

**Group:**

- 1 Differentiation genes
- 2 Genes correlated to pluripotency
- 3 Genes involved in the maintenance of pluripotency

**Samples:**

- 1 Ant(-);bFGF(+)
- 2 Ant(+);bFGF(+)
- 3 Ant(+);bFGF(-)
- 4 Ant(-);bFGF(-)

Group	Sample	Detector	delta ct exp 1	delta ct exp 2	delta ct exp 3
1	1	ACTC-Hs00606316_m1	8.270004	8.071516	8.924715
1	1	AFP-Hs00173490_m1	10.736845	10.091343	10.917534
1	1	CD34-Hs00156373_m1	14.435814	12.81189	14.515696
1	1	CDH5-Hs00174344_m1	15.651201	15.749922	16.84316
1	1	CDX2-Hs00230919_m1	11.5304985	11.026041	11.985125
1	1	CGB-Hs00361224_gH	11.548985	10.658838	11.6805935
1	1	COL1A1-Hs00164004_m1	7.7808933	8.535362	8.177116
1	1	DDX4-Hs00251859_m1	17.044184	16.987375	17.627756
1	1	DES-Hs00157258_m1	11.897966	11.750553	12.111856
1	1	EOMES-Hs00172872_m1	7.80764	9.494413	8.332354
1	1	FLT1-Hs00176573_m1	9.199202	8.18289	9.958521
1	1	FN1-Hs00277509_m1	4.349678	3.150093	4.554783
1	1	FOXA2-Hs00232764_m1	8.5048065	9.009106	8.9646
1	1	GATA4-Hs00171403_m1	9.392057	9.654871	9.573166
1	1	GATA6-Hs00232018_m1	9.582731	10.149612	9.795666
1	1	GFAP-Hs00157674_m1	13.875441	12.051243	13.576273
1	1	HBZ-Hs00744391_s1	17.666025	15.225426	17.317076
1	1	HLXB9-Hs00232128_m1	11.861193	12.693861	12.335241
1	1	IAPP-Hs00169095_m1	13.464985	12.664972	14.060013
1	1	ISL1-Hs00158126_m1	13.195557	13.775385	11.970312
1	1	LAMA1-Hs00300550_m1	7.390335	7.358822	7.5080185
1	1	LAMB1-Hs00158620_m1	5.4123383	5.083309	5.6123962
1	1	LAMC1-Hs00267056_m1	5.252268	4.8025036	5.553856
1	1	MYOD1-Hs00159528_m1	16.132383	15.644262	17.02049
1	1	NES-Hs00707120_s1	5.900036	5.630684	5.9809055
1	1	NEUROD1-Hs00159598_m1	13.584019	14.340923	15.253138
1	1	NPPA-Hs00383230_g1	16.38774	18.797552	16.914335
1	1	OLIG2-Hs00377820_m1	11.754919	12.2767315	13.178133
1	1	PAX4-Hs00173014_m1	18.1368	18.94139	18.39187
1	1	PAX6-Hs00240871_m1	9.461536	9.534494	9.775881
1	1	PECAM1-Hs00169777_m1	15.703093	14.511341	15.727095
1	1	PTF1A-Hs00603586_g1	18.476233	18.892313	19.239992
1	1	RUNX2-Hs00231692_m1	13.348932	13.123936	14.192623
1	1	SERPINA1-Hs00165475_m1	15.380175	15.5423565	16.221418

