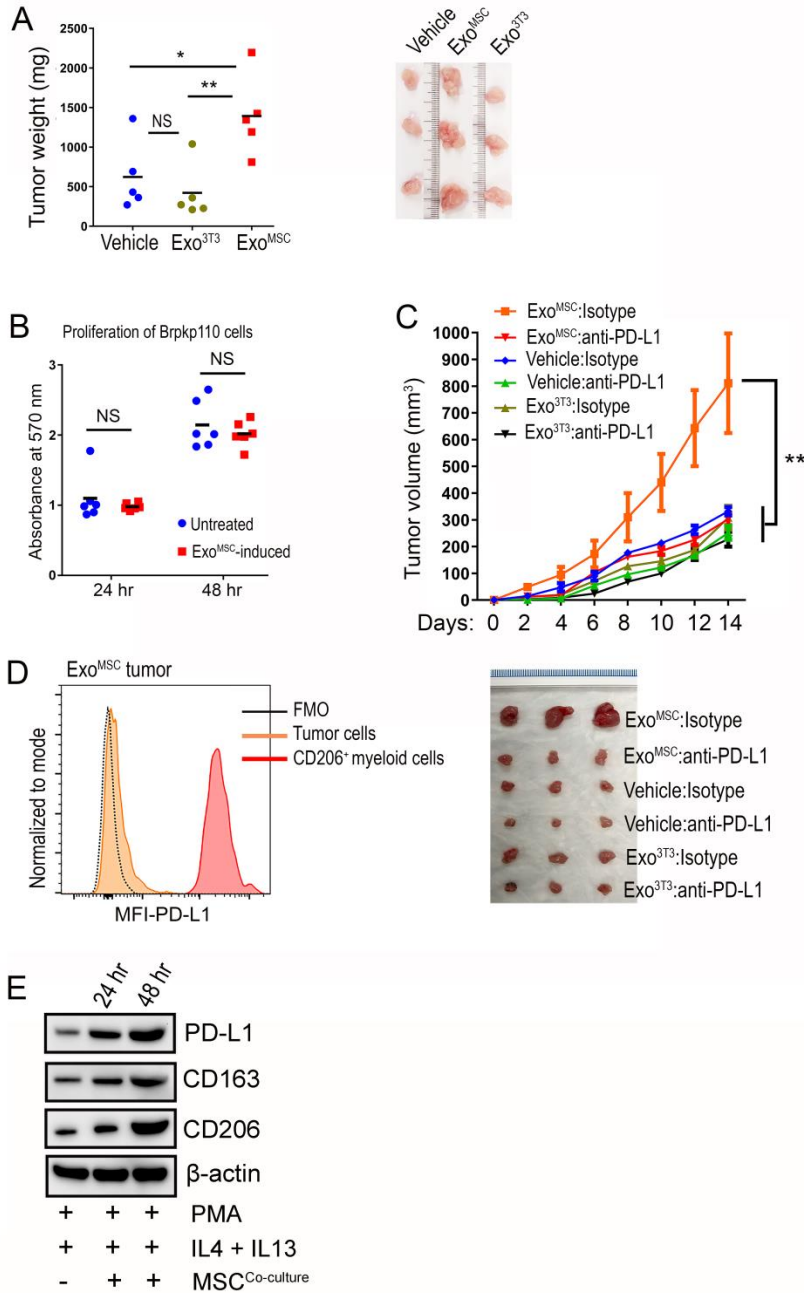


Supplemental Figure 1



Supplemental Figure 1. (A) Comparison of tumor weight between Exo^{MSC}, Exo^{3T3} and Vehicle group after 14 days of PBS or exosome administration (n=5/ group, one experiment). Representative tumors are depicted. (B) Scatter graph showing MTT assay-absorbance at 570 nm for *in vitro* treated Brpkp110 cells with or without MSC-derived exosomes for 24 hr and 48 hr. (C) Exo^{MSC}, Exo^{3T3} and Vehicle group mice administered with anti-PD-L1 neutralizing antibodies or anti-isotype control antibodies. Volume comparison at different time points (n=5/group, one experiment) starting from day of intra-tumor exosome or PBS administration (Day 0). (D) Representative comparison of MFI of PD-L1 expression in CD206⁺ myeloid cells and tumor cells in Exo^{MSC} tumors. (E) Western blot analysis showing expressions of PD-L1, CD206, CD163 and β-actin in M0 THP-1 cells treated stimulated with IL-4 and IL-13, and co-cultured with or without human MSCs for 24 hr or 48 hr.

Supplemental Table I. RNA sequencing data from Exosomes-treated mouse bone marrow-derived myeloid cells.

	CD163	Arg1	CD206	H2-DMa	H2-DMb1
Untreated_1	4.773051	4.179699	13.62254	11.55077	10.36281
Untreated_2	2.825899	0	13.51193	11.61546	10.49632
Untreated_3	3.016221	0	13.52282	11.0098	10.47075
Exo_Epcam_1	4.0519	5.372477	11.95318	11.68841	10.70746
Exo_Epcam_2	4.675584	5.539725	11.85633	11.64514	10.66435
Exo_Epcam_3	4.756594	5.17565	11.48189	11.62074	10.61123
Exo_3T3_1	3.810291	0	13.0685	11.10514	10.10657
Exo_3T3_2	3.921082	3.676971	13.12916	11.07982	10.03663
Exo_3T3_3	0	0	13.32306	10.94665	10.42439
Exo_MSC_1	6.421951	13.19755	15.07218	12.65616	11.94721
Exo_MSC_2	5.51572	13.02734	14.95649	12.62781	12.02493
Exo_MSC_3	5.584819	12.95458	15.02803	12.39748	11.68639
Exo_Brp_1	3.302971	7.442566	11.88774	10.71766	9.755995
Exo_Brp_2	4.846539	7.398262	11.58438	10.62833	9.836423
Exo_Brp_3	4.178581	5.886753	11.56525	10.78021	9.867239

Supplemental Table II. Pathway analysis from RNA sequencing data from exosomes-treated mouse bone marrow-derived myeloid cells.

Pathway	Total number of network objects in pathway	pValue	FDR	Number of network objects in data	Network Objects from Active Data
Macrophage-induced immunosuppression in the tumor microenvironment	96	6.00E-06	8.63E-04	9	KLF4, PPAR-gamma, CAT-2, PD-L2, ARG1, Angiopoietin 2, CD163, CCR2, MANR
Myeloid-derived suppressor cells and M2 macrophages in cancer	64	2.25E-04	1.49E-02	6	KLF4, PPAR-gamma, CAT-2, TLR4, ARG1, VEGFR-1
Macrophage and dendritic cell phenotype shift in cancer	100	4.19E-04	2.41E-02	7	IL-1RI, TLR4, ARG1, PERC, IRF4, SOCS1, MHC class II
L-Arginine metabolism	79	4.38E-03	1.26E-01	5	ARG1, GAMT, GATM, KCRB, AL1A1
Transcription_HIF-1 targets	95	9.48E-03	1.57E-01	5	Galectin-1, LOXL4, Angiopoietin 2, Adipophilin, VEGFR-1

Supplemental Table III. LC-MS/MS analysis of exosomes.

Protein IDs	Fasta headers	Peptides	3T3	Brpkp110	EpCAM	MSC
CDR2L_MO	>sp A2A6T1 CDR2L	3	0	0	0	0
UBR4_MO	>sp A2AN08 UBR4	2	0	0	0	0
LGR4_MO	>sp A2ARI4 LGR4	1	1.07E+08	1.49E+08	0	66180767
AGRIN_MO	>sp A2ASQ1 AGRIN	11	73459691	61723718	2.09E+08	1.39E+08
SVEP1_MO	>sp A2AVA0 SVEP	10	1.07E+08	78998488	86069053	1.18E+08
PTPRS_MO	>sp B0V2N1 PTPRS	6	0	29532669	27187271	22610766
RRN3_MO	>sp B2RS91 RRN3	1	2.04E+08	69094800	1.28E+08	1.46E+08
OTU7B_MO	>sp B2RUR8 OTU7B	1	0	0	0	0
PLXB2_MO	>sp B2RXS4 PLXB2	7	0	5721893	18444144	26439318
H2A1H_MO	>sp Q8CGP6 H2A1H	4	7.81E+08	3.61E+08	2.88E+08	1.67E+09
IFI5A_MO	>sp Q8CGE8 IFI5A	2	0	0	0	0
HMCN1_MC	>sp D3YXG0 HMCN1	16	70891178	76333262	1.23E+08	1.81E+08
GLSK_MO	>sp D3Z7P3 GLSK	4	0	0	6249355	0
FIBA_MO	>sp E9PV24 FIBA	3	2.29E+08	35068467	2.29E+08	1.89E+08
GCN1_MO	>sp E9PVA8 GCN1	4	0	2362682	0	0
APOB_MO	>sp E9Q414 APOB	5	8.33E+09	4.50E+09	8.69E+09	5.34E+09
RN213_MO	>sp E9Q555 RN213	14	62354587	40396779	0	7415718
KIF23_MO	>sp E9Q5G3 KIF23	6	0	3238656	0	8072630
TPR_MO	>sp F6ZDS4 TPR	3	0	0	0	2164226
TEX15_MO	>sp F8VPN2 TEX15	1	0	0	14537144	0
FARP1_MO	>sp F8VPU2 FARP1	4	0	0	0	26392796
HXK2_MO	>sp O08528 HXK2	1	0	0	0	0
CAN2_MO	>sp O08529 CAN2	6	0	0	10786988	0
CA2D1_MO	>sp O08532 CA2D1	1	0	0	0	9499588
SC22B_MO	>sp O08547 SC22B	3	1.82E+08	1.70E+08	7.36E+08	1.22E+08
DPYL2_MO	>sp O08553 DPYL2	13	2.44E+08	1.05E+08	1.84E+08	1.14E+08
ALRF2_MO	>sp Q9JJW6 ALRF2	1	0	0	0	0
PRDX6_MO	>sp O08709 PRDX6	4	26776340	10768282	17849600	30635817
THYG_MO	>sp O08710 THYG	2	1.27E+08	0	62672642	78669818
MATN2_MC	>sp O08746 MATN2	16	1.02E+08	69069132	1.81E+08	0
DLDH_MO	>sp O08749 DLDH	4	0	14163771	16471649	0
HCD2_MO	>sp O08756 HCD2	2	0	0	0	0
TCOF_MO	>sp O08784 TCOF	1	0	0	0	0
DCTN1_MO	>sp O08788 DCTN1	1	0	0	0	0
GLU2B_MO	>sp O08795 GLU2B	1	0	0	22951114	0
PRDX4_MO	>sp O08807 PRDX4	9	15829187	2.85E+08	4.47E+08	70013548
U5S1_MO	>sp O08810 U5S1	10	2444320	3306249	8104895	2864066
TSG6_MO	>sp O08859 TSG6	6	52583293	9278665	0	0
SDCB1_MO	>sp O08992 SDCB1	6	60228956	18178294	3.41E+08	1.05E+08
LTBP2_MO	>sp O08999 LTBP2	1	28602586	0	0	0
PSB1_MO	>sp O09061 PSB1	9	4.00E+08	4.00E+08	4.68E+08	2.76E+08
HDAC1_MC	>sp O09106 HDAC1	1	0	5412590	7638703	0
NDUBB_MC	>sp O09111 NDUBB	1	0	0	0	0
GSTO1_MO	>sp O09131 GSTO1	3	0	0	15599778	0

SODE_MOU	>sp O09164 SODE_	5	0	1.01E+08	62566813	0
RL21_MOU	>sp O09167 RL21_M	2	47763201	33605373	56952434	39415794
HGD_MOU	>sp O09173 HGD_M	3	46170268	54964398	67014356	48312076
PTGIS_MOU	>sp O35074 PTGIS_	12	22785233	0	58453039	3.06E+08
OMD_MOU	>sp O35103 OMD_M	2	45258694	7249585	1.86E+08	87476228
SCR2_MOU	>sp O35114 SCR2_	1	0	0	0	0
PHB2_MOU	>sp O35129 PHB2_M	3	32867268	46322735	59972639	88044008
COFA1_MO	>sp O35206 COFA1_	1	67872555	13679923	78449345	71109988
PSMD4_MO	>sp O35226 PSMD4_	1	0	0	17682987	0
DHX15_MO	>sp O35286 DHX15_	4	0	18323320	8369196	8327656
PURB_MOU	>sp O35295 PURB_	3	0	0	0	0
NMI_MOUS	>sp O35309 NMI_M	1	0	0	0	0
SRSF5_MO	>sp O35326 SRSF5_	1	0	0	0	0
IMA3_MOU	>sp O35343 IMA3_M	3	0	0	0	0
IMA4_MOU	>sp O35344 IMA4_M	2	0	0	0	0
CAN1_MOU	>sp O35350 CAN1_	1	0	0	0	0
NRP2_MOU	>sp O35375 NRP2_M	5	49242574	23671739	65071439	34151403
AN32A_MO	>sp O35381 AN32A_	3	60002869	33754249	37243766	59372690
EXOC4_MO	>sp O35382 EXOC4_	1	0	0	0	0
EDIL3_MO	>sp O35474 EDIL3_	2	0	11659400	22213837	0
BHMT1_MC	>sp O35490 BHMT1_	2	27154184	21168651	27605160	29576384
PSDE_MOU	>sp O35593 PSDE_M	2	0	0	4965293	0
ANXA3_MO	>sp O35639 ANXA3_	10	12582412	0	27165562	2.98E+08
ANXA8_MO	>sp O35640 ANXA8_	1	0	0	0	0
AP1B1_MO	>sp O35643 AP1B1_	8	0	0	0	0
C1QBP_MO	>sp O35658 C1QBP_	5	23727779	80658372	47444080	1.21E+08
MYADM_M	>sp O35682 MYADI	3	7491016	4930454	52740971	8267600
HNRH1_MC	>sp O35737 HNRH1_	9	0	1.16E+08	95276201	73140040
API5_MOU	>sp O35841 API5_M	1	0	0	0	0
BCAT2_MO	>sp O35855 BCAT2_	2	0	0	0	0
CSN5_MOU	>sp O35864 CSN5_M	1	0	0	8062563	0
CALU_MOU	>sp O35887 CALU_	8	0	53017885	88885740	27432141
LSM2_MOU	>sp O35900 LSM2_	1	0	0	0	0
FRDA_MOU	>sp O35943 FRDA_	1	0	0	0	0
OST48_MO	>sp O54734 OST48_	5	20268338	51255328	22524541	17233242
CSK22_MO	>sp O54833 CSK22_	4	0	9996522	0	0
BAF_MOUS	>sp O54962 BAF_M	6	0	38575613	18107390	85648123
LEG7_MOU	>sp O54974 LEG7_M	1	0	0	0	0
ASNA_MOU	>sp O54984 ASNA_	1	0	0	0	0
SLK_MOUS	>sp O54988 SLK_M	1	0	0	0	0
COPB2_MO	>sp O55029 COPB2_	10	0	21914744	18007802	0
NIPS1_MOU	>sp O55125 NIPS1_	2	65053178	0	2.34E+08	56512642
SEPT7_MO	>sp O55131 SEPT7_	7	69253854	74314022	1.12E+08	90987584
IF6_MOUSE	>sp O55135 IF6_MC	4	0	0	0	0
AT2A2_MO	>sp O55143 AT2A2_	5	0	50429664	16488744	12067181
ILK_MOUS	>sp O55222 ILK_M	9	2.45E+08	27287120	2.04E+08	2.91E+08
CHAD_MOU	>sp O55226 CHAD_	3	97345421	1.22E+08	40787690	99764389

PSB5_MOU	>sp O55234 PSB5_N	8	95628605	94309632	2.34E+08	57352153
DHX9_MOU	>sp O70133 DHX9_N	8	0	14522699	29558932	0
EIF3D_MOU	>sp O70194 EIF3D_N	11	20166134	35723436	0	23637423
EF1B_MOU	>sp O70251 EF1B_N	2	0	11037371	0	0
NMT1_MOU	>sp O70310 NMT1_N	2	3667771	6783705	7139949	5320852
E41L2_MOU	>sp O70318 E41L2_N	2	2016717	1126154	5595655	1899579
GREM2_MC	>sp O88273 GREM2	1	10558985	42156341	10021490	0
EMC8_MOU	>sp O70378 EMC8_N	1	0	14339599	0	0
PDLI1_MOU	>sp O70400 PDLI1_N	1	0	0	0	0
PSA3_MOU	>sp O70435 PSA3_N	7	2.80E+08	1.05E+08	4.10E+08	1.16E+08
UGDH_MOU	>sp O70475 UGDH_N	13	81566820	1.54E+08	1.08E+08	23921842
SNX3_MOU	>sp O70492 SNX3_N	1	15537029	3632664	0	0
DHB12_MO	>sp O70503 DHB12_N	4	0	50143035	16571237	17399241
CLC11_MO	>sp O88200 CLC11_N	3	5.55E+08	3.75E+08	3.02E+08	7.12E+08
CO5A1_MO	>sp O88207 CO5A1_N	13	2.94E+08	2.70E+08	2.32E+08	1.09E+08
NID2_MOU	>sp O88322 NID2_N	3	0	0	0	0
WDR1_MOU	>sp O88342 WDR1_N	7	1.80E+08	68949346	2.28E+08	1.65E+08
TGBR3_MO	>sp O88393 TGBR3_N	1	32803262	0	31045969	24674653
MTX2_MOU	>sp O88441 MTX2_N	1	0	0	0	0
KLC1_MOU	>sp O88447 KLC1_N	2	0	0	7055014	0
CPNS1_MO	>sp O88456 CPNS1_N	4	0	1190624	9018554	2161583
DC1I2_MOU	>sp O88487 DC1I2_N	4	0	0	0	0
AP1G2_MO	>sp O88512 AP1G2_N	1	1.24E+09	2.22E+09	1.57E+09	1.41E+09
CSN3_MOU	>sp O88543 CSN3_N	2	0	0	27293100	0
CSN4_MOU	>sp O88544 CSN4_N	4	1.53E+08	2.75E+08	1.73E+08	1.42E+08
CSN6_MOU	>sp O88545 CSN6_N	2	23142430	0	0	0
ROA2_MOU	>sp O88569 ROA2_N	10	2.22E+08	27945512	11740809	6578427
COMT_MO	>sp O88587 COMT_N	1	0	0	0	0
PRS6A_MO	>sp O88685 PRS6A_N	8	14048365	68217800	67367120	77255125
CTBP1_MO	>sp O88712 CTBP1_N	1	0	0	0	0
JAM1_MOU	>sp O88792 JAM1_N	2	0	0	0	0
FA10_MOU	>sp O88947 FA10_N	1	0	0	53012328	0
KBL_MOU	>sp O88986 KBL_N	2	16769667	0	0	0
LG MN_MO	>sp O89017 LG MN_N	1	16587972	0	0	34098537
COR1A_MC	>sp O89053 COR1A	5	70328541	4134266	1.10E+08	45233163
COPE_MOU	>sp O89079 COPE_N	3	0	0	0	0
DYR_MOU	>sp P00375 DYR_M	3	0	0	0	20385110
COX1_MOU	>sp P00397 COX1_N	1	0	0	0	0
COX2_MOU	>sp P00405 COX2_N	2	0	16761831	0	76133310
HPRT_MOU	>sp P00493 HPRT_N	3	0	0	0	0
CO3_MOUS	>sp P01027 CO3_M	89	5.66E+08	3.85E+09	3.22E+09	5.93E+09
CO4B_MOU	>sp P01029 CO4B_N	11	7.54E+09	4.84E+09	7.70E+09	1.14E+10
HA11_MOU	>sp P01899 HA11_N	3	0	37525779	31523557	13814930
HA1B_MOU	>sp P01901 HA1B_N	2	0	0	0	0
HA1D_MOU	>sp P01902 HA1D_N	1	1.11E+08	0	23315547	84945006
HBA_MOU	>sp P01942 HBA_M	2	6.55E+08	0	35463663	4.77E+08
H33_MOUS	>sp P84244 H33_MC	3	0	0	34836828	0

