Supplementary Table 1. List of differentially expressed genes derived with Cuffdiff.

transcript	gene	desc	A/R.fc	A/R.fc.sd	R.mean	A.mean	R.sd
NM_001199149	LTF	lactotransferrin	-10.17110357	2.398776926	7.029306886	3.68290257	1.633127559
NM_001925	DEFA4	defensin, alpha 4, corticostatin	-10.1105141	2.297684724	6.007257226	2.669472774	1.695115362
NM_001972	ELANE	elastase, neutrophil expressed	-9.615088856	1.939759323	5.627860544	2.362560354	1.525426791
NM_001700	AZU1	azurocidin 1	-8.658371507	1.88504198	5.18715908	2.073063376	1.486160233
NM_004345	CAMP	cathelicidin antimicrobial peptide	-7.929560335	2.264584914	6.09472973	3.107488854	1.741984018
NM_005564	LCN2	lipocalin 2	-7.756966451	2.262295873	6.647121694	3.691629132	1.601137369
NM_001911	CTSG	cathepsin G	-7.181021789	1.538956964	4.503634836	1.659445696	1.248315447
NM_002777	PRTN3	proteinase 3	-7.065156784	1.693033742	3.679550408	0.858828832	1.548391569
NM_005091	PGLYRP1	peptidoglycan recognition protein 1	-6.374096293	2.052685872	4.70761784	2.035397026	1.583021909
NM_002424	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	-6.127678816	2.175637149	3.941240328	1.325899648	1.877647737
NM_001725	BPI	bactericidal/permeability-increasing protein	-6.1197735	1.971349739	5.526451078	2.91297282	1.615381743
NM_004566	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-5.746427983	1.586788746	4.243786604	1.721121158	1.427938462
NM_001816	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	-5.499430834	1.996011588	3.92675293	1.467470616	1.654623436
NM_000250	MPO	myeloperoxidase	-5.324718061	1.81256785	4.433239866	2.020534728	1.449422921
NM_002483	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	-5.200636205	1.709503581	3.431342718	1.052654596	1.439422448
NM_001276	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	-5.115006112	1.881084519	3.527624494	1.17288853	1.556279352
NM_006061	CRISP3	cysteine-rich secretory protein 3	-5.070410548	1.614891935	3.354509666	1.0124071	1.422696319
NM_002935	RNASE3	ribonuclease, RNase A family, 3	-4.93457239	1.827106725	3.8612428	1.558317728	1.494854233
NM_003064	SLPI	secretory leukocyte peptidase inhibitor	-4.904941868	1.968832058	3.807115446	1.512879408	1.494676489
NM_005139	ANXA3	annexin A3	-4.349489284	1.860525205	3.387149984	1.266303974	1.517627567
NM_005980	S100P	S100 calcium binding protein P	-4.147923636	1.603075987	4.774031546	2.721642212	1.275553952
NM_006418	OLFM4	olfactomedin 4	-3.976879315	1.591111413	2.781867636	0.790230854	1.5520116
NM_014999	RAB21	RAB21, member RAS oncogene family	-3.866871497	0.997128219	4.289545574	2.338378752	0.211712904
NM_017817	RAB20	RAB20, member RAS oncogene family	-3.735355776	0.960465571	4.534754776	2.633509116	0.834907687
NM_006290	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-3.604946827	1.505433348	5.722349036	3.872371056	1.26239796
NM_005006	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	-3.504279621	0.786774913	3.451076294	1.641958396	0.332046339
NM_002165	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-3.277029095	1.450819837	2.904031538	1.191643056	0.76588905
NM_002983	CCL3	chemokine (C-C motif) ligand 3	-3.218647798	1.019134317	5.017591496	3.331136778	0.926570116
NM_015054	UHRF1BP1L	UHRF1 binding protein 1-like	-3.071766406	0.926168626	3.214635682	1.595567172	0.788354441
NM_002922	RGS1	regulator of G-protein signaling 1	-3.003921162	1.516965463	4.254307434	2.667460484	1.207232062
NM_017923	01-Mar	membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase	-2.835441773	1.340219159	3.77985505	2.27628152	0.993483604
NM_032864	PRPF38A	pre-mRNA processing factor 38A	-2.740265518	1.078328991	3.237623416	1.783307726	1.06743775
NM_001781	CD69	CD69 molecule	-2.675261125	1.241230434	6.470594238	5.050914522	0.896567025
NM_000201	ICAM1	intercellular adhesion molecule 1	-2.668115425	0.92323951	4.788279072	3.372457992	0.696716223
NM_020529	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	-2.665440793	1.023743614	7.977795816	6.56342168	0.754850179
NM_003486	SLC7A5	solute carrier family 7 (amino acid transporter light chain, L system), member 5	-2.659956724	1.101917469	3.53888264	2.127479866	0.833328183
NM_001674	ATF3	activating transcription factor 3	-2.534431381	1.000944824	2.521158278	1.179496174	0.9486628
NM_025079	ZC3H12A	zinc finger CCCH-type containing 12A	-2.51297588	1.196606124	4.365303858	3.035907034	0.911511418
NM_144669	GLT1D1	glycosyltransferase 1 domain containing 1	-2.50508054	1.075697792	3.88025698	2.555399992	0.58266031
NM_024731	KLHL36	kelch-like family member 36	-2.47917776	0.697489686	4.354000918	3.0441392	0.239418198
NM_002852	PTX3	pentraxin 3, long	-2.456954887	1.036123067	2.552964436	1.256093068	0.944902379
NM_001135776	ZBTB43	zinc finger and BTB domain containing 43	-2.429416717	1.147393667	2.645187276	1.3645773	0.876150146
NM_001206	KLF9	Kruppel-like factor 9	-2.394528917	1.105972213	4.638223212	3.378481354	0.93125044
