Identification of gene expression signatures in the chicken intestinal intraepithelial lymphocytes (IELs) in response to herb additive supplementations

Supplemental Table 1. Detailed information for common DEGs was described.

Anethol

Up-regulated

GeneName	Agilent ID	logFC	AveExpr	t	P-Value	Adj. P-Val	B
GDF2	A_87_P009507	3.588156	8.844506	9.330589	3.54E-05	0.048313	2.733757
BU415738	A_87_P027727	3.073602	6.845288	6.298285	0.000418	0.086348	0.593204
BX277386	A_87_P037368	2.85969	7.799524	6.398924	0.00038	0.086348	0.686047
CO503580	A_87_P041957	2.824056	7.078729	7.05126	0.00021	0.07965	1.225623
CR386395	A_87_P016505	2.756209	8.743256	6.313067	0.000412	0.086348	0.603324
LOC419671	A_87_P011329	2.742353	7.322559	7.092789	0.000202	0.079009	1.256861
MDK	A_87_P029081	2.68125	7.159742	6.492546	0.000348	0.086348	0.757694
TC198879	A_87_P006998	2.6585	7.363867	7.105818	0.0002	0.079009	1.281987
TC200204	A_87_P006807	2.556263	8.072637	7.132555	0.000195	0.078983	1.294766
CRH	A_87_P037220	2.540519	6.730633	6.833465	0.000254	0.083063	1.044728
TC210123	A_87_P003854	2.440955	8.914388	7.961465	9.79E-05	0.067942	1.89888
CR390040	A_87_P014407	2.430733	8.328124	6.019467	0.000548	0.090346	0.334332
BU479212	A_87_P025451	2.421219	8.588658	5.71204	0.000746	0.097039	0.041887
BU226241	A_87_P032548	2.409227	6.561791	6.271577	0.000428	0.086348	0.563639
CR390009	A_87_P014428	2.405584	9.182793	7.631772	0.000128	0.075518	1.656898
APOB	A_87_P022123	2.403839	8.427088	5.058336	0.0015	0.115403	-0.3911
CR386893	A_87_P016179	2.398479	9.32154	7.959767	9.81E-05	0.067942	1.887938
OPCML	A_87_P037717	2.371633	6.824025	6.41061	0.000375	0.086348	0.687815
BU423426	A_87_P027415	2.369735	10.30395	6.598943	0.000315	0.085477	0.850419
TC186301	A_87_P008359	2.357052	14.53735	6.271982	0.000428	0.086348	0.574459
CN236254	A_87_P020473	2.351936	7.208837	6.6739	0.000294	0.085477	0.916488

BU247950	A_87_P031712	2.347479	9.674958	6.57894	0.000321	0.085477	0.835869
TC194119	A_87_P007570	2.314791	8.275533	6.016172	0.000549	0.090346	0.333665
FZR1	A_87_P037626	2.299591	15.15082	7.268558	0.000174	0.076686	1.394834
M27663	A_87_P009373	2.255433	7.924457	7.279008	0.000172	0.076686	1.403311
CR406944	A_87_P012419	2.21909	7.435867	6.490538	0.000348	0.086348	0.757147
BU104894	A_87_P034768	2.207061	6.423518	5.589815	0.000847	0.099574	-0.07766
LOC421179	A_87_P026850	2.200907	8.179382	5.798062	0.000684	0.097029	0.124379
CO771160	A_87_P019220	2.198366	6.566678	5.552347	0.000881	0.099916	-0.11365
LOC395210	A_87_P017952	2.193343	7.102583	7.172012	0.000189	0.078409	1.352446
RCJMB04_21j5	A_87_P012102	2.183237	10.45699	14.63524	1.78E-06	0.007192	4.797705
TC203225	A_87_P005875	2.17043	14.69902	10.74599	1.4E-05	0.026857	3.4435
HCRT	A_87_P014389	2.155708	8.788928	8.399576	6.96E-05	0.067942	2.199138
LFNG	A_87_P008992	2.12722	7.951289	8.080736	8.91E-05	0.067942	1.970016
TC210304	A_87_P003832	2.119006	9.830926	9.759057	2.64E-05	0.044472	2.964463
ABHD6	A_87_P026925	2.10777	6.361032	6.634556	0.000305	0.085477	0.882713
AJ455964	A_87_P037269	2.080655	7.851321	5.977741	0.000571	0.091014	0.297599
AJ728686	A_87_P035890	2.069296	6.565869	5.949401	0.000587	0.092215	0.27224
CR386260	A_87_P016602	2.068276	8.196046	8.483269	6.54E-05	0.067942	2.404434
CO770158	A_87_P019319	2.054021	6.291328	6.020185	0.000547	0.090346	0.335759
PHOX2	A_87_P008691	2.052143	7.076713	6.24684	0.000439	0.086348	0.547996
CV858659	A_87_P010532	2.04848	7.476356	6.835216	0.000254	0.083063	1.060871
TC207295	A_87_P004132	2.019629	6.849754	6.208783	0.000455	0.087483	0.508601
TC206022	A_87_P004642	1.996117	7.048458	6.622625	0.000308	0.085477	0.878216
TC202794	A_87_P006118	1.993664	7.037863	5.90432	0.000614	0.095047	0.243364
TNNT3	A_87_P034373	1.982154	7.181178	6.465095	0.000357	0.086348	0.741877
CR390868	A_87_P013879	1.972242	6.670342	5.740135	0.000725	0.097039	0.07057
LOC423162	A_87_P023103	1.959043	7.492054	9.564628	3.01E-05	0.045273	2.861598

TC221798	A_87_P002470	1.956084	7.539481	6.10745	0.000502	0.089473	0.421928
BU470394	A_87_P025748	1.949767	7.051337	6.074588	0.000519	0.089473	0.386078
TNPO3	A_87_P016263	1.936908	7.527136	8.916763	4.74E-05	0.05874	2.532564
TC203827	A_87_P005544	1.931267	6.785104	8.036471	9.23E-05	0.067942	1.968875
ARC	A_87_P037475	1.9235	7.985849	6.902054	0.000239	0.082384	1.10266
LOC420585	A_87_P028929	1.919875	7.739128	5.793343	0.000687	0.097029	0.124352
MDK	A_87_P009319	1.909597	6.518566	5.283509	0.001172	0.109872	-0.11663
CN237892	A_87_P040742	1.905446	7.728358	8.24514	7.84E-05	0.067942	2.11723
LOC423636	A_87_P030019	1.90392	6.904272	6.508516	0.000342	0.086348	0.802589
BX262701	A_87_P025099	1.889939	7.666799	6.929627	0.000233	0.082384	1.126286
ZDHHC5	A_87_P035034	1.889719	6.815334	6.076138	0.000518	0.089473	0.392712
TC223018	A_87_P002214	1.871087	9.922726	7.479067	0.000145	0.075518	1.56846
CR385621	A_87_P017031	1.869029	6.845923	5.974786	0.000572	0.091014	0.294774
BU268923	A_87_P031191	1.865009	6.810877	6.698134	0.000287	0.085477	0.932006
CR390688	A_87_P013990	1.854372	8.913598	10.90366	1.27E-05	0.026691	3.513855
AKT2	A_87_P037817	1.847453	7.446635	10.86802	1.3E-05	0.026691	3.498093
BU373614	A_87_P028711	1.846066	8.163094	6.698686	0.000287	0.085477	0.976232
TC224651	A_87_P001292	1.841672	7.535536	5.645683	0.000799	0.098651	-0.01443
BU414476	A_87_P027750	1.840702	6.296522	5.816072	0.000671	0.097029	0.146895
CD760819	A_87_P021203	1.832628	6.716274	5.93641	0.000595	0.092766	0.268213
CDON	A_87_P015827	1.830065	6.648162	6.218217	0.000451	0.087483	0.522514
BU305794	A_87_P030191	1.822992	7.504305	7.977461	9.67E-05	0.067942	1.922181
TC227335	A_87_P000158	1.822138	6.88685	7.434658	0.000151	0.075518	1.512266
TC227424	A_87_P000116	1.802957	7.217393	6.751903	0.000274	0.085477	0.980897
GBE	A_87_P035833	1.800988	7.483263	6.295295	0.000419	0.086348	0.58707
CR390166	A_87_P014333	1.793541	8.688592	6.832037	0.000255	0.083063	1.043298
IRS-1	A_87_P009216	1.780841	6.759091	6.194661	0.000461	0.088112	0.506938