CO4A1_MO	>sp P02463 CO4A1_	7	2.19E+08	2.99E+08	4.96E+08	1.30E+09
LAMC1_MC	>sp P02468 LAMC1_	47	1.94E+09	8.31E+08	2.61E+09	1.33E+09
LAMB1_MC	>sp P02469 LAMB1_	55	1.74E+09	8.87E+08	2.72E+09	1.02E+09
NU5M_MOI	>sp P03921 NU5M_	1	0	0	0	0
PR2C3_MOI	>sp P04768 PR2C3_	3	0	1.05E+08	0	0
TGFB1_MO	>sp P04202 TGFB1_	2	0	0	0	0
ALDOA_MC	>sp P05064 ALDOA_	12	4.84E+08	7.24E+08	5.12E+08	3.90E+08
AATC_MOI	>sp P05201 AATC_	6	0	0	0	0
AATM_MOI	>sp P05202 AATM_	15	26368557	3.47E+08	2.98E+08	2.85E+08
TBA1B_MO	>sp P05213 TBA1B_	32	5.24E+09	4.02E+09	5.82E+09	6.89E+09
MYL1_MOI	>sp P05977 MYL1_	1	19984439	31663138	68626217	38421914
LDHA_MOI	>sp P06151 LDHA_	15	4.42E+08	6.67E+08	6.59E+08	3.88E+08
G6PI_MOU	>sp P06745 G6PI_M	14	2.08E+08	58433897	2.05E+08	1.92E+08
MDR1A_MC	>sp P21447 MDR1A_	2	0	0	36853011	0
CATL1_MO	>sp P06797 CATL1_	8	3.07E+08	2.54E+08	2.04E+08	1.22E+08
MAOX_MO	>sp P06801 MAOX_	10	0	37229310	43959854	22554728
CFAH_MOI	>sp P06909 CFAH_	10	0	37231021	0	0
S10A4_MOI	>sp P07091 S10A4_	3	1.03E+08	52320562	65435057	0
CSF1_MOU	>sp P07141 CSF1_M	2	0	0	0	0
SPRC_MOI	>sp P07214 SPRC_M	5	1.13E+08	45685306	76302910	8.31E+08
KCRM_MO	>sp P07310 KCRM_	7	5.86E+08	0	2.59E+08	5.46E+08
ANXA2_MC	>sp P07356 ANXA2_	29	8.47E+08	2.48E+09	5.71E+09	1.77E+09
ALBU_MOI	>sp P07724 ALBU_	3	0	9666256	0	0
HS90A_MOI	>sp P07901 HS90A_	36	9.84E+08	3.88E+08	6.41E+08	9.62E+08
PDIA4_MOI	>sp P08003 PDIA4_	8	0	92589856	24000181	50097888
APT_MOUS	>sp P08030 APT_M	3	0	3667060	13650620	0
CBR2_MOU	>sp P08074 CBR2_M	1	0	0	0	0
ENPL_MOI	>sp P08113 ENPL_M	27	2.16E+08	7.36E+08	6.52E+08	5.53E+08
CO3A1_MO	>sp P08121 CO3A1_	15	1.43E+09	98698912	8.43E+08	2.00E+08
CO4A2_MO	>sp P08122 CO4A2_	20	7.80E+08	1.70E+08	1.51E+08	2.86E+09
S10AA_MOI	>sp P08207 S10AA_	2	0	65377174	90961622	69316775
MDHM_MC	>sp P08249 MDHM_	14	54138028	4.54E+08	4.93E+08	5.81E+08
RASH_MOI	>sp Q61411 RASH_	1	0	0	0	0
GNAI2_MO	>sp P08752 GNAI2_	9	2.71E+08	45993325	1.94E+08	83866541
RPB1_MOU	>sp P08775 RPB1_M	1	0	0	0	0
ITB1_MOU	>sp P09055 ITB1_M	15	1.75E+08	3.33E+08	4.52E+08	5.87E+08
PDIA1_MOI	>sp P09103 PDIA1_	28	1.79E+08	9.94E+08	1.04E+09	8.54E+08
NUCL_MOI	>sp P09405 NUCL_	20	2.78E+08	2.67E+08	1.63E+08	6.25E+08
PGK1_MOU	>sp P09411 PGK1_M	20	1.22E+09	1.42E+09	1.62E+09	1.35E+09
ACE_MOUS	>sp P09470 ACE_M	1	44489585	19215293	34386375	0
FRIH_MOU	>sp P09528 FRIH_M	2	0	0	0	0
IGF2_MOU	>sp P09535 IGF2_M	2	4.59E+08	2.33E+08	1.95E+08	3.65E+08
SODM_MOI	>sp P09671 SODM_	5	7037087	94014447	1.07E+08	0
CALM3_MC	>sp P0DP28 CALM3_	6	1.19E+08	1.47E+08	1.62E+08	3.62E+08
MYOD1_MC	>sp P10085 MYOD1_	1	2.72E+08	54446754	52605293	3.25E+08
ANXA1_MC	>sp P10107 ANXA1_	28	1.07E+08	1.26E+09	1.56E+09	2.24E+09
EF1A1_MOI	>sp P10126 EF1A1_	23	1.61E+09	2.46E+09	2.41E+09	2.32E+09

NID1_MOU!>sp P10493 NID1_M	61	2.53E+10	1.25E+08	3.45E+10	6.37E+08
HEM2_MOU>sp P10518 HEM2_I	6	0	0	0	0
CATB_MOU>sp P10605 CATB_I	11	1.93E+08	5.71E+08	3.39E+08	1.65E+08
IF4A2_MOU>sp P10630 IF4A2_M	7	9468503	4577087	0	0
THIO_MOU>sp P10639 THIO_M	4	0	15760340	17075961	0
GSTA2_MO>sp P10648 GSTA2_	2	2.10E+08	17310277	91338809	74968144
GSTM1_MC>sp P10649 GSTM1_	2	0	0	15285276	11625222
TCEA1_MO>sp P10711 TCEA1_	1	0	0	0	0
4F2_MOUSI>sp P10852 4F2_MC	10	17371534	55828564	2.24E+08	2.47E+08
H2B1P_MO!>sp Q8CGP2 H2B1P	4	1.41E+09	9.87E+08	3.38E+08	3.92E+09
TCP4_MOU>sp P11031 TCP4_M	1	0	0	0	0
CO1A1_MO>sp P11087 CO1A1_	31	6.76E+09	3.29E+08	6.11E+09	1.31E+09
PARP1_MO>sp P11103 PARP1_	1	0	0	0	0
LIPL_MOU!>sp P11152 LIPL_M	10	50318294	16799050	30394712	3.64E+08
TPA_MOUS>sp P11214 TPA_M	2	0	5764246	17172293	14403856
LORF1_MO>sp P11260 LORF1_	1	0	0	40136433	10748705
FINC_MOU>sp P11276 FINC_M	143	8.50E+10	5.80E+10	1.49E+11	1.02E+11
CDK1_MOU>sp P11440 CDK1_M	2	0	13519069	11643392	0
HS90B_MO!>sp P11499 HS90B_	42	2.01E+09	2.53E+09	2.30E+09	2.68E+09
NGAL_MOU>sp P11672 NGAL_I	4	0	1.03E+08	0	0
K2C8_MOU>sp P11679 K2C8_M	17	2.74E+08	1.80E+08	1.19E+08	7.09E+08
ITA5_MOU!>sp P11688 ITA5_M	2	0	26326697	0	54142133
TCPA_MOU>sp P11983 TCPA_M	17	44567012	2.65E+08	1.82E+08	58115537
A4_MOUSE>sp P12023 A4_MO	3	0	1.10E+08	0	77858855
TIMP1_MO>sp P12032 TIMP1_	4	0	1.43E+08	1.03E+08	73878049
PFKAL_MC>sp P12382 PFKAL_	9	58903405	1.18E+08	70324913	44808121
COX5A_MC>sp P12787 COX5A_	3	0	26837069	7381185	89683910
PDCD6_MO>sp P12815 PDCD6_	3	0	0	0	0
semaphorin >sp P12960 CNTN1_	7	3.66E+08	79584581	2.19E+08	4.23E+08
GELS_MOU>sp P13020 GELS_M	16	26834152	39607051	48998956	0
UMPS_MOU>sp P13439 UMPS_I	4	0	0	0	0
S10A6_MOU>sp P14069 S10A6_I	3	0	0	0	0
AT1B1_MO!>sp P14094 AT1B1_	2	0	0	0	0
RL27A_MO>sp P14115 RL27A_	3	13572446	18464923	73708736	18350828
RS16_MOU!>sp P14131 RS16_M	1	13614773	32360460	23202391	33011613
RL7_MOUS>sp P14148 RL7_MC	7	0	64662739	64029428	64867576
MDHC_MO>sp P14152 MDHC_	4	0	28343371	0	0
RSSA_MOU>sp P14206 RSSA_M	10	35280927	1.69E+08	1.17E+08	99501117
CALR_MOU>sp P14211 CALR_I	18	94603471	5.95E+08	4.80E+08	2.15E+08
HSPB1_MO>sp P14602 HSPB1_	3	2.00E+08	0	58491029	2.09E+08
PSMD3_MO>sp P14685 PSMD3_	8	32807391	99550244	1.04E+08	63165293
ILRL1_MOU>sp P14719 ILRL1_I	3	40073146	0	26431541	0
LMNB1_MC>sp P14733 LMNB1_	4	0	0	0	0
ANXA6_MO>sp P14824 ANXA6_	27	9334606	5.08E+08	5.35E+08	17665685
RLA0_MOU>sp P14869 RLA0_M	8	46560501	1.71E+08	1.17E+08	1.58E+08
MAP1B_MC>sp P14873 MAP1B_	11	2.26E+08	1.21E+08	0	1.62E+08
CD44_MOU>sp P15379 CD44_M	1	34925795	38022033	0	58497230

NDKA_MOI>sp P15532 NDKA_	5	0	0	18045792	0
B4GT1_MO>sp P15535 B4GT1_	5	73413235	12941960	62626511	70468195
Semaphorin >sp P16045 LEG1_N	7	1.81E+08	2.77E+08	5.46E+08	4.44E+08
LEG3_MOU>sp P16110 LEG3_N	3	16796509	37844494	56702785	0
LDHB_MOI>sp P16125 LDHB_I	6	4.07E+08	1.63E+08	2.90E+08	3.55E+08
SRP14_MOI>sp P16254 SRP14_I	1	0	0	0	0
LCAT_MOI>sp P16301 LCAT_M	1	3982951	0	88375589	0
ASSY_MOU>sp P16460 ASSY_M	4	1.94E+08	1.47E+08	1.88E+08	2.56E+08
SPTN1_MOI>sp P16546 SPTN1_	19	1.88E+08	16479052	1.54E+08	2.57E+08
HS71L_MOI>sp P16627 HS71L_	7	1.48E+08	29012458	53815545	1.48E+08
PPGB_MOI>sp P16675 PPGB_M	1	0	29364114	11044506	0
G3P_MOUS>sp P16858 G3P_MC	21	1.54E+09	3.40E+09	3.55E+09	1.95E+09
LAMP2_MC>sp P17047 LAMP2_	1	0	26798566	0	0
TGFB3_MO>sp P17125 TGFB3_	6	0	0	0	1.90E+08
ENOA_MOI>sp P17182 ENOA_I	19	1.61E+09	8.17E+08	1.21E+09	1.18E+09
PTBP1_MOI>sp P17225 PTBP1_	10	0	10587748	0	0
AP2A1_MOI>sp P17426 AP2A1_	5	0	0	0	0
AP2A2_MOI>sp P17427 AP2A2_	7	8.05E+08	59995386	73697882	14352048
GLCM_MOI>sp P17439 GLCM_	1	0	0	0	0
HXK1_MOI>sp P17710 HXK1_I	5	39389723	46399740	48220161	0
PPIA_MOU>sp P17742 PPIA_M	9	1.04E+09	5.54E+08	7.02E+08	1.47E+09
TPIS_MOU>sp P17751 TPIS_M	14	2.74E+08	2.04E+08	2.93E+08	3.24E+08
GTR1_MOI>sp P17809 GTR1_M	2	25474533	60679874	34120445	45339952
HS71A_MOI>sp Q61696 HS71A_	16	1.23E+09	3.57E+08	5.62E+08	1.12E+09
PCNA_MOI>sp P17918 PCNA_I	4	0	0	0	0
MTDC_MOI>sp P18155 MTDC_	1	0	0	0	0
CATD_MOI>sp P18242 CATD_I	8	1.31E+08	1.43E+08	27033411	32841385
KS6A3_MOI>sp P18654 KS6A3_	1	0	0	0	0
COF1_MOU>sp P18760 COF1_N	9	99626938	2.60E+08	3.93E+08	7.42E+08
FAS_MOUS>sp P19096 FAS_MC	35	50311067	1.42E+08	3.86E+08	92686696
GSTP1_MOI>sp P19157 GSTP1_	5	0	1.25E+08	59497764	35241499
RL13A_MOI>sp P19253 RL13A_	2	0	0	39213818	0
SERPH_MOI>sp P19324 SERPH_	19	1.59E+08	9.14E+08	7.59E+08	2.75E+08
COX5B_MC>sp P19536 COX5B_	2	0	0	0	0
BIP_MOUSI>sp P20029 BIP_MC	31	6.50E+08	1.54E+09	3.37E+09	1.96E+09
HEXB_MOI>sp P20060 HEXB_I	2	0	40039134	7201818	41884634
PRDX3_MOI>sp P20108 PRDX3_	6	14723529	0	28288980	2.15E+08
VIME_MOI>sp P20152 VIME_M	48	2.18E+09	3.47E+09	4.39E+09	3.38E+09
MTAP2_MC>sp P20357 MTAP2_	1	0	17241401	51495442	0
KPCA_MOI>sp P20444 KPCA_I	4	0	0	0	0
GNAQ_MOI>sp P21279 GNAQ_	2	0	0	0	0
CYTC_MOI>sp P21460 CYTC_I	2	10876952	0	10935149	0
ENOB_MOI>sp P21550 ENOB_I	7	1.52E+08	26641990	58553441	1.50E+08
MFGM_MOI>sp P21956 MFGM_	16	6.06E+08	3.60E+08	6.09E+08	1.09E+09
TGM2_MOI>sp P21981 TGM2_I	5	0	34260771	0	0
PGH1_MOI>sp P22437 PGH1_N	2	0	0	0	0
PAI1_MOU>sp P22777 PAI1_M	5	36811918	19135722	11314778	0

AP1G1_MO	>sp P22892 AP1G1_	1	0	0	0	0
EIF3A_MOU	>sp P23116 EIF3A_	9	1.34E+08	1.01E+08	41932817	70127738
CBX3_MOU	>sp P23198 CBX3_M	2	0	0	0	0
CXA1_MOU	>sp P23242 CXA1_M	1	0	0	31602251	0
PNPH_MOU	>sp P23492 PNPH_M	2	0	0	0	0
PIMT_MOU	>sp P23506 PIMT_M	1	0	0	0	0
FCL_MOUS	>sp P23591 FCL_M	1	0	0	0	0
CRYAB_MC	>sp P23927 CRYAB	3	86146372	10946249	50529411	78093579
CATA_MOU	>sp P24270 CATA_	1	0	0	0	0
PPIB_MOU	>sp P24369 PPIB_M	5	16788250	98022980	1.19E+08	28962081
CAPG_MOU	>sp P24452 CAPG_	1	0	0	39900352	0
LKHA4_MC	>sp P24527 LKHA4_	2	0	0	0	0
IMDH2_MO	>sp P24547 IMDH2_	3	0	43268207	18428134	0
AL1A1_MO	>sp P24549 AL1A1_	3	0	21508329	17452334	23487284
MCM3_MO	>sp P25206 MCM3_	7	0	0	0	0
RS2_MOUS	>sp P25444 RS2_MC	4	9952061	1.08E+08	29116620	58351320
TIMP2_MO	>sp P25785 TIMP2_	7	70080775	9581978	88931871	42224033
UBF1_MOU	>sp P25976 UBF1_M	1	0	0	0	0
TLN1_MOU	>sp P26039 TLN1_M	72	4.90E+09	9.34E+08	2.33E+09	5.31E+09
EZRI_MOU	>sp P26040 EZRI_M	17	19251463	13152867	7532060	3.32E+08
MOES_MOI	>sp P26041 MOES_	21	3.75E+08	4.36E+08	6.35E+08	1.40E+09
CTNA1_MO	>sp P26231 CTNA1_	7	0	0	21839636	0
U2AF2_MO	>sp P26369 U2AF2_	4	7961979	0	32505870	0
DHE3_MOU	>sp P26443 DHE3_M	11	0	71961094	1.48E+08	18534802
PSMD7_MO	>sp P26516 PSMD7_	3	18033277	97894639	61641485	21783943
SYSC_MOU	>sp P26638 SYSC_M	8	43051507	32801527	10054867	33308720
FKB1A_MO	>sp P26883 FKB1A_	1	0	0	0	0
TGFB2_MO	>sp P27090 TGFB2_	3	0	0	0	0
RL3_MOUS	>sp P27659 RL3_MC	9	0	28721123	85851968	0
PDIA3_MOI	>sp P27773 PDIA3_	21	1.47E+08	1.27E+09	9.26E+08	4.57E+08
ACOC_MOI	>sp P28271 ACOC_	7	80067832	40784370	12458006	65324338
LYOX_MOI	>sp P28301 LYOX_	4	29200323	2047047	17359801	3546776
APEX1_MO	>sp P28352 APEX1_	3	0	0	0	23046382
ADHX_MOI	>sp P28474 ADHX_	4	0	0	0	0
CO2A1_MO	>sp P28481 CO2A1_	4	9.30E+08	1.10E+09	1.25E+09	1.50E+09
PGS1_MOU	>sp P28653 PGS1_M	18	3.03E+09	1.16E+08	3.11E+09	0
PGS2_MOU	>sp P28654 PGS2_M	13	2.77E+08	80346074	4.89E+08	3.19E+08
NP1L1_MOI	>sp P28656 NP1L1_	9	1.01E+08	1.83E+08	67462095	1.07E+08
ATX10_MO	>sp P28658 ATX10_	1	0	0	0	0
NCKP1_MO	>sp P28660 NCKP1_	1	0	0	0	0
GRN_MOU	>sp P28798 GRN_M	1	0	24227458	44212217	0
CTGF_MOU	>sp P29268 CTGF_M	3	0	2476949	8459287	1.07E+08
PABP1_MO	>sp P29341 PABP1_	6	30966692	1.09E+08	23218944	97799890
FRIL2_MOI	>sp P49945 FRIL2_	2	36133657	24647990	63199075	28968425
HEXA_MOI	>sp P29416 HEXA_	4	50578449	4722968	0	22820115
NOS2_MOU	>sp P29477 NOS2_M	1	0	0	0	0
OAT_MOUS	>sp P29758 OAT_M	7	0	0	36220749	9466283

