.10	0.44	-0.02	0.45	0.35	-0.21	0.32	0.24	-0.05	-0.11	-0.06	0.14	0.30	0.65	0.39	0.64	0.59	0.54	0.55	1.13	0.65	0.90	0.0189	-0.8906	-4.2297	0.0002	0.0149		
MODULE_156	0.47	-0.01	0.99	0.43	0.16	1.05	-0.03	-0.05	0.45	0.58	0.83	1.20	0.47	-0.77	-0.34	0.69	0.51	0.47	-0.35	-1.03	-0.14	-1.61	-1.75	-1.52	0.33	0.65	0.35	-0.82	-0.63	-0.59	-0.9886	0.9861	4.1683	0.0003	0.0149		
MODULE_56	0.12	0.35	-0.16	0.63	0.67	0.49	0.66	0.27	0.53	-0.10	0.08	0.35	0.63	0.66	0.74	0.30	0.22	0.27	0.87	0.65	0.65	-0.84	-0.62	-1.39	0.18	0.10	0.26	2.14	-1.71	-1.90	-0.9846	0.9462	3.7047	0.0009	0.0385		
MODULE_152	0.02	-0.61	-0.70	-0.30	-0.50	-0.39	0.79	1.13	1.12	0.57	0.86	1.29	0.49	-0.20	0.22	1.12	1.23	1.21	-0.31	-0.90	0.71	0.67	0.08	-0.34	0.75	-0.35	0.48	-0.81	-1.33	-1.21	0.9925	0.9249	0.9593	0.0012	0.0410		
MODULE_129	-0.96	-1.34	-1.28	-0.65	-0.02	0.24	-1.06	-0.67	-1.15	0.24	0.89	0.57	-0.37	0.08	-0.06	-0.44	-0.58	0.08	-0.06	0.71	0.63	0.92	1.85	0.99	0.51	0.87	0.70	-0.09	-0.04	-0.92	0.8844	-0.8440	-3.3517	0.0023	0.0566		
MODULE_54	-0.12	-0.30	-0.18	-0.29	-0.35	0.15	0.61	0.40	0.70	-0.26	-1.53	0.19	0.17	-0.67	-0.15	-1.56	-1.01	-1.59	0.31	0.76	0.09	0.55	-0.41	0.20	0.73	0.61	0.30	0.73	0.63	0.90	0.7560	-0.7505	-3.3414	0.0024	0.0566		
MODULE_75	0.87	0.81	0.24	0.64	0.46	0.47	0.92	0.82	0.27	-0.61	0.25	0.14	0.55	-0.17	-0.26	-0.53	0.76	0.31	0.64	0.06	0.46	-0.14	-1.14	-1.25	-1.56	-1.41	-0.79	-1.17	-0.76	0.7674	0.7640	3.0831	0.0046	0.0906			
MODULE_108	0.19	0.20	0.64	-0.20	-0.27	0.20	0.24	-1.68	0.51	-1.32	-1.75	-0.97	-1.18	-1.61	-0.64	0.47	0.72	0.72	0.36	0.29	0.41	0.53	0.31	0.76	0.49	0.23	0.64	0.44	0.62	0.64	-0.7954	-0.7953	-3.0654	0.0049	0.0906		
MODULE_63	0.30	0.14	0.20	0.93	-0.37	-0.17	-1.20	-0.13	0.70	-0.26	-1.04	0.19	1.33	-0.30	0.29	0.67	0.69	0.93	1.34	0.46	0.01	-1.10	-1.16	-1.61	-0.12	-0.42	-0.41	-0.51	-0.87	-0.88	-0.7388	0.7376	2.9341	0.0066	0.1103		
MODULE_144	0.62	0.38	1.26	1.36	0.40	0.93	1.58	0.73	1.18	0.81	-0.96	1.11	0.76	-0.69	-1.16	-0.65	-0.66	0.96	1.34	-0.81	-0.54	-0.39	-0.68	-0.96	-0.56	-0.61	-0.32	-0.29	-0.11	0.51	-0.0764	0.7640	2.7973	0.0092	0.1337		
MODULE_127	-0.56	-0.15	-1.19	-0.71	-0.57	-0.62	0.95	-0.34	-1.04	1.33	0.22	0.75	0.66	-0.47	-0.27	0.32	-0.46	-0.33	0.12	-0.55	1.21	0.20	0.94	-0.06	0.09	-0.46	1.36	0.37	0.79	-0.7194	-2.7264	0.0109	0.1337				
MODULE_116	-1.45	-1.39	-0.73	0.42	1.12	0.78	0.29	0.50	0.26	-0.55	-1.04	-1.24	-0.96	-0.24	-0.80	-0.59	0.40	-0.18	0.15	0.23	0.32	-0.53	-0.36	-0.54	1.24	1.20	0.82	1.01	0.77	0.82	0.0750	-0.7503	-2.7166	0.0112	0.1337		
MODULE_106	-0.76	-0.48	-0.49	-1.13	-1.28	-1.35	0.57	0.68	-0.23	-0.60	-1.64	-1.23	0.64	0.10	-0.48	0.98	0.65	0.82	0.51	0.30	0.39	-0.27	-0.08	-0.32	0.78	1.03	0.74	0.77	0.63	0.77	-0.7288	-0.7277	-2.7049	0.0115	0.1337		
MODULE_164	0.43	0.70	0.40	-0.47	1.02	0.48	-0.21	-0.19	0.18	0.85	0.11	0.44	0.48	-0.23	-0.47	-0.43	-0.11	0.24	0.08	0.18	0.03	-1.51	-2.21	-3.24	0.09	0.11	-0.03	0.14	0.31	0.36	0.0788	0.7884	2.6793	0.0122	0.1337		
MODULE_26	0.63	0.52	0.50	1.99	1.62	1.72	0.87	0.89	0.70	-0.60	-0.69	-0.37	-0.53	-0.90	-0.68	0.05	-0.24	-0.41	-0.29	-0.48	-0.64	-0.41	-0.70	-0.35	-0.31	0.16	-0.54	-0.62	-0.56	-0.32	0.0705	0.7047	2.6377	0.0135	0.1337		
MODULE_124	1.27	1.73	-2.46	0.61	0.09	0.16	0.46	0.69	0.01	-0.99	-0.35	-1.43	0.49	0.55	-0.29	0.26	0.17	-0.11	0.50	0.79	0.21	0.00	0.18	0.48	0.55	0.39	0.66	0.22	0.50	0.67	0.0714	-0.7142	-2.6335	0.0136	0.1337		