NM_001025370	VEGFA	vascular endothelial growth factor A	-2.361572309	0.642342833	2.720119406	1.480371696	0.598910962
NM_014330	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	-2.324769273	0.861190337	6.57484132	5.35775378	0.780547172
NM_080491	GAB2	GRB2-associated binding protein 2	-2.298012781	0.678650313	4.24583202	3.045445198	0.470710361
NM_001001794	DENND6B	DENN/MADD domain containing 6B	-2.246504086	0.353225807	2.356076868	1.188395182	0.251480101
NM_001002796	MCTP1	multiple C2 domains, transmembrane 1	-2.228517336	0.489192121	2.316406824	1.16032264	0.309280743
NM_025065	RPF1	ribosome production factor 1 homolog (S. cerevisiae)	-2.224644431	0.390274204	4.179613996	3.02603923	0.274572557
NM_001085400	RELL1	RELT-like 1	-2.224533588	0.735052308	3.236663354	2.083160472	0.64721528
NM_001001852	PIM3	pim-3 oncogene	-2.207362122	1.008530296	6.526809344	5.384486018	0.496218913
NM_018476	BEX1	brain expressed, X-linked 1	-2.188648302	0.890020544	1.650528832	0.520488688	0.863830941
NM_015675	GADD45B	growth arrest and DNA-damage-inducible, beta	-2.165217549	0.820281118	5.990815492	4.876303506	0.430084323
NM_007313	ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	-2.142760906	0.544806947	3.070156848	1.970685968	0.100947722
NM_152346	SLC43A2	solute carrier family 43 (amino acid system L transporter), member 2	-2.124628962	0.932585843	3.886927528	2.799716612	0.706110889
NM_002033	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	-2.121989139	0.737029695	3.680848072	2.5954308	0.611579414
NM_002659	PLAUR	plasminogen activator, urokinase receptor	-2.087748169	0.825020221	5.313475392	4.251527692	0.513984266
NM_004073	PLK3	polo-like kinase 3	-2.075627064	0.905188304	4.439717344	3.386170092	0.81037079
NM_017633	FAM46A	family with sequence similarity 46, member A	-2.073166114	0.893102197	3.522364676	2.470528958	0.784977177
NM_018566	YOD1	YOD1 deubiquitinase	-2.059628879	0.851729989	3.385930052	2.343545648	0.652412127
NM_032047	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	-2.05630353	0.870266635	1.817204862	0.777151626	0.800551092
NM_012118	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	-2.0302441	0.599812004	1.700159106	0.67850591	0.557314259
NR_045406	HIF1A-AS2	HIF1A antisense RNA 2	-2.025549051	0.851194954	4.582706118	3.564393096	0.725939435
NM_012329	MMD	monocyte to macrophage differentiation-associated	2.011005515	0.475834145	4.215757568	5.223674606	0.227605248
NM_001112736	FAM208A	family with sequence similarity 208, member A	2.035377897	0.654419801	2.760814092	3.786110768	0.258920681
NM_015935	METTL13	methyltransferase like 13	2.04322577	0.873952473	1.844180762	2.875029388	0.582408447
NM_021636	LGR6	leucine-rich repeat containing G protein-coupled receptor 6	2.056082968	0.967252639	1.567415662	2.607314144	0.82051892
NM_001197249	BTN3A2	butyrophilin, subfamily 3, member A2	2.065486757	0.665254796	3.19440855	4.24089036	0.593070612
NM_024830	LPCAT1	lysophosphatidylcholine acyltransferase 1	2.074284397	0.802876559	4.53275096	5.58536467	0.686526146
NM_003277	CLDN5	claudin 5	2.079007698	0.675896917	1.980325996	3.036221096	0.375381285
NM_004513	IL16	interleukin 16	2.091255514	0.576993179	3.76675984	4.831129184	0.484569254
NM_198457	ZNF600	zinc finger protein 600	2.098691553	0.974840183	2.342373028	3.411863176	0.744451332
NM_130782	RGS18	regulator of G-protein signaling 18	2.099048946	0.641967682	4.892641058	5.962376866	0.401763057
NM_007360	KLRK1	killer cell lectin-like receptor subfamily K, member 1	2.118744495	0.928371767	5.760341332	6.843550952	0.80997879
NM_138565	CTTN	cortactin	2.128518123	0.635099236	1.570924436	2.66077381	0.450465202
NM_001039933	CD79B	CD79b molecule, immunoglobulin-associated beta	2.159791351	0.684686175	3.359638916	4.470530862	0.434623791
NM_001098725	TCL1A	T-cell leukemia/lymphoma 1A	2.160479419	1.013011231	2.702370282	3.81372177	0.777917791
NM_004380	CREBBP	CREB binding protein	2.163416124	0.722944585	3.313521992	4.42683318	0.707947151
NM_001286624	MAP3K7CL	MAP3K7 C-terminal like	2.170448986	0.882907326	5.713656108	6.831649622	0.517288065
NM_005828	DCAF7	DDB1 and CUL4 associated factor 7	2.182275147	1.022942626	2.876733762	4.002566774	0.802400037
NM_024901	DENND2D	DENN/MADD domain containing 2D	2.218228233	0.940530216	3.693776726	4.843184538	0.720862724
NM_152687	GAPT	GRB2-binding adaptor protein, transmembrane	2.222852482	1.042489296	2.022914538	3.175326746	0.764852406
NM_018326	GIMAP4	GTPase, IMAP family member 4	2.234569379	1.037335909	5.520683652	6.68068049	0.698506887
NM_007145	ZNF146	zinc finger protein 146	2.236744703	1.008140465	1.749241046	2.910641646	0.478142037
NM_032383	HPS3	Hermansky-Pudlak syndrome 3	2.274396768	0.901877487	1.877485084	3.062969038	0.764623398
NM_001278182	EOMES	eomesodermin	2.293912062	1.063208077	2.038088852	3.235898938	0.834261899
NM_003006	SELPLG	selectin P ligand	2.315989435	1.013309122	5.534496022	6.746124694	0.791426757