NKTR_MOU>sp P30415 NKTR_I	1	1.16E+08	66104442	1.46E+08	1.02E+08
FKBP4_MO >sp P30416 FKBP4_	1	0	0	0	0
CTND1_MO >sp P30999 CTND1_	3	0	0	0	0
AIMP1_MO >sp P31230 AIMP1_	2	1.23E+08	69903352	0	63771137
ACBP_MOU >sp P31786 ACBP_M	1	0	0	0	0
MP2K1_MO >sp P31938 MP2K1_	2	0	9120377	0	0
LA_MOUSE >sp P32067 LA_MO	2	0	11037799	0	0
ANT3_MOU >sp P32261 ANT3_M	8	1.20E+08	11834800	1.27E+08	2.38E+08
SYWC_MOU >sp P32921 SYWC_	4	35508047	11616619	0	76323627
MMP2_MOU >sp P33434 MMP2_	28	1.21E+09	80932167	9.13E+08	68414881
MMP13_MC >sp P33435 MMP13.	3	0	10932987	0	0
RANG_MOU >sp P34022 RANG_	3	17219777	20496570	0	17720666
MIF_MOUS >sp P34884 MIF_MC	3	0	22572280	0	0
MMP12_MC >sp P34960 MMP12.	1	80988698	21821054	39837940	0
UBP4_MOU >sp P35123 UBP4_M	1	0	0	0	0
PTN11_MOU >sp P35235 PTN11_	2	0	0	0	13542141
RAB5C_MO >sp P35278 RAB5C_	2	16277231	11664534	18050405	23458736
RAB6B_MO >sp P61294 RAB6B_	1	45124487	97770575	1.27E+08	91915910
RAB18_MO >sp P35293 RAB18_	2	0	0	0	0
PPARD_MC >sp P35396 PPARD_	1	1.10E+08	80782435	67437673	2.79E+08
TSP1_MOU! >sp P35441 TSP1_M	54	97124496	9.67E+08	1.51E+09	3954690
ODPA_MOU >sp P35486 ODPA_I	1	0	0	0	0
FBRL_MOU >sp P35550 FBRL_M	2	0	0	0	0
CALX_MOU >sp P35564 CALX_I	12	3.26E+08	2.52E+08	9.37E+08	5.73E+08
PRDX1_MO >sp P35700 PRDX1_	15	1.23E+08	8.21E+08	9.56E+08	3.77E+08
CD81_MOU >sp P35762 CD81_M	3	6.96E+08	1.59E+08	6.09E+08	9.09E+08
LDLR_MOU >sp P35951 LDLR_M	4	0	0	0	83126418
RL12_MOU! >sp P35979 RL12_M	2	0	65184662	46168702	0
RL18_MOU! >sp P35980 RL18_M	2	0	67978229	58919773	27858240
SAR1A_MO >sp P36536 SAR1A_	2	0	22133780	34866677	0
NCPR_MOU >sp P37040 NCPR_M	2	0	0	0	0
FBLN2_MO >sp P37889 FBLN2_	42	6.55E+09	6.08E+08	1.07E+10	2.96E+09
GRP75_MO >sp P38647 GRP75_	16	0	3.08E+08	2.23E+08	2.42E+08
COIA1_MO >sp P39061 COIA1_	3	0	31192980	0	48541514
TIMP3_MO >sp P39876 TIMP3_	1	0	0	0	64708978
CAP1_MOU >sp P40124 CAP1_M	11	4.87E+08	57539785	1.61E+08	4.39E+08
TKT_MOUS >sp P40142 TKT_M	14	16983366	37600217	55061075	28416505
CD9_MOUS >sp P40240 CD9_M	3	57176266	1.22E+08	3.02E+08	61062285
VP26A_MO >sp P40336 VP26A_	1	0	12746453	0	0
CD63_MOU >sp P41731 CD63_M	2	83118458	68033843	78647436	63316489
ECI1_MOU! >sp P42125 ECI1_M	2	0	6964239	0	0
SEPT2_MOU >sp P42208 SEPT2_	6	75088757	85911818	67212447	89471389
TCPQ_MOU >sp P42932 TCPQ_M	12	1.01E+08	2.53E+08	1.68E+08	1.59E+08
GDF6_MOU >sp P43028 GDF6_M	3	0	0	0	0
MSH2_MOU >sp P43247 MSH2_I	1	3405552	0	0	0
ALDR_MOU >sp P45376 ALDR_I	3	32712414	2032887	30565667	28212442
ALD2_MOU >sp P45377 ALD2_M	1	0	0	0	0

COF2_MOU	>sp P45591 COF2_M	3	0	0	0	0
MA1A1_MC	>sp P45700 MA1A1_	1	15946876	6189484	18541561	11264676
FKBP2_MO	>sp P45878 FKBP2_	1	0	0	0	0
RAGP1_MO	>sp P46061 RAGP1_	2	0	0	0	0
NSF_MOUS	>sp P46460 NSF_M	2	0	20300207	6722059	0
PRS7_MOU	>sp P46471 PRS7_M	4	0	0	18014857	0
RB11B_MO	>sp P46638 RB11B_	6	89694596	39228016	61299575	69989229
PURA2_MO	>sp P46664 PURA2_	1	0	0	0	0
NEDD4_MO	>sp P46935 NEDD4_	2	11161884	10113740	0	11754215
STT3A_MO	>sp P46978 STT3A_	2	10968833	0	8626443	0
TES_MOUS	>sp P47226 TES_M	1	0	0	0	0
PA24A_MO	>sp P47713 PA24A_	1	0	0	0	0
ALDH2_MC	>sp P47738 ALDH2_	5	0	20734857	24711137	35871661
CAZA1_MO	>sp P47753 CAZA1_	3	0	0	0	0
CAZA2_MO	>sp P47754 CAZA2_	5	81563723	58006092	23587176	1.15E+08
SRPRB_MO	>sp P47758 SRPRB_	2	16521901	0	0	0
GFPT1_MO	>sp P47856 GFPT1_	4	0	0	0	0
IBP2_MOUS	>sp P47877 IBP2_M	1	69227012	0	0	94219808
IBP6_MOUS	>sp P47880 IBP6_M	1	78287010	0	0	95152364
RL6_MOUS	>sp P47911 RL6_M	3	5856582	36006643	18728526	23512659
RLA1_MOU	>sp P47955 RLA1_M	2	36913090	1.52E+08	13732841	1.03E+08
RL5_MOUS	>sp P47962 RL5_M	6	14497442	1.11E+08	1.08E+08	33415509
EIF1_MOUS	>sp P48024 EIF1_M	2	0	0	0	0
ANXA5_MC	>sp P48036 ANXA5_	24	3.07E+08	7.98E+08	1.34E+09	2.04E+09
LMNA_MO	>sp P48678 LMNA_	17	2.77E+08	1.65E+08	1.53E+08	4.91E+08
HS74L_MO	>sp P48722 HS74L_	2	0	0	0	0
PTX3_MOU	>sp P48759 PTX3_M	20	37108206	1.38E+09	9.01E+08	37566543
ADT1_MOU	>sp P48962 ADT1_M	16	23993095	5.30E+08	6.00E+08	3.24E+08
ROA1_MOU	>sp P49312 ROA1_M	9	0	37408988	9868173	18459732
HPPD_MOU	>sp P49429 HPPD_M	1	31125676	4530456	17558163	0
MCM4_MO	>sp P49717 MCM4_	8	0	0	19544226	0
MCM5_MO	>sp P49718 MCM5_	3	0	0	0	0
PSA2_MOU	>sp P49722 PSA2_M	5	1.78E+08	1.75E+08	4.20E+08	1.80E+08
CAV1_MOU	>sp P49817 CAV1_M	3	0	0	14497797	0
SRP09_MOU	>sp P49962 SRP09_	1	45439357	29504006	0	81703266
SAHH_MOU	>sp P50247 SAHH_	11	6.51E+08	2.02E+08	5.38E+08	5.96E+08
GDIA_MOU	>sp P50396 GDIA_M	6	0	7340708	70262501	14874363
VATA_MOU	>sp P50516 VATA_	10	29225099	60230679	30945567	1.04E+08
VATE1_MO	>sp P50518 VATE1_	1	0	7082313	29089484	34562700
S10AB_MO	>sp P50543 S10AB_	7	30241975	2.52E+08	3.23E+08	2.34E+08
PA2G4_MO	>sp P50580 PA2G4_	5	0	0	0	0
FMOD_MO	>sp P50608 FMOD_	4	2.90E+08	32714255	2.38E+08	2.56E+08
TSPO_MOU	>sp P50637 TSPO_M	2	0	0	9296424	0
RAB7A_MO	>sp P51150 RAB7A_	5	0	58023204	61003796	37872108
ACADL_MC	>sp P51174 ACADL_	1	0	0	0	0
RL9_MOUS	>sp P51410 RL9_M	6	77099795	35138627	51348909	7318445
DHB4_MOU	>sp P51660 DHB4_M	1	0	0	0	0

DYLT1_MO	>sp P51807 DYLT1_	1	0	4919331	0	0
HDGF_MOU	>sp P51859 HDGF_I	2	0	15806542	0	0
VA0D1_MO	>sp P51863 VA0D1_	1	0	0	10758225	0
ADT2_MOU	>sp P51881 ADT2_M	14	2.19E+08	2.54E+08	1.63E+08	2.99E+08
AAAT_MOU	>sp P51912 AAAT_I	1	27349300	17077124	13649806	0
IMA1_MOU	>sp P52293 IMA1_N	8	0	18721179	3742557	0
KPYM_MO	>sp P52480 KPYM_	38	2.27E+09	3.45E+09	4.27E+09	2.38E+09
RL10A_MO	>sp P53026 RL10A_	1	0	0	0	0
RAB2A_MO	>sp P53994 RAB2A_	6	0	70331157	19875553	78699423
IDHP_MOU	>sp P54071 IDHP_M	5	22336156	39004273	32622554	0
MSH6_MOU	>sp P54276 MSH6_I	1	0	0	0	0
PRS6B_MO	>sp P54775 PRS6B_	10	2.27E+08	1.55E+08	1.31E+08	2.26E+08
PUR8_MOU	>sp P54822 PUR8_N	5	33880014	21391966	33976626	32407884
DDX6_MOU	>sp P54823 DDX6_I	2	0	0	0	0
ADK_MOU	>sp P55264 ADK_M	3	0	13559710	21323514	0
ATPK_MOU	>sp P56135 ATPK_M	1	0	0	25639992	81140773
CX6B1_MO	>sp P56391 CX6B1_	2	0	12244637	25913520	0
CYB5_MOU	>sp P56395 CYB5_N	1	0	0	0	0
UBP5_MOU	>sp P56399 UBP5_N	8	0	16947926	19315200	14260061
ATPB_MOU	>sp P56480 ATPB_M	25	79582623	1.19E+09	1.60E+09	1.21E+09
FUS_MOUS	>sp P56959 FUS_M	3	0	0	0	0
NICA_MOU	>sp P57716 NICA_N	2	0	5260719	0	13147761
ERP29_MO	>sp P57759 ERP29_	1	0	9048505	0	0
EF1D_MOU	>sp P57776 EF1D_N	5	0	71777138	30796320	1.79E+08
ACTN4_MO	>sp P57780 ACTN4_	37	1.97E+08	3.70E+08	3.98E+08	2.40E+08
RU2A_MOU	>sp P57784 RU2A_M	3	1.09E+08	0	25303509	64770303
LOXL2_MO	>sp P58022 LOXL2_	13	0	0	0	8.46E+08
IDI1_MOUS	>sp P58044 IDI1_M	2	0	9445509	0	0
EF2_MOUS	>sp P58252 EF2_M	33	9.64E+08	1.10E+09	1.21E+09	7.50E+08
TPM1_MOU	>sp P58771 TPM1_M	3	26666910	58900205	80625629	56243025
ARPC4_MO	>sp P59999 ARPC4_	3	37991907	26785304	59353944	31920460
RUVB1_MO	>sp P60122 RUVB1_	4	0	13611902	0	0
EIF3E_MO	>sp P60229 EIF3E_M	7	12810564	41620302	29879133	40368438
PCBP1_MO	>sp P60335 PCBP1_	3	0	0	0	0
NPL4_MOU	>sp P60670 NPL4_N	3	0	18052947	0	22868752
ACTG_MOU	>sp P63260 ACTG_I	31	6.83E+09	5.93E+09	1.24E+10	1.11E+10
CDC42_MO	>sp P60766 CDC42_	4	40095858	15000985	49015238	64249045
IF4A1_MO	>sp P60843 IF4A1_M	12	1.70E+08	1.82E+08	2.60E+08	1.32E+08
RAB10_MO	>sp P61027 RAB10_	3	20298276	25650765	7275085	0
UB2D2_MO	>sp P62838 UB2D2_	2	0	0	0	0
UBC12_MO	>sp P61082 UBC12_	1	0	0	21719696	0
UBE2N_MO	>sp P61089 UBE2N_	1	0	0	0	0
ARP2_MOU	>sp P61161 ARP2_N	9	70214982	1.12E+08	1.84E+08	1.11E+08
ACTZ_MOU	>sp P61164 ACTZ_M	6	0	16545362	34212707	4603567
CSN2_MOU	>sp P61202 CSN2_N	5	0	0	0	0
ARL1_MOU	>sp P61211 ARL1_N	2	0	8032041	0	0
ABCE1_MO	>sp P61222 ABCE1_	3	0	0	5640972	0

PSME3_MO	>sp P61290 PSME3_	3	0	0	0	0
S61A1_MOU	>sp P61620 S61A1_	2	0	0	21094218	0
ARF4_MOU	>sp P61750 ARF4_M	8	0	0	15598422	0
PFD3_MOU	>sp P61759 PFD3_M	2	0	0	0	0
WDR5_MOI	>sp P61965 WDR5_	1	0	0	0	0
NTF2_MOU	>sp P61971 NTF2_M	3	1.42E+08	41895808	81439701	1.29E+08
HNRPK_MC	>sp P61979 HNRPK	8	1.04E+08	1.11E+08	73374967	1.40E+08
1433G_MOI	>sp P61982 1433G_	10	12872506	14011045	54588913	17813710
RRAS2_MO	>sp P62071 RRAS2_	1	0	0	6927747	80410165
TIM13_MOI	>sp P62075 TIM13_	1	0	0	0	0
RS7_MOUSE	>sp P62082 RS7_MC	8	6183531	50883137	64707820	38902994
PP1A_MOU	>sp P62137 PP1A_M	10	86840119	77407053	36928991	89604611
PRS4_MOI	>sp P62192 PRS4_M	5	53129412	93710705	53777555	75295913
PRS8_MOI	>sp P62196 PRS8_M	7	54340371	97988756	95064542	76882949
RS8_MOUSE	>sp P62242 RS8_MC	10	1.95E+08	1.72E+08	1.71E+08	1.73E+08
RS15A_MOI	>sp P62245 RS15A_	5	13849119	32837463	48288001	57581591
1433E_MOU	>sp P62259 1433E_M	9	74270095	53989002	1.35E+08	66914546
RS14_MOI	>sp P62264 RS14_M	2	0	20944054	20891242	0
RS23_MOI	>sp P62267 RS23_M	4	0	23417195	0	0
RS18_MOI	>sp P62270 RS18_M	2	0	0	0	0
RS11_MOI	>sp P62281 RS11_M	2	0	65586798	28071895	0
RS13_MOI	>sp P62301 RS13_M	2	7975709	15473710	9003629	18806533
RUXE_MOI	>sp P62305 RUXE_	2	0	12192445	0	8092296
RUXG_MOI	>sp P62309 RUXG_	1	0	0	0	0
SMD2_MOI	>sp P62317 SMD2_	1	0	0	0	0
SMD3_MOI	>sp P62320 SMD3_	1	0	0	0	13808586
LSM5_MOI	>sp P62322 LSM5_M	1	0	0	0	0
ARF6_MOI	>sp P62331 ARF6_M	2	0	0	0	0
PRS10_MOI	>sp P62334 PRS10_	12	48208148	1.48E+08	1.01E+08	1.08E+08
RS4X_MOI	>sp P62702 RS4X_M	8	18625852	1.17E+08	75187633	54749034
RL18A_MO	>sp P62717 RL18A_	3	0	42651740	37962862	42102442
RL23A_MO	>sp P62751 RL23A_	1	1.25E+08	47336633	0	0
RS6_MOUSE	>sp P62754 RS6_MC	3	0	66433852	0	0
MTPN_MOI	>sp P62774 MTPN_	1	0	0	0	0
H4_MOUSE	>sp P62806 H4_MO	15	3.46E+09	1.29E+09	9.23E+08	1.05E+10
VATB2_MO	>sp P62814 VATB2_	6	0	16013172	8472312	4550172
RAB1A_MO	>sp P62821 RAB1A_	8	55712378	1.00E+08	1.25E+08	2.05E+08
RAN_MOI	>sp P62827 RAN_M	8	6.11E+08	2.78E+08	3.71E+08	5.92E+08
RL23_MOI	>sp P62830 RL23_M	2	0	29492883	28671594	20823897
RS15_MOI	>sp P62843 RS15_M	2	0	0	0	2529847
RS24_MOI	>sp P62849 RS24_M	4	0	0	40177136	0
RS26_MOI	>sp P62855 RS26_M	3	10541435	41291319	30489687	0
RS28_MOI	>sp P62858 RS28_M	2	0	0	0	0
ELOB_MOI	>sp P62869 ELOB_M	1	0	0	0	0
GBB1_MOI	>sp P62874 GBB1_M	11	72664774	1.03E+08	2.19E+08	1.28E+08
RPAB5_MO	>sp P62876 RPAB5_	1	0	0	0	0
RBX1_MOI	>sp P62878 RBX1_M	1	0	0	0	0