MODULE_10	-0.32	-0.38	-0.47	-0.22	0.04	0.01	-0.17	-0.52	-0.51	-0.42	-0.43	-0.31	-0.11	-0.45	-0.30	-0.11	-0.01	-0.12	-0.08	0.01	-0.13	-0.33	-0.40	-0.41	-0.14	-0.40	1.93	2.03	0.28	0.0675	-0.6171	-2.5412	0.0169	0.1549			
MODULE_142	0.09	0.01	0.15	0.64	-0.69	0.65	0.15	-0.20	-0.35	1.39	2.46	1.09	0.63	-0.42	-0.65	1.34	1.49	1.15	0.52	-0.26	-0.50	-0.45	-0.63	-0.63	-0.25	0.02	-0.46	-0.37	-0.39	0.66	0.7088	0.7080	2.5142	0.0180	0.1549		
MODULE_58	-0.59	-1.78	-0.32	0.13	0.79	0.02	-0.49	-1.52	-0.26	0.45	-0.79	-0.13	0.36	-1.66	0.04	0.89	0.60	0.92	0.39	0.19	0.60	-0.15	-0.75	-0.34	0.88	0.30	0.63	1.46	0.61	0.14	0.6993	-0.6927	-2.5000	0.0185	0.1549		
MODULE_113	-0.13	-1.24	-0.37	-1.27	-1.59	-0.22	-0.06	-0.30	0.47	0.15	0.64	0.20	-1.15	0.52	0.59	0.74	0.51	0.60	0.24	0.08	0.15	0.16	1.10	0.18	-0.28	-0.20	0.86	0.47	1.13	0.0683	-0.6835	-2.3776	0.0245	0.1880			
MODULE_147	0.73	1.32	0.46	0.00	0.03	-0.32	1.20	0.94	0.98	-0.40	0.54	-1.49	0.34	1.02	0.27	-0.62	0.29	-0.54	0.68	1.05	-0.07	-0.45	-1.13	-1.36	-0.47	0.38	-1.09	-0.82	-0.58	-0.87	-0.6567	0.6569	2.3066	0.0254	0.1880		
MODULE_111	-0.06	-0.26	-0.08	-0.01	-0.58	-0.44	-0.02	-0.40	-0.58	-1.15	-1.81	-1.19	0.68	0.42	0.72	0.32	0.16	0.22	0.71	0.75	0.80	-0.27	-0.59	-0.69	0.15	0.14	0.23	0.87	0.93	1.05	0.0624	-0.5642	-2.3527	0.0259	0.1880		
MODULE_21	1.04	1.25	1.42	1.18	1.90	0.31	-0.51	-0.31	-0.62	-0.62	-0.39	-0.23	-0.13	0.03	-0.43	-0.36	-0.50	-0.23	-0.20	-0.31	-0.46	-0.61	-0.64	0.02	-0.13	-0.66	-0.46	-0.44	-0.05	0.6247	2.3020	0.0290	0.1961				
MODULE_165	-0.59	-1.11	-1.60	-1.57	-1.06	-1.74	-0.92	-1.29	-0.40	0.67	1.05	0.08	0.37	0.56	0.45	0.01	0.54	0.67	-0.37	0.36	0.28	0.61	1.17	0.80	0.13	-0.26	-0.63	1.26	0.89	0.67	0.6881	-0.6812	-2.2884	0.0299	0.1961		
MODULE_66	1.10	1.07	0.40	1.17	0.48	1.23	0.29	-0.88	-0.89	0.48	1.05	1.09	0.78	-0.57	-0.64	0.92	0.41	0.24	-0.49	-0.43	-0.50	-0.55	-0.48	-0.78	-0.01	0.49	-0.24	-0.41	-0.44	-0.24	0.0565	0.5646	2.2511	0.0308	0.1961		
MODULE_125	-0.62	-0.54	0.47	-0.70	-1.09	-0.76	-0.72	-0.31	0.49	1.49	0.79	1.04	-0.64	-0.96	-0.05	-0.16	-0.59	-0.06	-0.14	0.12	0.29	0.55	-0.58	-0.67	0.16	0.27	0.40	0.48	1.96	0.76	1.58	-0.0626	-0.6246	-2.2573	0.0320	0.1961	
MODULE_161	0.40	1.02	0.71	1.13	0.45	0.69	0.77	-0.14	-0.55	-1.00	-0.89	-1.12	1.22	0.07	1.03	1.02	-0.10	-0.14	1.02	0.33	0.60	-1.02	-1.15	-1.05	-0.21	-0.09	-0.13	-1.25	-1.34	-1.45	0.0656	0.6556	2.2349	0.0336	0.1961		
MODULE_110	0.52	-0.45	0.63	1.19	-0.38	-0.93	1.13	-1.12	-0.67	-0.32	-0.52	-1.43	0.81	0.05	0.30	0.21	0.25	0.59	0.06	0.46	0.79	-0.74	-1.30	-0.37	1.12	0.81	0.06	1.43	1.12	1.28	0.0647	-0.6468	-2.2284	0.0341	0.1961		
MODULE_110	-0.59	-1.78	-1.32	0.38	0.14	0.36	0.17	-0.06	-0.27	1.78	1.12	-1.27	0.82	0.13	0.38	0.70	0.69	0.77	0.53	0.30	0.10	-0.19	-0.15	0.31	0.61	0.83	0.98	0.38	0.24	0.42	0.0560	0.0101	-1.8738	0.0372	0.2068		
MODULE_134	0.10	0.06	0.42	0.65	1.05	1.22	0.64	0.36	0.64	-0.55	-1.43	-0.27	0.45	0.16	0.44	0.73	0.22	0.02	0.45	0.19	0.57	-1.41	-1.64	-0.69	0.67	0.64	0.86	-1.52	-0.94	-1.84	0.0646	0.6458	2.1535	0.0400	0.2068		
MODULE_111	0.74	0.05	0.23	-0.77	-1.08	1.20	0.29	-0.40	0.13	0.42	0.99	0.66	1.00	0.91	0.73	0.26	0.35	0.28	0.57	0.53	0.54	0.35	0.21	-1.04	-0.76	-0.72	-1.50	-1.93	-1.37	-0.0638	0.6381	2.1458	0.0407	0.2068			
