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Supplementary Table 3. Genes induced by Ox-PAPC (40ug/ml, 4hrs) in HAECs by 1.5 fold.

Values are represented as log2 scale.

cutoff by log2(1.5)

ProbeSetID	Gene.Symbol	log2(sc+C)	log2(sc+Ox40)	log2(ADAM10si+C)	log2(ADAM10si+Ox50)	Fold induction log2[(sc+Ox40)/(sc+C)]	log2[(ADAM10si+Ox40)/(ADAM10si+C)]	The effects ADAM10si on Fold induction by Ox40 (H-G))
219270_at	CHAC1	4.803703742	8.198312686	5.385948444	8.006949548	**3.394608944**	2.621001104	-0.773607839
219475_at	OSGIN1	3.995688686	7.268037665	3.882302196	6.714567231	**3.272348979**	2.832265035	-0.440083944
221841_s_at	KLF4	4.017792971	7.190641298	4.487485295	7.681254381	**3.172848327**	3.193769086	0.020920759
202672_s_at	ATF3	6.659700456	9.828723785	6.748311257	9.785887857	**3.169023329**	3.0375766	-0.131446729
204748_at	PTGS2	7.097004713	10.20680854	7.888435709	10.65440501	**3.109803831**	2.765969301	-0.34383453
210118_s_at	IL1A	4.615137895	7.368468764	6.096681246	8.178840689	**2.753330869**	2.082159442	-0.671171427
219371_s_at	KLF2	5.781491767	8.32906882	6.392785262	8.049214092	**2.547577053**	1.65642883	-0.891148223
201195_s_at	SLC7A5	5.943054797	8.420933332	6.652820379	8.456062926	**2.477878535**	1.803242546	-0.674635989
203438_at	STC2	6.460635532	8.884899541	6.985337525	8.427216885	**2.424264009**	1.44187936	-0.982384649
203665_at	HMOX1	9.991974246	12.39845324	9.273143534	12.29486364	**2.406478996**	3.021720102	0.615241107
220266_s_at	KLF4	3.327283865	5.638876011	3.434915178	5.99137933	**2.311592146**	2.556464152	0.244872006
207029_at	KITLG	3.151881632	5.357321076	3.359027062	4.275864385	**2.205439444**	0.916837323	-1.288602121
211124_s_at	KITLG	2.964011187	5.155668728	3.110940088	4.220911211	**2.191657541**	1.109971123	-1.081686418
222162_s_at	ADAMTS1	7.127516346	9.297423055	7.882476838	9.343380988	**2.169906709**	1.46090415	-0.709002559
202241_at	TRIB1	4.524613826	6.659960764	5.051607393	6.90562254	**2.135346938**	1.854015147	-0.281331791
218145_at	TRIB3	7.617767845	9.743675	8.027678792	9.582506542	**2.125907155**	1.55482775	-0.571079405
205047_s_at	ASNS	6.880706694	8.878131624	6.83699635	8.209876714	**1.99742493**	1.372880364	-0.624544567
200907_s_at	PALLD	6.845936804	8.838042951	6.949864627	8.349376126	**1.992106147**	1.399511499	-0.592594648
202581_at	HSPA1A /// HSPA1B	6.378141669	8.226010579	6.285587962	8.179144583	**1.84786891**	1.893556621	0.045687711
200897_s_at	PALLD	7.538453403	9.370555858	7.316199841	8.773709917	**1.832102455**	1.457510076	-0.374592379
200906_s_at	PALLD	5.74476219	7.56297506	5.969141836	7.497157284	**1.81821287**	1.528015448	-0.290197422
221489_s_at	SPRY4	5.020900733	6.8263897	6.171394812	7.242014586	**1.805488968**	1.070619774	-0.734869194
200800_s_at	HSPA1A /// HSPA1B	8.273306436	10.03764847	8.158319026	10.2185278	**1.764342038**	2.060208774	0.295866736
212501_at	CEBPB	7.368199722	9.127343051	7.803010894	8.937675116	**1.759143329**	1.134664222	-0.624479107
204823_at	NAV3	7.238248609	8.988451277	7.334071892	8.53976908	**1.750202668**	1.205697188	-0.54450548
213112_s_at	SQSTM1	6.417749539	8.167627466	5.842723418	7.509443698	**1.749877927**	1.66672028	-0.083157647
206942_s_at	PMCH	4.003389709	5.696800404	3.590252153	3.899857078	**1.693410695**	0.309604925	-1.38380577
204977_at	DDX10	7.724663217	9.41372041	7.638149622	8.793905548	**1.689057193**	1.155755926	-0.533301267
205193_at	MAFF	8.155717098	9.803938397	9.291781409	10.46288084	**1.648221299**	1.171099434	-0.477121864
211506_s_at	IL8	9.982336135	11.6083431	8.724611639	11.23306171	**1.62600696**	2.508450067	0.882443107
209383_at	DDIT3	6.436087749	8.05633899	6.469105548	8.31074763	**1.620251241**	1.841642083	0.221390842
204363_at	F3	4.52562969	6.112285987	5.00821857	6.547386234	**1.586656297**	1.539167663	-0.047488634
220655_at	TNIP3	3.546038592	5.108458015	3.635570626	4.513530687	**1.562419423**	0.877960062	-0.684459361
201041_s_at	DUSP1	7.849153795	9.407591251	8.389343052	9.627746798	**1.558437455**	1.238403747	-0.320033708
36711_at	MAFF	9.550314263	11.10768707	10.5605574	11.47075859	**1.557372805**	0.910201187	-0.647171618
204285_s_at	PMAIP1	7.584912955	9.133786321	8.390146174	9.193560124	**1.548873365**	0.80341395	-0.745459415
200799_at	HSPA1A	8.682120636	10.20093176	8.450194861	10.23118421	**1.518811128**	1.780989353	0.262178225
201044_x_at	DUSP1	4.133257166	5.638476273	4.612788748	5.909849741	**1.505219107**	1.297060993	-0.208158114
209457_at	DUSP5	6.027687755	7.5202526	6.001241743	7.365449368	**1.492564845**	1.364207625	-0.12835722
202887_s_at	DDIT4	8.258191832	9.708188437	8.553813129	9.652333405	**1.449996605**	1.098520276	-0.351476329
202014_at	PPP1R15A	7.844319198	9.291631465	8.066037616	9.459148674	**1.447312268**	1.393111058	-0.05420121
37028_at	PPP1R15A	8.046292648	9.487122439	8.367028875	9.741154735	**1.440829791**	1.37412586	-0.06670393
203925_at	GCLM	9.54680657	10.98307426	9.121337026	10.48324519	**1.436267687**	1.361908168	-0.07435952

209850_s_at	CDC42EP2	5.402179937	6.794284898	5.778767564	7.031876471	**1.392104962**	1.253108906	-0.138996055
201694_s_at	EGR1	6.059755078	7.440331573	6.192773846	7.549859632	**1.380576495**	1.357085786	-0.02349071
217173_s_at	LDLR	5.377604472	6.756737979	4.677621919	6.615407239	**1.379133507**	1.93778532	0.558651813
205463_s_at	PDGFA	5.987412264	7.365871619	5.815323313	7.426928301	**1.378459355**	1.611604988	0.233145633
204286_s_at	PMAIP1	6.10257409	7.479016111	6.318293861	7.31927861	**1.376442021**	1.00098475	-0.375457271
216466_at	NAV3	3.371634502	4.738998481	3.290180084	4.620706048	**1.367363979**	1.330525964	-0.036838015
207528_s_at	SLC7A11	6.905154874	8.271923662	6.564274654	7.862093839	**1.366768789**	1.297819185	-0.068949604
202068_s_at	LDLR	7.888751546	9.255385501	7.220328977	9.103519234	**1.366633955**	1.883190257	0.516556302
202847_at	PCK2	6.042034131	7.393921132	6.166758246	7.252837652	**1.351887002**	1.086079406	-0.265807596
220892_s_at	PSAT1	6.729436491	8.062018562	6.833180385	7.627260539	**1.332582072**	0.794080155	-0.538501917
214014_at	CDC42EP2	4.372255081	5.693698349	4.604397487	5.813893848	**1.321443268**	1.209496361	-0.111946907
203349_s_at	ETV5	5.845109733	7.161735469	6.673321868	7.460053067	**1.316625736**	0.786731199	-0.529894537
220955_x_at	RAB23	6.149432173	7.457611417	6.300507819	7.508238501	**1.308179244**	1.207730682	-0.100448562
204341_at	TRIM16	7.689668753	8.996536156	7.220336703	8.115015753	**1.306867403**	0.894679051	-0.412188352
221371_at	TNFSF18	7.800580675	9.101611872	7.603451668	8.814589217	**1.301031197**	1.211137549	-0.089893647
210538_s_at	BIRC3	4.726490967	6.023350114	3.964674114	5.113062339	**1.296859147**	1.148388225	-0.148470922
212290_at	SLC7A1	5.056550354	6.351847006	5.555100963	6.576485316	**1.295296652**	1.021384354	-0.273912298
202067_s_at	LDLR	6.56078292	7.833967023	5.800173809	7.648151531	**1.273184103**	1.847977722	0.574793619
202147_s_at	IFRD1	5.987024455	7.25296117	5.933253205	7.234538119	**1.265936715**	1.301284915	0.035348199
212295_s_at	SLC7A1	9.097856178	10.35089404	9.368853225	10.26061381	**1.253037859**	0.891760582	-0.361277277
215253_s_at	RCAN1	4.641582605	5.891784653	4.723788598	5.822058823	**1.250202048**	1.098270225	-0.151931823
208230_s_at	NRG1	5.611029387	6.85550089	5.746318853	6.893793705	**1.244471503**	1.147474853	-0.09699665
206765_at	KCNJ2	6.685117747	7.927117803	6.756573392	7.174655082	**1.242000057**	0.41808169	-0.823918367
206237_s_at	NRG1	7.512481557	8.747038747	7.659678477	8.790071247	**1.23455719**	1.13039277	-0.10416442
204495_s_at	C15orf39	5.036629764	6.267022478	5.299199414	6.317532337	**1.230392713**	1.018332923	-0.212059791
201761_at	MTHFD2	8.574370636	9.803732099	8.854332694	9.565177728	**1.229361462**	0.710845033	-0.518516429
202146_at	IFRD1	7.107730661	8.33481698	6.975430893	8.298043759	**1.227086319**	1.322612866	0.095526547
204970_s_at	MAFG	6.16811373	7.368066595	6.535323666	7.294971121	**1.199952865**	0.759647455	-0.44030541
211668_s_at	PLAU	6.053880153	7.24674174	5.833346757	6.743180772	**1.192861588**	0.909834015	-0.283027573
210845_s_at	PLAUR	6.549023425	7.741737337	7.538951628	8.177797681	**1.192713913**	0.638846053	-0.55386786
202679_at	NPC1	7.511201564	8.702067305	7.7351651	8.765200777	**1.190865741**	1.030035677	-0.160830065
214696_at	C17orf91	8.75698586	9.944112643	8.819470133	9.747474276	**1.187126783**	0.928004143	-0.25912264
205207_at	IL6	7.985424626	9.158568637	7.934905395	9.607110465	**1.173144011**	1.672205071	0.49906106
212722_s_at	JMJD6	5.868131667	7.036888788	6.263054354	7.316771573	**1.168757121**	1.053717219	-0.115039902
211924_s_at	PLAUR	7.026525418	8.190238001	8.03048998	8.509269875	**1.163712583**	0.478779894	-0.684932689
203439_s_at	STC2	5.572923946	6.735232101	6.006554844	6.528358902	**1.162308155**	0.521804059	-0.640504096
202207_at	ARL4C	3.781792594	4.940814809	4.37749579	5.147552545	**1.159022216**	0.770056755	-0.388965461
200924_s_at	SLC3A2	7.228586145	8.381770666	6.998165446	8.359894777	**1.153184521**	1.361729331	0.20854481
210512_s_at	VEGFA	6.3412984	7.481072406	6.379017202	7.250435848	**1.139774005**	0.871418645	-0.26835536
201625_s_at	INSIG1	4.94691553	6.084976611	4.703862105	5.959489779	**1.13806108**	1.255627674	0.117566594
205931_s_at	CREB5	3.579397309	4.714042283	3.650587293	4.630615034	**1.134644974**	0.980027741	-0.154617233
205659_at	HDAC9	6.193253522	7.327193991	6.852609937	7.821652989	**1.133940469**	0.969043052	-0.164897417
205547_s_at	TAGLN	7.629521032	8.756715382	7.681911099	8.214031737	**1.12719435**	0.532120639	-0.595073711
201170_s_at	BHLHE40	4.855815262	5.982113332	5.312291547	6.275574038	**1.12629807**	0.963282491	-0.163015579
201466_s_at	JUN	7.594421865	8.716922727	8.004132596	8.881430187	**1.122500863**	0.877297591	-0.245203272
213895_at	EMP1	6.019047081	7.13740129	6.37417122	7.106376554	**1.11835421**	0.732205334	-0.386148875
206715_at	TFEC	6.387204682	7.503321741	7.003905602	7.4811301	**1.116117059**	0.477224498	-0.638892561
204224_s_at	GCH1	6.778943623	7.89430718	7.115325085	7.742587721	**1.115363557**	0.627262636	-0.488100921
204011_at	SPRY2	7.219994508	8.319706598	7.79789932	8.739675247	**1.09971209**	0.941775926	-0.157936164
204203_at	CEBPG	6.825894513	7.923400628	7.050643407	7.749652528	**1.097506115**	0.699009121	-0.398496993

210139_s_at	PMP22	9.133708107	10.23016622	9.684054396	10.10281248	**1.096458117**	0.418758087	-0.677700029
203574_at	NFIL3	6.809116276	7.901970852	6.907849951	7.81297271	**1.092854577**	0.905122759	-0.187731817
204420_at	FOSL1	7.180282775	8.2662772	7.694623763	8.309649068	**1.085994425**	0.615025305	-0.47096912
215401_at	---	3.38800449	4.468679005	3.378783178	4.391153345	**1.080674515**	1.012370166	-0.068304349
202393_s_at	KLF10	7.817420422	8.893599645	7.920048332	8.831780965	**1.076179223**	0.911732633	-0.16444659
218691_s_at	PDLIM4	4.225373591	5.290098752	4.569204248	5.195238662	**1.064725162**	0.626034414	-0.438690747
200670_at	XBP1	6.332170663	7.390437723	6.520149924	7.151337181	**1.05826706**	0.631187257	-0.427079803
222016_s_at	ZNF323	8.227284055	9.283390722	7.525805418	8.708055997	**1.056106667**	1.182250579	0.126143912
201626_at	INSIG1	7.688680779	8.743785248	7.254154993	8.784264562	**1.055104469**	1.530109569	0.4750051
211434_s_at	CCRL2	4.467928142	5.519258552	5.047090218	5.639408765	**1.051330411**	0.592318547	-0.459011863
201465_s_at	JUN	6.641914558	7.691346854	7.211515081	8.092734861	**1.049432296**	0.88121978	-0.168212516
208241_at	NRG1	6.211075762	7.252763915	5.91626135	7.166258911	**1.041688154**	1.249997561	0.208309408
200632_s_at	NDRG1	7.773793717	8.812785805	7.727421789	8.73844028	**1.038992088**	1.01101849	-0.027973598
203723_at	ITPKB	7.012316796	8.050603134	7.787351944	8.469368696	**1.038286338**	0.682016752	-0.356269587
203467_at	PMM1	4.734778371	5.76624775	4.855009233	5.894884395	**1.031469378**	1.039875163	0.008405784
218881_s_at	FOSL2	5.393612636	6.422407589	5.123916641	6.099566838	**1.028794954**	0.975650197	-0.053144757
208370_s_at	RCAN1	6.001844218	7.028068149	6.084739347	6.971473859	**1.026223931**	0.886734511	-0.139489419
202081_at	IER2	8.318471555	9.337610795	8.363879849	9.410352155	**1.019139241**	1.046472306	0.027333066
209884_s_at	SLC4A7	5.301351306	6.309792247	5.879052898	6.629486086	**1.008440941**	0.750433188	-0.258007753
210190_at	STX11	3.725533203	4.728598892	3.957635613	4.78857307	**1.00306569**	0.830937458	-0.172128232
205379_at	CBR3	7.316516588	8.317244669	6.723157917	7.56910253	**1.000728081**	0.845944613	-0.154783469
209287_s_at	CDC42EP3	6.241207554	7.227174376	7.245292533	7.737206251	**0.985966822**	0.491913718	-0.494053104
201693_s_at	EGR1	3.863294812	4.848281148	4.051680691	4.818669168	**0.984986336**	0.766988477	-0.217997858
204194_at	BACH1	4.32878418	5.31311595	4.490123835	5.132959592	**0.984331769**	0.642835757	-0.341496012
200664_s_at	DNAJB1	7.321840294	8.305465524	7.331704555	8.423756621	**0.98362523**	1.092052066	0.108426836
209631_s_at	GPR37	3.656039313	4.638850004	4.094111104	4.840141853	**0.982810691**	0.746030749	-0.236779943
218880_at	FOSL2	5.771544389	6.752342252	5.731571471	6.534562723	**0.980797864**	0.802991253	-0.177806611
212374_at	FEM1B	4.900966422	5.881253079	4.976064418	6.05538158	**0.980286657**	1.079317162	0.099030506
222235_s_at	CSGALNACT2 /// LOC	6.285414778	7.265632094	7.033735665	7.828453793	**0.980217316**	0.794718128	-0.185499188
208231_at	NRG1	3.831196113	4.809965189	3.640125816	4.65264282	**0.978769076**	1.012517004	0.033747928
201627_s_at	INSIG1	7.31822636	8.296018753	6.899567856	8.237175226	**0.977792393**	1.33760737	0.359814978
204614_at	SERPINB2	9.664535705	10.64232257	9.546940959	10.35228361	**0.977786869**	0.805342648	-0.172444221
205680_at	MMP10	7.402322403	8.379593845	8.580563544	8.850461783	**0.977271442**	0.269898239	-0.707373204
208025_s_at	HMGA2	6.195136142	7.171297679	7.734954416	8.131786342	**0.976161537**	0.396831926	-0.579329611
208078_s_at	SIK1	4.43870402	5.414541099	4.60956213	5.591750338	**0.97583708**	0.982188208	0.006351129
208960_s_at	KLF6	8.504437246	9.478188711	8.712865552	9.824286416	**0.973751465**	1.111420864	0.137669399
205479_s_at	PLAU	5.286687084	6.259863672	5.091624636	5.901557413	**0.973176589**	0.809932777	-0.163243812
204494_s_at	C15orf39	4.135587081	5.107478407	4.429519852	5.286678308	**0.971891326**	0.857158456	-0.11473287
205770_at	GSR	6.988649993	7.955545341	6.974578035	7.596648486	**0.966895349**	0.622070451	-0.344824897
203348_s_at	ETV5	5.302752492	6.267597358	5.90228593	6.782813379	**0.964844866**	0.880527449	-0.084317417
213407_at	PHLPP2	5.64217685	6.602435927	5.830244131	6.769229723	**0.960259077**	0.938985591	-0.021273486
214967_at	---	4.223105	5.18087394	3.994114421	5.265541574	**0.95776894**	1.271427153	0.313658213
206917_at	GNA13	5.297767046	6.253232755	4.61879072	5.605917306	**0.955465709**	0.987126586	0.031660877
200666_s_at	DNAJB1	7.612700953	8.55939866	7.603938866	8.994223396	**0.946697708**	1.39028453	0.443586822
214844_s_at	DOK5	6.805299893	7.746667834	6.755061336	7.347706089	**0.941367941**	0.592644754	-0.348723188
217127_at	CTH	3.674204336	4.614734359	3.518038347	4.129348444	**0.940530023**	0.611310096	-0.329219927
209882_at	RIT1	8.2249714	9.165417682	8.20907207	9.053024868	**0.940446282**	0.843952799	-0.096493483
202859_x_at	IL8	11.51681028	12.45254928	10.7617759	12.28037408	**0.935739**	1.518598173	0.582859173
209406_at	BAG2	6.122166806	7.057767721	5.907454835	6.309792085	**0.935600914**	0.40233725	-0.533263665
213672_at	MARS	5.124895166	6.05963948	5.36605773	6.266527181	**0.934744314**	0.900469451	-0.034274863

201471_s_at	SQSTM1	10.72571472	11.65455853	10.20001846	11.24350503	**0.928843812**	1.04348657	0.114642758
202150_s_at	NEDD9	6.831145603	7.759358576	7.651236564	8.340308932	**0.928212973**	0.689072369	-0.239140604
218651_s_at	LARP6	5.391296221	6.313956349	5.625250113	6.556164352	**0.922660127**	0.930914239	0.008254112
212723_at	JMJD6	7.409357756	8.329881485	7.590255742	8.582155788	**0.920523729**	0.991900046	0.071376317
204141_at	TUBB2A	8.479040055	9.399264128	8.426143942	9.064470241	**0.920224073**	0.638326299	-0.281897774
209355_s_at	PPAP2B	6.320122587	7.237775579	7.198100107	7.513844288	**0.917652992**	0.315744182	-0.60190881
212171_x_at	VEGFA	5.46880831	6.386187447	5.640749003	6.3513025	**0.917379137**	0.710553497	-0.206825641
210513_s_at	VEGFA	3.670938708	4.587294381	3.787147008	4.420561738	**0.916355673**	0.63341473	-0.282940943
202149_at	NEDD9	7.73425997	8.6473137	8.576233843	8.94643391	**0.91305373**	0.370200067	-0.542853663
214326_x_at	JUND	5.303261842	6.215640746	5.216998203	5.973528229	**0.912378904**	0.756530026	-0.155848878
202459_s_at	LPIN2	5.700299162	6.608100145	6.042186483	6.70474116	**0.907800983**	0.662554677	-0.245246305
219908_at	DKK2	3.622643313	4.528405227	3.43654688	3.337783196	**0.905761915**	-0.098763685	-1.004525599
208744_x_at	HSPH1	8.893101067	9.796726173	8.923039069	9.938777431	**0.903625106**	1.015738362	0.112113257
201695_s_at	PNP	9.419443088	10.31951309	9.588057862	10.26347497	**0.900070006**	0.675417105	-0.224652901
221577_x_at	GDF15 /// LOC10029	10.5359737	11.43321061	10.82576031	11.72309283	**0.897236903**	0.897332513	9.561E-05
201325_s_at	EMP1	9.341950038	10.23589601	9.798803109	10.31648087	**0.893945969**	0.517677761	-0.376268208
203751_x_at	JUND	4.650385364	5.543970863	4.454695083	5.405962371	**0.893585499**	0.951267288	0.057681789
205579_at	HRH1	5.183012855	6.076330241	5.059870271	5.985553627	**0.893317386**	0.925683356	0.03236597
207630_s_at	CREM	7.220307127	8.110051984	7.47286968	8.124777917	**0.889744858**	0.651908237	-0.237836621
208961_s_at	KLF6	9.234697468	10.11588702	9.543230578	10.45135921	**0.881189552**	0.908128635	0.026939083
206907_at	TNFSF9	3.696716442	4.574198979	3.78609545	4.374562016	**0.877482537**	0.588466565	-0.289015972
212226_s_at	PPAP2B	7.174642961	8.047572569	8.11391829	8.277188515	**0.872929608**	0.163270225	-0.709659383
209339_at	SIAH2	6.119008541	6.986827869	6.452028522	6.981785414	**0.867819327**	0.529756892	-0.338062435
212803_at	NAB2	4.442701378	5.309566897	4.608350148	5.663089349	**0.866865518**	1.054739201	0.187873683
202286_s_at	TACSTD2	6.513447758	7.376544964	6.016039991	6.867564421	**0.863097206**	0.851524431	-0.011572775
205205_at	RELB	4.803952621	5.666936584	4.598107959	5.632648815	**0.862983963**	1.034540856	0.171556893
205681_at	BCL2A1	4.992185092	5.851521673	5.657808617	6.437367495	**0.859336581**	0.779558878	-0.079777703
221752_at	SSH1	8.633678582	9.492983373	8.866842864	9.554003992	**0.859304791**	0.687161128	-0.172143663
204334_at	KLF7	7.064042267	7.922113496	7.260520821	7.9887606	**0.858071229**	0.728239779	-0.12983145
216375_s_at	ETV5	4.212407235	5.06556748	4.890459933	5.305515245	**0.853160245**	0.415055311	-0.438104933
204436_at	PLEKHO2	6.410798805	7.263129457	6.376223638	7.37382182	**0.852330652**	0.997598183	0.145267531
204937_s_at	ZNF274	7.109208688	7.960241467	7.363969789	8.328191841	**0.851032779**	0.964222052	0.113189273
205746_s_at	ADAM17	7.003301711	7.853085493	6.985068525	7.887933691	**0.849783782**	0.902865166	0.053081384
214056_at	---	4.753965266	5.601291378	4.404827423	4.971854631	**0.847326112**	0.567027208	-0.280298904
212458_at	SPRED2	5.02347773	5.869722997	5.059387633	5.755085793	**0.846245267**	0.695698161	-0.150547106
211527_x_at	VEGFA	3.752790162	4.598739436	4.062923235	4.37855972	**0.845949273**	0.315636485	-0.530312788
209921_at	SLC7A11	10.50488088	11.34875332	9.911034848	10.96059384	**0.843872437**	1.049558992	0.205686556
217678_at	SLC7A11	10.32445149	11.16530446	9.770085805	10.80998875	**0.840852972**	1.039902945	0.199049974
212978_at	LRRC8B	6.825437577	7.664169138	7.16210165	7.854001697	**0.838731561**	0.691900047	-0.146831514
209286_at	CDC42EP3	7.779521495	8.61666269	8.978583126	9.256560852	**0.837141195**	0.277977726	-0.559163469
209288_s_at	CDC42EP3	7.943967644	8.781018739	8.932339328	9.180414339	**0.837051095**	0.248075011	-0.588976084
209193_at	PIM1	3.774072563	4.606502718	3.805523492	4.37083866	**0.832430154**	0.565315167	-0.267114987
205580_s_at	HRH1	4.736641795	5.56729342	4.984424677	5.81733267	**0.830651625**	0.832907993	0.002256368
215350_at	SYNE1	2.956350604	3.784268783	2.980206631	3.601307194	**0.82791818**	0.621100563	-0.206817617
218522_s_at	MAP1S	5.479225573	6.30271389	6.193585913	6.749731996	**0.823488317**	0.556146083	-0.267342234
212373_at	FEM1B	5.834772218	6.657238302	5.659676093	6.440325823	**0.822466084**	0.78064973	-0.041816354
210286_s_at	SLC4A7	3.674941407	4.494833351	3.776974137	4.745344542	**0.819891944**	0.968370405	0.148478461
212230_at	PPAP2B	6.245812238	7.065571948	6.51548167	6.918376405	**0.81975971**	0.402894735	-0.416864974
201920_at	SLC20A1	8.398950711	9.214993811	9.014125308	9.607188854	**0.8160431**	0.593063547	-0.222979553
211031_s_at	CLIP2	5.319013744	6.134303238	5.743680114	6.52594826	**0.815289494**	0.782268146	-0.033021348

218647_s_at	YRDC	6.069270472	6.881682343	6.54692332	7.036645724	**0.812411872**	0.489722404	-0.322689468
221753_at	SSH1	7.381827199	8.190719885	8.045457408	8.746607408	**0.808892686**	0.70115	-0.107742686
202206_at	ARL4C	3.325334347	4.13068286	3.690574317	4.2388339	**0.805348514**	0.548259583	-0.257088931
208893_s_at	DUSP6	7.38565978	8.188515825	7.81743024	8.15902572	**0.802856045**	0.34159548	-0.461260565
206976_s_at	HSPH1	9.07168978	9.870619508	8.933511614	9.815765403	**0.798929729**	0.882253789	0.083324061
201464_x_at	JUN	9.127609025	9.925629682	9.476819329	9.998178767	**0.798020658**	0.521359438	-0.276661219
212274_at	LPIN1	7.803377004	8.601048609	8.106885155	8.767094047	**0.797671605**	0.660208892	-0.137462712
217655_at	LOC100127972	3.661397634	4.456198764	3.649569132	4.073067926	**0.79480113**	0.423498795	-0.371302335
216017_s_at	NAB2	4.114090772	4.90599158	4.180546136	5.155266809	**0.791900808**	0.974720673	0.182819865
209209_s_at	FERMT2	8.348797565	9.140140632	7.389547758	8.162842399	**0.791343068**	0.773294642	-0.018048426
212860_at	ZDHHC18	5.222189108	6.006755345	5.405182925	6.122592464	**0.784566237**	0.717409539	-0.067156698
203068_at	KLHL21	6.819065605	7.602012246	6.835744934	7.838899144	**0.782946642**	1.003154209	0.220207568
217168_s_at	HERPUD1	8.406506793	9.188355987	8.444705599	9.144714063	**0.781849194**	0.700008464	-0.08184073
202497_x_at	SLC2A3	6.016862433	6.796523249	6.015532712	6.710530548	**0.779660815**	0.694997836	-0.08466298
212665_at	TIPARP	8.640932028	9.41954181	9.536352402	10.01998109	**0.778609782**	0.483628686	-0.294981096
213327_s_at	USP12	6.993955981	7.768790567	7.201715846	7.876679714	**0.774834586**	0.674963869	-0.099870718
202464_s_at	PFKFB3	6.365306636	7.138857525	6.458157999	6.979005783	**0.773550889**	0.520847784	-0.252703105
206636_at	RASA2	5.448784203	6.218749152	5.291848459	5.622694611	**0.769964949**	0.330846152	-0.439118797
203100_s_at	CDYL	6.325856185	7.095665242	6.19065454	7.089897207	**0.769809057**	0.899242667	0.12943361
203752_s_at	JUND	9.61610087	10.3853088	9.339320478	10.04248382	**0.769207926**	0.703163342	-0.066044584
209447_at	SYNE1	7.637977086	8.406180322	7.972960848	8.584847611	**0.768203236**	0.611886763	-0.156316473
203343_at	UGDH	7.55499714	8.322536991	7.342977984	7.879174074	**0.767539851**	0.53619609	-0.231343761
212272_at	LPIN1	5.640009349	6.407050398	5.569394218	6.361607772	**0.767041049**	0.792213554	0.025172505
203098_at	CDYL	7.114032906	7.880608314	7.104097766	8.032768989	**0.766575408**	0.928671223	0.162095816
212810_s_at	SLC1A4	5.485159075	6.250595941	5.873811249	6.506091473	**0.765436866**	0.632280225	-0.133156641
205525_at	CALD1	5.999355491	6.763387512	5.761715991	6.80266503	**0.764032021**	1.040949038	0.276917018
208916_at	SLC1A5	6.029173844	6.793133953	6.330595624	6.808120171	**0.763960109**	0.477524546	-0.286435562
207535_s_at	NFKB2	5.325886358	6.089380215	4.947109176	5.779720203	**0.763493858**	0.832611026	0.069117169
204346_s_at	RASSF1	6.380199573	7.142739299	6.490060893	6.817650958	**0.762539726**	0.327590065	-0.434949661
213281_at	LOC100288387	5.14668571	5.909132383	5.427424419	5.750214934	**0.762446673**	0.322790515	-0.439656158
218871_x_at	CSGALNACT2	6.909711186	7.670315716	7.74361978	8.170136883	**0.76060453**	0.426517103	-0.334087426
208892_s_at	DUSP6	7.986254652	8.74262666	8.337615106	8.569289794	**0.756372008**	0.231674688	-0.52469732
206474_at	CDK17	6.848781566	7.604244405	6.844335826	7.435884101	**0.755462839**	0.591548275	-0.163914564
212724_at	RND3	9.254153229	10.00828198	9.31454763	10.11426472	**0.754128754**	0.799717086	0.045588333
209948_at	KCNMB1	3.676331853	4.429961724	3.764436354	3.758305486	**0.753629871**	-0.006130868	-0.759760739
206411_s_at	ABL2	4.956258965	5.709655436	5.018971977	5.599721662	**0.753396471**	0.580749685	-0.172646786
209239_at	NFKB1	7.799482735	8.552560136	7.639225437	8.442625297	**0.753077401**	0.80339986	0.050322459
214446_at	ELL2	5.958060163	6.707939438	6.340254689	7.107179473	**0.749879275**	0.766924785	0.01704551
206034_at	SERPINB8	7.393226591	8.141487725	7.529878934	8.085185046	**0.748261135**	0.555306113	-0.192955022
221050_s_at	GTPBP2	7.008727928	7.754299692	7.189253114	7.745333095	**0.745571764**	0.556079981	-0.189491783
201468_s_at	NQO1	10.63643257	11.38082662	10.07872851	10.80872452	**0.744394053**	0.72999601	-0.014398043
212276_at	LPIN1	6.871636187	7.614852946	6.933361153	7.50125367	**0.743216759**	0.567892517	-0.175324242
219279_at	DOCK10	4.076536756	4.818541929	4.626644484	5.23659419	**0.742005174**	0.609949706	-0.132055468
58367_s_at	ZNF419	5.329928857	6.0703621	5.591857298	6.129622598	**0.740433243**	0.5377653	-0.202667943
221276_s_at	SYNC	5.013503141	5.753694508	4.854274444	5.304840979	**0.740191367**	0.450566536	-0.289624832
212367_at	FEM1B	6.711881521	7.451648226	6.473901539	7.372385989	**0.739766705**	0.89848445	0.158717744
209699_x_at	AKR1C2	3.95142814	4.691009596	3.771422527	4.013378375	**0.739581456**	0.241955847	-0.497625609
202638_s_at	ICAM1	7.209096039	7.948533384	7.733464792	7.867722316	**0.739437345**	0.134257525	-0.60517982
213324_at	SRC	5.659005203	6.396592323	5.794955912	6.214850167	**0.73758712**	0.419894255	-0.317692865
213310_at	EIF2C2	6.621975166	7.358540704	6.725939793	7.206533848	**0.736565538**	0.480594055	-0.255971483

38037_at	HBEGF	6.719581785	7.455262496	6.610007002	7.767531054	**0.735680712**	1.157524053	0.421843341
207604_s_at	SLC4A7	7.224949195	7.960284887	7.916574643	8.764558731	**0.735335693**	0.847984088	0.112648396
221571_at	TRAF3	7.276349677	8.010065971	7.656653415	8.177641667	**0.733716293**	0.520988252	-0.212728041
215037_s_at	BCL2L1	6.120294876	6.853429827	6.098382203	6.806161753	**0.733134951**	0.70777955	-0.025355401
218223_s_at	PLEKHO1	6.710777105	7.440389707	7.029186169	7.838739979	**0.729612602**	0.80955381	0.079941208
210942_s_at	ST3GAL6	7.120580034	7.849016922	6.714560262	7.656600195	**0.728436888**	0.942039933	0.213603045
214430_at	GLA	7.998661246	8.723894014	8.4989402	9.014562849	**0.725232768**	0.515622649	-0.209610118
216060_s_at	DAAM1	6.482254561	7.205911983	6.299726863	6.897731191	**0.723657422**	0.598004328	-0.125653095
214965_at	SPATA2L	5.618258734	6.340811955	5.5170365	6.231423874	**0.722553222**	0.714387375	-0.008165847
209785_s_at	PLA2G4C	7.895434653	8.616141561	8.814954598	9.134101122	**0.720706908**	0.319146525	-0.401560383
202499_s_at	SLC2A3	7.038288213	7.757684197	7.134200744	7.590065789	**0.719395985**	0.455865046	-0.263530939
214508_x_at	CREM	7.195515868	7.914642327	7.378127015	8.024175258	**0.719126458**	0.646048243	-0.073078215
207000_s_at	PPP3CC	6.434345547	7.153317612	6.705479882	7.161547902	**0.718972065**	0.45606802	-0.262904045
206109_at	FUT1	4.958886603	5.677214958	5.193218566	5.602731865	**0.718328355**	0.409513299	-0.308815056
212791_at	C1orf216	6.243618655	6.960980203	6.174200839	6.923068293	**0.717361548**	0.748867454	0.031505906
202820_at	AHR	7.636723574	8.353928496	7.27082317	7.743030084	**0.717204922**	0.472206915	-0.244998007
204151_x_at	AKR1C1	4.319586369	5.03676304	4.016470886	4.389928846	**0.717176671**	0.37345796	-0.343718711
206374_at	DUSP8	4.358646501	5.075008946	4.448341848	5.158742995	**0.716362445**	0.710401146	-0.005961298
209653_at	KPNA4	7.790517257	8.500759684	7.794351268	8.387753234	**0.710242427**	0.593401966	-0.116840461
210479_s_at	RORA	5.578746565	6.287553522	5.930852526	6.64294011	**0.708806957**	0.712087584	0.003280627
201751_at	JOSD1	8.513380071	9.220775293	8.569773449	9.261786458	**0.707395222**	0.692013009	-0.015382213
203320_at	SH2B3	8.352131258	9.057050301	8.557665542	9.030710984	**0.704919043**	0.473045443	-0.2318736
221778_at	JHDM1D	5.488027708	6.190907568	5.338971646	6.025958072	**0.702879859**	0.686986426	-0.015893433
205409_at	FOSL2	3.832327566	4.535129323	4.053392018	4.518522688	**0.702801758**	0.46513067	-0.237671088
213262_at	SACS	7.935747623	8.637989537	7.585031079	8.030450635	**0.702241914**	0.445419555	-0.256822358
215707_s_at	PRNP	7.095185812	7.795641153	6.953217123	7.629368317	**0.70045534**	0.676151194	-0.024304147
219496_at	ANKRD57	4.296040705	4.994692808	4.421223931	4.783311988	**0.698652104**	0.362088057	-0.336564047
204507_s_at	PPP3R1	6.613071215	7.311252877	6.842576454	7.293471985	**0.698181662**	0.450895531	-0.247286131
206748_s_at	SPAG9	5.740477479	6.437327997	5.743662288	6.256763969	**0.696850518**	0.513101681	-0.183748837
201397_at	PHGDH	3.508937532	4.205360446	3.713132289	4.180353563	**0.696422914**	0.467221274	-0.229201641
213355_at	ST3GAL6	7.066411818	7.761602704	6.739653746	7.473999814	**0.695190887**	0.734346068	0.039155181
218318_s_at	NLK	6.038414031	6.733299986	5.829583618	6.502909595	**0.694885954**	0.673325977	-0.021559977
204222_s_at	GLIPR1	9.265372665	9.959961723	9.377445703	9.918348428	**0.694589057**	0.540902724	-0.153686333
212923_s_at	C6orf145	8.007059067	8.70103769	8.081176837	8.716723242	**0.693978624**	0.635546405	-0.058432218
203821_at	HBEGF	7.789286779	8.480348652	7.676211015	8.791914071	**0.691061873**	1.115703056	0.424641183
219423_x_at	TNFRSF25	6.384184927	7.073802011	6.892317775	7.384590257	**0.689617085**	0.492272482	-0.197344603
200798_x_at	MCL1	7.902857771	8.59079413	7.563860113	8.047014167	**0.687936359**	0.483154054	-0.204782305
212111_at	STX12	8.891995416	9.579869404	9.134728827	9.640057463	**0.687873988**	0.505328637	-0.182545351
204642_at	S1PR1	7.869507851	8.556983655	7.817032236	8.329023895	**0.687475804**	0.511991659	-0.175484146
219474_at	C3orf52	4.006820313	4.692957735	4.056346387	4.781293817	**0.686137422**	0.72494743	0.038810008
208707_at	EIF5	4.733252203	5.418200826	4.6808635	5.271799891	**0.684948623**	0.590936392	-0.094012231
219973_at	ARSJ	6.49462402	7.177761823	6.401662763	6.996684602	**0.683137804**	0.595021839	-0.088115965
221823_at	C5orf30	6.347993453	7.030008194	6.559874554	6.716375244	**0.682014741**	0.15650069	-0.525514051
215198_s_at	CALD1	5.029099408	5.709111863	4.594509443	5.747810783	**0.680012455**	1.15330134	0.473288885
218478_s_at	ZCCHC8	7.028910061	7.708691939	6.799044646	7.532500305	**0.679781878**	0.73345566	0.053673782
208813_at	GOT1	7.872004871	8.551526686	7.951037389	8.495690151	**0.679521815**	0.544652762	-0.134869052
212441_at	KIAA0232	7.792743237	8.469587525	7.61049261	8.384968995	**0.676844288**	0.774476385	0.097632097
216283_s_at	PVR	5.602473198	6.277765998	6.065200392	6.653882136	**0.675292799**	0.588681744	-0.086611056
209610_s_at	SLC1A4	6.613788692	7.287687269	6.85393596	7.381178939	**0.673898577**	0.527242979	-0.146655598
206649_s_at	TFE3	5.003465231	5.67670306	4.91544067	5.58923796	**0.673237829**	0.67379729	0.000559461

202763_at	CASP3	7.490459414	8.163088556	7.555430662	8.031195579	**0.672629142**	0.475764917	-0.196864225
214682_at	LOC399491	4.011672475	4.684134545	4.221306885	5.209175301	**0.67246207**	0.987868415	0.315406345
221904_at	FAM131A	5.064376641	5.735914628	5.899610511	6.250082911	**0.671537987**	0.3504724	-0.321065587
204958_at	PLK3	5.038423339	5.709234713	5.205535991	5.751060693	**0.670811373**	0.545524702	-0.125286671
213005_s_at	KANK1	7.22478099	7.89219837	7.904342972	8.525863359	**0.66741738**	0.621520387	-0.045896993
218442_at	TTC4	6.141548438	6.808721954	6.146315309	6.638965785	**0.667173516**	0.492650476	-0.17452304
201844_s_at	RYBP	7.173765336	7.840803902	7.18948571	7.8136748	**0.667038566**	0.62418909	-0.042849477
219053_s_at	VPS37C	8.08077577	8.744958683	8.126272181	8.7263039	**0.664182913**	0.600031719	-0.064151194
209373_at	MALL	8.496484942	9.158880254	8.512908763	8.829645992	**0.662395313**	0.316737229	-0.345658084
220471_s_at	MYCT1	7.390697002	8.048914432	7.490300702	8.08167992	**0.658217429**	0.591379218	-0.066838211
201324_at	EMP1	10.27336442	10.9307417	10.59325345	10.98295947	**0.657377275**	0.38970602	-0.267671255
215199_at	CALD1	4.515173059	5.170773941	4.049158914	5.014685043	**0.655600882**	0.965526129	0.309925247
209674_at	CRY1	6.463390089	7.116728088	6.233429474	6.754372741	**0.653337999**	0.520943267	-0.132394732
214577_at	MAP1B	7.226425333	7.875939726	7.077073295	7.708022868	**0.649514394**	0.630949573	-0.018564821
202208_s_at	ARL4C	3.84908899	4.498264637	4.244125474	4.756363157	**0.649175647**	0.512237683	-0.136937964
201467_s_at	NQO1	8.573500504	9.221534935	8.048306229	8.751487381	**0.648034431**	0.703181151	0.05514672
210756_s_at	NOTCH2	5.425334481	6.073045502	6.056494054	6.392148939	**0.64771102**	0.335654885	-0.312056135
209210_s_at	FERMT2	10.26036791	10.90745721	9.166184433	9.821253602	**0.647089295**	0.655069169	0.007979874
220027_s_at	RASIP1	7.742541041	8.386902921	7.805644332	8.149760169	**0.644361879**	0.344115837	-0.300246043
212434_at	GRPEL1	6.898231526	7.542016288	6.96070376	7.391970206	**0.643784762**	0.431266446	-0.212518316
218486_at	KLF11	4.797949719	5.440869165	4.584560623	5.12829517	**0.642919446**	0.543734547	-0.099184899
221064_s_at	UNKL	5.492745404	6.135590076	5.346328121	5.868170422	**0.642844672**	0.521842301	-0.121002371
205599_at	TRAF1	3.435737712	4.078492655	3.217284725	3.299913935	**0.642754943**	0.08262921	-0.560125733
201118_at	PGD	10.07559716	10.71736995	10.16372389	10.57994005	**0.641772791**	0.416216157	-0.225556634
214212_x_at	FERMT2	7.574515542	8.21627366	6.910878155	7.637062235	**0.641758118**	0.72618408	0.084425962
208891_at	DUSP6	8.591371853	9.232636247	8.803048558	9.049283073	**0.641264394**	0.246234516	-0.395029878
219492_at	CHIC2	8.918770997	9.559762263	9.061283919	9.647124884	**0.640991266**	0.585840965	-0.055150301
202401_s_at	SRF	6.971600518	7.611090163	7.033734373	7.586108661	**0.639489645**	0.552374287	-0.087115358
203935_at	ACVR1	8.182886369	8.821962394	8.098821308	8.614686384	**0.639076025**	0.515865076	-0.123210949
212112_s_at	STX12	9.365915908	10.0044877	9.57553586	10.03827852	**0.638571796**	0.462742657	-0.175829139
220030_at	STYK1	5.957759357	6.596125463	5.81648427	6.086322242	**0.638366106**	0.269837972	-0.368528133
212470_at	SPAG9	7.496384922	8.134705668	7.437881691	8.207448696	**0.638320746**	0.769567004	0.131246258
202123_s_at	ABL1	8.441767613	9.079495854	9.136197459	9.424996343	**0.637728241**	0.288798884	-0.348929357
216236_s_at	SLC2A14 /// SLC2A3	6.438334425	7.075213746	6.441952244	7.113041026	**0.636879321**	0.671088782	0.034209461
212816_s_at	CBS	6.076266059	6.713028453	5.930813767	6.455083561	**0.636762393**	0.524269794	-0.112492599
206085_s_at	CTH	3.410395165	4.047058248	3.240632876	3.727638125	**0.636663084**	0.487005248	-0.149657835
204896_s_at	PTGER4	5.067830555	5.702646391	5.246550735	5.504295483	**0.634815836**	0.257744748	-0.377071088
215120_s_at	SAMD4A	3.479876128	4.112740129	3.601364049	3.849604425	**0.632864002**	0.248240376	-0.384623626
204094_s_at	TSC22D2	7.404292195	8.036984487	7.362765173	7.800472927	**0.632692292**	0.437707755	-0.194984537
212666_at	SMURF1	6.197140308	6.829155079	6.372055957	6.969069171	**0.632014771**	0.597013215	-0.035001557
209061_at	NCOA3	6.202082909	6.833506798	6.185346212	6.673286925	**0.631423888**	0.487940713	-0.143483176
222088_s_at	SLC2A14 /// SLC2A3	6.077431202	6.708691855	6.221128733	6.601804175	**0.631260654**	0.380675442	-0.250585212
204729_s_at	STX1A	4.305046257	4.934534966	4.464420692	5.217071789	**0.629488709**	0.752651097	0.123162388
202402_s_at	CARS	7.469519687	8.098862947	7.626595255	8.148321484	**0.629343261**	0.521726229	-0.107617032
200779_at	ATF4	10.90193683	11.53073065	10.76255834	11.52403013	**0.628793823**	0.76147179	0.132677967
215485_s_at	ICAM1	5.948630497	6.576678654	6.253043131	6.604667073	**0.628048157**	0.351623943	-0.276424214
221944_at	FLJ42627	4.512739078	5.140667739	4.473649173	5.171418665	**0.627928661**	0.697769492	0.069840831
221011_s_at	LBH	2.960052138	3.587857115	3.066625154	3.619617118	**0.627804976**	0.552991964	-0.074813012
209020_at	C20orf111	7.40502063	8.032373594	7.091066507	7.833636535	**0.627352964**	0.742570027	0.115217064
200796_s_at	MCL1	5.548503624	6.1749721	5.383402292	5.891107118	**0.626468475**	0.507704826	-0.118763649

202260_s_at	STXBP1	6.907939319	7.534379673	7.141136646	7.451803244	**0.626440353**	0.310666598	-0.315773755
212233_at	MAP1B	10.33254088	10.95895522	10.20084702	10.75896291	**0.626414338**	0.55811589	-0.068298448
201845_s_at	RYBP	6.483155058	7.109531273	6.671808862	7.287256169	**0.626376215**	0.615447308	-0.010928907
202695_s_at	STK17A	5.077701476	5.703210504	4.984730446	5.251998735	**0.625509028**	0.267268289	-0.358240739
212110_at	SLC39A14	8.256081201	8.881473429	8.398881385	8.668670241	**0.625392229**	0.269788857	-0.355603372
215977_x_at	GK	3.637136562	4.262167449	3.801125478	3.845053091	**0.625030887**	0.043927613	-0.581103274
216607_s_at	CYP51A1	7.193450668	7.81781484	6.443368064	7.265131636	**0.624364172**	0.821763572	0.1973994
219326_s_at	B3GNT2	6.361114866	6.98500906	6.470749169	6.878171568	**0.623894193**	0.407422399	-0.216471794
204506_at	PPP3R1	6.880640969	7.503735508	7.209084483	7.550209084	**0.623094539**	0.341124601	-0.281969939
211352_s_at	NCOA3	6.333239657	6.956141885	6.191620139	6.986173842	**0.622902228**	0.794553702	0.171651474
219569_s_at	TMEM22	7.783715874	8.405749599	7.853082422	8.427868437	**0.622033725**	0.574786016	-0.04724771
219558_at	ATP13A3	7.785431588	8.407101834	7.670605797	8.055469537	**0.621670246**	0.38486374	-0.236806506
202071_at	SDC4	6.218060661	6.838611703	6.055107684	6.205449259	**0.620551042**	0.150341575	-0.470209467
213567_at	---	6.948098412	7.568454746	6.700096084	7.167360705	**0.620356334**	0.467264621	-0.153091713
218368_s_at	TNFRSF12A	7.30572816	7.925906187	7.335192864	8.059728507	**0.620178027**	0.724535643	0.104357616
213191_at	TICAM1	5.705929579	6.325208028	5.799391423	6.3625997	**0.619278449**	0.563208277	-0.056070172
213532_at	ADAM17	8.886237153	9.505207719	9.048633606	9.517403506	**0.618970566**	0.4687699	-0.150200665
219240_s_at	C10orf88	5.85524996	6.473667907	5.736307645	6.369430437	**0.618417947**	0.633122792	0.014704844
209967_s_at	CREM	6.995788999	7.612283125	6.993551801	7.523983343	**0.616494126**	0.530431542	-0.086062584
204221_x_at	GLIPR1	7.471423793	8.08790077	7.700481417	8.191010361	**0.616476977**	0.490528944	-0.125948034
219826_at	ZNF419	5.862792039	6.478915815	5.825858165	6.412774679	**0.616123776**	0.586916514	-0.029207262
215493_x_at	BTN2A1	6.730427567	7.346187708	7.169131484	7.760564339	**0.615760141**	0.591432855	-0.024327285
212468_at	SPAG9	5.671016704	6.28583957	5.775020456	6.336029577	**0.614822866**	0.561009121	-0.053813745
212444_at	---	6.886924687	7.501705164	6.902859526	7.147114793	**0.614780477**	0.244255267	-0.37052521
202097_at	NUP153	7.684681899	8.298768434	7.362408353	7.811729173	**0.614086536**	0.44932082	-0.164765716
200808_s_at	ZYX	9.075496233	9.689088275	9.025306151	9.536394139	**0.613592042**	0.511087988	-0.102504054
215886_x_at	USP12	3.864422913	4.47796801	3.973813077	4.298972035	**0.613545097**	0.325158958	-0.288386139
202719_s_at	TES	8.013350863	8.625749988	8.077210819	8.58679257	**0.612399125**	0.509581751	-0.102817374
213700_s_at	---	4.931190442	5.543322026	5.078348348	5.804133708	**0.612131583**	0.725785359	0.113653776
218611_at	IER5	7.855245395	8.466793365	7.70998588	8.189756906	**0.611547969**	0.479771026	-0.131776943
206867_at	GCKR	4.281105858	4.89231772	4.754836995	5.077291068	**0.611211862**	0.322454073	-0.288757788
200769_s_at	MAT2A	6.085679937	6.696519896	6.04945004	6.591514883	**0.610839958**	0.542064843	-0.068775116
211841_s_at	TNFRSF25	4.639237864	5.249460619	4.893395067	5.475052517	**0.610222755**	0.581657449	-0.028565306
201846_s_at	RYBP	6.747895794	7.357688677	7.076949069	7.742338114	**0.609792883**	0.665389045	0.055596162
200797_s_at	MCL1	9.327063101	9.935791017	9.233344962	9.730427922	**0.608727916**	0.49708296	-0.111644956
201866_s_at	NR3C1	6.357040048	6.965551134	6.731065355	7.197351132	**0.608511086**	0.466285777	-0.142225309
218566_s_at	CHORDC1	7.265235845	7.873360493	6.892978311	7.477497467	**0.608124648**	0.584519157	-0.023605491
208775_at	XPO1	9.113084524	9.720673163	9.03806016	9.646169449	**0.607588639**	0.608109289	0.00052065
213793_s_at	HOMER1	3.760843695	4.367536068	4.128453045	4.750656099	**0.606692373**	0.622203054	0.015510682
219092_s_at	IPPK	5.011048648	5.617560172	5.462964123	5.822191246	**0.606511524**	0.359227123	-0.247284401
203192_at	ABCB6	4.620555702	5.226521409	4.65565643	4.948680765	**0.605965707**	0.293024335	-0.312941372
205282_at	LRP8	4.468334264	5.07413501	4.271951763	4.574733103	**0.605800746**	0.302781341	-0.303019406
210847_x_at	TNFRSF25	4.251346501	4.856300846	4.486153908	5.047016386	**0.604954345**	0.560862478	-0.044091866
210426_x_at	RORA	6.278140125	6.883070944	6.500190788	7.311102429	**0.604930819**	0.810911641	0.205980822
202656_s_at	SERTAD2	6.670736817	7.275437515	6.855893449	7.408106403	**0.604700698**	0.552212954	-0.052487744
201531_at	ZFP36	6.640098575	7.244050055	6.44763924	7.368716725	**0.603951481**	0.921077485	0.317126005
212635_at	TNPO1	9.331534616	9.935170375	9.224220259	9.555104025	**0.603635759**	0.330883766	-0.272751993
220494_s_at	---	5.138082465	5.739170106	5.570917732	5.666921306	**0.601087641**	0.096003574	-0.505084068
201739_at	SGK1	9.176473863	9.776544355	9.304519913	9.982204555	**0.600070493**	0.677684642	0.077614149
219778_at	ZFPM2	7.061532389	7.661242128	6.607963161	6.880603482	**0.599709739**	0.272640322	-0.327069417