APOB	A_87_P034149	1.769869	8.584946	5.712907	0.000746	0.097039	0.041942
CSPG5	A_87_P008748	1.769304	6.166809	7.302733	0.000169	0.076686	1.426966
TC224509	A_87_P001374	1.75378	6.756692	5.891841	0.000622	0.095892	0.225718
BU452711	A_87_P026454	1.72602	6.30809	5.734334	0.00073	0.097039	0.06639
LOC425139	A_87_P014925	1.706878	9.1819	7.088894	0.000203	0.079009	1.250895
HBD	A_87_P009554	1.705073	12.83512	9.162324	3.98E-05	0.052362	2.639034
BU415119	A_87_P027742	1.69864	6.82061	5.814261	0.000673	0.097029	0.141652
TC219891	A_87_P002751	1.696874	6.877864	7.807604	0.000111	0.071748	1.814234
CD727362	A_87_P021327	1.6915	6.531663	5.605648	0.000833	0.099014	-0.05602
BX260117	A_87_P025154	1.656703	7.028143	6.906544	0.000238	0.082384	1.108304
CO768011	A_87_P019527	1.650364	6.596461	6.596703	0.000315	0.085477	0.848109
TC226737	A_87_P000466	1.636989	7.763476	6.388054	0.000383	0.086348	0.667342
GLT25D2	A_87_P017120	1.618886	7.149251	5.719695	0.000741	0.097039	0.05089
CO757296	A_87_P020145	1.609191	6.223491	6.146565	0.000483	0.089473	0.45541
VAX1	A_87_P038172	1.608225	6.249451	6.246269	0.000439	0.086348	0.54115
BU424987	A_87_P041883	1.604188	6.308624	6.090902	0.00051	0.089473	0.40256
OLIG3	A_87_P037632	1.592316	6.704635	6.481658	0.000351	0.086348	0.755415
TC220349	A_87_P002688	1.587422	7.059313	5.712963	0.000746	0.097039	0.043555
CR406193	A_87_P012941	1.583236	9.072681	8.011658	9.41E-05	0.067942	1.939011
AJ739127	A_87_P035851	1.581738	7.439919	6.100811	0.000506	0.089473	0.414837
BU387573	A_87_P028278	1.566462	7.037257	5.574577	0.00086	0.099586	-0.09321
DYNC1H1	A_87_P008241	1.559896	10.70518	8.978146	4.54E-05	0.057899	2.532564
MGAT5	A_87_P016016	1.558693	8.754848	6.618124	0.000309	0.085477	0.868148
LOC425289	A_87_P012241	1.548216	7.239367	5.800808	0.000682	0.097029	0.127784
WHSC1L1	A_87_P013214	1.543161	9.44192	5.678486	0.000773	0.097658	0.010406
DYNC1H1	A_87_P038038	1.524044	7.552734	6.495052	0.000347	0.086348	0.759306
DN829968	A_87_P009752	1.521387	6.157345	5.722149	0.000739	0.097039	0.05578

BU120493	A_87_P034283	1.519967	6.804688	5.727174	0.000735	0.097039	0.06274
CR390671	A_87_P014002	1.519435	7.690412	7.435064	0.000151	0.075518	1.512744
RCJMB04_20d5	A_87_P036326	1.511338	7.193692	6.125401	0.000494	0.089473	0.432518
KIF5B	A_87_P022772	1.510213	10.54807	6.370116	0.00039	0.086348	0.655305
LOC427758	A_87_P007751	1.504371	7.146365	5.555331	0.000878	0.099874	-0.11246
BU205361	A_87_P033349	1.500232	5.990556	7.321331	0.000166	0.076686	1.435026
BU455240	A_87_P026343	1.498661	7.580348	5.63297	0.00081	0.098798	-0.03621
CV859110	A_87_P010492	1.498212	8.213298	5.982636	0.000568	0.091014	0.30201
LOC427434	A_87_P022431	1.493964	8.637726	6.506442	0.000343	0.086348	0.770897
TC186792	A_87_P008265	1.47477	8.0653	6.45958	0.000358	0.086348	0.733428
AM067107	A_87_P035373	1.470295	6.862038	6.861555	0.000248	0.083063	1.099032
CRYBA1	A_87_P009400	1.461856	7.182145	5.690526	0.000763	0.097039	0.021683
LOC426613	A_87_P023334	1.461766	7.334105	6.380346	0.000386	0.086348	0.661881
BU295088	A_87_P030477	1.458997	6.369213	5.591441	0.000845	0.099574	-0.06943
RCJMB04_19e2	A_87_P035599	1.436466	11.19889	6.270822	0.000429	0.086348	0.563277
BU460481	A_87_P026133	1.432495	7.71433	7.359445	0.000161	0.076686	1.511964
TC226823	A_87_P000414	1.424276	7.131516	6.855012	0.000249	0.083063	1.066196
NKX-2.2	A_87_P037886	1.420833	7.488328	5.719655	0.000741	0.097039	0.048501
LOC419750	A_87_P015390	1.420091	6.147698	6.087101	0.000512	0.089473	0.399655
BU417989	A_87_P027684	1.417371	6.413987	5.603326	0.000835	0.099014	-0.06356
GRB2	A_87_P009495	1.413722	9.467102	6.383001	0.000385	0.086348	0.663941
CR385664	A_87_P017003	1.405559	6.755644	5.95369	0.000585	0.092166	0.284928
CN234081	A_87_P020521	1.40503	6.349822	6.935865	0.000232	0.082384	1.157745
TC205715	A_87_P004815	1.404161	6.062793	6.921597	0.000235	0.082384	1.121268
LOC419436	A_87_P002536	1.39013	6.364257	5.613263	0.000826	0.098833	-0.05107
PLEKHQ1	A_87_P012444	1.389024	7.2908	6.255961	0.000435	0.086348	0.562603
LOC418607	A_87_P017318	1.387334	8.679819	7.854736	0.000107	0.070151	1.846759

ELMOD2	A_87_P023542	1.38582	8.189453	6.006753	0.000555	0.090837	0.330603
RCJMB04_11l17	A_87_P036602	1.385593	11.47125	6.603716	0.000313	0.085477	0.857146
U76305	A_87_P009023	1.383621	8.199186	6.115195	0.000498	0.089473	0.421949
CV862615	A_87_P009876	1.378644	8.374657	5.845068	0.000652	0.097029	0.172922
BU446674	A_87_P026707	1.366628	6.019076	5.6333	0.000809	0.098798	-0.024
BX277609	A_87_P024840	1.366506	8.908586	6.151891	0.000481	0.089473	0.471135
SPEN	A_87_P007302	1.361437	7.678228	5.973887	0.000573	0.091014	0.29201
CR353864	A_87_P017683	1.355605	7.090907	6.980925	0.000223	0.082384	1.20212
BU462788	A_87_P026028	1.344111	7.376784	7.954668	9.85E-05	0.067942	1.886775
CR391365	A_87_P013511	1.342527	7.535799	5.873778	0.000633	0.097029	0.213901
CR523642	A_87_P011476	1.341913	6.81085	5.560209	0.000873	0.099874	-0.10389
NHSL1	A_87_P002050	1.340994	6.553987	7.511111	0.000141	0.075518	1.581157
BX931974	A_87_P023710	1.336622	7.308088	5.699416	0.000756	0.097039	0.033583
BU421848	A_87_P027483	1.332581	6.488086	6.073442	0.000519	0.089473	0.384651
RCJMB04_22k13	A_87_P009183	1.33121	7.357983	5.742397	0.000724	0.097039	0.074667
LOC416214	A_87_P015049	1.314499	6.999075	6.494602	0.000347	0.086348	0.759306
AADAC	A_87_P034264	1.303529	6.686007	5.802494	0.000681	0.097029	0.132983
BX934358	A_87_P022627	1.303268	6.75994	7.290145	0.00017	0.076686	1.412873
CR388868	A_87_P015174	1.302289	7.894729	5.565099	0.000869	0.099822	-0.09859
BU391107	A_87_P028183	1.282306	6.958768	6.021721	0.000546	0.090346	0.34094
TC207604	A_87_P004074	1.279857	7.306998	7.231129	0.000179	0.076686	1.363166
TC193639	A_87_P007630	1.271465	7.109907	6.233973	0.000444	0.08697	0.540638
CR353938	A_87_P017639	1.267241	9.818816	8.853669	4.97E-05	0.059734	2.496416
BU228800	A_87_P032464	1.259823	5.97449	5.772018	0.000702	0.097039	0.10584
CASZ1	A_87_P023401	1.257562	6.413517	5.738091	0.000727	0.097039	0.068081
CR338795	A_87_P018837	1.23002	8.141499	6.545476	0.000331	0.086348	0.808141
LOC415553	A_87_P021890	1.228892	8.779147	7.930837	0.0001	0.068129	1.88328

CR523450	A_87_P011601	1.228428	7.711953	6.117745	0.000497	0.089473	0.43126
LARP1	A_87_P015360	1.221218	7.451497	5.855621	0.000645	0.097029	0.1905
HS1BP3	A_87_P018137	1.20385	7.953201	5.808004	0.000677	0.097029	0.139915
TC225719	A_87_P000887	1.199451	7.156528	6.1824	0.000467	0.088136	0.487547
CTCF	A_87_P008703	1.189698	9.822619	7.632652	0.000128	0.075518	1.713043
LOC425243	A_87_P021357	1.188633	7.480518	6.288759	0.000421	0.086348	0.583198
BU332246	A_87_P029583	1.184938	6.096583	7.163319	0.00019	0.078409	1.312645
ANKRD11	A_87_P028441	1.165922	10.30644	8.171477	8.3E-05	0.067942	2.078024
LOC419672	A_87_P027565	1.155371	6.314449	6.474859	0.000353	0.086348	0.747751
CR386677	A_87_P016317	1.154625	6.429055	5.82363	0.000666	0.097029	0.15858
BX935775	A_87_P021947	1.143107	9.059871	7.1004	0.000201	0.079009	1.261103
LOC419037	A_87_P015156	1.142997	12.52331	7.435708	0.000151	0.075518	1.540566
RCJMB04_7d18	A_87_P036813	1.135897	9.673969	7.223731	0.00018	0.076686	1.358227
MYOG	A_87_P009757	1.134265	5.906094	5.980762	0.000569	0.091014	0.29935
TC222502	A_87_P002382	1.128253	8.892461	5.798949	0.000683	0.097029	0.126992
BU461582	A_87_P026084	1.12468	9.215992	8.432569	6.79E-05	0.067942	2.231306
BX930578	A_87_P024243	1.123381	10.19514	7.572954	0.000134	0.075518	1.646038
TEAD3	A_87_P009075	1.118697	7.782432	6.36501	0.000392	0.086348	0.650567
LOC417506	A_87_P017838	1.117494	6.06158	7.331991	0.000164	0.076686	1.455721
UBXD2	A_87_P022336	1.117154	9.896447	8.305223	7.48E-05	0.067942	2.178071
BU476696	A_87_P025525	1.115695	6.479473	5.755239	0.000714	0.097039	0.083658
LOC430010	A_87_P021512	1.11306	8.707549	5.801631	0.000681	0.097029	0.128613
BRD1	A_87_P034947	1.103087	9.767223	6.350307	0.000397	0.086348	0.646078
CDC42BPB	A_87_P032380	1.099127	9.222297	7.237568	0.000178	0.076686	1.386868
APOB	A_87_P012184	1.09547	9.614417	3.977466	0.005425	0.16791	-0.66244
LOC396450	A_87_P009378	1.088027	6.499232	6.584522	0.000319	0.085477	0.842836
BM426314	A_87_P034888	1.087344	6.203328	5.838829	0.000656	0.097029	0.169403