GBB2_MOU>sp P62880 GBB2_M	10	5711949	0	53237555	7510031
RL30_MOU!>sp P62889 RL30_M	3	0	38560640	35640045	25508878
RL31_MOU!>sp P62900 RL31_M	1	0	0	0	0
RS3_MOUS!>sp P62908 RS3_MC	10	1.10E+08	1.79E+08	79274271	61447149
RL32_MOU!>sp P62911 RL32_M	3	6178679	5356548	54594340	5521637
RL8_MOUS>sp P62918 RL8_MC	4	9784818	4495376	14975928	7407894
PROF1_MO>sp P62962 PROF1_	6	21254242	70027415	73524213	82304881
RS27A_MO!>sp P62983 RS27A_	6	2.40E+08	2.14E+08	3.86E+08	4.12E+08
TRA2B_MO>sp P62996 TRA2B_	1	50948034	14167621	0	0
RAC1_MOU>sp P63001 RAC1_M	2	44044638	12118863	56293036	36584294
LIS1_MOUS>sp P63005 LIS1_M	4	11631608	29910848	51894337	17596960
HSP7C_MO>sp P63017 HSP7C_	25	1.91E+09	1.12E+09	1.50E+09	2.08E+09
TCTP_MOU>sp P63028 TCTP_M	5	54755380	66998555	34948084	1.04E+08
MPC1_MOU>sp P63030 MPC1_M	1	0	0	0	0
DNJA1_MO>sp P63037 DNJA1_	4	0	7913539	0	0
CH60_MOU>sp P63038 CH60_M	34	1.80E+08	1.03E+09	1.40E+09	1.18E+09
IF4E_MOUS!>sp P63073 IF4E_M	1	0	0	0	0
VATL_MOU>sp P63082 VATL_M	1	0	0	0	0
MK01_MOU>sp P63085 MK01_M	1	0	0	0	0
PP1G_MOU>sp P63087 PP1G_M	9	27043721	15542159	16875971	0
GNAS2_MO>sp P63094 GNAS2_	2	0	0	0	0
1433Z_MOU>sp P63101 1433Z_M	13	6.19E+09	1.27E+09	5.90E+08	6.36E+09
HMGB1_MC>sp P63158 HMGB1	2	51422920	11314589	0	1.22E+08
DYL1_MOU>sp P63168 DYL1_M	2	0	0	33138132	0
IF5A1_MOU>sp P63242 IF5A1_M	4	15016719	39584377	1.00E+08	83448900
RS17_MOUS!>sp P63276 RS17_M	6	7953307	4730241	12376599	5212265
UBC9_MOU>sp P63280 UBC9_M	2	0	0	0	0
RALB_MOU>sp Q9JIW9 RALB_	2	0	15427935	7448210	17038695
RS12_MOUS!>sp P63323 RS12_M	2	0	19020642	37455424	0
RS10_MOUS!>sp P63325 RS10_M	3	0	0	36956127	28862693
PP2AA_MO>sp P63330 PP2AA_	13	1.19E+08	1.89E+08	2.20E+08	1.72E+08
PHB_MOUS>sp P67778 PHB_M	14	0	1.01E+08	1.80E+08	2.57E+08
CSK2B_MO>sp P67871 CSK2B_	3	0	0	0	0
RL22_MOU!>sp P67984 RL22_M	1	0	0	0	0
ACTC_MOU>sp P68033 ACTC_M	25	1.64E+09	8.94E+08	1.68E+09	2.07E+09
UB2L3_MO!>sp P68037 UB2L3_	2	0	0	0	0
RACK1_MC>sp P68040 RACK1_	20	37563477	3.84E+08	3.29E+08	1.46E+08
1433T_MOU>sp P68254 1433T_M	9	93147843	36057552	76644820	27663694
TBA4A_MO>sp P68368 TBA4A_	28	7.61E+08	1.28E+08	5.90E+08	5.45E+08
TBA1A_MO>sp P68369 TBA1A_	32	1.30E+08	2.26E+08	2.03E+08	1.84E+08
TBB4B_MO>sp P68372 TBB4B_	28	3.67E+09	3.65E+09	4.29E+09	4.77E+09
TBA1C_MO>sp P68373 TBA1C_	31	0	95349198	0	0
H31_MOUS!>sp P68433 H31_MC	3	0	0	51614839	0
1433F_MOU>sp P68510 1433F_M	6	0	0	22820320	0
IMB1_MOU>sp P70168 IMB1_M	18	75122825	98775917	88603529	98245022
PSB7_MOU!>sp P70195 PSB7_M	4	4243725	3732343	35056627	0
SEM3E_MO>sp P70275 SEM3E_	1	0	0	0	0

HDAC2_MC>sp P70288 HDAC2	1	0	2723065	0	0
PEBP1_MO>sp P70296 PEBP1_	1	0	0	0	0
STAM1_MC>sp P70297 STAM1_	2	1.93E+08	34505475	1.08E+08	1.63E+08
HNRH2_MC>sp P70333 HNRH2_	4	0	0	0	0
ROCK1_MC>sp P70335 ROCK1_	1	0	0	8600935	4043399
HINT1_MO>sp P70349 HINT1_	3	0	0	0	0
ELAV1_MO>sp P70372 ELAV1_	3	0	0	0	0
ALS_MOUS>sp P70389 ALS_M	2	4.17E+08	77034863	2.26E+08	4.56E+08
IDHG1_MO>sp P70404 IDHG1_	4	1.75E+08	31366241	93181324	1.85E+08
EXT2_MOU>sp P70428 EXT2_N	10	1.68E+08	1.25E+08	1.19E+08	1.81E+08
NACAM_M<>sp P70670 NACAM	2	0	0	0	0
CASP3_MO>sp P70677 CASP3_	2	0	0	0	0
AK1CL_MC>sp Q91WR5 AK1C	1	22433198	5063501	19245190	19696795
PYRG1_MO>sp P70698 PYRG1_	1	0	7209799	0	0
LYAG_MOU>sp P70699 LYAG_	1	0	4021068	0	0
TCPH_MOU>sp P80313 TCPH_N	13	27029268	1.19E+08	1.42E+08	68622116
TCPB_MOU>sp P80314 TCPB_N	25	1.22E+08	3.60E+08	3.17E+08	2.74E+08
TCPD_MOU>sp P80315 TCPD_N	13	56228559	2.43E+08	2.58E+08	1.16E+08
TCPE_MOU>sp P80316 TCPE_N	16	47149979	1.93E+08	1.19E+08	1.45E+08
TCPZ_MOU>sp P80317 TCPZ_N	16	99308971	1.88E+08	1.00E+08	1.10E+08
TCPG_MOU>sp P80318 TCPG_N	16	2.21E+10	1.03E+10	3.87E+08	2.49E+10
NUCB2_MO>sp P81117 NUCB2_	1	0	0	0	0
BGH3_MOU>sp P82198 BGH3_N	25	1.10E+09	9.90E+08	9.84E+08	6.28E+08
TNIK_MOU>sp P83510 TNIK_N	2	0	14683126	34098737	16629513
ARF1_MOU>sp P84078 ARF1_N	12	4.77E+08	3.38E+08	4.74E+08	5.45E+08
ARF5_MOU>sp P84084 ARF5_N	8	64876644	0	33390494	0
AP2M1_MO>sp P84091 AP2M1_	2	0	0	24133960	0
RHOG_MO>sp P84096 RHOG_	2	0	0	0	0
SERF2_MO>sp P84102 SERF2_	1	0	0	32421749	0
SRSF3_MO>sp P84104 SRSF3_	2	45188493	11904960	7660140	43220028
H32_MOUS>sp P84228 H32_MC	3	0	0	62889728	0
ISC2A_MOU>sp P85094 ISC2A_	2	0	0	0	0
PEDF_MOU>sp P97298 PEDF_N	14	3.92E+08	80243401	2.12E+09	3.33E+08
MCM2_MO>sp P97310 MCM2_	5	0	0	0	0
MCM6_MO>sp P97311 MCM6_	9	0	0	0	26744883
SEPR_MOU>sp P97321 SEPR_N	2	32120871	41357629	20994630	82342944
NRP1_MOU>sp P97333 NRP1_N	10	1.97E+08	3.05E+08	3.03E+08	1.66E+08
RS3A_MOU>sp P97351 RS3A_N	6	20925952	1.09E+08	90931773	1.56E+08
AT1B3_MO>sp P97370 AT1B3_	1	0	0	69613957	0
PSME1_MO>sp P97371 PSME1_	2	4300918	5102004	0	0
PSME2_MO>sp P97372 PSME2_	2	0	0	0	0
ANX11_MO>sp P97384 ANX11_	4	29331433	36914018	25267147	1.10E+08
ANXA4_MC>sp P97429 ANXA4_	11	19528135	1.03E+08	1.85E+08	0
ATP5J_MO>sp P97450 ATP5J_	2	0	29204970	25388444	13771580
BOP1_MOU>sp P97452 BOP1_N	2	0	0	0	0
RS5_MOUS>sp P97461 RS5_MC	7	61694909	63139753	0	51029386
EXT1_MOU>sp P97464 EXT1_N	14	3.29E+08	2.19E+08	3.09E+08	3.55E+08

THIOM_MC>sp P97493 THIOM_	2	0	0	0	0
SMRC1_MC>sp P97496 SMRC1_	1	0	0	0	0
RPB3_MOU>sp P97760 RPB3_N	2	0	0	0	0
NEO1_MOU>sp P97798 NEO1_M	2	74581867	0	0	1.06E+08
FUMH_MO>sp P97807 FUMH_	7	0	0	0	0
AN32E_MO>sp P97822 AN32E_	2	22230856	0	0	0
LYPA1_MO>sp P97823 LYPA1_	3	0	0	6703064	14132125
G3BP1_MO>sp P97855 G3BP1_	4	0	0	0	0
LOXL1_MO>sp P97873 LOXL1_	1	35391390	0	0	19717942
LAMA4_MC>sp P97927 LAMA4	42	1.12E+09	96307482	1.57E+09	2.80E+08
KTHY_MO>sp P97930 KTHY_	2	0	0	0	0
BMP1_MO>sp P98063 BMP1_M	4	34789524	0	21497454	0
MASP1_MO>sp P98064 MASP1_	5	1.71E+08	1.26E+08	2.26E+08	1.62E+08
TBB5_MOU>sp P99024 TBB5_M	27	8.59E+08	8.90E+08	1.15E+09	1.34E+09
PSB4_MOU>sp P99026 PSB4_M	4	5109256	49308815	61299575	45685696
RLA2_MOU>sp P99027 RLA2_M	5	71612798	1.57E+08	1.68E+08	1.57E+08
QCR6_MOU>sp P99028 QCR6_M	1	0	17535731	31816623	62282431
PRDX5_MO>sp P99029 PRDX5_	7	99139664	45672471	49099358	23444991
CBPE_MOU>sp Q00493 CBPE_I	13	1.49E+08	48881010	33401349	40546068
G6PD1_MO>sp Q00612 G6PD1_	9	27187219	1.10E+08	50955441	59096729
RET4_MOU>sp Q00724 RET4_M	1	0	27246051	98565049	0
VEGFA_MC>sp Q00731 VEGFA	1	0	0	0	0
HNRL2_MC>sp Q00PI9 HNRL2_	4	38523572	0	38315626	47970562
CO1A2_MO>sp Q01149 CO1A2_	36	1.37E+10	1.09E+08	3.71E+09	4.88E+08
TOP2A_MO>sp Q01320 TOP2A_	3	0	0	16349538	0
RSU1_MOU>sp Q01730 RSU1_M	3	0	0	25451399	0
TCP11_MO>sp Q01755 TCP11_	1	86045201	10432027	96437609	51604567
NDKB_MO>sp Q01768 NDKB_	6	51991750	84230544	1.09E+08	1.29E+08
TERA_MO>sp Q01853 TERA_	39	2.94E+08	1.44E+09	1.61E+09	8.73E+08
AQP1_MOU>sp Q02013 AQP1_I	4	0	0	58558868	0
UBA1_MOU>sp Q02053 UBA1_	32	2.58E+08	3.81E+08	2.51E+08	1.73E+08
PLAK_MO>sp Q02257 PLAK_	4	0	4790561	0	29794191
CO6A2_MO>sp Q02788 CO6A2_	32	2.48E+09	9.00E+08	3.22E+09	2.67E+08
NUCB1_MO>sp Q02819 NUCB1	6	0	0	0	10968627
EPHA2_MO>sp Q03145 EPHA2_	3	0	0	0	6532962
ATPA_MO>sp Q03265 ATPA_	26	5.95E+08	8.20E+08	1.23E+09	1.01E+09
TSP2_MO>sp Q03350 TSP2_M	36	6.81E+08	18601393	2.41E+09	4458291
CCL7_MOU>sp Q03366 CCL7_M	1	29329368	0	0	0
CRIS1_MO>sp Q03401 CRIS1_	1	0	41254956	0	0
PFD6_MOU>sp Q03958 PFD6_M	1	0	0	0	0
KCRB_MO>sp Q04447 KCRB_	3	36010806	0	29743455	35334543
ASM_MO>sp Q04519 ASM_M	2	70094195	49484215	77192962	1.02E+08
CO6A1_MO>sp Q04857 CO6A1_	31	2.72E+09	2.71E+09	3.80E+09	6.71E+08
INHBB_MO>sp Q04999 INHBB_	2	0	0	0	0
CO9A1_MO>sp Q05722 CO9A1_	2	38512216	10790956	19047642	24324680
PGH2_MO>sp Q05769 PGH2_I	3	0	1.31E+08	5616278	0
PGBM_MO>sp Q05793 PGBM_	122	6.39E+09	4.03E+09	1.34E+10	2.65E+10

TSP3_MOU	>sp Q05895 TSP3_M	5	35637092	92170607	1.05E+08	23331858
PYC_MOUS	>sp Q05920 PYC_M	2	0	0	0	0
IF2P_MOUS	>sp Q05D44 IF2P_M	1	0	0	0	0
APLP2_MO	>sp Q06335 APLP2_	4	0	12682710	15876020	0
TIE1_MOUS	>sp Q06806 TIE1_M	2	1.03E+08	34291573	75920297	97572567
CLUS_MOU	>sp Q06890 CLUS_I	9	50913966	1.46E+08	1.32E+08	1.05E+09
ANXA7_MO	>sp Q07076 ANXA7	3	0	24162004	15941688	0
MPRI_MOU	>sp Q07113 MPRI_M	10	2.75E+09	2.59E+09	1.64E+09	2.58E+09
GDN_MOUS	>sp Q07235 GDN_M	1	0	0	0	0
LG3BP_MO	>sp Q07797 LG3BP_	13	45541561	1.93E+08	7.15E+08	39673780
CNN2_MOU	>sp Q08093 CNN2_I	1	0	12728485	0	0
FBLN1_MO	>sp Q08879 FBLN1_	9	0	8962089	0	0
SSRP1_MOI	>sp Q08943 SSRP1_	4	0	62326924	52070719	24445215
CTR1_MOU	>sp Q09143 CTR1_M	2	0	0	0	45427710
INF2_MOUS	>sp Q0GNC1 INF2_I	2	0	0	0	0
PSA_MOUS	>sp Q11011 PSA_M	2	0	26876855	25783811	0
PEPD_MOU	>sp Q11136 PEPD_M	2	0	0	0	0
NSUN2_MO	>sp Q1HFZ0 NSUN2_	4	0	0	0	0
FAT4_MOU	>sp Q2PZL6 FAT4_I	4	79882007	78125766	47829407	1.35E+08
OSBP1_MO	>sp Q3B7Z2 OSBP1_	1	0	0	0	0
PLBL2_MO	>sp Q3TCN2 PLBL2_	1	0	0	0	0
FAF2_MOU	>sp Q3TDN2 FAF2_I	2	0	6126597	3906729	0
STT3B_MOI	>sp Q3TDQ1 STT3E	2	5.56E+08	1.37E+08	4350397	5.30E+08
TTYH2_MO	>sp Q3TH73 TTYH2_	1	0	0	0	0
ML12B_MO	>sp Q3THE2 ML12I	9	43752479	3.77E+08	3.12E+09	1.77E+08
GUAA_MOI	>sp Q3THK7 GUAA_	6	0	0	0	0
METK2_MC	>sp Q3THS6 METK_	3	35621606	6042747	12007281	30060636
SRSF6_MOI	>sp Q3TWW8 SRSF_	1	0	0	0	0
PSMD1_MO	>sp Q3TXS7 PSMD_	11	0	52500241	40901660	7864339
SC31B_MOI	>sp Q3TZ89 SC31B_	1	0	14131258	0	6237019
TRADD_MC	>sp Q3U0V2 TRADD_	1	0	0	0	0
DDB1_MOU	>sp Q3U1J4 DDB1_I	3	0	7386483	0	0
CO5A2_MO	>sp Q3U962 CO5A2_	6	1.55E+08	0	39927488	45038616
PCH2_MOU	>sp Q3UA06 PCH2_	3	0	0	0	0
TTL12_MOI	>sp Q3UDE2 TTL12_	6	0	0	0	0
PUF60_MOI	>sp Q3UEB3 PUF60_	3	0	0	0	0
FRMD8_MC	>sp Q3UFK8 FRMD_	1	0	0	0	0
ZY11B_MOI	>sp Q3UFS0 ZY11B_	1	87209704	35481299	74066928	58455994
EI3JA_MOU	>sp Q3UGC7 EI3JA_	2	0	1955369	0	0
GREB1_MO	>sp Q3UHK3 GREB_	1	0	3852855	14934411	0
TEN4_MOU	>sp Q3UHK6 TEN4_	11	27263614	0	60610328	23231412
EDC4_MOU	>sp Q3UJB9 EDC4_	1	0	0	0	0
SMU1_MOU	>sp Q3UKJ7 SMU1_	1	0	0	0	0
MCU_MOU	>sp Q3UMR5 MCU_	1	0	0	0	0
PRRC1_MO	>sp Q3UPH1 PRRC_	1	0	0	0	0
SC31A_MOI	>sp Q3UPL0 SC31A_	5	0	0	0	15317380
PXDN_MOU	>sp Q3UQ28 PXDN_	32	8.56E+08	3.96E+08	1.07E+09	19334135