NM_030915	LBH	limb bud and heart development	2.325020247	1.087821682	5.103397856	6.320641136	0.905135621
NM_000387	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	2.393696672	0.633403364	2.780998142	4.040238488	0.41029172
NM_017523	XAF1	XIAP associated factor 1	2.411617424	0.978483903	2.936227392	4.20622845	0.707418276
NM_133367	PAQR8	progestin and adipoQ receptor family member VIII	2.434679053	1.099857286	1.4215969	2.705328504	0.827686803
NM_001184714	SLAMF6	SLAM family member 6	2.434727089	0.700721709	2.74982833	4.033588398	0.516953076
NM_000626	CD79B	CD79b molecule, immunoglobulin-associated beta	2.504807421	0.81688345	2.8021187	4.126818388	0.50778268
NM_002535	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	2.558927079	1.014877052	3.05661988	4.412158916	0.966223784
NM_002534	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	2.755562416	0.946797387	2.510106544	3.97245335	0.619600496
NM_000954	PTGDS	prostaglandin D2 synthase 21kDa (brain)	2.769966872	1.216482506	5.015483964	6.485352686	1.082426928
NR_038446	LINC00861	long intergenic non-protein coding RNA 861	2.854287855	1.061012474	2.93501099	4.448141828	0.845569356
NM_006272	S100B	S100 calcium binding protein B	3.316600502	1.389300398	1.994228634	3.723933878	0.898305396

transcript	A.sd	A/R.volume	A/R.stat_results	A/R.raw.pval	A/R.bh.pval	N_1214401_1	N_1248683	N_345100	N_634160	N_709307	N_1202403	N_1214401_2	N_1248683_2
NM_001199149	1.756993203	5.08804996	-3.119417838	0.014335606	0.437580038	3.931581	6.11877053	2.9503774	4.10528751	1.30849641	6.85575082	7.2863359	9.65318688
NM_001925	1.551108958	4.004523643	-3.248275471	0.011856099	0.437580038	3.21519083	4.66228139	1.56329698	3.1993355	0.70725917	5.55753471	6.88933962	8.33648818
NM_001972	1.198223408	3.646390023	-3.764092331	0.006088583	0.437580038	2.86954725	3.99958948	1.27951959	2.56359365	1.1005518	5.54584875	6.36543345	7.60333119
NM_001700	1.159616759	3.27922392	-3.693991835	0.006742978	0.437580038	2.39666206	3.61300534	1.36878589	2.42476268	0.56210091	4.59418217	5.83104971	7.29282891
NM_004345	1.447009507	4.351931147	-2.949623846	0.019124261	0.437580038	3.55019598	5.16306988	2.31784506	3.22029464	1.28603871	5.86788837	6.76005295	8.71765582
NM_005564	1.598230817	4.953656033	-2.9212281	0.019255094	0.437580038	3.82257493	5.96471331	3.2322471	3.92997622	1.5086341	6.4546176	6.95524578	9.19024597
NM_001911	0.900053933	2.733777139	-4.13253938	0.004039169	0.437580038	1.96228566	2.89011588	1.0669951	1.83711841	0.54071343	4.06244837	5.11690803	6.31709128
NM_002777	0.684723885	1.77766813	-3.725457464	0.011441389	0.437580038	0.83081413	1.78459034	0.2017486	1.26615707	0.21083402	3.66550863	4.31386245	5.44022581
NM_005091	1.306736745	3.095459796	-2.910950708	0.020317392	0.437580038	2.19517619	4.11380664	1.27406845	1.93522571	0.65870814	4.52430326	5.08853609	7.17257464
NM_002424	1.099015914	2.285976632	-2.687984781	0.033682461	0.437580038	1.26136966	3.12620895	0.55424479	1.35659809	0.33107675	4.00548394	3.74230249	7.02400386
NM_001725	1.129938768	4.012281369	-2.964423271	0.020440141	0.437580038	3.29890299	4.54894939	2.40972002	2.8151845	1.4921072	5.34821237	5.99602408	8.03052671
NM_004566	0.692018983	2.702604469	-3.554884944	0.012774249	0.437580038	1.87278078	2.03190173	2.63168391	1.14480774	0.92443163	4.98288307	1.79084279	5.26869598
NM_001816	1.116370702	2.400498811	-2.755055363	0.02823065	0.437580038	1.60967837	3.12177711	0.54583641	1.73574442	0.32431677	3.54344808	4.69468263	6.4009249
NM_000250	1.088382013	2.992910808	-2.97642524	0.019267863	0.437580038	2.55962252	3.32373597	1.64626305	2.16166482	0.41138728	3.34937844	4.87680388	6.72872299
NM_002483	0.92220687	1.900531158	-3.111375956	0.01765809	0.437580038	1.16444903	2.4591331	0.23707283	1.20086942	0.2017486	3.1071114	4.01799696	5.60709685
NM_001276	1.056633118	2.034087094	-2.799103194	0.026398527	0.437580038	1.19834294	2.92917974	0.55567101	0.99166508	0.18958388	3.2595862	3.27818064	6.20238855
NM_006061	0.764075353	1.84285903	-3.243003717	0.017092506	0.437580038	1.13038933	2.17954628	0.50166321	1.07154855	0.17888813	3.38231646	3.29102038	5.68814418
NM_002935	1.050585458	2.452966186	-2.818388734	0.02517585	0.437580038	1.14725877	3.27657919	0.97672171	1.78374105	0.60728792	2.69796978	4.12355661	6.30033545
NM_003064	1.28149985	2.399938866	-2.605640088	0.031953101	0.437580038	1.64030528	3.51853747	0.46502804	1.61957372	0.32095253	3.45652323	4.05311495	6.2289367
NM_005139	1.076271624	2.071029088	-2.548933943	0.037232491	0.437580038	1.35610344	3.0316651	0.69896885	1.04533463	0.19944785	3.01809995	3.69093006	5.85376071
NM_005980	0.970986476	3.604608963	-2.862797587	0.022619972	0.437580038	2.06993506	4.13649865	1.60411595	2.77025869	3.02740271	4.089344	4.64869919	7.01121
NM_006418	0.350564577	1.482672465	-2.798946192	0.043791572	0.437580038	1.3065568	0.80595689	0.5325689	0.89870602	0.40736566	1.00068822	4.56431601	3.95583614