GBX-1	A_87_P038146	1.084931	6.663906	5.675369	0.000775	0.097679	0.008239
LOC424135	A_87_P030843	1.079261	8.621746	6.412634	0.000375	0.086348	0.708848
CD217788	A_87_P021367	1.077373	6.524163	6.169198	0.000473	0.088874	0.483101
CR353205	A_87_P018094	1.071299	7.355828	6.453976	0.00036	0.086348	0.728651
BU305923	A_87_P030186	1.069782	8.261443	6.187313	0.000465	0.088112	0.489003
UPP2	A_87_P022639	1.051648	6.786706	5.583277	0.000853	0.099586	-0.07928
TC194424	A_87_P007536	1.046128	8.169236	5.618258	0.000822	0.098833	-0.04935
LOC415476	A_87_P034974	1.034263	8.097802	5.575813	0.000859	0.099586	-0.08901
LOC419752	A_87_P008020	1.03038	8.024437	2.692739	0.031187	0.297013	-3.59001
ADIPOR2	A_87_P037108	1.030011	11.08546	6.29393	0.000419	0.086348	0.584028
BU467197	A_87_P025869	1.029769	7.158828	6.094065	0.000509	0.089473	0.404187
RCJMB04_30e3	A_87_P011423	1.025104	11.81114	7.711025	0.00012	0.075518	1.781296
BU397032	A_87_P040788	1.018715	6.597443	7.541407	0.000138	0.075518	1.594714
CR386490	A_87_P016444	1.015271	8.093747	5.852261	0.000647	0.097029	0.178495
CR389707	A_87_P014643	1.013316	7.115202	5.621275	0.00082	0.098833	-0.04269
BU425544	A_87_P027321	1.011832	7.753464	6.053381	0.00053	0.089898	0.373329
RRAS2	A_87_P014781	1.008904	10.9093	6.027303	0.000543	0.090346	0.34688
LOC418850	A_87_P010987	1.000907	10.18271	7.52842	0.000139	0.075518	1.590661
BX260970	A_87_P025138	0.99912	11.04211	6.596331	0.000316	0.085477	0.84621
LOC417598	A_87_P007248	0.998994	9.635278	6.757542	0.000272	0.085477	1.008879
LOC395818	A_87_P009087	0.995454	7.258798	6.791475	0.000264	0.084199	1.023939
LMO4	A_87_P037569	0.983679	8.768973	6.254483	0.000436	0.086348	0.549319
LOC416235	A_87_P018176	0.974674	8.182308	6.378465	0.000387	0.086348	0.659552
CR389142	A_87_P015005	0.97023	7.051845	6.639892	0.000303	0.085477	0.883782
LOC420679	A_87_P022679	0.964185	7.253527	5.696453	0.000758	0.097039	0.02872
LOC416529	A_87_P016175	0.960936	7.016567	6.305188	0.000415	0.086348	0.600197
BU377193	A_87_P041674	0.958737	7.32051	6.375508	0.000388	0.086348	0.657901

BG713524	A_87_P041329	0.957433	8.800377	5.692216	0.000762	0.097039	0.025825
MEF2A	A_87_P037524	0.952317	9.247953	6.390147	0.000383	0.086348	0.675832
CR390595	A_87_P014045	0.934185	12.75921	5.834543	0.000659	0.097029	0.163443
ABCD2	A_87_P012773	0.931848	9.228287	5.750899	0.000717	0.097039	0.08302
BU229541	A_87_P032429	0.929412	9.5082	6.680118	0.000292	0.085477	0.931546
LOC427047	A_87_P011568	0.922807	8.414633	5.704396	0.000752	0.097039	0.041041
CO635711	A_87_P020191	0.917505	6.975835	6.319283	0.000409	0.086348	0.608475
CR390958	A_87_P013821	0.900795	12.35613	5.626734	0.000815	0.098833	-0.03653
LOC419752	A_87_P025507	0.892069	8.934367	5.778847	0.000697	0.097039	0.11981
LGR5	A_87_P018440	0.891834	6.029103	6.389229	0.000383	0.086348	0.668146
CD733169	A_87_P021265	0.888991	6.585147	6.493181	0.000347	0.086348	0.758919
CR522893	A_87_P011989	0.886915	8.455516	5.570415	0.000864	0.09966	-0.09526
LHX1	A_87_P009469	0.878048	5.904062	5.807041	0.000677	0.097029	0.133909
LOC422838	A_87_P005240	0.877494	8.925267	6.316594	0.00041	0.086348	0.605707
MARK1	A_87_P021538	0.873065	9.128538	6.115218	0.000498	0.089473	0.424261
LOC420214	A_87_P023888	0.867584	9.555262	6.188922	0.000464	0.088112	0.494191
CR352797	A_87_P018359	0.863893	6.479242	5.714619	0.000744	0.097039	0.048462
BU439010	A_87_P041884	0.858269	6.582341	5.680697	0.000771	0.097658	0.020029
CR523552	A_87_P011535	0.840863	6.772858	5.62068	0.00082	0.098833	-0.04809
CR352651	A_87_P018456	0.833935	9.313825	5.82154	0.000668	0.097029	0.148898
TC223629	A_87_P001871	0.830793	6.396773	5.620004	0.000821	0.098833	-0.04868
WDR67	A_87_P015733	0.827721	7.068219	5.854597	0.000646	0.097029	0.179471
LOC430267	A_87_P021385	0.825773	6.102752	5.599738	0.000838	0.099105	-0.06587
BU223011	A_87_P032666	0.823434	6.517572	5.74662	0.00072	0.097039	0.075929
CR385965	A_87_P016795	0.81376	5.89569	6.000716	0.000558	0.091014	0.321842
RPLP2	A_87_P021942	0.812594	11.79978	5.985484	0.000566	0.091014	0.31622
CR352647	A_87_P018460	0.798797	8.590207	6.083348	0.000514	0.089473	0.396163

SLC24A2	A_87_P037824	0.781334	8.896764	5.670081	0.000779	0.09792	0.005183
ANKRD11	A_87_P016287	0.766597	10.29186	3.132386	0.016719	0.243609	-3.01018
TC188062	A_87_P008155	0.744613	6.77842	5.747922	0.000719	0.097039	0.078815
CR406691	A_87_P012600	0.743718	10.16275	5.739832	0.000725	0.097039	0.068375
NHSL1	A_87_P000961	0.737955	6.169901	3.783682	0.006958	0.181344	-1.89426
CUBN	A_87_P015770	0.734722	11.1799	5.55652	0.000877	0.099874	-0.10877
ABHD6	A_87_P013037	0.445399	13.33248	2.091813	0.075075	0.403165	-4.19736
APOB	A_87_P009392	0.424524	15.69096	1.864071	0.104909	0.455966	-4.54514
AADAC	A_87_P023433	0.416105	5.847187	2.60086	0.035619	0.310686	-3.63041
FZR1	A_87_P037627	0.394851	6.220306	2.293508	0.055801	0.361748	-4.15128
LOC418850	A_87_P003958	0.344575	7.096828	2.046067	0.080303	0.413044	-4.50375
LOC419671	A_87_P011480	0.315535	5.884477	1.711894	0.130979	0.496481	-4.92827
UPP2	A_87_P012718	0.309693	8.058923	1.79142	0.116664	0.474499	-4.79558
NHSL1	A_87_P023191	0.282104	6.55258	2.075769	0.076869	0.406701	-4.48135
PLEKHQ1	A_87_P027367	0.257251	5.346288	1.781834	0.118306	0.477101	-4.89365
BRD1	A_87_P031217	0.242178	5.796926	1.765536	0.12115	0.481149	-4.90649
LOC416214	A_87_P033333	0.203628	5.78895	1.510325	0.175034	0.557327	-5.13602
LOC422838	A_87_P026888	0.194569	6.023572	1.32277	0.227793	0.615731	-5.25868
AADAC	A_87_P024018	0.189028	7.966028	0.515435	0.622242	0.88549	-6.16412
SPEN	A_87_P007724	0.177515	6.01671	1.224774	0.260565	0.64893	-5.48528
CPA2	A_87_P019171	0.167855	5.384217	0.963547	0.367608	0.74067	-5.8485
ANKRD11	A_87_P041632	0.111169	5.987283	0.398662	0.702112	0.916227	-6.26063
SPEN	A_87_P033540	0.08863	5.609021	0.592812	0.572092	0.861868	-6.02776
CUBN	A_87_P006481	0.073723	5.561673	0.399001	0.701873	0.916227	-6.23531
LARP1	A_87_P014677	0.070828	6.327151	0.453968	0.663695	0.902982	-6.20337
SPEN	A_87_P015114	0.058758	5.995002	0.357638	0.731233	0.926262	-6.26078
CRYBA1	A_87_P019019	0.049637	5.441549	0.290538	0.779887	0.94178	-6.29888