215706_x_at	ZYX	9.467545944	10.06705304	9.538723533	10.00305967	**0.599507095**	0.464336141	-0.135170954
209360_s_at	RUNX1	4.776919151	5.376277869	4.892371415	5.602519198	**0.599358719**	0.710147783	0.110789064
200790_at	ODC1	10.2373813	10.83570272	10.15815644	10.71189763	**0.59832142**	0.55374119	-0.04458023
216959_x_at	NRCAM	6.811566385	7.408314014	7.485609859	7.596646084	**0.596747629**	0.111036225	-0.485711404
215359_x_at	ZNF44	5.011192608	5.606423031	4.858486558	5.786721451	**0.595230423**	0.928234894	0.333004471
206868_at	STARD8	4.592538574	5.1870528	4.740877874	4.796159673	**0.594514226**	0.055281799	-0.539232427
209372_x_at	TUBB2A /// TUBB2B	4.652590295	5.246420822	4.689632795	5.158119549	**0.593830527**	0.468486754	-0.125343773
33304_at	ISG20	6.100641476	6.694455855	7.515199708	7.83187973	**0.593814379**	0.316680022	-0.277134357
209621_s_at	PDLIM3	5.871874113	6.465356306	5.960133827	6.332788092	**0.593482193**	0.372654265	-0.220827928
215236_s_at	PICALM	7.911199471	8.504559945	7.736104119	8.304810459	**0.593360474**	0.56870634	-0.024654134
214085_x_at	GLIPR1	10.12842882	10.72132139	10.3079325	10.818917	**0.592892568**	0.5109845	-0.081908068
211282_x_at	TNFRSF25	5.486016475	6.07834737	6.053764125	6.492305873	**0.592330895**	0.438541748	-0.153789147
212971_at	CARS	9.844673912	10.43695823	10.11796639	10.55613859	**0.592284313**	0.438172203	-0.15411211
209446_s_at	C7orf44	3.144690787	3.736358847	3.208366474	3.925155006	**0.59166806**	0.716788532	0.125120472
32541_at	PPP3CC	5.533886146	6.125546907	5.569900157	6.03794515	**0.591660761**	0.468044993	-0.123615768
209212_s_at	KLF5	3.444572785	4.036156304	3.715590851	4.218726368	**0.59158352**	0.503135517	-0.088448003
202021_x_at	EIF1	10.97847451	11.56962275	11.21178115	11.68211152	**0.59114824**	0.47033037	-0.12081787
211564_s_at	PDLIM4	8.171851298	8.762111328	8.772876254	9.010127435	**0.59026003**	0.237251181	-0.353008849
212190_at	SERPINE2	7.152193864	7.740437803	7.983240229	8.219975081	**0.588243939**	0.236734852	-0.351509087
202460_s_at	LPIN2	4.735510346	5.322583622	4.891006732	5.434034355	**0.587073276**	0.543027624	-0.044045653
203099_s_at	CDYL	6.5634118	7.150220664	6.511125285	7.286567455	**0.586808864**	0.77544217	0.188633306
209062_x_at	NCOA3	6.220242688	6.805752958	6.207675494	6.96720807	**0.58551027**	0.759532576	0.174022306

Supplementary Table 4. Categories of genes induced by OxPAPC by 1.5 fold in HAECs.
DAVID analysis was used for the identification of gene categories.
http://david.abcc.ncifcrf.gov/home.jsp

Category	**Term**	**Count**	**%**	**PValue**	**Genes**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichment**	**Bonferroni**	**Benjamini**	**FDR**
SP_PIR_KEYWORDS	phosphoprotein	238	56	1.20E-15	201464_X_A	418	7263	19235	1.507914862	4.92E-13	4.92E-13	1.71E-12
UP_SEQ_FEATURE	domain:Leucine-zipper	22	5.176470588	2.50E-14	201464_X_A	418	110	19113	9.144976077	3.35E-11	3.35E-11	4.09E-11
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	61	14.35294118	5.76E-14	201464_X_A	350	804	13528	2.932508884	1.35E-10	1.35E-10	1.01E-10
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	17	4	5.98E-14	201464_X_A	401	53	16659	13.32531878	4.52E-11	4.52E-11	9.12E-11
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	61	14.35294118	8.89E-14	201464_X_A	350	812	13528	2.903617171	2.08E-10	1.04E-10	1.56E-10
GOTERM_BP_FAT	GO:0010941~regulation of cell death	61	14.35294118	1.05E-13	201464_X_A	350	815	13528	2.89292901	2.46E-10	8.18E-11	1.84E-10
SMART	SM00338:BRLZ	17	4	3.15E-13	201464_X_A	247	53	9079	11.7900084	5.39E-11	5.39E-11	3.85E-10
UP_SEQ_FEATURE	DNA-binding region:Basic motif	24	5.647058824	9.11E-13	201464_X_A	418	161	19113	6.816131237	1.22E-09	6.12E-10	1.49E-09
SP_PIR_KEYWORDS	cytoplasm	129	30.35294118	9.68E-12	209636_AT,	418	3332	19235	1.78156071	3.90E-09	1.95E-09	1.35E-08
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	35	8.235294118	3.65E-11	208230_S_A	350	354	13528	3.821468927	8.54E-08	2.13E-08	6.39E-08
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	35	8.235294118	5.35E-11	208230_S_A	350	359	13528	3.768245125	1.25E-07	2.50E-08	9.37E-08
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	35	8.235294118	5.74E-11	208230_S_A	350	360	13528	3.757777778	1.34E-07	2.24E-08	1.00E-07
SP_PIR_KEYWORDS	Apoptosis	32	7.529411765	3.01E-10	218000_S_A	418	381	19235	3.864923583	1.21E-07	4.04E-08	4.20E-07
GOTERM_BP_FAT	GO:0008219~cell death	50	11.76470588	3.83E-10	201464_X_A	350	719	13528	2.687860123	8.96E-07	1.28E-07	6.71E-07
GOTERM_BP_FAT	GO:0016265~death	50	11.76470588	4.82E-10	201464_X_A	350	724	13528	2.669297553	1.13E-06	1.41E-07	8.44E-07
GOTERM_BP_FAT	GO:0012501~programmed cell death	45	10.58823529	6.05E-10	201464_X_A	350	611	13528	2.846668225	1.42E-06	1.57E-07	1.06E-06
GOTERM_BP_FAT	GO:0006916~anti-apoptosis	25	5.882352941	6.58E-10	212171_X_A	350	206	13528	4.690707351	1.54E-06	1.54E-07	1.15E-06
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	48	11.29411765	7.37E-10	201464_X_A	350	685	13528	2.708421272	1.73E-06	1.57E-07	1.29E-06
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	48	11.29411765	1.18E-09	201464_X_A	350	695	13528	2.669451182	2.77E-06	2.31E-07	2.07E-06
GOTERM_BP_FAT	GO:0006915~apoptosis	44	10.35294118	1.24E-09	201464_X_A	350	602	13528	2.825021357	2.91E-06	2.24E-07	2.18E-06
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	45	10.58823529	3.11E-09	201464_X_A	350	644	13528	2.70079858	7.29E-06	5.20E-07	5.45E-06
GOTERM_BP_FAT	GO:0010033~response to organic substance	48	11.29411765	3.83E-09	201464_X_A	350	721	13528	2.573188032	8.96E-06	5.97E-07	6.70E-06
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	45	10.58823529	4.98E-09	201464_X_A	350	654	13528	2.659501966	1.17E-05	7.29E-07	8.72E-06
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	39	9.176470588	2.14E-08	201464_X_A	337	542	12983	2.77211011	1.39E-05	1.39E-05	3.19E-05
SP_PIR_KEYWORDS	activator	34	8	3.98E-08	209636_AT,	418	520	19235	3.008787265	1.60E-05	4.01E-06	5.56E-05
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	33	7.764705882	7.39E-08	201464_X_A	350	430	13528	2.966272425	1.73E-04	1.02E-05	1.29E-04
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	33	7.764705882	8.64E-08	201464_X_A	350	433	13528	2.945720884	2.02E-04	1.12E-05	1.51E-04
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	33	7.764705882	9.65E-08	201464_X_A	350	435	13528	2.93217734	2.26E-04	1.19E-05	1.69E-04
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nu	41	9.647058824	9.83E-08	201464_X_A	350	624	13528	2.53959707	2.30E-04	1.15E-05	1.72E-04
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	25	5.882352941	2.34E-07	201464_X_A	350	278	13528	3.475847893	5.47E-04	2.61E-05	4.10E-04
GOTERM_CC_FAT	GO:0005829~cytosol	60	14.11764706	2.65E-07	209636_AT,	290	1330	12782	1.988384755	7.29E-05	7.29E-05	3.50E-04
GOTERM_MF_FAT	GO:0008134~transcription factor binding	35	8.235294118	4.64E-07	209636_AT,	337	513	12983	2.62842649	3.02E-04	1.51E-04	6.93E-04
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	37	8.705882353	4.98E-07	201464_X_A	350	564	13528	2.535643364	0.00116367	5.29E-05	8.71E-04
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	9	2.117647059	5.01E-07	204194_AT,	401	31	16659	12.06105703	3.78E-04	1.89E-04	7.63E-04
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	48	11.29411765	7.15E-07	201464_X_A	350	857	13528	2.164840807	0.0016723	7.28E-05	0.001252
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	33	7.764705882	7.70E-07	201464_X_A	350	477	13528	2.673998203	0.00179991	7.51E-05	0.001348
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	33	7.764705882	9.24E-07	201464_X_A	350	481	13528	2.651761212	0.00216035	8.65E-05	0.001618
GOTERM_MF_FAT	GO:0003700~transcription factor activity	52	12.23529412	9.90E-07	209636_AT,	337	975	12983	2.054678536	6.44E-04	2.15E-04	0.001479
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	45	10.58823529	1.01E-06	201464_X_A	350	787	13528	2.210056272	0.00235069	9.05E-05	0.001761
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	37	8.705882353	1.01E-06	201464_X_A	350	581	13528	2.461450701	0.00235897	8.75E-05	0.001767
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	26	6.117647059	1.02E-06	201464_X_A	165	267	5085	3.00102145	1.37E-04	1.37E-04	0.001194
GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	17	4	1.06E-06	201845_S_A	337	145	12983	4.51675023	6.93E-04	1.73E-04	0.00159
UP_SEQ_FEATURE	mutagenesis site	78	18.35294118	1.19E-06	209636_AT,	418	2045	19113	1.744029667	0.0016006	5.34E-04	0.001955
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	14	3.294117647	1.33E-06	212470_AT,	350	98	13528	5.521632653	0.00311822	1.12E-04	0.002337
GOTERM_BP_FAT	GO:0001775~cell activation	24	5.647058824	1.54E-06	209636_AT,	350	287	13528	3.232175212	0.00359264	1.24E-04	0.002693
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	42	9.882352941	1.95E-06	201464_X_A	350	727	13528	2.232957359	0.00454882	1.52E-04	0.003411
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	21	4.941176471	2.02E-06	201464_X_A	350	229	13528	3.544454148	0.00471294	1.52E-04	0.003535
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	13	3.058823529	2.87E-06	205745_X_A	350	89	13528	5.645714286	0.00668703	2.10E-04	0.00502
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	69	16.23529412	3.08E-06	201464_X_A	337	1512	12983	1.758095474	0.00200456	4.01E-04	0.004603
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	29	6.823529412	3.28E-06	201464_X_A	350	414	13528	2.707467219	0.0076541	2.33E-04	0.005749

GOTERM_BP_FAT	GO:0051789~response to protein stimulus	14	3.294117647	3.65E-06	214577_AT,	350	107	13528	5.057196262	0.00850652	2.51E-04	0.006392
GOTERM_BP_FAT	GO:0001568~blood vessel development	21	4.941176471	5.67E-06	201464_X_A	350	245	13528	3.312979592	0.01317632	3.79E-04	0.009924
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	19	4.470588235	6.11E-06	201464_X_A	350	205	13528	3.582327526	0.01418664	3.97E-04	0.01069
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	17	4	7.74E-06	212470_AT,	350	169	13528	3.888013525	0.01794522	4.89E-04	0.013548
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	13	3.058823529	7.97E-06	205745_X_A	350	98	13528	5.127230321	0.01847606	4.91E-04	0.013952
GOTERM_BP_FAT	GO:0001944~vasculature development	21	4.941176471	8.15E-06	201464_X_A	350	251	13528	3.233784861	0.01889823	4.89E-04	0.014274
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	31	7.294117647	8.72E-06	201464_X_A	350	485	13528	2.470503682	0.02018972	5.10E-04	0.01526
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	31	7.294117647	8.72E-06	201464_X_A	350	485	13528	2.470503682	0.02018972	5.10E-04	0.01526
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	18	4.235294118	9.90E-06	212470_AT,	350	192	13528	3.623571429	0.02290057	5.65E-04	0.017332
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	30	7.058823529	1.10E-05	201464_X_A	350	466	13528	2.488289393	0.02551321	6.15E-04	0.019335
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II pron	26	6.117647059	1.18E-05	201464_X_A	350	371	13528	2.708725452	0.02723833	6.42E-04	0.020661
SP_PIR_KEYWORDS	stress response	10	2.352941176	1.20E-05	201739_AT,	418	66	19235	6.972234305	0.00484047	9.70E-04	0.016811
SP_PIR_KEYWORDS	kinase	34	8	1.89E-05	212470_AT,	418	688	19235	2.274083398	0.00758494	0.00126817	0.026377
INTERPRO	IPR011700:Basic leucine zipper	6	1.411764706	1.92E-05	209383_AT,	401	15	16659	16.61745636	0.01436473	0.00481136	0.029189
GOTERM_BP_FAT	GO:0048660~regulation of smooth muscle cell proliferation	9	2.117647059	2.01E-05	201464_X_A	350	46	13528	7.562236025	0.0458742	0.0010667	0.03513
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	25	5.882352941	2.54E-05	209636_AT,	337	363	12983	2.653252242	0.01640366	0.00275282	0.037935
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	23	5.411764706	2.96E-05	218000_S_A	350	320	13528	2.778071429	0.06702453	0.00154051	0.051895
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	23	5.411764706	3.08E-05	218000_S_A	350	321	13528	2.769417	0.06954089	0.00156567	0.053915
GOTERM_BP_FAT	GO:0002520~immune system development	21	4.941176471	3.25E-05	209636_AT,	350	276	13528	2.940869565	0.07315866	0.00161514	0.056828
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	17	4	4.07E-05	212470_AT,	350	193	13528	3.404529978	0.09077535	0.0019806	0.071177
GOTERM_BP_FAT	GO:0030097~hemopoiesis	19	4.470588235	4.14E-05	212171_X_A	350	236	13528	3.111767554	0.09222923	0.00197281	0.072374
GOTERM_BP_FAT	GO:0051098~regulation of binding	15	3.529411765	4.18E-05	209061_AT,	350	153	13528	3.789355742	0.09326309	0.00195614	0.073226
SP_PIR_KEYWORDS	Proto-oncogene	17	4	4.48E-05	201464_X_A	418	230	19235	3.401237778	0.01789121	0.0025757	0.062531
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	20	4.705882353	4.62E-05	209636_AT,	350	260	13528	2.973186813	0.10241555	0.00211635	0.080811
SP_PIR_KEYWORDS	nucleus	128	30.11764706	5.43E-05	201464_X_A	418	4283	19235	1.37523781	0.02163475	0.00273029	0.075755
SP_PIR_KEYWORDS	DNA binding	21	4.941176471	5.77E-05	201464_X_A	418	340	19235	2.842210808	0.02300415	0.00258253	0.080604
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	12	2.823529412	6.89E-05	203665_AT,	350	103	13528	4.503079057	0.14894454	0.00309669	0.120599
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	12	2.823529412	6.89E-05	205745_X_A	350	103	13528	4.503079057	0.14894454	0.00309669	0.120599
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	22	5.176470588	7.61E-05	213138_AT,	337	316	12983	2.682135747	0.04833294	0.00705216	0.113581
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	15	3.529411765	8.94E-05	201464_X_A	350	164	13528	3.535191638	0.18874788	0.00393895	0.156387
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	23	5.411764706	9.16E-05	204011_AT,	350	345	13528	2.576761905	0.19291268	0.00396109	0.160232
GOTERM_BP_FAT	GO:0048008~platelet-derived growth factor receptor signaling pathway	6	1.411764706	9.58E-05	212171_X_A	350	19	13528	12.20571429	0.20088559	0.00406899	0.167648
SP_PIR_KEYWORDS	transcription regulation	70	16.47058824	9.68E-05	201464_X_A	418	2026	19235	1.589917201	0.03826606	0.00389414	0.135097
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	73	17.17647059	9.96E-05	201464_X_A	350	1813	13528	1.556290284	0.20785771	0.00415232	0.174194
KEGG_PATHWAY	hsa05200:Pathways in cancer	25	5.882352941	1.11E-04	201464_X_A	165	328	5085	2.348946785	0.01491798	0.00748702	0.130442
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	17	4	1.18E-04	201464_X_A	350	211	13528	3.114096141	0.24074881	0.00482032	0.205864
GOTERM_BP_FAT	GO:0001525~angiogenesis	14	3.294117647	1.19E-04	201464_X_A	350	148	13528	3.656216216	0.24312659	0.00479123	0.208206
GOTERM_BP_FAT	GO:0048661~positive regulation of smooth muscle cell proliferation	7	1.647058824	1.20E-04	201464_X_A	350	31	13528	8.727741935	0.24564615	0.00476646	0.210696
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	55	12.94117647	1.22E-04	212470_AT,	350	1256	13528	1.692538672	0.24853392	0.00475083	0.21356
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	25	5.882352941	1.37E-04	214577_AT,	350	405	13528	2.385890653	0.27435725	0.00524354	0.239664
SP_PIR_KEYWORDS	amino-acid biosynthesis	6	1.411764706	1.41E-04	220346_AT,	418	24	19235	11.5041866	0.05539164	0.00516705	0.197248
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	23	5.411764706	1.49E-04	204011_AT,	350	357	13528	2.490148059	0.29479701	0.00561754	0.260989
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	71	16.70588235	1.54E-04	201464_X_A	350	1773	13528	1.547801144	0.30277673	0.00570824	0.269481
GOTERM_BP_FAT	GO:0008283~cell proliferation	26	6.117647059	1.66E-04	214211_AT,	350	436	13528	2.304901704	0.32269948	0.00606963	0.291112
GOTERM_BP_FAT	GO:0045321~leukocyte activation	18	4.235294118	1.84E-04	209307_AT,	350	242	13528	2.874899646	0.34981568	0.00660118	0.32159
SP_PIR_KEYWORDS	Transcription	70	16.47058824	1.88E-04	201464_X_A	418	2071	19235	1.555370473	0.07303394	0.00629993	0.262421
GOTERM_BP_FAT	GO:0034097~response to cytokine stimulus	10	2.352941176	1.92E-04	201464_X_A	350	79	13528	4.892585895	0.36130524	0.00676984	0.334886
GOTERM_BP_FAT	GO:0048520~positive regulation of behavior	7	1.647058824	2.06E-04	205745_X_A	350	34	13528	7.957647059	0.38271649	0.00717454	0.36031
SP_PIR_KEYWORDS	repressor	23	5.411764706	2.22E-04	213138_AT,	418	435	19235	2.43306935	0.08572819	0.0068707	0.310061
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	10	2.352941176	2.32E-04	200790_AT,	350	81	13528	4.771781305	0.41913377	0.00795692	0.405634
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	32	7.529411765	2.42E-04	201464_X_A	337	607	12983	2.030983726	0.14566082	0.01948602	0.36049
GOTERM_BP_FAT	GO:0042592~homeostatic process	37	8.705882353	2.52E-04	201464_X_A	350	751	13528	1.90426479	0.44515186	0.00850078	0.439777
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	23	5.411764706	2.69E-04	204011_AT,	350	372	13528	2.389738863	0.46773414	0.00896829	0.470725
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	12	2.823529412	2.92E-04	203665_AT,	350	121	13528	3.833199528	0.49533414	0.00958558	0.510369
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	8	1.882352941	3.12E-04	220346_AT,	350	51	13528	6.062969188	0.51838181	0.01009596	0.54516

KEGG_PATHWAY	hsa05219:Bladder cancer	8	1.882352941	3.32E-04	212171_X_A	165	42	5085	5.87012987	0.04387944	0.01484579	0.388914
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	21	4.941176471	3.54E-04	209061_AT,	350	329	13528	2.467112462	0.56365728	0.01129636	0.618597
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	9	2.117647059	3.84E-04	218871_X_A	350	69	13528	5.041490683	0.59312028	0.01207832	0.670569
UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase	8	1.882352941	3.91E-04	208892_S_A	418	62	19113	5.899984566	0.40885755	0.12315458	0.639631
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	10	2.352941176	3.99E-04	206374_AT,	350	87	13528	4.442692939	0.60661783	0.0123626	0.695638
GOTERM_CC_FAT	GO:0045121~membrane raft	12	2.823529412	4.01E-04	205745_X_A	290	143	12782	3.69867374	0.10445054	0.05366525	0.527551
GOTERM_BP_FAT	GO:0042060~wound healing	15	3.529411765	4.39E-04	205207_AT,	350	191	13528	3.035452506	0.64238408	0.01343908	0.766438
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	15	3.529411765	4.63E-04	217173_S_A	350	192	13528	3.019642857	0.66142025	0.01396643	0.807044
GOTERM_BP_FAT	GO:0048146~positive regulation of fibroblast proliferation	6	1.411764706	4.67E-04	205463_S_A	350	26	13528	8.91956044	0.66503953	0.01392449	0.81502
SP_PIR_KEYWORDS	transcription factor	8	1.882352941	5.05E-04	209636_AT,	418	65	19235	5.663599558	0.18402877	0.01442186	0.702185
SP_PIR_KEYWORDS	ubl conjugation	27	6.352941176	5.08E-04	209636_AT,	418	588	19235	2.113013866	0.18504747	0.01354907	0.706483
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	10	2.352941176	5.13E-04	206374_AT,	350	90	13528	4.294603175	0.69904354	0.01508493	0.89443
GOTERM_BP_FAT	GO:0051341~regulation of oxidoreductase activity	7	1.647058824	5.17E-04	201983_S_A	350	40	13528	6.764	0.70151145	0.01499917	0.900535
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	22	5.176470588	5.54E-04	214577_AT,	350	367	13528	2.316979369	0.7268073	0.01589185	0.966175
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	8	1.882352941	5.60E-04	201464_X_A	350	56	13528	5.521632653	0.73044769	0.01586059	0.976115
GOTERM_BP_FAT	GO:0009612~response to mechanical stimulus	8	1.882352941	5.60E-04	201464_X_A	350	56	13528	5.521632653	0.73044769	0.01586059	0.976115
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	12	2.823529412	5.78E-04	205745_X_A	350	131	13528	3.540588877	0.7414398	0.01616463	1.006957
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	21	4.941176471	5.78E-04	201464_X_A	350	342	13528	2.373333333	0.74155311	0.01597888	1.007282
GOTERM_MF_FAT	GO:0042802~identical protein binding	32	7.529411765	5.87E-04	212171_X_A	337	640	12983	1.926261128	0.31769649	0.04158618	0.873126
GOTERM_BP_FAT	GO:0045449~regulation of transcription	93	21.88235294	5.96E-04	209636_AT,	350	2601	13528	1.38200033	0.75214974	0.01627702	1.038286
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	16	3.764705882	5.96E-04	201464_X_A	350	220	13528	2.811012987	0.75234726	0.01609841	1.038876
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	30	7.058823529	6.08E-04	212470_AT,	350	586	13528	1.978742077	0.75913254	0.01622903	1.059444
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	15	3.529411765	6.62E-04	205745_X_A	350	199	13528	2.913424264	0.78770729	0.01745707	1.152885
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	19	4.470588235	6.64E-04	209061_AT,	350	295	13528	2.489414044	0.78853477	0.01730575	1.155773
GOTERM_BP_FAT	GO:0042113~B cell activation	9	2.117647059	7.41E-04	205745_X_A	350	76	13528	4.577142857	0.82363059	0.01909505	1.2899
UP_SEQ_FEATURE	domain:RHD	4	0.941176471	7.85E-04	209636_AT,	418	9	19113	20.32216906	0.65185898	0.19024984	1.279691
GOTERM_BP_FAT	GO:0050921~positive regulation of chemotaxis	6	1.411764706	7.92E-04	205745_X_A	350	29	13528	7.996847291	0.84331163	0.02016206	1.37725
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	10	2.352941176	8.23E-04	206374_AT,	350	96	13528	4.026190476	0.85432979	0.02072154	1.431039
UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	18	4.235294118	8.41E-04	209636_AT,	418	325	19113	2.532454914	0.67698504	0.17166927	1.369916
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activity	8	1.882352941	8.54E-04	209061_AT,	350	60	13528	5.15352381	0.86460495	0.02127114	1.484972
UP_SEQ_FEATURE	binding site:ATP	25	5.882352941	8.81E-04	206411_S_A	418	542	19113	2.109081198	0.69398755	0.15562735	1.434993
GOTERM_BP_FAT	GO:0051099~positive regulation of binding	9	2.117647059	8.82E-04	209061_AT,	350	78	13528	4.45978022	0.87303407	0.02171643	1.53234
SP_PIR_KEYWORDS	nucleotide-binding	57	13.41176471	8.93E-04	202847_AT,	418	1686	19235	1.555726302	0.30224759	0.0222421	1.239215
SMART	SM00195:DSPc	6	1.411764706	9.78E-04	206374_AT,	247	29	9079	7.604914142	0.15400426	0.08021973	1.187242
GOTERM_BP_FAT	GO:0002763~positive regulation of myeloid leukocyte differentiation	5	1.176470588	0.0010002	201464_X_A	350	18	13528	10.73650794	0.90383695	0.02434826	1.736852
GOTERM_BP_FAT	GO:0007584~response to nutrient	12	2.823529412	0.0010059	203665_AT,	350	140	13528	3.312979592	0.90509756	0.02423185	1.746554
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	12	2.823529412	0.0010664	204011_AT,	350	141	13528	3.289483283	0.91764699	0.02541115	1.850768
GOTERM_BP_FAT	GO:0050920~regulation of chemotaxis	6	1.411764706	0.001086	205745_X_A	350	31	13528	7.480921659	0.92134232	0.02561172	1.884477
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	20	4.705882353	0.0010953	201468_S_A	350	334	13528	2.314456801	0.9230389	0.02557097	1.900483
GOTERM_BP_FAT	GO:0050795~regulation of behavior	7	1.647058824	0.0011071	205745_X_A	350	46	13528	5.88173913	0.9251366	0.02558784	1.920765
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	21	4.941176471	0.001131	214211_AT,	350	361	13528	2.248421053	0.92920459	0.02587674	1.961758
SP_PIR_KEYWORDS	chromosomal rearrangement	16	3.764705882	0.0011957	209636_AT,	418	279	19235	2.638953199	0.38255766	0.02796447	1.656753
GOTERM_BP_FAT	GO:0009611~response to wounding	27	6.352941176	0.0012891	209785_S_A	350	530	13528	1.96903504	0.95112457	0.02915936	2.233172
KEGG_PATHWAY	hsa05120:Epithelial cell signaling in Helicobacter pylori infection	9	2.117647059	0.0014037	205745_X_A	165	68	5085	4.078877005	0.17273441	0.04630119	1.6333
INTERPRO	IPR000451:NF-kappa-B/Rel/dorsal	4	0.941176471	0.0014541	209636_AT,	401	10	16659	16.61745636	0.6666708	0.24016667	2.192253
INTERPRO	IPR008343:MAP kinase phosphatase	4	0.941176471	0.0014541	206374_AT,	401	10	16659	16.61745636	0.6666708	0.24016667	2.192253
INTERPRO	IPR011539:Rel homology	4	0.941176471	0.0014541	209636_AT,	401	10	16659	16.61745636	0.6666708	0.24016667	2.192253
GOTERM_BP_FAT	GO:0045639~positive regulation of myeloid cell differentiation	6	1.411764706	0.0014543	201464_X_A	350	33	13528	7.027532468	0.96681314	0.03252345	2.515946
GOTERM_BP_FAT	GO:0002685~regulation of leukocyte migration	5	1.176470588	0.0015205	205745_X_A	350	20	13528	9.662857143	0.97157934	0.03365746	2.628963
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	9	2.117647059	0.0015487	204420_AT,	350	85	13528	4.092504202	0.97339846	0.0339511	2.677143
GOTERM_CC_FAT	GO:0005886~plasma membrane	110	25.88235294	0.0015666	207528_S_A	290	3777	12782	1.283649676	0.35023321	0.13386451	2.046001
UP_SEQ_FEATURE	domain:Protein kinase	22	5.176470588	0.0015968	206411_S_A	418	469	19113	2.144877118	0.88307712	0.23530643	2.585756
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	9	2.117647059	0.0016701	201464_X_A	350	86	13528	4.044916944	0.97998365	0.03622573	2.884034
GOTERM_BP_FAT	GO:0044272~sulfur compound biosynthetic process	7	1.647058824	0.0017229	218871_X_A	350	50	13528	5.4112	0.98231649	0.0370092	2.974035
KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	19	4.470588235	0.0017645	201642_AT,	165	262	5085	2.234906315	0.21212801	0.04656491	2.049203

GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	10	2.352941176	0.0017779	218871_X_A	350	107	13528	3.612283044	0.98445321	0.03782087	3.067479
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	10	2.352941176	0.0017968	201464_X_A	165	87	5085	3.542319749	0.21555858	0.03965617	2.086315
GOTERM_BP_FAT	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	8	1.882352941	0.0017988	205266_AT,	350	68	13528	4.547226891	0.98519782	0.03791378	3.103069
INTERPRO	IPR000340:Protein-tyrosine phosphatase, dual specificity	6	1.411764706	0.001802	206374_AT,	401	37	16659	6.736806632	0.74378643	0.23841142	2.710122
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	14	3.294117647	0.0018229	201464_X_A	350	197	13528	2.74680203	0.98601139	0.03807014	3.144045
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	5	1.176470588	0.0018404	201464_X_A	350	21	13528	9.202721088	0.98657406	0.03808956	3.173792
GOTERM_MF_FAT	GO:0015175~neutral amino acid transmembrane transporter activity	5	1.176470588	0.0018608	212810_S_A	337	21	12983	9.172672036	0.70255745	0.11419055	2.74325
GOTERM_BP_FAT	GO:0048145~regulation of fibroblast proliferation	6	1.411764706	0.0019072	205463_S_A	350	35	13528	6.625959184	0.98851983	0.03910019	3.287155
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	13	3.058823529	0.0019588	220049_S_A	350	175	13528	2.87124898	0.98982818	0.0397897	3.374674
SP_PIR_KEYWORDS	dna-binding	60	14.11764706	0.0020731	209636_AT,	418	1868	19235	1.478053953	0.56669673	0.04539924	2.856109
SP_PIR_KEYWORDS	protein phosphatase	10	2.352941176	0.0021266	208892_S_A	418	130	19235	3.539749724	0.57596144	0.04414998	2.92883
GOTERM_BP_FAT	GO:0043388~positive regulation of DNA binding	8	1.882352941	0.002129	209061_AT,	350	70	13528	4.417306122	0.99317485	0.04280376	3.662713
GOTERM_BP_FAT	GO:0045637~regulation of myeloid cell differentiation	8	1.882352941	0.002129	201464_X_A	350	70	13528	4.417306122	0.99317485	0.04280376	3.662713
UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	8	1.882352941	0.0022362	208892_S_A	418	83	19113	4.407217386	0.95053705	0.2839885	3.603351
SP_PIR_KEYWORDS	growth factor	10	2.352941176	0.0022409	205266_AT,	418	131	19235	3.512728734	0.59508851	0.04419785	3.083944
INTERPRO	IPR000340:Dual specificity phosphatase, catalytic domain	6	1.411764706	0.0022887	206374_AT,	401	39	16659	6.391329369	0.8227103	0.25048456	3.43026
GOTERM_BP_FAT	GO:0006986~response to unfolded protein	8	1.882352941	0.0023107	208744_X_A	350	71	13528	4.355090543	0.99554315	0.04598157	3.969415
GOTERM_BP_FAT	GO:0009070~serine family amino acid biosynthetic process	4	0.941176471	0.0024077	201397_AT,	350	11	13528	14.05506494	0.99645007	0.04746441	4.132748
GOTERM_BP_FAT	GO:0060323~head morphogenesis	4	0.941176471	0.0024077	202310_S_A	350	11	13528	14.05506494	0.99645007	0.04746441	4.132748
BBID	114.Genomic_reformatting_Brain_Ischemia	5	1.176470588	0.0025161	201464_X_A	28	9	358	7.103174603	0.15104635	0.15104635	2.534922
GOTERM_BP_FAT	GO:0000096~sulfur amino acid metabolic process	5	1.176470588	0.0026146	220346_AT,	350	23	13528	8.402484472	0.99781491	0.05101264	4.4802
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	9	2.117647059	0.0026469	206665_S_A	165	75	5085	3.698181818	0.30079439	0.04983134	3.059527
GOTERM_BP_FAT	GO:0008361~regulation of cell size	14	3.294117647	0.0027019	214577_AT,	350	206	13528	2.626796117	0.99821996	0.0522396	4.626617
GOTERM_BP_FAT	GO:0045767~regulation of anti-apoptosis	6	1.411764706	0.0027687	206665_S_A	350	38	13528	6.102857143	0.99847788	0.05305862	4.738254
GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	8	1.882352941	0.0029282	203665_AT,	350	74	13528	4.178532819	0.99895329	0.05557989	5.004776
GOTERM_BP_FAT	GO:0000082~G1/S transition of mitotic cell cycle	7	1.647058824	0.0030939	205745_X_A	350	56	13528	4.831428571	0.99929056	0.05816566	5.280814
GOTERM_MF_FAT	GO:0008083~growth factor activity	12	2.823529412	0.0031303	205266_AT,	337	161	12983	2.871445159	0.87010707	0.1693523	4.574276
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	8	1.882352941	0.0031599	201464_X_A	350	75	13528	4.122819048	0.99939226	0.05889722	5.390406
INTERPRO	IPR000387:Protein-tyrosine phosphatase	8	1.882352941	0.003303	208892_S_A	401	81	16659	4.103075644	0.91773987	0.3001144	4.914933
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in SUMO)	8	1.882352941	0.0033211	204970_S_A	418	89	19113	4.110101607	0.98852592	0.36030671	5.307353
GOTERM_BP_FAT	GO:0045787~positive regulation of cell cycle	7	1.647058824	0.0033844	205745_X_A	350	57	13528	4.746666667	0.9996413	0.06246032	5.762922
INTERPRO	IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved region	8	1.882352941	0.0035385	208892_S_A	401	82	16659	4.053038136	0.93118369	0.28433229	5.256663
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	20	4.705882353	0.0035451	203665_AT,	350	370	13528	2.089266409	0.999754	0.06482119	6.02847
GOTERM_CC_FAT	GO:0005615~extracellular space	28	6.588235294	0.0035594	212171_X_A	290	685	12782	1.801641077	0.62490182	0.21740649	4.592775
GOTERM_BP_FAT	GO:0032768~regulation of monooxygenase activity	5	1.176470588	0.0035867	201983_S_A	350	25	13528	7.730285714	0.9997769	0.06505069	6.097137
GOTERM_BP_FAT	GO:0031657~regulation of cyclin-dependent protein kinase activity during G1/	3	0.705882353	0.0038473	205745_X_A	350	4	13528	28.98857143	0.99987903	0.06908486	6.526222
GOTERM_BP_FAT	GO:0031659~positive regulation of cyclin-dependent protein kinase activity d	3	0.705882353	0.0038473	205745_X_A	350	4	13528	28.98857143	0.99987903	0.06908486	6.526222
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	12	2.823529412	0.0038715	220049_S_A	350	166	13528	2.794079174	0.99988572	0.06897683	6.565974
GOTERM_BP_FAT	GO:0002761~regulation of myeloid leukocyte differentiation	6	1.411764706	0.0038814	201464_X_A	350	41	13528	5.65630662	0.99988836	0.0686272	6.582339
GOTERM_BP_FAT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	6	1.411764706	0.0038814	210018_X_A	350	41	13528	5.65630662	0.99988836	0.0686272	6.582339
GOTERM_BP_FAT	GO:0042493~response to drug	14	3.294117647	0.0040195	201464_X_A	350	216	13528	2.505185185	0.99991929	0.0704544	6.808824
GOTERM_MF_FAT	GO:0033549~MAP kinase phosphatase activity	4	0.941176471	0.0040511	206374_AT,	337	13	12983	11.85391463	0.92882795	0.19765874	5.882207
GOTERM_MF_FAT	GO:0017017~MAP kinase tyrosine/serine/threonine phosphatase activity	4	0.941176471	0.0040511	206374_AT,	337	13	12983	11.85391463	0.92882795	0.19765874	5.882207
GOTERM_MF_FAT	GO:0015171~amino acid transmembrane transporter activity	7	1.647058824	0.004084	212810_S_A	337	59	12983	4.570789116	0.93034072	0.18529875	5.928582
GOTERM_BP_FAT	GO:0009069~serine family amino acid metabolic process	5	1.176470588	0.0041538	201397_AT,	350	26	13528	7.432967033	0.99994113	0.07218637	7.02856
GOTERM_BP_FAT	GO:0045766~positive regulation of angiogenesis	5	1.176470588	0.0041538	209360_S_A	350	26	13528	7.432967033	0.99994113	0.07218637	7.02856
GOTERM_CC_FAT	GO:0031981~nuclear lumen	49	11.52941176	0.0042185	209636_AT,	290	1450	12782	1.489460166	0.68730956	0.20745684	5.421603
GOTERM_BP_FAT	GO:0030307~positive regulation of cell growth	6	1.411764706	0.0043146	205745_X_A	350	42	13528	5.521632653	0.99995965	0.07432935	7.29103
GOTERM_BP_FAT	GO:0051591~response to cAMP	6	1.411764706	0.0043146	201464_X_A	350	42	13528	5.521632653	0.99995965	0.07432935	7.29103
SP_PIR_KEYWORDS	LIM domain	7	1.647058824	0.0043779	215706_X_A	418	71	19235	4.536862322	0.82935391	0.08075102	5.942481
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	15	3.529411765	0.0044529	205745_X_A	350	244	13528	2.376112412	0.99997085	0.07606536	7.516214
GOTERM_BP_FAT	GO:0060348~bone development	10	2.352941176	0.0045629	214985_AT,	350	123	13528	3.142392567	0.99997749	0.07731182	7.695031
GOTERM_BP_FAT	GO:0001558~regulation of cell growth	13	3.058823529	0.0045648	205745_X_A	350	194	13528	2.590044183	0.99997759	0.07678822	7.6981
SP_PIR_KEYWORDS	protein kinase inhibitor	4	0.941176471	0.0045915	202241_AT,	418	16	19235	11.5041866	0.84349013	0.08084604	6.223867
GOTERM_BP_FAT	GO:0009636~response to toxin	7	1.647058824	0.0047528	201468_S_A	350	61	13528	4.435409836	0.9999856	0.07926041	8.002771

GOTERM_BP_FAT	GO:0045428~regulation of nitric oxide biosynthetic process	5	1.176470588	0.0047786	205580_S_A	350	27	13528	7.157671958	0.99998644	0.07911169	8.044484
GOTERM_BP_FAT	GO:0060322~head development	4	0.941176471	0.005015	202310_S_A	350	14	13528	11.04326531	0.99999223	0.08228943	8.426223
GOTERM_BP_FAT	GO:0010171~body morphogenesis	4	0.941176471	0.005015	202310_S_A	350	14	13528	11.04326531	0.99999223	0.08228943	8.426223
INTERPRO	IPR002293:Amino acid/polyamine transporter I	4	0.941176471	0.0050428	207528_S_A	401	15	16659	11.07830424	0.97800468	0.34564342	7.412145
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	6	1.411764706	0.0052824	202847_AT,	350	44	13528	5.270649351	0.99999586	0.08589427	8.856194
GOTERM_MF_FAT	GO:0008138~protein tyrosine/serine/threonine phosphatase activity	6	1.411764706	0.005349	206374_AT,	337	44	12983	5.253439439	0.96954552	0.22072746	7.697251
GOTERM_BP_FAT	GO:0016477~cell migration	16	3.764705882	0.0054144	216959_X_A	350	276	13528	2.240662526	0.99999696	0.08734425	9.067675
GOTERM_MF_FAT	GO:0048037~cofactor binding	15	3.529411765	0.0054455	201468_S_A	337	249	12983	2.320796539	0.97141094	0.21099458	7.830996
INTERPRO	IPR016130:Protein-tyrosine phosphatase, active site	8	1.882352941	0.0055631	208892_S_A	401	89	16659	3.734259856	0.98518169	0.34373408	8.147049
GOTERM_BP_FAT	GO:0045765~regulation of angiogenesis	7	1.647058824	0.0055721	203665_AT,	350	63	13528	4.294603175	0.9999979	0.08916488	9.319715
INTERPRO	IPR000719:Protein kinase, core	22	5.176470588	0.0056631	206411_S_A	401	476	16659	1.920084243	0.98626433	0.32280518	8.287544
GOTERM_CC_FAT	GO:0009986~cell surface	17	4	0.0057725	216959_X_A	290	348	12782	2.153131193	0.79648679	0.23305286	7.349309
GOTERM_BP_FAT	GO:0006928~cell motion	23	5.411764706	0.0059055	216959_X_A	350	475	13528	1.871542857	0.99999904	0.09361997	9.850596
GOTERM_BP_FAT	GO:0048511~rhythmic process	10	2.352941176	0.0059128	209674_AT,	350	128	13528	3.019642857	0.99999906	0.09310254	9.862234
GOTERM_BP_FAT	GO:0002687~positive regulation of leukocyte migration	4	0.941176471	0.0061502	205745_X_A	350	15	13528	10.30704762	0.99999946	0.09602159	10.23828
GOTERM_BP_FAT	GO:0032642~regulation of chemokine production	4	0.941176471	0.0061502	205745_X_A	350	15	13528	10.30704762	0.99999946	0.09602159	10.23828
GOTERM_BP_FAT	GO:0000097~sulfur amino acid biosynthetic process	4	0.941176471	0.0061502	220346_AT,	350	15	13528	10.30704762	0.99999946	0.09602159	10.23828
GOTERM_BP_FAT	GO:0051674~localization of cell	17	4	0.0061769	216959_X_A	350	307	13528	2.14030712	0.9999995	0.09578261	10.28051
GOTERM_BP_FAT	GO:0048870~cell motility	17	4	0.0061769	216959_X_A	350	307	13528	2.14030712	0.9999995	0.09578261	10.28051
GOTERM_BP_FAT	GO:0010038~response to metal ion	10	2.352941176	0.0062163	215707_S_A	350	129	13528	2.996234773	0.99999954	0.09573397	10.34284
PIR_SUPERFAMILY	PIRSF006060:AA_transporter	4	0.941176471	0.0063146	207528_S_A	194	15	7396	10.16632302	0.74545465	0.74545465	7.725063
SP_PIR_KEYWORDS	cytoskeleton	25	5.882352941	0.006335	200906_S_A	418	636	19235	1.808834372	0.92278116	0.10537683	8.491463
GOTERM_BP_FAT	GO:0007623~circadian rhythm	6	1.411764706	0.0063945	201464_X_A	350	46	13528	5.041490683	0.9999997	0.09770696	10.62383
PIR_SUPERFAMILY	PIRSF001719:fos transforming protein	3	0.705882353	0.0064319	204420_AT,	194	5	7396	22.8742268	0.75186327	0.50186676	7.863214
GOTERM_BP_FAT	GO:0030217~T cell differentiation	7	1.647058824	0.00649	205745_X_A	350	65	13528	4.162461538	0.99999976	0.09845694	10.77421
GOTERM_BP_FAT	GO:0006955~immune response	30	7.058823529	0.0066968	214211_AT,	350	690	13528	1.680496894	0.99999985	0.10078925	11.09875
GOTERM_BP_FAT	GO:0033273~response to vitamin	7	1.647058824	0.0069881	204341_AT,	350	66	13528	4.099393939	0.99999993	0.10428285	11.55407
GOTERM_BP_FAT	GO:0045768~positive regulation of anti-apoptosis	5	1.176470588	0.0070233	206665_S_A	350	30	13528	6.441904762	0.99999993	0.10412145	11.60904
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	24	5.647058824	0.0070558	214211_AT,	350	512	13528	1.811785714	0.99999994	0.10392258	11.65958
SP_PIR_KEYWORDS	lipoprotein	25	5.882352941	0.0070839	209785_S_A	418	642	19235	1.791929377	0.94301452	0.11252354	9.449789
INTERPRO	IPR017441:Protein kinase, ATP binding site	21	4.941176471	0.0071222	201739_AT,	401	455	16659	1.917398811	0.99546764	0.36218654	10.31644
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	19	4.470588235	0.0072064	201464_X_A	350	368	13528	1.995590062	0.99999996	0.10536787	11.89398
INTERPRO	IPR001395:Aldo/keto reductase	4	0.941176471	0.0072734	216594_X_A	401	17	16659	9.774974329	0.99595979	0.34554886	10.5242
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	12	2.823529412	0.0073498	205745_X_A	350	181	13528	2.562525651	0.99999997	0.10669247	12.11654
SP_PIR_KEYWORDS	amino-acid transport	5	1.176470588	0.0074139	207528_S_A	418	36	19235	6.391214779	0.95015939	0.11304143	9.869121
GOTERM_BP_FAT	GO:0050999~regulation of nitric-oxide synthase activity	4	0.941176471	0.0074264	201983_S_A	350	16	13528	9.662857143	0.99999997	0.1070853	12.23519
KEGG_PATHWAY	hsa05215:Prostate cancer	9	2.117647059	0.0075743	201983_S_A	165	89	5085	3.116445352	0.64171433	0.12041325	8.52798
SP_PIR_KEYWORDS	Chaperone	10	2.352941176	0.0076579	202843_AT,	418	158	19235	2.912452305	0.95486044	0.11232865	10.17798
GOTERM_BP_FAT	GO:0045793~positive regulation of cell size	6	1.411764706	0.0076612	205745_X_A	350	48	13528	4.831428571	0.99999998	0.10961809	12.59794
GOTERM_BP_FAT	GO:0030183~B cell differentiation	6	1.411764706	0.0076612	205745_X_A	350	48	13528	4.831428571	0.99999998	0.10961809	12.59794
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	14	3.294117647	0.0078482	205193_AT,	350	234	13528	2.312478632	0.99999999	0.11147069	12.88588
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	5	1.176470588	0.0079029	201464_X_A	350	31	13528	6.234101382	0.99999999	0.11153208	12.96995
GOTERM_MF_FAT	GO:0015296~anion:cation symporter activity	5	1.176470588	0.0079861	212810_S_A	337	31	12983	6.213745573	0.9945918	0.27836801	11.18527
GOTERM_MF_FAT	GO:0046982~protein heterodimerization activity	13	3.058823529	0.0079875	214985_AT,	337	208	12983	2.407826409	0.99459656	0.26442381	11.28706
INTERPRO	IPR001781:Zinc finger, LIM-type	7	1.647058824	0.008123	215706_X_A	401	73	16659	3.983636798	0.99788335	0.35586781	11.68368
GOTERM_CC_FAT	GO:0005794~Golgi apparatus	32	7.529411765	0.0081427	218871_X_A	290	872	12782	1.617462828	0.89443284	0.27472264	10.21981
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	11	2.588235294	0.0082392	205745_X_A	350	159	13528	2.673998203	1	0.11531945	13.48494
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	67	15.76470588	0.0083279	209307_AT,	337	1918	12983	1.345771591	0.99567861	0.26099781	11.74066
GOTERM_CC_FAT	GO:0005925~focal adhesion	8	1.882352941	0.0083464	205745_X_A	290	102	12782	3.456930358	0.9002297	0.25032132	10.4626
INTERPRO	IPR002909:Cell surface receptor IPT/TIG	5	1.176470588	0.008595	209636_AT,	401	34	16659	6.109358956	0.99852234	0.35240279	12.32174
GOTERM_BP_FAT	GO:0019221~cytokine-mediated signaling pathway	7	1.647058824	0.009259	205282_AT,	350	70	13528	3.865142857	1	0.12794202	15.0294
UP_SEQ_FEATURE	domain:SPR	3	0.705882353	0.0092739	204011_AT,	418	7	19113	19.59637731	0.99999632	0.67939424	14.16451
GOTERM_BP_FAT	GO:0006534~cysteine metabolic process	3	0.705882353	0.0092937	206085_S_A	350	6	13528	19.32571429	1	0.12764268	15.08151
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	22	5.176470588	0.0095588	214211_AT,	350	466	13528	1.824745555	1	0.13029176	15.47846
GOTERM_BP_FAT	GO:0001503~ossification	9	2.117647059	0.0098123	214985_AT,	350	115	13528	3.02489441	1	0.13275399	15.85635

GOTERM_BP_FAT	GO:0006790~sulfur metabolic process	9	2.117647059	0.0098123	218871_X_AT	350	115	13528	3.02489441	1	0.13275399	15.85635
SP_PIR_KEYWORDS	mitogen	5	1.176470588	0.0098403	208378_X_AT	418	39	19235	5.899582873	0.98141241	0.1372258	12.89728
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	8	1.882352941	0.0102114	205745_X_AT	290	106	12782	3.326480156	0.94054764	0.26920331	12.65776
UP_SEQ_FEATURE	domain:Rhodanese	4	0.941176471	0.0102409	206374_AT,	418	21	19113	8.709501025	0.99999901	0.68400823	15.52767
GOTERM_MF_FAT	GO:0016563~transcription activator activity	20	4.705882353	0.0104969	209636_AT,	337	410	12983	1.879279149	0.99896111	0.3034097	14.58001
GOTERM_MF_FAT	GO:0004721~phosphoprotein phosphatase activity	11	2.588235294	0.0107453	208892_S_AT	337	165	12983	2.56834817	0.99911774	0.29647459	14.89966
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	15	3.529411765	0.010836	214577_AT,	350	271	13528	2.139377965	1	0.14479057	17.36657
GOTERM_BP_FAT	GO:0034976~response to endoplasmic reticulum stress	5	1.176470588	0.0109659	209383_AT,	350	34	13528	5.684033613	1	0.14557727	17.55638
SP_PIR_KEYWORDS	pyridoxal phosphate	6	1.411764706	0.0110018	200790_AT,	418	62	19235	4.453233524	0.98841782	0.14719516	14.31322
INTERPRO	IPR007875:Sprouty	3	0.705882353	0.0111494	204011_AT,	401	7	16659	17.80441753	0.9997893	0.41084582	15.70062
INTERPRO	IPR014393:Dual specificity protein phosphatase (MAP kinase phosphatase)	3	0.705882353	0.0111494	208892_S_AT	401	7	16659	17.80441753	0.9997893	0.41084582	15.70062
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	22	5.176470588	0.0116167	201464_X_AT	350	474	13528	1.793948162	1	0.15270782	18.50095
GOTERM_BP_FAT	GO:0006984~ER-nuclear signaling pathway	5	1.176470588	0.0121348	209383_AT,	350	35	13528	5.521632653	1	0.15810755	19.24574
GOTERM_BP_FAT	GO:0050927~positive regulation of positive chemotaxis	4	0.941176471	0.0121376	212171_X_AT	350	19	13528	8.137142857	1	0.15727316	19.24977
GOTERM_BP_FAT	GO:0050926~regulation of positive chemotaxis	4	0.941176471	0.0121376	212171_X_AT	350	19	13528	8.137142857	1	0.15727316	19.24977
GOTERM_MF_FAT	GO:0005275~amine transmembrane transporter activity	7	1.647058824	0.0121773	212810_S_AT	337	74	12983	3.644277809	0.99965643	0.31601213	16.721
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	14	3.294117647	0.0123374	202241_AT,	350	248	13528	2.181935484	1	0.15878761	19.53523
GOTERM_BP_FAT	GO:0008360~regulation of cell shape	6	1.411764706	0.0124886	209209_S_AT	350	54	13528	4.294603175	1	0.15971027	19.7507
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	8	1.882352941	0.0125225	209061_AT,	418	114	19113	3.208763536	0.99999996	0.7279695	18.66383
GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	8	1.882352941	0.012676	220049_S_AT	350	97	13528	3.187746686	1	0.16104423	20.01691
GOTERM_BP_FAT	GO:0017085~response to insecticide	3	0.705882353	0.0127906	216594_X_AT	350	7	13528	16.56489796	1	0.16151443	20.1792
GOTERM_BP_FAT	GO:0051150~regulation of smooth muscle cell differentiation	3	0.705882353	0.0127906	215253_S_AT	350	7	13528	16.56489796	1	0.16151443	20.1792
GOTERM_MF_FAT	GO:0003690~double-stranded DNA binding	8	1.882352941	0.0128663	201464_X_AT	337	97	12983	3.177337942	0.99978184	0.31832046	17.5842
SMART	SM00429:IPT	5	1.176470588	0.0128859	209636_AT,	247	34	9079	5.405453679	0.8911525	0.52253726	14.64781
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	16	3.764705882	0.0129409	203665_AT,	350	305	13528	2.027615925	1	0.16239283	20.3918
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	15	3.529411765	0.0129445	201468_S_AT	350	277	13528	2.093037648	1	0.1615758	20.39688
UP_SEQ_FEATURE	domain:CH	5	1.176470588	0.0130047	204823_AT,	418	42	19113	5.443438141	0.99999998	0.71512501	19.31245
GOTERM_MF_FAT	GO:0016791~phosphatase activity	14	3.294117647	0.0130155	212272_AT,	337	249	12983	2.16607677	0.99980229	0.30982682	17.77
SP_PIR_KEYWORDS	gtp-binding	15	3.529411765	0.0130215	209882_AT,	418	329	19235	2.098027952	0.99491845	0.16651764	16.72457
PIR_SUPERFAMILY	PIRSF000939:MAPK_Ptase	3	0.705882353	0.0130491	208892_S_AT	194	7	7396	16.33873343	0.94140833	0.61160054	15.35524
PIR_SUPERFAMILY	PIRSF000939:dual specificity protein phosphatase (MAP kinase phosphatase)	3	0.705882353	0.0130491	208892_S_AT	194	7	7396	16.33873343	0.94140833	0.61160054	15.35524
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	14	3.294117647	0.0132131	209882_AT,	418	295	19113	2.169994323	0.99999998	0.69605103	19.59125
GOTERM_BP_FAT	GO:0043407~negative regulation of MAP kinase activity	5	1.176470588	0.0133805	206374_AT,	350	36	13528	5.368253968	1	0.16569817	21.01028
GOTERM_MF_FAT	GO:0042803~protein homodimerization activity	17	4	0.0134358	214985_AT,	337	334	12983	1.960864621	0.99985017	0.30713311	18.29148
GOTERM_MF_FAT	GO:0004860~protein kinase inhibitor activity	5	1.176470588	0.0135177	202241_AT,	337	36	12983	5.350725354	0.99985805	0.29840669	18.39267
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	8	1.882352941	0.0135538	205745_X_AT	290	112	12782	3.148275862	0.9765478	0.31290253	16.46775
INTERPRO	IPR017442:Serine/threonine protein kinase-related	17	4	0.0135563	201739_AT,	401	359	16659	1.967247619	0.99996653	0.45456733	18.77269
UP_SEQ_FEATURE	binding site:Substrate	14	3.294117647	0.0138972	213700_S_AT	418	297	19113	2.155381567	0.99999999	0.69108099	20.50022
SMART	SM00132:LIM	7	1.647058824	0.0139617	215706_X_AT	247	73	9079	3.524651988	0.90966941	0.45177516	15.77689
GOTERM_BP_FAT	GO:0051385~response to mineralocorticoid stimulus	4	0.941176471	0.0140112	204420_AT,	350	20	13528	7.730285714	1	0.17194431	21.88966
SP_PIR_KEYWORDS	ATP	12	2.823529412	0.014278	213198_AT,	418	236	19235	2.339834563	0.99695887	0.17566988	18.19277
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	11	2.588235294	0.0143471	205745_X_AT	350	173	13528	2.457605285	1	0.17480281	22.35424
GOTERM_BP_FAT	GO:0002250~adaptive immune response	7	1.647058824	0.0144258	209636_AT,	350	77	13528	3.513766234	1	0.17477829	22.46273
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recombination of i	7	1.647058824	0.0144258	209636_AT,	350	77	13528	3.513766234	1	0.17477829	22.46273
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	7	1.647058824	0.0144258	205745_X_AT	350	77	13528	3.513766234	1	0.17477829	22.46273
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	13	3.058823529	0.0144695	202149_AT,	350	226	13528	2.223312263	1	0.17436794	22.52282
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	10	2.352941176	0.0145773	220049_S_AT	350	148	13528	2.611583012	1	0.17466471	22.67106
SP_PIR_KEYWORDS	charcot-marie-tooth disease	4	0.941176471	0.0146032	221667_S_AT	418	24	19235	7.669457735	0.99733746	0.17406655	18.56874
INTERPRO	IPR000837:Fos transforming protein	3	0.705882353	0.0146314	204420_AT,	401	8	16659	15.57886534	0.99998531	0.46110853	20.11092
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	5	1.176470588	0.0147048	202847_AT,	350	37	13528	5.223166023	1	0.17517326	22.84612
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	8	1.882352941	0.0148036	203665_AT,	350	100	13528	3.092114286	1	0.17536516	22.98149
GOTERM_MF_FAT	GO:0019210~kinase inhibitor activity	5	1.176470588	0.0148547	202241_AT,	337	37	12983	5.206111156	0.99994129	0.31252451	20.02895
INTERPRO	IPR004841:Amino acid permease-associated region	4	0.941176471	0.0150779	207528_S_AT	401	22	16659	7.553389254	0.99998957	0.45322024	20.6605
INTERPRO	IPR000712:Apoptosis regulator Bcl-2, BH	4	0.941176471	0.0150779	206665_S_AT	401	22	16659	7.553389254	0.99998957	0.45322024	20.6605
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	7	1.647058824	0.0152997	204420_AT,	350	78	13528	3.468717949	1	0.17981943	23.65766