MODULE_47	-0.98	-1.63	-0.55	0.47	0.55	0.58	0.24	-0.31	0.12	-0.67	-2.38	-0.80	0.05	-0.90	-0.02	0.63	0.56	0.69	0.13	-0.29	-0.34	0.22	-0.55	0.29	0.62	0.48	0.61	-1.11	0.96	1.14	0.0607	-0.6065	-2.1405	0.0412	0.2068		
MODULE_14	0.10	-0.03	-0.20	-0.40	-0.47	-0.45	-0.42	0.13	-0.48	0.03	-0.36	-0.22	-0.38	-0.27	-0.16	-0.18	-0.23	0.05	-0.04	-0.15	0.23	1.14	1.90	2.19	-0.25	-0.61	-0.50	-0.26	-0.08	-0.42	0.0549	-0.5484	-2.1299	0.0421	0.2068		
MODULE_49	-0.04	0.11	0.48	-1.62	-1.63	-1.13	-0.85	-0.19	-0.06	0.72	0.94	0.79	-0.05	-1.10	-0.42	0.14	-0.05	0.02	-0.11	-0.01	0.24	0.58	0.91	1.06	-0.49	-0.31	-0.07	0.98	0.65	1.00	0.5597	-0.5497	-2.0933	0.0455	0.2143		
MODULE_166	0.60	0.15	0.36	0.66	1.05	0.86	1.42	1.30	0.58	-0.58	-1.02	-0.19	0.67	0.81	0.4																						

MODULE_17 -0.83 -0.97 -0.73 1.02 1.12 1.07 1.00 0.61 0.78 -0.61 -1.50 -0.60 -0.44 -1.35 -0.32 0.18 0.27 -0.12 0.54 0.06 0.28 0.04 -0.44 -0.13 0.65 0.74 0.80 -0.26 -0.28 -0.58 0.0196 -0.1965 -0.7153 0.4803 0.6915
MODULE_112 -0.70 -0.60 -0.70 -0.84 -0.99 -0.91 -0.67 -0.59 -0.42 1.28 2.26 2.00 0.17 -0.18 0.36 -0.51 -0.26 -0.28 0.74 0.21 0.96 0.69 0.74 0.25 -0.68 -0.78 -0.72 0.21 0.09 -0.12 0.0220 -0.2199 -0.6971 0.4915 0.7015
MODULE_6 0.12 0.23 0.38 0.73 0.83 0.75 0.35 0.30 0.38 -1.54 -2.32 -1.63 0.00 -0.24 -0.03 0.11 0.18 0.09 0.27 0.11 -0.06 -0.06 -0.39 -0.15 0.78 0.78 0.72 -0.35 -0.13 -0.18 0.0186 -0.1862 -0.6874 0.4975 0.7041
MODULE_154 -0.17 -0.61 -0.06 1.17 0.30 1.51 -1.02 -0.90 -0.96 0.26 -0.42 0.13 -0.47 -0.74 -0.82 0.47 0.58 0.34 0.15 0.44 -0.86 -0.93 -0.94 -0.33 1.21 1.15 1.54 -0.44 0.13 0.30 0.0197 -0.1968 -0.6711 0.5077 0.7119
MODULE_145 0.10 0.49 -0.49 0.97 0.19 -0.01 1.12 1.51 -0.45 -1.60 -1.26 -0.51 0.75 0.80 -0.31 -0.81 -0.99 -0.99 1.03 0.49 0.53 -0.31 -0.37 -1.26 0.75 0.73 0.80 -0.68 0.16 -0.40 0.0204 -0.2041 -0.6649 0.5116 0.7119
MODULE_132 0.32 0.87 0.73 0.02 1.08 1.05 0.40 -0.33 0.28 -0.99 -0.09 -0.97 -0.14 0.63 -0.39 0.13 0.11 -0.53 0.17 0.48 -0.15 -1.83 -1.38 -1.43 -0.25 0.40 -0.30 1.19 1.20 0.50 -0.0193 0.1928 0.6541 0.5184 0.7154
MODULE_85 0.33 0.54 -0.32 -1.22 -0.34 -0.59 -1.51 -1.95 -1.42 0.12 1.05 0.42 0.73 1.30 0.68 0.11 0.53 0.19 0.16 0.39 0.32 -0.39 0.35 0.64 0.06 0.01 -0.46 0.24 0.86 0.56 0.0186 -0.1864 -0.6442 0.5247 0.7182
MODULE_158 0.21 0.24 -1.13 1.16 0.39 -0.52 0.17 -1.13 -0.75 -0.27 -1.13 1.13 0.94 -0.20 0.76 0.79 0.50 0.11 1.16 0.85 0.80 -0.15 0.33 -1.13 -0.94 -0.92 -0.75 0.20 1.21 0.69 -0.0187 -0.1865 -0.6209 0.5397 0.7327
MODULE_38 -0.16 -0.04 -0.36 0.02 -0.19 -0.45 -0.43 -0.31 -0.47 -0.59 0.05 -0.33 1.90 1.86 2.12 -0.47 -0.61 -0.32 0.80 0.75 0.11 -0.44 0.20 -0.27 -0.42 -0.26 -0.10 -0.43 -0.61 -0.55 -0.0170 -0.1703 0.6038 0.5509 0.7419
MODULE_13 -0.50 -0.53 -0.25 -0.31 -0.02 -0.21 1.52 1.62 1.48 -0.38 -0.60 -0.60 -0.53 -0.64 -0.53 -0.24 -0.15 -0.38 -0.40 -0.56 -0.39 0.00 -0.21 -0.22 1.53 1.76 0.94 -0.37 -0.45 -0.39 0.0173 -0.1733 -0.5930 0.5579 0.7434
MODULE_15 MODULE_15 0.49 -0.72 -0.22 -0.44 -0.64 -0.43 0.64 0.56 0.46 1.59 1.96 1.82 -0.51 -0.58 -0.20 -0.41 -0.62 -0.59 -0.16 -0.51 -0.41 0.39 0.63 0.79 -0.34 -0.01 -0.09 -0.58 -0.46 -0.45 -0.0166 0.1661 0.5886 0.5609 0.7434
MODULE_41 0.63 0.99 0.57 0.19 0.36 0.49 0.53 0.67 0.31 -0.32 -0.03 -0.15 0.52 0.56 0.47 -1.69 -1.70 -1.24 -0.15 -0.26 -0.01 0.05 0.35 0.25 0.76 0.81 0.67 -1.46 -1.07 -1.11 -0.0162 0.1619 0.5507 0.5862 0.7677