BROMI_MC	>sp Q3URV1 BROM	1	0	0	1.04E+08	0
ERMP1_MC	>sp Q3UVK0 ERMF	5	0	0	0	5473423
NIBAN_MO	>sp Q3UW53 NIBA1	1	0	0	0	0
CI131_MOU	>sp Q3V0E1 CI131_	1	0	20996674	50274335	0
OLM2B_MC	>sp Q3V1G4 OLM2	2	0	0	24373297	12512313
P3H1_MOU	>sp Q3V1T4 P3H1_	2	0	0	0	0
C1TM_MOU	>sp Q3V3R1 C1TM_	1	0	0	0	0
TIM8A_MO	>sp Q9WVA2 TIM8	1	0	0	15774261	0
ABRAL_MC	>sp Q4KML4 ABRA	1	0	0	0	0
MUML1_M	>sp Q4VA55 MUMI	1	0	0	1.96E+09	3.61E+08
DDX17_MO	>sp Q501J6 DDX17_	2	0	0	0	0
A16A1_MOU	>sp Q571I9 A16A1_	1	16287555	7287232	13372479	13390945
AAPK1_MO	>sp Q5EG47 AAPK	2	0	0	0	0
RHG01_MO	>sp Q5FWK3 RHG0	3	0	0	0	0
FA20C_MO	>sp Q5MJS3 FA20C	2	39436179	30375445	80446534	31851734
ABCAD_MC	>sp Q5SSE9 ABCAI	2	1.31E+08	48166575	0	0
TEFM_MOU	>sp Q5SSK3 TEFM_	1	0	0	0	0
TENS3_MO	>sp Q5SSZ5 TENS3	3	0	0	0	0
LC7L3_MO	>sp Q5SUF2 LC7L3	2	0	0	0	0
PUR4_MOU	>sp Q5SUR0 PUR4_	2	0	0	0	0
MYO1D_MC	>sp Q5SYD0 MYO1	8	1.82E+08	0	55324291	38945287
COPD_MOU	>sp Q5XJY5 COPD_	2	0	0	16186995	0
ODO1_MOU	>sp Q60597 ODO1_	6	0	11866030	12808328	11852546
MYL6_MOU	>sp Q60605 MYL6_	9	3.22E+08	4.88E+08	5.73E+08	4.48E+08
FLOT2_MO	>sp Q60634 FLOT2_	1	0	0	0	0
SAP3_MOU	>sp Q60648 SAP3_M	2	0	0	0	0
HNRPD_MC	>sp Q60668 HNRPD	3	0	0	0	0
LAMA2_MC	>sp Q60675 LAMA2	10	2.43E+08	1.14E+08	1.50E+08	1.60E+08
PSB6_MOU	>sp Q60692 PSB6_M	6	35529726	53873495	1.18E+08	25672762
SAMH1_MC	>sp Q60710 SAMH1	4	1.09E+08	84718242	34573611	1.65E+08
P4HA1_MO	>sp Q60715 P4HA1_	6	41897327	33000029	99205452	10313512
P4HA2_MO	>sp Q60716 P4HA2_	2	0	0	0	0
CSK21_MO	>sp Q60737 CSK21_	5	27011718	0	0	0
KHDR1_MC	>sp Q60749 KHDR1	2	0	0	0	0
RELN_MOU	>sp Q60841 RELN_	20	6.04E+08	3.68E+08	5.44E+08	4.88E+08
COCA1_MC	>sp Q60847 COCA1	68	6.19E+08	2.78E+09	1.92E+09	4.24E+08
SPB6_MOU	>sp Q60854 SPB6_M	8	0	32414792	17442836	0
STIP1_MOU	>sp Q60864 STIP1_	5	0	12548379	5483313	0
CAPR1_MO	>sp Q60865 CAPR1_	4	0	23548103	0	0
VDAC2_MC	>sp Q60930 VDAC2	10	0	1.51E+08	1.70E+08	1.53E+08
VDAC3_MC	>sp Q60931 VDAC3	6	0	88962068	96101126	25558572
VDAC1_MC	>sp Q60932 VDAC1	11	0	4.45E+08	5.98E+08	9.52E+08
PAFA_MOU	>sp Q60963 PAFA_	3	0	0	41322263	0
RBBP4_MO	>sp Q60972 RBBP4_	2	0	0	0	0
RBBP7_MO	>sp Q60973 RBBP7_	4	0	0	54941677	0
LAMA5_MC	>sp Q61001 LAMA5	40	1.01E+08	6.85E+08	1.51E+08	4.08E+08
ASNS_MOU	>sp Q61024 ASNS_	8	18910784	22460195	8576785	14449321

LAP2A_MO	>sp Q61033 LAP2A	3	0	12892762	0	0
CDC37_MO	>sp Q61081 CDC37	2	0	0	26365601	0
PRP4B_MO	>sp Q61136 PRP4B	2	0	0	0	0
MARE1_MC	>sp Q61166 MARE1	1	0	0	0	0
PRDX2_MO	>sp Q61171 PRDX2	6	2446488	68038122	44499855	69813715
PA1B2_MO	>sp Q61206 PA1B2	3	0	12773404	0	0
SAP_MOUS	>sp Q61207 SAP_M	14	95005060	4.26E+08	2.91E+08	74097971
SOAT1_MO	>sp Q61263 SOAT1	4	0	0	0	30972045
LAMB2_MC	>sp Q61292 LAMB2	1	0	0	0	0
HSP74_MO	>sp Q61316 HSP74	13	29798060	66831711	9061971	72591291
PCOC1_MO	>sp Q61398 PCOC1	27	3.32E+09	84589900	1.18E+09	1.08E+09
HCDH_MO	>sp Q61425 HCDH	3	0	0	0	0
SMRD3_MC	>sp Q6P9Z1 SMRD3	1	0	0	0	0
5NTD_MOU	>sp Q61503 5NTD_I	3	0	16573597	0	0
ECM1_MOU	>sp Q61508 ECM1_I	14	1.19E+08	3.96E+08	3.73E+08	92174953
GSLG1_MO	>sp Q61543 GSLG1	4	0	41686184	37775626	0
FSCN1_MO	>sp Q61553 FSCN1	7	0	1.36E+08	37748490	0
FBN1_MOU	>sp Q61554 FBN1_M	67	1.76E+09	3.72E+08	4.42E+09	80035874
FKB10_MO	>sp Q61576 FKB10	3	19388767	0	0	11240358
IBP7_MOU	>sp Q61581 IBP7_M	1	0	0	0	0
FXR1_MOU	>sp Q61584 FXR1_M	2	0	0	0	0
KTN1_MOU	>sp Q61595 KTN1_I	4	0	0	0	0
GDIB_MOU	>sp Q61598 GDIB_M	16	1.57E+08	1.46E+08	2.63E+08	1.87E+08
HPT_MOUS	>sp Q61646 HPT_M	1	29924008	42241902	34120445	0
DD19A_MO	>sp Q61655 DD19A	1	0	0	0	0
DDX5_MOU	>sp Q61656 DDX5_I	7	0	10991168	8970524	0
CBX5_MOU	>sp Q61686 CBX5_I	3	0	0	0	0
HS105_MO	>sp Q61699 HS105	5	0	10711384	11628196	0
CD47_MOU	>sp Q61735 CD47_M	1	0	35637875	35764869	30872657
SERA_MOU	>sp Q61753 SERA_I	7	37618192	55691667	59283391	46017694
KINH_MOU	>sp Q61768 KINH_I	2	0	0	0	0
LAMA3_MC	>sp Q61789 LAMA3	2	58370707	20479885	37561253	50744967
LTBP3_MO	>sp Q61810 LTBP3	2	11348741	0	0	31953237
PZP_MOUS	>sp Q61838 PZP_M	3	4.47E+08	1.49E+08	3.54E+08	3.35E+08
MYH10_MC	>sp Q61879 MYH10	16	5655995	9664973	13914651	0
MCM7_MO	>sp Q61881 MCM7	7	0	3594675	0	7954739
NPM_MOU	>sp Q61937 NPM_M	6	1.58E+08	3.16E+08	1.19E+08	5.66E+08
NNTM_MO	>sp Q61941 NNTM	1	0	0	0	0
NOTC3_MC	>sp Q61982 NOTC3	5	79820066	48008287	1.69E+08	95747634
PCBP2_MO	>sp Q61990 PCBP2	7	0	22496558	40288393	19303472
MIME_MO	>sp Q62000 MIME_I	3	1.72E+08	47636097	2.36E+08	1.47E+08
POSTN_MO	>sp Q62009 POSTN	20	0	7682952	7804502	0
CSPG2_MO	>sp Q62059 CSPG2	19	1.85E+09	1.47E+08	1.14E+09	3.48E+08
PON2_MOU	>sp Q62086 PON2_I	1	0	0	0	0
DDX3X_MC	>sp Q62167 DDX3X	11	7453851	49317371	16886554	49063830
SEM3C_MC	>sp Q62181 SEM3C	13	0	35603651	35935824	9.58E+08
SSRD_MOU	>sp Q62186 SSRD_I	3	0	65676637	47593326	41640393

DPYL3_MO	>sp Q62188 DPYL3	3	0	0	0	0
RFA2_MOU	>sp Q62193 RFA2_M	2	0	1.09E+08	36006377	70286336
SPTB2_MOI	>sp Q62261 SPTB2_	19	72243570	1.26E+08	46092722	81069932
TIF1B_MOI	>sp Q62318 TIF1B_	2	0	0	0	0
TSN_MOUS	>sp Q62348 TSN_M	2	0	0	0	0
TFR1_MOU	>sp Q62351 TFR1_M	4	1.20E+08	89984523	29035213	1.03E+08
FSTL1_MOI	>sp Q62356 FSTL1_	2	1.13E+08	44158041	43579955	85851129
TPD52_MOI	>sp Q62393 TPD52_	1	0	0	0	0
DBNL_MOU	>sp Q62418 DBNL_	2	0	0	0	0
SH3G1_MO	>sp Q62419 SH3G1_	1	0	3766653	0	0
OSTF1_MO	>sp Q62422 OSTF1_	1	0	1513318	0	3687611
NDRG1_MC	>sp Q62433 NDRG1	1	0	0	0	0
NPTX1_MO	>sp Q62443 NPTX1	3	1.41E+08	8743908	15127074	1.68E+08
VAT1_MOU	>sp Q62465 VAT1_	4	17027758	24215052	65530032	33510668
ITA3_MOU	>sp Q62470 ITA3_M	11	0	18333587	0	3.93E+08
NUP62_MOI	>sp Q63850 NUP62_	1	0	0	0	0
MP2K2_MO	>sp Q63932 MP2K2	2	0	0	0	0
CRK_MOU	>sp Q64010 CRK_M	1	0	0	92820419	0
MCF2L_MC	>sp Q64096 MCF2L	1	1.50E+09	1.73E+08	2.56E+08	1.05E+09
AEBP1_MO	>sp Q640N1 AEBP1	25	2.33E+09	1.39E+09	1.67E+09	3.62E+09
SPRE_MOU	>sp Q64105 SPRE_M	1	0	0	0	0
BTF3_MOU	>sp Q64152 BTF3_M	3	1843177	3143640	0	3172697
SF01_MOU	>sp Q64213 SF01_M	1	0	0	0	0
LY6E_MOU	>sp Q64253 LY6E_M	1	0	0	0	0
CDK6_MOU	>sp Q64261 CDK6_	2	0	0	0	0
IFIT1_MOU	>sp Q64282 IFIT1_M	1	0	0	0	0
SURF4_MO	>sp Q64310 SURF4_	3	0	0	0	0
CD34_MOU	>sp Q64314 CD34_M	1	0	0	0	0
SQSTM_MC	>sp Q64337 SQSTM	1	0	0	0	0
ISG15_MOU	>sp Q64339 ISG15_	2	0	0	27436919	0
ARF_MOUS	>sp Q64364 ARF_M	1	0	0	0	0
RGN_MOU	>sp Q64374 RGN_M	2	18160257	0	0	96390484
FKBP5_MO	>sp Q64378 FKBP5_	1	0	0	0	0
CP1B1_MOI	>sp Q64429 CP1B1_	3	0	0	0	0
CH10_MOU	>sp Q64433 CH10_M	9	8302864	3.21E+08	4.21E+08	6.61E+08
MRC2_MOU	>sp Q64449 MRC2_	10	3.41E+08	1.29E+08	4.56E+08	5.00E+08
PTPRD_MO	>sp Q64487 PTPRD_	4	87569998	76769623	73999088	1.19E+08
TPP2_MOU	>sp Q64514 TPP2_M	4	0	0	0	0
GPDM_MOI	>sp Q64521 GPDM_	4	0	65997491	2751833	0
H2A2C_MO	>sp Q64523 H2A2C_	4	0	0	0	0
SPEE_MOU	>sp Q64674 SPEE_M	3	0	0	0	0
VINC_MOU	>sp Q64727 VINC_M	8	1.87E+08	1.76E+08	1.49E+08	1.46E+08
PUR2_MOU	>sp Q64737 PUR2_M	4	0	0	0	0
CLH1_MOU	>sp Q68FD5 CLH1_	69	9.86E+08	1.29E+09	1.56E+09	1.24E+09
SYMC_MOI	>sp Q68FL6 SYMC_	1	0	0	0	0
MYOF_MO	>sp Q69ZN7 MYOF	15	1.19E+08	1.41E+08	62420280	1.41E+08
NOP58_MO	>sp Q6DFW4 NOP5	2	3821386	4940721	16634463	6561616

NOMO1_MC	>sp Q6GQT9 NOMC	1	0	0	0	0
C1QT6_MO	>sp Q6IR41 C1QT6_	2	0	0	0	22143431
TPM4_MOU	>sp Q6IRU2 TPM4_	6	0	31406455	0	0
SR140_MOU	>sp Q6NV83 SR140_	1	0	0	0	0
S23IP_MOU	>sp Q6NZC7 S23IP_	1	0	0	0	0
IF4G1_MOU	>sp Q6NZJ6 IF4G1_	3	0	0	0	0
SORCN_MC	>sp Q6P069 SORCN	2	0	1.44E+08	0	1.39E+08
XPP1_MOU	>sp Q6P1B1 XPP1_	8	40631653	9778341	21496912	24506539
2ABA_MOU	>sp Q6P1F6 2ABA_	7	5844917	37001718	57481580	4086749
TNPO3_MO	>sp Q6P2B1 TNPO3	1	0	0	0	0
U520_MOU	>sp Q6P4T2 U520_M	7	0	18686099	0	0
ABCF1_MO	>sp Q6P542 ABCF1_	1	0	0	0	0
UGGG1_MC	>sp Q6P5E4 UGGG1	11	0	46866048	40250403	0
TTYH3_MO	>sp Q6P5F7 TTYH3	1	0	0	0	0
XPO1_MOU	>sp Q6P5F9 XPO1_	6	0	10986463	12267242	13513594
SAT2_MOU	>sp Q6P8J2 SAT2_M	1	0	0	0	0
ANO6_MOU	>sp Q6P9J9 ANO6_	1	0	0	0	0
KIF11_MOU	>sp Q6P9P6 KIF11_	2	0	0	0	0
LPPRC_MO	>sp Q6PB66 LPPRC	5	0	7646588	0	0
ECM29_MO	>sp Q6PDI5 ECM29	2	0	0	6932903	0
SRSF1_MOI	>sp Q6PDM2 SRSF1	3	0	0	0	0
CHD4_MOU	>sp Q6PDQ2 CHD4_	2	0	20629189	0	0
PGFRL_MC	>sp Q6PE55 PGFRL	1	0	0	0	0
TRA2A_MO	>sp Q6PFR5 TRA2A	1	0	5512269	0	0
NAA50_MO	>sp Q6PGB6 NAA50	1	0	0	0	0
KCC2D_MC	>sp Q6PHZ2 KCC2I	2	7415963	9504546	11853693	4761953
RB15B_MOI	>sp Q6PHZ5 RB15B	1	0	0	0	0
NUDC1_MC	>sp Q6PIP5 NUDC1	2	0	0	0	0
DDX58_MO	>sp Q6Q899 DDX58	1	0	0	0	0
MYH14_MC	>sp Q6URW6 MYH	4	97550861	1.35E+08	84926640	1.52E+08
CAND1_MC	>sp Q6ZQ38 CAND	11	28312493	77389941	69027826	32309553
LARP1_MO	>sp Q6ZQ58 LARP1	1	0	0	0	0
MLEC_MOI	>sp Q6ZQI3 MLEC_	1	0	0	0	0
WDR43_MC	>sp Q6ZQL4 WDR4	1	0	0	17828435	0
LSM8_MOU	>sp Q6ZWM4 LSM8	1	0	0	0	0
SYNE1_MO	>sp Q6ZWR6 SYNE	1	0	0	33819239	0
RL10_MOU	>sp Q6ZWV3 RL10_	4	0	45368730	56132935	0
IF2A_MOU	>sp Q6ZWX6 IF2A_	5	0	13761206	12055583	0
SNED1_MO	>sp Q70E20 SNED1_	11	56014860	2561611	2.10E+08	0
2AAA_MOU	>sp Q76MZ3 2AAA_	9	46477912	74523647	64458172	90374339
SND1_MOU	>sp Q78PY7 SND1_	14	0	16245043	42510807	12616987
NP1L4_MOI	>sp Q78ZA7 NP1L4_	2	7482860	7831400	0	4382376
PICAL_MO	>sp Q7M6Y3 PICAL	1	0	0	0	0
CYFP1_MO	>sp Q7TMB8 CYFP	3	7375288	11115232	18039279	9577935
HNRPQ_MC	>sp Q7TMK9 HNRP	8	0	23193881	11857492	24647163
TBB2A_MO	>sp Q7TMM9 TBB2	24	3.36E+08	1.42E+08	1.05E+08	1.10E+08
HUWE1_MC	>sp Q7TMY8 HUW1	2	43038086	99545966	0	43926317

LC7L2_MO	>sp Q7TNC4 LC7L2	1	0	0	0	0
ACTN1_MO	>sp Q7TPR4 ACTN1	39	1.26E+09	1.55E+09	1.87E+09	2.02E+09
MBB1A_MC	>sp Q7TPV4 MBB1A	12	0	58626410	8721418	49144186
ATX2L_MO	>sp Q7TQH0 ATX2L	1	0	0	0	0
OTUB1_MO	>sp Q7TQI3 OTUB1	4	33412355	41743509	7142391	25587119
ATL4_MOU	>sp Q80T21 ATL4_M	1	0	0	30343154	26180275
SDCG8_MO	>sp Q80UF4 SDCG8	1	1.73E+08	1.03E+09	7.02E+08	0
SEPT9_MO	>sp Q80UG5 SEPT9	6	0	0	0	0
NAA15_MO	>sp Q80UM3 NAA15	4	2.06E+08	1.19E+08	0	2.43E+08
FACE1_MO	>sp Q80W54 FACE1	3	0	0	0	0
LYRIC_MO	>sp Q80WJ7 LYRIC	1	0	0	0	0
VRK1_MOU	>sp Q80X41 VRK1_M	1	0	0	0	0
FLNB_MOU	>sp Q80X90 FLNB_M	56	5.06E+08	9.20E+08	6.56E+08	1.01E+09
GLRX5_MO	>sp Q80Y14 GLRX5	1	0	0	8214523	0
TENA_MOU	>sp Q80YX1 TENA_M	41	6.24E+08	1.76E+08	1.20E+09	1.44E+08
TENN_MOU	>sp Q80Z71 TENN_M	8	0	53809324	7997166	0
PKHL1_MO	>sp Q80ZA4 PKHL1	14	0	0	0	28837318
EFTU_MOU	>sp Q8BFR5 EFTU_M	2	0	0	0	0
TNPO1_MO	>sp Q8BFY9 TNPO1	2	0	9621336	8949087	0
ROA3_MOU	>sp Q8BG05 ROA3_M	8	0	16262155	30704059	0
PSD11_MOU	>sp Q8BG32 PSD11	8	32110548	1.28E+08	20141483	37254634
PDIP3_MOU	>sp Q8BG81 PDIP3	1	0	0	0	0
IF4B_MOU	>sp Q8BGD9 IF4B_M	2	0	0	0	0
SAM50_MO	>sp Q8BGH2 SAM50	1	0	0	0	0
SYAC_MOU	>sp Q8BGQ7 SYAC_M	16	1.41E+08	99203722	52011020	72614552
UBCP1_MO	>sp Q8BGR9 UBCP1	1	0	0	0	0
MAK16_MC	>sp Q8BGS0 MAK16	1	0	0	0	0
ALAT2_MO	>sp Q8BGT5 ALAT2	1	0	0	0	0
PCKGM_M	>sp Q8BH04 PCKGM	7	15797184	0	0	18802303
SEM3D_MC	>sp Q8BH34 SEM3D	12	0	0	0	2.81E+08
CO8B_MOU	>sp Q8BH35 CO8B_M	3	56386510	27755566	2.56E+08	35004659
F13A_MOU	>sp Q8BH61 F13A_M	2	5.56E+08	2.61E+08	2.90E+08	5.74E+08
EHD2_MOU	>sp Q8BH64 EHD2_M	1	0	3865946	9069569	0
PTBP3_MO	>sp Q8BHD7 PTBP3	2	0	0	0	0
RAI3_MOU	>sp Q8BHL4 RAI3_M	1	0	0	0	0
GANAB_MC	>sp Q8BHN3 GANAB	25	1.60E+08	1.63E+08	3.56E+08	8.85E+08
CEMIP_MO	>sp Q8BI06 CEMIP	1	14265160	2.63E+08	3.45E+08	0
SYIM_MOU	>sp Q8BIJ6 SYIM_M	3	0	515719	20997072	0
CSTF2_MO	>sp Q8BIQ5 CSTF2	1	0	0	0	0
NUP93_MO	>sp Q8BJ71 NUP93	3	40608941	65338671	0	48990875
SUN2_MOU	>sp Q8BJS4 SUN2_M	4	0	0	7756472	0
SGTA_MOU	>sp Q8BJU0 SGTA_M	1	0	0	0	0
TSN9_MOU	>sp Q8BJU2 TSN9_M	1	0	0	0	1.22E+08
NOL11_MO	>sp Q8BJW5 NOL11	1	0	0	0	0
OLFL3_MO	>sp Q8BK62 OLFL3	8	2.63E+08	64384666	1.28E+08	1.60E+08
RCC2_MOU	>sp Q8BK67 RCC2_M	5	6881820	17493806	0	0
RT27_MOU	>sp Q8BK72 RT27_M	3	0	0	0	0