UP_SEQ_FEATURE	domain:PH	12	2.823529412	0.0153107	218000_S_AT	418	237	19113	2.315183817	1	0.70444425	22.34784
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	63	14.82352941	0.0155112	209307_AT,	337	1836	12983	1.321943911	0.99996196	0.31403083	20.82111
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	63	14.82352941	0.0155112	209307_AT,	337	1836	12983	1.321943911	0.99996196	0.31403083	20.82111
GOTERM_MF_FAT	GO:0010843~promoter binding	6	1.411764706	0.0157215	201464_X_AT	337	57	12983	4.055286584	0.9999669	0.30817878	21.07331
GOTERM_BP_FAT	GO:0040008~regulation of growth	17	4	0.0157604	214577_AT,	350	341	13528	1.926904064	1	0.18382905	24.28061
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	23	5.411764706	0.0159519	212470_AT,	350	520	13528	1.709582418	1	0.18494643	24.53807
SP_PIR_KEYWORDS	ank repeat	12	2.823529412	0.0159907	209636_AT,	418	240	19235	2.300837321	0.99849102	0.18372987	20.15522
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	11	2.588235294	0.0160091	213198_AT,	350	176	13528	2.415714286	1	0.18464553	24.61494
GOTERM_BP_FAT	GO:0034620~cellular response to unfolded protein	4	0.941176471	0.0160397	209383_AT,	350	21	13528	7.362176871	1	0.18406891	24.6559
GOTERM_BP_FAT	GO:0030968~endoplasmic reticulum unfolded protein response	4	0.941176471	0.0160397	209383_AT,	350	21	13528	7.362176871	1	0.18406891	24.6559
GOTERM_BP_FAT	GO:0015804~neutral amino acid transport	4	0.941176471	0.0160397	212810_S_AT	350	21	13528	7.362176871	1	0.18406891	24.6559
GOTERM_BP_FAT	GO:0001569~patterning of blood vessels	4	0.941176471	0.0160397	203935_AT,	350	21	13528	7.362176871	1	0.18406891	24.6559
GOTERM_BP_FAT	GO:0045429~positive regulation of nitric oxide biosynthetic process	4	0.941176471	0.0160397	205580_S_AT	350	21	13528	7.362176871	1	0.18406891	24.6559
GOTERM_MF_FAT	GO:0015179~L-amino acid transmembrane transporter activity	5	1.176470588	0.0162724	212810_S_AT	337	38	12983	5.069108231	0.99997701	0.30808454	21.73048
GOTERM_BP_FAT	GO:0042110~T cell activation	9	2.117647059	0.016371	205745_X_AT	350	126	13528	2.760816327	1	0.1866162	25.0989
GOTERM_BP_FAT	GO:0006563~L-serine metabolic process	3	0.705882353	0.0167655	201397_AT,	350	8	13528	14.49428571	1	0.18977765	25.62312
GOTERM_BP_FAT	GO:0045737~positive regulation of cyclin-dependent protein kinase activity	3	0.705882353	0.0167655	205745_X_AT	350	8	13528	14.49428571	1	0.18977765	25.62312
GOTERM_MF_FAT	GO:0030275~LRR domain binding	3	0.705882353	0.0168649	218364_AT,	337	8	12983	14.44695846	0.99998447	0.30863596	22.43154
GOTERM_BP_FAT	GO:0007050~cell cycle arrest	8	1.882352941	0.0171743	202443_X_AT	350	103	13528	3.002052705	1	0.19304059	26.16271
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	8	1.882352941	0.0171743	205745_X_AT	350	103	13528	3.002052705	1	0.19304059	26.16271
GOTERM_BP_FAT	GO:0007178~transmembrane receptor protein serine/threonine kinase signali	8	1.882352941	0.0171743	201464_X_AT	350	103	13528	3.002052705	1	0.19304059	26.16271
GOTERM_BP_FAT	GO:0051147~regulation of muscle cell differentiation	5	1.176470588	0.0175947	215253_S_AT	350	39	13528	4.955311355	1	0.1963741	26.71365
GOTERM_BP_FAT	GO:0051781~positive regulation of cell division	5	1.176470588	0.0175947	208378_X_AT	350	39	13528	4.955311355	1	0.1963741	26.71365
GOTERM_BP_FAT	GO:0051100~negative regulation of binding	6	1.411764706	0.0178236	209193_AT,	350	59	13528	3.930653753	1	0.19774763	27.01208
SP_PIR_KEYWORDS	manganese	9	2.117647059	0.0179517	204698_AT,	418	152	19235	2.724675774	0.99932463	0.19845955	22.34861
KEGG_PATHWAY	hsa05222:Small cell lung cancer	8	1.882352941	0.0180326	206665_S_AT	165	84	5085	2.935064935	0.91427525	0.23887454	19.21169
GOTERM_BP_FAT	GO:0045682~regulation of epidermis development	4	0.941176471	0.0182242	204970_S_AT	350	22	13528	7.027532468	1	0.2008101	27.53157
GOTERM_MF_FAT	GO:0004725~protein tyrosine phosphatase activity	8	1.882352941	0.0182844	208892_S_AT	337	104	12983	2.963478658	0.99999394	0.32126541	24.08738
INTERPRO	IPR000072:Platelet-derived growth factor (PDGF)	3	0.705882353	0.0185158	212171_X_AT	401	9	16659	13.8478803	0.99999926	0.50614935	24.77596
INTERPRO	IPR018459:RII binding domain	3	0.705882353	0.0185158	202759_S_AT	401	9	16659	13.8478803	0.99999926	0.50614935	24.77596
GOTERM_BP_FAT	GO:0007179~transforming growth factor beta receptor signaling pathway	6	1.411764706	0.0190459	201464_X_AT	350	60	13528	3.865142857	1	0.20796281	28.58619
INTERPRO	IPR001763:Rhodanese-like	4	0.941176471	0.0191309	206374_AT,	401	24	16659	6.92394015	0.99999954	0.50065899	25.49097
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	10	2.352941176	0.0191464	220346_AT,	350	155	13528	2.493640553	1	0.20798974	28.71418
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	10	2.352941176	0.0191464	220346_AT,	350	155	13528	2.493640553	1	0.20798974	28.71418
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	24	5.647058824	0.0192585	213138_AT,	350	561	13528	1.653537051	1	0.20812833	28.85661
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	13	3.058823529	0.0196654	205745_X_AT	350	236	13528	2.129104116	1	0.21110323	29.37165
GOTERM_MF_FAT	GO:0000166~nucleotide binding	74	17.41176471	0.019762	209307_AT,	337	2245	12983	1.269873705	0.99999773	0.33372946	25.77602
GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	8	1.882352941	0.0198013	220049_S_AT	350	106	13528	2.917088949	1	0.21145274	29.54288
GOTERM_BP_FAT	GO:0051325~interphase	8	1.882352941	0.0198013	205745_X_AT	350	106	13528	2.917088949	1	0.21145274	29.54288
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	8	1.882352941	0.0200629	209061_AT,	401	114	16659	2.915343221	0.99999977	0.5011863	26.56215
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	9	2.117647059	0.0202151	214577_AT,	350	131	13528	2.655441658	1	0.21443585	30.06182
GOTERM_CC_FAT	GO:0043233~organelle lumen	55	12.94117647	0.0204174	209636_AT,	290	1820	12782	1.331962865	0.99656209	0.40292788	23.8147
SP_PIR_KEYWORDS	nadp	9	2.117647059	0.0206343	201468_S_AT	418	156	19235	2.654812293	0.99977572	0.21896548	25.25858
SP_PIR_KEYWORDS	prenylation	9	2.117647059	0.0206343	218360_AT,	418	156	19235	2.654812293	0.99977572	0.21896548	25.25858
SMART	SM00337:BCL	4	0.941176471	0.0206854	206665_S_AT	247	22	9079	6.683106367	0.97196476	0.51073871	22.52827
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	13	3.058823529	0.0208475	220049_S_AT	350	238	13528	2.111212485	1	0.21943132	30.84798
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	12	2.823529412	0.0211648	212171_X_AT	350	211	13528	2.198185511	1	0.22142164	31.23925
GOTERM_BP_FAT	GO:0060325~face morphogenesis	3	0.705882353	0.0211918	202310_S_AT	350	9	13528	12.88380952	1	0.22070196	31.27246
GOTERM_MF_FAT	GO:0008195~phosphatidate phosphatase activity	3	0.705882353	0.0213162	202459_S_AT	337	9	12983	12.84174085	0.99999919	0.34626811	27.51426
SP_PIR_KEYWORDS	atp-binding	41	9.647058824	0.0213725	206411_S_AT	418	1326	19235	1.422840575	0.9998345	0.22023095	26.04142
KEGG_PATHWAY	hsa04210:Apoptosis	8	1.882352941	0.021479	206665_S_AT	165	87	5085	2.833855799	0.94667007	0.25407167	22.47402
GOTERM_MF_FAT	GO:0003924~GTPase activity	12	2.823529412	0.0215549	209882_AT,	337	211	12983	2.191007918	0.99999931	0.3411281	27.7778
SP_PIR_KEYWORDS	isopeptide bond	14	3.294117647	0.0222196	209636_AT,	418	319	19235	2.01954373	0.99988325	0.22239876	26.93031
GOTERM_BP_FAT	GO:0033189~response to vitamin A	5	1.176470588	0.0225519	204341_AT,	350	42	13528	4.601360544	1	0.23220728	32.9255
GOTERM_BP_FAT	GO:0030029~actin filament-based process	13	3.058823529	0.022719	202149_AT,	350	241	13528	2.084931832	1	0.23272061	33.12595

GOTERM_BP_FAT	GO:0002252~immune effector process	9	2.117647059	0.022808	205745_X_AT	350	134	13528	2.595991471	1	0.23252592	33.23251
UP_SEQ_FEATURE	short sequence motif:BH1	3	0.705882353	0.0229284	206665_S_AT	418	11	19113	12.47042192	1	0.82282775	31.63058
GOTERM_BP_FAT	GO:0010243~response to organic nitrogen	6	1.411764706	0.0230392	206665_S_AT	350	63	13528	3.681088435	1	0.23360779	33.50862
GOTERM_BP_FAT	GO:0009066~aspartate family amino acid metabolic process	4	0.941176471	0.0230644	220346_AT,	350	24	13528	6.441904762	1	0.23284214	33.53864
SMART	SM00141:PDGF	3	0.705882353	0.0232151	212171_X_AT	247	9	9079	12.25236167	0.98198551	0.48799959	24.93703
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	24	5.647058824	0.0240988	213138_AT,	350	573	13528	1.618908003	1	0.24100268	34.75993
GOTERM_BP_FAT	GO:0032103~positive regulation of response to external stimulus	6	1.411764706	0.0244817	205745_X_AT	350	64	13528	3.623571429	1	0.24334384	35.20667
GOTERM_BP_FAT	GO:0048167~regulation of synaptic plasticity	6	1.411764706	0.0244817	214577_AT,	350	64	13528	3.623571429	1	0.24334384	35.20667
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	9	2.117647059	0.0246616	204729_S_AT	350	136	13528	2.557815126	1	0.24389682	35.41559
GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	8	1.882352941	0.0247822	220049_S_AT	350	111	13528	2.785688546	1	0.24393222	35.55529
UP_SEQ_FEATURE	lipid moiety-binding region:S-farnesyl cysteine	5	1.176470588	0.0249412	209785_S_AT	418	51	19113	4.48283141	1	0.83225401	33.90312
KEGG_PATHWAY	hsa05020:Prion diseases	5	1.176470588	0.0250803	201694_S_AT	165	35	5085	4.402597403	0.96758135	0.26782024	25.75383
UP_SEQ_FEATURE	compositionally biased region:Ser-rich	17	4	0.0252754	209061_AT,	418	425	19113	1.828995215	1	0.82076526	34.27353
GOTERM_BP_FAT	GO:0006350~transcription	69	16.23529412	0.0256956	201464_X_AT	350	2101	13528	1.269371048	1	0.25075583	36.60389
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	8	1.882352941	0.0258727	216017_S_AT	350	112	13528	2.760816327	1	0.2512387	36.80534
GOTERM_BP_FAT	GO:0009396~folic acid and derivative biosynthetic process	3	0.705882353	0.0260435	201761_AT,	350	10	13528	11.59542857	1	0.25166371	36.99903
GOTERM_BP_FAT	GO:0045073~regulation of chemokine biosynthetic process	3	0.705882353	0.0260435	203665_AT,	350	10	13528	11.59542857	1	0.25166371	36.99903
SMART	SM00450:RHOD	4	0.941176471	0.0261336	206374_AT,	247	24	9079	6.126180837	0.98920071	0.47633151	27.63051
INTERPRO	IPR001715:Calponin-like actin-binding	6	1.411764706	0.026383	204823_AT,	401	70	16659	3.560883506	1	0.58425355	33.45526
GOTERM_BP_FAT	GO:0051241~negative regulation of multicellular organismal process	10	2.352941176	0.0264434	205745_X_AT	350	164	13528	2.356794425	1	0.25400697	37.45044
UP_SEQ_FEATURE	site:Lowers pKa of active site Tyr	3	0.705882353	0.0271223	216594_X_AT	418	12	19113	11.4312201	1	0.82769579	36.28564
UP_SEQ_FEATURE	domain:LDL-receptor class A 5	3	0.705882353	0.0271223	217173_S_AT	418	12	19113	11.4312201	1	0.82769579	36.28564
KEGG_PATHWAY	hsa04630:Jak-STAT signaling pathway	11	2.588235294	0.0273298	209193_AT,	165	155	5085	2.187096774	0.97626681	0.26782817	27.73763
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	11	2.588235294	0.0273783	213700_S_AT	350	192	13528	2.214404762	1	0.26076022	38.49383
INTERPRO	IPR018170:Aldo/keto reductase, conserved site	3	0.705882353	0.0274073	216594_X_AT	401	11	16659	11.33008388	1	0.58281351	34.51374
KEGG_PATHWAY	hsa05212:Pancreatic cancer	7	1.647058824	0.0277794	206665_S_AT	165	72	5085	2.996212121	0.97770285	0.25365049	28.12825
GOTERM_CC_FAT	GO:0005856~cytoskeleton	43	10.11764706	0.0280329	212810_S_AT	290	1381	12782	1.37238383	0.99959804	0.47878714	31.2649
GOTERM_BP_FAT	GO:0043433~negative regulation of transcription factor activity	5	1.176470588	0.0282802	209193_AT,	350	45	13528	4.294603175	1	0.2671283	39.4848
GOTERM_BP_FAT	GO:0051353~positive regulation of oxidoreductase activity	4	0.941176471	0.0285335	206411_S_AT	350	26	13528	5.946373626	1	0.26813842	39.76041
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	55	12.94117647	0.0286095	209636_AT,	290	1856	12782	1.306127378	0.99965857	0.45883333	31.80066
GOTERM_BP_FAT	GO:0006865~amino acid transport	7	1.647058824	0.0287751	212810_S_AT	350	90	13528	3.006222222	1	0.26904379	40.02217
SP_PIR_KEYWORDS	transferase	42	9.882352941	0.0287973	218871_X_AT	418	1394	19235	1.386444296	0.99999231	0.27258795	33.50257
GOTERM_MF_FAT	GO:0005516~calmodulin binding	9	2.117647059	0.0291174	209882_AT,	337	140	12983	2.47662145	1	0.42283387	35.67991
INTERPRO	IPR002110:Ankyrin	12	2.823529412	0.0291404	209636_AT,	401	238	16659	2.094637356	1	0.59062246	36.26904
SP_PIR_KEYWORDS	metal-binding	80	18.82352941	0.0291765	204334_AT,	418	2972	19235	1.238674197	0.99999343	0.26950124	33.86413
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase cascade	10	2.352941176	0.0292618	203665_AT,	350	167	13528	2.314456801	1	0.2719066	40.54618
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	12	2.823529412	0.0293103	213700_S_AT	350	222	13528	2.089266409	1	0.27124323	40.59819
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	53	12.47058824	0.0293139	209636_AT,	290	1779	12782	1.313108876	0.99972031	0.44256918	32.44983
SP_PIR_KEYWORDS	microtubule	11	2.588235294	0.0296306	209372_X_AT	418	231	19235	2.191273639	0.99999456	0.26714706	34.29476
GOTERM_CC_FAT	GO:0005901~caveola	5	1.176470588	0.0296591	217173_S_AT	290	52	12782	4.23806366	0.99974638	0.4241901	32.76594
BIOCARTA	h_arenrf2Pathway:Oxidative Stress Induced Gene Expression Via Nrf2	5	1.176470588	0.0300659	201464_X_AT	94	19	1437	4.022956327	0.99678234	0.99678234	31.5281
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	12	2.823529412	0.0301882	205745_X_AT	350	223	13528	2.079897502	1	0.27715779	41.53185
GOTERM_BP_FAT	GO:0002274~myeloid leukocyte activation	5	1.176470588	0.0303646	212722_S_AT	350	46	13528	4.201242236	1	0.27748636	41.7177
UP_SEQ_FEATURE	repeat:ANK 1	11	2.588235294	0.0308481	209636_AT,	418	231	19113	2.177375256	1	0.85233226	40.16981
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	31	7.294117647	0.0310248	206411_S_AT	418	962	19113	1.473462881	1	0.84122587	40.34838
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathw	12	2.823529412	0.0310579	205745_X_AT	350	224	13528	2.070612245	1	0.28184276	42.443
SP_PIR_KEYWORDS	s-nitrosylation	3	0.705882353	0.0312299	200790_AT,	418	13	19235	10.61924917	0.9999972	0.27360346	35.79086
GOTERM_BP_FAT	GO:0031293~membrane protein intracellular domain proteolysis	3	0.705882353	0.0312958	205745_X_AT	350	11	13528	10.5412987	1	0.28262377	42.69001
GOTERM_BP_FAT	GO:0060324~face development	3	0.705882353	0.0312958	202310_S_AT	350	11	13528	10.5412987	1	0.28262377	42.69001
GOTERM_BP_FAT	GO:0046686~response to cadmium ion	3	0.705882353	0.0312958	202679_AT,	350	11	13528	10.5412987	1	0.28262377	42.69001
GOTERM_BP_FAT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	3	0.705882353	0.0312958	205266_AT,	350	11	13528	10.5412987	1	0.28262377	42.69001
GOTERM_MF_FAT	GO:0019899~enzyme binding	22	5.176470588	0.031357	214211_AT,	337	523	12983	1.620563855	1	0.43792473	37.86042
GOTERM_MF_FAT	GO:0005161~platelet-derived growth factor receptor binding	3	0.705882353	0.0314765	212171_X_AT	337	11	12983	10.50687888	1	0.4303427	37.97485
GOTERM_MF_FAT	GO:0048185~activin binding	3	0.705882353	0.0314765	203935_AT,	337	11	12983	10.50687888	1	0.4303427	37.97485
SP_PIR_KEYWORDS	neuropathy	4	0.941176471	0.0315287	221667_S_AT	418	32	19235	5.752093301	0.99999753	0.2701346	36.06687

UP_SEQ_FEATURE	repeat:ANK 2	11	2.588235294	0.0315972	209636_AT,	418	232	19113	2.167990018	1	0.83414851	40.92346
UP_SEQ_FEATURE	short sequence motif:BH2	3	0.705882353	0.0315981	206665_S_AT	418	13	19113	10.55189547	1	0.8217994	40.92435
SP_PIR_KEYWORDS	phosphotransferase	10	2.352941176	0.0316062	209193_AT,	418	201	19235	2.289390369	0.99999761	0.26520566	36.13819
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	8	1.882352941	0.0318176	220049_S_AT	350	117	13528	2.642832723	1	0.28557786	43.22802
INTERPRO	IPR011993:Pleckstrin homology-type	14	3.294117647	0.031856	212717_AT,	401	303	16659	1.91950816	1	0.60941229	38.93111
INTERPRO	IPR013322:TRAF-type	3	0.705882353	0.0323743	205599_AT,	401	12	16659	10.38591022	1	0.60158395	39.42725
INTERPRO	IPR002475:BCL2-like apoptosis inhibitor	3	0.705882353	0.0323743	206665_S_AT	401	12	16659	10.38591022	1	0.60158395	39.42725
INTERPRO	IPR006011:Syntaxin, N-terminal	3	0.705882353	0.0323743	204729_S_AT	401	12	16659	10.38591022	1	0.60158395	39.42725
UP_SEQ_FEATURE	compositionally biased region:Poly-Ser	18	4.235294118	0.032465	204011_AT,	418	475	19113	1.732732309	1	0.81818571	41.7854
GOTERM_BP_FAT	GO:0051302~regulation of cell division	5	1.176470588	0.0325373	208378_X_AT	350	47	13528	4.111854103	1	0.29000207	43.96242
GOTERM_BP_FAT	GO:0031099~regeneration	6	1.411764706	0.0325589	202443_X_AT	350	69	13528	3.360993789	1	0.28909357	43.98431
GOTERM_MF_FAT	GO:0019207~kinase regulator activity	7	1.647058824	0.0334887	210018_X_AT	337	93	12983	2.899747934	1	0.44208062	39.87166
GOTERM_BP_FAT	GO:0007369~gastrulation	6	1.411764706	0.0343512	203935_AT,	350	70	13528	3.312979592	1	0.30145051	45.77373
KEGG_PATHWAY	hsa04144:Endocytosis	12	2.823529412	0.0345406	217173_S_AT	165	184	5085	2.009881423	0.99130858	0.287488	33.77439
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	4	0.941176471	0.0346276	205745_X_AT	350	28	13528	5.521632653	1	0.30239939	46.0449
GOTERM_BP_FAT	GO:0045740~positive regulation of DNA replication	4	0.941176471	0.0346276	201464_X_AT	350	28	13528	5.521632653	1	0.30239939	46.0449
GOTERM_BP_FAT	GO:0042108~positive regulation of cytokine biosynthetic process	5	1.176470588	0.0347988	203665_AT,	350	48	13528	4.026190476	1	0.30256529	46.2121
SMART	SM00353:HLH	8	1.882352941	0.0350301	209061_AT,	247	114	9079	2.579444563	0.99775172	0.53336066	35.30313
GOTERM_BP_FAT	GO:0030182~neuron differentiation	19	4.470588235	0.0353806	212171_X_AT	350	438	13528	1.676660144	1	0.30573034	46.77699
GOTERM_CC_FAT	GO:0044459~plasma membrane part	63	14.82352941	0.0353933	212810_S_AT	290	2203	12782	1.260453613	0.9999503	0.46170485	37.82022
INTERPRO	IPR001849:Pleckstrin homology	13	3.058823529	0.0358245	218000_S_AT	401	277	16659	1.949701558	1	0.62607904	42.63522
GOTERM_MF_FAT	GO:0015294~solute:cation symporter activity	7	1.647058824	0.0366081	212810_S_AT	337	95	12983	2.838700609	1	0.46342001	42.70555
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	9	2.117647059	0.0367619	204729_S_AT	350	147	13528	2.366413994	1	0.31461587	48.09573
SP_PIR_KEYWORDS	transforming protein	4	0.941176471	0.0368592	209193_AT,	418	34	19235	5.413734872	0.99999973	0.29670274	40.80889
GOTERM_BP_FAT	GO:0006809~nitric oxide biosynthetic process	3	0.705882353	0.0369251	201468_S_AT	350	12	13528	9.662857143	1	0.31467095	48.24949
GOTERM_BP_FAT	GO:0034101~erythrocyte homeostasis	5	1.176470588	0.0371493	203665_AT,	350	49	13528	3.944023324	1	0.31515904	48.45992
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	21	4.941176471	0.0375609	213138_AT,	350	504	13528	1.61047619	1	0.31696974	48.84439
GOTERM_BP_FAT	GO:0001501~skeletal system development	15	3.529411765	0.0375995	214985_AT,	350	319	13528	1.817465293	1	0.31613715	48.88025
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	12	2.823529412	0.0376105	205745_X_AT	350	231	13528	2.007866419	1	0.31511751	48.89054
GOTERM_BP_FAT	GO:0043393~regulation of protein binding	4	0.941176471	0.0379065	215199_AT,	350	29	13528	5.331231527	1	0.31609867	49.16502
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	17	4	0.0380163	201464_X_AT	350	380	13528	1.729142857	1	0.31577531	49.26646
KEGG_PATHWAY	hsa05221:Acute myeloid leukemia	6	1.411764706	0.0380682	209193_AT,	165	58	5085	3.188087774	0.99469751	0.29482212	36.55627
GOTERM_MF_FAT	GO:0016831~carboxy-lyase activity	4	0.941176471	0.0382013	200790_AT,	337	29	12983	5.3138238	1	0.46948791	44.10435
GOTERM_MF_FAT	GO:0043498~cell surface binding	4	0.941176471	0.0382013	212171_X_AT	337	29	12983	5.3138238	1	0.46948791	44.10435
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	21	4.941176471	0.0385185	200906_S_AT	337	504	12983	1.605217606	1	0.4640366	44.37905
SP_PIR_KEYWORDS	serine/threonine-protein kinase	15	3.529411765	0.0394297	201739_AT,	418	381	19235	1.81168293	0.99999991	0.3081964	42.97695
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	28	6.588235294	0.0395936	201464_X_AT	350	734	13528	1.474441417	1	0.32557032	50.70338
GOTERM_BP_FAT	GO:0006351~transcription, DNA-dependent	14	3.294117647	0.0401628	205193_AT,	350	292	13528	1.853150685	1	0.32834453	51.21243
UP_SEQ_FEATURE	domain:Death	4	0.941176471	0.0403207	209636_AT,	418	35	19113	5.225700615	1	0.87089559	49.06788
SMART	SM00503:SynN	3	0.705882353	0.0403529	204729_S_AT	247	12	9079	9.189271255	0.99912688	0.5427861	39.52891
SMART	SM00033:CH	6	1.411764706	0.0408366	204823_AT,	247	70	9079	3.150607287	0.999199	0.50981114	39.90006
GOTERM_BP_FAT	GO:0007566~embryo implantation	4	0.941176471	0.041338	205266_AT,	350	30	13528	5.15352381	1	0.3351613	52.24773
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	5	1.176470588	0.0421179	216594_X_AT	350	51	13528	3.789355742	1	0.33924283	52.9234
GOTERM_BP_FAT	GO:0043392~negative regulation of DNA binding	5	1.176470588	0.0421179	209193_AT,	350	51	13528	3.789355742	1	0.33924283	52.9234
GOTERM_MF_FAT	GO:0031072~heat shock protein binding	6	1.411764706	0.0425844	202843_AT,	337	74	12983	3.123666693	1	0.49060179	47.79008
GOTERM_MF_FAT	GO:0004672~protein kinase activity	24	5.647058824	0.0428168	206411_S_AT	337	606	12983	1.525751388	1	0.48444593	47.97898
SP_PIR_KEYWORDS	Cysteine biosynthesis	2	0.470588235	0.0428896	206085_S_AT	418	2	19235	46.01674641	0.99999998	0.32468787	45.77884
GOTERM_BP_FAT	GO:0046209~nitric oxide metabolic process	3	0.705882353	0.0429085	201468_S_AT	350	13	13528	8.91956044	1	0.34334034	53.59909
UP_SEQ_FEATURE	site:Cleavage (when cotranslationally processed)	2	0.470588235	0.0431603	209636_AT,	418	2	19113	45.72488038	1	0.87950623	51.48296
UP_SEQ_FEATURE	short sequence motif:Kinase activation loop	2	0.470588235	0.0431603	206411_S_AT	418	2	19113	45.72488038	1	0.87950623	51.48296
UP_SEQ_FEATURE	region of interest:GRR	2	0.470588235	0.0431603	209636_AT,	418	2	19113	45.72488038	1	0.87950623	51.48296
UP_SEQ_FEATURE	short sequence motif:TRAF6-binding	2	0.470588235	0.0431603	213112_S_AT	418	2	19113	45.72488038	1	0.87950623	51.48296
UP_SEQ_FEATURE	region of interest:CAP	2	0.470588235	0.0431603	206411_S_AT	418	2	19113	45.72488038	1	0.87950623	51.48296
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependent	16	3.764705882	0.0434306	213138_AT,	350	356	13528	1.737142857	1	0.34563086	54.04022
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II pro	13	3.058823529	0.0435222	203957_AT,	350	266	13528	1.888979592	1	0.34509882	54.11724

GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	14	3.294117647	0.0437154	205193_AT,	350	296	13528	1.828108108	1	0.34522969	54.27921
GOTERM_CC_FAT	GO:0044421~extracellular region part	31	7.294117647	0.043746	212171_X_A	290	960	12782	1.423283046	0.99999545	0.51499736	44.55696
GOTERM_BP_FAT	GO:0030522~intracellular receptor-mediated signaling pathway	6	1.411764706	0.04422	214508_X_A	350	75	13528	3.092114286	1	0.34736919	54.69979
GOTERM_CC_FAT	GO:0005730~nucleolus	24	5.647058824	0.0447717	218000_S_A	290	698	12782	1.515502421	0.99999662	0.50331419	45.33603
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	9	2.117647059	0.0448077	204729_S_A	350	153	13528	2.273613445	1	0.35001784	55.18504
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	4	0.941176471	0.0449203	202847_AT,	350	31	13528	4.987281106	1	0.34961449	55.27739
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	22	5.176470588	0.0451738	213138_AT,	350	547	13528	1.554536432	1	0.35010957	55.48482
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	9	2.117647059	0.0460331	201464_X_A	165	124	5085	2.236803519	0.99827417	0.32808804	42.44877
GOTERM_BP_FAT	GO:0050870~positive regulation of T cell activation	6	1.411764706	0.0463773	220049_S_A	350	76	13528	3.051428571	1	0.35657634	56.45696
UP_SEQ_FEATURE	domain:LDL-receptor class A 4	3	0.705882353	0.0465766	217173_S_A	418	16	19113	8.573415072	1	0.89017047	54.2459
SP_PIR_KEYWORDS	calmodulin-binding	7	1.647058824	0.0466726	207000_S_A	418	120	19235	2.684310207	1	0.34212651	48.69589
SP_PIR_KEYWORDS	host-virus interaction	12	2.823529412	0.0469101	217173_S_A	418	285	19235	1.937547217	1	0.33765545	48.87405
GOTERM_MF_FAT	GO:0030145~manganese ion binding	9	2.117647059	0.0469219	204698_AT,	337	154	12983	2.251474045	1	0.50886975	51.21308
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	12	2.823529412	0.0471348	205745_X_A	350	240	13528	1.932571429	1	0.36017391	57.05859
GOTERM_CC_FAT	GO:0005874~microtubule	12	2.823529412	0.0472327	204011_AT,	290	274	12782	1.930329726	0.99999834	0.50356512	47.1641
INTERPRO	IPR004978:Stanniocalcin	2	0.470588235	0.047447	203439_S_A	401	2	16659	41.5436409	1	0.7179083	52.31155
INTERPRO	IPR015015:F-actin binding	2	0.470588235	0.047447	206411_S_A	401	2	16659	41.5436409	1	0.7179083	52.31155
INTERPRO	IPR005874:Eukaryotic translation initiation factor SUI1	2	0.470588235	0.047447	212227_X_A	401	2	16659	41.5436409	1	0.7179083	52.31155
INTERPRO	IPR002945:Glucose transporter, type 3 (GLUT3)	2	0.470588235	0.047447	216236_S_A	401	2	16659	41.5436409	1	0.7179083	52.31155
INTERPRO	IPR001204:Phosphate transporter	2	0.470588235	0.047447	201920_AT,	401	2	16659	41.5436409	1	0.7179083	52.31155
INTERPRO	IPR008271:Serine/threonine protein kinase, active site	15	3.529411765	0.0477311	201739_AT,	401	354	16659	1.760323767	1	0.70795474	52.52777
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	16	3.764705882	0.0479097	213138_AT,	350	362	13528	1.708350434	1	0.36383453	57.66598
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	15	3.529411765	0.0480033	201464_X_A	350	331	13528	1.751575313	1	0.3632797	57.73877
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	15	3.529411765	0.0480033	213198_AT,	350	331	13528	1.751575313	1	0.3632797	57.73877
INTERPRO	IPR002290:Serine/threonine protein kinase	12	2.823529412	0.0488114	201739_AT,	401	259	16659	1.924801895	1	0.70441177	53.3416
INTERPRO	IPR011600:Peptidase C14, caspase catalytic	3	0.705882353	0.049135	210018_X_A	401	15	16659	8.30872818	1	0.6953917	53.58281
INTERPRO	IPR001309:Peptidase C14, ICE, catalytic subunit p20	3	0.705882353	0.049135	210018_X_A	401	15	16659	8.30872818	1	0.6953917	53.58281
GOTERM_BP_FAT	GO:0045604~regulation of epidermal cell differentiation	3	0.705882353	0.0492241	204970_S_A	350	14	13528	8.28244898	1	0.36959369	58.67766
GOTERM_CC_FAT	GO:0005667~transcription factor complex	10	2.352941176	0.0493121	201464_X_A	290	210	12782	2.098850575	0.99999909	0.50108995	48.66451
SP_PIR_KEYWORDS	zinc finger	8	1.882352941	0.0494182	210426_X_A	418	153	19235	2.406104388	1	0.34656345	50.72095
KEGG_PATHWAY	hsa00450:Selenoamino acid metabolism	4	0.941176471	0.0497517	201475_X_A	165	26	5085	4.741258741	0.99898139	0.3331925	45.02457
SP_PIR_KEYWORDS	alternative initiation	5	1.176470588	0.050058	209193_AT,	418	64	19235	3.595058313	1	0.34450403	51.18204
GOTERM_BP_FAT	GO:0000079~regulation of cyclin-dependent protein kinase activity	5	1.176470588	0.05024	205745_X_A	350	54	13528	3.578835979	1	0.37457834	59.44391
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	5	1.176470588	0.05024	203665_AT,	350	54	13528	3.578835979	1	0.37457834	59.44391
GOTERM_CC_FAT	GO:0012505~endomembrane system	26	6.117647059	0.0503704	218871_X_A	290	782	12782	1.465437869	0.99999933	0.4917613	49.41292
GOTERM_MF_FAT	GO:0030170~pyridoxal phosphate binding	5	1.176470588	0.0507054	212322_AT,	337	54	12983	3.567150236	1	0.52894898	54.02678
GOTERM_MF_FAT	GO:0070279~vitamin B6 binding	5	1.176470588	0.0507054	212322_AT,	337	54	12983	3.567150236	1	0.52894898	54.02678
OMIM_DISEASE	Leukemia, acute myeloid	3	0.705882353	0.0507445	219492_AT,	91	15	3671	8.068131868	0.99990577	0.99990577	47.28469
GOTERM_BP_FAT	GO:0019344~cysteine biosynthetic process	2	0.470588235	0.050933	206085_S_A	350	2	13528	38.65142857	1	0.37757368	59.95888
GOTERM_BP_FAT	GO:0070814~hydrogen sulfide biosynthetic process	2	0.470588235	0.050933	206085_S_A	350	2	13528	38.65142857	1	0.37757368	59.95888
GOTERM_BP_FAT	GO:0070813~hydrogen sulfide metabolic process	2	0.470588235	0.050933	206085_S_A	350	2	13528	38.65142857	1	0.37757368	59.95888
GOTERM_BP_FAT	GO:0031915~positive regulation of synaptic plasticity	2	0.470588235	0.050933	214577_AT,	350	2	13528	38.65142857	1	0.37757368	59.95888
GOTERM_MF_FAT	GO:0004487~methylenetetrahydrofolate dehydrogenase (NAD+) activity	2	0.470588235	0.0510922	201761_AT,	337	2	12983	38.52522255	1	0.52393027	54.30571
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	15	3.529411765	0.0513829	213198_AT,	350	334	13528	1.735842601	1	0.37909893	60.28993
SP_PIR_KEYWORDS	one-carbon metabolism	3	0.705882353	0.0514541	201761_AT,	418	17	19235	8.120602308	1	0.34673372	52.17439
PIR_SUPERFAMILY	PIRSF004499:translation initiation factor 1, eukaryotic type	2	0.470588235	0.0515129	212227_X_A	194	2	7396	38.12371134	0.99998907	0.94249596	48.89213
PIR_SUPERFAMILY	PIRSF000633:tyrosine-protein kinase, ABL type	2	0.470588235	0.0515129	206411_S_A	194	2	7396	38.12371134	0.99998907	0.94249596	48.89213
PIR_SUPERFAMILY	PIRSF036310:transcription factor NF-kappa-B2	2	0.470588235	0.0515129	209636_AT,	194	2	7396	38.12371134	0.99998907	0.94249596	48.89213
PIR_SUPERFAMILY	PIRSF004499:SUI1_euk	2	0.470588235	0.0515129	212227_X_A	194	2	7396	38.12371134	0.99998907	0.94249596	48.89213
INTERPRO	IPR011598:Helix-loop-helix DNA-binding	6	1.411764706	0.0515277	206649_S_A	401	84	16659	2.967402921	1	0.70190703	55.33056
UP_SEQ_FEATURE	short sequence motif:BH3	3	0.705882353	0.0520422	206665_S_A	418	17	19113	8.069096538	1	0.90860532	58.36109
SP_PIR_KEYWORDS	heparin-binding	5	1.176470588	0.0524666	212171_X_A	418	65	19235	3.539749724	1	0.34679279	52.88228
GOTERM_BP_FAT	GO:0032526~response to retinoic acid	4	0.941176471	0.0525294	204341_AT,	350	33	13528	4.685021645	1	0.3846934	61.1219
GOTERM_BP_FAT	GO:0001709~cell fate determination	4	0.941176471	0.0525294	214056_AT,	350	33	13528	4.685021645	1	0.3846934	61.1219
UP_SEQ_FEATURE	active site:Proton acceptor	22	5.176470588	0.0525851	201739_AT,	418	658	19113	1.528795393	1	0.90369213	58.75027

GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	12	2.823529412	0.0528852	201464_X_A	337	244	12983	1.894683076	1	0.52885832	55.57829
GOTERM_BP_FAT	GO:0017038~protein import	8	1.882352941	0.0531097	201464_X_A	350	131	13528	2.360392585	1	0.38692413	61.53669
GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferation	5	1.176470588	0.0531251	220049_S_A	350	55	13528	3.513766234	1	0.38586738	61.54764
SMART	SM00808:FABD	2	0.470588235	0.0534597	206411_S_A	247	2	9079	36.75708502	0.99991686	0.5743316	48.87742
GOTERM_MF_FAT	GO:0001882~nucleoside binding	53	12.47058824	0.0537108	209307_AT,	337	1612	12983	1.266648136	1	0.52704079	56.15314
GOTERM_BP_FAT	GO:0043627~response to estrogen stimulus	7	1.647058824	0.0543086	217173_S_A	350	105	13528	2.576761905	1	0.39153638	62.38048
GOTERM_MF_FAT	GO:0019838~growth factor binding	7	1.647058824	0.0549558	205798_AT,	337	105	12983	2.56834817	1	0.52808494	57.00678
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	18	4.235294118	0.0550247	201739_AT,	337	430	12983	1.612683735	1	0.52139832	57.05358
SP_PIR_KEYWORDS	golgi apparatus	20	4.705882353	0.055419	218871_X_A	418	588	19235	1.565195456	1	0.35715875	54.89141
GOTERM_BP_FAT	GO:0045927~positive regulation of growth	6	1.411764706	0.0556232	205745_X_A	350	80	13528	2.898857143	1	0.39786074	63.28567
GOTERM_BP_FAT	GO:0009067~aspartate family amino acid biosynthetic process	3	0.705882353	0.0558509	220346_AT,	350	15	13528	7.730285714	1	0.39799012	63.44033
GOTERM_BP_FAT	GO:0051054~positive regulation of DNA metabolic process	5	1.176470588	0.0560985	201464_X_A	350	56	13528	3.451020408	1	0.39823047	63.60782
GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferation	5	1.176470588	0.0560985	220049_S_A	350	56	13528	3.451020408	1	0.39823047	63.60782
GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell proliferation	5	1.176470588	0.0560985	220049_S_A	350	56	13528	3.451020408	1	0.39823047	63.60782
GOTERM_MF_FAT	GO:0030228~lipoprotein receptor activity	3	0.705882353	0.0561623	217173_S_A	337	15	12983	7.70504451	1	0.52184176	57.81922
GOTERM_MF_FAT	GO:0042301~phosphate binding	3	0.705882353	0.0561623	201761_AT,	337	15	12983	7.70504451	1	0.52184176	57.81922
GOTERM_BP_FAT	GO:0000060~protein import into nucleus, translocation	4	0.941176471	0.0565517	201464_X_A	350	34	13528	4.547226891	1	0.39961706	63.91255
GOTERM_BP_FAT	GO:0006470~protein amino acid dephosphorylation	8	1.882352941	0.0567373	208892_S_A	350	133	13528	2.324897959	1	0.39950562	64.03666
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	22	5.176470588	0.0572861	218000_S_A	290	642	12782	1.510387797	0.99999991	0.52164638	54.06073
UP_SEQ_FEATURE	domain:LIM zinc-binding	3	0.705882353	0.0577232	55081_AT, 2	418	18	19113	7.620813397	1	0.91752866	62.26844
GOTERM_BP_FAT	GO:0044057~regulation of system process	14	3.294117647	0.0579109	204729_S_A	350	309	13528	1.751197411	1	0.40484607	64.81203
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	7	1.647058824	0.0584964	203665_AT,	350	107	13528	2.528598131	1	0.40690569	65.19301
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	12	2.823529412	0.0585313	203665_AT,	350	249	13528	1.862719449	1	0.4059511	65.21555
SMART	SM00248:ANK	12	2.823529412	0.0586387	209636_AT,	247	238	9079	1.853298404	0.99996747	0.57730406	52.19042
GOTERM_MF_FAT	GO:0019887~protein kinase regulator activity	6	1.411764706	0.0587016	202241_AT,	337	81	12983	2.853720189	1	0.53109377	59.48261
GOTERM_MF_FAT	GO:0005525~GTP binding	16	3.764705882	0.0609911	213923_AT,	337	372	12983	1.656998819	1	0.53836213	60.92966
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	16	3.764705882	0.0609923	201464_X_A	350	374	13528	1.653537051	1	0.41806498	66.77363
INTERPRO	IPR006012:Syntaxin/epimorphin, conserved site	3	0.705882353	0.0616846	204729_S_A	401	17	16659	7.331230747	1	0.75678989	62.08747
SP_PIR_KEYWORDS	zinc	59	13.88235294	0.0618353	221841_S_A	418	2189	19235	1.240286906	1	0.38451632	58.9865
GOTERM_CC_FAT	GO:0005912~adherens junction	8	1.882352941	0.0622659	205745_X_A	290	155	12782	2.274883204	0.99999998	0.53637135	57.15954
GOTERM_BP_FAT	GO:0030518~steroid hormone receptor signaling pathway	5	1.176470588	0.0623083	209061_AT,	350	58	13528	3.332019704	1	0.42387731	67.57958
GOTERM_BP_FAT	GO:0006760~folic acid and derivative metabolic process	3	0.705882353	0.0627687	201761_AT,	350	16	13528	7.247142857	1	0.42513288	67.85716
GOTERM_BP_FAT	GO:0046579~positive regulation of Ras protein signal transduction	3	0.705882353	0.0627687	202443_X_A	350	16	13528	7.247142857	1	0.42513288	67.85716
SP_PIR_KEYWORDS	polymorphism	267	62.82352941	0.0628089	201464_X_A	418	11550	19235	1.063763748	1	0.3837533	59.57684
GOTERM_BP_FAT	GO:0009615~response to virus	7	1.647058824	0.0628724	204698_AT,	350	109	13528	2.482201835	1	0.42451635	67.91935
SP_PIR_KEYWORDS	placenta	3	0.705882353	0.0629	202464_S_A	418	19	19235	7.265802065	1	0.37874779	59.63166
UP_SEQ_FEATURE	repeat:ANK 3	9	2.117647059	0.0630854	212373_AT,	418	194	19113	2.121257337	1	0.92948599	65.6383
GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	6	1.411764706	0.0632063	220049_S_A	350	83	13528	2.794079174	1	0.42510298	68.11892
SP_PIR_KEYWORDS	Serine biosynthesis	2	0.470588235	0.0636412	201397_AT,	418	3	19235	30.67783094	1	0.37700194	60.07521
KEGG_PATHWAY	hsa04710:Circadian rhythm	3	0.705882353	0.0638828	209674_AT,	165	13	5085	7.111888112	0.99986523	0.39049577	53.88056
PIR_SUPERFAMILY	PIRSF037165:ras protein	3	0.705882353	0.063967	213923_AT,	194	16	7396	7.148195876	0.99999937	0.94248545	56.78514
UP_SEQ_FEATURE	binding site:Pyridoxal phosphate	2	0.470588235	0.0640385	220892_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
UP_SEQ_FEATURE	region of interest:N-LIP	2	0.470588235	0.0640385	202459_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
UP_SEQ_FEATURE	region of interest:Clustered O-linked oligosaccharides	2	0.470588235	0.0640385	217173_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
UP_SEQ_FEATURE	region of interest:C-LIP	2	0.470588235	0.0640385	202459_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
UP_SEQ_FEATURE	region of interest:Pyridoxal phosphate binding	2	0.470588235	0.0640385	220892_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
UP_SEQ_FEATURE	short sequence motif:DXDXT motif	2	0.470588235	0.0640385	202459_S_A	418	3	19113	30.48325359	1	0.92676968	66.20682
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	34	8	0.0642688	212470_AT,	350	973	13528	1.350615181	1	0.42944902	68.74613
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	34	8	0.0642688	212470_AT,	350	973	13528	1.350615181	1	0.42944902	68.74613
BIOCARTA	h_nthiPathway:NFkB activation by Nontypeable Hemophilus influenzae	5	1.176470588	0.0644133	209878_S_A	94	24	1437	3.184840426	0.99999634	0.99808619	56.22332
BIOCARTA	h_p53hypoxiaPathway:Hypoxia and p53 in the Cardiovascular system	5	1.176470588	0.0644133	201468_S_A	94	24	1437	3.184840426	0.99999634	0.99808619	56.22332
GOTERM_BP_FAT	GO:0006417~regulation of translation	8	1.882352941	0.0644442	205207_AT,	350	137	13528	2.257017727	1	0.42919717	68.84849
GOTERM_CC_FAT	GO:0005884~actin filament	4	0.941176471	0.0649783	200906_S_A	290	41	12782	4.300084104	0.99999999	0.53691018	58.76494
GOTERM_BP_FAT	GO:0055072~iron ion homeostasis	4	0.941176471	0.065019	214211_AT,	350	36	13528	4.294603175	1	0.43098963	69.18192
GOTERM_BP_FAT	GO:0048168~regulation of neuronal synaptic plasticity	4	0.941176471	0.065019	201694_S_A	350	36	13528	4.294603175	1	0.43098963	69.18192

GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	0.941176471	0.0655007	201266_AT,	337	36	12983	4.280580284	1	0.55811081	63.63996
GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	6	1.411764706	0.0658572	220049_S_A	350	84	13528	2.760816327	1	0.4341002	69.66207
GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	6	1.411764706	0.0658572	220049_S_A	350	84	13528	2.760816327	1	0.4341002	69.66207
SP_PIR_KEYWORDS	oxidoreductase	19	4.470588235	0.0659856	214211_AT,	418	562	19235	1.555726302	1	0.3828447	61.44861
GOTERM_BP_FAT	GO:0050801~ion homeostasis	17	4	0.0660277	201464_X_A	350	409	13528	1.606538596	1	0.43381406	69.75891
GOTERM_CC_FAT	GO:0048179~activin receptor complex	2	0.470588235	0.0663128	203935_AT,	290	3	12782	29.38390805	0.99999999	0.52987251	59.53421
KEGG_PATHWAY	hsa04540:Gap junction	7	1.647058824	0.0664853	209372_X_A	165	89	5085	2.423901941	0.99990745	0.3866576	55.36154
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	52	12.23529412	0.0667157	209307_AT,	337	1601	12983	1.251287678	1	0.55835385	64.3396
UP_SEQ_FEATURE	zinc finger region:Phorbol-ester/DAG-type	4	0.941176471	0.0670441	212717_AT,	418	43	19113	4.253477245	1	0.93025251	67.94247
SP_PIR_KEYWORDS	transmembrane protein	21	4.941176471	0.0676467	212810_S_A	418	642	19235	1.505220677	1	0.38533691	62.39496
GOTERM_BP_FAT	GO:0007049~cell cycle	28	6.588235294	0.0693454	203957_AT,	350	776	13528	1.394639175	1	0.44917799	71.58554
GOTERM_BP_FAT	GO:0030301~cholesterol transport	4	0.941176471	0.0694585	216594_X_A	350	37	13528	4.178532819	1	0.44857048	71.64594
GOTERM_BP_FAT	GO:0019722~calcium-mediated signaling	4	0.941176471	0.0694585	215253_S_A	350	37	13528	4.178532819	1	0.44857048	71.64594
GOTERM_BP_FAT	GO:0015918~sterol transport	4	0.941176471	0.0694585	216594_X_A	350	37	13528	4.178532819	1	0.44857048	71.64594
GOTERM_BP_FAT	GO:0008624~induction of apoptosis by extracellular signals	7	1.647058824	0.0697892	211282_X_A	350	112	13528	2.415714286	1	0.44902983	71.82188
GOTERM_BP_FAT	GO:0046466~membrane lipid catabolic process	3	0.705882353	0.0699582	219257_S_A	350	17	13528	6.820840336	1	0.44869892	71.91133
GOTERM_BP_FAT	GO:0018205~peptidyl-lysine modification	3	0.705882353	0.0699582	212722_S_A	350	17	13528	6.820840336	1	0.44869892	71.91133
GOTERM_BP_FAT	GO:0042516~regulation of tyrosine phosphorylation of Stat3 protein	3	0.705882353	0.0699582	205266_AT,	350	17	13528	6.820840336	1	0.44869892	71.91133
GOTERM_BP_FAT	GO:0030149~sphingolipid catabolic process	3	0.705882353	0.0699582	219257_S_A	350	17	13528	6.820840336	1	0.44869892	71.91133
GOTERM_BP_FAT	GO:0051057~positive regulation of small GTPase mediated signal transductior	3	0.705882353	0.0699582	202443_X_A	350	17	13528	6.820840336	1	0.44869892	71.91133
INTERPRO	IPR007651:Lipin, N-terminal conserved region	2	0.470588235	0.0703215	202459_S_A	401	3	16659	27.6957606	1	0.7925598	67.06899
INTERPRO	IPR004760:L-type amino acid transporter	2	0.470588235	0.0703215	207528_S_A	401	3	16659	27.6957606	1	0.7925598	67.06899
INTERPRO	IPR002112:Transcription factor Jun	2	0.470588235	0.0703215	201464_X_A	401	3	16659	27.6957606	1	0.7925598	67.06899
INTERPRO	IPR005643:Jun-like transcription factor	2	0.470588235	0.0703215	201464_X_A	401	3	16659	27.6957606	1	0.7925598	67.06899
INTERPRO	IPR004755:Cationic amino acid transport permease	2	0.470588235	0.0703215	212290_AT,	401	3	16659	27.6957606	1	0.7925598	67.06899
INTERPRO	IPR008653:Immediate early response	2	0.470588235	0.0703215	218611_AT,	401	3	16659	27.6957606	1	0.7925598	67.06899
GOTERM_MF_FAT	GO:0030291~protein serine/threonine kinase inhibitor activity	3	0.705882353	0.0703414	202763_AT,	337	17	12983	6.798568686	1	0.57168748	66.35343
INTERPRO	IPR014729:Rossmann-like alpha/beta/alpha sandwich fold	4	0.941176471	0.0706973	209674_AT,	401	40	16659	4.15436409	1	0.78512523	67.27119
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	6	1.411764706	0.0713427	205745_X_A	350	86	13528	2.696611296	1	0.45424283	72.63451
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	6	1.411764706	0.0713427	201464_X_A	350	86	13528	2.696611296	1	0.45424283	72.63451
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	16	3.764705882	0.0723925	213923_AT,	337	382	12983	1.613621887	1	0.57609789	67.44517
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	16	3.764705882	0.0723925	213923_AT,	337	382	12983	1.613621887	1	0.57609789	67.44517
GOTERM_BP_FAT	GO:0070482~response to oxygen levels	8	1.882352941	0.0727566	205745_X_A	350	141	13528	2.192988855	1	0.45984219	73.35488
GOTERM_CC_FAT	GO:0030173~integral to Golgi membrane	4	0.941176471	0.0728319	218871_X_A	290	43	12782	4.100080192	1	0.55059521	63.10522
KEGG_PATHWAY	hsa00603:Glycosphingolipid biosynthesis	3	0.705882353	0.0729922	208322_S_A	165	14	5085	6.603896104	0.999964	0.40046741	58.87602
SP_PIR_KEYWORDS	heterodimer	6	1.411764706	0.0734258	209372_X_A	418	103	19235	2.68058717	1	0.40601554	65.52208
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	51	12	0.0735467	209307_AT,	337	1577	12983	1.2459013	1	0.57574906	68.04491
GOTERM_CC_FAT	GO:0030027~lamellipodium	5	1.176470588	0.0737054	202149_AT,	290	70	12782	3.148275862	1	0.54150596	63.56091
SMART	SM00233:PH	13	3.058823529	0.0739277	218000_S_A	247	277	9079	1.725061752	0.99999802	0.63587356	60.85552
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	4	0.941176471	0.0740313	216594_X_A	350	38	13528	4.068571429	1	0.4647027	73.98899
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	4	0.941176471	0.0740313	216594_X_A	350	38	13528	4.068571429	1	0.4647027	73.98899
GOTERM_MF_FAT	GO:0017048~Rho GTPase binding	4	0.941176471	0.074572	214014_AT,	337	38	12983	4.055286584	1	0.57476616	68.56902
GOTERM_BP_FAT	GO:0051052~regulation of DNA metabolic process	7	1.647058824	0.0746354	201464_X_A	350	114	13528	2.373333333	1	0.46637143	74.28453
INTERPRO	IPR015421:Pyridoxal phosphate-dependent transferase, major region, subdor	4	0.941176471	0.0749786	212322_AT,	401	41	16659	4.053038136	1	0.79614874	69.49428
GOTERM_BP_FAT	GO:0032227~negative regulation of synaptic transmission, dopaminergic	2	0.470588235	0.075421	204748_AT,	350	3	13528	25.76761905	1	0.46886658	74.66406
GOTERM_BP_FAT	GO:0050667~homocysteine metabolic process	2	0.470588235	0.075421	206085_S_A	350	3	13528	25.76761905	1	0.46886658	74.66406
GOTERM_BP_FAT	GO:0006564~L-serine biosynthetic process	2	0.470588235	0.075421	201397_AT,	350	3	13528	25.76761905	1	0.46886658	74.66406
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	70	16.47058824	0.0754703	201464_X_A	290	2596	12782	1.188486265	1	0.53730547	64.4658
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	70	16.47058824	0.0754703	201464_X_A	290	2596	12782	1.188486265	1	0.53730547	64.4658
GOTERM_MF_FAT	GO:0005315~inorganic phosphate transmembrane transporter activity	2	0.470588235	0.0756537	201920_AT,	337	3	12983	25.6834817	1	0.57410093	69.1132
GOTERM_MF_FAT	GO:0043008~ATP-dependent protein binding	2	0.470588235	0.0756537	204729_S_A	337	3	12983	25.6834817	1	0.57410093	69.1132
GOTERM_MF_FAT	GO:0004477~methenyltetrahydrofolate cyclohydrolase activity	2	0.470588235	0.0756537	201761_AT,	337	3	12983	25.6834817	1	0.57410093	69.1132
GOTERM_MF_FAT	GO:0004486~methylenetetrahydrofolate dehydrogenase activity	2	0.470588235	0.0756537	201761_AT,	337	3	12983	25.6834817	1	0.57410093	69.1132
GOTERM_MF_FAT	GO:0005173~stem cell factor receptor binding	2	0.470588235	0.0756537	207029_AT,	337	3	12983	25.6834817	1	0.57410093	69.1132
UP_SEQ_FEATURE	domain:LDL-receptor class A 3	3	0.705882353	0.0759413	217173_S_A	418	21	19113	6.532125769	1	0.94747052	72.60262