MODULE_48 -0.79 -1.10 -0.46 0.25 0.05 0.07 0.40 0.54 0.45 -0.61 -1.70 -0.73 0.57 -0.57 -0.12 0.94 0.87 0.84 0.43 0.20 -0.07 -0.12 -1.68 -0.72 -0.36 0.30 0.05 0.93 1.03 1.13 0.0153 -0.1530 -0.5363 0.5960 0.7677
MODULE_167 0.40 0.60 0.39 1.22 1.46 1.31 0.82 0.99 -0.10 -1.65 -0.54 -1.15 -0.31 -0.50 -0.69 -0.57 0.32 0.75 0.02 0.42 -0.66 -0.14 -0.88 -1.11 1.35 1.23 0.16 -1.07 0.10 -0.67 -0.0174 0.1737 0.5358 0.5963 0.7677
MODULE_61 -0.43 -1.01 -1.00 1.03 0.97 1.21 0.38 0.16 0.26 0.38 -0.97 0.46 -0.16 -0.71 -0.30 0.29 0.13 0.37 -0.44 -0.57 -0.52 0.64 0.28 0.38 0.81 0.64 1.02 -1.17 -0.94 -1.17 -0.0146 0.1459 0.5339 0.5976 0.7677
MODULE_51 -0.66 -0.73 -0.68 0.97 0.99 1.14 1.28 1.08 1.26 -0.14 -0.08 0.31 -0.57 -0.95 -0.54 -0.45 -0.54 -0.49 -0.08 -0.39 -0.29 -0.54 -0.42 -0.32 1.21 1.23 1.40 -1.00 -1.05 -0.95 -0.0165 0.1653 0.5254 0.6035 0.7693
MODULE_120 0.20 0.12 0.17 -1.28 -1.06 -0.66 -0.82 -1.04 -0.55 0.31 -1.04 0.64 0.49 -0.41 0.88 0.95 0.92 1.11 -0.23 -0.39 -0.16 1.09 1.02 1.63 -0.94 -1.08 -0.64 0.29 0.09 0.39 0.0149 -0.1488 -0.4885 0.6290 0.7957
MODULE_84 -0.43 -0.17 -0.42 -0.25 -0.37 0.33 -1.10 -1.65 -0.82 -0.13 1.36 0.75 0.34 0.96 0.56 0.05 0.12 0.00 0.17 -0.33 -0.16 0.70 0.98 1.09 -1.18 -0.99 -0.40 0.35 0.10 0.56 0.0124 -0.1237 -0.4571 0.6511 0.8124
MODULE_36 1.45 1.38 1.49 0.56 0.37 0.01 -0.25 -1.28 -0.48 -1.09 -1.63 -1.08 0.60 0.52 0.40 0.14 -0.04 -0.09 0.74 0.52 0.28 -0.73 -0.97 -1.09 -0.12 0.03 -0.34 -0.08 0.61 0.14 -0.0138 0.1377 0.4560 0.6519 0.8124
MODULE_3 0.50 0.26 0.51 0.37 0.29 0.41 0.26 0.02 0.30 -1.12 -2.65 -1.02 0.28 -0.31 0.10 0.43 0.20 0.31 0.38 0.26 0.41 -0.49 -1.45 -0.78 0.56 0.32 0.35 0.53 0.24 0.51 0.0119 -0.1193 -0.4330 0.6684 0.8268
MODULE_114 0.49 0.78 -0.38 0.20 -0.11 -0.11 -0.04 0.17 -0.69 0.59 1.64 1.11 0.02 0.44 0.19 1.68 -1.52 2.00 0.42 0.79 0.01 0.57 0.89 0.73 -0.10 -0.37 -0.90 -0.54 0.06 -0.64 -0.0126 -0.1260 -0.4078 0.6865 0.8430
MODULE_118 0.93 1.21 0.86 0.69 0.63 0.30 0.11 -0.18 -0.30 -1.97 -1.33 -1.42 0.94 0.97 0.79 -0.55 -0.32 -0.43 0.29 0.42 -0.09 0.51 0.89 0.49 0.02 0.17 -0.09 -1.19 -1.16 -1.18 -0.0128 0.1277 0.4005 0.6918 0.8433
MODULE_163 2.17 1.44 1.97 -0.35 -0.96 -0.25 -0.21 -0.79 -0.17 0.30 -1.02 -0.34 0.09 -1.19 0.79 -0.44 -0.17 0.05 1.03 -0.80 0.71 -0.24 -0.84 -0.53 -0.45 -0.66 -0.72 0.32 0.56 0.70 -0.0127 0.1269 0.3912 0.6986 0.8452
MODULE_140 0.58 1.02 1.12 0.89 0.45 -0.81 1.02 1.15 0.19 -1.02 -0.85 -1.35 0.25 -1.06 0.43 -1.10 -1.01 -0.71 0.49 0.53 0.41 0.27 0.92 0.52 -0.40 0.63 -0.40 -0.79 -0.45 -0.90 0.0116 -0.1165 -0.3845 0.7035 0.8452
MODULE_121 -0.84 -0.01 -0.85 -0.01 0.62 0.26 -0.57 -0.33 -0.54 0.92 1.91 0.89 -0.51 -0.74 -0.76 0.26 -0.09 -0.40 -0.02 -0.60 -0.27 0.80 1.00 1.18 0.65 1.07 1.04 -0.98 -0.88 -1.19 0.0110 -0.1102 -0.3760 0.7098 0.8466
MODULE_155 0.15 0.19 0.44 1.09 1.40 1.47 0.96 -0.33 0.93 -1.27 -1.65 -1.88 0.22 -0.07 0.25 -0.58 0.05 -0.56 0.25 0.25 0.50 -0.51 -0.90 -0.31 0.15 1.05 0.71 -0.34 -0.26 -1.40 -0.0112 0.1123 0.3456 0.7322 0.8558
MODULE_74 0.17 0.48 0.51 0.66 0.71 0.95 0.22 -0.38 0.14 -0.76 -1.80 -1.30 -0.92 -1.48 -0.56 0.73 1.03 0.83 -0.67 -0.75 -0.61 -0.19 -1.12 -0.15 0.85 0.66 0.92 0.83 0.37 0.64 -0.0107 -0.1070 -0.3432 0.7340 0.8558