NM_014999	0.974393315	3.167109443	-4.375507147	0.009740324	0.437580038	2.01488561	1.56146302	3.99087102	2.38358052	1.74109359	4.37320858	4.02012322	4.59374416
NM_017817	0.474787602	3.455765912	-4.426306019	0.003884939	0.437580038	2.81132419	2.94940841	3.1197928	2.30723637	1.97978381	5.05180715	3.11804827	5.21111101
NM_006290	0.820171298	4.707340946	-2.747831064	0.029143115	0.437580038	3.56133718	3.74878615	5.22904867	3.01571673	3.80696655	6.27594063	3.63085279	6.96294165
NM_005006	0.713274135	2.380446113	-5.141636488	0.002541807	0.437580038	1.20490926	1.34145938	2.91117589	1.34892842	1.40331903	3.55470608	3.64817578	3.57323362
NM_002165	1.232189986	1.86026047	-2.639209192	0.034869968	0.437580038	1.94147592	0.52505028	2.99442038	0.11072772	0.38654098	3.51075309	1.58029544	2.99973668
NM_002983	0.424384938	4.088310601	-3.700226092	0.011389978	0.437580038	3.15386913	2.91214487	3.57109274	3.06635671	3.95222044	5.40169583	3.53417224	4.92447964
NM_015054	0.486092172	2.26476647	-3.908950428	0.006437213	0.437580038	1.50438882	1.64993305	1.56075791	0.94943349	2.31332259	3.53494114	1.82021122	3.66220858
NM_002922	0.918572242	3.368708501	-2.339076094	0.049681561	0.437580038	2.40337515	2.50681118	4.2390094	1.81819731	2.36990938	5.17996498	2.13747271	4.57495494
NM_017923	0.899543063	2.933259995	-2.508614058	0.036722865	0.437580038	3.43146569	3.05951521	1.76756879	1.6246286	1.49822931	4.15571523	3.91800313	4.8909333
NM_032864	0.152872695	2.402848071	-3.015729682	0.037346258	0.437580038	1.68695263	1.87186081	1.56146302	1.91775771	1.87850446	1.3903263	3.65502769	3.97805597
NM_001781	0.858382526	5.71685389	-2.557543115	0.033826935	0.437580038	5.50584041	4.74644927	6.16597332	3.86883716	4.96747245	7.27745489	5.00170342	6.3141706
NM_000201	0.605770334	4.018491013	-3.429090876	0.009230561	0.437580038	3.5912475	3.1673839	4.31862939	2.99733561	2.78769356	4.96069633	3.5706664	5.33400447
NM_020529	0.691557803	7.23613419	-3.089285901	0.015044385	0.437580038	7.08247443	6.26494141	7.49636942	5.88969091	6.08363223	8.2124868	6.77262908	8.85084013
NM_003486	0.720962029	2.743884393	-2.864091582	0.021469589	0.437580038	1.91775771	2.13071183	3.34103823	1.79027994	1.45761162	4.09623209	2.15359485	3.91477833
NM_001674	0.319263892	1.724440936	-2.997215826	0.031013953	0.437580038	1.05395338	0.7806589	1.40460861	1.0669951	1.59126488	2.94341559	0.94179935	3.39903867
NM_025079	0.775250379	3.640419851	-2.484210643	0.03859277	0.437580038	3.33675385	3.02393015	4.15727322	2.15535342	2.50622453	4.95958966	2.77117029	4.76567084
NM_144669	0.904230447	3.148905946	-2.753998668	0.029026047	0.437580038	2.15592822	4.09143707	1.72568462	2.49152157	2.31242848	4.11432022	4.30285579	4.46068372
NM_024731	0.65511128	3.640629736	-4.199259001	0.008314244	0.437580038	4.03351975	2.3108765	2.74792118	2.8279839	3.30039467	4.49110224	4.47632692	4.35567753
NM_002852	0.425100582	1.790743123	-2.7987916	0.033904916	0.437580038	1.11285936	1.25973086	1.96149514	0.82377027	1.12260971	2.37554211	1.5979598	4.14108423
NM_001135776	0.740859736	1.899884868	-2.495683079	0.037968782	0.437580038	1.31470054	0.4838482	2.54219148	1.24551386	1.23663242	3.32275189	1.11878095	3.06840147
NM_001206	0.596613068	3.958554109	-2.546961303	0.039164558	0.437580038	3.4584188	2.92966505	4.26594609	2.73584573	3.5025311	4.68335493	3.50902935	6.09416975
NM_001025370	0.232185217	2.00668577	-4.315701854	0.007027742	0.437580038	1.3451281	1.44986111	1.85762733	1.50057717	1.24866477	3.47407288	1.80364281	2.83239386
NM_014330	0.363861112	5.935181626	-3.160149804	0.021171173	0.437580038	5.73150489	5.16364571	5.66253706	4.84909689	5.38198435	7.23256179	5.27075751	6.82250095
NM_080491	0.488874221	3.595893316	-3.955124577	0.004217711	0.437580038	3.4788388	3.17342885	3.44644642	2.31137848	2.81713344	4.72136028	3.6371499	4.66524614
NM_001001794	0.248044814	1.673305232	-7.391916364	7.69E-05	0.21407149	1.49321512	1.3645375	1.04260148	0.87124683	1.17037498	2.33444305	2.6322636	2.28367713
NM_001002796	0.379017616	1.639444809	-5.284391781	0.00084386	0.437580038	0.89502324	1.70376587	0.90983521	1.41647287	0.87651601	2.33836207	2.42889755	2.71032552
NM_025065	0.277351519	3.556357113	-6.609382754	0.000167815	0.29759194	2.8404812	2.71121657	3.38134129	3.23530256	2.96185453	4.16126306	3.70930838	4.32715332
NM_001085400	0.348445514	2.596630347	-3.509016746	0.012219757	0.437580038	2.3379702	1.97570168	2.53841064	1.68095444	1.88275936	3.06919774	2.34077576	4.14054456
NM_001001852	0.878009196	5.928196493	-2.532707861	0.042579222	0.437580038	6.1256011	4.88919168	6.52884992	4.77050206	4.60828533	6.80139581	5.64248314	6.68598253
NM_018476	0.214319093	0.926866542	-2.839087926	0.041028685	0.437580038	0.62996202	0.6814276	0.64565426	0.4838482	0.16155136	1.57507162	1.59985759	3.08681387
NM_015675	0.69849082	5.404908379	-3.038134742	0.020111716	0.437580038	5.56611164	4.49484049	5.68980226	4.45530654	4.1754566	6.10269628	5.25336682	6.01195244