BRD1	A_87_P018384	0.045186	7.330342	0.249728	0.810021	0.952432	-6.30139
SPEN	A_87_P005488	0.03828	5.398131	0.209138	0.840341	0.961019	-6.31349
CDON	A_87_P020225	0.025987	6.587412	0.138237	0.893975	0.972653	-6.32374
Anethol							
Down regulated genes							
LARP1	A_87_P034758	-0.00358	5.313377	-0.02521	0.980597	0.994518	-6.33734
ANKRD11	A_87_P038543	-0.05038	5.858476	-0.30765	0.767364	0.93754	-6.27763
LOC421179	A_87_P038022	-0.0603	5.467891	-0.29833	0.774175	0.939923	-6.29578
DYNC1H1	A_87_P008121	-0.08909	5.870267	-0.58274	0.578482	0.86411	-6.16412
GRB2	A_87_P029728	-0.11515	5.315705	-0.77623	0.463217	0.80583	-5.86542
TNNT3	A_87_P009388	-0.13219	5.292242	-0.98143	0.359318	0.73363	-5.59675
GLT25D2	A_87_P027152	-0.30383	5.81651	-1.60707	0.152403	0.527947	-4.99945
BU308605	A_87_P030118	-0.34726	9.532341	-2.38732	0.048627	0.343887	-3.98925
LOC419037	A_87_P017184	-0.35478	10.36378	-2.32603	0.053199	0.356699	-4.06431
LOC420585	A_87_P024094	-0.39163	5.403571	-2.72125	0.029932	0.293397	-3.4993
LOC418850	A_87_P010115	-0.4078	6.268512	-2.94052	0.021887	0.264463	-3.02095
DYNC1H1	A_87_P019789	-0.41912	10.70052	-2.44015	0.04501	0.335573	-3.98925
CDC42BPB	A_87_P018639	-0.45147	6.698886	-2.78538	0.027299	0.283947	-3.28098
LOC418607	A_87_P033600	-0.51507	9.179022	-3.12728	0.016839	0.244288	-3.0139
KIF5B	A_87_P007853	-0.57485	6.491169	-3.13508	0.016657	0.243538	-2.14155
BU273071	A_87_P031048	-0.8169	7.72065	-5.84875	0.000649	0.097029	0.176267
MORF4L1	A_87_P016244	-0.8651	10.55829	-6.38535	0.000384	0.086348	0.666313
TC208562	A_87_P003961	-0.86766	8.650317	-6.04579	0.000534	0.090209	0.365087
LOC425610	A_87_P024269	-0.88469	10.08882	-6.59273	0.000317	0.085477	0.845894
CO764135	A_87_P019795	-0.88498	8.928574	-5.83374	0.000659	0.097029	0.159344
CR732995	A_87_P010849	-0.8861	7.634547	-6.03911	0.000537	0.090346	0.358069

LOC415445	A_87_P019604	-0.89443	10.07785	-6.03371	0.00054	0.090346	0.351884
GNPDA1	A_87_P036824	-0.9231	9.819387	-6.33255	0.000404	0.086348	0.633128
LOC427054	A_87_P036130	-0.93781	9.837849	-6.43677	0.000366	0.086348	0.723792
UGP2	A_87_P036732	-0.94837	11.4386	-5.96722	0.000577	0.091275	0.291169
SOCS3	A_87_P037625	-0.95225	11.52355	-7.14897	0.000192	0.07862	1.305907
LOC415531	A_87_P024595	-0.95968	8.695207	-5.79844	0.000683	0.097029	0.125205
GSTA1	A_87_P009500	-0.9607	11.77119	-6.60961	0.000312	0.085477	0.864345
BU308605	A_87_P030119	-0.96711	8.052488	-6.13655	0.000488	0.089473	0.450563
NUDT6	A_87_P032440	-0.98851	8.152001	-5.8672	0.000637	0.097029	0.196755
CR385677	A_87_P016995	-1.00566	7.449435	-6.97512	0.000224	0.082384	1.162382
FABP3	A_87_P021934	-1.00763	10.53447	-5.02828	0.001551	0.116808	-0.62993
CR389027	A_87_P015076	-1.02452	7.508749	-6.09584	0.000508	0.089473	0.404251
CR523002	A_87_P011912	-1.02507	9.70337	-6.22608	0.000448	0.087228	0.529606
BU296863	A_87_P030431	-1.04575	7.194878	-6.29486	0.000419	0.086348	0.584412
BU484898	A_87_P039937	-1.04646	10.40774	-6.55197	0.000329	0.086348	0.831124
NOXO1	A_87_P010984	-1.05554	6.788754	-5.923	0.000603	0.09363	0.255592
BLMH	A_87_P038228	-1.06134	9.45922	-5.6554	0.000791	0.097953	-4.7E-06
SLC37A2	A_87_P023260	-1.06202	9.498505	-6.64116	0.000303	0.085477	0.906682
C-16	A_87_P009336	-1.07516	7.303363	-6.06596	0.000523	0.089473	0.383595
BU129127	A_87_P034022	-1.12502	7.144141	-5.57376	0.000861	0.099586	-0.09444
BU123654	A_87_P034186	-1.14116	7.78349	-6.81573	0.000258	0.083449	1.042131
MLF1	A_87_P010877	-1.14159	6.256189	-6.21063	0.000454	0.087483	0.515439
FABP3	A_87_P021933	-1.14241	9.764458	-5.58004	0.000856	0.099586	-0.08578
CR389681	A_87_P014658	-1.15207	10.46053	-7.0309	0.000213	0.080161	1.218217
CR353647	A_87_P017801	-1.17466	7.063261	-6.80981	0.00026	0.083449	1.028789
RCJMB04_7d1	A_87_P036816	-1.17523	10.38491	-6.32241	0.000408	0.086348	0.617447
TC191392	A_87_P034248	-1.17678	6.120014	-6.28411	0.000423	0.086348	0.578596

1700012B18RIK	A_87_P011567	-1.17796	11.22739	-6.09591	0.000508	0.089473	0.408751
TC206107	A_87_P004587	-1.20014	9.360992	-5.79809	0.000684	0.097029	0.124717
GSTT1	A_87_P009143	-1.20746	10.94061	-9.32235	3.56E-05	0.048313	2.729175
TC220248	A_87_P002700	-1.22657	7.208018	-5.93598	0.000595	0.092766	0.255998
TC199001	A_87_P006979	-1.23195	9.871338	-5.7559	0.000714	0.097039	0.099248
BU490772	A_87_P025233	-1.28838	7.050169	-6.06231	0.000525	0.089473	0.376694
GCG	A_87_P008759	-1.29049	7.222154	-6.60167	0.000314	0.085477	0.852154
CR523709	A_87_P011424	-1.33025	6.544542	-7.2236	0.00018	0.076686	1.352546
LOC418700	A_87_P019694	-1.35654	7.713938	-7.6176	0.000129	0.075518	1.656263
TC202539	A_87_P006253	-1.39052	9.717155	-7.90162	0.000103	0.068632	1.866912
TC191391	A_87_P007845	-1.42504	7.693566	-10.4968	1.64E-05	0.029984	3.328977
LOC418060	A_87_P021136	-1.44567	7.909738	-7.47325	0.000146	0.075518	1.544862
TC193806	A_87_P007610	-1.44895	8.416028	-6.91354	0.000237	0.082384	1.114803
BU417024	A_87_P039183	-1.46128	6.133697	-6.66841	0.000295	0.085477	0.911282
LOC395708	A_87_P008896	-1.66586	8.434461	-11.2793	1.02E-05	0.025232	3.675195
CR387293	A_87_P015918	-1.71259	9.202857	-8.08243	8.9E-05	0.067942	1.990331
LOC422306	A_87_P030446	-1.71323	7.996071	-7.54695	0.000137	0.075518	1.613669
LOC418790	A_87_P021778	-1.83449	12.14388	-8.11273	8.69E-05	0.067942	2.029461
CV862752	A_87_P009844	-1.87884	9.642913	-8.7631	5.31E-05	0.060373	2.458908
FGG	A_87_P037916	-1.9518	7.065645	-6.12678	0.000493	0.089473	0.441441
ELA1	A_87_P023858	-2.10205	10.67685	-11.7671	7.69E-06	0.021588	3.872248
TC193162	A_87_P007669	-2.10231	11.02518	-10.0962	2.12E-05	0.037098	3.135977
TC197901	A_87_P007125	-2.12509	9.163066	-14.5202	1.88E-06	0.007192	4.767016
PRSS3	A_87_P009139	-2.72757	6.613198	-7.06065	0.000208	0.07965	1.247839
K123	A_87_P008724	-2.89887	7.23779	-9.56666	3.01E-05	0.045273	2.862688
CPB1	A_87_P022185	-3.38717	9.01057	-18.063	4.27E-07	0.002248	5.535204
CPA1	A_87_P008876	-4.00424	13.40686	-18.8308	3.22E-07	0.001934	5.6625

LOC430670	A_87_P021646	-4.11023	8.782912	-15.4323	1.24E-06	0.005823	4.998362
CPA2	A_87_P021751	-4.30228	10.21274	-26.0532	3.47E-08	0.000365	6.456055
PNLIP	A_87_P023861	-4.36029	10.82498	-10.8322	1.33E-05	0.026691	3.482149