MODULE_159 0.71 0.45 0.33 0.69 0.47 0.36 0.55 -0.16 -0.09 -1.24 -2.06 -1.27 0.49 0.67 0.28 0.09 0.73 0.01 0.65 0.42 0.38 -0.11 -1.30 0.04 -1.70 -1.25 -0.47 0.76 0.70 1.12 -0.0106 0.1062 0.3392 0.7370 0.8558
MODULE_34 0.51 0.70 -0.01 -1.22 -1.32 -1.75 -0.80 -0.92 -1.23 0.56 1.12 0.60 0.43 1.08 0.50 0.26 0.48 0.31 0.44 0.65 0.47 0.31 0.60 0.04 -0.71 -0.61 -0.74 0.00 0.26 0.00 0.0097 -0.0972 -0.3380 0.7379 0.8558
MODULE_78 -0.30 -0.37 0.46 1.40 0.77 0.57 0.57 -0.21 -0.25 -0.75 -1.17 -1.08 -0.32 -0.54 -0.46 1.20 0.23 0.94 0.10 -0.33 0.00 -0.57 -0.84 -0.92 1.27 1.56 1.19 -0.68 -0.88 -0.57 -0.0094 0.0944 0.3092 0.7595 0.8747
MODULE_45 -0.06 0.25 -0.17 1.72 1.91 1.35 0.58 -0.08 -0.61 -1.18 -0.81 -0.85 -0.06 -0.60 -0.72 -0.19 0.31 -0.18 0.69 0.40 -0.31 -0.41 -0.59 -0.75 0.67 1.02 0.41 -0.67 -0.34 -0.74 -0.0085 0.0847 0.2868 0.7764 0.8880
MODULE_29 0.68 0.31 0.70 -0.40 -0.85 -1.03 -0.84 -1.80 -1.15 0.28 0.25 0.42 1.09 0.77 1.12 0.09 -0.12 -0.07 0.74 0.63 0.89 -0.22 -0.56 -0.63 -0.41 -0.53 -0.73 0.32 0.46 0.59 0.0077 -0.0775 -0.2776 0.7834 0.8900
MODULE_82 -0.58 -0.83 -0.82 0.59 0.39 -0.18 -0.29 -0.94 -0.77 1.04 1.29 1.33 -0.66 -0.61 -0.88 1.29 0.59 0.56 0.16 -0.41 -0.25 -0.24 0.26 -0.92 -0.87 -0.49 -0.57 1.00 0.74 1.07 -0.0073 0.0729 0.2480 0.8060 0.9092
MODULE_143 0.74 0.59 0.01 -1.35 -1.32 -0.98 -1.31 -0.14 -0.73 1.21 1.90 1.24 -0.28 0.73 -0.02 -0.29 -0.45 -0.08 -0.73 0.75 0.02 -0.30 -0.83 -0.29 0.08 -0.39 0.29 0.77 0.51 0.63 0.0073 -0.0732 -0.2412 0.8112 0.9092
MODULE_18 0.26 0.27 0.56 0.35 0.18 0.17 0.22 0.27 0.28 -1.65 -2.16 -1.85 0.50 0.30 0.47 0.37 0.51 0.47 0.48 0.56 0.68 0.28 -0.29 0.13 0.48 0.39 0.48 -1.05 -0.84 -0.82 0.0067 -0.0674 -0.2318 0.8184 0.9111
MODULE_89 0.16 -0.09 -0.15 1.19 -0.24 -0.78 0.92 0.16 0.25 -1.35 -1.26 -1.12 1.18 1.38 0.60 -0.05 -0.37 0.06 1.41 0.48 0.41 -0.57 -0.79 -1.32 -0.17 -0.35 -0.90 0.36 0.29 0.67 -0.0067 0.0673 0.2206 0.8247 0.9121
MODULE_7 -0.54 -0.57 -0.49 1.41 1.28 1.48 0.79 -0.09 0.51 -0.59 -0.42 -0.35 -0.59 -0.62 -0.40 -0.48 -0.45 -0.30 -0.29 -0.48 -0.62 0.18 0.00 -0.01 1.06 1.10 1.29 -0.61 -0.58 -0.63 0.0058 -0.0582 -0.2134 0.8349 0.9173
MODULE_141 -1.01 -1.02 -0.99 0.17 -0.21 -0.61 0.31 1.01 0.25 0.25 1.99 1.04 -0.11 0.62 -1.18 0.06 -0.21 0.08 0.02 0.40 -0.54 0.70 0.97 1.03 -1.48 -0.86 -1.38 0.73 -0.01 -0.01 -0.0061 0.0607 0.1934 0.8480 0.9212
MODULE_37 0.01 0.04 0.02 -0.89 -0.79 -1.01 -0.41 -0.26 -0.77 0.95 1.96 0.77 -0.47 0.07 0.40 -0.20 -0.05 0.26 -0.64 -0.44 -0.62 0.80 1.42 0.48 -0.59 -0.59 -0.83 0.58 1.06 -0.25 0.0054 -0.0537 -0.1915 0.8495 0.9212
MODULE_117 -0.31 -0.30 -0.55 2.64 1.03 1.73 -0.33 -0.55 -0.55 -0.55 -0.55 -0.16 -0.26 -0.08 -0.55 -0.37 -0.10 -0.09 -0.41 -0.02 0.55 1.98 0.72 -0.55 -0.30 -0.55 -0.17 -0.27 -0.55 -0.0047 -0.0472 -0.1511 0.8810 0.9422
MODULE_73 0.88 1.00 0.60 -0.69 -0.52 -0.36 -0.96 -0.24 -0.34 1.00 2.01 0.44 -0.84 0.33 0.09 -1.02 -0.30 -0.77 -0.38 -0.54 -0.29 1.02 1.14 0.67 -0.54 -0.68 -1.21 -0.16 0.44 0.23 0.0044 0.0437 0.1476 0.8837 0.9422
MODULE_105 -0.55 -0.13 0.22 -0.45 -1.61 -1.62 0.05 -0.04 0.21 0.85 1.28 0.84 0.94 0.06 0.69 -0.43 0.17 -0.19 0.61 0.67 0.55 0.47 0.77 0.79 -1.45 -0.83 -0.81 -0.90 0.17 -0.34 -0.0043 0.0426 0.1449 0.8858 0.9422
MODULE_130 0.58 0.67 0.09 -1.06 -0.83 -0.71 -0.31 -0.43 -0.30 -1.09 -0.81 -0.93 0.49 1.19 -0.50 1.38 1.49 1.38 0.76 0.82 -0.20 0.09 0.55 -0.46 -0.25 0.24 -0.28 -0.74 0.16 -0.98 -0.0039 0.0391 0.1323 0.8957 0.9467