NM_007313	0.535372924	2.459738811	-4.512592283	0.009137529	0.437580038	1.66433897	2.71911671	2.119812	2.05946145	1.29070071	3.13438196	3.14400989	3.06882653
NM_152346	0.609199284	3.298832456	-2.606813659	0.03184749	0.437580038	3.13003941	2.42545206	3.64148088	2.72366794	2.07794277	4.39917959	2.70168914	4.15664387
NM_002033	0.411319087	3.090855295	-3.293038015	0.01323622	0.437580038	3.12068889	2.43289379	2.93755829	2.30994773	2.1760653	3.57945127	3.14094621	4.73415652
NM_002659	0.645351485	4.752934648	-2.878217025	0.021652456	0.437580038	4.39298166	4.26403649	5.24446502	3.64541258	3.71074271	5.48099828	4.44459928	5.37403263
NM_004073	0.403317552	3.877323573	-2.602556024	0.041367651	0.437580038	3.44994714	3.523493	3.89548448	3.2717841	2.79014174	4.60883692	3.10995373	5.31627761
NM_017633	0.425960522	2.949932869	-2.633490517	0.037886275	0.437580038	2.83656746	2.54556553	2.90667179	2.10668161	1.9571584	3.61437144	2.77641172	4.80450811
NM_018566	0.547542136	2.816927695	-2.736597768	0.026304713	0.437580038	2.68839555	2.31372673	3.07057823	1.75976705	1.88526068	3.22286307	2.4265924	4.21572083
NM_032047	0.341294542	1.188378607	-2.672318624	0.040881505	0.437580038	1.26733456	0.46789544	0.83222459	0.43652181	0.88178173	1.69846888	0.86814272	3.08769311
NM_012118	0.221754949	1.07404283	-3.808670016	0.011478846	0.437580038	1.02078701	0.42692987	0.60112741	0.6005056	0.74317966	1.9045962	1.24925862	2.57313406
NR_045406	0.444460107	4.04160439	-2.675082986	0.033424538	0.437580038	3.55182832	3.23375	4.32285273	3.25874072	3.45479371	4.82730657	3.30854431	5.14386646
NM_012329	0.417868382	4.692733292	4.736463399	0.002958493	0.437580038	5.0574947	5.53380922	5.07314952	5.75230602	4.70161357	4.10477369	4.54573001	3.95165928
NM_001112736	0.601020263	3.23307098	3.503306383	0.015018147	0.437580038	4.13407559	3.62997233	2.88228612	3.80367753	4.48054227	2.86987581	2.94209738	2.9936152
NM_015935	0.651608261	2.302623262	2.63749766	0.030149346	0.437580038	2.60384802	3.19046817	1.85476136	3.42662374	3.29944565	1.68768151	2.76078565	1.20490926
NM_021636	0.512178065	2.021569941	2.404008633	0.04870486	0.437580038	3.28420269	2.87438256	2.44506042	2.52301235	1.9099127	1.48584053	1.83895725	0.35738059
NM_001197249	0.301382136	3.68064348	3.517455988	0.012778009	0.437580038	4.34781187	4.28817205	3.71489728	4.38277154	4.47079906	3.28709871	3.93998304	2.28560765
NM_024830	0.416284302	5.031606808	2.931603597	0.0235301	0.437580038	5.21619147	5.76051037	5.15293322	5.63121497	6.16597332	5.1287897	4.95620223	3.42473408
NM_003277	0.562072534	2.452082292	3.49321496	0.010140126	0.437580038	2.72570801	4.02239731	2.82324919	2.9503774	2.65937357	2.02782423	2.56306749	2.01145155
NM_004513	0.313231172	4.265876626	4.124835945	0.004651111	0.437580038	5.13847918	4.51644195	4.51380177	5.14439649	4.84252653	3.65656402	4.42672334	3.25772105
NM_198457	0.629369205	2.826987138	2.453174084	0.040539188	0.437580038	2.99314114	3.05552131	3.38776261	3.11783098	4.50505984	2.021299	2.70756171	2.119812
NM_130782	0.500708449	5.401089692	3.726047354	0.006317988	0.437580038	5.53704501	6.65195818	5.67091711	6.33729022	5.61467381	4.48291975	5.29407921	4.52710256
NM_007360	0.453661214	6.27862958	2.609009054	0.038502774	0.437580038	6.70050261	6.99260058	6.34321054	6.63904073	7.5424003	5.74494464	6.23363422	4.60952426
NM_138565	0.447696484	2.044474161	3.837159843	0.004967524	0.437580038	2.39962076	3.15266031	3.14585704	2.3088996	2.29683134	1.56146302	2.26618031	1.19665374
NM_001039933	0.529053228	3.875483126	3.627983151	0.007138794	0.437580038	3.90516817	5.13603661	4.23515345	4.92058085	4.15571523	3.19323503	4.0654541	3.36734698
NM_001098725	0.648872611	3.210309701	2.453139114	0.0406721	0.437580038	3.22853412	4.62571522	3.93784974	4.18842745	3.08808232	3.11938707	3.29782392	3.33085021
NM_004380	0.146491315	3.829935913	3.443472082	0.023004518	0.437580038	4.57274549	4.40387567	4.42732061	4.19718032	4.53304381	2.45762321	4.40387567	3.37060484
NM_001286624	0.71549871	6.247695302	2.831451752	0.024322505	0.437580038	6.36757645	7.90215641	6.25637798	7.2373654	6.39477187	4.95156422	5.5542654	5.76895897
NM_005828	0.63448073	3.393275552	2.460977851	0.04079079	0.437580038	3.94434214	4.19805997	2.9362576	4.46068372	4.47349044	2.84258403	4.23466772	2.1639418
NM_024901	0.604114244	4.229614915	2.732664999	0.026474603	0.437580038	4.69780778	4.66574382	3.99434891	5.44103293	5.41698925	3.38189777	4.54653721	2.66034458
NM_152687	0.708367651	2.534445627	2.471845077	0.038766447	0.437580038	3.08624596	3.77905524	2.00799456	3.67350101	3.32983696	1.56265789	3.09299281	2.55775392
NM_018326	0.766911936	6.073048951	2.500474302	0.037157935	0.437580038	6.22403187	6.68598253	5.65540281	7.45543213	7.38255311	5.47677089	6.68598253	4.84734347
NM_007145	0.887540078	2.256416149	2.576000847	0.041127916	0.437580038	2.93327913	3.45433557	1.46351039	3.78272488	2.91935826	1.95081004	2.40562797	1.39208897