1	1 SOX17-Hs00751752_s1	10.05051	10.127617	10.178951
1	1 SST-Hs00174949_m1	11.041954	11.243547	12.5570965
1	1 SYCP3-Hs00538143_m1	16.969229	15.714941	16.680262
1	1 SYP-Hs00300531_m1	11.201639	10.574081	11.438953
1	1 T-Hs00610080_m1	8.726309	9.907145	9.178326
1	1 TAT-Hs00356930_m1	16.900476	16.824373	18.143564
1	1 TH-Hs00165941_m1	11.759951	11.599878	12.646034
1	2 ACTC-Hs00606316_m1	7.754922	7.4032288	8.014792
1	2 AFP-Hs00173490_m1	14.884664	12.279079	17.554577
1	2 CD34-Hs00156373_m1	15.01508	13.023802	15.83565
1	2 CDH5-Hs00174344_m1	17.421604	19.371948	17.795708
1	2 CDX2-Hs00230919_m1	16.12444	15.513065	17.584965
1	2 CGB-Hs00361224_gH	12.813109	11.784071	12.151059
1	2 COL1A1-Hs00164004_m1	7.284631	8.318457	7.832013
1	2 COL2A1-Hs00156568_m1	12.929704	11.003159	13.118567
1	2 DDX4-Hs00251859_m1	19.67965	17.911259	18.62498
1	2 DES-Hs00157258_m1	12.98784	12.936674	12.522346
1	2 EOMES-Hs00172872_m1	10.586654	8.326782	12.904691
1	2 FLT1-Hs00176573_m1	9.860095	9.080219	9.1455965
1	2 FN1-Hs00277509_m1	5.210183	3.8203812	6.1170073
1	2 FOXA2-Hs00232764_m1	10.11485	8.842218	11.995528
1	2 GATA4-Hs00171403_m1	10.853065	9.822163	12.8692465
1	2 GATA6-Hs00232018_m1	11.175506	9.647928	13.604291
1	2 GFAP-Hs00157674_m1	13.064237	12.954561	12.891896
1	2 HBZ-Hs00744391_s1	18.173946	16.62946	17.568237
1	2 HLXB9-Hs00232128_m1	15.529584	13.791773	16.377846
1	2 IAPP-Hs00169095_m1	19.13734	17.84415	19.158283
1	2 ISL1-Hs00158126_m1	15.65244	13.607668	15.083941
1	2 LAMA1-Hs00300550_m1	9.228551	8.47674	9.111476
1	2 LAMB1-Hs00158620_m1	6.3581114	5.587221	5.9739523
1	2 LAMC1-Hs00267056_m1	5.9538107	5.354059	5.555133
1	2 MYOD1-Hs00159528_m1	19.419983	24.144703	20.707436
1	2 NES-Hs00707120_s1	6.9862146	6.3527584	6.8748045
1	2 NEUROD1-Hs00159598_m1	18.918053	19.338337	19.453682
1	2 NPPA-Hs00383230_g1	24.212925	18.59782	24.83107
1	2 OLIG2-Hs00377820_m1	14.514918	14.049446	14.160258
1	2 PAX4-Hs00173014_m1	20.695778	19.151249	20.778152
1	2 PAX6-Hs00240871_m1	14.064242	12.766115	16.464397
1	2 PECAM1-Hs00169777_m1	17.961357	16.70694	18.658325
1	2 PTF1A-Hs00603586_g1	16.168018	17.64981	16.335201
1	2 RUNX2-Hs00231692_m1	14.454185	14.3094635	15.582744
1	2 SERPINA1-Hs00165475_m1	17.770226	15.590738	18.044281
1	2 SOX17-Hs00751752_s1	11.694018	9.598652	14.568715
1	2 SST-Hs00174949_m1	17.53107	16.243122	19.97517
1	2 SYCP3-Hs00538143_m1	16.727272	16.102001	16.261917
1	2 SYP-Hs00300531_m1	11.999259	11.792799	12.454034
1	2 T-Hs00610080_m1	12.968825	10.605637	15.127736