Garlic

Up-regulated

GeneName	**Agilent ID**	logFC	AveExpr	t	PValue	adjPVal	B
TC223018	A_87_P002214	5.417267	9.922726	21.65377	1.24E-07	0.002485	7.664505
TC210123	A_87_P003854	4.36885	8.914388	14.24953	2.13E-06	0.002807	5.557162
CR386395	A_87_P016505	3.62175	8.743256	8.295579	7.54E-05	0.010005	2.238525
PLEKHQ1	A_87_P027367	3.472835	7.2908	15.64114	1.14E-06	0.00272	6.073271
LOC420585	A_87_P028929	3.381939	7.739128	10.20521	1.97E-05	0.005308	3.5532
GDF2	A_87_P009507	3.192406	8.844506	8.301486	7.51E-05	0.010005	2.243076
CR390009	A_87_P014428	3.182333	9.182793	10.09602	2.12E-05	0.005397	3.48574
CR386260	A_87_P016602	3.143616	8.196046	12.8939	4.18E-06	0.003255	4.979359
ARC	A_87_P037475	3.142328	7.985849	11.27555	1.02E-05	0.004019	4.171977
CN236254	A_87_P020473	3.052023	7.208837	8.660481	5.72E-05	0.008924	2.51356
BU479212	A_87_P025451	3.027008	8.588658	7.141192	0.000194	0.013667	1.281258
CO503580	A_87_P041957	2.992013	7.078729	7.470625	0.000146	0.012484	1.568831
CR406944	A_87_P012419	2.987838	7.435867	8.73902	5.4E-05	0.008548	2.57117
APOB	A_87_P034149	2.953624	8.427088	6.215236	0.000452	0.020298	0.40416
RCJMB04_21j5	A_87_P012102	2.938946	10.45699	19.70112	2.36E-07	0.002485	7.239298
CD760819	A_87_P021203	2.896273	6.716274	9.381864	3.41E-05	0.007046	3.022757
DYNC1H1	A_87_P038038	2.864114	7.552734	12.20606	6.03E-06	0.003338	4.653319
BU455240	A_87_P026343	2.820383	7.580348	10.60088	1.54E-05	0.004896	3.790704
BU247950	A_87_P031712	2.820165	9.674958	7.903669	0.000103	0.011183	1.928998
TC186301	A_87_P008359	2.812524	14.53735	7.483966	0.000145	0.012484	1.580224
CR390040	A_87_P014407	2.809063	8.328124	6.956364	0.000228	0.014727	1.114508
BU415738	A_87_P027727	2.79161	6.845288	5.720439	0.00074	0.02526	-0.11003

BX931974	A_87_P023710	2.766386	7.308088	11.79599	7.57E-06	0.003598	4.447201
BX277386	A_87_P037368	2.75407	7.799524	6.162587	0.000476	0.020914	0.351027
TC200204	A_87_P006807	2.697556	8.072637	7.526793	0.00014	0.012363	1.616668
LOC425139	A_87_P014925	2.693621	9.1819	11.18697	1.08E-05	0.004057	4.123544
CRH	A_87_P037220	2.672877	6.730633	7.189482	0.000186	0.013504	1.324174
CR390166	A_87_P014333	2.661301	8.688592	10.13755	2.06E-05	0.005397	3.511494
FZR1	A_87_P037626	2.65754	15.15082	8.399965	6.96E-05	0.009762	2.318465
CR391365	A_87_P013511	2.646549	7.535799	11.57909	8.56E-06	0.00373	4.334403
LOC419671	A_87_P011329	2.629356	7.322559	6.800534	0.000262	0.015526	0.970792
TC194119	A_87_P007570	2.607279	8.275533	6.776351	0.000268	0.015631	0.948227
TC198879	A_87_P006998	2.599557	7.363867	6.94827	0.000229	0.014768	1.107115
CN237892	A_87_P040742	2.572242	7.728358	11.13046	1.11E-05	0.004109	4.092393
BU423426	A_87_P027415	2.564211	10.30395	7.140496	0.000194	0.013667	1.280636
LOC421179	A_87_P026850	2.509674	8.179382	6.611477	0.000311	0.016687	0.792481
MDK	A_87_P009319	2.497724	7.159742	6.048145	0.000532	0.021842	0.234256
AJ455964	A_87_P037269	2.483443	7.851321	7.134953	0.000195	0.013667	1.275693
LOC423636	A_87_P030019	2.457692	6.904272	8.401575	6.95E-05	0.009762	2.31969
CO771160	A_87_P019220	2.454038	6.566678	6.19809	0.00046	0.020506	0.386897
LOC425289	A_87_P012241	2.429191	7.239367	9.101617	4.16E-05	0.007534	2.830159
TC226737	A_87_P000466	2.42582	7.763476	9.466326	3.22E-05	0.006847	3.079557
BU104894	A_87_P034768	2.424214	6.423518	6.139797	0.000487	0.021039	0.327914
TC221798	A_87_P002470	2.41321	7.539481	7.534729	0.000139	0.012358	1.623399
GLT25D2	A_87_P017120	2.401886	7.149251	8.48612	6.52E-05	0.00966	2.383674
LFNG	A_87_P008992	2.390865	7.951289	9.082252	4.21E-05	0.007534	2.816611
CV858659	A_87_P010532	2.350559	7.476356	7.843168	0.000108	0.011582	1.879852
AJ739127	A_87_P035851	2.32505	7.439919	8.967787	4.57E-05	0.007889	2.735884
M27663	A_87_P009373	2.316347	7.924457	7.475596	0.000146	0.012484	1.573079

LOC423162	A_87_P023103	2.314943	7.492054	11.30224	1.01E-05	0.004019	4.186479
TNNT3	A_87_P009388	2.310754	7.181178	7.536874	0.000138	0.012358	1.625217
BU226241	A_87_P032548	2.283567	6.561791	5.944466	0.00059	0.022836	0.126936
WHSC1L1	A_87_P013214	2.2701	9.44192	8.35346	7.21E-05	0.009762	2.282978
DYNC1H1	A_87_P008121	2.266514	10.70518	13.04516	3.86E-06	0.003253	5.047927
ZDHHC5	A_87_P035034	2.261976	6.815334	7.273081	0.000173	0.013035	1.397845
CR388868	A_87_P015174	2.258443	7.894729	9.651052	2.84E-05	0.006497	3.201828
BU417989	A_87_P027684	2.226168	6.413987	8.800759	5.16E-05	0.008358	2.616072
CR390868	A_87_P013879	2.201505	6.670342	6.407396	0.000376	0.018153	0.594997
PHOX2	A_87_P008691	2.199162	7.076713	6.694375	0.000288	0.016116	0.871208
CDON	A_87_P020225	2.181635	6.648162	7.412787	0.000154	0.012734	1.519214
AJ728686	A_87_P035890	2.176365	6.565869	6.257233	0.000434	0.019879	0.446281
SPEN	A_87_P033540	2.160839	7.678228	9.481601	3.19E-05	0.00682	3.089769
BU373614	A_87_P028711	2.158572	8.163094	7.832652	0.000109	0.011582	1.871272
CR386893	A_87_P016179	2.155938	9.32154	7.154854	0.000191	0.013667	1.293426
TNPO3	A_87_P016263	2.144692	7.527136	9.87332	2.45E-05	0.005922	3.345482
HCRT	A_87_P014389	2.113268	8.788928	8.234214	7.91E-05	0.010115	2.191048
CR406193	A_87_P012941	2.105225	9.072681	10.65308	1.49E-05	0.004857	3.821244
CN234081	A_87_P020521	2.101173	6.349822	10.37234	1.77E-05	0.005218	3.654832
BU268923	A_87_P031191	2.097826	6.810877	7.534287	0.000139	0.012358	1.623024
TC203225	A_87_P005875	2.091986	14.69902	10.3576	1.79E-05	0.005228	3.645946
MGAT5	A_87_P016016	2.084338	8.754848	8.849984	4.98E-05	0.008237	2.651634
TC207295	A_87_P004132	2.08427	6.849754	6.407505	0.000376	0.018153	0.595104
LOC418607	A_87_P017318	2.082023	8.679819	11.78789	7.6E-06	0.003598	4.443033
BU470394	A_87_P025748	2.062785	7.051337	6.4267	0.00037	0.018011	0.613905
TC224509	A_87_P001374	2.052643	6.756692	6.895874	0.00024	0.015028	1.059064
BU387573	A_87_P028278	2.007733	7.037257	7.144932	0.000193	0.013667	1.28459