NM_032383	0.478261498	2.398057272	2.939227052	0.02279461	0.437580038	3.67150214	3.1430755	3.03951026	3.12813712	2.33262017	1.04533463	3.02393015	1.51027016
NM_001278182	0.659104315	2.568082855	2.519153903	0.037345079	0.437580038	2.57355995	3.13003941	2.63958725	3.89322274	3.94308534	2.73646599	2.1760653	0.91574366
NM_003006	0.632802549	6.110351895	2.673699481	0.029415742	0.437580038	7.11871037	5.63431236	6.82570555	7.11409275	7.03780244	5.2577748	5.90537464	4.88109135
NM_030915	0.603394994	5.679502304	2.502100083	0.041012675	0.437580038	5.50997722	6.1926727	6.11617841	6.68284209	7.10153526	5.40294477	5.67170185	3.49900619
NM_000387	0.482556241	3.351998766	4.445424789	0.002291928	0.437580038	3.88068263	4.17429876	3.58249553	3.75189384	4.81182168	2.49152157	3.27051191	2.77580991
NM_017523	0.676010451	3.514319734	2.902253874	0.019866511	0.437580038	4.4378996	3.38351952	3.65628828	4.50830591	5.04512894	3.2778846	3.36184535	1.68590683
NM_133367	0.724306983	1.961093219	2.609894182	0.031595083	0.437580038	2.20195465	2.72291535	1.7889506	3.30151529	3.51130663	0.98888093	2.81219324	0.9653303
NM_001184714	0.473043793	3.330416738	4.096597469	0.00351186	0.437580038	3.58022111	4.09266227	3.523493	4.39387736	4.57768825	2.57541847	3.44456632	2.24349246
NM_000626	0.639886959	3.40056392	3.626121393	0.007321908	0.437580038	3.29838082	4.82534707	3.67220768	4.62652418	4.21163219	2.84927354	3.59787897	2.67025558
NM_002535	0.310462605	3.672368807	2.986644959	0.032019203	0.437580038	4.45346033	4.22164251	4.02378619	4.84252653	4.51937902	2.90043617	4.65831535	2.32430155
NM_002534	0.715905383	3.157733546	3.453650074	0.008923394	0.437580038	4.54464676	2.84428414	3.9970096	4.63065811	3.84566814	2.75601471	2.57416887	1.81782148
NM_000954	0.555141092	5.703260681	2.701827906	0.035677844	0.437580038	7.15546749	6.75316457	5.92963681	6.70050261	5.88799195	4.75024913	6.39784063	3.84287315
NR_038446	0.640905558	3.613218116	3.188900691	0.014067966	0.437580038	4.30437214	4.02660417	3.69348477	5.15293322	5.06331484	2.60384802	4.02854633	1.80549784
NM_006272	1.059812724	2.725137716	2.783946879	0.02440084	0.437580038	3.5171903	4.65124019	4.14603975	1.97804583	4.32715332	2.05478611	2.54284036	2.64445074

transcript	N_479260	N_748605	FPKM_1214401_1	FPKM_1248683	FPKM_345100	FPKM_634160	FPKM_709307	FPKM_1202403	FPKM_1214401_2	FPKM_1248683_2	FPKM_479260	FPKM_748605
NM_001199149	5.56930384	5.78195699	14.795712	69.779465	6.520752	17.369986	1.729611	119.525624	168.301734	872.762286	44.98604	55.235399
NM_001925	3.82807723	5.42484639	8.548621	24.965593	1.885213	9.103051	0.72899	45.646448	128.765751	339.605075	12.726078	42.652754
NM_001972	3.4776832	5.14700613	6.419537	15.484704	1.385621	5.636679	1.317021	45.155092	89.386573	200.438613	9.821026	34.6084
NM_001700	3.29979362	4.91794099	4.394316	11.51524	1.541609	4.991095	0.551217	22.814926	60.420463	155.416016	8.514074	29.210845
NM_004345	4.3664521	4.76159941	11.049369	35.809039	3.901345	9.240376	1.687414	56.030875	115.243426	443.552822	19.110193	26.002636
NM_005564	5.07216496	5.56333416	13.568297	62.077992	8.189763	15.339948	2.153186	87.778369	134.157944	645.27583	31.393481	47.418234
NM_001911	3.0621979	3.9595286	2.960084	6.648577	1.087902	3.039262	0.530353	14.930476	36.566854	74.772806	6.919291	13.94955
NM_002777	1.21371726	3.76443789	0.80472	2.623995	0.158091	1.667851	0.182214	11.123828	20.421364	39.633828	1.191152	12.090463
NM_005091	3.04129704	3.71137817	3.672167	16.745215	1.378226	3.293185	0.668327	21.466846	35.933076	143.150356	6.80591	11.630462
NM_002424	2.14351347	2.79089788	1.446756	8.001444	0.478169	1.867398	0.291775	14.354845	13.284101	127.636795	3.198828	5.471004
NM_001725	4.0654541	4.19203813	9.12653	22.884795	4.207423	6.831914	2.106087	38.77072	69.719377	266.534641	15.347849	16.701932
NM_004566	4.97881869	4.19769249	2.733723	3.291441	5.048057	1.437044	1.019881	30.106229	2.714174	35.125682	29.552665	16.805203
NM_001816	2.55475513	2.43995391	2.111313	7.975441	0.47012	2.780166	0.286515	10.148473	26.760837	79.899538	4.556635	4.10746
NM_000250	3.16251049	4.04878353	5.020558	9.277382	2.055248	4.056944	0.37207	8.773239	30.753808	100.991553	7.606883	14.912846
NM_002483	1.9551559	2.46935248	1.271355	4.683951	0.192522	1.54048	0.172677	7.296358	16.308819	44.082225	2.692419	4.193013
NM_001276	2.25837983	2.63958725	1.348574	6.851324	0.481345	1.179758	0.161787	8.232235	9.467748	68.801206	3.529857	4.815031
NM_006061	2.25707668	2.15399063	1.21559	3.703345	0.433549	1.311314	0.150413	8.99312	9.587809	46.695102	3.525129	3.154427
NM_002935	2.65385892	3.53049324	1.239836	8.940995	0.973076	2.899475	0.608255	5.194747	17.636158	74.00609	4.991896	10.067566
NM_003064	2.33006097	2.96694138	2.18008	10.758644	0.399647	2.463885	0.285387	9.482442	16.742018	70.469868	3.751086	6.386633
NM_005139	2.09453872	2.27842048	1.584578	7.438229	0.638156	1.263118	0.16844	6.791995	12.824674	53.007169	3.052929	3.532758
NM_005980	4.0724544	4.04845014	3.27504	17.099576	1.982062	6.60079	7.797285	15.27378	25.88785	125.438625	15.422365	14.911893