1	2 TAT-Hs00356930_m1	17.930672	16.55885	17.915016
1	2 TH-Hs00165941_m1	20.038773	18.28566	20.379784
1	3 ACTC-Hs00606316_m1	7.698488	7.6748524	7.804944
1	3 AFP-Hs00173490_m1	14.766491	12.14308	13.882333
1	3 CD34-Hs00156373_m1	15.612003	13.769411	15.144107
1	3 CDH5-Hs00174344_m1	17.955608	17.087467	17.981209
1	3 CDX2-Hs00230919_m1	12.928326	11.337124	15.817668
1	3 CGB-Hs00361224_gH	12.267471	11.108356	12.127749
1	3 COL1A1-Hs00164004_m1	9.105944	8.918705	9.4184065
1	3 COL2A1-Hs00156568_m1	8.400942	7.406355	12.407292
1	3 DDX4-Hs00251859_m1	19.916214	17.428196	17.555676
1	3 DES-Hs00157258_m1	12.205013	11.787764	12.144666
1	3 EOMES-Hs00172872_m1	8.233519	7.984329	9.410632
1	3 FLT1-Hs00176573_m1	9.2418	8.937298	8.917436
1	3 FN1-Hs00277509_m1	4.686283	3.9465637	5.677518
1	3 FOXA2-Hs00232764_m1	9.559711	8.712585	10.692958
1	3 GATA4-Hs00171403_m1	9.716507	8.634581	10.964917
1	3 GATA6-Hs00232018_m1	10.21834	9.60261	11.803517
1	3 GFAP-Hs00157674_m1	13.346178	12.930721	13.619067
1	3 HBZ-Hs00744391_s1	18.957775	15.367111	18.529198
1	3 HLXB9-Hs00232128_m1	12.741926	11.747747	14.450063
1	3 IAPP-Hs00169095_m1	15.967667	14.650457	17.422855
1	3 ISL1-Hs00158126_m1	13.4621105	13.501114	13.99064
1	3 LAMA1-Hs00300550_m1	8.412596	7.734453	8.473506
1	3 LAMB1-Hs00158620_m1	5.774416	5.3347874	5.788743
1	3 LAMC1-Hs00267056_m1	5.3445168	5.296028	5.931079
1	3 MYOD1-Hs00159528_m1	16.96495	16.325222	19.081131
1	3 NES-Hs00707120_s1	6.2369175	6.1650352	6.7055845
1	3 NEUROD1-Hs00159598_m1	18.165531	15.435114	19.476341
1	3 NPPA-Hs00383230_g1	19.222672	16.617382	20.213219
1	3 OLIG2-Hs00377820_m1	14.01598	12.664579	15.094451
1	3 PAX4-Hs00173014_m1	19.639618	20.297573	19.010845
1	3 PAX6-Hs00240871_m1	12.670731	11.762558	14.053693
1	3 PECAM1-Hs00169777_m1	17.274063	15.4736	17.010502
1	3 PTF1A-Hs00603586_g1	18.601742	17.57014	18.236141
1	3 RUNX2-Hs00231692_m1	14.760197	13.296556	14.958333
1	3 SERPINA1-Hs00165475_m1	17.369602	17.364471	17.115833
1	3 SOX17-Hs00751752_s1	10.605158	9.420801	11.916474
1	3 SST-Hs00174949_m1	14.959637	13.273788	18.406975
1	3 SYCP3-Hs00538143_m1	17.030888	17.070728	16.818169
1	3 SYP-Hs00300531_m1	13.176878	12.436752	13.075797
1	3 T-Hs00610080_m1	9.756102	8.734428	10.903819
1	3 TAT-Hs00356930_m1	17.955666	17.421307	17.299267
1	3 TH-Hs00165941_m1	13.609423	12.700245	18.175056
1	4 ACTC-Hs00606316_m1	8.070229	7.775381	7.0455723
1	4 AFP-Hs00173490_m1	6.426489	6.0409393	6.206415
1	4 CD34-Hs00156373_m1	12.38796	12.294838	11.621334