IPO5_MOU	>sp Q8BKC5 IPO5_	10	98148598	1.10E+08	40958645	0
SRSF7_MOI	>sp Q8BL97 SRSF7_	1	0	22496131	0	0
COGA1_MC	>sp Q8BLX7 COGA	3	0	0	9410937	0
HSP13_MOI	>sp Q8BM72 HSP13	2	66070053	27950646	65066012	60203742
SRP68_MOI	>sp Q8BMA6 SRP68	3	0	0	0	0
SCMC1_MC	>sp Q8BMD8 SCMC	2	0	0	0	0
ODP2_MOU	>sp Q8BMF4 ODP2_	4	0	0	16124583	0
SYLC_MOU	>sp Q8BMJ2 SYLC_	14	82390644	1.88E+08	1.24E+08	1.50E+08
CKAP4_MO	>sp Q8BMK4 CKAF	8	1.12E+08	3.29E+08	1.47E+08	97954259
SYQ_MOUS	>sp Q8BML9 SYQ_	5	0	0	0	0
QSOX1_MO	>sp Q8BND5 QSOX	3	1.85E+08	1.45E+08	1.44E+08	1.58E+08
SYNC_MOI	>sp Q8BP47 SYNC_	11	4.68E+08	1.86E+08	1.39E+08	36439441
MAP11_MO	>sp Q8BP48 MAP11	2	0	0	0	0
RL24_MOU	>sp Q8BP67 RL24_	2	9557079	43717402	46684280	30388405
RCN2_MOU	>sp Q8BP92 RCN2_	4	0	0	24762423	0
FBLN3_MO	>sp Q8BPB5 FBLN3	18	3.32E+09	99263615	1.19E+09	1.07E+09
SCFD1_MO	>sp Q8BRF7 SCFD1	2	0	0	0	0
FLNA_MOU	>sp Q8BTM8 FLNA	55	2.16E+09	9.89E+08	1.19E+09	2.31E+09
GMPPB_MC	>sp Q8BTZ7 GMPP	1	0	0	8008834	0
SYIC_MOU	>sp Q8BU30 SYIC_	14	2126766	1.02E+08	40836534	19889227
SRCRL_MO	>sp Q8BV57 SRCRI	3	51135923	0	0	45344181
VATH_MOI	>sp Q8BVE3 VATH	3	0	9540909	0	0
RL1D1_MO	>sp Q8BVY0 RL1D	1	0	0	0	0
STEAM2_MO	>sp Q8BWB6 STEAM	1	0	0	0	0
B4GA1_MO	>sp Q8BWP8 B4GA	5	2.10E+08	6751620	2.38E+08	1.82E+08
ERF1_MOU	>sp Q8BWW3 ERF1_	1	0	0	0	0
FA53C_MO	>sp Q8BXQ8 FA53C	1	0	0	16320503	0
BRI3B_MOI	>sp Q8BXV2 BRI3B	1	0	0	0	0
TMX3_MOI	>sp Q8BXZ1 TMX3	1	0	13539175	0	0
CTL2_MOU	>sp Q8BY89 CTL2_	1	0	0	0	19712655
TBCD_MOI	>sp Q8BYA0 TBCD	1	0	0	3976467	0
TENR_MOI	>sp Q8BYI9 TENR_	5	0	0	22778531	33628030
SYFA_MOU	>sp Q8C0C7 SYFA_	3	0	0	0	0
SIIL1_MOU	>sp Q8C0T5 SIIL1_	1	4123145	4236939	0	0
SEP11_MOI	>sp Q8C1B7 SEP11_	1	0	6763171	11905251	0
T120A_MOI	>sp Q8C1E7 T120A_	1	0	0	0	0
HDAC7_MC	>sp Q8C2B3 HDAC7	1	2.10E+08	65719418	59793543	2.00E+08
LMF2_MOI	>sp Q8C3X8 LMF2_	3	25548863	0	0	0
CNOT2_MC	>sp Q8C5L3 CNOT2	1	0	0	0	0
SEP10_MOI	>sp Q8C650 SEP10_	1	0	0	0	0
K0556_MOI	>sp Q8C753 K0556_	2	0	0	3.39E+08	31138044
EMC1_MOI	>sp Q8C7X2 EMC1_	1	0	0	0	0
LIPB1_MOI	>sp Q8C8U0 LIPB1_	1	0	0	0	0
MIC60_MOI	>sp Q8CAQ8 MIC60	2	0	0	0	0
TSK_MOUS	>sp Q8CBR6 TSK_M	1	0	0	0	0
VWA8_MOI	>sp Q8CC88 VWA8_	1	88095469	52543021	0	1.00E+08
PRP31_MOI	>sp Q8CCF0 PRP31_	1	0	0	0	0

PABP2_MO	>sp Q8CCS6 PABP2	1	0	0	0	0
TXNL1_MO	>sp Q8CDN6 TXNL	3	0	6912902	0	0
COL10_MO	>sp Q8CF98 COL10	3	6.01E+08	2.73E+08	6.26E+08	4.83E+08
C1RB_MOU	>sp Q8CFG9 C1RB_	8	0	0	0	0
RIFK_MOU	>sp Q8CFV9 RIFK_	1	0	0	0	0
CS1A_MOU	>sp Q8CG14 CS1A_	8	1.76E+08	1.61E+08	1.05E+08	2.39E+08
C1RA_MOU	>sp Q8CG16 C1RA_	9	1.36E+08	1.49E+08	22419797	47799276
LTBP1_MO	>sp Q8CG19 LTBP1	7	77796639	0	0	29151341
SMC2_MOU	>sp Q8CG48 SMC2_	1	0	0	0	0
SYEP_MOU	>sp Q8CGC7 SYEP_	18	20121743	35406005	74807733	26087231
LONM_MO	>sp Q8CGK3 LONM	11	0	9617486	0	12108417
SEPT8_MO	>sp Q8CHH9 SEPT8	3	0	0	0	0
MBOA7_MC	>sp Q8CHK3 MBOA	1	0	0	0	0
GNL3_MOU	>sp Q8CI11 GNL3_I	1	0	0	0	0
PYGB_MOU	>sp Q8CI94 PYGB_	6	1.16E+08	47730214	75269040	1.48E+08
COPA_MOU	>sp Q8CIE6 COPA_	10	8791997	2.75E+08	4.13E+08	3685602
ANM5_MOU	>sp Q8CIG8 ANM5_	2	0	57514116	28402950	0
VWF_MOU	>sp Q8CIZ8 VWF_M	1	15059046	4482970	2.37E+08	0
BMPER_MC	>sp Q8CJ69 BMPER	5	0	0	0	1.25E+08
HMCS1_MC	>sp Q8JZK9 HMCS1	1	0	0	44380458	0
EIF3B_MOU	>sp Q8JZQ9 EIF3B_	9	0	55623218	4.76E+08	0
ACSL5_MO	>sp Q8JZR0 ACSL5	1	0	0	0	0
TXTP_MOU	>sp Q8JZU2 TXTP_	1	0	0	0	0
SULF1_MO	>sp Q8K007 SULF1	3	17829902	0	0	35347231
AL1L2_MO	>sp Q8K009 AL1L2	3	0	0	0	0
CP51A_MO	>sp Q8K0C4 CP51A	6	0	0	0	0
URP2_MOU	>sp Q8K1B8 URP2_	6	36934769	28445188	83105834	56953544
SPP24_MOU	>sp Q8K1I3 SPP24_	1	0	2.09E+08	1.46E+08	0
TRNT1_MO	>sp Q8K1J6 TRNT1	1	0	0	0	0
DNM1L_MC	>sp Q8K1M6 DNM1	2	0	7866052	17671590	6844343
NAT10_MO	>sp Q8K224 NAT10	1	0	0	0	0
MTMR3_MC	>sp Q8K296 MTMR	1	0	0	50217350	0
GT251_MO	>sp Q8K297 GT251_	2	0	8245515	0	0
ANLN_MOU	>sp Q8K298 ANLN_	2	0	0	0	0
SDHA_MOU	>sp Q8K2B3 SDHA_	4	0	0	7994181	0
S38A1_MOU	>sp Q8K2P7 S38A1_	2	0	0	0	0
IPO11_MOU	>sp Q8K2V6 IPO11_	1	0	0	0	0
EVA1B_MO	>sp Q8K2Y3 EVA1B	1	0	0	0	0
CND1_MOU	>sp Q8K2Z4 CND1_	1	0	0	0	0
MATR3_MC	>sp Q8K310 MATR3	4	5840787	5250024	0	4201257
CHAP1_MO	>sp Q8K327 CHAP1	1	7.32E+08	3.10E+08	0	0
PREP_MOU	>sp Q8K411 PREP_	7	93554593	42678264	35081049	23722008
EMIL2_MO	>sp Q8K482 EMIL2	6	36476401	0	1.25E+08	0
LTBP4_MO	>sp Q8K4G1 LTBP4	15	1.10E+09	71841309	1.31E+08	1.25E+09
SF3A1_MOU	>sp Q8K4Z5 SF3A1	2	0	0	3.12E+08	9.94E+08
MCFD2_MC	>sp Q8K5B2 MCFD	1	0	0	0	0
OAF_MOUS	>sp Q8QZR4 OAF_M	3	0	0	9846193	0

ALAT1_MO	>sp Q8QZR5 ALAT	2	0	0	0	0
HIBCH_MO	>sp Q8QZS1 HIBCH	1	0	0	0	0
THIL_MOU	>sp Q8QZT1 THIL_	2	0	0	0	0
EIF3L_MOI	>sp Q8QZY1 EIF3L	5	11917572	13831794	5384268	0
SF3B4_MOI	>sp Q8QZY9 SF3B4	1	0	0	0	0
MARE2_MC	>sp Q8R001 MARE2	4	2.00E+08	12731907	35748588	1.21E+08
AIMP2_MO	>sp Q8R010 AIMP2	2	0	12702817	0	0
BLMH_MOI	>sp Q8R016 BLMH	4	0	0	0	0
ERF3A_MO	>sp Q8R050 ERF3A	5	0	1.13E+08	0	0
HNRPL_MC	>sp Q8R081 HNRPL	7	43654405	49899186	9612012	46943905
NU133_MOI	>sp Q8R0G9 NU133	1	1.16E+08	78600629	44985584	1.03E+08
GGA1_MOI	>sp Q8R0H9 GGA1_	1	0	0	0	0
AL1L1_MOI	>sp Q8R0Y6 AL1L1	3	1.20E+08	77976034	19785734	49144186
ERO1A_MC	>sp Q8R180 ERO1A	11	4.97E+08	2.08E+08	96651981	0
EIF3C_MOI	>sp Q8R1B4 EIF3C_	4	0	18664280	9895580	0
NIBL1_MOI	>sp Q8R1F1 NIBL1_	7	45041898	4.02E+08	22854783	14982210
DC1L1_MO	>sp Q8R1Q8 DC1L1	2	0	0	13484278	0
RRF2M_MC	>sp Q8R2Q4 RRF2M	2	0	41290464	52276950	0
PTH2_MOU	>sp Q8R2Y8 PTH2_	4	0	0	0	0
PSPC1_MOI	>sp Q8R326 PSPC1_	1	0	0	0	0
IGSF8_MOI	>sp Q8R366 IGSF8_	1	0	0	0	0
TSN8_MOU	>sp Q8R3G9 TSN8_	1	0	0	0	2.66E+08
MIC13_MOI	>sp Q8R404 MIC13_	1	0	0	0	0
CD109_MOI	>sp Q8R422 CD109_	4	4085155	0	0	15212705
NUP85_MOI	>sp Q8R480 NUP85_	2	26694783	5789058	43986990	20761515
OIT3_MOU	>sp Q8R4V5 OIT3_I	1	36429945	7842523	0	57319376
ACTY_MOI	>sp Q8R5C5 ACTY_	6	0	0	0	0
PRAF3_MO	>sp Q8R5J9 PRAF3_	3	0	29130532	12463976	15885160
FIBG_MOU	>sp Q8VCM7 FIBG_	8	2.45E+09	1.92E+09	1.38E+09	1.90E+09
NCLN_MOI	>sp Q8VCM8 NCLN	3	0	0	0	0
CGL_MOU	>sp Q8VCN5 CGL_	2	0	0	0	0
MYH9_MOI	>sp Q8VDD5 MYH9	111	3.19E+09	4.37E+09	6.35E+09	4.69E+09
VIGLN_MO	>sp Q8VDJ3 VIGLN	3	0	0	0	0
PSMD2_MO	>sp Q8VDM4 PSMI	14	88877999	1.08E+08	52830519	81097423
HNRL1_MC	>sp Q8VDM6 HNRI	2	0	0	0	0
AT1A1_MO	>sp Q8VDN2 AT1A	10	10601312	41345223	95520422	56372018
DX39A_MO	>sp Q8VDW0 DX39	8	0	5344997	0	0
RCC1_MOU	>sp Q8VE37 RCC1_	4	0	0	0	0
CC115_MOI	>sp Q8VE99 CC115_	1	0	0	0	0
LEGL_MOU	>sp Q8VED9 LEGL_	2	0	10033313	0	20815439
RFA1_MOU	>sp Q8VEE4 RFA1_	4	0	0	0	0
ARL8B_MO	>sp Q9CQW2 ARL8	1	0	4255762	5874610	0
EPMIP_MO	>sp Q8VEH5 EPMII	1	1.02E+09	4.20E+08	3.00E+08	9.96E+08
CBWD1_MC	>sp Q8VEH6 CBWI	1	0	0	0	0
HNRPU_MC	>sp Q8VEK3 HNRP	14	7771921	71558957	31409587	0
MPCP_MOI	>sp Q8VEM8 MPCF	8	0	95173798	1.30E+08	3.16E+08
RBM39_MO	>sp Q8VH51 RBM39	2	0	0	0	0

FLNC_MOU	>sp Q8VHX6 FLNC	12	92616177	1.47E+08	36332006	22696409
CSPG4_MO	>sp Q8VHY0 CSPG	21	1.13E+08	0	64979178	76380723
PAXI_MOU	>sp Q8VI36 PAXI_M	1	0	0	0	0
IPO4_MOU	>sp Q8VI75 IPO4_M	2	0	4500082	0	0
SFPQ_MOU	>sp Q8VIJ6 SFPQ_M	5	15151958	27819737	7295708	15584882
BACH_MOU	>sp Q91V12 BACH_	2	8745644	19442886	11636065	30733091
RAB14_MO	>sp Q91V41 RAB14	1	0	0	0	0
SFXN3_MO	>sp Q91V61 SFXN3	2	0	0	0	0
ACLY_MOU	>sp Q91V92 ACLY_	24	3.44E+08	3.23E+08	1.01E+09	2.63E+08
PDIP2_MOU	>sp Q91VA6 PDIP2_	1	0	0	0	0
IF4A3_MOU	>sp Q91VC3 IF4A3_	3	0	0	0	0
NDUS1_MO	>sp Q91VD9 NDUS	4	0	0	0	0
MEMO1_M	>sp Q91VH6 MEMC	1	0	38773687	0	0
RINI_MOU	>sp Q91VI7 RINI_M	7	0	0	0	0
RMXL1_MC	>sp Q91VM5 RMXI	1	0	0	0	0
ATPG_MOU	>sp Q91VR2 ATPG_	5	0	4299869	54778863	0
DDX1_MOU	>sp Q91VR5 DDX1_	4	0	0	0	0
FAM3C_MC	>sp Q91VU0 FAM3C	1	0	0	0	0
SH3L3_MO	>sp Q91VW3 SH3L3	1	0	17980648	0	0
TXND5_MO	>sp Q91W90 TXND	10	23706099	1.83E+08	1.11E+08	7979903
NDUS2_MO	>sp Q91WD5 NDUS	1	0	0	0	0
FUBP1_MO	>sp Q91WJ8 FUBP1	1	0	0	0	0
EIF3H_MO	>sp Q91WK2 EIF3H	8	0	31027420	22626843	7220008
DNJC9_MO	>sp Q91WN1 DNJC9	1	0	0	0	0
SYYC_MOU	>sp Q91WQ3 SYYC	1	0	0	0	0
UXS1_MOU	>sp Q91XL3 UXS1_	1	0	0	0	12832680
FA11_MOU	>sp Q91Y47 FA11_M	1	30805644	41942439	35653613	34041442
WASL_MOU	>sp Q91YD9 WASL	1	3.14E+08	4.56E+08	4.54E+08	2.01E+08
ATLA3_MO	>sp Q91YH5 ATLA3	3	0	6156115	8767006	0
SNX4_MOU	>sp Q91YJ2 SNX4_M	1	0	0	0	0
NEUL_MOU	>sp Q91YP2 NEUL_	1	0	0	0	0
RPN1_MOU	>sp Q91YQ5 RPN1_	12	0	1.42E+08	1.13E+08	49865277
TWF1_MOU	>sp Q91YR1 TWF1_	3	0	0	0	0
NDUV1_MC	>sp Q91YT0 NDUV	3	0	0	31528985	0
DNJC3_MO	>sp Q91YW3 DNJC3	3	0	0	0	0
PTBP2_MO	>sp Q91Z31 PTBP2_	2	0	0	0	0
GRHPR_MC	>sp Q91Z53 GRHPR	1	0	0	0	0
SRGP2_MO	>sp Q91Z67 SRGP2_	2	0	0	0	0
UGPA_MOU	>sp Q91ZJ5 UGPA_	11	98952807	41809391	55313437	19793011
DYST_MOU	>sp Q91ZU6 DYST_	3	0	22742119	7120411	0
LRP1_MOU	>sp Q91ZX7 LRP1_	78	2.90E+09	3.03E+09	3.16E+09	3.15E+09
RISC_MOU	>sp Q920A5 RISC_M	3	5844194	15372748	18235742	8719498
SP16H_MO	>sp Q920B9 SP16H_	2	7.00E+08	2.93E+08	0	0
FPPS_MOU	>sp Q920E5 FPPS_M	3	0	0	0	3614022
BICD2_MO	>sp Q921C5 BICD2_	1	4.45E+08	0	40234121	3.78E+08
TADBP_MC	>sp Q921F2 TADBP	5	0	15658094	12188277	0
TRFE_MOU	>sp Q921I1 TRFE_M	15	74729495	0	0	2.86E+08