NM_006418	1.41436298	2.97413483	1.509074	0.841213	0.457767	1.034342	0.368838	0.90962	24.373093	13.181099	1.521481	6.419061
NM_014999	4.2390094	4.22164251	3.113687	2.152695	14.389601	4.820948	2.704441	19.192034	16.342142	21.446842	17.398644	17.146662
NM_017817	4.52091633	4.77189112	6.152618	6.965437	7.505504	4.532816	3.319288	31.852312	8.283012	34.0391	21.535032	26.27246
NM_006290	6.10606566	5.63594445	11.138525	12.881906	34.966392	7.931009	13.543574	75.784532	12.329721	119.462921	65.392855	49.950048
NM_005006	2.86075782	3.61850817	1.363126	1.694933	6.31983	1.855933	1.92034	10.201277	12.478104	9.548633	5.917001	10.816215
NM_002165	3.32373597	3.10563651	2.899736	0.492445	6.766804	0.096414	0.35058	9.855304	2.179837	6.035151	8.667868	7.114432
NM_002983	6.04185235	5.18575742	8.147107	6.782538	10.599939	8.262698	15.045411	40.349013	11.489709	27.239361	62.146206	35.634324
NM_015054	3.67350101	3.38231646	1.873318	2.331107	1.879448	1.104468	4.492902	10.068809	2.786624	10.351116	11.320758	8.902521
NM_002922	4.61857899	4.76056555	4.426365	4.874939	17.343764	2.984254	4.704161	34.656663	3.697627	21.264057	23.181551	25.996595
NM_017923	3.75240254	2.18222105	10.149314	7.618182	2.339331	2.479644	2.123278	16.077637	15.185437	26.538495	12.046513	3.232652
NM_032864	3.88652648	3.27818064	2.273219	2.835374	1.8799	3.245853	3.045887	1.45904	12.52338	13.427861	13.340887	8.173529
NM_001781	6.72609459	7.03354769	47.372261	26.610377	69.37595	14.660163	29.449853	156.689351	33.511904	74.646517	102.5584	133.794558
NM_000201	4.97972904	5.09629912	11.340842	8.213006	18.470953	7.802626	6.48822	29.682802	11.783802	37.066438	29.561962	33.567613
NM_020529	8.07517175	7.97785132	149.353173	76.464951	183.250106	57.952907	62.828448	317.71078	118.146963	488.985454	268.265707	281.537638
NM_003486	4.15516921	3.37463872	2.843118	3.561204	8.889772	2.916632	2.027322	15.324359	3.737242	12.762808	16.390551	8.862599
NM_001674	2.41837217	2.90316561	1.093016	0.802991	1.609217	1.302403	2.348341	6.397168	1.007709	8.268507	4.054919	6.03409
NM_025079	4.87598558	4.45410292	9.402978	7.413182	16.265099	4.041224	5.24332	29.672943	6.292325	24.082091	27.726542	20.405648
NM_144669	3.15562947	3.3677957	3.532461	16.449437	2.235556	5.307508	4.489608	15.523036	20.265304	19.388941	7.549592	8.809679
NM_024731	3.93934208	4.50755582	15.953604	4.172413	5.573286	6.894092	9.450005	20.970155	23.010386	17.951371	13.926184	21.255701
NM_002852	2.35591596	2.29432008	1.190714	1.551615	2.850999	0.917099	1.344899	3.901705	2.232565	15.217062	3.833237	3.590891
NM_001135776	2.78100561	2.93499646	1.52233	0.448918	4.691445	1.625439	1.584444	8.59672	1.278078	6.363102	5.550404	6.225966
NM_001206	4.41443555	4.49012648	10.354645	6.852966	17.733681	6.412716	10.981139	24.152682	11.253069	64.305721	19.784045	20.999236
NM_001025370	2.66607888	2.8244086	1.565281	1.901108	2.550629	2.175815	1.604729	9.583263	2.741864	5.256071	5.045938	5.616508
NM_014330	6.48873991	7.05964644	55.533381	35.84271	48.854781	28.50222	39.17967	151.71172	41.785494	108.449906	85.810238	136.814362
NM_080491	3.91195172	4.29345206	10.526998	8.237713	9.590636	4.558146	6.635219	24.82583	12.38363	22.490474	13.630959	18.262007
NM_001001794	2.54284036	1.9871602	1.858475	1.737249	1.05624	0.989726	1.432201	3.767323	5.625553	3.271674	4.51408	2.694752
NM_001002796	2.24551904	1.85892994	0.874974	2.455892	0.891096	1.994147	0.955663	3.771862	4.688211	4.756298	3.487414	2.343315
NM_025065	4.35680186	4.34354336	6.295361	5.766406	9.11127	9.341515	7.418377	16.153807	12.974127	17.545888	18.963154	18.947289
NM_001085400	3.40350351	3.2292952	4.174937	3.11598	4.674906	2.622271	3.055668	7.094503	4.370026	15.20604	9.29041	7.832031
NM_001001852	6.73391208	6.77027316	73.10163	29.244611	89.897531	27.265693	23.096647	113.889071	53.21622	98.249081	102.837226	111.842611
NM_018476	0.82904086	1.16186022	0.574733	0.667666	0.576528	0.47967	0.140228	1.775824	2.235146	6.452122	0.679716	1.067631
NM_015675	6.27841765	6.30764427	49.029009	21.997216	49.869436	22.059401	17.334974	66.935262	41.192408	59.96604	74.753688	80.723376
NM_007313	2.89730595	3.10625991	2.224505	5.787265	3.256126	3.707121	1.698935	7.460794	8.461607	6.367015	6.098912	7.117322
NM_152346	3.7943535	4.38277154	7.985684	4.570593	11.216988	6.351664	3.621289	19.488465	5.937782	15.413842	12.438989	19.433875
NM_002033	3.47291062	3.47677574	7.937797	4.591893	6.443046	4.552345	3.9588	10.408646	8.440276	23.552295	9.770541	9.618459
NM_002659	5.4539668	5.81377997	20.724274	18.798102	35.330916	12.606812	12.702407	42.606206	22.439823	38.037251	41.829746	56.62531
NM_004073	4.47875225	4.68476621	10.288735	10.783656	13.505446	9.575232	6.49239	23.014882	8.22885	36.444103	20.914446	24.483064
NM_017633	3.03703822	3.37949389	6.277541	5.033778	6.298219	3.877449	3.25533	10.6812	6.31554	24.764015	6.779679	8.889463