UP_SEQ_FEATURE	domain:PLAT	3	0.705882353	0.0759413	212561_AT,	418	21	19113	6.532125769	1	0.94747052	72.60262
PIR_SUPERFAMILY	PIRSF001715:rel-related protein	2	0.470588235	0.0762705	209878_S_AT	194	3	7396	25.41580756	0.99999996	0.94250721	63.46562
PIR_SUPERFAMILY	PIRSF001961:LDL receptor	2	0.470588235	0.0762705	217173_S_AT	194	3	7396	25.41580756	0.99999996	0.94250721	63.46562
PIR_SUPERFAMILY	PIRSF005475:glutamate/aspartate transport protein	2	0.470588235	0.0762705	212810_S_AT	194	3	7396	25.41580756	0.99999996	0.94250721	63.46562
PIR_SUPERFAMILY	PIRSF037826:transcription factor MafK	2	0.470588235	0.0762705	204970_S_AT	194	3	7396	25.41580756	0.99999996	0.94250721	63.46562
PIR_SUPERFAMILY	PIRSF015614:TNF receptor-associated factor (TRAF)	2	0.470588235	0.0762705	205599_AT,	194	3	7396	25.41580756	0.99999996	0.94250721	63.46562
KEGG_PATHWAY	hsa00260:Glycine, serine and threonine metabolism	4	0.941176471	0.0766375	201397_AT,	165	31	5085	3.976539589	0.99997885	0.40104681	60.73242
GOTERM_CC_FAT	GO:0005905~coated pit	4	0.941176471	0.0769103	217173_S_AT	290	44	12782	4.006896552	1	0.53181637	65.18871
GOTERM_BP_FAT	GO:0051170~nuclear import	6	1.411764706	0.0770715	201464_X_AT	350	88	13528	2.635324675	1	0.4753037	75.44439
UP_SEQ_FEATURE	sequence variant	277	65.17647059	0.077177	201464_X_AT	418	11992	19113	1.05618678	1	0.94581328	73.19708
INTERPRO	IPR011029:DEATH-like	5	1.176470588	0.0772699	209636_AT,	401	67	16659	3.100271709	1	0.79765649	70.62528
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol binding	5	1.176470588	0.0772699	212717_AT,	401	67	16659	3.100271709	1	0.79765649	70.62528
GOTERM_BP_FAT	GO:0010464~regulation of mesenchymal cell proliferation	3	0.705882353	0.0774008	212171_X_AT	350	18	13528	6.441904762	1	0.47564505	75.59732
GOTERM_BP_FAT	GO:0045987~positive regulation of smooth muscle contraction	3	0.705882353	0.0774008	219257_S_AT	350	18	13528	6.441904762	1	0.47564505	75.59732
KEGG_PATHWAY	hsa05218:Melanoma	6	1.411764706	0.0779033	208378_X_AT	165	71	5085	2.604353393	0.99998243	0.39206708	61.35888
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	14	3.294117647	0.079018	201468_S_AT	350	325	13528	1.664984615	1	0.48180012	76.33549
BIOCARTA	h_LairPathway:Cells and Molecules involved in local acute inflammatory respo	4	0.941176471	0.0795579	205207_AT,	94	16	1437	3.821808511	0.99999983	0.99445655	64.24734
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	36	8.470588235	0.0803222	212810_S_AT	290	1215	12782	1.305951469	1	0.53584757	66.84759
GOTERM_CC_FAT	GO:0031982~vesicle	22	5.176470588	0.0805457	218000_S_AT	290	670	12782	1.447267113	1	0.52523691	66.95368
INTERPRO	IPR013753:Ras	7	1.647058824	0.0808404	218360_AT,	401	125	16659	2.32644389	1	0.80443744	72.30991
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	13	3.058823529	0.0811405	201464_X_AT	350	295	13528	1.703283293	1	0.49009087	77.27243
UP_SEQ_FEATURE	domain:t-SNARE coiled-coil homology	3	0.705882353	0.0823685	204729_S_AT	418	22	19113	6.235210961	1	0.95206869	75.56473
UP_SEQ_FEATURE	region of interest:Hinge	3	0.705882353	0.0823685	210426_X_AT	418	22	19113	6.235210961	1	0.95206869	75.56473
GOTERM_MF_FAT	GO:0043566~structure-specific DNA binding	8	1.882352941	0.0826858	201464_X_AT	337	145	12983	2.12552952	1	0.60190342	72.44232
GOTERM_BP_FAT	GO:0031668~cellular response to extracellular stimulus	5	1.176470588	0.0829936	201464_X_AT	350	64	13528	3.019642857	1	0.49704424	78.06172
GOTERM_BP_FAT	GO:0001819~positive regulation of cytokine production	6	1.411764706	0.0830412	205745_X_AT	350	90	13528	2.576761905	1	0.49608188	78.08164
GOTERM_BP_FAT	GO:0043523~regulation of neuron apoptosis	6	1.411764706	0.0830412	201464_X_AT	350	90	13528	2.576761905	1	0.49608188	78.08164
SP_PIR_KEYWORDS	Flavoprotein	6	1.411764706	0.0833181	201468_S_AT	418	107	19235	2.580378303	1	0.44251222	70.3209
SP_PIR_KEYWORDS	amino acid transport	2	0.470588235	0.0839439	212810_S_AT	418	4	19235	23.00837321	1	0.43968001	70.60255
SP_PIR_KEYWORDS	phosphate transport	2	0.470588235	0.0839439	201920_AT,	418	4	19235	23.00837321	1	0.43968001	70.60255
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	8	1.882352941	0.0839996	201464_X_AT	350	146	13528	2.117886497	1	0.49906205	78.47929
UP_SEQ_FEATURE	domain:BAG	2	0.470588235	0.0844621	217911_S_AT	418	4	19113	22.86244019	1	0.95210507	76.46277
UP_SEQ_FEATURE	region of interest:Defines substrate specificity	2	0.470588235	0.0844621	216236_S_AT	418	4	19113	22.86244019	1	0.95210507	76.46277
UP_SEQ_FEATURE	domain:VPS37 C-terminal	2	0.470588235	0.0844621	219053_S_AT	418	4	19113	22.86244019	1	0.95210507	76.46277
UP_SEQ_FEATURE	domain:WHEP-TRS	2	0.470588235	0.0844621	208693_S_AT	418	4	19113	22.86244019	1	0.95210507	76.46277
UP_SEQ_FEATURE	short sequence motif:LXXIL motif	2	0.470588235	0.0844621	202459_S_AT	418	4	19113	22.86244019	1	0.95210507	76.46277
GOTERM_BP_FAT	GO:0015837~amine transport	7	1.647058824	0.0848883	212810_S_AT	350	118	13528	2.292881356	1	0.50171102	78.84193
GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	11	2.588235294	0.0849767	205745_X_AT	290	269	12782	1.802358672	1	0.53381573	68.99298
GOTERM_BP_FAT	GO:0046626~regulation of insulin receptor signaling pathway	3	0.705882353	0.0850788	202545_AT,	350	19	13528	6.102857143	1	0.50136198	78.91892
GOTERM_CC_FAT	GO:0031228~intrinsic to Golgi membrane	4	0.941176471	0.0853598	218871_X_AT	290	46	12782	3.832683658	1	0.52457104	69.16373
GOTERM_CC_FAT	GO:0030018~Z disc	4	0.941176471	0.0853598	202949_S_AT	290	46	12782	3.832683658	1	0.52457104	69.16373
GOTERM_BP_FAT	GO:0046942~carboxylic acid transport	8	1.882352941	0.0863615	212810_S_AT	350	147	13528	2.103479106	1	0.50564351	79.43044
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	5	1.176470588	0.0867322	203935_AT,	350	65	13528	2.973186813	1	0.50604584	79.57606
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	18	4.235294118	0.0867335	213138_AT,	350	459	13528	1.515742297	1	0.50489645	79.57658
GOTERM_CC_FAT	GO:0033256~I-kappaB/NF-kappaB complex	2	0.470588235	0.0874283	209636_AT,	290	4	12782	22.03793103	1	0.52287731	70.07069
GOTERM_BP_FAT	GO:0001570~vasculogenesis	4	0.941176471	0.0885183	219778_AT,	350	41	13528	3.77087108	1	0.51118735	80.26426
GOTERM_BP_FAT	GO:0006446~regulation of translational initiation	4	0.941176471	0.0885183	212227_X_AT	350	41	13528	3.77087108	1	0.51118735	80.26426
GOTERM_BP_FAT	GO:0015849~organic acid transport	8	1.882352941	0.088761	212810_S_AT	350	148	13528	2.089266409	1	0.51103803	80.35603
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase activity	4	0.941176471	0.0891512	206411_S_AT	337	41	12983	3.758558298	1	0.62486647	75.20481
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	9	2.117647059	0.0893723	205745_X_AT	290	203	12782	1.954102259	1	0.52077954	70.90053
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	35	8.235294118	0.0898905	212810_S_AT	290	1188	12782	1.29853129	1	0.5130091	71.11813
BBID	51.CD40_and_EBV	3	0.705882353	0.0909455	205599_AT,	28	7	358	5.479591837	0.99796603	0.95490042	62.16014
BBID	110.CRHandLC-NA	3	0.705882353	0.0909455	205266_AT,	28	7	358	5.479591837	0.99796603	0.95490042	62.16014
UP_SEQ_FEATURE	domain:J	4	0.941176471	0.0911603	202843_AT,	418	49	19113	3.732643297	1	0.9596158	79.13215
BIOCARTA	h_tnfr2Pathway:TNFR2 Signaling Pathway	4	0.941176471	0.0922366	205599_AT,	94	17	1437	3.596996245	0.99999999	0.98941438	69.89963

GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	6	1.411764706	0.0924406	212171_X_A	350	93	13528	2.493640553	1	0.52487037	81.6995
INTERPRO	IPR000580:TSC-22 / Dip / Bun	2	0.470588235	0.0926481	204094_S_A	401	4	16659	20.77182045	1	0.84040565	77.26017
INTERPRO	IPR000672:Tetrahydrofolate dehydrogenase/cyclohydrolase	2	0.470588235	0.0926481	201761_AT,	401	4	16659	20.77182045	1	0.84040565	77.26017
INTERPRO	IPR009851:Modifier of rudimentary, Modr	2	0.470588235	0.0926481	219053_S_A	401	4	16659	20.77182045	1	0.84040565	77.26017
GOTERM_BP_FAT	GO:0051607~defense response to virus	3	0.705882353	0.0929752	205207_AT,	350	20	13528	5.797714286	1	0.52585495	81.88734
GOTERM_BP_FAT	GO:0033619~membrane protein proteolysis	3	0.705882353	0.0929752	205745_X_A	350	20	13528	5.797714286	1	0.52585495	81.88734
GOTERM_BP_FAT	GO:0000188~inactivation of MAPK activity	3	0.705882353	0.0929752	206374_AT,	350	20	13528	5.797714286	1	0.52585495	81.88734
GOTERM_BP_FAT	GO:0030516~regulation of axon extension	3	0.705882353	0.0929752	216959_X_A	350	20	13528	5.797714286	1	0.52585495	81.88734
GOTERM_CC_FAT	GO:0031252~cell leading edge	7	1.647058824	0.0930526	205745_X_A	290	138	12782	2.235732134	1	0.51612637	72.4136
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	7	1.647058824	0.0930632	202146_AT,	350	121	13528	2.236033058	1	0.52505257	81.9181
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	7	1.647058824	0.0930632	201464_X_A	350	121	13528	2.236033058	1	0.52505257	81.9181
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	6	1.411764706	0.0934288	207000_S_A	165	75	5085	2.465454545	0.99999822	0.43770034	68.33404
KEGG_PATHWAY	hsa04662:B cell receptor signaling pathway	6	1.411764706	0.0934288	201464_X_A	165	75	5085	2.465454545	0.99999822	0.43770034	68.33404
GOTERM_BP_FAT	GO:0022405~hair cycle process	4	0.941176471	0.0935927	213198_AT,	350	42	13528	3.681088435	1	0.52601055	82.10202
GOTERM_BP_FAT	GO:0022404~molting cycle process	4	0.941176471	0.0935927	213198_AT,	350	42	13528	3.681088435	1	0.52601055	82.10202
GOTERM_BP_FAT	GO:0001942~hair follicle development	4	0.941176471	0.0935927	213198_AT,	350	42	13528	3.681088435	1	0.52601055	82.10202
SMART	SM00220:S_TKc	12	2.823529412	0.093795	201739_AT,	247	259	9079	1.703030966	0.99999995	0.69970268	69.96325
SP_PIR_KEYWORDS	Symport	6	1.411764706	0.093878	212810_S_A	418	111	19235	2.487391698	1	0.47311801	74.75428
GOTERM_BP_FAT	GO:0022402~cell cycle process	21	4.941176471	0.0941973	203957_AT,	350	565	13528	1.43660177	1	0.52725866	82.30989
SP_PIR_KEYWORDS	cell shape	3	0.705882353	0.0946682	209209_S_A	418	24	19235	5.752093301	1	0.47069408	75.05997
KEGG_PATHWAY	hsa00270:Cysteine and methionine metabolism	4	0.941176471	0.0952464	200768_S_A	165	34	5085	3.625668449	0.99999865	0.43051398	69.0704
UP_SEQ_FEATURE	domain:LIM zinc-binding 2	4	0.941176471	0.095487	215706_X_A	418	50	19113	3.657990431	1	0.96264748	80.7024
UP_SEQ_FEATURE	domain:LIM zinc-binding 1	4	0.941176471	0.095487	215706_X_A	418	50	19113	3.657990431	1	0.96264748	80.7024
KEGG_PATHWAY	hsa04912:GnRH signaling pathway	7	1.647058824	0.0955844	201464_X_A	165	98	5085	2.201298701	0.99999871	0.41871713	69.20559
GOTERM_CC_FAT	GO:0070161~anchoring junction	8	1.882352941	0.0956305	205745_X_A	290	172	12782	2.050040096	1	0.51684956	73.42978
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	6	1.411764706	0.0956904	201464_X_A	350	94	13528	2.467112462	1	0.53197959	82.81356
GOTERM_MF_FAT	GO:0050662~coenzyme binding	9	2.117647059	0.0982949	201468_S_A	337	181	12983	1.915618801	1	0.65670538	78.67297
GOTERM_BP_FAT	GO:0030218~erythrocyte differentiation	4	0.941176471	0.0987841	212171_X_A	350	43	13528	3.595481728	1	0.54277795	83.8144
GOTERM_BP_FAT	GO:0042633~hair cycle	4	0.941176471	0.0987841	213198_AT,	350	43	13528	3.595481728	1	0.54277795	83.8144
GOTERM_BP_FAT	GO:0042303~molting cycle	4	0.941176471	0.0987841	213198_AT,	350	43	13528	3.595481728	1	0.54277795	83.8144
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	5	1.176470588	0.0992643	212717_AT,	337	68	12983	2.832736952	1	0.65472095	79.01284
GOTERM_BP_FAT	GO:0034383~low-density lipoprotein particle clearance	2	0.470588235	0.0992789	217173_S_A	350	4	13528	19.32571429	1	0.54351382	83.96929
GOTERM_BP_FAT	GO:0002467~germinal center formation	2	0.470588235	0.0992789	205745_X_A	350	4	13528	19.32571429	1	0.54351382	83.96929
GOTERM_BP_FAT	GO:0046683~response to organophosphorus	2	0.470588235	0.0992789	216594_X_A	350	4	13528	19.32571429	1	0.54351382	83.96929
GOTERM_MF_FAT	GO:0003704~specific RNA polymerase II transcription factor activity	4	0.941176471	0.0994802	202443_X_A	337	43	12983	3.583741633	1	0.64986745	79.08785
GOTERM_MF_FAT	GO:0034189~very-low-density lipoprotein binding	2	0.470588235	0.0995813	217173_S_A	337	4	12983	19.26261128	1	0.64464925	79.12287
GOTERM_MF_FAT	GO:0016361~activin receptor activity, type I	2	0.470588235	0.0995813	203935_AT,	337	4	12983	19.26261128	1	0.64464925	79.12287
GOTERM_MF_FAT	GO:0030229~very-low-density lipoprotein receptor activity	2	0.470588235	0.0995813	217173_S_A	337	4	12983	19.26261128	1	0.64464925	79.12287
GOTERM_MF_FAT	GO:0047115~trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	2	0.470588235	0.0995813	216594_X_A	337	4	12983	19.26261128	1	0.64464925	79.12287
SP_PIR_KEYWORDS	cytokine	8	1.882352941	0.0995861	205266_AT,	418	181	19235	2.033889344	1	0.48343119	76.88648
GOTERM_CC_FAT	GO:0005654~nucleoplasm	27	6.352941176	0.0997489	201464_X_A	290	882	12782	1.349261084	1	0.52334376	74.98171

Supplementary Table 5. Genes induced by Ox-PAPC by 1.5 fold and the indcution was reversed by 1.2 fold by ADAM10 silencing.

Values are represented as log2 scale.

						cutoff by log2(1.5) value		**cutoff by -log2(1.2) value**
ProbeSetID	**Gene.Symbol**	**log2(sc+C)**	**log2(sc+Ox40)**	**log2(ADAM10si+C)**	**log2(ADAM10si+Ox50)**	**log2[(sc+Ox40)/(sc+C)]**	**log2[(ADAM10si+Ox40) /(ADAM10si+C)]**	**The effects ADAM10si on Fold induction by Ox40 (H-G))**
206942_s_at	PMCH	4.003389709	5.696800404	3.590252153	3.899857078	1.693410695	0.309604925	-1.38380577
207029_at	KITLG	3.151881632	5.357321076	3.359027062	4.275864385	2.205439444	0.916837323	-1.288602121
211124_s_at	KITLG	2.964011187	5.155668728	3.110940088	4.220911211	2.191657541	1.109971123	-1.081686418
219908_at	DKK2	3.622643313	4.528405227	3.43654688	3.337783196	0.905761915	-0.098763685	-1.004525599
203438_at	STC2	6.460635532	8.884899541	6.985337525	8.427216885	2.424264009	1.44187936	-0.982384649
219371_s_at	KLF2	5.781491767	8.32906882	6.392785262	8.049214092	2.547577053	1.65642883	-0.891148223
206765_at	KCNJ2	6.685117747	7.927117803	6.756573392	7.174655082	1.242000057	0.41808169	-0.823918367
219270_at	CHAC1	4.803703742	8.198312686	5.385948444	8.006949548	3.394608944	2.621001104	-0.773607839
209948_at	KCNMB1	3.676331853	4.429961724	3.764436354	3.758305486	0.753629871	-0.006130868	-0.759760739
204285_s_at	PMAIP1	7.584912955	9.133786321	8.390146174	9.193560124	1.548873365	0.80341395	-0.745459415
221489_s_at	SPRY4	5.020900733	6.8263897	6.171394812	7.242014586	1.805488968	1.070619774	-0.734869194
212226_s_at	PPAP2B	7.174642961	8.047572569	8.11391829	8.277188515	0.872929608	0.163270225	-0.709659383
222162_s_at	ADAMTS1	7.127516346	9.297423055	7.882476838	9.343380988	2.169906709	1.46090415	-0.709002559
205680_at	MMP10	7.402322403	8.379593845	8.580563544	8.850461783	0.977271442	0.269898239	-0.707373204
211924_s_at	PLAUR	7.026525418	8.190238001	8.03048998	8.509269875	1.163712583	0.478779894	-0.684932689
220655_at	TNIP3	3.546038592	5.108458015	3.635570626	4.513530687	1.562419423	0.877960062	-0.684459361
210139_s_at	PMP22	9.133708107	10.23016622	9.684054396	10.10281248	1.096458117	0.418758087	-0.677700029
201195_s_at	SLC7A5	5.943054797	8.420933332	6.652820379	8.456062926	2.477878535	1.803242546	-0.674635989
210118_s_at	IL1A	4.615137895	7.368468764	6.096681246	8.178840689	2.753330869	2.082159442	-0.671171427
36711_at	MAFF	9.550314263	11.10768707	10.5605574	11.47075859	1.557372805	0.910201187	-0.647171618
203439_s_at	STC2	5.572923946	6.735232101	6.006554844	6.528358902	1.162308155	0.521804059	-0.640504096
206715_at	TFEC	6.387204682	7.503321741	7.003905602	7.4811301	1.116117059	0.477224498	-0.638892561
205047_s_at	ASNS	6.880706694	8.878131624	6.83699635	8.209876714	1.99742493	1.372880364	-0.624544567
212501_at	CEBPB	7.368199722	9.127343051	7.803010894	8.937675116	1.759143329	1.134664222	-0.624479107
202638_s_at	ICAM1	7.209096039	7.948533384	7.733464792	7.867722316	0.739437345	0.134257525	-0.60517982
209355_s_at	PPAP2B	6.320122587	7.237775579	7.198100107	7.513844288	0.917652992	0.315744182	-0.60190881
205547_s_at	TAGLN	7.629521032	8.756715382	7.681911099	8.214031737	1.12719435	0.532120639	-0.595073711
200907_s_at	PALLD	6.845936804	8.838042951	6.949864627	8.349376126	1.992106147	1.399511499	-0.592594648
209288_s_at	CDC42EP3	7.943967644	8.781018739	8.932339328	9.180414339	0.837051095	0.248075011	-0.588976084
215977_x_at	GK	3.637136562	4.262167449	3.801125478	3.845053091	0.625030887	0.043927613	-0.581103274
208025_s_at	HMGA2	6.195136142	7.171297679	7.734954416	8.131786342	0.976161537	0.396831926	-0.579329611
218145_at	TRIB3	7.617767845	9.743675	8.027678792	9.582506542	2.125907155	1.55482775	-0.571079405
205599_at	TRAF1	3.435737712	4.078492655	3.217284725	3.299913935	0.642754943	0.08262921	-0.560125733
209286_at	CDC42EP3	7.779521495	8.61666269	8.978583126	9.256560852	0.837141195	0.277977726	-0.559163469
210845_s_at	PLAUR	6.549023425	7.741737337	7.538951628	8.177797681	1.192713913	0.638846053	-0.55386786
204823_at	NAV3	7.238248609	8.988451277	7.334071892	8.53976908	1.750202668	1.205697188	-0.54450548
202149_at	NEDD9	7.73425997	8.6473137	8.576233843	8.94643391	0.91305373	0.370200067	-0.542853663
206868_at	STARD8	4.592538574	5.1870528	4.740877874	4.796159673	0.594514226	0.055281799	-0.539232427
220892_s_at	PSAT1	6.729436491	8.062018562	6.833180385	7.627260539	1.332582072	0.794080155	-0.538501917

204977_at	DDX10	7.724663217	9.41372041	7.638149622	8.793905548	1.689057193	1.155755926	-0.533301267
209406_at	BAG2	6.122166806	7.057767721	5.907454835	6.309792085	0.935600914	0.40233725	-0.533263665
211527_x_at	VEGFA	3.752790162	4.598739436	4.062923235	4.37855972	0.845949273	0.315636485	-0.530312788
203349_s_at	ETV5	5.845109733	7.161735469	6.673321868	7.460053067	1.316625736	0.786731199	-0.529894537
221823_at	C5orf30	6.347993453	7.030008194	6.559874554	6.716375244	0.682014741	0.15650069	-0.525514051
208892_s_at	DUSP6	7.986254652	8.74262666	8.337615106	8.569289794	0.756372008	0.231674688	-0.52469732
201761_at	MTHFD2	8.574370636	9.803732099	8.854332694	9.565177728	1.229361462	0.710845033	-0.518516429
220494_s_at	---	5.138082465	5.739170106	5.570917732	5.666921306	0.601087641	0.096003574	-0.505084068
209699_x_at	AKR1C2	3.95142814	4.691009596	3.771422527	4.013378375	0.739581456	0.241955847	-0.497625609
209287_s_at	CDC42EP3	6.241207554	7.227174376	7.245292533	7.737206251	0.985966822	0.491913718	-0.494053104
204224_s_at	GCH1	6.778943623	7.89430718	7.115325085	7.742587721	1.115363557	0.627262636	-0.488100921
216959_x_at	NRCAM	6.811566385	7.408314014	7.485609859	7.596646084	0.596747629	0.111036225	-0.485711404
205193_at	MAFF	8.155717098	9.803938397	9.291781409	10.46288084	1.648221299	1.171099434	-0.477121864
204420_at	FOSL1	7.180282775	8.2662772	7.694623763	8.309649068	1.085994425	0.615025305	-0.47096912
202071_at	SDC4	6.218060661	6.838611703	6.055107684	6.205449259	0.620551042	0.150341575	-0.470209467
208893_s_at	DUSP6	7.38565978	8.188515825	7.81743024	8.15902572	0.802856045	0.34159548	-0.461260565
211434_s_at	CCRL2	4.467928142	5.519258552	5.047090218	5.639408765	1.051330411	0.592318547	-0.459011863
204970_s_at	MAFG	6.16811373	7.368066595	6.535323666	7.294971121	1.199952865	0.759647455	-0.44030541
219475_at	OSGIN1	3.995688686	7.268037665	3.882302196	6.714567231	3.272348979	2.832265035	-0.440083944
213281_at	LOC100288387	5.14668571	5.909132383	5.427424419	5.750214934	0.762446673	0.322790515	-0.439656158
206636_at	RASA2	5.448784203	6.218749152	5.291848459	5.622694611	0.769964949	0.330846152	-0.439118797
218691_s_at	PDLIM4	4.225373591	5.290098752	4.569204248	5.195238662	1.064725162	0.626034414	-0.438690747
216375_s_at	ETV5	4.212407235	5.06556748	4.890459933	5.305515245	0.853160245	0.415055311	-0.438104933
204346_s_at	RASSF1	6.380199573	7.142739299	6.490060893	6.817650958	0.762539726	0.327590065	-0.434949661
200670_at	XBP1	6.332170663	7.390437723	6.520149924	7.151337181	1.05826706	0.631187257	-0.427079803
212230_at	PPAP2B	6.245812238	7.065571948	6.51548167	6.918376405	0.81975971	0.402894735	-0.416864974
204341_at	TRIM16	7.689668753	8.996536156	7.220336703	8.115015753	1.306867403	0.894679051	-0.412188352
209785_s_at	PLA2G4C	7.895434653	8.616141561	8.814954598	9.134101122	0.720706908	0.319146525	-0.401560383
204203_at	CEBPG	6.825894513	7.923400628	7.050643407	7.749652528	1.097506115	0.699009121	-0.398496993
208891_at	DUSP6	8.591371853	9.232636247	8.803048558	9.049283073	0.641264394	0.246234516	-0.395029878
202207_at	ARL4C	3.781792594	4.940814809	4.37749579	5.147552545	1.159022216	0.770056755	-0.388965461
213895_at	EMP1	6.019047081	7.13740129	6.37417122	7.106376554	1.11835421	0.732205334	-0.386148875
215120_s_at	SAMD4A	3.479876128	4.112740129	3.601364049	3.849604425	0.632864002	0.248240376	-0.384623626
204896_s_at	PTGER4	5.067830555	5.702646391	5.246550735	5.504295483	0.634815836	0.257744748	-0.377071088
201325_s_at	EMP1	9.341950038	10.23589601	9.798803109	10.31648087	0.893945969	0.517677761	-0.376268208
204286_s_at	PMAIP1	6.10257409	7.479016111	6.318293861	7.31927861	1.376442021	1.00098475	-0.375457271
200897_s_at	PALLD	7.538453403	9.370555858	7.316199841	8.773709917	1.832102455	1.457510076	-0.374592379
217655_at	LOC100127972	3.661397634	4.456198764	3.649569132	4.073067926	0.79480113	0.423498795	-0.371302335
212444_at	---	6.886924687	7.501705164	6.902859526	7.147114793	0.614780477	0.244255267	-0.37052521
220030_at	STYK1	5.957759357	6.596125463	5.81648427	6.086322242	0.638366106	0.269837972	-0.368528133
212295_s_at	SLC7A1	9.097856178	10.35089404	9.368853225	10.26061381	1.253037859	0.891760582	-0.361277277
202695_s_at	STK17A	5.077701476	5.703210504	4.984730446	5.251998735	0.625509028	0.267268289	-0.358240739
203723_at	ITPKB	7.012316796	8.050603134	7.787351944	8.469368696	1.038286338	0.682016752	-0.356269587
212110_at	SLC39A14	8.256081201	8.881473429	8.398881385	8.668670241	0.625392229	0.269788857	-0.355603372
211564_s_at	PDLIM4	8.171851298	8.762111328	8.772876254	9.010127435	0.59026003	0.237251181	-0.353008849

212190_at	SERPINE2	7.152193864	7.740437803	7.983240229	8.219975081	0.588243939	0.236734852	-0.351509087
202887_s_at	DDIT4	8.258191832	9.708188437	8.553813129	9.652333405	1.449996605	1.098520276	-0.351476329
202123_s_at	ABL1	8.441767613	9.079495854	9.136197459	9.424996343	0.637728241	0.288798884	-0.348929357
214844_s_at	DOK5	6.805299893	7.746667834	6.755061336	7.347706089	0.941367941	0.592644754	-0.348723188
209373_at	MALL	8.496484942	9.158880254	8.512908763	8.829645992	0.662395313	0.316737229	-0.345658084
205770_at	GSR	6.988649993	7.955545341	6.974578035	7.596648486	0.966895349	0.622070451	-0.344824897
204748_at	PTGS2	7.097004713	10.20680854	7.888435709	10.65440501	3.109803831	2.765969301	-0.34383453
204151_x_at	AKR1C1	4.319586369	5.03676304	4.016470886	4.389928846	0.717176671	0.37345796	-0.343718711
204194_at	BACH1	4.32878418	5.31311595	4.490123835	5.132959592	0.984331769	0.642835757	-0.341496012
209339_at	SIAH2	6.119008541	6.986827869	6.452028522	6.981785414	0.867819327	0.529756892	-0.338062435
219496_at	ANKRD57	4.296040705	4.994692808	4.421223931	4.783311988	0.698652104	0.362088057	-0.336564047
218871_x_at	CSGALNACT2	6.909711186	7.670315716	7.74361978	8.170136883	0.76060453	0.426517103	-0.334087426
217127_at	CTH	3.674204336	4.614734359	3.518038347	4.129348444	0.940530023	0.611310096	-0.329219927
219778_at	ZFPM2	7.061532389	7.661242128	6.607963161	6.880603482	0.599709739	0.272640322	-0.327069417
218647_s_at	YRDC	6.069270472	6.881682343	6.54692332	7.036645724	0.812411872	0.489722404	-0.322689468
221904_at	FAM131A	5.064376641	5.735914628	5.899610511	6.250082911	0.671537987	0.3504724	-0.321065587
201041_s_at	DUSP1	7.849153795	9.407591251	8.389343052	9.627746798	1.558437455	1.238403747	-0.320033708
213324_at	SRC	5.659005203	6.396592323	5.794955912	6.214850167	0.73758712	0.419894255	-0.317692865
202260_s_at	STXBP1	6.907939319	7.534379673	7.141136646	7.451803244	0.626440353	0.310666598	-0.315773755
203192_at	ABCB6	4.620555702	5.226521409	4.65565643	4.948680765	0.605965707	0.293024335	-0.312941372
210756_s_at	NOTCH2	5.425334481	6.073045502	6.056494054	6.392148939	0.64771102	0.335654885	-0.312056135
206109_at	FUT1	4.958886603	5.677214958	5.193218566	5.602731865	0.718328355	0.409513299	-0.308815056
205282_at	LRP8	4.468334264	5.07413501	4.271951763	4.574733103	0.605800746	0.302781341	-0.303019406
220027_s_at	RASIP1	7.742541041	8.386902921	7.805644332	8.149760169	0.644361879	0.344115837	-0.300246043
212665_at	TIPARP	8.640932028	9.41954181	9.536352402	10.01998109	0.778609782	0.483628686	-0.294981096
200906_s_at	PALLD	5.74476219	7.56297506	5.969141836	7.497157284	1.81821287	1.528015448	-0.290197422
221276_s_at	SYNC	5.013503141	5.753694508	4.854274444	5.304840979	0.740191367	0.450566536	-0.289624832
206907_at	TNFSF9	3.696716442	4.574198979	3.78609545	4.374562016	0.877482537	0.588466565	-0.289015972
206867_at	GCKR	4.281105858	4.89231772	4.754836995	5.077291068	0.611211862	0.322454073	-0.288757788
215886_x_at	USP12	3.864422913	4.47796801	3.973813077	4.298972035	0.613545097	0.325158958	-0.288386139
208916_at	SLC1A5	6.029173844	6.793133953	6.330595624	6.808120171	0.763960109	0.477524546	-0.286435562
211668_s_at	PLAU	6.053880153	7.24674174	5.833346757	6.743180772	1.192861588	0.909834015	-0.283027573
210513_s_at	VEGFA	3.670938708	4.587294381	3.787147008	4.420561738	0.916355673	0.63341473	-0.282940943
204506_at	PPP3R1	6.880640969	7.503735508	7.209084483	7.550209084	0.623094539	0.341124601	-0.281969939
204141_at	TUBB2A	8.479040055	9.399264128	8.426143942	9.064470241	0.920224073	0.638326299	-0.281897774
202241_at	TRIB1	4.524613826	6.659960764	5.051607393	6.90562254	2.135346938	1.854015147	-0.281331791
214056_at	---	4.753965266	5.601291378	4.404827423	4.971854631	0.847326112	0.567027208	-0.280298904
33304_at	ISG20	6.100641476	6.694455855	7.515199708	7.83187973	0.593814379	0.316680022	-0.277134357
201464_x_at	JUN	9.127609025	9.925629682	9.476819329	9.998178767	0.798020658	0.521359438	-0.276661219
215485_s_at	ICAM1	5.948630497	6.576678654	6.253043131	6.604667073	0.628048157	0.351623943	-0.276424214
212290_at	SLC7A1	5.056550354	6.351847006	5.555100963	6.576485316	1.295296652	1.021384354	-0.273912298
212635_at	TNPO1	9.331534616	9.935170375	9.224220259	9.555104025	0.603635759	0.330883766	-0.272751993
210512_s_at	VEGFA	6.3412984	7.481072406	6.379017202	7.250435848	1.139774005	0.871418645	-0.26835536
201324_at	EMP1	10.27336442	10.9307417	10.59325345	10.98295947	0.657377275	0.38970602	-0.267671255
218522_s_at	MAP1S	5.479225573	6.30271389	6.193585913	6.749731996	0.823488317	0.556146083	-0.267342234

209193_at	PIM1	3.774072563	4.606502718	3.805523492	4.37083866	0.832430154	0.565315167	-0.267114987
202847_at	PCK2	6.042034131	7.393921132	6.166758246	7.252837652	1.351887002	1.086079406	-0.265807596
202499_s_at	SLC2A3	7.038288213	7.757684197	7.134200744	7.590065789	0.719395985	0.455865046	-0.263530939

Supplementary Table 6. Gene categories of genes induced by Ox-PAPC by 1.5 fold and the induction was reversed by 1.2 fold by ADAM10 silencing.

DAVID analysis used for the identification of gene categories.

http://david.abcc.ncifcrf.gov/home.jsp

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
INTERPRO	IPR004827:Basic-leucine zipper (bZIP) transcription factor	8	5.673758865	1.90E-07	201464_X_A	133	53	16659	18.9065116	6.28E-05	6.28E-05	2.58E-04
SMART	SM00338:BRLZ	8	5.673758865	3.22E-07	201464_X_A	80	53	9079	17.1301887	2.48E-05	2.48E-05	3.40E-04
SP_PIR_KEYWORDS	Apoptosis	14	9.929078014	3.73E-06	204286_S_A	139	381	19235	5.08487698	9.68E-04	9.68E-04	0.00486897
GOTERM_BP_FAT	GO:0034097~response to cytokine stimulus	8	5.673758865	5.86E-06	201464_X_A	120	79	13528	11.4160338	0.00770106	0.00770106	0.00958655
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	22	15.60283688	6.26E-06	201464_X_A	120	804	13528	3.08474295	0.0082201	0.00411853	0.01023531
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	22	15.60283688	7.29E-06	201464_X_A	120	812	13528	3.0543514	0.00956886	0.00319985	0.01192273
GOTERM_BP_FAT	GO:0010941~regulation of cell death	22	15.60283688	7.71E-06	201464_X_A	120	815	13528	3.04310838	0.01012409	0.00254069	0.01261802
UP_SEQ_FEATURE	domain:Leucine-zipper	8	5.673758865	1.50E-05	201464_X_A	139	110	19113	10.0002616	0.00791362	0.00791362	0.02183266
UP_SEQ_FEATURE	DNA-binding region:Basic motif	9	6.382978723	2.24E-05	201464_X_A	139	161	19113	7.68653649	0.01174156	0.00588811	0.0324543
GOTERM_BP_FAT	GO:0006915~apoptosis	17	12.05673759	7.35E-05	201464_X_A	120	602	13528	3.18349945	0.09236307	0.01919554	0.1201065
GOTERM_BP_FAT	GO:0012501~programmed cell death	17	12.05673759	8.75E-05	201464_X_A	120	611	13528	3.13660666	0.10894788	0.01904176	0.14294565
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	14	9.929078014	1.03E-04	201464_X_A	120	430	13528	3.6703876	0.12732618	0.01926815	0.16875029
GOTERM_BP_FAT	GO:0060323~head morphogenesis	4	2.836879433	1.04E-04	202310_S_A	120	11	13528	40.9939394	0.12820854	0.01700439	0.17000265
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	14	9.929078014	1.11E-04	201464_X_A	120	433	13528	3.64495766	0.13584357	0.01609151	0.18089194
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	14	9.929078014	1.16E-04	201464_X_A	120	435	13528	3.62819923	0.1417629	0.01517123	0.18939983
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	6	4.255319149	1.29E-04	201464_X_A	120	56	13528	12.0785714	0.15673491	0.01537816	0.2111806
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	10	7.092198582	1.39E-04	201464_X_A	120	220	13528	5.12424242	0.16749542	0.01516029	0.22707181
GOTERM_BP_FAT	GO:0060322~head development	4	2.836879433	2.25E-04	202310_S_A	120	14	13528	32.2095238	0.25689396	0.02258088	0.36752776
GOTERM_BP_FAT	GO:0010171~body morphogenesis	4	2.836879433	2.25E-04	202310_S_A	120	14	13528	32.2095238	0.25689396	0.02258088	0.36752776
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	15	10.63829787	2.30E-04	201464_X_A	113	542	12983	3.17971786	0.07894881	0.07894881	0.31474191
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	9	6.382978723	3.46E-04	201464_X_A	120	197	13528	5.15025381	0.36669969	0.03210273	0.56488711
GOTERM_BP_FAT	GO:0051591~response to cAMP	5	3.546099291	4.92E-04	201464_X_A	120	42	13528	13.4206349	0.47759999	0.04236456	0.80198758
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	6	4.255319149	5.11E-04	201464_X_A	120	75	13528	9.01866667	0.49066226	0.04128866	0.83313285
GOTERM_BP_FAT	GO:0008219~cell death	17	12.05673759	5.50E-04	201464_X_A	120	719	13528	2.66546129	0.51582032	0.04176733	0.89540729
GOTERM_BP_FAT	GO:0048008~platelet-derived growth factor receptor signalin	4	2.836879433	5.80E-04	210513_S_A	120	19	13528	23.7333333	0.53493512	0.04164033	0.94489767
GOTERM_BP_FAT	GO:0016265~death	17	12.05673759	5.93E-04	201464_X_A	120	724	13528	2.64705341	0.54247795	0.04031888	0.96498187
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	8	5.673758865	6.08E-04	201464_X_A	120	164	13528	5.49918699	0.5519358	0.03934596	0.99063237
SP_PIR_KEYWORDS	amino-acid biosynthesis	4	2.836879433	6.55E-04	220346_AT,	139	24	19235	23.0635492	0.15660524	0.08163474	0.85260225
SP_PIR_KEYWORDS	phosphoprotein	71	50.35460993	0.001253808	201464_X_A	139	7263	19235	1.3527567	0.2783353	0.10302883	1.62651915
GOTERM_BP_FAT	GO:0007584~response to nutrient	7	4.964539007	0.001470267	204341_AT,	120	140	13528	5.63666667	0.85639798	0.08827306	2.37793556
SP_PIR_KEYWORDS	cytoplasm	39	27.65957447	0.001817295	200906_S_A	139	3332	19235	1.61970903	0.37682412	0.11150976	2.34952192
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	8	5.673758865	0.002218351	201464_X_A	120	205	13528	4.39934959	0.94656318	0.12466444	3.56737016
GOTERM_BP_FAT	GO:0006916~anti-apoptosis	8	5.673758865	0.002279969	206665_S_A	120	206	13528	4.37799353	0.95074344	0.12269498	3.66473239
GOTERM_BP_FAT	GO:0042592~homeostatic process	16	11.34751773	0.002411241	201464_X_A	120	751	13528	2.40177541	0.95859141	0.12425278	3.87184574
GOTERM_BP_FAT	GO:0060325~face morphogenesis	3	2.127659574	0.002653079	202310_S_A	120	9	13528	37.5777778	0.969925	0.13078297	4.25231133
UP_SEQ_FEATURE	site:Lowers pKa of active site Tyr	3	2.127659574	0.003257675	206561_S_A	139	12	19113	34.3758993	0.82144527	0.43689361	4.62448914
INTERPRO	IPR018170:Aldo/keto reductase, conserved site	3	2.127659574	0.003270365	206561_S_A	133	11	16659	34.1606288	0.66074016	0.41753984	4.3437673
GOTERM_BP_FAT	GO:0009396~folic acid and derivative biosynthetic process	3	2.127659574	0.003297314	201761_AT,	120	10	13528	33.82	0.9871748	0.15426708	5.25895042
UP_SEQ_FEATURE	domain:CH	4	2.836879433	0.003441371	204823_AT,	139	42	19113	13.0955807	0.83800302	0.3655802	4.87923187
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	16	11.34751773	0.003754173	220049_S_A	120	787	13528	2.29191021	0.99299458	0.16785069	5.96677604
INTERPRO	IPR013322:TRAF-type	3	2.127659574	0.003904131	205599_AT,	133	12	16659	31.3139098	0.72497269	0.34968275	5.16506217
GOTERM_BP_FAT	GO:0060324~face development	3	2.127659574	0.004006936	202310_S_A	120	11	13528	30.7454545	0.99498722	0.1723248	6.35625373
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	10	7.092198582	0.004024788	210118_S_A	120	354	13528	3.18455744	0.99510434	0.16758804	6.38370405
GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	5	3.546099291	0.004077961	216493_S_A	120	74	13528	7.61711712	0.99543724	0.16444653	6.46542267
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	10	7.092198582	0.00440947	210118_S_A	120	359	13528	3.14020427	0.99705884	0.17141072	6.97338494
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	10	7.092198582	0.004489746	210118_S_A	120	360	13528	3.13148148	0.99735559	0.16929323	7.09600058
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	10	7.092198582	0.004571161	201464_X_A	120	361	13528	3.12280702	0.99762601	0.16733743	7.22020039
GOTERM_BP_FAT	GO:0032496~response to lipopolysaccharide	5	3.546099291	0.004700616	201464_X_A	120	77	13528	7.32034632	0.99800025	0.16705378	7.41736458
GOTERM_BP_FAT	GO:0001570~vasculogenesis	4	2.836879433	0.005546531	219778_AT,	120	41	13528	10.998374	0.9993485	0.18909697	8.6960692
GOTERM_BP_FAT	GO:0040007~growth	7	4.964539007	0.00555264	201325_S_A	120	183	13528	4.31220401	0.99935376	0.18454536	8.70524382

GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	5	3.546099291	0.005626152	220346_AT,	120	81	13528	6.95884774	0.9994138	0.18219476	8.81556978
GOTERM_BP_FAT	GO:0001568~blood vessel development	8	5.673758865	0.00590119	201464_X_A	120	245	13528	3.68108844	0.99959301	0.18571119	9.22723152
INTERPRO	IPR011700:Basic leucine zipper	3	2.127659574	0.006115319	212501_AT,	133	15	16659	25.0511278	0.86790726	0.39713547	7.97965999
GOTERM_BP_FAT	GO:0045604~regulation of epidermal cell differentiation	3	2.127659574	0.006516389	204970_S_A	120	14	13528	24.1571429	0.99982012	0.19837055	10.1417216
UP_SEQ_FEATURE	short sequence motif:BH3	3	2.127659574	0.006556105	206665_S_A	139	17	19113	24.2653407	0.96897682	0.50072793	9.10334254
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	5	3.546099291	0.006666146	204420_AT,	120	85	13528	6.63137255	0.99985256	0.19792415	10.3630218
GOTERM_BP_FAT	GO:0001944~vasculature development	8	5.673758865	0.006710954	201464_X_A	120	251	13528	3.59309429	0.99986108	0.19476732	10.4291368
GOTERM_CC_FAT	GO:0031968~organelle outer membrane	5	3.546099291	0.006941353	206665_S_A	94	104	12782	6.53743863	0.67419444	0.67419444	8.07505517
GOTERM_BP_FAT	GO:0002237~response to molecule of bacterial origin	5	3.546099291	0.006944706	201464_X_A	120	86	13528	6.55426357	0.99989815	0.19656393	10.7732972
KEGG_PATHWAY	hsa05200:Pathways in cancer	10	7.092198582	0.006959558	201464_X_A	55	328	5085	2.81873614	0.46663539	0.46663539	7.31614976
GOTERM_CC_FAT	GO:0005886~plasma membrane	40	28.36879433	0.007156844	216959_X_A	94	3777	12782	1.4400712	0.68538166	0.4390915	8.31588553
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic proce	14	9.929078014	0.007169347	201464_X_A	120	685	13528	2.30403893	0.99992443	0.19804891	11.1028738
GOTERM_BP_FAT	GO:0048660~regulation of smooth muscle cell proliferation	4	2.836879433	0.007651392	201464_X_A	120	46	13528	9.80289855	0.99996017	0.2056649	11.8062411
INTERPRO	IPR001395:Aldo/keto reductase	3	2.127659574	0.007839264	206561_S_A	133	17	16659	22.1039363	0.92551447	0.40514052	10.1201557
GOTERM_CC_FAT	GO:0019867~outer membrane	5	3.546099291	0.00791466	206665_S_A	94	108	12782	6.29531127	0.72177625	0.34717306	9.15821993
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	14	9.929078014	0.008053861	201464_X_A	120	695	13528	2.27088729	0.99997668	0.21102715	12.3894892
GOTERM_BP_FAT	GO:0006760~folic acid and derivative metabolic process	3	2.127659574	0.008495052	201761_AT,	120	16	13528	21.1375	0.99998703	0.21700339	13.0246912
GOTERM_MF_FAT	GO:0042802~identical protein binding	13	9.219858156	0.00907454	210513_S_A	113	640	12983	2.33378042	0.96174631	0.8044145	11.7587777
GOTERM_MF_FAT	GO:0046982~protein heterodimerization activity	7	4.964539007	0.009236202	206665_S_A	113	208	12983	3.86661845	0.96391669	0.66955278	11.9561234
GOTERM_BP_FAT	GO:0044272~sulfur compound biosynthetic process	4	2.836879433	0.00963183	218871_X_A	120	50	13528	9.01866667	0.99999714	0.2378533	14.6414958
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	4	2.836879433	0.010169196	220346_AT,	120	51	13528	8.84183007	0.9999986	0.24487469	15.3959129
GOTERM_BP_FAT	GO:0010033~response to organic substance	14	9.929078014	0.010762345	201464_X_A	120	721	13528	2.18899676	0.99999937	0.25268985	16.2213755
SP_PIR_KEYWORDS	alternative initiation	4	2.836879433	0.010944619	209193_AT,	139	64	19235	8.64883094	0.94280492	0.43574978	13.3979509
GOTERM_BP_FAT	GO:0016477~cell migration	8	5.673758865	0.010998828	205282_AT,	120	276	13528	3.26763285	0.99999954	0.25304963	16.5483662
KEGG_PATHWAY	hsa05222:Small cell lung cancer	5	3.546099291	0.011708076	206665_S_A	55	84	5085	5.50324675	0.65352478	0.41137854	12.025278
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthe	13	9.219858156	0.012438646	201464_X_A	120	654	13528	2.24087666	0.99999993	0.27654361	18.5135236
SP_PIR_KEYWORDS	activator	10	7.092198582	0.012779561	204194_AT,	139	520	19235	2.66117875	0.96470803	0.4272752	15.4747043
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	5	3.546099291	0.012908204	209193_AT,	120	103	13528	5.47249191	0.99999996	0.28075493	19.1449545
INTERPRO	IPR000712:Apoptosis regulator Bcl-2, BH	3	2.127659574	0.012975959	206665_S_A	133	22	16659	17.0803144	0.98656768	0.51244323	16.2276957
GOTERM_BP_FAT	GO:0009612~response to mechanical stimulus	4	2.836879433	0.013114639	201464_X_A	120	56	13528	8.05238095	0.99999997	0.28002615	19.4210989
GOTERM_CC_FAT	GO:0009986~cell surface	8	5.673758865	0.013389931	216959_X_A	94	348	12782	3.12594766	0.88586142	0.41875649	15.0363991
GOTERM_BP_FAT	GO:0045787~positive regulation of cell cycle	4	2.836879433	0.013756033	209193_AT,	120	57	13528	7.91111111	0.99999999	0.28704452	20.2734399
GOTERM_BP_FAT	GO:0050805~negative regulation of synaptic transmission	3	2.127659574	0.014447149	204748_AT,	120	21	13528	16.1047619	1	0.29460406	21.1823778
GOTERM_BP_FAT	GO:0001836~release of cytochrome c from mitochondria	3	2.127659574	0.014447149	201464_X_A	120	21	13528	16.1047619	1	0.29460406	21.1823778
GOTERM_CC_FAT	GO:0005829~cytosol	18	12.76595745	0.014674964	201464_X_A	94	1330	12782	1.84031355	0.90746577	0.37875847	16.3644437
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	11	7.80141844	0.014798762	201464_X_A	120	512	13528	2.42200521	1	0.29613491	21.6410666
SMART	SM00337:BCL	3	2.127659574	0.015429169	206665_S_A	80	22	9079	15.4755682	0.69799349	0.45044881	15.1305289
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	12	8.510638298	0.015585281	204194_AT,	113	607	12983	2.27137671	0.9963879	0.75484552	19.3907535
INTERPRO	IPR004978:Stanniocalcin	2	1.418439716	0.015784978	203439_S_A	133	2	16659	125.255639	0.99475559	0.52767344	19.4027404
GOTERM_BP_FAT	GO:0045682~regulation of epidermis development	3	2.127659574	0.015801403	204970_S_A	120	22	13528	15.3727273	1	0.308277	22.9353179
GOTERM_MF_FAT	GO:0004487~methylenetetrahydrofolate dehydrogenase (NA	2	1.418439716	0.017179571	201761_AT,	113	2	12983	114.893805	0.99797812	0.71083152	21.1639044
GOTERM_BP_FAT	GO:0030097~hemopoiesis	7	4.964539007	0.017937327	202443_X_A	120	236	13528	3.34378531	1	0.33742558	25.6258379
GOTERM_BP_FAT	GO:0010243~response to organic nitrogen	4	2.836879433	0.017975821	206665_S_A	120	63	13528	7.15767196	1	0.3333713	25.6735083
INTERPRO	IPR001715:Calponin-like actin-binding	4	2.836879433	0.018100903	204823_AT,	133	70	16659	7.15746509	0.99758974	0.52928505	21.9362142
GOTERM_BP_FAT	GO:0006790~sulfur metabolic process	5	3.546099291	0.018636663	218871_X_A	120	115	13528	4.90144928	1	0.33870931	26.4874176
GOTERM_BP_FAT	GO:0001101~response to acid	3	2.127659574	0.018665497	209878_S_A	120	24	13528	14.0916667	1	0.33463359	26.5227397
GOTERM_BP_FAT	GO:0051674~localization of cell	8	5.673758865	0.01873381	205282_AT,	120	307	13528	2.93767644	1	0.33123807	26.6063591
GOTERM_BP_FAT	GO:0048870~cell motility	8	5.673758865	0.01873381	205282_AT,	120	307	13528	2.93767644	1	0.33123807	26.6063591
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	6	4.255319149	0.019587846	206665_S_A	120	176	13528	3.84318182	1	0.33911195	27.6442396
GOTERM_BP_FAT	GO:0051970~negative regulation of transmission of nerve im	3	2.127659574	0.020173338	204748_AT,	120	25	13528	13.528	1	0.34296026	28.3477895
GOTERM_BP_FAT	GO:0033273~response to vitamin	4	2.836879433	0.020326342	204341_AT,	120	66	13528	6.83232323	1	0.34079326	28.5305846
GOTERM_CC_FAT	GO:0045121~membrane raft	5	3.546099291	0.020376459	205282_AT,	94	143	12782	4.75450082	0.96364758	0.42444229	22.0302427
UP_SEQ_FEATURE	domain:Protein kinase	9	6.382978723	0.020654267	209193_AT,	139	469	19113	2.63866178	0.99998362	0.84064301	26.1287517
UP_SEQ_FEATURE	binding site:Substrate	7	4.964539007	0.020930356	203723_AT,	139	297	19113	3.24082552	0.99998589	0.79719349	26.4303644
GOTERM_CC_FAT	GO:0044421~extracellular region part	14	9.929078014	0.021299485	205282_AT,	94	960	12782	1.98302305	0.96876651	0.39053918	22.9136442