TC202794	A_87_P006118	1.984307	7.037863	5.876608	0.000631	0.023524	0.055896
ABHD6	A_87_P013037	1.98111	6.361032	6.235872	0.000443	0.020124	0.424886
BX262701	A_87_P025099	1.97955	7.666799	7.258194	0.000175	0.01306	1.384783
LOC424135	A_87_P030843	1.973145	8.621746	11.72381	7.88E-06	0.003607	4.409961
MDK	A_87_P029081	1.967867	6.518566	5.444731	0.000986	0.028242	-0.41143
LOC430010	A_87_P021512	1.965178	8.707549	10.24315	1.92E-05	0.005308	3.576439
TC210304	A_87_P003832	1.963803	9.830926	9.044273	4.33E-05	0.007689	2.789949
BX277609	A_87_P024840	1.94855	8.908586	8.772201	5.27E-05	0.008446	2.595344
OPCML	A_87_P037717	1.947096	6.824025	5.26307	0.001198	0.030688	-0.61607
LOC427434	A_87_P022431	1.943261	8.637726	8.463197	6.64E-05	0.009696	2.366392
BRD1	A_87_P031217	1.942316	9.767223	11.18162	1.08E-05	0.004057	4.120602
TC203827	A_87_P005544	1.925507	6.785104	8.012501	9.4E-05	0.010717	2.016472
BU120493	A_87_P034283	1.908308	6.804688	7.190428	0.000186	0.013504	1.325012
KIF5B	A_87_P007853	1.864352	10.54807	7.863883	0.000106	0.011428	1.896721
LOC417598	A_87_P007248	1.860532	9.635278	12.58528	4.91E-06	0.003255	4.836018
CTCF	A_87_P008703	1.853838	9.822619	11.89352	7.16E-06	0.003598	4.497055
TC224651	A_87_P001292	1.847881	7.535536	5.664719	0.000784	0.025918	-0.17006
NKX-2.2	A_87_P037886	1.837636	7.488328	7.397523	0.000155	0.012759	1.506058
CO770158	A_87_P019319	1.836656	6.291328	5.383104	0.001053	0.028955	-0.4803
TC206022	A_87_P004642	1.828047	7.048458	6.065012	0.000524	0.02163	0.251576
CDC42BPB	A_87_P018639	1.826955	9.222297	12.03019	6.64E-06	0.003493	4.56604
TC227424	A_87_P000116	1.825614	7.217393	6.836751	0.000253	0.015254	1.004453
CR338795	A_87_P018837	1.821955	8.141499	9.69542	2.76E-05	0.006402	3.230803
CR385664	A_87_P017003	1.816715	6.755644	7.695271	0.000121	0.011879	1.758127
LOC420214	A_87_P023888	1.816255	9.555262	12.95627	4.05E-06	0.003255	5.007766
RCJMB04_11l17	A_87_P036602	1.804636	11.47125	8.600873	5.98E-05	0.009145	2.469467

BU461582	A_87_P026084	1.798394	9.215992	13.4839	3.09E-06	0.003144	5.240803
RCJMB04_30e3	A_87_P011423	1.783615	11.81114	13.41669	3.2E-06	0.003144	5.211822
CD727362	A_87_P021327	1.774074	6.531663	5.879299	0.00063	0.023523	0.058725
APOB	A_87_P022123	1.766774	8.584946	5.702916	0.000753	0.025473	-0.12886
TC227335	A_87_P000158	1.758278	6.88685	7.174095	0.000188	0.013591	1.310528
RCJMB04_19e2	A_87_P035599	1.751931	11.19889	7.64797	0.000126	0.011996	1.718716
TC207604	A_87_P004074	1.744403	7.306998	9.855792	2.48E-05	0.005957	3.334289
CO635711	A_87_P020191	1.711356	6.975835	11.7869	7.61E-06	0.003598	4.442524
ADIPOR2	A_87_P037108	1.709929	11.08546	10.4486	1.69E-05	0.005127	3.700559
BU415119	A_87_P027742	1.702494	6.82061	5.827456	0.000664	0.024048	0.004041
OLIG3	A_87_P037632	1.699857	6.704635	6.919412	0.000235	0.014931	1.080691
BU391107	A_87_P028183	1.683482	6.958768	7.905645	0.000102	0.011183	1.930596
AADAC	A_87_P023433	1.679254	6.686007	7.474987	0.000146	0.012484	1.572558
CR389707	A_87_P014643	1.677874	7.115202	9.307844	3.59E-05	0.007057	2.97251
CV859110	A_87_P010492	1.672093	8.213298	6.676978	0.000293	0.016147	0.854756
BU421848	A_87_P027483	1.665532	6.488086	7.590919	0.000132	0.012186	1.670866
UBXD2	A_87_P022336	1.648795	9.896447	12.25758	5.86E-06	0.003319	4.678578
CSPG5	A_87_P008748	1.646708	6.166809	6.796723	0.000263	0.015558	0.967241
LOC418850	A_87_P003958	1.646565	10.18271	12.38481	5.47E-06	0.003319	4.740357
BU305794	A_87_P030191	1.634162	7.504305	7.151137	0.000192	0.013667	1.290118
CO757296	A_87_P020145	1.633027	6.223491	6.237613	0.000443	0.020124	0.426631
CR385621	A_87_P017031	1.632155	6.845923	5.217563	0.001259	0.031508	-0.6681
RCJMB04_22k13	A_87_P009183	1.632036	7.357983	7.040059	0.000212	0.014372	1.19051
BU295088	A_87_P030477	1.613234	6.369213	6.182537	0.000467	0.020624	0.371204
TC220349	A_87_P002688	1.608801	7.059313	5.789902	0.000689	0.024466	-0.0358
CRYBA1	A_87_P009400	1.598227	7.182145	6.221372	0.00045	0.020265	0.410329

IRS-1	A_87_P009216	1.591721	6.759091	5.536807	0.000895	0.027309	-0.30955
LOC416529	A_87_P016175	1.572861	7.016567	10.32034	1.83E-05	0.005242	3.623414
ANKRD11	A_87_P041632	1.534698	10.30644	10.75608	1.39E-05	0.004624	3.880983
BU414476	A_87_P027750	1.517179	6.296522	4.793834	0.002023	0.039493	-1.1676
CASZ1	A_87_P023401	1.512518	6.413517	6.901425	0.000239	0.015028	1.064171
TC219891	A_87_P002751	1.508501	6.877864	6.940866	0.000231	0.014825	1.100344
RCJMB04_20d5	A_87_P036326	1.507354	7.193692	6.109252	0.000501	0.021297	0.296826
BU424987	A_87_P041883	1.505333	6.308624	5.715562	0.000744	0.02526	-0.11527
TC225719	A_87_P000887	1.499034	7.156528	7.726556	0.000118	0.011823	1.784066
CR523642	A_87_P011476	1.490371	6.81085	6.175345	0.00047	0.020722	0.363936
BU446674	A_87_P026707	1.481507	6.019076	6.106836	0.000503	0.021304	0.294361
TC222502	A_87_P002382	1.481365	8.892461	7.613862	0.00013	0.012149	1.69015
LOC416214	A_87_P033333	1.474362	6.999075	7.284445	0.000171	0.01303	1.407799
BM426314	A_87_P034888	1.458408	6.203328	7.831374	0.000109	0.011582	1.870227
BX930578	A_87_P024243	1.456957	10.19514	9.821661	2.53E-05	0.006036	3.312426
BX260117	A_87_P025154	1.456351	7.028143	6.071308	0.00052	0.02156	0.258032
AM067107	A_87_P035373	1.442052	6.862038	6.729752	0.000279	0.015929	0.904547
BX934358	A_87_P022627	1.438792	6.75994	8.048236	9.14E-05	0.010646	2.044936
TC186792	A_87_P008265	1.43868	8.0653	6.301505	0.000416	0.019343	0.490431
MEF2A	A_87_P037524	1.436489	9.247953	9.638986	2.86E-05	0.006514	3.193923
TC194424	A_87_P007536	1.404065	8.169236	7.540572	0.000138	0.012358	1.62835
LOC426613	A_87_P023334	1.401208	7.334105	6.116024	0.000498	0.021242	0.303728
HBD	A_87_P009554	1.397616	12.83512	7.510181	0.000141	0.012483	1.602555
CR352651	A_87_P018456	1.385618	9.313825	9.672726	2.8E-05	0.006438	3.216002
CO768011	A_87_P019527	1.384532	6.596461	5.534143	0.000898	0.027319	-0.31248
BU228800	A_87_P032464	1.372774	5.97449	6.289517	0.000421	0.019522	0.478501
LARP1	A_87_P034758	1.36637	7.451497	6.551608	0.000329	0.016988	0.735093

LOC419436	A_87_P002536	1.362553	6.364257	5.501911	0.000928	0.027523	-0.34802
RRAS2	A_87_P014781	1.360997	10.9093	8.13075	8.57E-05	0.010335	2.110179
DN829968	A_87_P009752	1.358651	6.157345	5.110078	0.001417	0.033669	-0.79222
BU476696	A_87_P025525	1.357989	6.479473	7.005094	0.000218	0.014595	1.158859
VAX1	A_87_P038172	1.352599	6.249451	5.25343	0.001211	0.030783	-0.62706
LOC425243	A_87_P021357	1.351836	7.480518	7.152227	0.000192	0.013667	1.291088
CR390671	A_87_P014002	1.348874	7.690412	6.60046	0.000314	0.016759	0.781954
LOC419037	A_87_P017184	1.348352	12.52331	8.771632	5.27E-05	0.008446	2.594931
CV862615	A_87_P009876	1.332883	8.374657	5.651054	0.000795	0.026095	-0.18485
LOC427047	A_87_P011568	1.32753	8.414633	8.206221	8.08E-05	0.010138	2.16927
AKT2	A_87_P037817	1.312046	7.446635	7.718385	0.000119	0.011823	1.777301
TC193639	A_87_P007630	1.307296	7.109907	6.409651	0.000376	0.018153	0.597208
BU462788	A_87_P026028	1.30336	7.376784	7.713497	0.00012	0.011823	1.773251
CD217788	A_87_P021367	1.297697	6.524163	7.430803	0.000151	0.012703	1.534709
BX935775	A_87_P021947	1.296274	9.059871	8.051797	9.12E-05	0.010646	2.047766
U76305	A_87_P009023	1.294854	8.199186	5.72287	0.000738	0.02526	-0.10742
WDR67	A_87_P015733	1.285835	7.068219	9.094908	4.18E-05	0.007534	2.825469
CR353864	A_87_P017683	1.283953	7.090907	6.611939	0.000311	0.016687	0.792922
HS1BP3	A_87_P018137	1.276394	7.953201	6.157995	0.000478	0.020944	0.346375
CR386490	A_87_P016444	1.26986	8.093747	7.319776	0.000166	0.012981	1.438652
TEAD3	A_87_P009075	1.244151	7.782432	7.078804	0.000205	0.014159	1.225416
NHSL1	A_87_P002050	1.2312	6.553987	6.896143	0.00024	0.015028	1.059312
LOC419750	A_87_P015390	1.210357	6.147698	5.188096	0.0013	0.032059	-0.70195
TC205715	A_87_P004815	1.204017	6.062793	5.935018	0.000596	0.022876	0.117083
CR389142	A_87_P015005	1.18251	7.051845	8.092663	8.83E-05	0.010497	2.080147
GBE	A_87_P035833	1.174279	7.483263	4.104652	0.004622	0.061693	-2.03907
BU467197	A_87_P025869	1.168849	7.158828	6.917129	0.000236	0.014931	1.078596