1	4	CDH5-Hs00174344_m1	14.781042	13.730841	12.4412
1	4	CDX2-Hs00230919_m1	10.955046	10.7805	10.027
1	4	CGB-Hs00361224_gH	10.113937	10.571049	10.416363
1	4	COL1A1-Hs00164004_m1	9.094896	7.460047	6.2284355
1	4	COL2A1-Hs00156568_m1	8.99988	8.468048	7.2782536
1	4	DDX4-Hs00251859_m1	18.25613	18.001007	19.066587
1	4	DES-Hs00157258_m1	11.26972	10.974068	11.071592
1	4	EOMES-Hs00172872_m1	6.4995995	7.7992134	6.9949894
1	4	FLT1-Hs00176573_m1	9.12178	8.582487	9.029995
1	4	FN1-Hs00277509_m1	2.546938	3.104601	2.5346375
1	4	FOXA2-Hs00232764_m1	7.536995	8.369034	8.088497
1	4	GATA4-Hs00171403_m1	7.876766	8.48633	8.131899
1	4	GATA6-Hs00232018_m1	7.780718	8.984234	8.245251
1	4	GFAP-Hs00157674_m1	14.348934	12.746248	14.121153
1	4	HBZ-Hs00744391_s1	17.302265	14.7920685	16.30396
1	4	HLXB9-Hs00232128_m1	11.362656	11.626564	11.481499
1	4	IAPP-Hs00169095_m1	16.81984	14.49017	13.717953
1	4	ISL1-Hs00158126_m1	11.403641	12.359375	12.430532
1	4	LAMA1-Hs00300550_m1	7.2192955	7.235384	6.8290615
1	4	LAMB1-Hs00158620_m1	5.25012	5.070078	5.143938
1	4	LAMC1-Hs00267056_m1	5.4942627	5.477068	5.402607
1	4	MYOD1-Hs00159528_m1	15.614897	15.84791	15.079357
1	4	NES-Hs00707120_s1	6.661804	6.5901337	6.0475388
1	4	NEUROD1-Hs00159598_m1	17.51381	15.345024	14.751978
1	4	NPPA-Hs00383230_g1	17.494682	17.697311	13.931126
1	4	OLIG2-Hs00377820_m1	14.361248	13.35289	12.80756
1	4	PAX4-Hs00173014_m1	20.268562	19.244164	18.50942
1	4	PAX6-Hs00240871_m1	11.63888	11.644924	9.896971
1	4	PECAM1-Hs00169777_m1	14.756294	13.390085	13.26297
1	4	PTF1A-Hs00603586_g1	21.337795	21.45129	15.761515
1	4	RUNX2-Hs00231692_m1	13.620512	13.219465	12.863926
1	4	SERPINA1-Hs00165475_m1	13.185036	11.8190155	12.138016
1	4	SOX17-Hs00751752_s1	8.276396	9.001291	8.445456
1	4	SST-Hs00174949_m1	14.057926	12.583244	12.406427
1	4	SYCP3-Hs00538143_m1	16.30972	16.76672	16.17864
1	4	SYP-Hs00300531_m1	12.083588	11.809902	11.190855
1	4	T-Hs00610080_m1	8.965904	9.421783	8.691715
1	4	TAT-Hs00356930_m1	17.757454	17.652729	18.303755
1	4	TH-Hs00165941_m1	16.188967	13.275574	12.331709
2	1	BRIX-Hs00217848_m1	7.330473	6.631569	7.2374306
2	1	CD9-Hs00233521_m1	5.523554	5.0245914	5.46233
2	1	COL2A1-Hs00156568_m1	7.1453476	7.3765335	7.535658
2	1	COMMD3-Hs00201350_m1	10.26343	10.051344	10.7443695
2	1	CRABP2-Hs00275636_m1	3.0560951	2.8308372	3.9151363
2	1	EBAF-Hs00745761_s1	9.246645	8.873724	9.217163
2	1	FGF4-Hs00173564_m1	13.502655	13.794666	14.262335
2	1	FOXD3-Hs00255287_s1	8.721155	8.123589	8.868296