GOTERM_BP_FAT	GO:0019725~cellular homeostasis	10	7.092198582	0.021734061	201464_X_A	120	466	13528	2.41917024	1	0.35541048	30.1919662
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	10	7.092198582	0.021734061	201464_X_A	120	466	13528	2.41917024	1	0.35541048	30.1919662
GOTERM_BP_FAT	GO:0001817~regulation of cytokine production	6	4.255319149	0.021809995	204341_AT,	120	181	13528	3.73701657	1	0.35216248	30.2805435
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	5	3.546099291	0.022008514	209193_AT,	120	121	13528	4.6584022	1	0.35057522	30.5116208
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	5	3.546099291	0.022008514	201464_X_A	120	121	13528	4.6584022	1	0.35057522	30.5116208
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	7	4.964539007	0.022280942	202241_AT,	120	248	13528	3.18198925	1	0.34997069	30.8275566
SMART	SM00033:CH	4	2.836879433	0.022874514	204823_AT,	80	70	9079	6.485	0.83166429	0.44784787	21.6624174
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	8	5.673758865	0.022903354	202443_X_A	120	320	13528	2.81833333	1	0.3537595	31.5443202
GOTERM_BP_FAT	GO:0060348~bone development	5	3.546099291	0.023210021	202310_S_A	120	123	13528	4.58265583	1	0.35355427	31.8949039
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	8	5.673758865	0.023248651	202443_X_A	120	321	13528	2.80955348	1	0.35009644	31.9389468
GOTERM_BP_FAT	GO:0006928~cell motion	10	7.092198582	0.024228179	205282_AT,	120	475	13528	2.37333333	1	0.35799364	33.0468199
SP_PIR_KEYWORDS	transforming protein	3	2.127659574	0.024677591	209193_AT,	139	34	19235	12.2101143	0.99849154	0.60469415	27.8634807
INTERPRO	IPR011616:bZIP transcription factor, bZIP-1	3	2.127659574	0.024939854	201464_X_A	133	31	16659	12.1215135	0.99975992	0.60388781	28.9935772
GOTERM_BP_FAT	GO:0031645~negative regulation of neurological system proc	3	2.127659574	0.024988306	204748_AT,	120	28	13528	12.0785714	1	0.36304677	33.8948547
SP_PIR_KEYWORDS	Proto-oncogene	6	4.255319149	0.025222759	209193_AT,	139	230	19235	3.60994683	0.99869564	0.56406185	28.388753
UP_SEQ_FEATURE	sequence variant	99	70.21276596	0.02539328	201464_X_A	139	11992	19113	1.13516145	0.99999874	0.816878	31.1495654
GOTERM_MF_FAT	GO:0004486~methylenetetrahydrofolate dehydrogenase activ	2	1.418439716	0.02565934	201761_AT,	113	3	12983	76.5958702	0.99990912	0.78796252	30.0026387
GOTERM_MF_FAT	GO:0004477~methenyltetrahydrofolate cyclohydrolase activit	2	1.418439716	0.02565934	201761_AT,	113	3	12983	76.5958702	0.99990912	0.78796252	30.0026387
GOTERM_MF_FAT	GO:0016645~oxidoreductase activity, acting on the CH-NH gro	3	2.127659574	0.025733068	201761_AT,	113	29	12983	11.8855661	0.99991155	0.73639197	30.0752883
PIR_SUPERFAMILY	PIRSF015614:TNF receptor-associated factor (TRAF)	2	1.418439716	0.025739436	205599_AT,	65	3	7396	75.8564103	0.86918437	0.86918437	24.105961
PIR_SUPERFAMILY	PIRSF037826:transcription factor MafK	2	1.418439716	0.025739436	204970_S_A	65	3	7396	75.8564103	0.86918437	0.86918437	24.105961
GOTERM_BP_FAT	GO:0032227~negative regulation of synaptic transmission, do	2	1.418439716	0.026160169	204748_AT,	120	3	13528	75.1555556	1	0.37261505	35.1825067
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metal	12	8.510638298	0.026344518	201464_X_A	120	644	13528	2.10062112	1	0.37082543	35.3829148
GOTERM_BP_FAT	GO:0048511~rhythmic process	5	3.546099291	0.026386103	201464_X_A	120	128	13528	4.40364583	1	0.3674909	35.428042
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	9	6.382978723	0.026520151	206665_S_A	120	405	13528	2.50518519	1	0.36524519	35.5733058
SP_PIR_KEYWORDS	kinase	11	7.80141844	0.02658308	211924_S_A	139	688	19235	2.21249163	0.99909278	0.54083586	29.6840654
GOTERM_CC_FAT	GO:0005615~extracellular space	11	7.80141844	0.026899712	205282_AT,	94	685	12782	2.18359994	0.98760137	0.42234076	28.0795683
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	10	7.092198582	0.027232917	201464_X_A	120	485	13528	2.32439863	1	0.36934244	36.3405712
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	10	7.092198582	0.027232917	201464_X_A	120	485	13528	2.32439863	1	0.36934244	36.3405712
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	6	4.255319149	0.027261107	204420_AT,	120	192	13528	3.52291667	1	0.36600085	36.3707402
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	7	4.964539007	0.027286377	202443_X_A	120	260	13528	3.03512821	1	0.36269356	36.3977714
GOTERM_CC_FAT	GO:0005741~mitochondrial outer membrane	4	2.836879433	0.027804736	206665_S_A	94	90	12782	6.04349882	0.98932633	0.39615741	28.883949
GOTERM_BP_FAT	GO:0007566~embryo implantation	3	2.127659574	0.028431648	203542_S_A	120	30	13528	11.2733333	1	0.37121177	37.6116461
GOTERM_MF_FAT	GO:0016814~hydrolase activity, acting on carbon-nitrogen (bu	3	2.127659574	0.029146605	201761_AT,	113	31	12983	11.1187554	0.99997482	0.73385029	33.3633738
GOTERM_BP_FAT	GO:0048661~positive regulation of smooth muscle cell prolife	3	2.127659574	0.030220542	201464_X_A	120	31	13528	10.9096774	1	0.3859372	39.4642613
GOTERM_BP_FAT	GO:0008637~apoptotic mitochondrial changes	3	2.127659574	0.030220542	201464_X_A	120	31	13528	10.9096774	1	0.3859372	39.4642613
SP_PIR_KEYWORDS	polymorphism	95	67.37588652	0.030566838	201464_X_A	139	11550	19235	1.13820113	0.99968765	0.55386667	33.35403
INTERPRO	IPR000672:Tetrahydrofolate dehydrogenase/cyclohydrolase	2	1.418439716	0.031322648	201761_AT,	133	4	16659	62.6278195	0.99997251	0.65012588	35.0425066
GOTERM_BP_FAT	GO:0042246~tissue regeneration	3	2.127659574	0.032053041	202443_X_A	120	32	13528	10.56875	1	0.40043565	41.3083955
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	8	5.673758865	0.032649441	209193_AT,	120	345	13528	2.61410628	1	0.40255787	41.8971153
GOTERM_MF_FAT	GO:0008134~transcription factor binding	10	7.092198582	0.033155749	209193_AT,	113	513	12983	2.23964533	0.99999428	0.73847399	37.0419301
GOTERM_MF_FAT	GO:0047115~trans-1,2-dihydrobenzene-1,2-diol dehydrogena	2	1.418439716	0.034066594	209699_X_A	113	4	12983	57.4469027	0.99999592	0.71085928	37.8509873
GOTERM_BP_FAT	GO:0046683~response to organophosphorus	2	1.418439716	0.034728519	204341_AT,	120	4	13528	56.3666667	1	0.41847849	43.9063562
GOTERM_BP_FAT	GO:0002520~immune system development	7	4.964539007	0.035049545	202443_X_A	120	276	13528	2.85917874	1	0.41778715	44.2107215
INTERPRO	IPR000719:Protein kinase, core	9	6.382978723	0.035768108	209193_AT,	133	476	16659	2.36827889	0.99999398	0.66469136	38.9695112
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	5	3.546099291	0.035816215	208892_S_A	120	141	13528	3.99763593	1	0.42113491	44.9313418
GOTERM_BP_FAT	GO:0000060~protein import into nucleus, translocation	3	2.127659574	0.035845302	201464_X_A	120	34	13528	9.94705882	1	0.41782861	44.9585086
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	7	4.964539007	0.03611056	201464_X_A	120	278	13528	2.83860911	1	0.4166757	45.2056787
GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	5	3.546099291	0.036732623	219778_AT,	113	145	12983	3.96185536	0.99999848	0.70417565	40.1640246
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	8	5.673758865	0.038189612	209193_AT,	120	357	13528	2.52623716	1	0.43129096	47.1071753
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	6	4.255319149	0.038579436	201464_X_A	120	211	13528	3.2056872	1	0.43110743	47.4567375
GOTERM_BP_FAT	GO:0048589~developmental growth	4	2.836879433	0.041278675	202443_X_A	120	87	13528	5.18314176	1	0.45002003	49.8183435
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	4	2.836879433	0.041278675	208892_S_A	120	87	13528	5.18314176	1	0.45002003	49.8183435
INTERPRO	IPR015421:Pyridoxal phosphate-dependent transferase, majo	3	2.127659574	0.041790031	212322_AT,	133	41	16659	9.16504676	0.99999924	0.6908503	43.9390324
GOTERM_BP_FAT	GO:0044236~multicellular organismal metabolic process	3	2.127659574	0.041838834	205680_AT,	120	37	13528	9.14054054	1	0.45103137	50.2957806

UP_SEQ_FEATURE	binding site:ATP	9	6.382978723	0.043076001	209193_AT,	139	542	19113	2.28327006	1	0.92446582	47.214071
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	8	5.673758865	0.043254949	206665_S_AT	120	367	13528	2.45740236	1	0.45878386	51.483822
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	8	5.673758865	0.043784347	201464_X_AT	120	368	13528	2.45072464	1	0.45943806	51.9210702
GOTERM_BP_FAT	GO:0045767~regulation of anti-apoptosis	3	2.127659574	0.04391466	206665_S_AT	120	38	13528	8.9	1	0.45700632	52.0281319
BIOCARTA	h_tnfr2Pathway:TNFR2 Signaling Pathway	3	2.127659574	0.044349656	205599_AT,	30	17	1437	8.45294118	0.99349584	0.99349584	40.1530595
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	4	2.836879433	0.044904103	208892_S_AT	120	90	13528	5.01037037	1	0.46117389	52.8337563
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	8	5.673758865	0.045943968	209193_AT,	120	372	13528	2.42437276	1	0.4656103	53.6667357
GOTERM_BP_FAT	GO:0051098~regulation of binding	5	3.546099291	0.046046515	209193_AT,	120	153	13528	3.68409586	1	0.46301302	53.7481281
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	5	3.546099291	0.046046515	201761_AT,	120	153	13528	3.68409586	1	0.46301302	53.7481281
INTERPRO	IPR012227:TNF receptor-associated factor TRAF	2	1.418439716	0.046616856	205599_AT,	133	6	16659	41.7518797	0.99999986	0.70234534	47.6487634
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	5	3.546099291	0.047894543	220346_AT,	120	155	13528	3.63655914	1	0.47320764	55.1921122
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	5	3.546099291	0.047894543	220346_AT,	120	155	13528	3.63655914	1	0.47320764	55.1921122
SP_PIR_KEYWORDS	differentiation	8	5.673758865	0.048193829	214056_AT,	139	460	19235	2.40663122	0.99999735	0.6888535	47.5668769
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nu	11	7.80141844	0.048210244	201464_X_AT	120	624	13528	1.98728632	1	0.47215548	55.4345158
GOTERM_MF_FAT	GO:0004715~non-membrane spanning protein tyrosine kinase	3	2.127659574	0.048629224	202123_S_AT	113	41	12983	8.4068638	0.99999998	0.77400306	49.5454719
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	8	5.673758865	0.050466643	201464_X_AT	120	380	13528	2.37333333	1	0.48477149	57.1315308
GOTERM_MF_FAT	GO:0032052~bile acid binding	2	1.418439716	0.050666007	209699_X_AT	113	6	12983	38.2979351	0.99999999	0.7611337	51.0077514
PIR_SUPERFAMILY	PIRSF015614:TRAF	2	1.418439716	0.050826443	205599_AT,	65	6	7396	37.9282051	0.98290145	0.86923859	42.4074241
GOTERM_CC_FAT	GO:0005794~Golgi apparatus	12	8.510638298	0.051352695	218871_X_AT	94	872	12782	1.87126684	0.999794	0.57205602	47.1251998
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	6	4.255319149	0.051615589	201464_X_AT	120	229	13528	2.95371179	1	0.48937707	57.972145
GOTERM_BP_FAT	GO:0019369~arachidonic acid metabolic process	2	1.418439716	0.051641585	209785_S_AT	120	6	13528	37.5777778	1	0.48627492	57.9909843
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	4	2.836879433	0.052612651	208892_S_AT	120	96	13528	4.69722222	1	0.48958504	58.6890681
INTERPRO	IPR014393:Dual specificity protein phosphatase (MAP kinase p	2	1.418439716	0.054173847	208892_S_AT	133	7	16659	35.7873255	0.99999999	0.73094676	53.0028469
INTERPRO	IPR004826:Maf transcription factor	2	1.418439716	0.054173847	204970_S_AT	133	7	16659	35.7873255	0.99999999	0.73094676	53.0028469
SP_PIR_KEYWORDS	myristate	4	2.836879433	0.054265675	202207_AT,	139	119	19235	4.6514721	0.9999995	0.70146291	51.7745366
BIOCARTA	h_arenrf2Pathway:Oxidative Stress Induced Gene Expression	3	2.127659574	0.054397032	201464_X_AT	30	19	1437	7.56315789	0.99798776	0.955142	46.900033
GOTERM_CC_FAT	GO:0005901~caveola	3	2.127659574	0.054918507	205282_AT,	94	52	12782	7.84492635	0.99988766	0.56251905	49.4781751
SP_PIR_KEYWORDS	growth regulation	3	2.127659574	0.055527198	219475_AT,	139	53	19235	7.83290349	0.99999965	0.68100114	52.608642
GOTERM_BP_FAT	GO:0051241~negative regulation of multicellular organismal p	5	3.546099291	0.056713809	210513_S_AT	120	164	13528	3.43699187	1	0.51311373	61.5189453
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	20	14.18439716	0.058633455	201464_X_AT	113	1512	12983	1.51975933	1	0.78670828	56.3586242
GOTERM_MF_FAT	GO:0051393~alpha-actinin binding	2	1.418439716	0.058859381	200906_S_AT	113	7	12983	32.8268015	1	0.76491704	56.5021345
PIR_SUPERFAMILY	PIRSF000939:dual specificity protein phosphatase (MAP kinase	2	1.418439716	0.05904662	208892_S_AT	65	7	7396	32.5098901	0.99132414	0.79451943	47.469856
PIR_SUPERFAMILY	PIRSF000939:MAPK_Ptase	2	1.418439716	0.05904662	208892_S_AT	65	7	7396	32.5098901	0.99132414	0.79451943	47.469856
GOTERM_BP_FAT	GO:0043433~negative regulation of transcription factor activit	3	2.127659574	0.059454023	209193_AT,	120	45	13528	7.51555556	1	0.52696716	63.3071918
GOTERM_MF_FAT	GO:0008201~heparin binding	4	2.836879433	0.059479433	210513_S_AT	113	103	12983	4.46189535	1	0.74641962	56.8937527
GOTERM_BP_FAT	GO:0021700~developmental maturation	4	2.836879433	0.059491565	216959_X_AT	120	101	13528	4.46468647	1	0.52393729	63.3311409
UP_SEQ_FEATURE	region of interest:Calmodulin-binding	3	2.127659574	0.059958527	203723_AT,	139	55	19113	7.50019621	1	0.96179129	59.2296812
UP_SEQ_FEATURE	domain:Ig-like C2-type 5	3	2.127659574	0.059958527	200906_S_AT	139	55	19113	7.50019621	1	0.96179129	59.2296812
GOTERM_BP_FAT	GO:0046653~tetrahydrofolate metabolic process	2	1.418439716	0.059987587	201761_AT,	120	7	13528	32.2095238	1	0.5237365	63.6461897
GOTERM_BP_FAT	GO:0017085~response to insecticide	2	1.418439716	0.059987587	204341_AT,	120	7	13528	32.2095238	1	0.5237365	63.6461897
COG_ONTOLOGY	Coenzyme metabolism	2	1.418439716	0.060481291	201761_AT,	12	11	1950	29.5454545	0.39292344	0.39292344	28.9328184
GOTERM_BP_FAT	GO:0001501~skeletal system development	7	4.964539007	0.062506614	202310_S_AT	120	319	13528	2.4737722	1	0.53559001	65.2073067
GOTERM_BP_FAT	GO:0006690~icosanoid metabolic process	3	2.127659574	0.064194791	209785_S_AT	120	47	13528	7.19574468	1	0.54221947	66.2180546
GOTERM_MF_FAT	GO:0048037~cofactor binding	6	4.255319149	0.064309403	205770_AT,	113	249	12983	2.76852543	1	0.75335094	59.8342627
GOTERM_BP_FAT	GO:0042108~positive regulation of cytokine biosynthetic proc	3	2.127659574	0.066611606	210118_S_AT	120	48	13528	7.04583333	1	0.55274898	67.6171633
GOTERM_BP_FAT	GO:0060343~trabecula formation	2	1.418439716	0.068260753	202310_S_AT	120	8	13528	28.1833333	1	0.55870328	68.5404357
INTERPRO	IPR004032:PMP-22/EMP/MP20	2	1.418439716	0.069109943	201325_S_AT	133	9	16659	27.8345865	1	0.79309803	62.1250308
GOTERM_CC_FAT	GO:0044459~plasma membrane part	23	16.31205674	0.069881495	216959_X_AT	94	2203	12782	1.41965984	0.9999914	0.62165443	58.3419157
INTERPRO	IPR017441:Protein kinase, ATP binding site	8	5.673758865	0.07017417	209193_AT,	133	455	16659	2.20229695	1	0.77701116	62.7078589
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	7	4.964539007	0.070318688	202443_X_AT	120	329	13528	2.39858156	1	0.56668282	69.657916
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	7	4.964539007	0.071946291	206665_S_AT	120	331	13528	2.38408862	1	0.57215752	70.5152128
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	8	5.673758865	0.072778819	220049_S_AT	120	414	13528	2.1784219	1	0.57337993	70.9448824
GOTERM_BP_FAT	GO:0007565~female pregnancy	4	2.836879433	0.072874774	204420_AT,	120	110	13528	4.09939394	1	0.57078575	70.9940252
SP_PIR_KEYWORDS	pyridoxal phosphate	3	2.127659574	0.07312396	212322_AT,	139	62	19235	6.69586911	1	0.75591278	62.9372962
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	10	7.092198582	0.073288996	205282_AT,	120	586	13528	1.92377702	1	0.5698601	71.2052737

GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic	13	9.219858156	0.073905484	201464_X_AT	120	857	13528	1.7100739	1	0.56998232	71.5170018
GOTERM_BP_FAT	GO:0043392~negative regulation of DNA binding	3	2.127659574	0.074039235	209193_AT,	120	51	13528	6.63137255	1	0.56765388	71.5842137
GOTERM_BP_FAT	GO:0033559~unsaturated fatty acid metabolic process	3	2.127659574	0.074039235	209785_S_AT	120	51	13528	6.63137255	1	0.56765388	71.5842137
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg h	7	4.964539007	0.074428372	206665_S_AT	120	334	13528	2.36267465	1	0.56664591	71.7789148
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	4	2.836879433	0.076017222	202310_S_AT	120	112	13528	4.02619048	1	0.57165478	72.560959
INTERPRO	IPR008343:MAP kinase phosphatase	2	1.418439716	0.076489972	208892_S_AT	133	10	16659	25.0511278	1	0.78661653	65.9992562
UP_SEQ_FEATURE	short sequence motif:BH1	2	1.418439716	0.076635699	206665_S_AT	139	11	19113	25.000654	1	0.97822752	68.5559266
GOTERM_MF_FAT	GO:0070279~vitamin B6 binding	3	2.127659574	0.079015194	212322_AT,	113	54	12983	6.38298918	1	0.80545447	67.6818805
GOTERM_MF_FAT	GO:0030170~pyridoxal phosphate binding	3	2.127659574	0.079015194	212322_AT,	113	54	12983	6.38298918	1	0.80545447	67.6818805
UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	7	4.964539007	0.079180911	200906_S_AT	139	413	19113	2.33056944	1	0.97347412	69.7904783
SP_PIR_KEYWORDS	heparin-binding	3	2.127659574	0.079339698	210513_S_AT	139	65	19235	6.386829	1	0.76137099	66.057779
GOTERM_BP_FAT	GO:0001503~ossification	4	2.836879433	0.080841628	202310_S_AT	120	115	13528	3.92115942	1	0.5920757	74.812728
SP_PIR_KEYWORDS	stress response	3	2.127659574	0.081447286	205193_AT,	139	66	19235	6.29005886	1	0.74855594	67.0595009
GOTERM_BP_FAT	GO:0006955~immune response	11	7.80141844	0.082418757	220049_S_AT	120	690	13528	1.79719807	1	0.59651717	75.5103903
GOTERM_MF_FAT	GO:0042805~actinin binding	2	1.418439716	0.083021344	200906_S_AT	113	10	12983	22.9787611	1	0.80467016	69.5585263
UP_SEQ_FEATURE	domain:MATH	2	1.418439716	0.083306428	205599_AT,	139	12	19113	22.9172662	1	0.97077727	71.696111
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	17	12.05673759	0.083864663	209785_S_AT	120	1256	13528	1.52584926	1	0.6002543	76.1340254
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	6	4.255319149	0.084229057	206665_S_AT	113	270	12983	2.55319567	1	0.79299312	70.1041279
GOTERM_BP_FAT	GO:0032225~regulation of synaptic transmission, dopaminerg	2	1.418439716	0.08459109	204748_AT,	120	10	13528	22.5466667	1	0.60066126	76.4416842
GOTERM_BP_FAT	GO:0043403~skeletal muscle regeneration	2	1.418439716	0.08459109	211924_S_AT	120	10	13528	22.5466667	1	0.60066126	76.4416842
GOTERM_MF_FAT	GO:0010843~promoter binding	3	2.127659574	0.086693882	201464_X_AT	113	57	12983	6.04704238	1	0.78689049	71.1896282
GOTERM_BP_FAT	GO:0051054~positive regulation of DNA metabolic process	3	2.127659574	0.086968134	201464_X_AT	120	56	13528	6.03928571	1	0.60842053	77.4225919
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	12	8.510638298	0.08848463	203192_AT,	139	962	19113	1.71522159	1	0.96962419	73.9296413
GOTERM_BP_FAT	GO:0008283~cell proliferation	8	5.673758865	0.089917628	206907_AT,	120	436	13528	2.06850153	1	0.61840022	78.5864394
UP_SEQ_FEATURE	short sequence motif:BH2	2	1.418439716	0.089929312	206665_S_AT	139	13	19113	21.1543996	1	0.96373861	74.5228396
GOTERM_BP_FAT	GO:0009617~response to bacterium	5	3.546099291	0.090582744	201464_X_AT	120	193	13528	2.92055268	1	0.61840297	78.8409877
GOTERM_MF_FAT	GO:0043027~caspase inhibitor activity	2	1.418439716	0.09093791	206665_S_AT	113	11	12983	20.8897828	1	0.78806432	72.9734725
INTERPRO	IPR015422:Pyridoxal phosphate-dependent transferase, majo	2	1.418439716	0.091076278	217127_AT,	133	12	16659	20.8759398	1	0.82635203	72.5998967
INTERPRO	IPR002475:BCL2-like apoptosis inhibitor	2	1.418439716	0.091076278	206665_S_AT	133	12	16659	20.8759398	1	0.82635203	72.5998967
INTERPRO	IPR002083:MATH	2	1.418439716	0.091076278	205599_AT,	133	12	16659	20.8759398	1	0.82635203	72.5998967
SP_PIR_KEYWORDS	transmembrane protein	9	6.382978723	0.091266618	214056_AT,	139	642	19235	1.9399247	1	0.76862168	71.3767119
GOTERM_CC_FAT	GO:0005819~spindle	4	2.836879433	0.091792736	218522_S_AT	94	147	12782	3.70010132	0.99999981	0.6965152	68.771492
GOTERM_MF_FAT	GO:0015171~amino acid transmembrane transporter activity	3	2.127659574	0.091932833	212290_AT,	113	59	12983	5.8420579	1	0.77710663	73.376566
SP_PIR_KEYWORDS	LIM domain	3	2.127659574	0.09223688	202193_AT,	139	71	19235	5.84709697	1	0.75286366	71.7736174
GOTERM_BP_FAT	GO:0009070~serine family amino acid biosynthetic process	2	1.418439716	0.092649506	217127_AT,	120	11	13528	20.4969697	1	0.62429251	79.6139536
GOTERM_BP_FAT	GO:0007567~parturition	2	1.418439716	0.092649506	209785_S_AT	120	11	13528	20.4969697	1	0.62429251	79.6139536
GOTERM_CC_FAT	GO:0000267~cell fraction	13	9.219858156	0.093108528	218647_S_AT	94	1083	12782	1.63224691	0.99999985	0.67499791	69.3140086
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	5	3.546099291	0.093212704	201761_AT,	120	195	13528	2.89059829	1	0.62383689	79.8199456
GOTERM_BP_FAT	GO:0051100~negative regulation of binding	3	2.127659574	0.095026303	209193_AT,	120	59	13528	5.73220339	1	0.62851091	80.4700771
UP_SEQ_FEATURE	nucleotide phosphate-binding region:NADP	3	2.127659574	0.095458118	206561_S_AT	139	72	19113	5.72931655	1	0.9635123	76.6788904
SP_PIR_KEYWORDS	nucleotide-binding	18	12.76595745	0.095771798	203192_AT,	139	1686	19235	1.47738037	1	0.74782641	73.1770563
SP_PIR_KEYWORDS	manganese	4	2.836879433	0.096290501	209193_AT,	139	152	19235	3.64161303	1	0.73185172	73.3774829
GOTERM_BP_FAT	GO:0051091~positive regulation of transcription factor activit	3	2.127659574	0.097758726	202637_S_AT	120	60	13528	5.63666667	1	0.6367308	81.4125582
SMART	SM00061:MATH	2	1.418439716	0.099619286	205599_AT,	80	12	9079	18.9145833	0.99969039	0.86735098	66.9501612

Supplementary Table 7. Genes inhibited by Ox-PAPC (50ug/ml, 4hrs) in HAECs by 1.5 fold.

Values are represented as log2 scale.

						cutoff by -log2(1.5) value		
ProbeSetID	Gene.Symbol	log2(sc+C)	log2(sc+Ox40)	log2(ADAM10si+C)	log2(ADAM10si+Ox 50)	log2[(sc+Ox40)/(sc+C)]	log2[(ADAM10si+Ox40)/(ADAM10si+C)]	The effects ADAM10si on Fold induction by Ox40 (H-G))
219825_at	CYP26B1	8.388583579	3.874179133	6.405008194	3.705304775	**-4.514404446**	-2.69970342	1.814701026
211518_s_at	BMP4	9.730159116	7.535330536	9.172036037	6.800500834	**-2.194828579**	-2.371535202	-0.176706623
202687_s_at	TNFSF10	8.100263694	5.92531378	7.891517735	6.691890896	**-2.174949913**	-1.199626839	0.975323074
209182_s_at	C10orf10	9.710113249	7.574637023	9.805716166	7.629806408	**-2.135476226**	-2.175909758	-0.040433533
202688_at	TNFSF10	10.00585203	7.918398744	9.931076725	8.87316092	**-2.087453291**	-1.057915805	1.029537486
219684_at	RTP4	4.921763329	2.934174067	6.638645288	3.797859713	**-1.987589262**	-2.840785575	-0.853196313
204072_s_at	FRY	7.360591798	5.382644371	7.333915739	5.140346518	**-1.977947427**	-2.193569221	-0.215621794
214329_x_at	TNFSF10	6.577768737	4.658339698	6.488819738	5.559067062	**-1.919429039**	-0.929752676	0.989676363
218736_s_at	PALMD	9.872387001	7.961946976	9.964117478	8.896719754	**-1.910440025**	-1.067397724	0.843042301
220319_s_at	MYLIP	5.856473911	3.952880731	5.54902285	3.766269027	**-1.90359318**	-1.782753823	0.120839357
202023_at	EFNA1	8.186285186	6.395832448	7.779739709	6.16756089	**-1.790452738**	-1.612178819	0.178273919
220351_at	CCRL1	5.58923612	3.833576082	4.937351575	3.998474307	**-1.755660038**	-0.938877268	0.81678277
218589_at	LPAR6	8.181315618	6.428764471	7.98664591	6.411123611	**-1.752551146**	-1.575522299	0.177028847
201340_s_at	ENC1	6.989831111	5.244481146	7.412316003	5.414259541	**-1.745349965**	-1.998056463	-0.252706498
209200_at	MEF2C	7.322932412	5.581554544	7.315545713	5.484232447	**-1.741377869**	-1.831313266	-0.089935397
209183_s_at	C10orf10	11.11590487	9.376347935	11.26247281	9.431499179	**-1.739556933**	-1.830973635	-0.091416702
217502_at	IFIT2	5.127427357	3.413431574	5.288333692	3.889822268	**-1.713995782**	-1.398511425	0.315484358
218711_s_at	SDPR	8.986571412	7.284239337	8.192686451	7.034226551	**-1.702332074**	-1.1584599	0.543872174
214059_at	IFI44	5.360548984	3.698386873	6.990870709	4.065533008	**-1.662162111**	-2.925337701	-1.26317559
218559_s_at	MAFB	6.178769687	4.552070662	4.996160792	3.970683428	**-1.626699024**	-1.025477364	0.60122166
203153_at	IFIT1	6.755179647	5.128565071	8.93863775	7.744305482	**-1.626614576**	-1.194332269	0.432282307
205883_at	ZBTB16	4.620074776	3.032091855	5.718066716	3.277251331	**-1.587982922**	-2.440815385	-0.852832464
205960_at	PDK4	5.069533491	3.522816119	4.850751466	3.484042009	**-1.546717372**	-1.366709457	0.180007915
201341_at	ENC1	8.470869614	6.938132072	8.580698851	6.754586993	**-1.532737542**	-1.826111859	-0.293374317
205529_s_at	RUNX1T1	6.63998722	5.111485079	6.658759494	5.294574401	**-1.52850214**	-1.364185093	0.164317047
219243_at	GIMAP4	9.09261922	7.57859098	9.122584133	7.821571483	**-1.51402824**	-1.30101265	0.21301559
213844_at	HOXA5	6.145689141	4.651462949	6.322751944	4.948114679	**-1.494226192**	-1.374637265	0.119588927
212907_at	SLC30A1	8.705847982	7.221042385	8.822865212	7.415615019	**-1.484805597**	-1.407250193	0.077555404
221756_at	PIK3IP1	6.398640194	4.917792485	6.205370136	5.191715421	**-1.480847708**	-1.013654715	0.467192993
205528_s_at	RUNX1T1	6.575935984	5.1158491	6.521932545	5.72974096	**-1.460086884**	-0.792191586	0.667895299
221757_at	PIK3IP1	5.483937543	4.024141133	5.294936684	3.949259224	**-1.45979641**	-1.345677459	0.114118951
40687_at	GJA4	5.219621926	3.780723815	4.388183284	3.48444866	**-1.438898111**	-0.903734624	0.535163487
204731_at	TGFBR3	7.590578345	6.152856167	6.629897656	5.091649729	**-1.437722178**	-1.538247927	-0.100525749
202481_at	DHRS3	7.658698697	6.223374954	7.586713937	6.426657018	**-1.435323743**	-1.160056919	0.275266823
204747_at	IFIT3	5.769683064	4.335072564	7.581926024	5.908629271	**-1.4346105**	-1.673296753	-0.238686253
207354_at	CCL16	4.925519905	3.511236004	4.318421411	3.462159344	**-1.414283901**	-0.856262067	0.558021835
220751_s_at	C5orf4	5.586742546	4.176352579	4.78385966	3.779427263	**-1.410389967**	-1.004432397	0.40595757
206932_at	CH25H	4.902128632	3.492004581	3.305145563	3.032174062	**-1.410124051**	-0.272971501	1.137152551
222108_at	AMIGO2	8.016859194	6.624432393	7.720007366	6.540207667	**-1.3924268**	-1.179799699	0.212627101

202743_at	PIK3R3	7.034185019	5.645566296	7.197673822	5.908506119	**-1.388618723**	-1.289167703	0.09945102
209201_x_at	CXCR4	9.193491101	7.850086312	10.05970085	9.107454797	**-1.343404789**	-0.952246049	0.39115874
201368_at	ZFP36L2	9.254404722	7.915923119	8.769023562	7.754696234	**-1.338481603**	-1.014327328	0.324154275
204069_at	MEIS1	5.515307553	4.201112454	5.764887623	4.304459402	**-1.314195099**	-1.46042822	-0.146233122
211919_s_at	CXCR4	9.238278346	7.930104811	10.14813145	9.100107631	**-1.308173535**	-1.048023816	0.26014972
209683_at	FAM49A	5.568207105	4.269816402	5.539144366	4.305331038	**-1.298390703**	-1.233813328	0.064577375
217028_at	CXCR4	9.168396251	7.870083624	9.729104608	8.865188808	**-1.298312627**	-0.8639158	0.434396827
221773_at	ELK3	8.325945683	7.028717861	8.174725187	6.975736271	**-1.297227822**	-1.198988916	0.098238906
203504_s_at	ABCA1	5.82027563	4.537585177	5.223060063	4.527634938	**-1.282690454**	-0.695425125	0.587265328
206638_at	HTR2B	6.321534065	5.047591115	5.93139585	4.434146702	**-1.27394295**	-1.497249148	-0.223306198
208530_s_at	RARB	8.054411271	6.787652059	7.731879449	6.853821704	**-1.266759212**	-0.878057745	0.388701467
204904_at	GJA4	6.567220234	5.302604681	5.753143787	4.935297198	**-1.264615552**	-0.817846589	0.446768963
212750_at	PPP1R16B	8.19643968	6.94833304	7.920536171	6.793697425	**-1.248106641**	-1.126838745	0.121267895
202668_at	EFNB2	9.128544305	7.885280615	8.192280733	6.813784994	**-1.24326369**	-1.378495739	-0.135232049
204589_at	NUAK1	9.415043235	8.191022683	9.465056999	8.525443065	**-1.224020552**	-0.939613934	0.284406617
212093_s_at	MTUS1	9.532434691	8.310260553	9.529887295	8.587978565	**-1.222174139**	-0.94190873	0.280265408
205020_s_at	ARL4A	8.121296661	6.900595243	8.26419611	6.768142119	**-1.220701418**	-1.496053991	-0.275352573
213668_s_at	SOX4	6.549002297	5.332413824	7.002752507	5.373653578	**-1.216588472**	-1.62909893	-0.412510458
202669_s_at	EFNB2	8.279978924	7.066760278	7.82194825	6.312726003	**-1.213218645**	-1.509222247	-0.296003602
218999_at	TMEM140	8.186651709	6.974415048	8.541039483	7.837502282	**-1.212236661**	-0.703537201	0.50869946
41577_at	PPP1R16B	8.276569597	7.06495937	7.917653462	6.866195253	**-1.211610227**	-1.051458209	0.160152018
220300_at	RGS3	5.238302743	4.027837927	4.802134939	3.775829174	**-1.210464816**	-1.026305765	0.184159051
206127_at	ELK3	5.277435106	4.069172981	5.174075106	4.439662807	**-1.208262125**	-0.734412299	0.473849826
207480_s_at	MEIS2	9.086333019	7.88452414	9.060210787	8.086575086	**-1.201808879**	-0.973635701	0.228173178
212399_s_at	VGLL4	8.776410436	7.582597038	9.102488457	7.815101297	**-1.193813398**	-1.28738716	-0.093573763
207220_at	ART4	6.055558984	4.86241372	6.594490327	5.671897576	**-1.193145264**	-0.922592751	0.270552513
212095_s_at	MTUS1	8.627630812	7.438351547	8.519103305	7.722012328	**-1.189279265**	-0.797090977	0.392188288
209050_s_at	RALGDS	7.624500766	6.438319708	7.301922361	6.456316694	**-1.186181059**	-0.845605667	0.340575391
209199_s_at	MEF2C	8.012979974	6.826958537	8.203890702	6.889624266	**-1.186021437**	-1.314266436	-0.128245
212183_at	NUDT4	8.30886265	7.12795236	8.182630901	7.248611199	**-1.18091029**	-0.934019702	0.246890588
210174_at	NR5A2	6.859203146	5.679771264	5.88677227	5.37979164	**-1.179431882**	-0.50698063	0.672451252
209969_s_at	STAT1	7.90036024	6.725277399	8.419523305	7.458542953	**-1.175082842**	-0.960980352	0.214102489
212096_s_at	MTUS1	10.55375565	9.37930607	10.64392677	9.617054581	**-1.174449579**	-1.026872193	0.147577386
213094_at	GPR126	7.205384144	6.038900098	5.695781707	4.830745567	**-1.166484046**	-0.865036141	0.301447905
208337_s_at	NR5A2	5.092764069	3.927312061	3.917792351	3.653257786	**-1.165452009**	-0.264534565	0.900917444
214004_s_at	VGLL4	8.689303735	7.535349202	9.173362386	8.014659532	**-1.153954533**	-1.158702854	-0.004748322
201416_at	SOX4	8.894995016	7.75178313	9.185558223	8.195330535	**-1.143211887**	-0.990227687	0.152984199
202869_at	OAS1	7.165479841	6.028120412	9.123966918	8.209686483	**-1.137359429**	-0.914280435	0.223078994
204633_s_at	RPS6KA5	7.429742472	6.31612804	7.147618759	6.254041677	**-1.113614433**	-0.893577082	0.220037351
219427_at	FAT4	5.64566854	4.533326471	5.048825141	4.302269333	**-1.112342069**	-0.746555808	0.365786261
216831_s_at	RUNX1T1	5.230463501	4.119330803	5.424472614	4.486852066	**-1.111132699**	-0.937620548	0.173512151
204249_s_at	LMO2	9.59814078	8.488072873	9.189193959	8.58056346	**-1.110067907**	-0.608630499	0.501437408
212677_s_at	CEP68	6.522501233	5.423917128	6.172697985	4.758526921	**-1.098584105**	-1.414171063	-0.315586959
205080_at	RARB	7.308940054	6.215011609	7.079795667	6.125138714	**-1.093928445**	-0.954656953	0.139271492
201295_s_at	WSB1	8.65114204	7.567572216	7.355393998	6.785817343	**-1.083569824**	-0.569576655	0.513993169

203505_at	ABCA1	4.790210373	3.707748229	4.343797002	3.499316633	**-1.082462144**	-0.844480369	0.237981775
207112_s_at	GAB1	5.128364431	4.046812101	5.268899742	4.205994504	**-1.08155233**	-1.062905237	0.018647093
219777_at	GIMAP6	9.619405819	8.538358042	9.550593378	8.48792796	**-1.081047778**	-1.062665418	0.01838236
211742_s_at	EVI2B	4.992504072	3.929400706	4.989319459	4.036676287	**-1.063103367**	-0.952643172	0.110460195
207761_s_at	METTL7A	7.867728901	6.808454177	6.798723484	5.774481136	**-1.059274724**	-1.024242347	0.035032376
212909_at	LYPD1	5.969289007	4.910058417	5.868567909	5.093242568	**-1.05923059**	-0.775325341	0.283905249
212181_s_at	NUDT4 /// NUDT	10.33301507	9.277931023	10.11040308	9.224410976	**-1.055084047**	-0.8859921	0.169091947
209051_s_at	RALGDS	5.588744177	4.541156026	4.905130662	4.149138192	**-1.04758815**	-0.755992469	0.291595681
204067_at	SUOX	6.351615004	5.305189329	6.083016837	5.212413144	**-1.046425675**	-0.870603694	0.175821981
212353_at	SULF1	6.855906098	5.810023145	5.93881689	5.327721814	**-1.045882953**	-0.611095076	0.434787877
201294_s_at	WSB1	8.967550792	7.922024308	8.09657401	7.496520381	**-1.045526483**	-0.600053629	0.445472854
201418_s_at	SOX4	6.567776385	5.530539294	6.752626333	5.883359565	**-1.037237091**	-0.869266768	0.167970323
206302_s_at	NUDT4 /// NUDT	9.927966734	8.891295441	9.475702995	8.519529856	**-1.036671294**	-0.956173138	0.080498155
219494_at	RAD54B	5.682243842	4.651988898	5.481160565	4.331714021	**-1.030254944**	-1.149446544	-0.119191601
208343_s_at	NR5A2	5.576855258	4.552681106	4.811859613	4.338440935	**-1.024174153**	-0.473418678	0.550755475
201417_at	SOX4	10.1453015	9.138555069	10.16827551	9.14090075	**-1.006746428**	-1.027374764	-0.020628336
202625_at	LYN	7.457769656	6.461947047	7.158632348	6.094690805	**-0.995822609**	-1.063941543	-0.068118934
214295_at	KIAA0485	4.134713149	3.145977411	3.970197884	3.023240161	**-0.988735738**	-0.946957723	0.041778014
209049_s_at	ZMYND8	8.134547836	7.146786425	8.172755782	7.437516024	**-0.987761411**	-0.735239758	0.252521653
204159_at	CDKN2C	5.350781188	4.364504183	4.814646984	4.112209615	**-0.986277005**	-0.702437369	0.283839636
211538_s_at	HSPA2	5.679489779	4.696542777	5.040997279	4.347929205	**-0.982947001**	-0.693068074	0.289878927
204573_at	CROT	5.768667893	4.7894214	5.675794288	5.302245721	**-0.979246493**	-0.373548566	0.605697927
218346_s_at	SESN1	7.326374497	6.351204234	7.425811529	6.503332755	**-0.975170263**	-0.922478773	0.052691489
209048_s_at	ZMYND8	7.882412253	6.914897686	7.920908395	7.192185721	**-0.967514567**	-0.728722674	0.238791893
204635_at	RPS6KA5	5.683074432	4.716303266	5.12605279	4.71715187	**-0.966771166**	-0.40890092	0.557870247
203888_at	THBD	8.464023086	7.50405055	9.344500365	8.357649259	**-0.959972536**	-0.986851106	-0.02687857
206303_s_at	NUDT4	8.923246541	7.964207217	8.528036188	7.850447281	**-0.959039324**	-0.677588908	0.281450416
210754_s_at	LYN	8.540881736	7.586402929	8.506670084	7.279747863	**-0.954478807**	-1.226922222	-0.272443415
212182_at	NUDT4 /// NUDT	4.223351991	3.270118343	3.662695527	3.274764805	**-0.953233648**	-0.387930722	0.565302926
221884_at	MECOM	8.569163227	7.618990382	8.650087034	7.92991336	**-0.950172845**	-0.720173674	0.229999171
212675_s_at	CEP68	7.594694777	6.645335983	6.897569283	6.027454124	**-0.949358793**	-0.870115158	0.079243635
203917_at	CXADR	6.862480984	5.914302556	7.215690753	6.591601425	**-0.948178428**	-0.624089327	0.3240891
203394_s_at	HES1	6.293039147	5.347842881	6.296835403	5.353843749	**-0.945196266**	-0.942991655	0.002204611
203887_s_at	THBD	9.384122442	8.444027106	10.15572738	9.13468048	**-0.940095337**	-1.021046898	-0.080951562
202626_s_at	LYN	8.352726134	7.418233558	8.33737021	7.169065678	**-0.934492576**	-1.168304532	-0.233811957
220637_at	FAM124B	9.271350934	8.339416573	8.865807042	7.645364534	**-0.931934361**	-1.220442508	-0.288508147
219625_s_at	COL4A3BP	6.625303971	5.697603829	6.804516439	5.901247872	**-0.927700142**	-0.903268566	0.024431576
210056_at	RND1	5.885950267	4.967768572	5.728045536	4.924399474	**-0.918181696**	-0.803646062	0.114535634
212188_at	KCTD12	11.15293483	10.24056302	10.93959098	9.971538435	**-0.912371807**	-0.968052548	-0.055680742
221249_s_at	FAM117A	7.046591812	6.134279581	6.713002734	5.956939071	**-0.912312231**	-0.756063662	0.156248569
212354_at	SULF1	8.180550695	7.27524866	7.550223806	6.839193084	**-0.905302036**	-0.711030722	0.194271314
202540_s_at	HMGCR	6.110860472	5.205580138	5.901114097	5.493614957	**-0.905280334**	-0.40749914	0.497781193
221864_at	ORAI3	5.572427545	4.679290996	5.240667715	4.552132326	**-0.893136549**	-0.688535389	0.204601159
201369_s_at	ZFP36L2	4.577653628	3.688558279	4.305869968	3.491626806	**-0.889095349**	-0.814243162	0.074852187
205552_s_at	OAS1	6.016383743	5.130571778	7.809642158	6.941292947	**-0.885811964**	-0.868349211	0.017462754

201565_s_at	ID2	6.789876436	5.904185564	6.778758573	6.281124544	**-0.885690872**	-0.49763403	0.388056842
201818_at	LPCAT1	7.540364264	6.662163268	8.292062869	6.760300145	**-0.878200996**	-1.531762724	-0.653561729
203395_s_at	HES1	5.17190263	4.295061333	4.977285049	4.498700714	**-0.876841297**	-0.478584335	0.398256962
206133_at	XAF1	6.065623221	5.18881892	7.23102188	6.557966639	**-0.876804301**	-0.673055241	0.203749059
210102_at	VWA5A	6.011667453	5.136181882	5.441671876	4.715640899	**-0.875485571**	-0.726030977	0.149454594
222126_at	AGFG2	5.931399855	5.056773844	5.536739262	5.333108622	**-0.874626011**	-0.20363064	0.670995371
213761_at	MDM1	4.073682903	3.201203487	3.837958549	3.068644227	**-0.872479416**	-0.769314321	0.103165095
206756_at	CHST7	6.212649558	5.340818569	6.788490954	6.048738166	**-0.871830989**	-0.739752788	0.132078201
212192_at	KCTD12	10.97039568	10.10207623	10.40697816	9.451675182	**-0.868319451**	-0.955302975	-0.086983523
48031_r_at	C5orf4	5.02196417	4.154555391	4.510801792	4.042744089	**-0.867408779**	-0.468057703	0.399351076
218032_at	SNN	7.397931851	6.531780195	7.706127264	7.092526739	**-0.866151656**	-0.613600525	0.252551131
204200_s_at	PDGFB	6.153945261	5.292404042	5.818717339	5.566242715	**-0.861541219**	-0.252474624	0.609066595
205571_at	LIPT1	6.034334435	5.178092778	5.689142887	4.728669254	**-0.856241657**	-0.960473634	-0.104231976
218995_s_at	EDN1	10.46591325	9.610787847	10.45223578	9.658302987	**-0.855125407**	-0.793932797	0.06119261
221766_s_at	FAM46A	5.257118176	4.40557595	6.34131727	5.013053169	**-0.851542226**	-1.328264101	-0.476721875
219367_s_at	---	7.610506221	6.759894105	7.647347957	6.895132866	**-0.850612116**	-0.752215091	0.098397025
218350_s_at	GMNN	7.356476568	6.512730049	7.254162235	6.463688116	**-0.843746519**	-0.79047412	0.053272399
211341_at	POU4F1	7.218086171	6.37792612	6.893317299	5.935269746	**-0.840160051**	-0.958047553	-0.117887502
207968_s_at	MEF2C	4.38761606	3.554352901	4.581259637	3.447089476	**-0.833263159**	-1.134170161	-0.300907003
204288_s_at	SORBS2	7.68425462	6.860005227	7.677463506	6.885507024	**-0.824249393**	-0.791956482	0.032292911
222372_at	---	6.026834029	5.207008809	5.893422847	5.39233812	**-0.81982522**	-0.501084727	0.318740493
212344_at	SULF1	7.944694366	7.125295615	7.38551489	6.850395955	**-0.819398751**	-0.535118935	0.284279815
216061_x_at	PDGFB	5.947930189	5.130552322	5.744645627	5.435470066	**-0.817377868**	-0.309175561	0.508202307
202597_at	IRF6	5.363595734	4.54759881	5.755060801	5.072578665	**-0.815996923**	-0.682482137	0.133514787
201896_s_at	PSRC1	4.972352126	4.157060527	4.641498724	4.057495999	**-0.815291599**	-0.584002725	0.231288874
205051_s_at	KIT	4.627544341	3.812619947	6.495412197	5.221279752	**-0.814924394**	-1.274132444	-0.45920805
205013_s_at	ADORA2A /// CY	5.882795574	5.070196447	5.911543006	4.907728801	**-0.812599127**	-1.003814205	-0.191215078
203252_at	CDK2AP2	7.084372244	6.274029134	7.009351948	6.233301586	**-0.810343109**	-0.776050362	0.034292747
204315_s_at	GTSE1	4.71915756	3.912481748	4.077105924	3.699333729	**-0.806675812**	-0.377772195	0.428903617
209238_at	STX3	8.453144811	7.647456466	8.67225921	7.926434677	**-0.805688344**	-0.745824533	0.059863811
219147_s_at	C9orf95	8.076365295	7.271388057	7.289462972	6.761353211	**-0.804977239**	-0.528109761	0.276867477
202983_at	HLTF	7.233044361	6.42837712	6.9920318	6.172772863	**-0.804667241**	-0.819258936	-0.014591696
217504_at	ABCA6	5.33551132	4.531649994	4.919160732	4.432864654	**-0.803861326**	-0.486296078	0.317565248
211580_s_at	PIK3R3	4.405566023	3.606438792	4.463854243	3.628146536	**-0.799127231**	-0.835707707	-0.036580476
203632_s_at	GPRC5B	6.727643008	5.945705285	6.742332254	5.937433179	**-0.781937722**	-0.804899075	-0.022961352
200920_s_at	BTG1	10.29742377	9.519316468	10.46747827	9.643767541	**-0.778107297**	-0.823710726	-0.045603428
203980_at	FABP4	9.551390224	8.775171069	8.873671177	8.556276474	**-0.776219155**	-0.317394703	0.458824452
212914_at	CBX7	4.872461517	4.0963296	4.610036707	4.161873936	**-0.776131918**	-0.448162772	0.327969146
206382_s_at	BDNF	5.11913362	4.343523798	4.806221991	4.556533195	**-0.775609822**	-0.249688796	0.525921026
203625_x_at	SKP2	7.432081748	6.657277885	7.029691399	6.476084282	**-0.774803863**	-0.553607117	0.221196746
201009_s_at	TXNIP	7.879983251	7.106602098	7.731911725	7.256417543	**-0.773381153**	-0.475494182	0.29788697
202814_s_at	HEXIM1	7.270039176	6.497477304	7.116688513	6.34886204	**-0.772561871**	-0.767826473	0.004735399
221221_s_at	KLHL3	7.532158657	6.760815881	8.137157474	7.289231306	**-0.771342776**	-0.847926168	-0.076583392
206289_at	HOXA4	5.157402286	4.386646609	5.091557755	4.725101148	**-0.770755677**	-0.366456607	0.40429907
204510_at	CDC7	4.600088597	3.829621409	3.843249988	3.728640365	**-0.770467188**	-0.114609623	0.655857565

215073_s_at	NR2F2	7.872109494	7.101993542	7.758090307	7.227936461	**-0.770115952**	-0.530153846	0.239962106
213784_at	IFT27	5.196288644	4.42722882	5.336696383	4.533831373	**-0.769059824**	-0.80286501	-0.033805186
209757_s_at	MYCN	5.15135049	4.382610605	5.227322422	3.971580565	**-0.768739885**	-1.255741857	-0.487001972
209119_x_at	NR2F2	6.44602687	5.678844122	6.720700306	6.140335076	**-0.767182749**	-0.58036523	0.186817519
204821_at	BTN3A3	6.55009466	5.783396907	7.02724001	6.515688394	**-0.766697754**	-0.511551616	0.255146138
221123_x_at	ZNF395	5.966883225	5.205394821	5.681289691	5.377925557	**-0.761488405**	-0.303364133	0.458124272
217164_at	---	5.564255348	4.805740911	5.491066963	5.15751455	**-0.758514438**	-0.333552413	0.424962025
221044_s_at	TRIM34 /// TRIM	5.890570036	5.135197621	6.027068617	5.248767757	**-0.755372416**	-0.77830086	-0.022928444
213260_at	FOXC1	7.187449029	6.433393634	7.348028111	6.42487529	**-0.754055395**	-0.923152821	-0.169097426
201008_s_at	TXNIP	7.263343697	6.51167121	7.066111516	6.570025473	**-0.751672488**	-0.496086043	0.255586445
212774_at	ZNF238	8.368321762	7.617680642	8.20054718	7.509842455	**-0.75064112**	-0.690704725	0.059936395
213625_at	ZKSCAN4	5.201239213	4.452456355	5.103912196	4.460491493	**-0.748782858**	-0.643420703	0.105362154
218816_at	LRRC1	4.628217814	3.881072108	4.615009259	3.63363182	**-0.747145706**	-0.981377439	-0.234231732
213227_at	PGRMC2	7.782197311	7.037449962	8.022538239	7.274261409	**-0.744747349**	-0.74827683	-0.00352948
206940_s_at	POU4F1	8.723122785	7.979051907	8.254270125	7.459095142	**-0.744070878**	-0.795174984	-0.051104106
218149_s_at	ZNF395	7.426482907	6.683358604	7.120846671	6.639254827	**-0.743124303**	-0.481591844	0.261532459
209426_s_at	AMACR /// C1QT	5.326148188	4.583324215	5.161026976	4.437589665	**-0.742823972**	-0.723437311	0.019386661
206114_at	EPHA4	7.032820049	6.293261776	7.486984029	6.830777528	**-0.739558274**	-0.656206501	0.083351772
201367_s_at	ZFP36L2	5.492056686	4.753396279	5.186398	4.755773063	**-0.738660407**	-0.430624937	0.308035471
201010_s_at	TXNIP	8.444760104	7.713328182	8.014070624	7.598933037	**-0.731431921**	-0.415137588	0.316294334
205805_s_at	ROR1	5.311797857	4.588275602	6.491036014	5.120291212	**-0.723522256**	-1.370744802	-0.647222547
219470_x_at	CCNJ	7.513682848	6.790221492	7.778322354	7.108589531	**-0.723461356**	-0.669732823	0.053728532
212660_at	PHF15	5.590764461	4.869271738	6.110979333	5.315776295	**-0.721492723**	-0.795203038	-0.073710315
214453_s_at	IFI44	8.196923088	7.476223993	9.74922236	9.275261515	**-0.720699095**	-0.473960845	0.24673825
202190_at	CSTF1	6.199345103	5.483424131	6.145684695	5.424145232	**-0.715920972**	-0.721539463	-0.00561849
211163_s_at	TNFRSF10C	5.545931944	4.830300265	5.838291433	5.34445199	**-0.715631679**	-0.493839443	0.221792236
213348_at	CDKN1C	5.541727399	4.828329874	4.612126505	4.37437469	**-0.713397525**	-0.237751816	0.47564571
207574_s_at	GADD45B	7.19994109	6.489153134	6.590610483	6.248586564	**-0.710787956**	-0.342023919	0.368764037
216199_s_at	MAP3K4	6.559770368	5.849000111	6.452203248	5.759515747	**-0.710770257**	-0.692687502	0.018082756
217317_s_at	HERC2P2 /// HE	10.00146518	9.290747442	9.398807008	8.968387762	**-0.710717736**	-0.430419246	0.280298489
214457_at	HOXA2	4.329359997	3.619391569	3.972219557	3.547024676	**-0.709968427**	-0.425194881	0.284773546
218361_at	GOLPH3L	8.821941994	8.112544919	8.575614542	7.781905263	**-0.709397075**	-0.793709279	-0.084312204
204719_at	ABCA8	8.368336985	7.661080224	8.105206042	7.483689573	**-0.707256761**	-0.621516469	0.085740292
209761_s_at	SP110	5.912932651	5.207469805	7.137946333	6.480383429	**-0.705462846**	-0.657562904	0.047899942
218006_s_at	ZNF22	6.911715301	6.210651616	6.803813688	6.001527513	**-0.701063685**	-0.802286175	-0.10122249
202815_s_at	HEXIM1	6.154830458	5.456956529	5.995213769	5.311352097	**-0.697873929**	-0.683861672	0.014012258
204358_s_at	FLRT2	7.692398088	6.995535537	7.552280593	7.178880239	**-0.696862552**	-0.373400354	0.323462198
222344_at	---	4.732873684	4.036690795	4.396008578	3.885497905	**-0.696182889**	-0.510510673	0.185672216
219650_at	ERCC6L	4.338978653	3.642905627	3.965823966	3.366185663	**-0.696073027**	-0.599638303	0.096434723
212558_at	SPRY1	4.862231603	4.167885057	5.982117438	4.107168519	**-0.694346546**	-1.874948919	-1.180602373
204653_at	TFAP2A	6.639573699	5.945551823	6.966380316	6.548630424	**-0.694021876**	-0.417749892	0.276271984
210296_s_at	PEX2	7.636941802	6.944249753	7.14354875	6.414047268	**-0.69269205**	-0.729501482	-0.036809432
209305_s_at	GADD45B	7.266582753	6.574602086	6.578300271	6.570348807	**-0.691980667**	-0.007951464	0.684029203
212224_at	ALDH1A1	11.32294879	10.63246312	10.82480698	10.09439603	**-0.690485668**	-0.73041095	-0.039925282
212151_at	PBX1	5.175311466	4.485811241	4.515389855	4.119314304	**-0.689500225**	-0.396075551	0.293424674