MODULE_99 -0.12 -0.80 -0.78 1.10 0.76 0.95 1.38 0.79 0.75 -0.11 -0.85 -0.36 0.70 -0.37 0.62 -1.63 -1.03 -1.28 0.73 0.12 0.25 0.34 0.01 0.68 0.46 0.00 0.83 -1.13 -1.07 -0.96 0.0037 -0.0372 -0.1190 0.9061 0.9517
MODULE_98 0.57 0.73 -0.10 0.24 -0.83 -0.54 0.07 0.49 -0.20 0.45 1.00 0.65 0.06 1.09 0.71 -1.53 -1.83 -0.85 0.38 0.59 -0.08 0.60 0.88 -0.14 -0.69 -1.45 -1.32 -0.06 0.52 0.58 -0.0026 0.0260 0.0857 0.9323 0.9660
MODULE_8 -0.61 -0.75 -0.68 1.15 0.93 1.25 1.52 1.31 1.01 -0.86 -1.02 -0.68 -0.55 -0.76 -0.56 -0.26 -0.09 -0.23 -0.21 -0.42 -0.55 0.35 0.36 0.30 0.41 0.58 0.53 -0.58 -0.42 -0.49 -0.0020 0.0198 0.0699 0.9447 0.9660
MODULE_43 0.24 0.10 0.25 1.60 1.21 1.66 -0.17 0.43 -0.12 -0.73 -0.58 -0.75 -0.66 -0.69 -0.91 0.02 -0.15 -0.60 -0.21 -0.82 -0.86 -0.55 -0.69 -0.56 1.16 1.08 0.68 0.03 0.13 0.46 -0.0019 0.0194 0.0680 0.9462 0.9660
MODULE_139 -1.54 -1.44 -1.80 0.47 -0.02 -0.15 0.92 0.52 0.41 -0.49 0.37 1.33 0.08 -0.25 0.10 0.09 0.56 0.71 0.48 0.13 0.05 1.11 0.78 1.00 -0.73 -1.23 -0.32 -0.63 -0.42 -0.06 0.0020 -0.0200 -0.0667 0.9473 0.9660
MODULE_86 0.23 0.65 -0.16 0.42 -0.06 0.67 1.28 1.54 1.75 -0.51 -0.69 -0.32 -0.83 -0.83 -0.83 -0.83 -0.42 0.07 0.73 0.97 1.24 1.11 0.25 0.03 -0.29 -0.83 -0.64 -0.63 0.0020 -0.0201 -0.0650 0.9487 0.9660
MODULE_157 0.15 0.14 -0.18 0.62 -0.01 0.04 -0.28 -0.98 -0.54 -1.04 -1.31 -0.59 1.31 -0.15 -0.87 1.47 0.92 1.26 1.10 0.89 0.29 -0.26 -1.31 -1.01 0.64 0.38 0.97 -0.78 -0.26 -0.56 0.0010 -0.0097 -0.0312 0.9753 0.9872
MODULE_65 -1.28 -1.33 -1.56 -0.24 -0.87 -0.72 -0.20 0.23 -0.19 0.06 0.67 0.50 0.85 0.87 0.41 1.08 0.95 0.82 0.57 0.51 0.57 -0.44 -0.17 -0.47 -0.45 -0.60 -0.96 0.65 0.19 0.55 -0.0005 0.0054 0.0193 0.9847 0.9878
MODULE_104 -0.39 -0.45 0.08 -0.36 -0.57 -0.05 -0.56 -0.72 -0.45 0.29 -0.24 -0.52 1.93 1.04 1.26 -0.22 0.26 -0.32 1.98 1.14 0.77 -0.72 -0.53 -0.03 -0.45 0.50 -0.54 -0.72 -0.72 -0.0005 0.0046 0.0154 0.9878 0.9878

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ENSP00000382392:T538M:	LVPMLDFGQEGFTR	ENSP00000382392	T538M	538 ENSP00000382392_E68:	2	0	0	0	2	0	0	0	0	0	0
ENSP00000382695_3732:ATTTTT>ATTTT	RPKSESQGNATKM	ENSP00000382695	rs1050409 A73E	3732 ENSP00000382695_37:	1	0	0	0	1	0	0	0	0	0	0
ENSP00000383244:A73E:rs1050409	EPWVEQEPEYVDR	ENSP00000383244	rs1050409 A73E	73 ENSP00000383244_rs1:	1	0	0	0	0	0	0	0	0	1	0
ENSP00000383362:A36S:rs5748469	VSVVDYVEPSQGTGR	ENSP00000383362	rs5748469 A36S	36 ENSP00000383362_rs1:	4	0	0	0	0	0	0	1	0	3	0
ENSP00000384176:T310I:	DMELPIEK	ENSP00000384176	T310I	310 ENSP00000384176_rs1:	4	0	3	0	0	0	0	0	1	0	0
ENSP00000384176:T310I:	DMELPIEKVALVK	ENSP00000384176	T310I	310 ENSP00000384176_rs1:	1	0	1	0	0	0	0	0	0	0	0
ENSP00000384455:I193T:	LGTTDDCELVEGLVLTQK	ENSP00000384455	I193T	193 ENSP00000384455_I19:	5	0	3	2	0	0	0	0	0	0	0
ENSP00000384455:I193T:	LGTTDDCELVEGLVLTQK	ENSP00000384455	I193T	193 ENSP00000384455_I19:	3	0	2	1	0	0	0	0	0	0	0
ENSP00000385139:R79G:	ALANVNGSLICNVGAGGPAPAAGAAP	ENSP00000385139	R79G	79 ENSP00000385139_L11:	2	0	0	0	0	2	0	0	0	0	0
ENSP00000385139:L110F:	KEESKESDDDMGFGLFD	ENSP00000385139	L110F	110 ENSP00000385139_L11:	1	0	0	0	0	1	0	0	0	0	0
ENSP00000386006:K17M:	EMEDKVTSPK	ENSP00000386006	K17M	17 ENSP00000386006_K1:	1	0	0	0	1	0	0	0	0	0	0