2	1 GAL-Hs00544355_m1	5.956955	6.357914	6.5221977
2	1 GBX2-Hs00230965_m1	7.8125076	8.654245	8.459602
2	1 GRB7-Hs00917999_g1	7.7315445	6.860565	7.949404
2	1 IFITM1-Hs00705137_s1	2.2602158	1.7522697	2.7747498
2	1 IFITM2-Hs00829485_sH	5.496752	5.0695534	6.030367
2	1 IL6ST-Hs00174360_m1	8.985489	9.118046	9.471905
2	1 IMP2-Hs00538956_m1	6.2076626	5.344694	6.371786
2	1 KIT-Hs00174029_m1	7.847563	7.5205917	8.2680645
2	1 LEFTB-Hs00764128_s1	8.717346	9.148556	8.263468
2	1 LIFR-Hs00158730_m1	15.944571	14.229027	14.556339
2	1 LIN28-Hs00702808_s1	1.5198803	0.92993546	1.5689487
2	1 NODAL-Hs00415443_m1	6.81785	8.067982	6.8315716
2	1 NOG-Hs00271352_s1	10.365639	10.667929	10.609262
2	1 NR5A2-Hs00187067_m1	9.795689	9.589663	10.037836
2	1 NR6A1-Hs00265966_m1	5.3610725	5.635559	5.6753025
2	1 PODXL-Hs00193638_m1	3.3319492	3.2997932	3.8839378
2	1 PTEN-Hs00829813_s1	9.506378	8.463253	9.577211
2	1 REST-Hs00194498_m1	8.646357	8.699432	9.127062
2	1 SEMA3A-Hs00173810_m1	7.7100487	8.011923	8.046106
2	1 SFRP2-Hs00293258_m1	4.1377525	4.4318256	4.489403
2	1 TERT-Hs00162669_m1	9.927216	9.52858	10.204201
2	1 TFCP2L1-Hs00232708_m1	11.937431	10.638302	11.852373
2	1 UTF1-Hs00747497_g1	8.655764	7.7392635	9.461245
2	1 Xist-Hs01079824_m1	15.008677	13.5620365	15.975828
2	1 ZFP42-Hs00399279_m1	8.092361	7.6107063	8.112532
2	2 BRIX-Hs00217848_m1	7.24413	6.3247204	7.134366
2	2 CD9-Hs00233521_m1	5.661168	4.8515453	5.512458
2	2 COMMD3-Hs00201350_m1	11.814164	11.311958	11.459878
2	2 CRABP2-Hs00275636_m1	6.19847	4.952341	5.002639
2	2 EBAF-Hs00745761_s1	8.049779	5.694891	8.562905
2	2 FGF4-Hs00173564_m1	15.602498	14.215576	15.054753
2	2 FOXD3-Hs00255287_s1	7.3033495	7.2857018	7.7990026
2	2 GAL-Hs00544355_m1	6.3331957	5.5211143	6.9675455
2	2 GBX2-Hs00230965_m1	10.128221	10.718897	12.195329
2	2 GRB7-Hs00917999_g1	7.4195223	6.9465218	7.093047
2	2 IFITM1-Hs00705137_s1	3.1184263	2.264267	2.7844763
2	2 IFITM2-Hs00829485_sH	6.8712854	5.8004303	6.606904
2	2 IL6ST-Hs00174360_m1	10.372165	9.6282215	11.022044
2	2 IMP2-Hs00538956_m1	6.803931	6.026388	6.431714
2	2 KIT-Hs00174029_m1	9.323754	8.605528	9.285844
2	2 LEFTB-Hs00764128_s1	7.461814	5.115631	7.7136316
2	2 LIFR-Hs00158730_m1	13.963817	12.996136	17.89569
2	2 LIN28-Hs00702808_s1	2.6143522	1.813221	2.2115602
2	2 NODAL-Hs00415443_m1	6.252576	4.93894	7.065715
2	2 NOG-Hs00271352_s1	12.887778	11.054626	14.375741
2	2 NR5A2-Hs00187067_m1	10.005233	9.687653	10.649201
2	2 NR6A1-Hs00265966_m1	7.088414	6.4807186	6.7639933