219306_at	KIF15	4.634725049	3.945349174	3.929151732	3.449883529	**-0.689375874**	-0.479268203	0.210107671
214639_s_at	HOXA1	4.842408166	4.153298513	5.016934968	4.125288429	**-0.689109653**	-0.891646539	-0.202536887
219148_at	PBK	7.143798104	6.455806561	6.516958485	5.576713644	**-0.687991543**	-0.940244841	-0.252253299
219685_at	TMEM35	5.699017819	5.012442422	5.842616125	5.158865177	**-0.686575396**	-0.683750948	0.002824449
211792_s_at	CDKN2C	5.374801921	4.689999856	5.223896377	4.847657374	**-0.684802065**	-0.376239003	0.308563062
205677_s_at	DLEU1	6.870162951	6.18599487	6.600107777	5.777251825	**-0.68416808**	-0.822855952	-0.138687872
177_at	PLD1	7.432527869	6.750434034	7.145833243	6.644052045	**-0.682093835**	-0.501781197	0.180312638
201734_at	CLCN3	9.067394679	8.388820166	9.222833885	8.459172788	**-0.678574513**	-0.763661097	-0.085086584
218755_at	KIF20A	7.586070843	6.908294485	6.900246525	5.878820687	**-0.677776358**	-1.021425839	-0.343649481
214724_at	DIXDC1	5.836246959	5.159450137	5.757893103	4.843309064	**-0.676796822**	-0.914584039	-0.237787216
200921_s_at	BTG1	10.06299273	9.386992019	9.917040835	9.003160452	**-0.676000709**	-0.913880383	-0.237879674
202440_s_at	ST5	3.974039298	3.298918863	4.354914341	3.561424892	**-0.675120434**	-0.793489449	-0.118369014
213019_at	RANBP6	7.441997088	6.766909132	7.073810814	6.519869287	**-0.675087956**	-0.553941527	0.121146429
215775_at	---	7.707925002	7.033262335	7.598009469	7.470935301	**-0.674662667**	-0.127074168	0.547588498
221565_s_at	CALHM2	5.929790764	5.255176849	5.617722478	5.058844034	**-0.674613915**	-0.558878444	0.115735471
219863_at	HERC5	4.916543169	4.242461502	6.159555162	5.515534524	**-0.674081667**	-0.644020638	0.030061029
219901_at	FGD6	5.171130223	4.498066081	4.658349133	4.371595081	**-0.673064141**	-0.286754052	0.386310089
221436_s_at	CDCA3	5.466567135	4.793550428	5.023173256	4.25963932	**-0.673016707**	-0.763533936	-0.090517229
219209_at	IFIH1	6.834978612	6.162051829	7.927530004	7.396623118	**-0.672926784**	-0.530906886	0.142019897
203408_s_at	SATB1	8.163533151	7.49097368	7.879846124	7.576359468	**-0.672559471**	-0.303486656	0.369072815
209710_at	GATA2	5.908551438	5.23634281	5.52379661	4.910080839	**-0.672208628**	-0.613715772	0.058492856
203508_at	TNFRSF1B	5.033324674	4.36146959	5.145958078	4.892185991	**-0.671855085**	-0.253772088	0.418082997
212494_at	TENC1	5.715065515	5.043270899	5.624163134	5.028880551	**-0.671794616**	-0.595282583	0.076512032
204187_at	GMPR	7.48775934	6.816322832	7.601814381	7.057964121	**-0.671436508**	-0.54385026	0.127586248
203209_at	RFC5	5.953638146	5.28248646	5.270251733	4.412227073	**-0.671151686**	-0.85802466	-0.186872974
209662_at	CETN3	6.902853516	6.232713978	6.137874516	5.778875703	**-0.670139538**	-0.358998813	0.311140725
202227_s_at	BRD8	8.809453036	8.140607266	8.668328836	8.257470707	**-0.66884577**	-0.41085813	0.257987641
208012_x_at	SP110	6.954386972	6.285893133	8.0785566	7.339314489	**-0.668493839**	-0.739242111	-0.070748272
38241_at	BTN3A3	5.475581511	4.807485436	5.850350674	5.186074504	**-0.668096075**	-0.66427617	0.003819905
214466_at	GJA5	4.286631207	3.618682459	4.068913459	3.636658577	**-0.667948748**	-0.432254881	0.235693866
204967_at	SHROOM2	6.066990351	5.399096485	6.223535152	5.240054061	**-0.667893865**	-0.983481092	-0.315587226
218633_x_at	ABHD10	7.204564931	6.537883749	7.157660181	6.341233177	**-0.666681182**	-0.816427004	-0.149745822
219546_at	BMP2K	5.028567226	4.362001832	5.25992096	4.800809163	**-0.666565394**	-0.459111797	0.207453597
221012_s_at	TRIM8	8.673586593	8.007144841	9.010131006	8.364497953	**-0.666441752**	-0.645633053	0.020808699
210288_at	KLRG1	6.640426926	5.975630944	6.685849848	6.122945952	**-0.664795982**	-0.562903897	0.101892085
203764_at	DLGAP5	7.836673754	7.173265835	7.399284806	6.803698662	**-0.663407919**	-0.595586143	0.067821776
218326_s_at	LGR4	4.865531759	4.202577534	5.104551019	4.044984135	**-0.662954225**	-1.059566884	-0.396612659
218862_at	ASB13	4.378226327	3.715335407	4.128702129	3.666684352	**-0.66289092**	-0.462017777	0.200873143
218573_at	MAGEH1	6.912234844	6.250040866	6.799134456	6.339373361	**-0.662193978**	-0.459761095	0.202432882
221589_s_at	ALDH6A1	5.877838733	5.215864783	4.821476396	4.029665203	**-0.66197395**	-0.791811193	-0.129837243
218005_at	ZNF22	8.623535404	7.961970702	8.547494066	7.626613912	**-0.661564702**	-0.920880154	-0.259315453
204917_s_at	MLLT3	4.678187493	4.016838419	4.605165363	4.316111928	**-0.661349074**	-0.289053434	0.37229564
219568_x_at	SOX18	5.299917639	4.639321946	4.996951287	4.302566849	**-0.660595693**	-0.694384437	-0.033788744
205466_s_at	HS3ST1	3.81994569	3.160238065	3.34849638	3.045166868	**-0.659707625**	-0.303329513	0.356378113
221640_s_at	LRDD	5.559230197	4.899610464	5.73805334	5.273507555	**-0.659619733**	-0.464545785	0.195073948

203432_at	TMPO	6.616064588	5.957325489	6.268096156	5.710801861	**-0.658739099**	-0.557294294	0.101444804
202326_at	EHMT2	7.080490311	6.422958982	6.981813932	6.48978392	**-0.657531329**	-0.492030012	0.165501317
204089_x_at	MAP3K4	6.056732656	5.400184361	6.118367598	5.074740174	**-0.656548295**	-1.043627424	-0.387079129
209121_x_at	NR2F2	9.834215135	9.179241282	10.13301369	9.634042508	**-0.654973852**	-0.498971185	0.156002667
213373_s_at	CASP8	4.467352143	3.814213085	4.461603649	3.741961041	**-0.653139058**	-0.719642607	-0.066503549
220952_s_at	PLEKHA5	6.635364527	5.982942948	6.54670769	5.889638868	**-0.652421579**	-0.657068822	-0.004647243
209304_x_at	GADD45B	5.777573616	5.127027171	5.29040807	4.941021355	**-0.650546445**	-0.349386715	0.30115973
204162_at	NDC80	6.37939333	5.729969464	5.861053185	5.324045172	**-0.649423866**	-0.537008013	0.112415853
203588_s_at	TFDP2	7.365631727	6.7168774	7.299789483	6.961992147	**-0.648754326**	-0.337797337	0.31095699
218534_s_at	AGGF1	6.562582195	5.914444805	6.465283871	5.658751102	**-0.64813739**	-0.806532769	-0.158395379
221213_s_at	ZNF280D	4.40785718	3.761281953	4.088208126	3.352144017	**-0.646575227**	-0.736064109	-0.089488881
202973_x_at	FAM13A	4.305373004	3.659117326	4.53686453	3.526551413	**-0.646255678**	-1.010313118	-0.364057439
202609_at	EPS8	8.251436679	7.606396841	7.809068175	7.337514471	**-0.645039839**	-0.471553704	0.173486135
205933_at	SETBP1	5.861641289	5.217035752	6.064323942	5.367710768	**-0.644605537**	-0.696613174	-0.052007637
200864_s_at	RAB11A	6.865293822	6.220827841	6.973143404	6.147172088	**-0.644465981**	-0.825971316	-0.181505335
204822_at	TTK	5.834998716	5.190824947	5.296398648	4.444066784	**-0.644173769**	-0.852331864	-0.208158095
57715_at	CALHM2	5.229205137	4.587909334	4.707258994	4.218692068	**-0.641295803**	-0.488566926	0.152728877
216614_at	---	3.950212039	3.309138572	3.529984341	3.211080856	**-0.641073467**	-0.318903485	0.322169982
204566_at	PPM1D	8.05960279	7.419053546	8.073538809	7.467447636	**-0.640549244**	-0.606091174	0.03445807
212875_s_at	C2CD2	7.593155036	6.952691899	7.327544537	6.87904	**-0.640463137**	-0.448504537	0.1919586
211814_s_at	CCNE2	4.470273161	3.829879031	4.544583599	4.040298268	**-0.640394129**	-0.504285332	0.136108798
214131_at	CYorf15B	5.185694346	4.545473813	5.309651943	4.734313207	**-0.640220533**	-0.575338735	0.064881797
218252_at	CKAP2	8.030200494	7.394431595	7.589180143	6.848771404	**-0.635768899**	-0.740408739	-0.10463984
205203_at	PLD1	8.123017583	7.489492742	7.843167724	7.362897363	**-0.633524842**	-0.480270361	0.153254481
221485_at	B4GALT5	9.057683991	8.424856902	9.150865669	8.278916592	**-0.632827088**	-0.871949077	-0.239121989
221688_s_at	IMP3	7.743991115	7.111215851	7.921478872	7.066164074	**-0.632775265**	-0.855314798	-0.222539533
215626_at	---	3.99918121	3.369461348	4.028224777	3.42592158	**-0.629719863**	-0.602303197	0.027416666
204318_s_at	GTSE1	5.824293827	5.195537834	5.495548162	4.298483538	**-0.628755993**	-1.197064624	-0.568308631
220183_s_at	NUDT6	5.134765883	4.506545591	5.123302018	4.575821457	**-0.628220292**	-0.547480561	0.080739731
59644_at	BMP2K	4.709920534	4.082054301	4.901150737	4.355073531	**-0.627866233**	-0.546077206	0.081789026
210658_s_at	GGA2	5.15733321	4.530489496	5.06193082	4.694187046	**-0.626843714**	-0.367743775	0.259099939
212632_at	STX7	8.230818803	7.604977081	8.350824574	7.936226138	**-0.625841723**	-0.414598435	0.211243287
218769_s_at	ANKRA2	6.59299283	5.967313983	6.060956387	5.441896808	**-0.625678847**	-0.619059579	0.006619267
219691_at	SAMD9	5.62614656	5.001661508	6.707512029	5.976448278	**-0.624485051**	-0.731063751	-0.1065787
219258_at	TIPIN	4.773640184	4.15052216	4.49482522	3.886544151	**-0.623118024**	-0.608281069	0.014836954
217047_s_at	FAM13A	4.107660494	3.48731015	4.387392754	3.893372995	**-0.620350345**	-0.494019759	0.126330586
203418_at	CCNA2	6.748345595	6.131234528	6.437460908	5.425065871	**-0.617111067**	-1.012395037	-0.39528397
203595_s_at	IFIT5	6.621788689	6.004742343	7.79878229	6.653197769	**-0.617046346**	-1.145584521	-0.528538175
218719_s_at	GINS3	6.22770176	5.611230231	6.182269875	5.603094475	**-0.61647153**	-0.5791754	0.03729613
212148_at	PBX1	4.763456575	4.147139188	4.127441295	3.563445281	**-0.616317387**	-0.563996013	0.052321374
221087_s_at	APOL3	7.399307426	6.785109185	7.420671769	6.734104907	**-0.614198242**	-0.686566862	-0.07236862
200887_s_at	STAT1	9.742152944	9.128915664	10.40955265	9.832131044	**-0.61323728**	-0.577421606	0.035815674
209682_at	CBLB	7.077430958	6.464228081	7.189666174	6.643195914	**-0.613202878**	-0.54647026	0.066732617
219872_at	FAM198B	7.778964924	7.165887407	7.469808649	7.099680613	**-0.613077517**	-0.370128036	0.242949481
206271_at	TLR3	4.752565305	4.141576076	5.198226058	4.714158226	**-0.610989229**	-0.484067832	0.126921397

213269_at	ZNF248	5.295442393	4.684525128	5.209403927	4.691296152	**-0.610917265**	-0.518107775	0.09280949
209732_at	CLEC2B	10.19845468	9.590932407	10.13457006	10.08964635	**-0.607522268**	-0.044923713	0.562598555
218259_at	MKL2	7.181731985	6.574823181	6.796081058	6.210802337	**-0.606908804**	-0.585278721	0.021630083
214318_s_at	FRY	6.754090876	6.147584403	6.548499169	6.079319074	**-0.606506473**	-0.469180095	0.137326378
209120_at	NR2F2	9.728375837	9.123056542	9.734506091	9.348610098	**-0.605319296**	-0.385895993	0.219423303
205601_s_at	HOXB5	5.007037457	4.402094758	5.276774759	4.709360527	**-0.604942699**	-0.567414232	0.037528467
204256_at	ELOVL6	4.031199969	3.426400804	4.11062244	3.50017695	**-0.604799165**	-0.610445491	-0.005646326
205600_x_at	HOXB5	5.337933286	4.733235669	5.599971128	5.064662591	**-0.604697617**	-0.535308537	0.06938908
204780_s_at	FAS	7.745968558	7.142596052	7.722378428	7.351296072	**-0.603372506**	-0.371082355	0.232290151
209642_at	BUB1	5.67948391	5.079061464	5.010157037	4.289084739	**-0.600422446**	-0.721072298	-0.120649852
215555_at	---	4.121189699	3.523980806	3.79111653	3.448197624	**-0.597208893**	-0.342918907	0.254289987
220934_s_at	TMEM223	6.088727867	5.491876511	6.180626567	5.545867346	**-0.596851357**	-0.634759221	-0.037907865
213261_at	TRANK1	4.827313182	4.231453891	5.442878669	4.6165249	**-0.595859291**	-0.826353769	-0.230494478
214250_at	NUMA1	4.086775378	3.491295224	4.191194566	3.47997614	**-0.595480155**	-0.711218426	-0.115738271
207559_s_at	ZMYM3	6.238409276	5.643307388	5.987153312	5.918685448	**-0.595101888**	-0.068467864	0.526634024
210567_s_at	SKP2	4.556791439	3.962071682	4.085193864	3.585310676	**-0.594719757**	-0.499883188	0.09483657
221484_at	B4GALT5	8.580112768	7.985732842	8.892438021	7.717021678	**-0.594379926**	-1.175416344	-0.581036418
210044_s_at	LYL1	7.609464614	7.015292707	7.803144596	7.027270269	**-0.594171907**	-0.775874327	-0.18170242
204112_s_at	HNMT	5.717777441	5.125063351	5.770792951	5.346691739	**-0.59271409**	-0.424101212	0.168612878
202870_s_at	CDC20	8.491879747	7.900462821	7.858511207	7.235599509	**-0.591416926**	-0.622911698	-0.031494772
201310_s_at	C5orf13	9.403734647	8.814629079	9.831002148	9.124608717	**-0.589105568**	-0.706393431	-0.117287863
219416_at	SCARA3	5.354622485	4.769157812	5.323441921	5.009287229	**-0.585464673**	-0.314154692	0.271309981
203409_at	DDB2	8.357365602	7.772334618	8.274856267	7.844315891	**-0.585030984**	-0.430540376	0.154490609

Supplementary Table 8. Gene categories of genes inhibited by Ox-PAPC by 1.5 fold in HAECs.
DAVID analysis used for the identification of gene categories.
http://david.abcc.ncifcrf.gov/home.jsp

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	49	12.25	1.47E-10	210754_S_AT, 204526_S_AT,	302	787	13528	2.78899669	3.38E-07	3.38E-07	2.57E-07
SP_PIR_KEYWORDS	phosphoprotein	210	52.5	3.48E-10	213625_AT, 203504_S_AT, 20	395	7263	19235	1.40798603	1.12E-07	1.12E-07	4.70E-07
GOTERM_BP_FAT	GO:0007049~cell cycle	47	11.75	9.42E-10	203362_S_AT, 205698_S_AT,	302	776	13528	2.71308118	2.17E-06	1.08E-06	1.65E-06
GOTERM_BP_FAT	GO:0022402~cell cycle process	39	9.75	1.03E-09	203362_S_AT, 205698_S_AT,	302	565	13528	3.09202368	2.37E-06	7.89E-07	1.80E-06
GOTERM_BP_FAT	GO:0022403~cell cycle phase	32	8	3.27E-09	204315_S_AT, 219534_X_AT,	302	414	13528	3.46239242	7.52E-06	1.88E-06	5.71E-06
SP_PIR_KEYWORDS	cell cycle	30	7.5	9.72E-08	219534_X_AT, 203362_S_AT,	395	461	19235	3.16895027	3.13E-05	1.56E-05	1.31E-04
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	26	6.5	9.97E-08	204315_S_AT, 207574_S_AT,	302	331	13528	3.51861707	2.29E-04	4.59E-05	1.74E-04
SP_PIR_KEYWORDS	Proto-oncogene	20	5	2.95E-07	204917_S_AT, 210754_S_AT,	395	230	19235	4.23445239	9.51E-05	3.17E-05	3.99E-04
GOTERM_BP_FAT	GO:0007507~heart development	20	5	3.32E-07	213373_S_AT, 213260_AT, 20	302	215	13528	4.16694902	7.64E-04	1.27E-04	5.80E-04
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	25	6.25	8.09E-07	202540_S_AT, 207574_S_AT,	302	345	13528	3.2459929	0.00186144	2.66E-04	0.0014144
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	26	6.5	8.15E-07	204315_S_AT, 219534_X_AT,	302	370	13528	3.14773582	0.00187476	2.35E-04	0.00142454
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	25	6.25	1.49E-06	202540_S_AT, 207574_S_AT,	302	357	13528	3.13688389	0.00341691	3.80E-04	0.00259833
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	29	7.25	1.82E-06	202540_S_AT, 210754_S_AT,	302	466	13528	2.78765313	0.00418298	4.19E-04	0.00318209
GOTERM_BP_FAT	GO:0003002~regionalization	18	4.5	1.95E-06	204917_S_AT, 207069_S_AT,	302	197	13528	4.09291693	0.00447815	4.08E-04	0.00340713
GOTERM_BP_FAT	GO:0035295~tube development	19	4.75	2.09E-06	213373_S_AT, 213844_AT, 21	302	220	13528	3.86863335	0.00479206	4.00E-04	0.00364654
GOTERM_BP_FAT	GO:0007389~pattern specification process	21	5.25	2.23E-06	204917_S_AT, 209119_X_AT,	302	267	13528	3.52317881	0.00512896	3.95E-04	0.00390356
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	25	6.25	3.06E-06	202540_S_AT, 207574_S_AT,	302	372	13528	3.01039664	0.00702042	5.03E-04	0.00534816
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	54	13.5	3.63E-06	203504_S_AT, 210754_S_AT,	302	1256	13528	1.92588687	0.00833051	5.58E-04	0.00635033
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic proce	29	7.25	3.93E-06	202540_S_AT, 210754_S_AT,	302	485	13528	2.6784461	0.00901522	5.66E-04	0.00687464
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic proces	29	7.25	3.93E-06	202540_S_AT, 210754_S_AT,	302	485	13528	2.6784461	0.00901522	5.66E-04	0.00687464
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	60	15	4.13E-06	213625_AT, 213260_AT, 2029	282	1512	12983	1.82694473	0.00222214	0.00222214	0.00601565
GOTERM_BP_FAT	GO:0000279~M phase	23	5.75	4.49E-06	203362_S_AT, 204444_AT, 20	302	329	13528	3.13154452	0.01027427	6.07E-04	0.00783968
SP_PIR_KEYWORDS	nucleus	127	31.75	4.50E-06	222108_AT, 213625_AT, 2021	395	4283	19235	1.4439453	0.00144803	3.62E-04	0.00607838
GOTERM_MF_FAT	GO:0003700~transcription factor activity	44	11	5.64E-06	213625_AT, 213260_AT, 2091	282	975	12983	2.07765776	0.00302785	0.00151507	0.00820003
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	24	6	6.07E-06	219534_X_AT, 202704_AT, 21	302	361	13528	2.97804113	0.01387562	7.76E-04	0.01060679
KEGG_PATHWAY	hsa04115:p53 signaling pathway	11	2.75	6.96E-06	204315_S_AT, 213373_S_AT,	131	68	5085	6.27918725	8.49E-04	8.49E-04	0.00801403
SP_PIR_KEYWORDS	dna-binding	67	16.75	7.63E-06	213625_AT, 221213_S_AT, 21	395	1868	19235	1.74659827	0.00245492	4.91E-04	0.01030997
GOTERM_BP_FAT	GO:0001944~vasculature development	19	4.75	1.32E-05	213373_S_AT, 40687_AT, 209	302	251	13528	3.39083401	0.02985786	0.00159413	0.02300902
KEGG_PATHWAY	hsa04110:Cell cycle	14	3.5	1.46E-05	203588_S_AT, 219534_X_AT,	131	125	5085	4.34748092	0.00178315	8.92E-04	0.01684197
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	22	5.5	1.66E-05	213373_S_AT, 203394_S_AT,	302	331	13528	2.97729137	0.03753603	0.0019111	0.02903957
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	21	5.25	1.80E-05	213373_S_AT, 203394_S_AT,	302	307	13528	3.06413271	0.04054933	0.00196922	0.03141932
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth o	22	5.5	1.89E-05	213373_S_AT, 203394_S_AT,	302	334	13528	2.95054923	0.04264245	0.00197887	0.03307673
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	23	5.75	2.60E-05	202540_S_AT, 218032_AT, 21	302	368	13528	2.79966887	0.058173	0.00260242	0.04548789
GOTERM_BP_FAT	GO:0048568~embryonic organ development	15	3.75	3.04E-05	205453_AT, 213844_AT, 2036	302	172	13528	3.90651471	0.06763834	0.00291385	0.05315208
GOTERM_BP_FAT	GO:0007067~mitosis	17	4.25	3.36E-05	214250_AT, 202870_S_AT, 20	302	220	13528	3.46140879	0.07447461	0.00309096	0.05873565
GOTERM_BP_FAT	GO:0000280~nuclear division	17	4.25	3.36E-05	214250_AT, 202870_S_AT, 20	302	220	13528	3.46140879	0.07447461	0.00309096	0.05873565
GOTERM_BP_FAT	GO:0001568~blood vessel development	18	4.5	3.50E-05	213373_S_AT, 40687_AT, 209	302	245	13528	3.29103933	0.07731783	0.00309023	0.06106994
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	17	4.25	4.18E-05	214250_AT, 202870_S_AT, 20	302	224	13528	3.39959792	0.09179955	0.00355995	0.07307131
UP_SEQ_FEATURE	mutagenesis site	69	17.25	4.74E-05	202869_AT, 210754_S_AT, 20	395	2045	19113	1.63262914	0.05621202	0.05621202	0.07679236
GOTERM_BP_FAT	GO:0045449~regulation of transcription	87	21.75	4.79E-05	213625_AT, 213260_AT, 2134	302	2601	13528	1.49832337	0.10430876	0.00392654	0.0835919
GOTERM_MF_FAT	GO:0003677~DNA binding	78	19.5	5.02E-05	213625_AT, 205875_S_AT, 21	282	2331	12983	1.5405588	0.02666529	0.00896862	0.0730608
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	66	16.5	5.23E-05	213625_AT, 213260_AT, 2029	302	1813	13528	1.63069516	0.11334286	0.00413958	0.09128089
GOTERM_BP_FAT	GO:0048285~organelle fission	17	4.25	5.46E-05	214250_AT, 202870_S_AT, 20	302	229	13528	3.32537089	0.11804335	0.00417833	0.09531232
GOTERM_BP_FAT	GO:0010941~regulation of cell death	37	9.25	6.35E-05	222108_AT, 213260_AT, 2056	302	815	13528	2.03362451	0.1360706	0.00470709	0.11097386
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	13	3.25	6.81E-05	204917_S_AT, 209119_X_AT,	302	140	13528	4.15950804	0.14500887	0.00488379	0.11885985
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	13	3.25	7.29E-05	202540_S_AT, 202730_S_AT,	302	141	13528	4.13000798	0.15455401	0.00507469	0.12737211
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA poly	34	8.5	7.77E-05	209199_S_AT, 209121_X_AT,	302	727	13528	2.09493792	0.16386566	0.00524988	0.13576855
UP_SEQ_FEATURE	short sequence motif:Antp-type hexapeptide	6	1.5	8.99E-05	205453_AT, 213844_AT, 2062	395	23	19113	12.6227848	0.10387698	0.05336226	0.14553085

GOTERM_BP_FAT	GO:0006260~DNA replication	15	3.75	9.03E-05	205875_S_AT, 221521_S_AT,	302	190	13528	3.53642384	0.18777895	0.00592474	0.1577641
PIR_SUPERFAMILY	PIRSF005680:interferon-induced 56K protein	4	1	1.22E-04	203596_S_AT, 204747_AT, 21	174	5	7396	34.0045977	0.02638214	0.02638214	0.15457956
INTERPRO	IPR001827:Homeobox protein, antennapedia type, cons	6	1.5	1.23E-04	205453_AT, 213844_AT, 2062	352	24	16659	11.8316761	0.08214482	0.08214482	0.18564109
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	36	9	1.31E-04	222108_AT, 213260_AT, 2056	302	812	13528	1.98597201	0.26086652	0.00836142	0.22920825
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	23	5.75	1.49E-04	210754_S_AT, 209757_S_AT,	302	414	13528	2.48859455	0.29043668	0.00923026	0.26012731
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-depende	63	15.75	1.66E-04	213625_AT, 213260_AT, 2029	302	1773	13528	1.59168992	0.31769048	0.01000936	0.28977841
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	10	2.5	1.73E-04	202540_S_AT, 202730_S_AT,	302	90	13528	4.97718911	0.32808959	0.01014385	0.30140317
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded org	76	19	1.79E-04	210754_S_AT, 203362_S_AT,	252	2596	12782	1.48493409	0.05184127	0.05184127	0.23886179
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	76	19	1.79E-04	210754_S_AT, 203362_S_AT,	252	2596	12782	1.48493409	0.05184127	0.05184127	0.23886179
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule me	33	8.25	2.08E-04	203362_S_AT, 209120_AT, 21	302	734	13528	2.01393074	0.38120198	0.0119277	0.36370775
GOTERM_BP_FAT	GO:0012501~programmed cell death	29	7.25	2.37E-04	213373_S_AT, 209199_S_AT,	302	611	13528	2.12609878	0.42022691	0.01320758	0.41296791
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	35	8.75	2.37E-04	222108_AT, 213260_AT, 2056	302	804	13528	1.95001812	0.42051904	0.01290699	0.41334893
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	10	2.5	2.82E-04	202540_S_AT, 202730_S_AT,	302	96	13528	4.66611479	0.47792821	0.01500146	0.49218999
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	22	5.5	2.92E-04	215719_X_AT, 211580_S_AT,	302	405	13528	2.43329245	0.48997689	0.01518577	0.50982647
SP_PIR_KEYWORDS	Transcription	66	16.5	3.07E-04	213625_AT, 221213_S_AT, 21	395	2071	19235	1.55188284	0.09422481	0.01635874	0.41427119
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosyntheti	27	6.75	3.33E-04	209199_S_AT, 209121_X_AT,	302	561	13528	2.15589475	0.53597226	0.01691773	0.58118299
GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	15	3.75	3.45E-04	203504_S_AT, 203920_AT, 20	302	216	13528	3.11074319	0.54836847	0.01713174	0.60161727
GOTERM_CC_FAT	GO:0031981~nuclear lumen	48	12	3.54E-04	205909_AT, 218006_S_AT, 20	252	1450	12782	1.67908046	0.09968999	0.05115333	0.47066727
GOTERM_BP_FAT	GO:0021546~rhombomere development	4	1	3.57E-04	205453_AT, 214639_S_AT, 21	302	7	13528	25.5969726	0.56064266	0.01734656	0.62240636
SP_PIR_KEYWORDS	mitosis	13	3.25	4.06E-04	214250_AT, 202870_S_AT, 20	395	183	19235	3.45929308	0.12251882	0.01849816	0.54675513
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic proces	27	6.75	4.63E-04	209199_S_AT, 209121_X_AT,	302	573	13528	2.11074512	0.65585732	0.02197779	0.80650735
GOTERM_BP_FAT	GO:0007050~cell cycle arrest	10	2.5	4.77E-04	203725_AT, 213348_AT, 2195	302	103	13528	4.34900019	0.66677969	0.02217795	0.83079115
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleo	25	6.25	4.86E-04	209199_S_AT, 209121_X_AT,	302	512	13528	2.18724131	0.67363977	0.02214616	0.84645049
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	19	4.75	5.01E-04	202540_S_AT, 207574_S_AT,	302	334	13528	2.54820161	0.68482147	0.02238518	0.87268865
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule bio	26	6.5	5.36E-04	209199_S_AT, 209121_X_AT,	302	547	13528	2.12918145	0.70862383	0.02343526	0.93176187
GOTERM_BP_FAT	GO:0060429~epithelium development	15	3.75	5.64E-04	213373_S_AT, 209119_X_AT,	302	227	13528	2.96000233	0.72728553	0.02421759	0.98152869
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	20	5	5.75E-04	215719_X_AT, 211580_S_AT,	302	367	13528	2.44112817	0.73412959	0.02423387	1.00063212
GOTERM_BP_FAT	GO:0051325~interphase	10	2.5	5.89E-04	204315_S_AT, 219534_X_AT,	302	106	13528	4.22591528	0.74258388	0.02437193	1.02491542
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compounc	25	6.25	5.92E-04	209199_S_AT, 209121_X_AT,	302	519	13528	2.15774094	0.7443032	0.02405877	1.02995061
GOTERM_CC_FAT	GO:0044427~chromosomal part	19	4.75	6.23E-04	205053_AT, 209757_S_AT, 20	252	386	12782	2.49668969	0.16896224	0.05982885	0.82801348
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic	30	7.5	6.74E-04	209199_S_AT, 203504_S_AT,	302	685	13528	1.96181177	0.78833958	0.02687391	1.17185597
INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	7	1.75	6.79E-04	203920_AT, 209119_X_AT, 20	352	51	16659	6.49582219	0.37617515	0.21017417	1.01773501
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activ	9	2.25	6.97E-04	202540_S_AT, 202730_S_AT,	302	87	13528	4.63393469	0.79927206	0.02730654	1.2116356
GOTERM_CC_FAT	GO:0005694~chromosome	21	5.25	7.56E-04	205053_AT, 209757_S_AT, 20	252	460	12782	2.31557971	0.20119898	0.05461294	1.0041212
GOTERM_BP_FAT	GO:0008283~cell proliferation	22	5.5	7.70E-04	201368_AT, 208965_S_AT, 21	302	436	13528	2.26028313	0.83025758	0.02961159	1.33729768
SP_PIR_KEYWORDS	transcription regulation	63	15.75	8.18E-04	213625_AT, 221213_S_AT, 21	395	2026	19235	1.51424519	0.23164062	0.03240069	1.09922585
GOTERM_BP_FAT	GO:0030097~hemopoiesis	15	3.75	8.33E-04	213373_S_AT, 215719_X_AT,	302	236	13528	2.84712089	0.85318916	0.03147099	1.44594425
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	30	7.5	8.52E-04	209199_S_AT, 203504_S_AT,	302	695	13528	1.93358426	0.85952986	0.03166425	1.47897029
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	14	3.5	8.90E-04	213373_S_AT, 209119_X_AT,	302	211	13528	2.97216032	0.87127977	0.03252564	1.54428182
GOTERM_BP_FAT	GO:0000075~cell cycle checkpoint	9	2.25	9.40E-04	204315_S_AT, 203362_S_AT,	302	91	13528	4.43024525	0.88512431	0.03376451	1.62929453
GOTERM_BP_FAT	GO:0051301~cell division	17	4.25	9.52E-04	202870_S_AT, 203362_S_AT,	302	295	13528	2.58138961	0.88846686	0.03369175	1.65134339
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	56	14	9.53E-04	210754_S_AT, 205909_AT, 21	252	1856	12782	1.53041188	0.24658652	0.05505468	1.26393806
GOTERM_BP_FAT	GO:0006915~apoptosis	27	6.75	9.62E-04	213373_S_AT, 209199_S_AT,	302	602	13528	2.00906471	0.89078651	0.03349468	1.66703375
GOTERM_BP_FAT	GO:0001657~ureteric bud development	6	1.5	9.90E-04	212558_AT, 206382_S_AT, 21	302	35	13528	7.67909177	0.89778427	0.03396537	1.716453
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell d	19	4.75	0.001142949	222108_AT, 209199_S_AT, 21	302	359	13528	2.37075024	0.92810673	0.0385302	1.97866187
SP_PIR_KEYWORDS	cell division	15	3.75	0.001151693	202870_S_AT, 203362_S_AT,	395	264	19235	2.76682969	0.30999676	0.04039043	1.54445565
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	19	4.75	0.001193663	222108_AT, 209199_S_AT, 21	302	360	13528	2.36416483	0.93603718	0.03962662	2.06559688
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound	28	7	0.001196682	209199_S_AT, 203504_S_AT,	302	644	13528	1.94759574	0.9364807	0.03916059	2.07076985
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	26	6.5	0.001262492	209199_S_AT, 209121_X_AT,	302	581	13528	2.00458219	0.94542023	0.04069304	2.18346776
GOTERM_BP_FAT	GO:0001822~kidney development	9	2.25	0.001332531	219658_AT, 212558_AT, 2063	302	96	13528	4.19950331	0.95355715	0.04231164	2.30327504
GOTERM_BP_FAT	GO:0008219~cell death	30	7.5	0.001420072	213373_S_AT, 209199_S_AT,	302	719	13528	1.86904181	0.96204403	0.0444184	2.45282389
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental proc	16	4	0.001429784	210754_S_AT, 203332_S_AT,	302	278	13528	2.57811234	0.96288436	0.04411667	2.46940159
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	17	4.25	0.001437834	209119_X_AT, 209121_X_AT,	282	316	12983	2.47678203	0.53888673	0.17595315	2.07160507

GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule met	34	8.5	0.001468787	210754_S_AT, 213260_AT, 20	302	857	13528	1.7771527	0.96607606	0.04469516	2.53595329
GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activi	14	3.5	0.001482695	205498_AT, 207574_S_AT, 20	302	223	13528	2.81222344	0.96714647	0.04452111	2.55967266
GOTERM_BP_FAT	GO:0010033~response to organic substance	30	7.5	0.001487495	213373_S_AT, 215719_X_AT,	302	721	13528	1.86385723	0.96750805	0.04408758	2.56785867
GOTERM_MF_FAT	GO:0004879~ligand-dependent nuclear receptor activit	7	1.75	0.001534715	203920_AT, 209119_X_AT, 20	282	58	12983	5.55643189	0.56233902	0.15232853	2.20974096
GOTERM_BP_FAT	GO:0016265~death	30	7.5	0.001557092	213373_S_AT, 209199_S_AT,	302	724	13528	1.85613406	0.97232479	0.04551872	2.68646706
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	26	6.5	0.00157691	209199_S_AT, 209121_X_AT,	282	607	12983	1.97201678	0.57217762	0.13195165	2.2698482
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleos	27	6.75	0.001598745	209199_S_AT, 203504_S_AT,	302	624	13528	1.9382323	0.97485901	0.04612365	2.75738892
GOTERM_BP_FAT	GO:0048738~cardiac muscle tissue development	7	1.75	0.00161492	219658_AT, 213260_AT, 2050	302	57	13528	5.50110375	0.97577937	0.04600378	2.78491628
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	19	4.75	0.001623429	207574_S_AT, 205698_S_AT,	302	370	13528	2.30026848	0.97624994	0.04567608	2.79939459
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling	18	4.5	0.001709214	205805_S_AT, 207069_S_AT,	302	342	13528	2.35761589	0.9805124	0.04745411	2.94524509
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	19	4.75	0.001762325	204315_S_AT, 205875_S_AT,	302	373	13528	2.28176766	0.98275875	0.04831167	3.03543957
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	21	5.25	0.001781744	213373_S_AT, 215719_X_AT,	302	435	13528	2.16250285	0.98351383	0.04825738	3.06839866
SP_PIR_KEYWORDS	DNA binding	17	4.25	0.00183726	209199_S_AT, 209119_X_AT,	395	340	19235	2.43481013	0.44685873	0.05749512	2.45330322
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	12	3	0.001955856	221884_AT, 213260_AT, 2033	302	176	13528	3.05418423	0.98896616	0.05223836	3.36343317
GOTERM_BP_FAT	GO:0043406~positive regulation of MAP kinase activity	9	2.25	0.001965617	211919_S_AT, 205498_AT, 20	302	102	13528	3.9524737	0.98921182	0.05189112	3.37994935
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	14	3.5	0.002033887	205498_AT, 207574_S_AT, 20	302	231	13528	2.71483042	0.99078364	0.05303901	3.49538251
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	23	5.75	0.002044101	209199_S_AT, 209119_X_AT,	302	504	13528	2.04420267	0.99099824	0.05270222	3.51264187
GOTERM_BP_FAT	GO:0008354~germ cell migration	4	1	0.002066944	202540_S_AT, 211919_S_AT,	302	12	13528	14.9315673	0.99146031	0.05268664	3.55123187
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ developm	15	3.75	0.002087676	213373_S_AT, 215719_X_AT,	302	260	13528	2.58430973	0.99185909	0.05261955	3.58624037
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	9	2.25	0.002090951	204315_S_AT, 219534_X_AT,	302	103	13528	3.91410017	0.99192037	0.05212997	3.59177108
GOTERM_BP_FAT	GO:0030902~hindbrain development	7	1.75	0.002107646	205453_AT, 211466_AT, 2033	302	60	13528	5.22604857	0.99222561	0.05197343	3.61995238
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	10	2.5	0.002122309	213373_S_AT, 209757_S_AT,	302	127	13528	3.52714189	0.99248419	0.05177198	3.64469801
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	8	2	0.002145553	202730_S_AT, 212593_S_AT,	302	81	13528	4.4241681	0.99287659	0.05177669	3.68391337
GOTERM_BP_FAT	GO:0006928~cell motion	22	5.5	0.002198755	202540_S_AT, 209119_X_AT,	302	475	13528	2.07470199	0.99369938	0.05247825	3.77361501
GOTERM_BP_FAT	GO:0050866~negative regulation of cell activation	7	1.75	0.002294745	204781_S_AT, 215719_X_AT,	302	61	13528	5.14037564	0.99495105	0.05414803	3.93526016
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-	22	5.5	0.002328356	209199_S_AT, 209119_X_AT,	302	477	13528	2.06600303	0.99532779	0.05436359	3.99179826
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	11	2.75	0.0023457	205498_AT, 204154_AT, 2115	302	154	13528	3.19962157	0.99551109	0.0542088	4.02096236
SP_PIR_KEYWORDS	ubl conjugation	24	6	0.002433085	209199_S_AT, 220183_S_AT,	395	588	19235	1.9876001	0.54361019	0.06882665	3.23686504
GOTERM_BP_FAT	GO:0045766~positive regulation of angiogenesis	5	1.25	0.002439978	209710_AT, 200921_S_AT, 20	302	26	13528	8.61436577	0.99638872	0.05576918	4.1793416
GOTERM_CC_FAT	GO:0005819~spindle	10	2.5	0.002466136	214250_AT, 200747_S_AT, 20	252	147	12782	3.45049131	0.51970125	0.11505032	3.24083751
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	18	4.5	0.002477981	222108_AT, 209199_S_AT, 21	302	354	13528	2.27769671	0.99669193	0.05605825	4.24311358
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from	15	3.75	0.002576421	209199_S_AT, 209121_X_AT,	302	266	13528	2.52601703	0.99736421	0.0576568	4.40811738
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic proc	22	5.5	0.00259769	209199_S_AT, 209119_X_AT,	302	481	13528	2.04882213	0.99749048	0.05756072	4.44373294
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-	18	4.5	0.002622522	209199_S_AT, 209119_X_AT,	302	356	13528	2.26490066	0.99763026	0.05754252	4.48529979
GOTERM_BP_FAT	GO:0001656~metanephros development	6	1.5	0.002814976	212558_AT, 206382_S_AT, 21	302	44	13528	6.10836845	0.99848025	0.06105846	4.80687034
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	14	3.5	0.00282989	205498_AT, 207574_S_AT, 20	302	240	13528	2.61302428	0.99853169	0.06080046	4.83174713
GOTERM_BP_FAT	GO:0021569~rhombomere 3 development	3	0.75	0.00287422	205453_AT, 214639_S_AT, 21	302	4	13528	33.5960265	0.99867452	0.06115472	4.90565522
GOTERM_BP_FAT	GO:0060428~lung epithelium development	3	0.75	0.00287422	213844_AT, 210002_AT, 2115	302	4	13528	33.5960265	0.99867452	0.06115472	4.90565522
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	10	2.5	0.002904061	205453_AT, 213844_AT, 2062	302	133	13528	3.36802271	0.99876276	0.06120598	4.95537584
GOTERM_CC_FAT	GO:0043233~organelle lumen	53	13.25	0.002987676	205909_AT, 218006_S_AT, 20	252	1820	12782	1.4770757	0.58879688	0.11922455	3.91364382
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule bios	27	6.75	0.003048248	209199_S_AT, 209121_X_AT,	302	654	13528	1.84932256	0.9991131	0.06356972	5.19527466
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	10	2.5	0.003053986	209199_S_AT, 203920_AT, 20	302	134	13528	3.34288821	0.99912478	0.06311501	5.2048106
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic proc	18	4.5	0.003112887	209199_S_AT, 209119_X_AT,	302	362	13528	2.22736087	0.99923608	0.06372349	5.30263715
GOTERM_BP_FAT	GO:0001655~urogenital system development	9	2.25	0.003153978	219658_AT, 212558_AT, 2063	302	110	13528	3.66502107	0.99930523	0.06397067	5.37082684
GOTERM_BP_FAT	GO:0043193~positive regulation of gene-specific transc	8	2	0.003221301	209199_S_AT, 203920_AT, 20	302	87	13528	4.11905306	0.99940527	0.06472396	5.48244837
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	21	5.25	0.003306334	209199_S_AT, 209119_X_AT,	302	459	13528	2.04943081	0.99951131	0.06580451	5.6232549
GOTERM_BP_FAT	GO:0048015~phosphoinositide-mediated signaling	8	2	0.003434652	206638_AT, 201042_AT, 2041	302	88	13528	4.07224564	0.99963666	0.06769015	5.83536353
GOTERM_MF_FAT	GO:0008022~protein C-terminus binding	10	2.5	0.003565776	215023_S_AT, 202870_S_AT,	282	141	12983	3.26517781	0.85365899	0.24008227	5.06426743
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	20	5	0.00356642	213373_S_AT, 215719_X_AT,	302	430	13528	2.08347451	0.99973201	0.06960437	6.052708
GOTERM_BP_FAT	GO:0002520~immune system development	15	3.75	0.003588595	213373_S_AT, 215719_X_AT,	302	276	13528	2.43449467	0.9997454	0.06943515	6.08923846
GOTERM_BP_FAT	GO:0016477~cell migration	15	3.75	0.003588595	202540_S_AT, 209119_X_AT,	302	276	13528	2.43449467	0.9997454	0.06943515	6.08923846
GOTERM_BP_FAT	GO:0048870~cell motility	16	4	0.003711773	202540_S_AT, 209119_X_AT,	302	307	13528	2.3345773	0.99980846	0.07113933	6.29191096
GOTERM_BP_FAT	GO:0051674~localization of cell	16	4	0.003711773	202540_S_AT, 209119_X_AT,	302	307	13528	2.3345773	0.99980846	0.07113933	6.29191096

GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	15	3.75	0.003723176	202540_S_AT, 202730_S_AT,	302	277	13528	2.42570588	0.99981344	0.07076256	6.31065294
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	24	6	0.003824882	209199_S_AT, 209119_X_AT,	302	564	13528	1.90615753	0.99985251	0.07203446	6.47765446
KEGG_PATHWAY	hsa05200:Pathways in cancer	18	4.5	0.003830797	213373_S_AT, 215719_X_AT,	131	328	5085	2.13018991	0.373906	0.14451346	4.32290209
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell de	20	5	0.003844878	213373_S_AT, 215719_X_AT,	302	433	13528	2.06903935	0.99985917	0.07181179	6.51045583
GOTERM_BP_FAT	GO:0010564~regulation of cell cycle process	9	2.25	0.003926748	204315_S_AT, 207069_S_AT,	302	114	13528	3.53642384	0.99988345	0.07269839	6.64463775
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from R	18	4.5	0.003948625	209199_S_AT, 203394_S_AT,	302	371	13528	2.17332786	0.99988919	0.07250741	6.68046216
GOTERM_BP_FAT	GO:0033554~cellular response to stress	24	6	0.004005772	204315_S_AT, 205875_S_AT,	302	566	13528	1.89942199	0.9999029	0.07293919	6.77398359
GOTERM_MF_FAT	GO:0003707~steroid hormone receptor activity	6	1.5	0.004014532	203920_AT, 209119_X_AT, 20	282	49	12983	5.63742944	0.88515422	0.23701785	5.68440849
GOTERM_BP_FAT	GO:0045638~negative regulation of myeloid cell differe	5	1.25	0.004171651	203332_S_AT, 205883_AT, 20	302	30	13528	7.46578366	0.99993383	0.07525534	7.04494377
GOTERM_CC_FAT	GO:0000922~spindle pole	5	1.25	0.004237701	214250_AT, 200747_S_AT, 20	252	34	12782	7.45915033	0.71670638	0.14585894	5.5086445
SP_PIR_KEYWORDS	kinase	26	6.5	0.004274984	210754_S_AT, 211580_S_AT,	395	688	19235	1.84026347	0.74829451	0.10859638	5.62242071
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine	13	3.25	0.0044294	205805_S_AT, 205498_AT, 21	302	224	13528	2.59969253	0.99996353	0.07910782	7.46449772
GOTERM_BP_FAT	GO:0045637~regulation of myeloid cell differentiation	7	1.75	0.004589714	204781_S_AT, 215719_X_AT,	302	70	13528	4.4794702	0.99997483	0.08122934	7.72455081
GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	8	2	0.004667144	213373_S_AT, 210754_S_AT,	302	93	13528	3.8533077	0.99997896	0.08191709	7.8499055
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	51	12.75	0.00505116	205909_AT, 218006_S_AT, 20	252	1779	12782	1.45409406	0.77775976	0.15389406	6.53340596
SP_PIR_KEYWORDS	chromosomal rearrangement	14	3.5	0.005163877	204917_S_AT, 205529_S_AT,	395	279	19235	2.44353704	0.81120176	0.12035481	6.7540908
GOTERM_MF_FAT	GO:0016538~cyclin-dependent protein kinase regulator	4	1	0.005447124	213348_AT, 219534_X_AT, 20	282	17	12983	10.8327076	0.94705826	0.27856069	7.63897057
SP_PIR_KEYWORDS	Apoptosis	17	4.25	0.005555315	213373_S_AT, 212354_AT, 20	395	381	19235	2.17279644	0.83367286	0.12025966	7.24844397
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	9	2.25	0.005622073	205498_AT, 210754_S_AT, 20	302	121	13528	3.33183734	0.99999769	0.09714484	9.38275204
GOTERM_BP_FAT	GO:0043200~response to amino acid stimulus	4	1	0.005883921	204154_AT, 210754_S_AT, 20	302	17	13528	10.5399299	0.99999874	0.10069333	9.79885059
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	21	5.25	0.005886059	204315_S_AT, 203362_S_AT,	252	549	12782	1.94019429	0.82680284	0.16082202	7.5744766
GOTERM_BP_FAT	GO:0001709~cell fate determination	5	1.25	0.005912566	209710_AT, 203394_S_AT, 21	302	33	13528	6.78707606	0.99999882	0.10041584	9.84426043
GOTERM_MF_FAT	GO:0033293~monocarboxylic acid binding	6	1.5	0.006101129	209238_AT, 216985_S_AT, 20	282	54	12983	5.11544523	0.96283774	0.28053411	8.51866574
GOTERM_BP_FAT	GO:0060284~regulation of cell development	12	3	0.006171408	210754_S_AT, 203394_S_AT,	302	205	13528	2.6221289	0.99999935	0.10382539	10.253617
GOTERM_BP_FAT	GO:0009967~positive regulation of signal transduction	15	3.75	0.006409834	213373_S_AT, 205498_AT, 21	302	295	13528	2.27769671	0.99999963	0.10684886	10.6291332
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	13	3.25	0.006445727	212183_AT, 201042_AT, 2027	302	235	13528	2.47800479	0.99999966	0.10664694	10.6855361
GOTERM_MF_FAT	GO:0032405~MutLalpha complex binding	3	0.75	0.0066105	205875_S_AT, 201202_AT, 20	282	6	12983	23.0195035	0.971795	0.27702954	9.19840215
GOTERM_BP_FAT	GO:0000079~regulation of cyclin-dependent protein kin	6	1.5	0.006847516	219863_AT, 203725_AT, 2133	302	54	13528	4.97718911	0.99999986	0.11212677	11.3146238
GOTERM_BP_FAT	GO:0032355~response to estradiol stimulus	6	1.5	0.006847516	205498_AT, 204200_S_AT, 21	302	54	13528	4.97718911	0.99999986	0.11212677	11.3146238
UP_SEQ_FEATURE	splice variant	179	44.75	0.006877948	202540_S_AT, 205875_S_AT,	395	7458	19113	1.16134811	0.9997796	0.93959573	10.5783395
GOTERM_CC_FAT	GO:0005829~cytosol	40	10	0.006912409	211580_S_AT, 210754_S_AT,	252	1330	12782	1.52548037	0.87256054	0.17079103	8.8395761
GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	16	4	0.006953453	213373_S_AT, 205498_AT, 21	302	329	13528	2.17846575	0.99999989	0.11296544	11.4797934
GOTERM_BP_FAT	GO:0006350~transcription	64	16	0.00708959	213625_AT, 221213_S_AT, 21	302	2101	13528	1.3645221	0.99999992	0.11425059	11.6916234
GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	7	1.75	0.007297355	205453_AT, 213844_AT, 2062	302	77	13528	4.07224564	0.99999995	0.11659484	12.0139859
SP_PIR_KEYWORDS	tumor suppressor	9	2.25	0.007307369	202730_S_AT, 219534_X_AT,	395	137	19235	3.1990206	0.90573184	0.1456726	9.43153983
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	26	6.5	0.007500993	210754_S_AT, 207574_S_AT,	302	667	13528	1.74612032	0.99999997	0.11883789	12.3288685
SP_PIR_KEYWORDS	SH2 domain	8	2	0.007887054	209682_AT, 211580_S_AT, 20	395	111	19235	3.50963622	0.92189486	0.14730743	10.1432988
GOTERM_MF_FAT	GO:0008134~transcription factor binding	21	5.25	0.008021558	209119_X_AT, 209121_X_AT,	282	513	12983	1.88463772	0.9868719	0.30307908	11.0569245
GOTERM_BP_FAT	GO:0048736~appendage development	8	2	0.00809741	209119_X_AT, 209121_X_AT,	302	103	13528	3.47920015	0.99999999	0.12682915	13.2449992
GOTERM_BP_FAT	GO:0060173~limb development	8	2	0.00809741	209119_X_AT, 209121_X_AT,	302	103	13528	3.47920015	0.99999999	0.12682915	13.2449992
SP_PIR_KEYWORDS	bromodomain	5	1.25	0.008100216	209762_X_AT, 209049_S_AT,	395	39	19235	6.24310289	0.92711633	0.14277289	10.4037221
SP_PIR_KEYWORDS	alternative splicing	178	44.5	0.008231412	202540_S_AT, 205875_S_AT,	395	7488	19235	1.15757533	0.93015549	0.13744831	10.563659
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	6	1.5	0.008591381	205453_AT, 213844_AT, 2062	302	57	13528	4.71523179	1	0.13315741	13.9969245
INTERPRO	IPR002087:Anti-proliferative protein	3	0.75	0.008667304	200921_S_AT, 200920_S_AT,	352	7	16659	20.2828734	0.99764222	0.86690306	12.2915596
GOTERM_MF_FAT	GO:0005504~fatty acid binding	5	1.25	0.008891936	209238_AT, 216985_S_AT, 20	282	38	12983	6.05776409	0.99181341	0.30901363	12.1855813
INTERPRO	IPR000980:SH2 motif	8	2	0.009098028	209682_AT, 211580_S_AT, 20	352	111	16659	3.41093366	0.99825686	0.79566967	12.8639566
GOTERM_MF_FAT	GO:0008289~lipid binding	19	4.75	0.009337156	209238_AT, 203504_S_AT, 21	282	450	12983	1.94386919	0.99357134	0.30267189	12.7577474
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	32	8	0.009337748	210754_S_AT, 218935_AT, 20	395	962	19113	1.60955815	0.9999893	0.94281098	14.09959
SP_PIR_KEYWORDS	dna replication	7	1.75	0.009415859	203209_AT, 221521_S_AT, 20	395	88	19235	3.87356157	0.95246413	0.14813741	11.9956564
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	21	5.25	0.009459698	205875_S_AT, 45633_AT, 201	302	506	13528	1.85906866	1	0.14468447	15.3038125
GOTERM_BP_FAT	GO:0001945~lymph vessel development	3	0.75	0.009623897	209121_X_AT, 209119_X_AT,	302	7	13528	19.1977294	1	0.14605033	15.5488309
GOTERM_BP_FAT	GO:0021783~preganglionic parasympathetic nervous sy	3	0.75	0.009623897	205453_AT, 203394_S_AT, 21	302	7	13528	19.1977294	1	0.14605033	15.5488309
GOTERM_CC_FAT	GO:0005730~nucleolus	24	6	0.01047522	213373_S_AT, 219534_X_AT,	252	698	12782	1.74403056	0.95617496	0.22943338	13.1079146