TMCO1_MC>sp Q921L3 TMCO1	1	0	0	0	0
SF3B3_MOU>sp Q921M3 SF3B3	4	0	0	0	0
DDX27_MO>sp Q921N6 DDX27	1	8.53E+09	4.44E+09	6.44E+09	8.30E+09
TOIP1_MO>sp Q921T2 TOIP1	1	0	0	0	0
PDIA5_MO>sp Q921X9 PDIA5	1	0	0	0	0
SYDC_MO>sp Q922B2 SYDC	5	42319563	48470317	41778143	35776502
PP6R3_MO>sp Q922D4 PP6R3	1	0	0	0	0
C1TC_MO>sp Q922D8 C1TC	5	0	0	0	0
TBB6_MO>sp Q922F4 TBB6	16	13881122	1.12E+08	54835848	13564345
LRC59_MO>sp Q922Q8 LRC59	7	0	1.07E+08	20378106	68014158
PDIA6_MO>sp Q922R8 PDIA6	10	0	48808283	1.10E+08	82757413
UBXN1_MO>sp Q922Y1 UBXN1	1	0	0	0	0
SF3B5_MO>sp Q923D4 SF3B5	1	0	0	0	0
TALDO_MC>sp Q93092 TALDO	2	0	0	0	0
ROAA_MO>sp Q99020 ROAA	5	0	40549933	5213042	35650681
MEP50_MO>sp Q99J09 MEP50	2	0	0	0	0
DERL1_MO>sp Q99J56 DERL1	1	0	6548840	0	0
RFC4_MO>sp Q99J62 RFC4	2	0	0	0	0
SIAS_MO>sp Q99J77 SIAS	3	0	0	0	0
THTM_MO>sp Q99J99 THTM	3	0	0	0	0
STML2_MO>sp Q99JB2 STML2	3	0	4343933	4090166	7611322
PSMD6_MO>sp Q99JI4 PSMD6	5	16113086	47931282	15317567	0
RAP1B_MO>sp Q99JI6 RAP1B	9	2.51E+08	99708532	3.30E+08	2.53E+08
SFXN1_MO>sp Q99JR1 SFXN1	5	0	0	0	4386182
TINAL_MO>sp Q99JR5 TINAL	17	1.57E+08	1.82E+08	4.75E+08	5.28E+09
STK26_MO>sp Q99JT2 STK26	2	0	0	0	0
LIMS1_MO>sp Q99JW4 LIMS1	3	18272785	41541158	3.76E+08	98823375
GORS2_MO>sp Q99JX3 GORS2	1	0	0	0	0
EIF3M_MO>sp Q99JX4 EIF3M	1	0	26325842	0	21255283
PLPP3_MO>sp Q99JY8 PLPP3	1	0	0	0	0
ARP3_MO>sp Q99JY9 ARP3	15	2.07E+08	2.30E+08	2.69E+08	3.38E+08
EMIL1_MO>sp Q99K41 EMIL1	2	57603663	0	0	0
PRC1_MO>sp Q99K43 PRC1	1	0	0	0	0
NONO_MO>sp Q99K48 NONO	4	0	0	30378430	0
PLST_MO>sp Q99K51 PLST	3	0	0	0	0
SERC_MO>sp Q99K85 SERC	6	46791749	13866874	83632266	50612802
MAOM_MC>sp Q99KE1 MAOM	12	0	0	3.24E+08	15231737
TMED9_MC>sp Q99KF1 TMED9	2	4481065	23515162	0	0
ACON_MO>sp Q99KI0 ACON	11	19847135	54211461	1.38E+08	39775282
DCTN2_MO>sp Q99KJ8 DCTN2	1	0	0	0	0
DPP3_MO>sp Q99KK7 DPP3	3	0	0	20006890	0
PRP19_MO>sp Q99KP6 PRP19	7	0	0	10678717	4190261
LACB2_MO>sp Q99KR3 LACB2	1	0	0	36980549	0
VMP1_MO>sp Q99KU0 VMP1	1	0	0	0	0
DJB11_MO>sp Q99KV1 DJB11	6	32701058	66476633	14892622	0
3HIDH_MO>sp Q99L13 3HIDH	1	0	0	0	0
IF2B_MO>sp Q99L45 IF2B	1	0	0	0	0

F10A1_MOU>sp Q99L47 F10A1_	3	39170863	23618263	16584533	51618312
MAT2B_MC>sp Q99LB6 MAT2I	2	0	0	0	0
NDUAA_MC>sp Q99LC3 NDUA.	2	0	28247970	18915491	0
ETF_A_MOU>sp Q99LC5 ETF_A_	6	0	0	13920621	0
CSN1_MOU>sp Q99LD4 CSN1_	1	0	5971731	12656368	0
ABCF2_MO>sp Q99LE6 ABCF2	1	0	0	0	0
RTCB_MOU>sp Q99LF4 RTCB_	6	22564308	0	53335243	0
GRPE1_MO>sp Q99LP6 GRPE1.	2	0	17031348	12297634	0
SERB_MOU>sp Q99LS3 SERB_	2	0	0	0	0
DPY30_MO>sp Q99LT0 DPY30	1	0	0	0	0
PARK7_MO>sp Q99LX0 PARK7	2	0	0	0	0
NDUS5_MO>sp Q99LY9 NDUS5	1	0	0	0	0
HSP7E_MO>sp Q99M31 HSP7E	2	0	0	0	0
EPDR1_MO>sp Q99M71 EPDR1	2	0	15429646	12270498	30752122
NASP_MOU>sp Q99MD9 NASP.	4	0	0	0	0
SYK_MOUS>sp Q99MN1 SYK_	3	0	6834614	6210822	0
ASPN_MOU>sp Q99MQ4 ASPN.	1	19598336	31720892	31762352	0
SRRT_MOU>sp Q99MR6 SRRT_	1	0	0	0	0
RM01_MOU>sp Q99N96 RM01_	1	0	0	0	0
SF3B1_MOU>sp Q99NB9 SF3B1.	4	0	7284665	0	14385882
RTN4_MOU>sp Q99P72 RTN4_	6	92938273	1.38E+08	4.74E+08	88482796
NU155_MOU>sp Q99P88 NU155_	3	0	0	0	0
RRBP1_MO>sp Q99PL5 RRBP1.	2	0	0	0	0
GDIR1_MO>sp Q99PT1 GDIR1_	9	41815771	0	1.21E+08	73967921
PRP8_MOU>sp Q99PV0 PRP8_	2	0	0	0	0
NPM3_MOU>sp Q99CPP0 NPM3_	1	0	0	0	0
NDUA5_MO>sp Q99CPP6 NDUA5	1	0	0	0	0
TOM22_MC>sp Q99CPQ3 TOM22	1	0	0	0	0
RL17_MOU>sp Q99CPR4 RL17_	2	0	0	0	0
GLOD4_MC>sp Q99CPV4 GLOD4	2	0	0	0	0
AMPL_MOU>sp Q99CPY7 AMPL.	6	0	10426466	0	0
NUDC2_MO>sp Q99CQ48 NUDC2	1	0	0	0	0
NDUC2_MO>sp Q99CQ54 NDUC2	1	0	0	0	0
DECR_MOU>sp Q99CQ62 DECR.	1	0	0	0	0
MTAP_MOU>sp Q99CQ65 MTAP.	6	47225341	55203969	58442184	59923553
RFA3_MOU>sp Q99CQ71 RFA3_	2	0	0	0	0
FIS1_MOUS>sp Q99CQ92 FIS1_M	1	0	0	0	0
BZW1_MOU>sp Q99CQC6 BZW1.	3	0	0	0	0
SAR1B_MO>sp Q99CQC9 SAR1B	2	0	0	4935443	0
NPS3B_MO>sp Q99CQE1 NPS3B	3	0	0	0	0
RTRAF_MC>sp Q99CQE8 RTRAF.	4	0	4104833	0	0
CPSF5_MO>sp Q99CQF3 CPSF5	2	0	0	0	0
PCYOX_MC>sp Q99CQF9 PCYOX.	3	3.04E+08	37768772	13954269	1.65E+08
COTL1_MO>sp Q99CQI6 COTL1	1	0	0	0	0
RU2B_MOU>sp Q99CQI7 RU2B_	1	0	0	0	0
NDUB9_MO>sp Q99CQJ8 NDUB9	3	0	0	0	0
RWDD1_MC>sp Q99CQK7 RWDD1	1	0	0	0	0

GLRX3_MO	>sp Q9CQM9 GLRX3	3	0	15351786	27162848	0
TRAP1_MO	>sp Q9CQN1 TRAP1	2	0	0	0	0
AT5F1_MO	>sp Q9CQ7 AT5F1	2	0	2771963	7529889	0
ACO13_MO	>sp Q9CQR4 ACO13	1	0	0	8735257	0
NOP10_MO	>sp Q9CQS2 NOP10	1	31334212	0	0	0
MTNA_MO	>sp Q9CQT1 MTNA	2	0	0	0	0
DESI1_MO	>sp Q9CQT7 DESI1	1	0	0	0	0
TXD12_MO	>sp Q9CQU0 TXD12	1	0	0	0	0
1433B_MO	>sp Q9CQV8 1433B	6	24566056	20629617	51517150	22289341
CYB5B_MO	>sp Q9CQX2 CYB5B	2	0	62010348	0	0
TMA16_MO	>sp Q9CR02 TMA16	1	0	0	0	0
PPID_MO	>sp Q9CR16 PPID_M	2	0	0	0	0
HYPK_MO	>sp Q9CR41 HYPK_M	1	0	0	0	0
VATG1_MO	>sp Q9CR51 VATG1	1	0	0	0	0
RL14_MO	>sp Q9CR57 RL14_M	3	0	39697746	31200642	33356299
UCRI_MO	>sp Q9CR68 UCRI_M	3	0	0	0	5167646
CHSP1_MO	>sp Q9CR86 CHSP1	2	0	0	0	0
LRC40_MO	>sp Q9CRC8 LRC40	1	0	1751862	0	0
OCAD1_MC	>sp Q9CRD0 OCAD1	1	0	0	0	0
EMC2_MO	>sp Q9CRD2 EMC2_M	3	0	0	0	0
PRPS2_MO	>sp Q9CS42 PRPS2_M	4	0	25404777	40828393	0
RRP44_MO	>sp Q9CSH3 RRP44	2	0	0	0	0
ARPC2_MO	>sp Q9CVB6 ARPC2	11	88831542	68453092	2.38E+08	89232435
SMC3_MO	>sp Q9CW03 SMC3_M	1	0	0	0	0
PUR9_MO	>sp Q9CWJ9 PUR9_M	8	1.35E+08	55028569	29887274	1.16E+08
RBM8A_MC	>sp Q9CWZ3 RBM8A	1	0	0	0	0
SGT1_MO	>sp Q9CX34 SGT1_M	1	0	0	0	0
PSMD8_MO	>sp Q9CX56 PSMD8	2	1.46E+08	73830602	3.95E+08	1.89E+08
TMED5_MC	>sp Q9CXE7 TMED5	1	0	0	0	0
MANF_MO	>sp Q9CXI5 MANF_M	2	35636060	0	0	28550784
NIP7_MO	>sp Q9CXK8 NIP7_M	2	0	0	0	0
MPPB_MO	>sp Q9CXT8 MPPB_M	2	0	0	0	0
RT22_MO	>sp Q9CXW2 RT22_M	1	0	0	0	0
CYBP_MO	>sp Q9CXW3 CYBP_M	2	0	0	0	0
RL11_MO	>sp Q9CXW4 RL11_M	3	0	21117743	22686270	0
ILF2_MO	>sp Q9CXY6 ILF2_M	1	0	0	0	0
RT28_MO	>sp Q9CY16 RT28_M	1	0	0	0	0
SSRA_MO	>sp Q9CY50 SSRA_M	1	0	22248432	0	0
PAIRB_MO	>sp Q9CY58 PAIRB_M	3	0	0	35390396	0
BIEA_MO	>sp Q9CY64 BIEA_M	1	0	0	0	0
CREL2_MO	>sp Q9CYA0 CREL2_M	2	0	0	0	0
TOM34_MC	>sp Q9CYG7 TOM34	1	15169508	16820013	0	0
GAPR1_MO	>sp Q9CYL5 GAPR1	1	0	0	0	0
RENR_MO	>sp Q9CYN9 RENR_M	3	0	0	0	10552783
TPD54_MO	>sp Q9CZZ2 TPD54	1	0	0	0	0
CSN7A_MO	>sp Q9CZ04 CSN7A	1	0	0	0	0
QCR1_MO	>sp Q9CZ13 QCR1_M	10	0	11877581	29564359	66815158

OLA1_MOU	>sp Q9CZ30 OLA1_	3	29511063	0	0	25592406
GARS_MOU	>sp Q9CZD3 GARS_	15	17039114	1.22E+08	1.15E+08	26190848
RL15_MOU	>sp Q9CZM2 RL15_	4	43336438	1.02E+08	47058753	30374659
GLYM_MO	>sp Q9CZN7 GLYM	17	0	58686302	58889924	13738803
EFTS_MOU	>sp Q9CZR8 EFTS_	2	0	0	0	0
CISY_MOU	>sp Q9CZU6 CISY_	9	19916303	1.13E+08	1.21E+08	67050940
TOM70_MC	>sp Q9CZW5 TOM7	1	0	0	0	0
RS19_MOU	>sp Q9CZX8 RS19_	2	0	14783233	12189362	7787577
UB2V2_MO	>sp Q9D2M8 UB2V	1	0	0	0	0
ODPB_MOU	>sp Q9D051 ODPB_	2	0	0	0	0
MMS19_MC	>sp Q9D071 MMS19	1	0	0	0	0
HNRPM_MC	>sp Q9D0E1 HNRPM	4	0	22430249	0	17094733
RFC5_MOU	>sp Q9D0F6 RFC5_	1	0	0	1.01E+08	0
PGM1_MOU	>sp Q9D0F9 PGM1_	10	2.14E+08	1.18E+08	1.65E+08	1.75E+08
SYRC_MOU	>sp Q9D0I9 SYRC_	8	0	38578607	49351721	26960577
SCOT1_MO	>sp Q9D0K2 SCOT1	5	44512297	15791569	20754750	0
ARM10_MC	>sp Q9D0L7 ARM10	1	0	0	0	0
CY1_MOUS	>sp Q9D0M3 CY1_1	1	0	17652521	31781347	0
SYTC_MOU	>sp Q9D0R2 SYTC_	12	47722939	1.77E+08	1.27E+08	1.74E+08
LSM12_MO	>sp Q9D0R8 LSM12	1	0	0	0	0
HINT2_MO	>sp Q9D0S9 HINT2	1	0	0	0	0
CNDP2_MO	>sp Q9D1A2 CNDP2	1	0	0	14152360	0
TMEDA_MC	>sp Q9D1D4 TMED	3	0	36768992	18281872	23912326
RAB1B_MO	>sp Q9D1G1 RAB1B	4	19162680	5989271	11918819	26656069
VATF_MOU	>sp Q9D1K2 VATF_	2	0	0	0	0
SEC13_MO	>sp Q9D1M0 SEC13	2	0	0	0	0
MCA3_MOU	>sp Q9D1M4 MCA3	3	0	0	0	0
FKB11_MO	>sp Q9D1M7 FKB11	1	0	0	0	0
CHRD1_MC	>sp Q9D1P4 CHRD1	1	0	0	0	0
ERP44_MO	>sp Q9D1Q6 ERP44	3	0	0	0	0
SPF27_MO	>sp Q9D287 SPF27_	2	0	0	0	0
ODO2_MOU	>sp Q9D2G2 ODO2_	3	0	18309202	14366732	17485941
HYEP_MOU	>sp Q9D379 HYEP_	7	0	0	5404077	56968346
ATPD_MOU	>sp Q9D3D9 ATPD_	1	21835461	3183683	13936631	2681149
SF3A3_MO	>sp Q9D554 SF3A3_	6	0	0	0	0
SC23B_MO	>sp Q9D662 SC23B_	5	0	9863046	0	0
IDH3A_MO	>sp Q9D6R2 IDH3A	3	0	23033026	0	0
F162A_MO	>sp Q9D6U8 F162A	3	0	28417809	7600984	0
PRS23_MO	>sp Q9D6X6 PRS23	1	0	0	0	0
NOP56_MO	>sp Q9D6Z1 NOP56	5	19948306	17922894	0	0
RTCA_MOU	>sp Q9D7H3 RTCA_	1	0	0	0	0
GID8_MOU	>sp Q9D7M1 GID8_	1	0	0	0	0
RT09_MOU	>sp Q9D7N3 RT09_	1	0	0	0	0
APMAP_MC	>sp Q9D7N9 APMA	1	0	0	0	0
RL22L_MO	>sp Q9D7S7 RL22L	1	0	0	0	0
IPYR_MOU	>sp Q9D819 IPYR_1	4	20326150	0	16138422	17148656
PRXD1_MO	>sp Q9D820 PRXD1	1	0	0	0	0