ENSP00000386423:P150A:rs4832242	FLEENADVSASEIR	ENSP00000386423	rs4832242 P150A	150 ENSP00000386423_rs4:	3	0	0	0	1	1	0	0	1	0	0
ENSP00000386465:N70S:rs11559078	SQDKDVSSEGETSDGVR	ENSP00000386465	rs11559078 N70S	70 ENSP00000386465_rs1:	1	0	0	1	0	0	0	0	0	0	0
ENSP00000386756:L248I:	GLGTTDDTIIR	ENSP00000386756	L248I	248 ENSP00000386756_M2:	14	0	8	6	0	0	0	0	0	0	0
ENSP00000386813:A852V:rs11542286	SVVSDVPEELDFLVPK	ENSP00000386813	rs11542286 A852V	852 ENSP00000386813_rs1:	1	0	0	0	0	0	0	0	0	0	1
ENSP00000387272:A280D:	SLGGNDELSDTFLEMK	ENSP00000387272	A280D	280 ENSP00000387272_C1:	2	0	1	1	0	0	0	0	0	0	0

S12 CO-EXPRESSION MODULE GENES

Cluster	Ensembl Gene ID	Associated Gene	GO Term Accession (GO Term Name (bp))	Class	
40	ENSG00000178921	PFAS	GO:0006164	purine nucleotide biosynthetic process	DNA/RNA synthesis & repair
40	ENSG00000204842	ATXN2	GO:0016070	RNA metabolic process	DNA/RNA synthesis & repair
40	ENSG00000109606	DHX15	GO:0006397	mRNA processing	DNA/RNA synthesis & repair
40	ENSG00000083520	DIS3	GO:0006364	rRNA processing	DNA/RNA synthesis & repair
42	ENSG00000126814	TRMT5	GO:0008033	tRNA processing	DNA/RNA synthesis & repair
42	ENSG00000120800	UTP20	GO:0006364	rRNA processing	DNA/RNA synthesis & repair
56	ENSG00000138772	ANXA3	GO:0051054	positive regulation of DNA metabolic process	DNA/RNA synthesis & repair
75	ENSG00000135336	ORC3L	GO:0006260	DNA replication	DNA/RNA synthesis & repair
75	ENSG0000020922	MRE11A	GO:0006281	DNA repair	DNA/RNA synthesis & repair
75	ENSG00000104320	NBN	GO:0006302	double-strand break repair	DNA/RNA synthesis & repair
75	ENSG00000113522	RAD50	GO:0006281	DNA repair	DNA/RNA synthesis & repair
129	ENSG00000116560	SFPQ	GO:0006281	DNA repair	DNA/RNA synthesis & repair
156	ENSG00000095002	MSH2	GO:0006281	DNA repair	DNA/RNA synthesis & repair
156	ENSG00000104413	ESRP1	GO:0043484	regulation of RNA splicing	DNA/RNA synthesis & repair
40	ENSG00000114480	GBE1	GO:0005975	carbohydrate metabolic process	Metabolism process
40	ENSG00000082212	ME2	GO:0006108	malate metabolic process	Metabolism process
40	ENSG00000146085	MUT	GO:0008152	metabolic process	Metabolism process
40	ENSG00000178057	NDUFAF3	GO:0032981	mitochondrial respiratory chain complex I assembly	Metabolism process
40	ENSG00000152256	PDK1	GO:0006006	glucose metabolic process	Metabolism process
40	ENSG00000185875	THNSL1	GO:0008152	metabolic process	Metabolism process
42	ENSG00000110955	ATP5B	GO:0006091	generation of precursor metabolites and energy	Metabolism process
42	ENSG00000069998	CECR5	GO:0008152	metabolic process	Metabolism process
42	ENSG00000115419	GLS	GO:0006541	glutamine metabolic process	Metabolism process
42	ENSG00000083720	OXCT1	GO:0008152	metabolic process	Metabolism process
54	ENSG00000159228	CBR1	GO:0008152	metabolic process	Metabolism process
54	ENSG00000159231	CBR3	GO:0008152	metabolic process	Metabolism process
54	ENSG00000095321	CRAT	GO:0006091	generation of precursor metabolites and energy	Metabolism process
108	ENSG00000122873	CISD1	GO:0043457	regulation of cellular respiration	Metabolism process
129	ENSG00000100889	PCK2	GO:0006094	gluconeogenesis	Metabolism process
156	ENSG00000150768	DLAT	GO:0008152	metabolic process	Metabolism process
40	ENSG00000162191	UBXN1	GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	Protein turnover/folding/transport