GOTERM_BP_FAT	GO:0014075~response to amine stimulus	5	1.25	0.01071195	204154_AT, 210754_S_AT, 205	302	39	13528	5.74291051	1	0.16019963	17.1556186
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	11	2.75	0.01086074	204154_AT, 215719_X_AT, 205	302	192	13528	2.56636313	1	0.16120712	17.3730907
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	8	2	0.011162305	212709_AT, 204739_AT, 2033	252	124	12782	3.27240143	0.9643443	0.22620609	13.9094866
GOTERM_MF_FAT	GO:0032404~mismatch repair complex binding	3	0.75	0.01199129	205875_S_AT, 201202_AT, 209	282	8	12983	17.2646277	0.99848192	0.35123652	16.097251
GOTERM_BP_FAT	GO:0030071~regulation of mitotic metaphase/anaphas	4	1	0.012278198	203764_AT, 203362_S_AT, 215	302	22	13528	8.14449127	1	0.17921624	19.4180487
SP_PIR_KEYWORDS	nucleotide-binding	49	12.25	0.012371987	203504_S_AT, 202869_AT, 210	395	1686	19235	1.41525144	0.98184172	0.1816224	15.4775245
SP_PIR_KEYWORDS	transferase	42	10.5	0.012514509	202869_AT, 210754_S_AT, 205	395	1394	19235	1.46717396	0.98266624	0.17560043	15.6421256
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	21	5.25	0.012521135	207574_S_AT, 205698_S_AT, 2	302	520	13528	1.80901681	1	0.18130101	19.7637051
GOTERM_BP_FAT	GO:0048486~parasympathetic nervous system develop	3	0.75	0.012644486	205453_AT, 203394_S_AT, 214	302	8	13528	16.7980132	1	0.18179172	19.938678
KEGG_PATHWAY	hsa03030:DNA replication	5	1.25	0.01275637	203209_AT, 205053_AT, 2012	131	36	5085	5.39122137	0.79118124	0.32400672	13.7411416
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	7	1.75	0.012942118	221884_AT, 214466_AT, 2050	302	87	13528	3.60417142	1	0.18453333	20.3593839
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	7	1.75	0.012942118	221884_AT, 214466_AT, 2050	302	87	13528	3.60417142	1	0.18453333	20.3593839
GOTERM_BP_FAT	GO:0010243~response to organic nitrogen	6	1.5	0.012955579	204154_AT, 210754_S_AT, 205	302	63	13528	4.26616209	1	0.18358176	20.3783624
SMART	SM00099:btg1	3	0.75	0.013067937	200921_S_AT, 200920_S_AT, 2	238	7	9079	16.3487395	0.91566563	0.91566563	15.0579681
UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	5	1.25	0.013622366	209121_X_AT, 209119_X_AT,	395	45	19113	5.37637131	0.99999995	0.96479983	19.9243455
UP_SEQ_FEATURE	zinc finger region:NR C4-type	5	1.25	0.013622366	209121_X_AT, 209119_X_AT,	395	45	19113	5.37637131	0.99999995	0.96479983	19.9243455
GOTERM_BP_FAT	GO:0051129~negative regulation of cellular component	9	2.25	0.014101024	207069_S_AT, 203920_AT, 203	302	142	13528	2.83910083	1	0.19700491	21.97774
GOTERM_CC_FAT	GO:0005654~nucleoplasm	28	7	0.014322213	209199_S_AT, 208965_S_AT, 2	252	882	12782	1.61022928	0.98621883	0.26363717	17.5086175
SP_PIR_KEYWORDS	atp-binding	40	10	0.014529574	203504_S_AT, 202869_AT, 210	395	1326	19235	1.46896539	0.9910208	0.19282936	17.9378181
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	6	1.5	0.014691292	211919_S_AT, 213844_AT, 209	302	65	13528	4.13489557	1	0.20318674	22.7900536
GOTERM_BP_FAT	GO:0007093~mitotic cell cycle checkpoint	5	1.25	0.015001166	204315_S_AT, 213226_AT, 203	302	43	13528	5.20868628	1	0.20580476	23.2132964
GOTERM_BP_FAT	GO:0001101~response to acid	4	1	0.015619421	204154_AT, 210754_S_AT, 205	302	24	13528	7.46578366	1	0.21212741	24.0512171
INTERPRO	IPR001628:Zinc finger, nuclear hormone receptor-type	5	1.25	0.015769926	209121_X_AT, 209119_X_AT,	352	46	16659	5.14420702	0.99998407	0.89024313	21.296719
SP_PIR_KEYWORDS	cytoplasm	86	21.5	0.016246138	210754_S_AT, 215723_S_AT, 2	395	3332	19235	1.25686477	0.99487803	0.20492096	19.847665
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	6	1.5	0.016576386	213373_S_AT, 213844_AT, 212	302	67	13528	4.01146585	1	0.2223622	25.3312123
INTERPRO	IPR001723:Steroid hormone receptor	5	1.25	0.016958213	209121_X_AT, 209119_X_AT,	352	47	16659	5.0347558	0.99999312	0.86209259	22.71622
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	8	2	0.017002782	209121_X_AT, 209119_X_AT,	302	119	13528	3.01140854	1	0.22612427	25.8949677
GOTERM_BP_FAT	GO:0006916~anti-apoptosis	11	2.75	0.017079751	222108_AT, 209199_S_AT, 215	302	206	13528	2.39195011	1	0.22574429	25.9963033
GOTERM_BP_FAT	GO:0021675~nerve development	4	1	0.017462848	205453_AT, 206382_S_AT, 203	302	25	13528	7.16715232	1	0.2289218	26.4987367
UP_SEQ_FEATURE	region of interest:Linker	4	1	0.017624275	202540_S_AT, 209682_AT, 203	395	27	19113	7.16849508	1	0.97309808	25.0281902
GOTERM_CC_FAT	GO:0000776~kinetochore	6	1.5	0.017629633	212709_AT, 204739_AT, 2033	252	77	12782	3.95238095	0.99492133	0.2968467	21.1262912
GOTERM_BP_FAT	GO:0001525~angiogenesis	9	2.25	0.017687793	211919_S_AT, 213373_S_AT, 2	302	148	13528	2.72400215	1	0.2302326	26.7922525
UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	14	3.5	0.01784254	204917_S_AT, 203588_S_AT, 2	395	325	19113	2.0843778	1	0.95662087	25.2975825
INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, c	5	1.25	0.018201005	209121_X_AT, 209119_X_AT,	352	48	16659	4.92986506	0.99999714	0.83858033	24.1752349
INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	5	1.25	0.018201005	209121_X_AT, 209119_X_AT,	352	48	16659	4.92986506	0.99999714	0.83858033	24.1752349
GOTERM_MF_FAT	GO:0003690~double-stranded DNA binding	7	1.75	0.018686295	208965_S_AT, 211466_AT, 201	282	97	12983	3.32240257	0.99996086	0.46967825	23.9997045
GOTERM_MF_FAT	GO:0004861~cyclin-dependent protein kinase inhibitor	3	0.75	0.018729681	213348_AT, 219534_X_AT, 204	282	10	12983	13.8117021	0.99996178	0.45028786	24.0485756
GOTERM_BP_FAT	GO:0048660~regulation of smooth muscle cell prolifera	5	1.25	0.018838916	204200_S_AT, 201042_AT, 216	302	46	13528	4.86898935	1	0.24201692	28.2770638
SP_PIR_KEYWORDS	golgi apparatus	21	5.25	0.018981648	212354_AT, 210754_S_AT, 202	395	588	19235	1.73915009	0.99791053	0.22672343	22.8063237
SP_PIR_KEYWORDS	cyclin	5	1.25	0.019041477	216831_S_AT, 205529_S_AT, 2	395	50	19235	4.86962025	0.99795116	0.21934291	22.8698879
SP_PIR_KEYWORDS	coenzyme A	4	1	0.019122207	202540_S_AT, 214440_AT, 204	395	28	19235	6.95660036	0.99800474	0.21267546	22.9555817
GOTERM_BP_FAT	GO:0043583~ear development	7	1.75	0.019251834	204967_AT, 206382_S_AT, 203	302	95	13528	3.30066225	1	0.24530815	28.8027242
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	10	2.5	0.019436194	213373_S_AT, 205453_AT, 213	302	180	13528	2.48859455	1	0.24602157	29.0362465
UP_SEQ_FEATURE	domain:Bromo	4	1	0.01944385	209762_X_AT, 209049_S_AT, 2	395	28	19113	6.9124774	1	0.94993302	27.2463901
GOTERM_BP_FAT	GO:0050673~epithelial cell proliferation	3	0.75	0.019733976	218326_S_AT, 205051_S_AT, 2	302	10	13528	13.4384106	1	0.24797095	29.4119129
GOTERM_BP_FAT	GO:0016310~phosphorylation	28	7	0.020129472	210754_S_AT, 207574_S_AT, 2	302	800	13528	1.56781457	1	0.25095441	29.9079517
GOTERM_BP_FAT	GO:0007346~regulation of mitotic cell cycle	9	2.25	0.020416527	204315_S_AT, 207069_S_AT, 2	302	152	13528	2.65231788	1	0.25272391	30.2659212
PIR_SUPERFAMILY	PIRSF002612:homeotic protein Hox A5/D4	3	0.75	0.021638324	213844_AT, 206289_AT, 2056	174	10	7396	12.7517241	0.99187403	0.90985585	24.3056386
GOTERM_BP_FAT	GO:0060537~muscle tissue development	8	2	0.021659425	209121_X_AT, 209119_X_AT,	302	125	13528	2.86686093	1	0.26461801	31.7960751
GOTERM_BP_FAT	GO:0000077~DNA damage checkpoint	5	1.25	0.021705652	204315_S_AT, 213226_AT, 219	302	48	13528	4.66611479	1	0.26373238	31.8523706
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	22	5.5	0.021714328	207574_S_AT, 205698_S_AT, 2	302	586	13528	1.68171236	1	0.2624639	31.8629313
SP_PIR_KEYWORDS	activator	19	4.75	0.021782993	204917_S_AT, 209199_S_AT, 2	395	520	19235	1.77928432	0.99916797	0.23099172	25.7311182
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	7	1.75	0.023080882	221884_AT, 214466_AT, 2050	302	99	13528	3.16730216	1	0.27521918	33.5072392

GOTERM_BP_FAT	GO:0030324~lung development	7	1.75	0.023080882	213844_AT, 209757_S_AT, 20	302	99	13528	3.16730216	1	0.27521918	33.5072392
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	7	1.75	0.023080882	221884_AT, 214466_AT, 2050	302	99	13528	3.16730216	1	0.27521918	33.5072392
GOTERM_BP_FAT	GO:0008015~blood circulation	10	2.5	0.023462157	206638_AT, 217518_AT, 2054	302	186	13528	2.40831731	1	0.27770299	33.9592906
GOTERM_BP_FAT	GO:0003013~circulatory system process	10	2.5	0.023462157	206638_AT, 217518_AT, 2054	302	186	13528	2.40831731	1	0.27770299	33.9592906
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	55	13.75	0.023568173	219885_AT, 203504_S_AT, 20	282	1918	12983	1.32020093	0.99999732	0.50976005	29.318825
GOTERM_BP_FAT	GO:0045841~negative regulation of mitotic metaphase/	3	0.75	0.023769076	203362_S_AT, 215509_S_AT,	302	11	13528	12.2167369	1	0.27940328	34.3210758
GOTERM_BP_FAT	GO:0007094~mitotic cell cycle spindle assembly checkp	3	0.75	0.023769076	203362_S_AT, 215509_S_AT,	302	11	13528	12.2167369	1	0.27940328	34.3210758
GOTERM_BP_FAT	GO:0007379~segment specification	3	0.75	0.023769076	204917_S_AT, 214457_AT, 21	302	11	13528	12.2167369	1	0.27940328	34.3210758
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	12	3	0.023879956	213373_S_AT, 202730_S_AT,	302	249	13528	2.15878082	1	0.27912262	34.4513173
GOTERM_BP_FAT	GO:0048872~homeostasis of number of cells	7	1.75	0.024112512	215719_X_AT, 210754_S_AT,	302	100	13528	3.13562914	1	0.2800546	34.7236911
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	6	1.5	0.024417493	211919_S_AT, 213844_AT, 20	302	74	13528	3.63200286	1	0.28168914	35.0792733
GOTERM_BP_FAT	GO:0016202~regulation of striated muscle tissue devel	5	1.25	0.024825217	219743_AT, 200921_S_AT, 21	302	50	13528	4.4794702	1	0.28430608	35.5517939
SP_PIR_KEYWORDS	cell cycle control	4	1	0.025086992	210567_S_AT, 213226_AT, 20	395	31	19235	6.28338097	0.9997201	0.25336654	29.0487217
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	7	1.75	0.025174581	213373_S_AT, 205453_AT, 21	302	101	13528	3.10458331	1	0.28632016	35.9540978
INTERPRO	IPR017995:Homeobox protein, antennapedia type	3	0.75	0.025411989	213844_AT, 206289_AT, 2056	352	12	16659	11.8316761	0.99999998	0.89313635	32.145832
INTERPRO	IPR017970:Homeobox, conserved site	11	2.75	0.025792709	205453_AT, 213844_AT, 2113	352	232	16659	2.24393858	0.99999999	0.86706663	32.5440955
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulu	9	2.25	0.025890417	210029_AT, 204200_S_AT, 20	302	159	13528	2.53554917	1	0.29181952	36.7710226
SMART	SM00252:SH2	8	2	0.025936538	209682_AT, 211580_S_AT, 20	238	111	9079	2.74933757	0.99284839	0.91543284	27.822256
GOTERM_BP_FAT	GO:0030323~respiratory tube development	7	1.75	0.026267417	213844_AT, 209757_S_AT, 20	302	102	13528	3.07414621	1	0.29401323	37.1973021
GOTERM_BP_FAT	GO:0048634~regulation of muscle development	5	1.25	0.026481175	219743_AT, 200921_S_AT, 21	302	51	13528	4.39163745	1	0.29464013	37.4377961
GOTERM_CC_FAT	GO:0000777~condensed chromosome kinetochore	5	1.25	0.02693962	204739_AT, 203362_S_AT, 21	252	58	12782	4.37260536	0.99969973	0.39765564	30.5368183
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	8	2	0.027134924	213373_S_AT, 215719_X_AT,	302	131	13528	2.73555432	1	0.29936889	38.1679369
UP_SEQ_FEATURE	compositionally biased region:Ser/Thr-rich	4	1	0.027720805	205805_S_AT, 207480_S_AT,	395	32	19113	6.04841772	1	0.97786899	36.5816565
INTERPRO	IPR001356:Homeobox	11	2.75	0.027773243	205453_AT, 213844_AT, 2113	352	235	16659	2.21529255	1	0.85879631	34.580923
INTERPRO	IPR011993:Pleckstrin homology-type	13	3.25	0.027777478	215626_AT, 206204_AT, 2071	352	303	16659	2.03051868	1	0.83133955	34.5852158
SP_PIR_KEYWORDS	Homeobox	11	2.75	0.02795348	205453_AT, 213844_AT, 2113	395	242	19235	2.21346375	0.99989155	0.27006566	31.8152787
GOTERM_CC_FAT	GO:0005815~microtubule organizing center	11	2.75	0.027970229	203362_S_AT, 212675_S_AT,	252	253	12782	2.20531401	0.9997808	0.39080718	31.5120568
GOTERM_BP_FAT	GO:0051784~negative regulation of nuclear division	3	0.75	0.028109502	203362_S_AT, 215509_S_AT,	302	12	13528	11.1986755	1	0.3069656	39.2414977
GOTERM_BP_FAT	GO:0031577~spindle checkpoint	3	0.75	0.028109502	203362_S_AT, 215509_S_AT,	302	12	13528	11.1986755	1	0.3069656	39.2414977
GOTERM_BP_FAT	GO:0045839~negative regulation of mitosis	3	0.75	0.028109502	203362_S_AT, 215509_S_AT,	302	12	13528	11.1986755	1	0.3069656	39.2414977
GOTERM_BP_FAT	GO:0031570~DNA integrity checkpoint	5	1.25	0.028201856	204315_S_AT, 213226_AT, 21	302	52	13528	4.30718288	1	0.30639586	39.3423152
GOTERM_BP_FAT	GO:0046620~regulation of organ growth	4	1	0.028425262	219743_AT, 213260_AT, 2066	302	30	13528	5.97262693	1	0.30702178	39.5855415
GOTERM_BP_FAT	GO:0006954~inflammatory response	14	3.5	0.029598698	204154_AT, 210754_S_AT, 21	302	325	13528	1.92961793	1	0.31615709	40.8480598
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	6	1.5	0.029813643	205498_AT, 204781_S_AT, 21	302	78	13528	3.44574631	1	0.31664243	41.0766098
GOTERM_BP_FAT	GO:0001889~liver development	5	1.25	0.029987641	219658_AT, 203394_S_AT, 21	302	53	13528	4.22591528	1	0.31676183	41.2610114
SP_PIR_KEYWORDS	developmental protein	25	6.25	0.030729674	209199_S_AT, 207574_S_AT,	395	779	19235	1.56277929	0.99995682	0.28466615	34.3991619
GOTERM_CC_FAT	GO:0005856~cytoskeleton	38	9.5	0.030942729	204315_S_AT, 213373_S_AT,	252	1381	12782	1.39568751	0.99991174	0.40465894	34.254366
GOTERM_BP_FAT	GO:0048661~positive regulation of smooth muscle cell	4	1	0.030966493	204200_S_AT, 201042_AT, 21	302	31	13528	5.77996155	1	0.323901	42.2882912
GOTERM_BP_FAT	GO:0048732~gland development	8	2	0.031267774	209710_AT, 204154_AT, 2138	302	135	13528	2.65450086	1	0.32507917	42.6010534
SMART	SM00399:ZnF_C4	5	1.25	0.031390457	209121_X_AT, 209119_X_AT,	238	46	9079	4.14641944	0.99751135	0.86448483	32.679244
GOTERM_BP_FAT	GO:0051250~negative regulation of lymphocyte activati	5	1.25	0.031838851	204781_S_AT, 215719_X_AT,	302	54	13528	4.14765759	1	0.32855054	43.1895122
UP_SEQ_FEATURE	binding site:ATP	19	4.75	0.032199029	210754_S_AT, 218935_AT, 20	395	542	19113	1.69623523	1	0.98155416	41.1515523
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	9	2.25	0.032313849	210754_S_AT, 203394_S_AT,	302	166	13528	2.42862842	1	0.33115756	43.6746303
GOTERM_BP_FAT	GO:0007423~sensory organ development	11	2.75	0.032475226	213260_AT, 203394_S_AT, 20	302	229	13528	2.15171058	1	0.33109287	43.8385544
GOTERM_BP_FAT	GO:0010595~positive regulation of endothelial cell migr	3	0.75	0.032739765	204200_S_AT, 216061_X_AT,	302	13	13528	10.3372389	1	0.33189291	44.1062968
GOTERM_BP_FAT	GO:0034605~cellular response to heat	3	0.75	0.032739765	217518_AT, 210754_S_AT, 20	302	13	13528	10.3372389	1	0.33189291	44.1062968
GOTERM_BP_FAT	GO:0008045~motor axon guidance	3	0.75	0.032739765	211919_S_AT, 209201_X_AT,	302	13	13528	10.3372389	1	0.33189291	44.1062968
UP_SEQ_FEATURE	binding site:Coenzyme A	3	0.75	0.032750509	214440_AT, 204573_AT, 2021	395	14	19113	10.3687161	1	0.97510631	41.6924467
GOTERM_BP_FAT	GO:0042770~DNA damage response, signal transductio	6	1.5	0.032771983	204315_S_AT, 213226_AT, 20	302	80	13528	3.35960265	1	0.33074941	44.1388233
GOTERM_BP_FAT	GO:0010740~positive regulation of protein kinase casca	9	2.25	0.033312765	213373_S_AT, 205498_AT, 21	302	167	13528	2.41408574	1	0.33382999	44.6821146
GOTERM_BP_FAT	GO:0060541~respiratory system development	7	1.75	0.033487376	213844_AT, 209757_S_AT, 20	302	108	13528	2.90336031	1	0.33386324	44.8564698
INTERPRO	IPR004367:Cyclin, C-terminal	3	0.75	0.034083503	213226_AT, 219470_X_AT, 21	352	14	16659	10.1414367	1	0.86580051	40.6941456
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	52	13	0.034377928	219885_AT, 203504_S_AT, 20	282	1836	12983	1.30393702	0.99999999	0.62863289	39.8875174

GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	52	13	0.034377928	219885_AT, 203504_S_AT, 20	282	1836	12983	1.30393702	0.99999999	0.62863289	39.8875174
GOTERM_BP_FAT	GO:0009615~response to virus	7	1.75	0.034803751	211919_S_AT, 208965_S_AT,	302	109	13528	2.87672398	1	0.34317552	46.1543358
SP_PIR_KEYWORDS	repressor	16	4	0.034843099	208965_S_AT, 203394_S_AT,	395	435	19235	1.79112469	0.99998902	0.30814177	38.0613526
GOTERM_BP_FAT	GO:0009314~response to radiation	10	2.5	0.03515394	202540_S_AT, 203887_S_AT,	302	200	13528	2.2397351	1	0.34457195	46.4947201
GOTERM_BP_FAT	GO:0009612~response to mechanical stimulus	5	1.25	0.035738545	201009_S_AT, 203688_AT, 20	302	56	13528	3.99952696	1	0.34781678	47.0584408
GOTERM_BP_FAT	GO:0007088~regulation of mitosis	5	1.25	0.035738545	203764_AT, 203362_S_AT, 21	302	56	13528	3.99952696	1	0.34781678	47.0584408
GOTERM_BP_FAT	GO:0009408~response to heat	5	1.25	0.035738545	217518_AT, 210754_S_AT, 20	302	56	13528	3.99952696	1	0.34781678	47.0584408
GOTERM_BP_FAT	GO:0051783~regulation of nuclear division	5	1.25	0.035738545	203764_AT, 203362_S_AT, 21	302	56	13528	3.99952696	1	0.34781678	47.0584408
GOTERM_BP_FAT	GO:0045165~cell fate commitment	8	2	0.035803646	209710_AT, 209121_X_AT, 20	302	139	13528	2.57811234	1	0.34691566	47.1208684
GOTERM_BP_FAT	GO:0000187~activation of MAPK activity	6	1.5	0.035907208	211919_S_AT, 205498_AT, 20	302	82	13528	3.27766112	1	0.34632569	47.2200347
SMART	SM00430:HOLI	5	1.25	0.03596385	209121_X_AT, 209119_X_AT,	238	48	9079	3.97365196	0.99897778	0.82119238	36.5184435
GOTERM_CC_FAT	GO:0005794~Golgi apparatus	26	6.5	0.036388325	203504_S_AT, 212354_AT, 21	252	872	12782	1.51235984	0.99998345	0.43977346	39.0164776
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	8	2	0.037083545	209238_AT, 216985_S_AT, 21	282	144	12983	2.55772262	1	0.63814584	42.2920033
GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	6	1.5	0.037541805	217518_AT, 210754_S_AT, 20	302	83	13528	3.23817123	1	0.35766114	48.7622142
GOTERM_BP_FAT	GO:0002683~negative regulation of immune system pr	6	1.5	0.037541805	204781_S_AT, 215719_X_AT,	302	83	13528	3.23817123	1	0.35766114	48.7622142
SP_PIR_KEYWORDS	peroxisome	6	1.5	0.037563861	202540_S_AT, 209424_S_AT,	395	90	19235	3.2464135	0.99999558	0.31973212	40.3786274
GOTERM_BP_FAT	GO:0010552~positive regulation of specific transcriptio	5	1.25	0.037787388	209199_S_AT, 209710_AT, 20	302	57	13528	3.92935982	1	0.35812608	48.9902078
GOTERM_BP_FAT	GO:0002695~negative regulation of leukocyte activatio	5	1.25	0.037787388	204781_S_AT, 215719_X_AT,	302	57	13528	3.92935982	1	0.35812608	48.9902078
GOTERM_MF_FAT	GO:0043566~structure-specific DNA binding	8	2	0.038275802	205875_S_AT, 208965_S_AT,	282	145	12983	2.54008315	1	0.63206503	43.3228677
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	14	3.5	0.038838357	203920_AT, 207069_S_AT, 20	302	337	13528	1.8609075	1	0.36470994	49.9551432
GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	7	1.75	0.038951479	205498_AT, 205453_AT, 2138	302	112	13528	2.79966887	1	0.364135	50.0579728
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phospho	9	2.25	0.039749378	202730_S_AT, 207069_S_AT,	302	173	13528	2.33036022	1	0.36868942	50.7776373
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor act	11	2.75	0.039826903	209199_S_AT, 209119_X_AT,	282	244	12983	2.07552901	1	0.62986014	44.6383409
GOTERM_BP_FAT	GO:0006261~DNA-dependent DNA replication	5	1.25	0.039902374	205053_AT, 219258_AT, 2118	302	58	13528	3.86161224	1	0.36840108	50.9145102
SP_PIR_KEYWORDS	kinetochore	5	1.25	0.040133511	204739_AT, 203362_S_AT, 21	395	63	19235	3.86477798	0.99999813	0.32946597	42.4932379
GOTERM_CC_FAT	GO:0000779~condensed chromosome, centromeric reg	5	1.25	0.040591881	204739_AT, 203362_S_AT, 21	252	66	12782	3.84259259	0.99999548	0.45955646	42.4719696
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	6	1.5	0.04094606	205498_AT, 204781_S_AT, 21	302	85	13528	3.16197896	1	0.37466814	51.8386802
GOTERM_BP_FAT	GO:0032147~activation of protein kinase activity	7	1.75	0.041884161	205498_AT, 207574_S_AT, 20	302	114	13528	2.75055188	1	0.38005826	52.6553344
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	9	2.25	0.042067308	215719_X_AT, 203332_S_AT,	302	175	13528	2.30372753	1	0.37994428	52.81324
GOTERM_BP_FAT	GO:0045216~cell-cell junction organization	4	1	0.042276017	40687_AT, 204904_AT, 2049	302	35	13528	5.11939451	1	0.3800148	52.99258
GOTERM_BP_FAT	GO:0007052~mitotic spindle organization	3	0.75	0.042810495	204162_AT, 204444_AT, 2048	302	15	13528	8.9589404	1	0.38240403	53.4489208
GOTERM_CC_FAT	GO:0000785~chromatin	9	2.25	0.043805527	209757_S_AT, 219258_AT, 21	252	200	12782	2.2825	0.99999833	0.46927677	44.9905524
SP_PIR_KEYWORDS	transcription factor	5	1.25	0.044210672	209199_S_AT, 209121_X_AT,	395	65	19235	3.74586173	0.99999953	0.3483442	45.7063705
GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	5	1.25	0.044330894	207069_S_AT, 205453_AT, 21	302	60	13528	3.73289183	1	0.39167845	54.7243167
GOTERM_BP_FAT	GO:0030193~regulation of blood coagulation	4	1	0.045384751	204200_S_AT, 216061_X_AT,	302	36	13528	4.97718911	1	0.39753968	55.5889412
GOTERM_BP_FAT	GO:0043407~negative regulation of MAP kinase activity	4	1	0.045384751	202540_S_AT, 202730_S_AT,	302	36	13528	4.97718911	1	0.39753968	55.5889412
GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	4	1	0.045384751	203764_AT, 203362_S_AT, 20	302	36	13528	4.97718911	1	0.39753968	55.5889412
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	45	11.25	0.045419756	219885_AT, 203504_S_AT, 20	282	1577	12983	1.31373197	1	0.66287831	49.149201
PIR_SUPERFAMILY	PIRSF002610:homeotic protein Hox B2	2	0.5	0.046237994	205453_AT, 214457_AT	174	2	7396	42.5057471	0.99997002	0.96893524	45.2626352
KEGG_PATHWAY	hsa04360:Axon guidance	8	2	0.046283207	211919_S_AT, 210056_AT, 20	131	129	5085	2.40724303	0.9969156	0.6853454	42.0515063
SP_PIR_KEYWORDS	Endocytosis	6	1.5	0.047402123	205498_AT, 203887_S_AT, 20	395	96	19235	3.04351266	0.99999984	0.3603117	48.1046059
UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	15	3.75	0.048139975	201368_AT, 204917_S_AT, 36	395	413	19113	1.75740951	1	0.99336872	55.033876
UP_SEQ_FEATURE	domain:SH2	6	1.5	0.048473066	206204_AT, 210754_S_AT, 20	395	96	19113	3.02420886	1	0.99056152	55.2881102
GOTERM_BP_FAT	GO:0000819~sister chromatid segregation	4	1	0.048603649	203764_AT, 203362_S_AT, 20	302	37	13528	4.84267049	1	0.41784538	58.1344698
GOTERM_BP_FAT	GO:0009611~response to wounding	19	4.75	0.048783615	210754_S_AT, 221087_S_AT,	302	530	13528	1.60584781	1	0.41755688	58.2726479
GOTERM_BP_FAT	GO:0006275~regulation of DNA replication	5	1.25	0.049023819	204200_S_AT, 216061_X_AT,	302	62	13528	3.61247597	1	0.41766807	58.4564063
GOTERM_MF_FAT	GO:0019207~kinase regulator activity	6	1.5	0.051188795	213348_AT, 211580_S_AT, 21	282	93	12983	2.97025852	1	0.69207334	53.4417765
GOTERM_MF_FAT	GO:0030291~protein serine/threonine kinase inhibitor	3	0.75	0.051268566	213348_AT, 219534_X_AT, 20	282	17	12983	8.12453066	1	0.67780143	53.4986932
GOTERM_MF_FAT	GO:0005160~transforming growth factor beta receptor	3	0.75	0.051268566	207069_S_AT, 205210_AT, 20	282	17	12983	8.12453066	1	0.67780143	53.4986932
GOTERM_BP_FAT	GO:0045765~regulation of angiogenesis	5	1.25	0.051469123	209710_AT, 200921_S_AT, 20	302	63	13528	3.55513508	1	0.43207544	60.284177
INTERPRO	IPR001487:Bromodomain	4	1	0.051662434	209762_X_AT, 209049_S_AT,	352	40	16659	4.73267045	1	0.94133162	55.0302457
GOTERM_CC_FAT	GO:0042579~microbody	6	1.5	0.052175678	202540_S_AT, 209424_S_AT,	252	103	12782	2.95469256	0.99999988	0.51490593	51.0795552
GOTERM_CC_FAT	GO:0005777~peroxisome	6	1.5	0.052175678	202540_S_AT, 209424_S_AT,	252	103	12782	2.95469256	0.99999988	0.51490593	51.0795552

GOTERM_BP_FAT	GO:0001501~skeletal system development	13	3.25	0.052584925	205498_AT, 205453_AT, 2138	302	319	13528	1.82548942	1	0.43768416	61.0927606
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	14	3.5	0.052649553	203588_S_AT, 203920_AT, 20	282	363	12983	1.77560909	1	0.67344869	54.473812
GOTERM_BP_FAT	GO:0042493~response to drug	10	2.5	0.052679352	210754_S_AT, 203980_AT, 20	302	216	13528	2.0738288	1	0.43678621	61.1604709
UP_SEQ_FEATURE	sequence variant	264	66	0.052846946	219885_AT, 40687_AT, 21362	395	11992	19113	1.06523167	1	0.99118574	58.5038103
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	7	1.75	0.05322426	209119_X_AT, 209121_X_AT,	302	121	13528	2.59142904	1	0.43872162	61.5490441
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	9	2.25	0.053640014	205498_AT, 207574_S_AT, 20	302	184	13528	2.19104521	1	0.43983168	61.8430495
GOTERM_BP_FAT	GO:0060393~regulation of pathway-restricted SMAD pr	3	0.75	0.053867746	207069_S_AT, 204822_AT, 21	302	17	13528	7.90494741	1	0.43976675	62.0031931
GOTERM_BP_FAT	GO:0006297~nucleotide-excision repair, DNA gap filling	3	0.75	0.053867746	203209_AT, 201202_AT, 2059	302	17	13528	7.90494741	1	0.43976675	62.0031931
GOTERM_BP_FAT	GO:0032103~positive regulation of response to externa	5	1.25	0.05398006	210029_AT, 204200_S_AT, 20	302	64	13528	3.49958609	1	0.4389902	62.0819396
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	45	11.25	0.055728145	219885_AT, 203504_S_AT, 20	282	1601	12983	1.2940383	1	0.68100375	56.5794812
GOTERM_MF_FAT	GO:0005524~ATP binding	42	10.5	0.056181038	219885_AT, 203504_S_AT, 20	282	1477	12983	1.30916608	1	0.6707663	56.8814808
GOTERM_MF_FAT	GO:0060090~molecular adaptor activity	5	1.25	0.057036694	206204_AT, 207112_S_AT, 20	282	67	12983	3.4357468	1	0.66361669	57.4467203
UP_SEQ_FEATURE	DNA-binding region:Homeobox; TALE-type	3	0.75	0.057544211	207480_S_AT, 204069_AT, 21	395	19	19113	7.6401066	1	0.99193582	61.7149085
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	8	2	0.058201295	209424_S_AT, 204154_AT, 21	302	155	13528	2.31198462	1	0.46301543	64.9324671
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	8	2	0.058201295	209424_S_AT, 204154_AT, 21	302	155	13528	2.31198462	1	0.46301543	64.9324671
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from R	6	1.5	0.058520149	219743_AT, 209199_S_AT, 20	302	94	13528	2.8592363	1	0.46339506	65.1393656
SP_PIR_KEYWORDS	ubl conjugation pathway	17	4.25	0.059042986	201294_S_AT, 202870_S_AT,	395	509	19235	1.62639576	1	0.41977505	56.0455388
OMIM_DISEASE	Common variants at 30 loci contribute to polygenic dysl	4	1	0.059062618	202540_S_AT, 203504_S_AT,	74	45	3671	4.40960961	0.99996988	0.99996988	52.4527
INTERPRO	IPR017441:Protein kinase, ATP binding site	16	4	0.059138294	205805_S_AT, 59644_AT, 210	352	455	16659	1.66423576	1	0.95149967	60.085037
GOTERM_BP_FAT	GO:0045646~regulation of erythrocyte differentiation	3	0.75	0.059732988	203332_S_AT, 204249_S_AT,	302	18	13528	7.46578366	1	0.46898314	65.9158877
GOTERM_BP_FAT	GO:0035116~embryonic hindlimb morphogenesis	3	0.75	0.059732988	221884_AT, 205080_AT, 2058	302	18	13528	7.46578366	1	0.46898314	65.9158877
INTERPRO	IPR004182:GRAM	3	0.75	0.059801442	204526_S_AT, 218706_S_AT,	352	19	16659	7.47263756	1	0.94256536	60.5068025
GOTERM_MF_FAT	GO:0042803~protein homodimerization activity	13	3.25	0.059970089	202540_S_AT, 205875_S_AT,	282	334	12983	1.7919374	1	0.67013164	59.3325514
GOTERM_MF_FAT	GO:0001882~nucleoside binding	45	11.25	0.060996241	219885_AT, 203504_S_AT, 20	282	1612	12983	1.28520801	1	0.66453599	59.9736603
KEGG_PATHWAY	hsa00120:Primary bile acid biosynthesis	3	0.75	0.061608763	209424_S_AT, 206932_AT, 20	131	16	5085	7.27814885	0.99957259	0.7255435	51.9118687
INTERPRO	IPR013629:Zinc finger-associated region	2	0.5	0.06189027	209121_X_AT, 209119_X_AT,	352	3	16659	31.5511364	1	0.9376599	61.8082728
INTERPRO	IPR003068:Transcription factor COUP	2	0.5	0.06189027	209121_X_AT, 209119_X_AT,	352	3	16659	31.5511364	1	0.9376599	61.8082728
GOTERM_BP_FAT	GO:0050818~regulation of coagulation	4	1	0.062551539	204200_S_AT, 216061_X_AT,	302	41	13528	4.37021483	1	0.48359465	67.6579551
GOTERM_CC_FAT	GO:0019898~extrinsic to membrane	16	4	0.062654842	205498_AT, 206204_AT, 2189	252	494	12782	1.64282501	1	0.5663518	57.823698
GOTERM_MF_FAT	GO:0032139~dinucleotide insertion or deletion binding	2	0.5	0.063540643	201202_AT, 209421_AT	282	3	12983	30.6926714	1	0.66836703	61.5229506
GOTERM_BP_FAT	GO:0032869~cellular response to insulin stimulus	5	1.25	0.064674342	205498_AT, 211580_S_AT, 20	302	68	13528	3.29372809	1	0.49390482	68.9142065
GOTERM_BP_FAT	GO:0021915~neural tube development	5	1.25	0.064674342	213373_S_AT, 203394_S_AT,	302	68	13528	3.29372809	1	0.49390482	68.9142065
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	5	1.25	0.064674342	204154_AT, 210029_AT, 2042	302	68	13528	3.29372809	1	0.49390482	68.9142065
GOTERM_BP_FAT	GO:0043123~positive regulation of I-kappaB kinase/NF-	6	1.5	0.065201908	206638_AT, 213373_S_AT, 20	302	97	13528	2.77080631	1	0.49528026	69.2191983
GOTERM_BP_FAT	GO:0035283~central nervous system segmentation	2	0.5	0.065280969	214457_AT, 218559_S_AT	302	3	13528	29.8631347	1	0.4941965	69.2646608
GOTERM_BP_FAT	GO:0035284~brain segmentation	2	0.5	0.065280969	214457_AT, 218559_S_AT	302	3	13528	29.8631347	1	0.4941965	69.2646608
GOTERM_BP_FAT	GO:0021570~rhombomere 4 development	2	0.5	0.065280969	205453_AT, 214639_S_AT	302	3	13528	29.8631347	1	0.4941965	69.2646608
GOTERM_BP_FAT	GO:0060433~bronchus development	2	0.5	0.065280969	213844_AT, 211518_S_AT	302	3	13528	29.8631347	1	0.4941965	69.2646608
INTERPRO	IPR012287:Homeodomain-related	10	2.5	0.065349367	205453_AT, 213844_AT, 2113	352	238	16659	1.988517	1	0.93689344	63.8758077
GOTERM_BP_FAT	GO:0051960~regulation of nervous system developmen	9	2.25	0.065381963	210754_S_AT, 203394_S_AT,	302	192	13528	2.09975166	1	0.4932395	69.3226431
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	9	2.25	0.065381963	207112_S_AT, 215775_AT, 20	302	192	13528	2.09975166	1	0.4932395	69.3226431
GOTERM_BP_FAT	GO:0030182~neuron differentiation	16	4	0.065481774	209238_AT, 210056_AT, 2195	302	438	13528	1.63633615	1	0.49228266	69.3798448
GOTERM_BP_FAT	GO:0007098~centrosome cycle	3	0.75	0.065805801	203725_AT, 204444_AT, 2096	302	19	13528	7.07284768	1	0.4925474	69.5648522
GOTERM_BP_FAT	GO:0008206~bile acid metabolic process	3	0.75	0.065805801	209424_S_AT, 209426_S_AT,	302	19	13528	7.07284768	1	0.4925474	69.5648522
GOTERM_BP_FAT	GO:0021545~cranial nerve development	3	0.75	0.065805801	205453_AT, 203394_S_AT, 21	302	19	13528	7.07284768	1	0.4925474	69.5648522
GOTERM_BP_FAT	GO:0048483~autonomic nervous system development	3	0.75	0.065805801	205453_AT, 203394_S_AT, 21	302	19	13528	7.07284768	1	0.4925474	69.5648522
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	30	7.5	0.066028658	210754_S_AT, 207574_S_AT,	302	973	13528	1.38113161	1	0.49226487	69.6914835
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	30	7.5	0.066028658	210754_S_AT, 207574_S_AT,	302	973	13528	1.38113161	1	0.49226487	69.6914835
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	12	3	0.066125656	202730_S_AT, 207069_S_AT,	302	295	13528	1.82215737	1	0.49130797	69.746444
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	42	10.5	0.066480824	219885_AT, 203504_S_AT, 20	282	1497	12983	1.29167555	1	0.67422456	63.2436157
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	9	2.25	0.067024382	210754_S_AT, 207112_S_AT,	302	193	13528	2.08887211	1	0.49464589	70.2512268
GOTERM_BP_FAT	GO:0070302~regulation of stress-activated protein kina	5	1.25	0.067508719	202730_S_AT, 210754_S_AT,	302	69	13528	3.2459929	1	0.49574756	70.519959
GOTERM_BP_FAT	GO:0035270~endocrine system development	5	1.25	0.067508719	209710_AT, 213844_AT, 2033	302	69	13528	3.2459929	1	0.49574756	70.519959

GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	6	1.5	0.067520325	210754_S_AT, 204200_S_AT, 2	302	98	13528	2.74253277	1	0.4943439	70.5263701
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	11	2.75	0.068534928	202540_S_AT, 211538_S_AT, 2	302	262	13528	1.88069359	1	0.49822102	71.0818024
PIR_SUPERFAMILY	PIRSF500849:orphan nuclear receptor COUP-TF	2	0.5	0.068553496	209121_X_AT, 209119_X_AT, 2	174	3	7396	28.3371648	0.99999984	0.97987734	59.5052273
PIR_SUPERFAMILY	PIRSF010369:growth arrest and DNA-damage-inducible	2	0.5	0.068553496	203725_AT, 207574_S_AT, 209	174	3	7396	28.3371648	0.99999984	0.97987734	59.5052273
UP_SEQ_FEATURE	short sequence motif:PDZ-binding	5	1.25	0.069185686	206638_AT, 202669_S_AT, 203	395	75	19113	3.22582278	1	0.99577518	68.6971754
UP_SEQ_FEATURE	repeat:LRR 6	9	2.25	0.069984667	222108_AT, 210567_S_AT, 204	395	210	19113	2.07374322	1	0.99452099	69.1296288
SP_PIR_KEYWORDS	lipoprotein	20	5	0.070080832	209119_X_AT, 209121_X_AT, 2	395	642	19235	1.51701566	1	0.46864111	62.5213097
GOTERM_BP_FAT	GO:0030218~erythrocyte differentiation	4	1	0.070145718	210754_S_AT, 201565_S_AT, 2	302	43	13528	4.16694902	1	0.50511946	71.9433854
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	8	2	0.070224523	202540_S_AT, 211538_S_AT, 2	302	162	13528	2.21208405	1	0.50406577	71.9849094
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	10	2.5	0.070589705	210754_S_AT, 203332_S_AT, 2	302	229	13528	1.95610052	1	0.50448508	72.1765765
KEGG_PATHWAY	hsa04210:Apoptosis	6	1.5	0.070904886	213373_S_AT, 202687_S_AT, 2	131	87	5085	2.67702027	0.99987314	0.7224543	57.1199307
GOTERM_BP_FAT	GO:0033261~regulation of S phase	3	0.75	0.072074113	207069_S_AT, 219258_AT, 204	302	20	13528	6.7192053	1	0.51056923	72.9430211
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	6	1.5	0.072293157	205498_AT, 211580_S_AT, 210	302	100	13528	2.68768212	1	0.51022319	73.0544206
GOTERM_BP_FAT	GO:0051321~meiotic cell cycle	6	1.5	0.072293157	211538_S_AT, 214250_AT, 200	302	100	13528	2.68768212	1	0.51022319	73.0544206
SP_PIR_KEYWORDS	polymorphism	252	63	0.073495073	219885_AT, 213625_AT, 20254	395	11550	19235	1.0624626	1	0.47630532	64.3378781
GOTERM_BP_FAT	GO:0006720~isoprenoid metabolic process	4	1	0.074091518	202540_S_AT, 204488_AT, 202	302	44	13528	4.07224564	1	0.51772932	73.9528035
GOTERM_BP_FAT	GO:0007281~germ cell development	6	1.5	0.07474725	211538_S_AT, 211919_S_AT, 2	302	101	13528	2.66107141	1	0.51950808	74.2732948
GOTERM_BP_FAT	GO:0051276~chromosome organization	17	4.25	0.075726659	202326_AT, 203362_S_AT, 202	302	485	13528	1.57012357	1	0.52284047	74.745069
GOTERM_CC_FAT	GO:0005816~spindle pole body	2	0.5	0.076273117	203362_S_AT, 215509_S_AT, 2	252	4	12782	25.3611111	1	0.62537062	65.3052406
GOTERM_BP_FAT	GO:0032870~cellular response to hormone stimulus	7	1.75	0.076623746	205498_AT, 211580_S_AT, 207	302	133	13528	2.35761589	1	0.52573239	75.1700214
GOTERM_MF_FAT	GO:0046332~SMAD binding	4	1	0.077135049	207069_S_AT, 202704_AT, 205	282	46	12983	4.00339192	1	0.71922235	68.8967112
UP_SEQ_FEATURE	repeat:LRR 4	10	2.5	0.078039371	222108_AT, 204359_AT, 21833	395	252	19113	1.92013261	1	0.99594227	73.1871595
SP_PIR_KEYWORDS	tyrosine-protein kinase	6	1.5	0.078075231	205805_S_AT, 210754_S_AT, 2	395	111	19235	2.63222716	1	0.48889347	66.6468846
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	12	3	0.078344572	211538_S_AT, 209199_S_AT, 2	131	267	5085	1.74457501	0.99995243	0.7118153	60.9110088
GOTERM_BP_FAT	GO:0000086~G2/M transition of mitotic cell cycle	3	0.75	0.078526284	203725_AT, 208159_X_AT, 204	302	21	13528	6.39924314	1	0.53335473	76.0490529
GOTERM_BP_FAT	GO:0003007~heart morphogenesis	5	1.25	0.07947543	219658_AT, 213260_AT, 21825	302	73	13528	3.06813027	1	0.53637466	76.476538
GOTERM_BP_FAT	GO:0007178~transmembrane receptor protein serine/tl	6	1.5	0.079789826	207069_S_AT, 204200_S_AT, 2	302	103	13528	2.60940012	1	0.53640758	76.6165452
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	6	1.5	0.079789826	209121_X_AT, 209119_X_AT, 2	302	103	13528	2.60940012	1	0.53640758	76.6165452
GOTERM_MF_FAT	GO:0000166~nucleotide binding	59	14.75	0.079883242	202540_S_AT, 219885_AT, 203	282	2245	12983	1.20993382	1	0.72189145	70.2173942
UP_SEQ_FEATURE	repeat:TNFR-Cys 3	3	0.75	0.080719951	204781_S_AT, 215719_X_AT, 2	395	23	19113	6.31139241	1	0.99550255	74.4225437
GOTERM_BP_FAT	GO:0018108~peptidyl-tyrosine phosphorylation	4	1	0.082270714	205498_AT, 210754_S_AT, 202	302	46	13528	3.89519148	1	0.54639696	77.6941008
GOTERM_BP_FAT	GO:0001816~cytokine production	4	1	0.082270714	203504_S_AT, 210029_AT, 210	302	46	13528	3.89519148	1	0.54639696	77.6941008
INTERPRO	IPR001611:Leucine-rich repeat	9	2.25	0.08266296	222108_AT, 204359_AT, 21833	352	213	16659	1.99971991	1	0.96425623	72.7444225
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	26	6.5	0.083369538	204315_S_AT, 210754_S_AT, 2	252	952	12782	1.38527077	1	0.64447666	68.6977358
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	8	2	0.083625279	207112_S_AT, 215775_AT, 205	302	169	13528	2.12045927	1	0.55108877	78.2625106
GOTERM_BP_FAT	GO:0043627~response to estrogen stimulus	6	1.5	0.085010078	205498_AT, 204200_S_AT, 213	302	105	13528	2.55969726	1	0.55583835	78.8294729
GOTERM_BP_FAT	GO:0055010~ventricular cardiac muscle morphogenesis	3	0.75	0.085151092	219658_AT, 213260_AT, 20473	302	22	13528	6.10836845	1	0.55503574	78.8864179
GOTERM_BP_FAT	GO:0008633~activation of pro-apoptotic gene products	3	0.75	0.085151092	213373_S_AT, 202687_S_AT, 2	302	22	13528	6.10836845	1	0.55503574	78.8864179
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	7	1.75	0.085535661	209119_X_AT, 209121_X_AT, 2	302	137	13528	2.28878039	1	0.55531264	79.0409832
SMART	SM00297:BROMO	4	1	0.085736354	209762_X_AT, 209049_S_AT, 2	238	40	9079	3.81470588	0.99999995	0.96562153	67.1134902
GOTERM_BP_FAT	GO:0021610~facial nerve morphogenesis	2	0.5	0.086083219	205453_AT, 214639_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0021604~cranial nerve structural organization	2	0.5	0.086083219	205453_AT, 214639_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0021571~rhombomere 5 development	2	0.5	0.086083219	214639_S_AT, 218559_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0021612~facial nerve structural organization	2	0.5	0.086083219	205453_AT, 214639_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0010544~negative regulation of platelet activation	2	0.5	0.086083219	204200_S_AT, 216061_X_AT, 2	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0060438~trachea development	2	0.5	0.086083219	213844_AT, 211518_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
GOTERM_BP_FAT	GO:0060441~branching involved in lung morphogenesis	2	0.5	0.086083219	213844_AT, 211518_S_AT	302	4	13528	22.397351	1	0.55630277	79.2592174
SMART	SM00568:GRAM	3	0.75	0.086760388	204526_S_AT, 218706_S_AT, 2	238	19	9079	6.02321981	0.99999996	0.94179121	67.5675902
COG_ONTOLOGY	Cell division and chromosome partitioning	6	1.5	0.08685498	212096_S_AT, 211580_S_AT, 2	45	106	1950	2.45283019	0.74408466	0.74408466	46.8321702
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	6	1.5	0.087014817	219743_AT, 209757_S_AT, 207	395	114	19113	2.5467022	1	0.99612486	77.1168904
UP_SEQ_FEATURE	active site:Proton acceptor	20	5	0.087706678	210754_S_AT, 205698_S_AT, 2	395	658	19113	1.47073987	1	0.99516937	77.3961988
GOTERM_MF_FAT	GO:0019955~cytokine binding	6	1.5	0.087770583	211919_S_AT, 205498_AT, 203	282	109	12983	2.53425727	1	0.74661696	73.7235237
UP_SEQ_FEATURE	repeat:LRR 15	4	1	0.087806231	218326_S_AT, 218816_AT, 205	395	51	19113	3.79508563	1	0.99388145	77.4361246

SMART	SM00389:HOX	11	2.75	0.088100713	205453_AT, 213844_AT, 21134	238	235	9079	1.78560701	0.99999997	0.91599841	68.1532364
GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	5	1.25	0.089094902	210029_AT, 201042_AT, 20398	302	76	13528	2.94701987	1	0.56790941	80.4217572
GOTERM_MF_FAT	GO:0005070~SH3/SH2 adaptor activity	4	1	0.08939473	206204_AT, 207112_S_AT, 202	282	49	12983	3.75828629	1	0.74376495	74.3960067
PIR_SUPERFAMILY	PIRSF037625:HERC protein	2	0.5	0.090349823	219863_AT, 219352_AT	174	4	7396	21.2528736	1	0.98449492	70.043151
GOTERM_BP_FAT	GO:0043122~regulation of I-kappaB kinase/NF-kappaB c	6	1.5	0.090405922	206638_AT, 213373_S_AT, 202	302	107	13528	2.51185245	1	0.57205298	80.9083855
GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transc	4	1	0.090819638	219743_AT, 213348_AT, 20919	302	48	13528	3.73289183	1	0.57238213	81.0595676
GOTERM_BP_FAT	GO:0018212~peptidyl-tyrosine modification	4	1	0.090819638	205498_AT, 210754_S_AT, 202	302	48	13528	3.73289183	1	0.57238213	81.0595676
GOTERM_BP_FAT	GO:0006909~phagocytosis	4	1	0.090819638	203504_S_AT, 209710_AT, 203	302	48	13528	3.73289183	1	0.57238213	81.0595676
UP_SEQ_FEATURE	zinc finger region:PHD-type	4	1	0.091826761	209762_X_AT, 209049_S_AT, 2	395	52	19113	3.72210321	1	0.99395881	78.9943693
GOTERM_BP_FAT	GO:0030195~negative regulation of blood coagulation	3	0.75	0.091937722	204200_S_AT, 216061_X_AT, 2	302	23	13528	5.84278722	1	0.57564388	81.4625157
GOTERM_BP_FAT	GO:0001974~blood vessel remodeling	3	0.75	0.091937722	201042_AT, 205581_S_AT, 213	302	23	13528	5.84278722	1	0.57564388	81.4625157
GOTERM_BP_FAT	GO:0045321~leukocyte activation	10	2.5	0.092170511	215719_X_AT, 210754_S_AT, 2	302	242	13528	1.85102074	1	0.57520793	81.5453883
UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	7	1.75	0.092759989	201368_AT, 209119_X_AT, 209	395	151	19113	2.2431218	1	0.99290621	79.3413294
UP_SEQ_FEATURE	repeat:TNFR-Cys 1	3	0.75	0.093212371	204781_S_AT, 215719_X_AT, 2	395	25	19113	5.80648101	1	0.99156136	79.5075766
UP_SEQ_FEATURE	repeat:TNFR-Cys 2	3	0.75	0.093212371	204781_S_AT, 215719_X_AT, 2	395	25	19113	5.80648101	1	0.99156136	79.5075766
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bH	6	1.5	0.093273134	219743_AT, 209757_S_AT, 207	352	114	16659	2.49087919	1	0.97216863	77.1264006
GOTERM_CC_FAT	GO:0001950~plasma membrane enriched fraction	2	0.5	0.094418011	209238_AT, 216985_S_AT, 216	252	5	12782	20.2888889	1	0.67790597	73.3739257
GOTERM_CC_FAT	GO:0031264~death-inducing signaling complex	2	0.5	0.094418011	213373_S_AT, 204781_S_AT, 2	252	5	12782	20.2888889	1	0.67790597	73.3739257
SP_PIR_KEYWORDS	Acyltransferase	7	1.75	0.095076668	214440_AT, 204573_AT, 2018	395	153	19235	2.22793083	1	0.55257023	74.0612736
GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	7	1.75	0.095098044	209121_X_AT, 209119_X_AT,	282	145	12983	2.22257276	1	0.75702086	76.632636
GOTERM_BP_FAT	GO:0034101~erythrocyte homeostasis	4	1	0.095227427	210754_S_AT, 201565_S_AT, 2	302	49	13528	3.65671037	1	0.58630423	82.6017402
GOTERM_BP_FAT	GO:0009310~amine catabolic process	5	1.25	0.09580481	204154_AT, 210029_AT, 20429	302	78	13528	2.87145526	1	0.58722986	82.7947492
GOTERM_BP_FAT	GO:0007517~muscle organ development	9	2.25	0.098503735	209199_S_AT, 209119_X_AT, 2	302	211	13528	1.91067449	1	0.5965349	83.6704852
UP_SEQ_FEATURE	region of interest:Fatty acid binding	2	0.5	0.098918364	203980_AT, 202345_S_AT	395	5	19113	19.3549367	1	0.9924596	81.4995601
UP_SEQ_FEATURE	DNA-binding region:Homeobox	8	2	0.099013119	205453_AT, 213844_AT, 2062	395	190	19113	2.03736176	1	0.99100615	81.5310513
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	7	1.75	0.099918109	205053_AT, 219258_AT, 2155	252	162	12782	2.19170096	1	0.68587517	75.4525671

Supplementary Table 9. Genes inhibited by Ox-PAPC by 1.5 fold and the inhibition was reversed by ADAM10 silencing by 1.2 fold.