QCR7_MOU	>sp Q9D855 QCR7_	2	0	0	0	42012569
U2AF1_MO	>sp Q9D883 U2AF1	2	0	0	0	0
RL4_MOUS	>sp Q9D8E6 RL4_M	4	46922859	42662435	1.01E+08	34645171
EF1G_MOU	>sp Q9D8N0 EF1G_	13	82940892	2.49E+08	1.88E+08	2.35E+08
ORN_MOU	>sp Q9D8S4 ORN_M	1	0	0	0	0
GSDMD_MC	>sp Q9D8T2 GSDM	1	0	0	0	0
SLIRP_MO	>sp Q9D8T7 SLIRP_	1	0	0	0	0
HM13_MO	>sp Q9D8V0 HM13_	1	0	0	0	0
PSD12_MO	>sp Q9D8W5 PSD12	8	22347512	55007178	49142776	60071577
ACTT1_MO	>sp Q9D9J3 ACTT1	1	0	0	0	0
DCPS_MO	>sp Q9DAR7 DCPS_	1	0	0	0	0
PRP4_MO	>sp Q9DAW6 PRP4_	1	0	0	0	69030241
CNN3_MO	>sp Q9DAW9 CNN3_	4	0	17393699	0	0
SNAAMC	>sp Q9DB05 SNAAMC	4	3.44E+08	11858757	15493678	1.71E+08
ATPO_MO	>sp Q9DB20 ATPO_	6	0	79747147	5.11E+08	58194836
NB5R1_MO	>sp Q9DB73 NB5R1	1	0	0	0	0
QCR2_MO	>sp Q9DB77 QCR2_	6	0	0	19910015	0
KAP0_MO	>sp Q9DBC7 KAP0_	2	0	0	16759830	90962209
AP2B1_MO	>sp Q9DBG3 AP2B1	14	82126360	87434804	98231280	53740351
PLIN3_MO	>sp Q9DBG5 PLIN3	3	0	4337516	0	0
RPN2_MO	>sp Q9DBG6 RPN2_	12	65304042	82741782	78433064	12478479
SRPRA_MO	>sp Q9DBG7 SRPRA	1	0	0	0	0
TX1B3_MO	>sp Q9DBG9 TX1B3	1	0	0	0	0
LMAN2_MC	>sp Q9DBH5 LMAN2	3	19987536	23815054	62520682	18082269
PGAM1_MC	>sp Q9DBJ1 PGAM1	7	1.45E+08	1.50E+08	86378401	2.10E+08
BI2L1_MO	>sp Q9DBJ3 BI2L1_	3	0	0	1.29E+08	0
ACDSB_MC	>sp Q9DBL1 ACDSB	1	0	0	0	0
NPT2B_MO	>sp Q9DBP0 NPT2B	1	1.17E+08	51743026	22702823	1.33E+08
KCY_MO	>sp Q9DBP5 KCY_I	2	0	0	0	0
TMM43_MC	>sp Q9DBS1 TMM43	4	26874414	0	0	0
CP2S1_MO	>sp Q9DBX6 CP2S1	2	0	0	0	0
EIF3K_MO	>sp Q9DBZ5 EIF3K_	2	0	0	0	0
ERGI1_MO	>sp Q9DC16 ERGI1_	2	0	37103108	31377025	0
OCTC_MO	>sp Q9DC50 OCTC_	2	0	0	0	0
GNAI3_MO	>sp Q9DC51 GNAI3	5	0	0	0	0
MPPA_MO	>sp Q9DC61 MPPA_	1	0	0	0	0
NDUA9_MC	>sp Q9DC69 NDUA9	3	0	0	0	0
6PGD_MO	>sp Q9DCD0 6PGD_	12	2.05E+08	1.43E+08	1.85E+08	1.19E+08
SSRG_MO	>sp Q9DCF9 SSRG_	1	0	0	0	0
TR112_MO	>sp Q9DCG9 TR112	1	0	0	0	0
EIF3F_MO	>sp Q9DCH4 EIF3F_	5	0	22733990	0	0
NDUA8_MC	>sp Q9DCJ5 NDUA8	1	0	0	0	0
TSN4_MO	>sp Q9DCK3 TSN4_	1	0	0	0	18336026
PUR6_MO	>sp Q9DCL9 PUR6_	7	52553355	74352525	70816069	52339404
ETHE1_MO	>sp Q9DCM0 ETHE1	2	0	0	0	0
NB5R3_MO	>sp Q9DCN2 NB5R3	11	9323972	1.07E+08	2.47E+08	51346581
MECR_MO	>sp Q9DCS3 MECR_	2	0	0	0	0

NDUBA_MC	>sp Q9DCS9 NDUB	5	0	0	7230853	0
NDUS3_MO	>sp Q9DCT2 NDUS	1	0	0	0	0
ATP5H_MO	>sp Q9DCX2 ATP5I	6	20380865	25913010	93151474	61253660
GMPR1_MC	>sp Q9DCZ1 GMPR	1	0	0	0	0
PARVA_MC	>sp Q9EPC1 PARVA	1	0	0	0	0
CSTN1_MO	>sp Q9EPL2 CSTN1	1	0	0	0	0
IPO7_MO	>sp Q9EPL8 IPO7_M	7	0	22985540	0	9946411
GLCE_MO	>sp Q9EPS3 GLCE_	1	0	0	0	0
RENT1_MO	>sp Q9EPU0 RENT1	2	0	0	0	0
PPN_MO	>sp Q9EPX2 PPN_M	1	0	0	0	0
MMSA_MO	>sp Q9EQ20 MMSA	1	0	0	0	49938232
DPYL5_MO	>sp Q9EQF6 DPYL5	2	0	0	0	0
VPS35_MO	>sp Q9EQH3 VPS35	15	1.04E+08	1.62E+08	1.86E+08	68055393
RM46_MO	>sp Q9EQI8 RM46_	1	0	768209.6	0	0
MVP_MO	>sp Q9EQK5 MVP_	3	0	0	0	0
EHD4_MO	>sp Q9EQP2 EHD4_	6	0	0	83686538	1.04E+08
OGA_MO	>sp Q9EQQ9 OGA_	2	0	0	0	0
SET_MO	>sp Q9EQU5 SET_M	5	0	0	0	0
RPGF4_MO	>sp Q9EQZ6 RPGF4	1	0	28385296	1.04E+08	0
SYCC_MO	>sp Q9ER72 SYCC_	3	0	0	0	0
TBB3_MO	>sp Q9ERD7 TBB3_	15	0	0	0	0
MESD_MO	>sp Q9ERE7 MESD_	1	0	0	0	0
XPO2_MO	>sp Q9ERK4 XPO2_	3	10493947	22943187	11287371	0
SEP15_MO	>sp Q9ERR7 SEP15	2	0	0	6062118	0
UBE4B_MO	>sp Q9ES00 UBE4B	1	0	0	0	0
C1QT3_MO	>sp Q9ES30 C1QT3	2	7.06E+08	1.04E+09	1.34E+09	9.55E+08
PARVB_MC	>sp Q9ES46 PARVB	1	1.33E+09	5.42E+08	35379542	0
SDF2L_MO	>sp Q9ESP1 SDF2L	1	0	0	0	0
AN32B_MO	>sp Q9EST5 AN32B	3	0	0	0	0
PYGL_MO	>sp Q9ET01 PYGL_	8	2.29E+08	89030517	1.67E+08	2.19E+08
TM9S3_MO	>sp Q9ET30 TM9S3	1	0	0	0	0
TMOD3_MC	>sp Q9JHJ0 TMOD3	1	0	0	0	0
PLEK_MO	>sp Q9JHK5 PLEK_	1	73781788	11362075	70946321	80706215
IDE_MO	>sp Q9JHR7 IDE_M	2	2.13E+08	71122596	5.16E+08	0
DYHC1_MC	>sp Q9JHU4 DYHC	37	1.60E+08	3.15E+08	2.37E+08	1.61E+08
ANM1_MO	>sp Q9JIF0 ANM1_	5	0	0	0	0
COPB_MO	>sp Q9JIF7 COPB_M	6	0	18360967	45015434	38740167
DAZP1_MO	>sp Q9JII5 DAZP1_	3	0	0	0	0
AK1A1_MO	>sp Q9JII6 AK1A1_	3	86672876	41350784	65801390	56652208
DDX21_MO	>sp Q9JIK5 DDX21_	3	88892452	0	35322557	73496356
ACINU_MO	>sp Q9JIX8 ACINU_	2	0	0	5930239	0
RNAS4_MO	>sp Q9JJH1 RNAS4	1	51182380	6076116	22304199	88769329
NSMA2_MC	>sp Q9JJY3 NSMA2	1	0	0	0	0
DDX20_MO	>sp Q9JJY4 DDX20_	1	0	0	0	0
GNA1_MO	>sp Q9JK38 GNA1_	2	0	0	0	0
SHLB1_MO	>sp Q9JK48 SHLB1_	1	0	0	0	0
PRELP_MO	>sp Q9JK53 PRELP_	3	23951801	46673535	46407496	0

IQGA1_MO	>sp Q9JKF1 IQGA1	18	1.69E+08	2.89E+08	4.75E+08	1.29E+08
RM39_MOU	>sp Q9JKF7 RM39_	2	0	0	0	0
CHP3_MOU	>sp Q9JKL5 CHP3_	1	0	0	0	0
HYOU1_MC	>sp Q9JKR6 HYOU	16	6604115	62113021	82275481	24454731
SC5A3_MOI	>sp Q9JKZ2 SC5A3	1	0	33598528	72384513	2.64E+08
SACS_MOU	>sp Q9JLC8 SACS_	2	1.53E+09	5.17E+08	4.34E+08	1.64E+09
CAN15_MO	>sp Q9JLG8 CAN15	1	88648815	16834130	89314485	70300081
AL9A1_MO	>sp Q9JLJ2 AL9A1_	2	0	0	40882665	0
ARPC3_MO	>sp Q9JM76 ARPC3	2	10300895	43139865	23787437	22963911
UBP14_MOI	>sp Q9JMA1 UBP14	3	0	0	0	0
TRXR1_MO	>sp Q9JMH6 TRXR	3	0	10121013	0	0
MY18A_MC	>sp Q9JMH9 MY18	8	0	0	0	10414380
B4GT5_MO	>sp Q9JMK0 B4GT5	1	61446110	14363556	51066698	53984592
RHOA_MOI	>sp Q9QUI0 RHOA_	6	1.71E+08	1.01E+08	1.58E+08	2.00E+08
ACSL4_MO	>sp Q9QUJ7 ACSL4	3	0	0	0	0
PSA6_MOU	>sp Q9QUM9 PSA6	9	4.91E+08	3.63E+08	6.41E+08	2.73E+08
PPCE_MOU	>sp Q9QUR6 PPCE_	7	0	43477831	29390690	0
NAGAB_MC	>sp Q9QWR8 NAGAB	1	0	0	14027807	0
COPG2_MC	>sp Q9QXK3 COPG	3	0	0	0	0
PLEC_MOU	>sp Q9QXS1 PLEC_	82	4.51E+08	1.14E+09	8.83E+08	3.04E+08
CNPY2_MO	>sp Q9QXT0 CNPY	2	0	0	0	0
CMC2_MOU	>sp Q9QXX4 CMC2	5	0	0	0	0
EHD3_MOU	>sp Q9QXY6 EHD3	11	2.27E+08	71045591	1.02E+08	2.44E+08
TOM40_MC	>sp Q9QYA2 TOM4	2	0	0	0	0
CLIC4_MOI	>sp Q9QYB1 CLIC4	9	0	2656969	13314409	33460974
ADDG_MOI	>sp Q9QYB5 ADDC	1	0	0	0	0
ADDA_MOU	>sp Q9QYC0 ADDA	3	3604178	0	0	3026470
DNJA2_MO	>sp Q9QYJ0 DNJA2	3	0	0	9422605	0
ACOT2_MC	>sp Q9QYR9 ACOT	6	0	2907877	3118707	6815372
QKI_MOUS	>sp Q9QYS9 QKI_M	1	0	0	0	0
VPS29_MOI	>sp Q9QZ88 VPS29	1	0	0	22271908	0
DIC_MOUS	>sp Q9QZD8 DIC_M	1	0	0	0	0
EIF3I_MOU	>sp Q9QZD9 EIF3I_	4	8001312	15146011	11827914	18463961
COPG1_MC	>sp Q9QZE5 COPG	10	0	14779382	19795231	0
GPC1_MOU	>sp Q9QZF2 GPC1_	11	73921157	1.81E+08	3.98E+08	6.78E+08
AFAD_MOU	>sp Q9QZQ1 AFAD	2	0	0	0	0
H2AY_MOU	>sp Q9QZQ8 H2AY	2	0	0	5.79E+08	0
ANGL2_MC	>sp Q9R045 ANGL2	16	1.37E+09	67203902	4.85E+08	91293149
PLOD2_MO	>sp Q9R0B9 PLOD2	2	0	0	0	0
PLOD3_MO	>sp Q9R0E1 PLOD3	10	9.15E+08	4.47E+08	3.48E+08	3.18E+08
PLOD1_MO	>sp Q9R0E2 PLOD1	27	7.81E+08	2.69E+08	9.65E+08	60364455
COMP_MOI	>sp Q9R0G6 COMP	12	9.18E+08	4.92E+08	8.56E+08	6.66E+08
GALK1_MC	>sp Q9R0N0 GALK	3	48443527	37677650	1.02E+08	43518192
ESTD_MOU	>sp Q9R0P3 ESTD_	12	45554981	2.03E+08	3.26E+08	41794762
DEST_MOU	>sp Q9R0P5 DEST_	4	0	42694092	0	14828899
SC11A_MOI	>sp Q9R0P6 SC11A	1	0	0	9707258	0
TEBP_MOU	>sp Q9R0Q7 TEBP_	4	86753400	56453160	73716877	1.03E+08

ACOT9_MC>sp Q9R0X4 ACOT9	4	0	0	14114370	0
KAD1_MOU>sp Q9R0Y5 KAD1	2	0	0	0	0
HTRA1_MC>sp Q9R118 HTRA1	9	0	75345032	44915032	5.38E+08
ANGL3_MC>sp Q9R182 ANGL3	2	97038810	27301237	40695428	1.37E+08
MTA2_MOU>sp Q9R190 MTA2	1	0	0	0	0
SLIT2_MOU>sp Q9R1B9 SLIT2	4	1.69E+08	71751470	0	0
PR40A_MO>sp Q9R1C7 PR40A	1	0	0	0	0
ENPP2_MO>sp Q9R1E6 ENPP2	2	28349658	39995498	18287028	26116836
PSA4_MOU>sp Q9R1P0 PSA4_I	13	6.27E+08	4.63E+08	8.17E+08	4.29E+08
PSB3_MOU>sp Q9R1P1 PSB3_I	5	2.91E+08	2.53E+08	4.20E+08	2.30E+08
PSB2_MOU>sp Q9R1P3 PSB2_I	7	2.57E+08	2.10E+08	3.10E+08	1.50E+08
PSA1_MOU>sp Q9R1P4 PSA1_I	10	1.62E+08	2.15E+08	3.53E+08	97797776
CAN7_MOU>sp Q9R1S8 CAN7	1	0	0	0	0
SAE1_MOU>sp Q9R1T2 SAE1	4	41321270	0	0	0
MYO1C_MC>sp Q9WTI7 MYO1	7	0	57967590	5660510	72951837
RUVB2_MO>sp Q9WTM5 RUVB	6	0	0	0	0
KAD2_MOU>sp Q9WTP6 KAD2	2	0	0	0	0
KAD3_MOU>sp Q9WTP7 KAD3	1	0	0	0	0
PDC6I_MO>sp Q9WU78 PDC6I	16	81961182	53599700	1.29E+08	82389466
SYFB_MOU>sp Q9WUA2 SYFB	2	0	9042088	0	0
PFKAP_MO>sp Q9WUA3 PFKAP	5	0	14223664	0	0
CHIP_MOU>sp Q9WUD1 CHIP	1	0	0	0	0
COR1B_MC>sp Q9WUM3 COR1B	3	0	0	0	0
COR1C_MC>sp Q9WUM4 COR1C	8	1.72E+08	79122551	1.43E+08	2.02E+08
SUCA_MOU>sp Q9WUM5 SUC4	2	0	0	0	0
CATZ_MOU>sp Q9WUU7 CATZ	3	11002901	1618814	30329586	11654827
ARC1B_MO>sp Q9WV32 ARC1B	5	16297879	15338524	53278258	21350442
ASAH1_MO>sp Q9WV54 ASAH1	6	6730992	1.02E+08	15863266	28614223
FPRP_MOU>sp Q9WV91 FPRP	11	1.46E+08	48363365	1.21E+08	59416040
TIM9_MOU>sp Q9WV98 TIM9	2	0	0	0	0
TAGL2_MO>sp Q9WVA4 TAGL2	8	3.00E+08	1.34E+08	1.94E+08	3.76E+08
PACN2_MO>sp Q9WVE8 PACN2	4	0	0	0	43240117
FBLN5_MO>sp Q9WVH9 FBLN5	7	6.09E+08	63584671	1.80E+08	23861575
PSD13_MOU>sp Q9WVJ2 PSD13	8	1.49E+08	69766454	40356232	13958725
FBLN4_MO>sp Q9WVJ9 FBLN4	16	9.33E+08	34748468	1.39E+09	4.93E+08
EHD1_MOU>sp Q9WVK4 EHD1	16	1.07E+08	87729990	2.11E+08	2.25E+08
RGAP1_MO>sp Q9WVM1 RGAP1	9	0	0	0	0
ADA17_MO>sp Q9Z0F8 ADA17	1	0	0	0	0
NPC2_MOU>sp Q9Z0J0 NPC2_M	1	0	0	0	0
GDF15_MO>sp Q9Z0J7 GDF15	1	0	0	0	0
VNN1_MOU>sp Q9Z0K8 VNN1	1	31230976	8949682	38516431	20086946
IF2H_MOU>sp Q9Z0N2 IF2H_M	3	0	33101847	0	0
ZO2_MOUS>sp Q9Z0U1 ZO2_M	1	0	0	0	0
NU160_MO>sp Q9Z0W3 NU160	1	0	0	0	0
AIFM1_MO>sp Q9Z0X1 AIFM1	1	0	0	0	0
P5CS_MOU>sp Q9Z110 P5CS_M	7	0	1.19E+08	0	1.26E+08
LOXL3_MO>sp Q9Z175 LOXL3	12	6.50E+08	73663758	2.08E+08	4673879

EIF3G_MOI	>sp Q9Z1D1 EIF3G_	2	0	0	0	0
GYS1_MOU	>sp Q9Z1E4 GYS1_	1	0	0	17907671	0
VPP1_MOU	>sp Q9Z1G4 VPP1_	1	0	0	0	27169926
DX39B_MO	>sp Q9Z1N5 DX39B	9	8972866	68572878	50176646	55525106
KANK3_MC	>sp Q9Z1P7 KANK3	1	0	27877063	40462061	36524027
ANGL4_MO	>sp Q9Z1P8 ANGL4	2	0	7819849	0	17896181
CLIC1_MOI	>sp Q9Z1Q5 CLIC1_	10	48891571	1.25E+08	1.09E+08	1.29E+08
SYVC_MOU	>sp Q9Z1Q9 SYVC_	15	29984917	1.34E+08	1.11E+08	74610771
BAG6_MOU	>sp Q9Z1R2 BAG6_	3	0	9590107	0	0
APOM_MOI	>sp Q9Z1R3 APOM_	2	1.22E+09	1.24E+09	1.11E+09	9.68E+08
TSP4_MOU	>sp Q9Z1T2 TSP4_M	13	2.89E+09	1.49E+09	4.40E+09	2.73E+09
STRAP_MO	>sp Q9Z1Z2 STRAP	1	0	14280134	9699660	0
HNRPC_MC	>sp Q9Z204 HNRPC	2	0	37947595	0	24711659
GIPC2_MOI	>sp Q9Z2H7 GIPC2_	1	0	0	0	0
LETM1_MC	>sp Q9Z2I0 LETM1_	1	0	0	0	0
SUCB1_MO	>sp Q9Z2I9 SUCB1_	1	0	0	0	0
MINP1_MO	>sp Q9Z2L6 MINP1_	2	0	0	0	0
ACL6A_MO	>sp Q9Z2N8 ACL6A	1	0	0	0	0
VAMP5_MC	>sp Q9Z2P8 VAMP5	1	0	0	0	0
RM40_MOU	>sp Q9Z2Q5 RM40_	1	0	0	0	0
SEPT5_MOI	>sp Q9Z2Q6 SEPT5_	1	1.16E+09	1.26E+09	9.72E+08	0
PSA7_MOU	>sp Q9Z2U0 PSA7_	10	3.76E+08	3.62E+08	4.69E+08	2.92E+08
PSA5_MOU	>sp Q9Z2U1 PSA5_	9	3.28E+08	3.57E+08	7.45E+08	2.09E+08
DNPEP_MO	>sp Q9Z2W0 DNPEP	3	0	0	0	0
HNRPF_MC	>sp Q9Z2X1 HNRPF	9	20661667	46386906	13972993	70293737
GFPT2_MO	>sp Q9Z2Z9 GFPT2_	3	0	0	0	0