40	ENSG00000104325	DECR1	GO:0051289	protein homotetramerization	Protein turnover/folding/transport
40	ENSG00000126602	TRAP1	GO:0006457	protein folding	Protein turnover/folding/transport
40	ENSG00000140598	EFTUD1	GO:0006412	translation	Protein turnover/folding/transport
40	ENSG00000079805	DNM2	GO:0006892	post-Golgi vesicle-mediated transport	Protein turnover/folding/transport
54	ENSG00000105402	NAPA	GO:0006886	intracellular protein transport	Protein turnover/folding/transport
54	ENSG00000138297	TIMM23	GO:0015031	protein transport	Protein turnover/folding/transport
56	ENSG00000176978	DPP7	GO:0006508	proteolysis	Protein turnover/folding/transport
56	ENSG00000120694	HSPH1	GO:0006986	response to unfolded protein	Protein turnover/folding/transport
56	ENSG00000072274	TRFC	GO:0006508	proteolysis	Protein turnover/folding/transport
56	ENSG00000074695	LMAN1	GO:0006457	protein folding	Protein turnover/folding/transport
56	ENSG00000165813	C10orf118	GO:0006412	translation	Protein turnover/folding/transport
75	ENSG00000173486	FKBP2	GO:0006457	protein folding	Protein turnover/folding/transport
108	ENSG00000004478	FKBP4	GO:0006457	protein folding	Protein turnover/folding/transport
129	ENSG00000147475	ERLIN2	GO:0030433	ER-associated protein catabolic process	Protein turnover/folding/transport
129	ENSG00000106077	ABHD11	GO:0006886	intracellular protein transport	Protein turnover/folding/transport
152	ENSG00000147010	SH3KBP1	GO:0006897	endocytosis	Protein turnover/folding/transport
156	ENSG00000109501	WFS1	GO:0022417	protein maturation by protein folding	Protein turnover/folding/transport
40	ENSG00000111530	CAND1	GO:0045449	regulation of transcription	Transcription regulation
40	ENSG00000079805	DNM2	GO:0045449	regulation of transcription	Transcription regulation
42	ENSG00000067334	DNTTIP2	GO:0045449	regulation of transcription	Transcription regulation
42	ENSG00000121390	PSPC1	GO:0045449	regulation of transcription	Transcription regulation
54	ENSG00000088992	TESC	GO:0043193	positive regulation of gene-specific transcription	Transcription regulation
56	ENSG00000138772	ANXA3	GO:0051091	positive regulation of transcription factor activity	Transcription regulation
56	ENSG00000117713	ARID1A	GO:0045449	regulation of transcription	Transcription regulation
75	ENSG00000155508	CNOT8	GO:0006355	regulation of transcription, DNA-dependent	Transcription regulation
108	ENSG00000132382	MYBBP1A	GO:0006355	regulation of transcription, DNA-dependent	Transcription regulation
129	ENSG00000116560	SFPQ	GO:0045449	regulation of transcription	Transcription regulation
40	ENSG00000114023	FAM162A			Unmapped
42	ENSG00000079819	EPB41L2			Unmapped
54	ENSG00000180921	FAM83H			Unmapped
54	ENSG00000008394	MGST1			Unmapped
54	ENSG00000176422	SPRYD4			Unmapped
56	ENSG00000175866	BAIAP2			Unmapped
56	ENSG00000177106	EPS8L2			Unmapped
56	ENSG00000167468	GPX4			Unmapped
75	ENSG00000166145	SPINT1			Unmapped
108	ENSG00000178425	NT5DC1			Unmapped
108	ENSG00000124570	SERPINB6			Unmapped
108	ENSG00000138279	ANXA7			Unmapped
129	ENSG00000010278	CD9			Unmapped
129	ENSG00000184897	H1FX			Unmapped
152	ENSG00000057019	DCBLD2			Unmapped
152	ENSG00000147065	MSN			Unmapped
152	ENSG00000147394	ZNF185			Unmapped
156	ENSG00000163686	ABHD6			Unmapped
156	ENSG00000117868	FAM62B			Unmapped