Values are represented as log2 scale.

						cutoff by -log2(1.5)		**cutoff by log2(1.2)**
ProbeSetID	**Gene.Symbol**	**log2(sc+C)**	**log2(sc+Ox40)**	**log2(ADAM10si+C)**	**log2(ADAM10si+Ox50)**	**log2[(sc+Ox40)/(sc+C)]**	**log2[(ADAM10si+Ox40) /(ADAM10si+C)]**	**The effects ADAM10si on Fold induction by Ox40 (H-G))**
219825_at	CYP26B1	8.388583579	3.874179133	6.405008194	3.705304775	-4.514404446	-2.69970342	**1.814701026**
206932_at	CH25H	4.902128632	3.492004581	3.305145563	3.032174062	-1.410124051	-0.272971501	**1.137152551**
202688_at	TNFSF10	10.00585203	7.918398744	9.931076725	8.87316092	-2.087453291	-1.057915805	**1.029537486**
214329_x_at	TNFSF10	6.577768737	4.658339698	6.488819738	5.559067062	-1.919429039	-0.929752676	**0.989676363**
202687_s_at	TNFSF10	8.100263694	5.92531378	7.891517735	6.691890896	-2.174949913	-1.199626839	**0.975323074**
208337_s_at	NR5A2	5.092764069	3.927312061	3.917792351	3.653257786	-1.165452009	-0.264534565	**0.900917444**
218736_s_at	PALMD	9.872387001	7.961946976	9.964117478	8.896719754	-1.910440025	-1.067397724	**0.843042301**
220351_at	CCRL1	5.58923612	3.833576082	4.937351575	3.998474307	-1.755660038	-0.938877268	**0.81678277**
209305_s_at	GADD45B	7.266582753	6.574602086	6.578300271	6.570348807	-0.691980667	-0.007951464	**0.684029203**
210174_at	NR5A2	6.859203146	5.679771264	5.88677227	5.37979164	-1.179431882	-0.50698063	**0.672451252**
222126_at	AGFG2	5.931399855	5.056773844	5.536739262	5.333108622	-0.874626011	-0.20363064	**0.670995371**
205528_s_at	RUNX1T1	6.575935984	5.1158491	6.521932545	5.72974096	-1.460086884	-0.792191586	**0.667895299**
204510_at	CDC7	4.600088597	3.829621409	3.843249988	3.728640365	-0.770467188	-0.114609623	**0.655857565**
204200_s_at	PDGFB	6.153945261	5.292404042	5.818717339	5.566242715	-0.861541219	-0.252474624	**0.609066595**
204573_at	CROT	5.768667893	4.7894214	5.675794288	5.302245721	-0.979246493	-0.373548566	**0.605697927**
218559_s_at	MAFB	6.178769687	4.552070662	4.996160792	3.970683428	-1.626699024	-1.025477364	**0.60122166**
203504_s_at	ABCA1	5.82027563	4.537585177	5.223060063	4.527634938	-1.282690454	-0.695425125	**0.587265328**
212182_at	NUDT4 /// NUD	4.223351991	3.270118343	3.662695527	3.274764805	-0.953233648	-0.387930722	**0.565302926**
209732_at	CLEC2B	10.19845468	9.590932407	10.13457006	10.08964635	-0.607522268	-0.044923713	**0.562598555**
207354_at	CCL16	4.925519905	3.511236004	4.318421411	3.462159344	-1.414283901	-0.856262067	**0.558021835**
204635_at	RPS6KA5	5.683074432	4.716303266	5.12605279	4.71715187	-0.966771166	-0.40890092	**0.557870247**
208343_s_at	NR5A2	5.576855258	4.552681106	4.811859613	4.338440935	-1.024174153	-0.473418678	**0.550755475**
215775_at	---	7.707925002	7.033262335	7.598009469	7.470935301	-0.674662667	-0.127074168	**0.547588498**
218711_s_at	SDPR	8.986571412	7.284239337	8.192686451	7.034226551	-1.702332074	-1.1584599	**0.543872174**
40687_at	GJA4	5.219621926	3.780723815	4.388183284	3.48444866	-1.438898111	-0.903734624	**0.535163487**
207559_s_at	ZMYM3	6.238409276	5.643307388	5.987153312	5.918685448	-0.595101888	-0.068467864	**0.526634024**
206382_s_at	BDNF	5.11913362	4.343523798	4.806221991	4.556533195	-0.775609822	-0.249688796	**0.525921026**
201295_s_at	WSB1	8.65114204	7.567572216	7.355393998	6.785817343	-1.083569824	-0.569576655	**0.513993169**
218999_at	TMEM140	8.186651709	6.974415048	8.541039483	7.837502282	-1.212236661	-0.703537201	**0.50869946**
216061_x_at	PDGFB	5.947930189	5.130552322	5.744645627	5.435470066	-0.817377868	-0.309175561	**0.508202307**
204249_s_at	LMO2	9.59814078	8.488072873	9.189193959	8.58056346	-1.110067907	-0.608630499	**0.501437408**
202540_s_at	HMGCR	6.110860472	5.205580138	5.901114097	5.493614957	-0.905280334	-0.40749914	**0.497781193**
213348_at	CDKN1C	5.541727399	4.828329874	4.612126505	4.37437469	-0.713397525	-0.237751816	**0.47564571**
206127_at	ELK3	5.277435106	4.069172981	5.174075106	4.439662807	-1.208262125	-0.734412299	**0.473849826**
221756_at	PIK3IP1	6.398640194	4.917792485	6.205370136	5.191715421	-1.480847708	-1.013654715	**0.467192993**
203980_at	FABP4	9.551390224	8.775171069	8.873671177	8.556276474	-0.776219155	-0.317394703	**0.458824452**
221123_x_at	ZNF395	5.966883225	5.205394821	5.681289691	5.377925557	-0.761488405	-0.303364133	**0.458124272**
204904_at	GJA4	6.567220234	5.302604681	5.753143787	4.935297198	-1.264615552	-0.817846589	**0.446768963**

201294_s_at	WSB1	8.967550792	7.922024308	8.09657401	7.496520381	-1.045526483	-0.600053629	**0.445472854**
212353_at	SULF1	6.855906098	5.810023145	5.93881689	5.327721814	-1.045882953	-0.611095076	**0.434787877**
217028_at	CXCR4	9.168396251	7.870083624	9.729104608	8.865188808	-1.298312627	-0.8639158	**0.434396827**
203153_at	IFIT1	6.755179647	5.128565071	8.93863775	7.744305482	-1.626614576	-1.194332269	**0.432282307**
204315_s_at	GTSE1	4.71915756	3.912481748	4.077105924	3.699333729	-0.806675812	-0.377772195	**0.428903617**
217164_at	---	5.564255348	4.805740911	5.491066963	5.15751455	-0.758514438	-0.333552413	**0.424962025**
203508_at	TNFRSF1B	5.033324674	4.36146959	5.145958078	4.892185991	-0.671855085	-0.253772088	**0.418082997**
220751_s_at	C5orf4	5.586742546	4.176352579	4.78385966	3.779427263	-1.410389967	-1.004432397	**0.40595757**
206289_at	HOXA4	5.157402286	4.386646609	5.091557755	4.725101148	-0.770755677	-0.366456607	**0.40429907**
48031_r_at	C5orf4	5.02196417	4.154555391	4.510801792	4.042744089	-0.867408779	-0.468057703	**0.399351076**
203395_s_at	HES1	5.17190263	4.295061333	4.977285049	4.498700714	-0.876841297	-0.478584335	**0.398256962**
212095_s_at	MTUS1	8.627630812	7.438351547	8.519103305	7.722012328	-1.189279265	-0.797090977	**0.392188288**
209201_x_at	CXCR4	9.193491101	7.850086312	10.05970085	9.107454797	-1.343404789	-0.952246049	**0.39115874**
208530_s_at	RARB	8.054411271	6.787652059	7.731879449	6.853821704	-1.266759212	-0.878057745	**0.388701467**
201565_s_at	ID2	6.789876436	5.904185564	6.778758573	6.281124544	-0.885690872	-0.49763403	**0.388056842**
219901_at	FGD6	5.171130223	4.498066081	4.658349133	4.371595081	-0.673064141	-0.286754052	**0.386310089**
204917_s_at	MLLT3	4.678187493	4.016838419	4.605165363	4.316111928	-0.661349074	-0.289053434	**0.37229564**
203408_s_at	SATB1	8.163533151	7.49097368	7.879846124	7.576359468	-0.672559471	-0.303486656	**0.369072815**
207574_s_at	GADD45B	7.19994109	6.489153134	6.590610483	6.248586564	-0.710787956	-0.342023919	**0.368764037**
219427_at	FAT4	5.64566854	4.533326471	5.048825141	4.302269333	-1.112342069	-0.746555808	**0.365786261**
205466_s_at	HS3ST1	3.81994569	3.160238065	3.34849638	3.045166868	-0.659707625	-0.303329513	**0.356378113**
209050_s_at	RALGDS	7.624500766	6.438319708	7.301922361	6.456316694	-1.186181059	-0.845605667	**0.340575391**
212914_at	CBX7	4.872461517	4.0963296	4.610036707	4.161873936	-0.776131918	-0.448162772	**0.327969146**
201368_at	ZFP36L2	9.254404722	7.915923119	8.769023562	7.754696234	-1.338481603	-1.014327328	**0.324154275**
203917_at	CXADR	6.862480984	5.914302556	7.215690753	6.591601425	-0.948178428	-0.624089327	**0.3240891**
204358_s_at	FLRT2	7.692398088	6.995535537	7.552280593	7.178880239	-0.696862552	-0.373400354	**0.323462198**
216614_at	---	3.950212039	3.309138572	3.529984341	3.211080856	-0.641073467	-0.318903485	**0.322169982**
222372_at	---	6.026834029	5.207008809	5.893422847	5.39233812	-0.81982522	-0.501084727	**0.318740493**
217504_at	ABCA6	5.33551132	4.531649994	4.919160732	4.432864654	-0.803861326	-0.486296078	**0.317565248**
201010_s_at	TXNIP	8.444760104	7.713328182	8.014070624	7.598933037	-0.731431921	-0.415137588	**0.316294334**
217502_at	IFIT2	5.127427357	3.413431574	5.288333692	3.889822268	-1.713995782	-1.398511425	**0.315484358**
209662_at	CETN3	6.902853516	6.232713978	6.137874516	5.778875703	-0.670139538	-0.358998813	**0.311140725**
203588_s_at	TFDP2	7.365631727	6.7168774	7.299789483	6.961992147	-0.648754326	-0.337797337	**0.31095699**
211792_s_at	CDKN2C	5.374801921	4.689999856	5.223896377	4.847657374	-0.684802065	-0.376239003	**0.308563062**
201367_s_at	ZFP36L2	5.492056686	4.753396279	5.186398	4.755773063	-0.738660407	-0.430624937	**0.308035471**
213094_at	GPR126	7.205384144	6.038900098	5.695781707	4.830745567	-1.166484046	-0.865036141	**0.301447905**
209304_x_at	GADD45B	5.777573616	5.127027171	5.29040807	4.941021355	-0.650546445	-0.349386715	**0.30115973**
201009_s_at	TXNIP	7.879983251	7.106602098	7.731911725	7.256417543	-0.773381153	-0.475494182	**0.29788697**
212151_at	PBX1	5.175311466	4.485811241	4.515389855	4.119314304	-0.689500225	-0.396075551	**0.293424674**
209051_s_at	RALGDS	5.588744177	4.541156026	4.905130662	4.149138192	-1.04758815	-0.755992469	**0.291595681**
211538_s_at	HSPA2	5.679489779	4.696542777	5.040997279	4.347929205	-0.982947001	-0.693068074	**0.289878927**
214457_at	HOXA2	4.329359997	3.619391569	3.972219557	3.547024676	-0.709968427	-0.425194881	**0.284773546**
204589_at	NUAK1	9.415043235	8.191022683	9.465056999	8.525443065	-1.224020552	-0.939613934	**0.284406617**
212344_at	SULF1	7.944694366	7.125295615	7.38551489	6.850395955	-0.819398751	-0.535118935	**0.284279815**
212909_at	LYPD1	5.969289007	4.910058417	5.868567909	5.093242568	-1.05923059	-0.775325341	**0.283905249**

204159_at	CDKN2C	5.350781188	4.364504183	4.814646984	4.112209615	-0.986277005	-0.702437369	**0.283839636**
206303_s_at	NUDT4	8.923246541	7.964207217	8.528036188	7.850447281	-0.959039324	-0.677588908	**0.281450416**
217317_s_at	HERC2P2 /// HE	10.00146518	9.290747442	9.398807008	8.968387762	-0.710717736	-0.430419246	**0.280298489**
212093_s_at	MTUS1	9.532434691	8.310260553	9.529887295	8.587978565	-1.222174139	-0.94190873	**0.280265408**
219147_s_at	C9orf95	8.076365295	7.271388057	7.289462972	6.761353211	-0.804977239	-0.528109761	**0.276867477**
204653_at	TFAP2A	6.639573699	5.945551823	6.966380316	6.548630424	-0.694021876	-0.417749892	**0.276271984**
202481_at	DHRS3	7.658698697	6.223374954	7.586713937	6.426657018	-1.435323743	-1.160056919	**0.275266823**
219416_at	SCARA3	5.354622485	4.769157812	5.323441921	5.009287229	-0.585464673	-0.314154692	**0.271309981**
207220_at	ART4	6.055558984	4.86241372	6.594490327	5.671897576	-1.193145264	-0.922592751	**0.270552513**

Supplementary Table 10. Gene categories of genes inhibited by Ox-PAPC by 1.5 fold and the inhibition was reversed by ADAM10 silencing by 1.2 fold.

DAVID analysis used for the identification of gene categories.

http://david.abcc.ncifcrf.gov/home.jsp

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	chromosomal rearrangement	10	10.30927835	9.88E-06	204917_S_AT, 204200_S_AT, 2160	96	279	19235	7.18152628	0.00159871	0.00159871	0.01195033
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	17	17.5257732	1.01E-05	219534_X_AT, 204526_S_AT, 2039	80	787	13528	3.65273189	0.00992102	0.00992102	0.01591873
SP_PIR_KEYWORDS	Proto-oncogene	9	9.278350515	1.84E-05	204917_S_AT, 204200_S_AT, 2160	96	230	19235	7.84035326	0.00297591	0.00148906	0.02225906
GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	9	9.278350515	3.66E-05	203504_S_AT, 203920_AT, 206382	80	216	13528	7.04583333	0.035503	0.01791192	0.05770175
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	9	9.278350515	3.83E-04	213348_AT, 219534_X_AT, 207826	74	316	12983	4.99687821	0.07839493	0.07839493	0.48417571
GOTERM_BP_FAT	GO:0048568~embryonic organ development	7	7.216494845	5.00E-04	206289_AT, 208530_S_AT, 214457	80	172	13528	6.88197674	0.38966487	0.15175211	0.78526664
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	20	20.6185567	5.27E-04	201368_AT, 219534_X_AT, 202704	74	1512	12983	2.32071357	0.10617853	0.05457868	0.66511482
GOTERM_BP_FAT	GO:0007389~pattern specification process	8	8.24742268	9.31E-04	204917_S_AT, 206289_AT, 209201	80	267	13528	5.06666667	0.60172522	0.20558817	1.45919227
GOTERM_BP_FAT	GO:0003002~regionalization	7	7.216494845	0.001016704	204917_S_AT, 206289_AT, 214457	80	197	13528	6.00862944	0.63396057	0.1820899	1.59189964
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	22	22.68041237	0.001320192	201368_AT, 204917_S_AT, 219534	80	1813	13528	2.05195808	0.72888481	0.19550075	2.06246566
GOTERM_BP_FAT	GO:0007379~segment specification	3	3.092783505	0.001789832	204917_S_AT, 214457_AT, 218559	80	11	13528	46.1181818	0.82965652	0.22341435	2.7865015
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	8	8.24742268	0.002076665	206289_AT, 208530_S_AT, 214457	80	307	13528	4.40651466	0.87176336	0.22642662	3.22623722
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polyme	12	12.37113402	0.003205474	203920_AT, 219534_X_AT, 201565	80	727	13528	2.7911967	0.95808433	0.29703984	4.93875872
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	8	8.24742268	0.003971274	202540_S_AT, 207574_S_AT, 2195	80	345	13528	3.92115942	0.9803844	0.32506779	6.08435088
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RN	7	7.216494845	0.00457981	213348_AT, 219534_X_AT, 207826	80	266	13528	4.45	0.98927573	0.33787112	6.98545236
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	8	8.24742268	0.00478227	202540_S_AT, 207574_S_AT, 2195	80	357	13528	3.78935574	0.99122823	0.32610752	7.28344839
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	8	8.24742268	0.005078667	213348_AT, 219534_X_AT, 204159	80	361	13528	3.74736842	0.99346451	0.32088322	7.71809765
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	9	9.278350515	0.005239351	213348_AT, 219534_X_AT, 207826	80	459	13528	3.31568627	0.99442848	0.30976316	7.95293183
GOTERM_BP_FAT	GO:0048545~response to steroid hormone stimulus	6	6.18556701	0.0052755	215719_X_AT, 204200_S_AT, 2160	80	192	13528	5.284375	0.99462497	0.29418309	8.00568578
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic p	10	10.30927835	0.00528499	219534_X_AT, 203980_AT, 201565	80	561	13528	3.01426025	0.9946754	0.27907024	8.01953037
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	20	20.6185567	0.005673596	204917_S_AT, 203588_S_AT, 2039	80	1773	13528	1.90750141	0.9963807	0.28156139	8.58477162
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	8	8.24742268	0.005965445	202540_S_AT, 207574_S_AT, 2195	80	372	13528	3.63655914	0.9972919	0.27993746	9.00713518
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	10	10.30927835	0.006052648	219534_X_AT, 203980_AT, 201565	80	573	13528	2.95113438	0.99751675	0.27071745	9.13297938
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	6	6.18556701	0.006518078	202540_S_AT, 203504_S_AT, 2094	80	202	13528	5.02277228	0.99843668	0.2760602	9.80190292
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	5	5.154639175	0.007598865	206289_AT, 208530_S_AT, 214457	80	133	13528	6.35714286	0.99946666	0.30153749	11.3374777
GOTERM_MF_FAT	GO:0003700~transcription factor activity	13	13.40206186	0.007780193	201368_AT, 203588_S_AT, 203920	74	975	12983	2.33927928	0.81055592	0.42567153	9.4172946
GOTERM_BP_FAT	GO:0045637~regulation of myeloid cell differentiation	4	4.12371134	0.007924291	215719_X_AT, 201565_S_AT, 2042	80	70	13528	9.66285714	0.99961427	0.30043057	11.7950223
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	9	9.278350515	0.009026752	213348_AT, 219534_X_AT, 207826	80	504	13528	3.01964286	0.99987142	0.3226171	13.3286853
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	5	5.154639175	0.009069501	204917_S_AT, 206289_AT, 214457	80	140	13528	6.03928571	0.99987678	0.31275506	13.3876478
GOTERM_BP_FAT	GO:0035295~tube development	6	6.18556701	0.009250268	206382_S_AT, 209201_X_AT, 2170	80	220	13528	4.61181818	0.9998971	0.3073787	13.6365627
SP_PIR_KEYWORDS	transcription regulation	19	19.58762887	0.009686545	204917_S_AT, 203588_S_AT, 2039	96	2026	19235	1.87903607	0.79337918	0.40881325	11.1111443
UP_SEQ_FEATURE	region of interest:Ligand-binding	3	3.092783505	0.009713802	203920_AT, 208337_S_AT, 208530	96	30	19113	19.909375	0.9853986	0.9853986	12.8658209
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleosid	9	9.278350515	0.009872982	213348_AT, 219534_X_AT, 207826	80	512	13528	2.97246094	0.99994471	0.31410974	14.4889159
SP_PIR_KEYWORDS	peroxisome	4	4.12371134	0.010057446	202540_S_AT, 209424_S_AT, 2045	96	90	19235	8.90509259	0.8055451	0.33594397	11.5131509
GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	4	4.12371134	0.010285903	206289_AT, 214457_AT, 204653_A	80	77	13528	8.78441558	0.99996339	0.31500037	15.0497593
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound m	9	9.278350515	0.010660987	213348_AT, 219534_X_AT, 207826	80	519	13528	2.93236994	0.99997482	0.31490661	15.556222
KEGG_PATHWAY	hsa04110:Cell cycle	5	5.154639175	0.011159648	213348_AT, 203588_S_AT, 219534	37	125	5085	5.4972973	0.46658392	0.46658392	10.4894807
KEGG_PATHWAY	hsa04115:p53 signaling pathway	4	4.12371134	0.011917746	204315_S_AT, 215719_X_AT, 2075	37	68	5085	8.08426073	0.48900864	0.2851634	11.1647951
SP_PIR_KEYWORDS	Transcription	19	19.58762887	0.012004098	204917_S_AT, 203588_S_AT, 2039	96	2071	19235	1.83820719	0.85863783	0.32381328	13.5958466
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	7	7.216494845	0.012775576	204315_S_AT, 213348_AT, 219534	80	331	13528	3.57613293	0.99999696	0.35470961	18.3589723
GOTERM_CC_FAT	GO:0005777~peroxisome	4	4.12371134	0.013044551	202540_S_AT, 209424_S_AT, 2045	62	103	12782	8.0062637	0.80371094	0.80371094	14.0687165
GOTERM_CC_FAT	GO:0042579~microbody	4	4.12371134	0.013044551	202540_S_AT, 209424_S_AT, 2045	62	103	12782	8.0062637	0.80371094	0.80371094	14.0687165
GOTERM_BP_FAT	GO:0044092~negative regulation of molecular function	7	7.216494845	0.013308535	202540_S_AT, 213348_AT, 219534	80	334	13528	3.54401198	0.99999822	0.35675981	19.0514975
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	4	4.12371134	0.013435353	202540_S_AT, 209424_S_AT, 2069	80	85	13528	7.95764706	0.99999843	0.35020622	19.2154725
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosyr	9	9.278350515	0.014288476	213348_AT, 219534_X_AT, 207826	80	547	13528	2.78226691	0.99999933	0.35875186	20.3104934
GOTERM_BP_FAT	GO:0007049~cell cycle	11	11.34020619	0.014540078	211538_S_AT, 204315_S_AT, 2035	80	776	13528	2.39703608	0.99999948	0.35500773	20.6307712
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	4	4.12371134	0.015653102	202540_S_AT, 213348_AT, 219534	80	90	13528	7.51555556	0.99999983	0.36774236	22.0331902
GOTERM_BP_FAT	GO:0045665~negative regulation of neuron differentiation	3	3.092783505	0.015814517	214457_AT, 203395_S_AT, 212151	80	33	13528	15.3727273	0.99999986	0.36236475	22.2346372
GOTERM_BP_FAT	GO:0001709~cell fate determination	3	3.092783505	0.015814517	214457_AT, 203395_S_AT, 219825	80	33	13528	15.3727273	0.99999986	0.36236475	22.2346372
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal tı	6	6.18556701	0.015897901	204526_S_AT, 209051_S_AT, 2127	80	252	13528	4.02619048	0.99999987	0.35584408	22.3385101

GOTERM_BP_FAT	GO:0035284~brain segmentation	2	2.06185567	0.017418391	214457_AT, 218559_S_AT	80	3	13528	112.733333	0.99999997	0.3745079	24.2099634
GOTERM_BP_FAT	GO:0035283~central nervous system segmentation	2	2.06185567	0.017418391	214457_AT, 218559_S_AT	80	3	13528	112.733333	0.99999997	0.3745079	24.2099634
GOTERM_BP_FAT	GO:0001657~ureteric bud development	3	3.092783505	0.017688088	206382_S_AT, 208530_S_AT, 2121	80	35	13528	14.4942857	0.99999998	0.37124034	24.5374702
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-de	7	7.216494845	0.017703261	213348_AT, 219534_X_AT, 207826	80	356	13528	3.325	0.99999998	0.36396386	24.5558557
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic pr	10	10.30927835	0.018056717	203504_S_AT, 203920_AT, 215775	80	685	13528	2.46861314	0.99999998	0.36242075	24.9829696
GOTERM_BP_FAT	GO:0043583~ear development	4	4.12371134	0.018065238	206382_S_AT, 214457_AT, 203395	80	95	13528	7.12	0.99999998	0.35551797	24.9932389
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	4	4.12371134	0.018571124	202540_S_AT, 213348_AT, 219534	80	96	13528	7.04583333	0.99999999	0.35658866	25.6005322
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	6	6.18556701	0.018912816	204526_S_AT, 209051_S_AT, 2127	74	274	12983	3.84188203	0.9828715	0.63823226	21.4778344
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	8	8.24742268	0.01892557	202540_S_AT, 207574_S_AT, 2195	80	466	13528	2.90300429	0.99999999	0.35532922	26.0232815
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic proces	7	7.216494845	0.019057073	213348_AT, 219534_X_AT, 207826	80	362	13528	3.2698895	0.99999999	0.35082172	26.1795528
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	10	10.30927835	0.019648031	203504_S_AT, 203920_AT, 215775	80	695	13528	2.43309353	1	0.35317383	26.8780072
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	9	9.278350515	0.020250579	203920_AT, 206289_AT, 208337_S	74	607	12983	2.60134022	0.9871915	0.58168865	22.8229352
SP_PIR_KEYWORDS	dna-binding	17	17.5257732	0.020251364	201368_AT, 203588_S_AT, 203920	96	1868	19235	1.82344642	0.96364399	0.42443281	21.9302027
GOTERM_BP_FAT	GO:0055092~sterol homeostasis	3	3.092783505	0.020665102	203504_S_AT, 203980_AT, 208337	80	38	13528	13.35	1	0.36141516	28.0656126
GOTERM_BP_FAT	GO:0042632~cholesterol homeostasis	3	3.092783505	0.020665102	203504_S_AT, 203980_AT, 208337	80	38	13528	13.35	1	0.36141516	28.0656126
SP_PIR_KEYWORDS	repressor	7	7.216494845	0.020798409	209431_S_AT, 203395_S_AT, 2034	96	435	19235	3.22425766	0.96678901	0.3851707	22.4560379
UP_SEQ_FEATURE	zinc finger region:NR C4-type	3	3.092783505	0.021068997	203920_AT, 208337_S_AT, 208530	96	45	19113	13.2729167	0.999901	0.99004993	25.9504977
UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	3	3.092783505	0.021068997	203920_AT, 208337_S_AT, 208530	96	45	19113	13.2729167	0.999901	0.99004993	25.9504977
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA	7	7.216494845	0.021218644	203920_AT, 208337_S_AT, 208530	80	371	13528	3.19056604	1	0.36290929	28.7043524
GOTERM_BP_FAT	GO:0045449~regulation of transcription	24	24.74226804	0.021947172	204917_S_AT, 219534_X_AT, 2033	80	2601	13528	1.56032295	1	0.36667844	29.5369159
OMIM_DISEASE	Common variants at 30 loci contribute to polygenic dyslipi	3	3.092783505	0.022012432	202540_S_AT, 203504_S_AT, 2185	20	45	3671	12.2366667	0.64080245	0.64080245	18.9724846
GOTERM_BP_FAT	GO:0051329~interphase of mitotic cell cycle	4	4.12371134	0.02233217	204315_S_AT, 213348_AT, 219534	80	103	13528	6.56699029	1	0.36580168	29.9732059
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	4	4.12371134	0.022900917	204526_S_AT, 212796_S_AT, 2199	80	104	13528	6.50384615	1	0.367316	30.6130981
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	8	8.24742268	0.022978845	202540_S_AT, 207574_S_AT, 2195	80	485	13528	2.78927835	1	0.36259699	30.7003468
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	8	8.24742268	0.022978845	202540_S_AT, 207574_S_AT, 2195	80	485	13528	2.78927835	1	0.36259699	30.7003468
GOTERM_MF_FAT	GO:0019955~cytokine binding	4	4.12371134	0.023418513	203508_AT, 209201_X_AT, 217028	74	109	12983	6.43838334	0.99357449	0.56882726	25.9240545
GOTERM_BP_FAT	GO:0006915~apoptosis	9	9.278350515	0.023929345	215719_X_AT, 207574_S_AT, 2026	80	602	13528	2.52807309	1	0.36883361	31.7562911
INTERPRO	IPR001628:Zinc finger, nuclear hormone receptor-type	3	3.092783505	0.024049719	203920_AT, 208337_S_AT, 208530	88	46	16659	12.3460968	0.99755296	0.99755296	27.0682736
GOTERM_BP_FAT	GO:0051325~interphase	4	4.12371134	0.024062017	204315_S_AT, 213348_AT, 219534	80	106	13528	6.38113208	1	0.36494077	31.9024762
GOTERM_BP_FAT	GO:0051789~response to protein stimulus	4	4.12371134	0.024654368	211538_S_AT, 215719_X_AT, 2078	80	107	13528	6.32149533	1	0.36665332	32.551592
GOTERM_MF_FAT	GO:0008134~transcription factor binding	8	8.24742268	0.024885843	203588_S_AT, 203920_AT, 207826	74	513	12983	2.73599916	0.99533541	0.53551325	27.3211822
INTERPRO	IPR001723:Steroid hormone receptor	3	3.092783505	0.025034608	203920_AT, 208337_S_AT, 208530	88	47	16659	12.0834139	0.99809308	0.95633171	28.0168474
GOTERM_BP_FAT	GO:0012501~programmed cell death	9	9.278350515	0.02586137	215719_X_AT, 207574_S_AT, 2026	80	611	13528	2.4908347	1	0.37542071	33.8563662
INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	3	3.092783505	0.026035759	203920_AT, 208337_S_AT, 208530	88	48	16659	11.8316761	0.99852047	0.88605166	28.9694027
INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, core	3	3.092783505	0.026035759	203920_AT, 208337_S_AT, 208530	88	48	16659	11.8316761	0.99852047	0.88605166	28.9694027
SP_PIR_KEYWORDS	cell cycle	7	7.216494845	0.026693081	213348_AT, 203588_S_AT, 219534	96	461	19235	3.04241233	0.98751268	0.42182586	27.9196553
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metab	10	10.30927835	0.026841601	213348_AT, 219534_X_AT, 207826	80	734	13528	2.30381471	1	0.38123776	34.8985648
GOTERM_BP_FAT	GO:0006720~isoprenoid metabolic process	3	3.092783505	0.027191271	202540_S_AT, 202481_AT, 219825	80	44	13528	11.5295455	1	0.3798797	35.2666039
GOTERM_BP_FAT	GO:0001656~metanephros development	3	3.092783505	0.027191271	206382_S_AT, 208530_S_AT, 2121	80	44	13528	11.5295455	1	0.3798797	35.2666039
GOTERM_BP_FAT	GO:0046890~regulation of lipid biosynthetic process	3	3.092783505	0.02834994	203920_AT, 204200_S_AT, 216061	80	45	13528	11.2733333	1	0.38731493	36.4722591
GOTERM_BP_FAT	GO:0043433~negative regulation of transcription factor ac	3	3.092783505	0.02834994	207826_S_AT, 201565_S_AT, 2139	80	45	13528	11.2733333	1	0.38731493	36.4722591
PIR_SUPERFAMILY	PIRSF005680:interferon-induced 56K protein	2	2.06185567	0.028741389	217502_AT, 203153_AT	44	5	7396	67.2363636	0.81029085	0.81029085	25.1036308
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside	9	9.278350515	0.028842359	203504_S_AT, 203920_AT, 204200	80	624	13528	2.43894231	1	0.3874284	36.9782512
GOTERM_BP_FAT	GO:0045647~negative regulation of erythrocyte differenti	2	2.06185567	0.028863877	204249_S_AT, 218559_S_AT	80	5	13528	67.64	1	0.38262962	37.0002757
INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	3	3.092783505	0.029134864	203920_AT, 208337_S_AT, 208530	88	51	16659	11.1356952	0.99932664	0.83891228	31.8448377
SP_PIR_KEYWORDS	tumor suppressor	4	4.12371134	0.030430813	213348_AT, 219534_X_AT, 204159	96	137	19235	5.85006083	0.99330476	0.42665175	31.1986666
SP_PIR_KEYWORDS	metal-binding	23	23.71134021	0.030815317	201368_AT, 202688_AT, 207559_S	96	2972	19235	1.55060075	0.99372144	0.39773728	31.5280989
INTERPRO	IPR006694:Fatty acid hydroxylase	2	2.06185567	0.030932731	206932_AT, 220751_S_AT, 48031_	88	6	16659	63.1022727	0.99957399	0.78822051	33.4633162
GOTERM_MF_FAT	GO:0003707~steroid hormone receptor activity	3	3.092783505	0.030937102	203920_AT, 208337_S_AT, 208530	74	49	12983	10.7415885	0.99876129	0.56686717	32.8303424
GOTERM_BP_FAT	GO:0035282~segmentation	3	3.092783505	0.031942296	204917_S_AT, 214457_AT, 218559	80	48	13528	10.56875	1	0.40891981	40.0779682
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	4	4.12371134	0.033770575	207826_S_AT, 201565_S_AT, 2139	80	121	13528	5.59008264	1	0.42157546	41.8385609
GOTERM_BP_FAT	GO:0022403~cell cycle phase	7	7.216494845	0.033852871	211538_S_AT, 204315_S_AT, 2133	80	414	13528	2.85917874	1	0.41730613	41.9166593
GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	7	7.216494845	0.033852871	204200_S_AT, 204526_S_AT, 2160	80	414	13528	2.85917874	1	0.41730613	41.9166593
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound me	9	9.278350515	0.033883977	203504_S_AT, 203920_AT, 204200	80	644	13528	2.36319876	1	0.41265999	41.9461531
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	5	5.154639175	0.034388223	204526_S_AT, 212796_S_AT, 2199	80	210	13528	4.02619048	1	0.41251224	42.4223103

GOTERM_BP_FAT	GO:0010887~negative regulation of cholesterol storage	2	2.06185567	0.034537156	203504_S_AT, 203920_AT	80	6	13528	56.3666667	1	0.40912444	42.562246
SMART	SM00399:ZnF_C4	3	3.092783505	0.034690381	203920_AT, 208337_S_AT, 208530	59	46	9079	10.0357406	0.91846745	0.91846745	30.6809945
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	4	4.12371134	0.035197588	204526_S_AT, 212796_S_AT, 2199	80	123	13528	5.49918699	1	0.4104452	43.1789499
KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	6	6.18556701	0.035599083	202687_S_AT, 215719_X_AT, 2042	37	262	5085	3.14730761	0.86865111	0.49167422	30.0876695
GOTERM_BP_FAT	GO:0043392~negative regulation of DNA binding	3	3.092783505	0.035703754	207826_S_AT, 201565_S_AT, 2139	80	51	13528	9.94705882	1	0.41035923	43.6473988
GOTERM_BP_FAT	GO:0055088~lipid homeostasis	3	3.092783505	0.035703754	203504_S_AT, 203980_AT, 208337	80	51	13528	9.94705882	1	0.41035923	43.6473988
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosyn	9	9.278350515	0.036618947	203920_AT, 204200_S_AT, 216061	80	654	13528	2.32706422	1	0.4138516	44.4852252
SP_PIR_KEYWORDS	alternative splicing	47	48.45360825	0.037259819	202540_S_AT, 204526_S_AT, 2045	96	7488	19235	1.25763026	0.99786954	0.42834502	36.8385822
SMART	SM00430:HOLI	3	3.092783505	0.037503287	203920_AT, 208337_S_AT, 208530	59	48	9079	9.61758475	0.9337254	0.74256146	32.7491192
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	6	6.18556701	0.038173689	211538_S_AT, 215719_X_AT, 2075	37	267	5085	3.08836927	0.88691303	0.42009995	31.9089533
UP_SEQ_FEATURE	compositionally biased region:Poly-Gln	4	4.12371134	0.039504268	201368_AT, 202704_AT, 201367_S	96	151	19113	5.27400662	0.99999997	0.99702485	43.3721519
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	7	7.216494845	0.039587027	202687_S_AT, 215719_X_AT, 2078	80	430	13528	2.7527907	1	0.43453276	47.1228252
BIOCARTA	h_nuclearRsPathway:Nuclear Receptors in Lipid Metabolis	3	3.092783505	0.04002901	203504_S_AT, 203920_AT, 208530	14	36	1437	8.55357143	0.69416642	0.69416642	29.1732305
GOTERM_BP_FAT	GO:0021546~rhombomere development	2	2.06185567	0.040177709	214457_AT, 218559_S_AT	80	7	13528	48.3142857	1	0.4348332	47.6335331
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell deat	7	7.216494845	0.040727261	202687_S_AT, 215719_X_AT, 2078	80	433	13528	2.73371824	1	0.43479562	48.1045268
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	7	7.216494845	0.041498964	202687_S_AT, 215719_X_AT, 2078	80	435	13528	2.72114943	1	0.43653165	48.7592213
GOTERM_MF_FAT	GO:0004879~ligand-dependent nuclear receptor activity	3	3.092783505	0.042108194	203920_AT, 208337_S_AT, 208530	74	58	12983	9.07479031	0.99989519	0.63873753	42.0026932
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	4	4.12371134	0.042793449	206382_S_AT, 214457_AT, 203395	80	133	13528	5.08571429	1	0.44230093	49.8400892
GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	4	4.12371134	0.043594859	213348_AT, 203920_AT, 219534_X	80	134	13528	5.04776119	1	0.44410941	50.4985075
GOTERM_BP_FAT	GO:0001666~response to hypoxia	4	4.12371134	0.043594859	204200_S_AT, 216061_X_AT, 2092	80	134	13528	5.04776119	1	0.44410941	50.4985075
GOTERM_BP_FAT	GO:0048704~embryonic skeletal system morphogenesis	3	3.092783505	0.043706875	206289_AT, 214457_AT, 204653_A	80	57	13528	8.9	1	0.44065026	50.5898897
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	10	10.30927835	0.044150806	215719_X_AT, 202688_AT, 211792	80	804	13528	2.10323383	1	0.43976169	50.9504947
GOTERM_BP_FAT	GO:0007423~sensory organ development	5	5.154639175	0.044917099	206382_S_AT, 208530_S_AT, 2144	80	229	13528	3.69213974	1	0.44128943	51.5671607
GOTERM_BP_FAT	GO:0051100~negative regulation of binding	3	3.092783505	0.046509731	207826_S_AT, 201565_S_AT, 2139	80	59	13528	8.59830508	1	0.44878325	52.8256592
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	10	10.30927835	0.046521017	215719_X_AT, 202688_AT, 211792	80	812	13528	2.08251232	1	0.44474512	52.834467
GOTERM_BP_FAT	GO:0022402~cell cycle process	8	8.24742268	0.046634948	211538_S_AT, 204315_S_AT, 2133	80	565	13528	2.39433628	1	0.44151207	52.923295
GOTERM_BP_FAT	GO:0010941~regulation of cell death	10	10.30927835	0.047431589	215719_X_AT, 202688_AT, 211792	80	815	13528	2.07484663	1	0.4431674	53.5400475
GOTERM_BP_FAT	GO:0030902~hindbrain development	3	3.092783505	0.047935435	214457_AT, 203395_S_AT, 218559	80	60	13528	8.455	1	0.44274616	53.9262053
GOTERM_BP_FAT	GO:0030097~hemopoiesis	5	5.154639175	0.049205092	215719_X_AT, 201565_S_AT, 2094	80	236	13528	3.58262712	1	0.44759248	54.8860055
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	4	4.12371134	0.049414236	202540_S_AT, 204200_S_AT, 2160	80	141	13528	4.79716312	1	0.44514271	55.0423001
GOTERM_BP_FAT	GO:0070482~response to oxygen levels	4	4.12371134	0.049414236	204200_S_AT, 216061_X_AT, 2092	80	141	13528	4.79716312	1	0.44514271	55.0423001
GOTERM_BP_FAT	GO:0035162~embryonic hemopoiesis	2	2.06185567	0.051361384	204249_S_AT, 212151_AT	80	9	13528	37.5777778	1	0.4543358	56.4732755
GOTERM_BP_FAT	GO:0043536~positive regulation of blood vessel endotheli	2	2.06185567	0.051361384	204200_S_AT, 216061_X_AT, 2157	80	9	13528	37.5777778	1	0.4543358	56.4732755
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	6	6.18556701	0.053310697	203588_S_AT, 203920_AT, 207826	74	363	12983	2.89993299	0.99999145	0.68867134	50.0296921
GOTERM_BP_FAT	GO:0032103~positive regulation of response to external st	3	3.092783505	0.053794725	204200_S_AT, 216061_X_AT, 2039	80	64	13528	7.9265625	1	0.46631859	58.201609
GOTERM_MF_FAT	GO:0004861~cyclin-dependent protein kinase inhibitor act	2	2.06185567	0.054844348	213348_AT, 219534_X_AT, 204159	74	10	12983	35.0891892	0.99999394	0.6645286	51.0451772
GOTERM_BP_FAT	GO:0001568~blood vessel development	5	5.154639175	0.05504077	40687_AT, 204904_AT, 209201_X_	80	245	13528	3.45102041	1	0.4703904	59.0615489
UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	6	6.18556701	0.055063693	201368_AT, 204917_S_AT, 205642	96	413	19113	2.89240315	1	0.99782567	55.026462
GOTERM_BP_FAT	GO:0006911~phagocytosis, engulfment	2	2.06185567	0.056904875	203504_S_AT, 215775_AT	80	10	13528	33.82	1	0.47815989	60.3171481
GOTERM_BP_FAT	GO:0008219~cell death	9	9.278350515	0.05809067	215719_X_AT, 207574_S_AT, 2026	80	719	13528	2.11668985	1	0.48158488	61.0969925
GOTERM_BP_FAT	GO:0010033~response to organic substance	9	9.278350515	0.05885675	211538_S_AT, 215719_X_AT, 2042	80	721	13528	2.11081831	1	0.48242116	61.5931514
GOTERM_BP_FAT	GO:0006928~cell motion	7	7.216494845	0.058908256	202540_S_AT, 204200_S_AT, 2191	80	475	13528	2.492	1	0.47900901	61.6262963
GOTERM_BP_FAT	GO:0001944~vasculature development	5	5.154639175	0.059131666	40687_AT, 204904_AT, 209201_X_	80	251	13528	3.3685259	1	0.47666518	61.7697535
UP_SEQ_FEATURE	splice variant	46	47.42268041	0.059626925	202540_S_AT, 204526_S_AT, 2191	96	7458	19113	1.22798505	1	0.995127	57.9955577
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dep	7	7.216494845	0.059878783	203920_AT, 208337_S_AT, 208530	80	477	13528	2.48155136	1	0.47742914	62.2458569
GOTERM_BP_FAT	GO:0016265~death	9	9.278350515	0.060017981	215719_X_AT, 207574_S_AT, 2026	80	724	13528	2.10207182	1	0.4746566	62.3339453
GOTERM_BP_FAT	GO:0051098~regulation of binding	4	4.12371134	0.060224963	207826_S_AT, 201565_S_AT, 2139	80	153	13528	4.42091503	1	0.47231953	62.4645736
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	7	7.216494845	0.061848682	203920_AT, 208337_S_AT, 208530	80	481	13528	2.46091476	1	0.47810433	63.4746961
GOTERM_BP_FAT	GO:0010885~regulation of cholesterol storage	2	2.06185567	0.062416379	203504_S_AT, 203920_AT	80	11	13528	30.7454545	1	0.47782603	63.8218141
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	6	6.18556701	0.063299359	215719_X_AT, 204200_S_AT, 2160	80	367	13528	2.76457766	1	0.47930681	64.3555778
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ developme	5	5.154639175	0.065565934	215719_X_AT, 201565_S_AT, 2094	80	260	13528	3.25192308	1	0.48829367	65.6921562
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	4	4.12371134	0.066013521	204200_S_AT, 216061_X_AT, 2039	80	159	13528	4.25408805	1	0.48729641	65.9504813
GOTERM_BP_FAT	GO:0006935~chemotaxis	4	4.12371134	0.06700246	204200_S_AT, 216061_X_AT, 2073	80	160	13528	4.2275	1	0.48919606	66.5148026
GOTERM_BP_FAT	GO:0042330~taxis	4	4.12371134	0.06700246	204200_S_AT, 216061_X_AT, 2073	80	160	13528	4.2275	1	0.48919606	66.5148026
GOTERM_BP_FAT	GO:0010888~negative regulation of lipid storage	2	2.06185567	0.067896079	203504_S_AT, 203920_AT	80	12	13528	28.1833333	1	0.49055796	67.0171852

GOTERM_BP_FAT	GO:0008354~germ cell migration	2	2.06185567	0.067896079	202540_S_AT, 209201_X_AT, 2170	80	12	13528	28.1833333	1	0.49055796	67.0171852
GOTERM_BP_FAT	GO:0010745~negative regulation of foam cell differentiatio	2	2.06185567	0.067896079	203504_S_AT, 203920_AT	80	12	13528	28.1833333	1	0.49055796	67.0171852
SP_PIR_KEYWORDS	magnesium	6	6.18556701	0.067934537	219147_S_AT, 212182_AT, 206303,	96	442	19235	2.71988122	0.99998877	0.61316424	57.313907
GOTERM_BP_FAT	GO:0006766~vitamin metabolic process	3	3.092783505	0.071101615	219147_S_AT, 202481_AT, 219825,	80	75	13528	6.764	1	0.50375291	68.7618202
UP_SEQ_FEATURE	cross-link:Glycyl lysine isopeptide (Lys-Gly) (interchain with	3	3.092783505	0.072489625	204653_AT, 203408_S_AT, 218559,	96	89	19113	6.71102528	1	0.99561969	65.4136952
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	4	4.12371134	0.07307828	206382_S_AT, 214457_AT, 203395,	80	166	13528	4.0746988	1	0.51034423	69.7941459
GOTERM_BP_FAT	GO:0010595~positive regulation of endothelial cell migrati	2	2.06185567	0.073344156	204200_S_AT, 216061_X_AT, 2157	80	13	13528	26.0153846	1	0.508351	69.9305374
GOTERM_BP_FAT	GO:0008045~motor axon guidance	2	2.06185567	0.073344156	209201_X_AT, 217028_AT, 214457,	80	13	13528	26.0153846	1	0.508351	69.9305374
GOTERM_BP_FAT	GO:0030511~positive regulation of transforming growth fa	2	2.06185567	0.073344156	213348_AT, 219534_X_AT, 215775,	80	13	13528	26.0153846	1	0.508351	69.9305374
SP_PIR_KEYWORDS	isopeptide bond	5	5.154639175	0.073385846	215023_S_AT, 201009_S_AT, 2046	96	319	19235	3.14051071	0.99999566	0.61317927	60.2387017
SP_PIR_KEYWORDS	lipid-binding	3	3.092783505	0.074508092	218711_S_AT, 203980_AT, 208337,	96	91	19235	6.60542582	0.99999643	0.59179037	60.8175113
GOTERM_BP_FAT	GO:0051384~response to glucocorticoid stimulus	3	3.092783505	0.076098945	215719_X_AT, 203980_AT, 213910	80	78	13528	6.50384615	1	0.5184984	71.3101694
SP_PIR_KEYWORDS	protein kinase inhibitor	2	2.06185567	0.076190488	213348_AT, 219534_X_AT, 204159	96	16	19235	25.0455729	0.99999734	0.57509657	61.6707563
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	6	6.18556701	0.076764925	204526_S_AT, 209051_S_AT, 2127	74	404	12983	2.60563286	0.99999996	0.75773357	63.6298589
GOTERM_BP_FAT	GO:0048839~inner ear development	3	3.092783505	0.077789107	206382_S_AT, 203395_S_AT, 2185	80	79	13528	6.42151899	1	0.52328162	72.1270364
GOTERM_BP_FAT	GO:0002520~immune system development	5	5.154639175	0.077872879	215719_X_AT, 201565_S_AT, 2094	80	276	13528	3.0634058	1	0.52042557	72.1669518
UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	5	5.154639175	0.078800049	204917_S_AT, 213348_AT, 203588,	96	325	19113	3.06298077	1	0.99376216	68.5896239
UP_SEQ_FEATURE	mutagenesis site	16	16.49484536	0.079798668	204589_AT, 212344_AT, 204635_A	96	2045	19113	1.55770171	1	0.98890417	69.0666355
INTERPRO	IPR000355:Chemokine receptor	2	2.06185567	0.080398842	209201_X_AT, 217028_AT, 220351,	88	16	16659	23.6633523	1	0.96826685	66.2696391
GOTERM_MF_FAT	GO:0016563~transcription activator activity	6	6.18556701	0.080603865	213348_AT, 203920_AT, 219534_X	74	410	12983	2.56750165	0.99999998	0.74764882	65.4991732
SP_PIR_KEYWORDS	phosphoprotein	44	45.36082474	0.080838352	203504_S_AT, 202704_AT, 204510,	96	7263	19235	1.21382923	0.99999883	0.57406538	63.9401685
COG_ONTOLOGY	Cell division and chromosome partitioning	3	3.092783505	0.082077528	212093_S_AT, 212796_S_AT, 2056	10	106	1950	5.51886792	0.40181432	0.40181432	33.6265738
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	6	6.18556701	0.082561725	204526_S_AT, 209051_S_AT, 2127	74	413	12983	2.54885151	0.99999999	0.73045357	66.4180635
GOTERM_BP_FAT	GO:0032369~negative regulation of lipid transport	2	2.06185567	0.084146161	203920_AT, 215775_AT	80	15	13528	22.5466667	1	0.5459229	75.0084826
GOTERM_CC_FAT	GO:0009986~cell surface	5	5.154639175	0.084240793	211538_S_AT, 215719_X_AT, 2042	62	348	12782	2.9620875	0.99998177	0.99572988	63.803062
GOTERM_MF_FAT	GO:0016493~C-C chemokine receptor activity	2	2.06185567	0.086315523	209201_X_AT, 217028_AT, 220351,	74	16	12983	21.9307432	1	0.72247207	68.1171118
GOTERM_MF_FAT	GO:0019957~C-C chemokine binding	2	2.06185567	0.086315523	209201_X_AT, 217028_AT, 220351,	74	16	12983	21.9307432	1	0.72247207	68.1171118
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	6	6.18556701	0.087891569	215719_X_AT, 204200_S_AT, 2160	80	405	13528	2.50518519	1	0.55906194	76.5729747
GOTERM_BP_FAT	GO:0031960~response to corticosteroid stimulus	3	3.092783505	0.088172646	215719_X_AT, 203980_AT, 213910	80	85	13528	5.96823529	1	0.55703235	76.6866031
GOTERM_BP_FAT	GO:0009611~response to wounding	7	7.216494845	0.089101363	204200_S_AT, 216061_X_AT, 2078	80	530	13528	2.23339623	1	0.55778654	77.0583882
GOTERM_BP_FAT	GO:0043535~regulation of blood vessel endothelial cell mi	2	2.06185567	0.089500446	204200_S_AT, 216061_X_AT, 2157	80	16	13528	21.1375	1	0.55629834	77.2164374
SP_PIR_KEYWORDS	fusion protein	2	2.06185567	0.089822831	205528_S_AT, 212151_AT	96	19	19235	21.0910088	0.99999976	0.59215586	67.9813159
GOTERM_MF_FAT	GO:0030291~protein serine/threonine kinase inhibitor acti	2	2.06185567	0.09145927	213348_AT, 219534_X_AT, 204159	74	17	12983	20.6406995	1	0.72109272	70.3168752
GOTERM_MF_FAT	GO:0016538~cyclin-dependent protein kinase regulator ac	2	2.06185567	0.09145927	213348_AT, 219534_X_AT, 204159	74	17	12983	20.6406995	1	0.72109272	70.3168752
GOTERM_BP_FAT	GO:0043193~positive regulation of gene-specific transcript	3	3.092783505	0.09172174	203920_AT, 208337_S_AT, 210174,	80	87	13528	5.83103448	1	0.56243153	78.0776652
GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	3	3.092783505	0.09172174	202540_S_AT, 207574_S_AT, 2039	80	87	13528	5.83103448	1	0.56243153	78.0776652
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	3	3.092783505	0.09172174	208530_S_AT, 219825_AT, 212151,	80	87	13528	5.83103448	1	0.56243153	78.0776652
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	3	3.092783505	0.09172174	208530_S_AT, 219825_AT, 212151,	80	87	13528	5.83103448	1	0.56243153	78.0776652
GOTERM_MF_FAT	GO:0003677~DNA binding	19	19.58762887	0.092939979	201368_AT, 203588_S_AT, 203920,	74	2331	12983	1.43006134	1	0.70541928	70.9236855
BBID	71.Id_proteins_G0-to-S_cell_cycle	2	2.06185567	0.094525028	207826_S_AT, 201565_S_AT, 2139	8	5	358	17.9	0.72496127	0.72496127	48.1802448
SP_PIR_KEYWORDS	nucleus	28	28.86597938	0.09548723	201368_AT, 204917_S_AT, 219534,	96	4283	19235	1.3098782	0.99999991	0.59474132	70.3109577
GOTERM_MF_FAT	GO:0046872~metal ion binding	30	30.92783505	0.095770289	201368_AT, 202688_AT, 217317_S	74	4140	12983	1.27134743	1	0.69616896	72.0519002
GOTERM_MF_FAT	GO:0019207~kinase regulator activity	3	3.092783505	0.096271362	213348_AT, 219534_X_AT, 204159	74	93	12983	5.65954664	1	0.67851305	72.2473849
GOTERM_BP_FAT	GO:0006350~transcription	18	18.55670103	0.097211579	204917_S_AT, 203588_S_AT, 2039	80	2101	13528	1.4487387	1	0.5814811	80.0771646