NM_018566	3.64242453	3.42204943	5.539033	4.17675	7.204091	2.836346	3.064875	8.013038	4.682416	16.111888	11.070474	9.182008
NM_032047	1.63210722	1.79961238	1.456516	0.426465	0.802516	0.428222	0.963095	2.009627	0.899956	6.454675	1.925434	2.212568
NM_012118	1.52645138	1.24735527	1.03975	0.373669	0.524695	0.622153	0.780011	2.536302	1.479624	4.211216	1.727481	1.199208
NR_045406	4.81279114	4.82102211	11.064654	8.624692	18.509858	9.500369	10.574115	26.880061	9.754413	32.108978	26.534499	27.217101
NM_012329	4.15098542	4.32563944	34.268953	45.155137	31.492907	53.151309	24.607536	15.407745	24.04955	13.122943	16.348934	18.785309
NM_001112736	2.37203195	2.62645012	17.244117	11.671768	6.186447	13.988261	21.217935	6.038697	7.230047	6.008771	3.897783	4.773822
NM_015935	1.5886056	1.97892179	5.206954	8.344397	2.544149	10.780657	9.446358	1.98501	6.250351	1.070076	1.849773	2.675615
NM_021636	2.63787882	1.51702112	9.050517	6.5831	4.343922	5.440735	3.123953	1.625109	2.848069	0.225951	4.901984	1.639321
NM_001197249	3.14585704	3.31349631	19.994418	19.057748	11.767091	21.039359	21.096295	8.393723	15.417912	3.282789	7.475566	8.415083
NM_024830	4.82102211	4.33300668	38.06626	54.287051	33.223998	49.211017	65.956328	33.523712	32.461515	8.440584	26.6332	18.860038
NM_003277	1.61700989	1.68227682	5.740867	15.703544	5.901925	7.552481	5.939187	2.86628	5.312279	2.46338	1.897284	1.955456
NM_004513	3.40611272	4.08667807	36.280367	22.286916	21.306134	35.331199	27.179513	11.030434	22.218162	7.410986	9.306989	15.388783
NM_198457	3.41009631	1.45309612	7.12724	7.603372	9.143293	8.587912	21.531785	2.846905	5.967457	2.771061	9.352681	1.535117
NM_130782	5.31739676	4.84170701	48.287285	99.240731	49.228441	79.044773	45.907901	20.779149	42.214215	20.547364	37.600586	27.569836
NM_007360	6.75316457	5.46043897	111.655761	124.438842	78.459692	95.375803	162.483345	51.650342	80.894714	21.641998	105.085371	43.792224
NM_138565	1.15096257	1.67936254	4.409911	8.142194	7.661497	4.547825	4.420279	1.756327	4.08733	1.060777	1.102031	1.949858
NM_001039933	3.28607526	2.88608321	14.578779	35.025965	17.247244	30.302285	17.083277	7.82736	16.842501	8.087862	8.418588	5.924782
NM_001098725	1.60729515	2.15649506	8.644543	24.204029	13.891805	18.462665	8.149193	7.359577	9.671428	7.827531	1.88089	3.163638
NM_004380	3.30480644	3.0306998	23.445859	20.541391	19.951998	18.539731	21.909486	4.212091	21.818728	8.106491	8.545905	6.701741
NM_001286624	6.3540697	5.93942225	88.38132	219.880168	74.480245	140.486992	75.620969	29.542291	50.614162	49.711659	78.475166	61.757545
NM_005828	2.7044748	2.43800046	14.954859	17.921512	6.437957	22.104376	21.116405	5.898156	19.195191	2.904409	5.236604	4.096794
NM_024901	4.12007743	3.76002664	25.599973	25.05364	14.42546	42.869649	40.21343	8.990286	24.050559	4.571902	15.94613	12.057294
NM_152687	1.30581603	1.59535204	7.695767	13.206313	2.984363	12.852701	9.623337	1.757525	8.141337	4.157025	1.338196	1.786567
NM_018326	5.15875112	5.43457025	77.811931	102.057795	48.767558	158.052918	143.425366	42.471761	110.399932	25.640318	33.443278	42.985591
NM_007145	1.80709675	1.1905815	6.758774	10.261634	1.717743	13.777425	7.20098	2.649543	4.601531	1.32815	2.314083	1.113429
NM_032383	1.59126488	2.2166256	12.05943	8.099834	7.022099	8.631182	4.552121	0.968021	7.704181	1.481844	1.853894	3.346987
NM_001278182	2.87988692	1.48228239	5.084447	8.01331	5.071123	14.921165	14.8818	5.412663	3.816981	0.718297	6.017315	1.579435
NM_003006	4.89000299	6.73823633	150.572311	48.993781	109.712441	130.649428	116.630692	36.639313	64.505065	26.334588	28.116895	109.629785
NM_030915	5.37403263	5.56930384	47.396182	73.161551	66.010233	100.173968	121.293292	40.380253	54.149856	9.011726	39.448546	47.710409
NM_000387	3.09034558	2.27680174	14.259628	17.632746	10.697575	13.515804	26.588786	4.338395	9.417093	4.987049	7.118275	3.529323
NM_017523	3.06840147	3.28709871	21.307579	9.743341	11.304538	22.733612	31.038684	8.338309	10.145947	1.792131	6.960285	8.213886
NM_133367	0.79311748	1.54846255	3.703021	5.815458	2.390496	9.799333	11.055241	0.892052	6.511932	0.778223	0.64661	1.699677
NM_001184714	3.12974844	2.35591596	11.254938	16.469264	10.222315	21.197607	22.661894	4.667347	10.7714	3.150988	7.383569	3.786113
NM_000626	2.1958641	2.69732131	9.12602	27.888439	11.434688	24.586615	17.772937	5.926504	12.009225	4.60516	3.333041	5.06024
NM_002535	2.27935744	3.12068889	21.521061	18.182316	14.746034	28.400492	21.740871	6.18088	26.067518	3.405644	3.58965	7.199733
NM_002534	2.02350891	3.37901875	22.967077	6.422263	14.433175	24.668798	13.915879	5.498792	5.357626	2.040241	2.856112	8.888834
NM_000954	5.85832879	4.22812812	155.644809	106.953599	58.363443	101.169771	55.790401	25.408574	91.4491	12.09199	54.828585	17.199836
NR_038446	2.79356941	3.44359335	19.254362	15.751463	11.621546	35.568805	31.225084	4.800116	16.47111	2.01342	5.612899	9.371454
NM_006272	0.44058864	2.28847732	10.822754	24.744566	16.110639	3.421256	19.178844	2.932458	5.190781	4.496042	0.310413	3.570931