ELMOD2	A_87_P023542	1.168116	8.189453	5.063129	0.001492	0.034398	-0.84699
BU397032	A_87_P040788	1.16758	6.597443	8.643434	5.8E-05	0.009004	2.500983
BU205361	A_87_P033349	1.162494	5.990556	5.673122	0.000777	0.02582	-0.16098
CR523552	A_87_P011535	1.161866	6.772858	7.766401	0.000115	0.011732	1.816952
BU305923	A_87_P030186	1.134254	8.261443	6.560201	0.000326	0.01693	0.743357
GRB2	A_87_P029728	1.11274	9.467102	5.024057	0.001559	0.035058	-0.89282
BU452711	A_87_P026454	1.110326	6.30809	3.688821	0.007875	0.082955	-2.59969
LGR5	A_87_P018440	1.099875	6.029103	7.879663	0.000105	0.011313	1.909542
CR523450	A_87_P011601	1.098468	7.711953	5.470527	0.00096	0.027919	-0.38276
MARK1	A_87_P021538	1.085638	9.128538	7.604146	0.000131	0.012158	1.681991
CR406691	A_87_P012600	1.084509	10.16275	8.369973	7.12E-05	0.009762	2.295602
LOC427758	A_87_P007751	1.080391	7.146365	3.989659	0.005342	0.066804	-2.19156
UPP2	A_87_P022639	1.071893	6.786706	5.690762	0.000763	0.025669	-0.14195
CR390958	A_87_P013821	1.061511	12.35613	6.630634	0.000306	0.016481	0.810749
LMO4	A_87_P037569	1.059354	8.768973	6.735645	0.000278	0.015928	0.910085
BU425544	A_87_P027321	1.05914	7.753464	6.336402	0.000403	0.01892	0.525052
CD733169	A_87_P021265	1.051037	6.585147	7.676766	0.000123	0.011899	1.742737
MYOG	A_87_P009757	1.032767	5.906094	5.445578	0.000985	0.028236	-0.41048
LOC420679	A_87_P022679	1.03243	7.253527	6.099652	0.000506	0.021327	0.287029
CR522893	A_87_P011989	1.03196	8.455516	6.481395	0.000351	0.017494	0.667214
LOC415476	A_87_P034974	1.02762	8.097802	5.540002	0.000892	0.027309	-0.30604
LOC422838	A_87_P026888	1.021924	8.925267	7.356268	0.000161	0.012903	1.470374
CR390688	A_87_P013990	1.017507	8.913598	5.982912	0.000568	0.022657	0.166903
LOC415553	A_87_P021890	1.008216	8.779147	6.506672	0.000343	0.017317	0.691723
APOB	A_87_P012184	1.004595	9.614417	3.647515	0.008315	0.085377	-2.65672
ELA1	A_87_P023858	0.987266	10.67685	5.526656	0.000905	0.027396	-0.32072
LOC395818	A_87_P009087	0.920015	7.258798	6.276797	0.000426	0.019697	0.465822

FZR1	A_87_P037627	0.907587	6.220306	5.271752	0.001187	0.030675	-0.60618
BU332246	A_87_P029583	0.904321	6.096583	5.4669	0.000963	0.027948	-0.38679
CR385965	A_87_P016795	0.899303	5.89569	6.631518	0.000305	0.016481	0.811592
CPA1	A_87_P008876	0.884935	13.40686	4.161598	0.004305	0.059338	-1.96429
BU460481	A_87_P026133	0.88388	7.71433	4.540935	0.002717	0.045969	-1.47886
LHX1	A_87_P009469	0.878037	5.904062	5.806967	0.000678	0.024292	-0.01767
BU229541	A_87_P032429	0.874057	9.5082	6.282254	0.000424	0.019616	0.471265
BX260970	A_87_P025138	0.866904	11.04211	5.723426	0.000738	0.02526	-0.10682
BG713524	A_87_P041329	0.859105	8.800377	5.107631	0.00142	0.033722	-0.79507
ANKRD11	A_87_P016287	0.829109	10.29186	3.387815	0.011769	0.102913	-3.02046
LOC418850	A_87_P010987	0.828382	7.096828	4.918889	0.001754	0.036715	-1.01733
LOC419752	A_87_P025507	0.824746	8.934367	5.342726	0.0011	0.029557	-0.52574
ABCD2	A_87_P012773	0.821795	9.228287	5.071709	0.001478	0.03424	-0.83695
GBX-1	A_87_P038146	0.820149	6.663906	4.290271	0.003674	0.054504	-1.79715
TC223629	A_87_P001871	0.789825	6.396773	5.342872	0.001099	0.029557	-0.52557
TC226823	A_87_P000414	0.781267	7.131516	3.760223	0.007173	0.07861	-2.50165
LOC419752	A_87_P008020	0.773261	8.024437	2.020798	0.083345	0.320754	-5.01003
CR353938	A_87_P017639	0.768199	9.818816	5.367078	0.001071	0.029216	-0.49831
CR352797	A_87_P018359	0.735624	6.479242	4.866124	0.001862	0.037936	-1.08044
BU223011	A_87_P032666	0.716286	6.517572	4.998849	0.001603	0.0354	-0.92251
GCG	A_87_P008759	0.709982	7.222154	3.632002	0.008487	0.086001	-2.6782
CR390595	A_87_P014045	0.704693	12.75921	4.401226	0.003211	0.050698	-1.65506
CR386677	A_87_P016317	0.699334	6.429055	3.527261	0.009754	0.092896	-2.82408
LOC416235	A_87_P018176	0.69185	8.182308	4.527607	0.00276	0.046421	-1.49554
LOC396450	A_87_P009378	0.686717	6.499232	4.155875	0.004336	0.059567	-1.97179
SLC24A2	A_87_P037824	0.655666	8.896764	4.758116	0.002108	0.040326	-1.21096
LOC419672	A_87_P027565	0.642339	6.314449	3.599755	0.008857	0.088175	-2.72296

CR353205	A_87_P018094	0.615056	7.355828	3.705369	0.007706	0.081808	-2.57691
RCJMB04_7d18	A_87_P036813	0.607024	9.673969	3.860362	0.006301	0.073329	-2.36537
LOC417506	A_87_P017838	0.600836	6.06158	3.942144	0.005674	0.068878	-2.25515
LOC419671	A_87_P011480	0.595238	5.884477	3.229389	0.014617	0.116225	-3.24635
RPLP2	A_87_P021942	0.582678	11.79978	4.291944	0.003666	0.054504	-1.79499
LOC430267	A_87_P021385	0.569409	6.102752	3.861279	0.006293	0.073323	-2.36413
CR352647	A_87_P018460	0.544033	8.590207	4.143156	0.004405	0.059953	-1.98845
NHSL1	A_87_P000961	0.536987	6.169901	2.75327	0.028586	0.171751	-3.93902
CUBN	A_87_P015770	0.528699	11.1799	3.998419	0.005283	0.06628	-2.17988
TC188062	A_87_P008155	0.510781	6.77842	3.942892	0.005669	0.068847	-2.25415
TC191391	A_87_P007845	0.505862	7.693566	3.726168	0.007499	0.080752	-2.54832
SPEN	A_87_P005488	0.477551	5.995002	2.906675	0.022963	0.151503	-3.71409
SPEN	A_87_P015114	0.436473	6.01671	3.01146	0.019802	0.13904	-3.56127
LARP1	A_87_P014677	0.428841	6.327151	2.748646	0.028776	0.172403	-3.94581
AADAC	A_87_P024018	0.395282	7.966028	1.077844	0.317103	0.648588	-6.21336
APOB	A_87_P009392	0.384118	15.69096	1.686649	0.135862	0.420324	-5.47517
CUBN	A_87_P006481	0.338671	5.561673	1.83295	0.109797	0.374043	-5.27495
CRYBA1	A_87_P019019	0.336732	5.441549	1.970971	0.08968	0.334929	-5.08101
ANKRD11	A_87_P038543	0.327275	5.987283	1.173634	0.279206	0.609622	-6.1105
LOC420585	A_87_P024094	0.268939	5.403571	1.868722	0.104197	0.363565	-5.2251
NHSL1	A_87_P023191	0.264609	6.55258	1.947044	0.092888	0.341176	-5.11493
LOC421179	A_87_P038022	0.212611	5.467891	1.051823	0.328088	0.659591	-6.24024
BRD1	A_87_P018384	0.212481	5.796926	1.549037	0.16563	0.470416	-5.65713
LOC422838	A_87_P005240	0.101275	6.023572	0.688516	0.513458	0.802074	-6.56091
SPEN	A_87_P007302	0.082917	5.609021	0.554598	0.596565	0.847875	-6.64995
ABHD6	A_87_P026925	0.076519	13.33248	0.35937	0.729994	0.909909	-6.74772
ANKRD11	A_87_P028441	0.069055	5.858476	0.421663	0.686013	0.890771	-6.72081

SPEN	A_87_P007724	0.068915	5.398131	0.376505	0.717778	0.904967	-6.74073
DYNC1H1	A_87_P008241	0.06566	5.870267	0.429503	0.680564	0.888354	-6.71714
LOC416214	A_87_P015049	0.056882	5.78895	0.421901	0.685847	0.890721	-6.7207
LARP1	A_87_P015360	0.044132	5.313377	0.310887	0.765008	0.924873	-6.76579
Garlic							
Down-regulated							
CPA2	A_87_P021751	-0.00313	5.384217	-0.01799	0.986153	0.99619	-6.81986
BRD1	A_87_P034947	-0.00595	7.330342	-0.03286	0.974711	0.993156	-6.81943
CDON	A_87_P015827	-0.02965	6.587412	-0.15771	0.879175	0.964002	-6.80601
CDC42BPB	A_87_P032380	-0.06275	6.698886	-0.38716	0.710223	0.901273	-6.73622
TNNT3	A_87_P034373	-0.10802	5.292242	-0.80195	0.449139	0.759738	-6.47253
GRB2	A_87_P009495	-0.10998	5.315705	-0.74136	0.48278	0.782394	-6.52117
PLEKHQ1	A_87_P012444	-0.12579	5.346288	-0.8713	0.412686	0.732583	-6.41301
UPP2	A_87_P012718	-0.19922	8.058923	-1.15236	0.287282	0.617512	-6.13386
LOC418607	A_87_P033600	-0.33404	9.179022	-2.02818	0.082445	0.318358	-4.99948
AADAC	A_87_P034264	-0.33828	5.847187	-2.11444	0.072615	0.296879	-4.8755
DYNC1H1	A_87_P019789	-0.39333	10.70052	-2.29002	0.056087	0.255429	-4.62023
KIF5B	A_87_P022772	-0.42251	6.491169	-2.30428	0.054925	0.252321	-4.59937
GLT25D2	A_87_P027152	-0.43103	5.81651	-2.27991	0.056926	0.257728	-4.63501
CR732995	A_87_P010849	-0.51583	7.634547	-3.51562	0.009907	0.093759	-2.84037
LOC419037	A_87_P015156	-0.57636	10.36378	-3.7788	0.007002	0.077935	-2.47627
UGP2	A_87_P036732	-0.59206	11.4386	-3.72528	0.007508	0.080759	-2.54954
C-16	A_87_P009336	-0.61711	7.303363	-3.48166	0.010369	0.096202	-2.88803
BU484898	A_87_P039937	-0.63087	10.40774	-3.94994	0.005618	0.068428	-2.24469
BU439010	A_87_P041884	-0.64843	6.582341	-4.29184	0.003667	0.054504	-1.79513

BU377193	A_87_P041674	-0.65849	7.32051	-4.3789	0.003299	0.051561	-1.6835
BLMH	A_87_P038228	-0.67959	9.45922	-3.6212	0.008609	0.086891	-2.69318
LOC415445	A_87_P019604	-0.6832	10.07785	-4.60875	0.002508	0.043866	-1.39442
GSTA1	A_87_P009500	-0.68823	11.77119	-4.735	0.002165	0.04086	-1.23913
BU308605	A_87_P030119	-0.70728	9.532341	-4.86231	0.00187	0.037936	-1.08502
TC193162	A_87_P007669	-0.73154	11.02518	-3.51321	0.009939	0.093915	-2.84375
CR523709	A_87_P011424	-0.73624	6.544542	-3.99795	0.005286	0.066299	-2.18051
CPB1	A_87_P022185	-0.74417	9.01057	-3.96849	0.005487	0.067694	-2.21985
MLF1	A_87_P010877	-0.74734	6.256189	-4.06577	0.004852	0.063199	-2.09041
LOC425610	A_87_P024269	-0.82095	10.08882	-6.11773	0.000497	0.021228	0.305465
SLC37A2	A_87_P023260	-0.82436	9.498505	-5.155	0.001348	0.032747	-0.74014
CR389681	A_87_P014658	-0.82438	10.46053	-5.03106	0.001546	0.035058	-0.88458
TC220248	A_87_P002700	-0.865	7.208018	-4.18619	0.004176	0.058359	-1.93215
NOXO1	A_87_P010984	-0.87278	6.788754	-4.89746	0.001797	0.037082	-1.04291
LOC430670	A_87_P021646	-0.92931	8.782912	-3.48922	0.010264	0.095674	-2.87741
TC199001	A_87_P006979	-0.93249	9.871338	-4.35674	0.003388	0.052238	-1.7118
TC197901	A_87_P007125	-0.9559	9.163066	-6.53146	0.000335	0.0171	0.715681
LOC418850	A_87_P010115	-0.96211	6.268512	-6.93752	0.000232	0.014825	1.097286
CR523002	A_87_P011912	-0.97241	9.70337	-5.90625	0.000613	0.023183	0.087002
BU273071	A_87_P031048	-0.98347	7.72065	-7.04131	0.000211	0.014372	1.191642
BU417024	A_87_P039183	-1.00518	6.133697	-4.58701	0.002573	0.044571	-1.42141
LOC422306	A_87_P030446	-1.00923	7.996071	-4.44574	0.003044	0.049181	-1.5986
CR385677	A_87_P016995	-1.03353	7.449435	-7.16842	0.000189	0.013611	1.30549
SOCS3	A_87_P037625	-1.04345	11.52355	-7.83365	0.000108	0.011582	1.872084
CR387293	A_87_P015918	-1.0473	9.202857	-4.94264	0.001708	0.036196	-0.98907
GNPDA1	A_87_P036824	-1.05309	9.819387	-7.22429	0.00018	0.013242	1.354944
TC191392	A_87_P034248	-1.05445	6.120014	-5.63085	0.000812	0.026247	-0.20677

TC206107	A_87_P004587	-1.07734	9.360992	-5.20482	0.001277	0.031737	-0.68272
FABP3	A_87_P021934	-1.08481	10.53447	-5.41343	0.00102	0.028699	-0.44634
LOC418700	A_87_P019694	-1.09423	7.713938	-6.14461	0.000484	0.021039	0.332801
FABP3	A_87_P021933	-1.09954	9.764458	-5.37064	0.001067	0.029171	-0.4943
K123	A_87_P008724	-1.10435	7.23779	-3.64448	0.008348	0.08548	-2.66092
CO764135	A_87_P019795	-1.11702	8.928574	-7.36333	0.00016	0.012903	1.476499
LOC395210	A_87_P017952	-1.12457	7.102583	-3.67722	0.007996	0.083547	-2.61569
BU123654	A_87_P034186	-1.1325	7.78349	-6.76399	0.000271	0.015631	0.936664
BU129127	A_87_P034022	-1.14673	7.144141	-5.68129	0.00077	0.025694	-0.15216
TC193806	A_87_P007610	-1.15524	8.416028	-5.51211	0.000919	0.027501	-0.33676
BU308605	A_87_P030118	-1.15963	8.052488	-7.35817	0.000161	0.012903	1.472026
TC208562	A_87_P003961	-1.1715	8.650317	-8.16295	8.36E-05	0.01028	2.135462
CPA2	A_87_P019171	-1.19304	10.21274	-7.22461	0.00018	0.013242	1.355227
MORF4L1	A_87_P016244	-1.21334	10.55829	-8.95579	4.61E-05	0.007893	2.727358
LOC415531	A_87_P024595	-1.25317	8.695207	-7.5717	0.000134	0.012278	1.654666
LOC418790	A_87_P021778	-1.26211	12.14388	-5.58145	0.000854	0.026962	-0.2606
FGG	A_87_P037916	-1.26612	7.065645	-3.9744	0.005446	0.067472	-2.21195
NUDT6	A_87_P032440	-1.3054	8.152001	-7.74807	0.000116	0.011792	1.801845
BU296863	A_87_P030431	-1.33615	7.194878	-8.04293	9.18E-05	0.010646	2.04072
RCJMB04_7d1	A_87_P036816	-1.36416	10.38491	-7.3388	0.000163	0.012907	1.455208
CR389027	A_87_P015076	-1.40327	7.508749	-8.34936	7.24E-05	0.009762	2.279839
CR353647	A_87_P017801	-1.44055	7.063261	-8.35125	7.23E-05	0.009762	2.281287
LOC395708	A_87_P008896	-1.51078	8.434461	-10.2293	1.94E-05	0.005308	3.567948
BU490772	A_87_P025233	-1.51876	7.050169	-7.14629	0.000193	0.013667	1.285797
TC202539	A_87_P006253	-1.65108	9.717155	-9.38224	3.41E-05	0.007046	3.023013
GSTT1	A_87_P009143	-1.72659	10.94061	-13.3304	3.34E-06	0.003197	5.174319
CV862752	A_87_P009844	-1.77023	9.642913	-8.25653	7.77E-05	0.010095	2.208356

1700012B18RIK	A_87_P011567	-1.807	11.22739	-9.35119	3.49E-05	0.007046	3.001986
LOC418060	A_87_P021136	-1.84282	7.909738	-9.5263	3.09E-05	0.006739	3.119545
PRSS3	A_87_P009139	-1.94406	6.613198	-5.03242	0.001544	0.035058	-0.88299
LOC427054	A_87_P036130	-2.14877	9.837849	-14.7484	1.69E-06	0.002739	5.750472
PNLIP	A_87_P023861	-2.21791	10.82498	-5.50991	0.000921	0.027504	-0.33919