2	2	PODXL-Hs00193638_m1	4.2740583	3.807455	3.8750448
2	2	PTEN-Hs00829813_s1	9.333398	8.865635	10.157041
2	2	REST-Hs00194498_m1	9.920091	9.466562	9.467925
2	2	SEMA3A-Hs00173810_m1	8.791665	7.3449135	8.757476
2	2	SFRP2-Hs00293258_m1	5.9958887	4.7963676	5.8231497
2	2	TERT-Hs00162669_m1	11.299216	10.001543	10.578546
2	2	TFCP2L1-Hs00232708_m1	10.731225	10.190388	10.871442
2	2	UTF1-Hs00747497_g1	8.585805	8.483162	8.828187
2	2	Xist-Hs01079824_m1	15.297269	14.6027355	15.0532675
2	2	ZFP42-Hs00399279_m1	8.638806	7.3032284	8.457322
2	3	BRIX-Hs00217848_m1	6.3877716	6.54805	6.7080107
2	3	CD9-Hs00233521_m1	5.3641605	5.2872963	5.336808
2	3	COMMD3-Hs00201350_m1	11.496515	10.828487	11.312116
2	3	CRABP2-Hs00275636_m1	4.8480015	3.8655014	5.0636797
2	3	EBAF-Hs00745761_s1	10.027487	9.138128	9.288243
2	3	FGF4-Hs00173564_m1	14.457594	14.145632	14.569222
2	3	FOXD3-Hs00255287_s1	8.034819	7.3957253	7.890483
2	3	GAL-Hs00544355_m1	5.4150524	5.3283005	6.1879816
2	3	GBX2-Hs00230965_m1	9.224159	9.966574	10.289399
2	3	GRB7-Hs00917999_g1	6.802595	6.6707096	7.3667173
2	3	IFITM1-Hs00705137_s1	2.1008568	1.4167519	2.5690012
2	3	IFITM2-Hs00829485_sH	5.8087807	5.1449203	6.143653
2	3	IL6ST-Hs00174360_m1	10.022186	9.653294	10.472594
2	3	IMP2-Hs00538956_m1	6.1707	4.90024	6.5246305
2	3	KIT-Hs00174029_m1	8.939196	8.347431	8.940585
2	3	LEFTB-Hs00764128_s1	8.225685	7.574196	7.896533
2	3	LIFR-Hs00158730_m1	16.00615	14.3415985	17.164566
2	3	LIN28-Hs00702808_s1	1.9648952	1.5854034	1.9850874
2	3	NODAL-Hs00415443_m1	5.82848	5.7901363	6.5600023
2	3	NOG-Hs00271352_s1	12.191877	11.204407	13.609849
2	3	NR5A2-Hs00187067_m1	9.573748	9.48637	9.637551
2	3	NR6A1-Hs00265966_m1	6.4213276	6.392536	6.581918
2	3	PODXL-Hs00193638_m1	3.9019585	3.5312939	3.9629126
2	3	PTEN-Hs00829813_s1	9.421885	9.138313	9.850318
2	3	REST-Hs00194498_m1	9.400297	8.970158	9.497672
2	3	SEMA3A-Hs00173810_m1	8.114841	7.7072506	8.277261
2	3	SFRP2-Hs00293258_m1	4.78438	4.536825	5.152175
2	3	TERT-Hs00162669_m1	10.78331	10.114229	10.385112
2	3	TFCP2L1-Hs00232708_m1	11.094782	10.445065	11.046691
2	3	UTF1-Hs00747497_g1	9.260054	9.04833	9.330529
2	3	Xist-Hs01079824_m1	15.415667	14.34347	15.788302
2	3	ZFP42-Hs00399279_m1	6.554653	6.5758476	6.404668
2	4	BRIX-Hs00217848_m1	6.6155777	6.5196323	6.5246525
2	4	CD9-Hs00233521_m1	4.917574	5.3516827	5.201519
2	4	COMMD3-Hs00201350_m1	10.832781	10.46788	10.06193
2	4	CRABP2-Hs00275636_m1	4.3353004	3.3573074	3.222334
2	4	EBAF-Hs00745761_s1	10.294886	10.502558	10.363483

2	4	FGF4-Hs00173564_m1	13.528267	13.3115635	13.103828
2	4	FOXD3-Hs00255287_s1	8.38488	8.63887	8.39612
2	4	GAL-Hs00544355_m1	5.4613113	6.0513515	5.569359
2	4	GBX2-Hs00230965_m1	8.930206	9.668964	8.026739
2	4	GRB7-Hs00917999_g1	7.6729164	6.928793	7.5445194
2	4	IFITM1-Hs00705137_s1	2.224804	1.8622952	2.1599674
2	4	IFITM2-Hs00829485_sH	5.3168144	5.467518	5.302273
2	4	IL6ST-Hs00174360_m1	8.896376	8.568901	8.329905
2	4	IMP2-Hs00538956_m1	6.6474037	5.568022	5.937044
2	4	KIT-Hs00174029_m1	7.836149	8.00124	7.9085064
2	4	LEFTB-Hs00764128_s1	7.5958996	8.495575	8.11982
2	4	LIFR-Hs00158730_m1	11.699884	13.090597	13.060486
2	4	LIN28-Hs00702808_s1	1.7223587	1.1329918	1.534277
2	4	NODAL-Hs00415443_m1	6.5349903	6.754633	6.395075
2	4	NOG-Hs00271352_s1	11.010441	11.1537895	10.462038
2	4	NR5A2-Hs00187067_m1	9.916025	9.9795265	9.8901825
2	4	NR6A1-Hs00265966_m1	5.5830193	5.4195557	5.5888824
2	4	PODXL-Hs00193638_m1	3.7402763	3.5036297	3.5952282
2	4	PTEN-Hs00829813_s1	9.781803	9.024754	8.935322
2	4	REST-Hs00194498_m1	9.463671	9.131153	9.222023
2	4	SEMA3A-Hs00173810_m1	7.4328003	7.8712616	7.559
2	4	SFRP2-Hs00293258_m1	4.189417	4.6784687	4.5535736
2	4	TERT-Hs00162669_m1	10.215645	9.842598	10.23259
2	4	TFCP2L1-Hs00232708_m1	11.564995	11.055618	11.6373825
2	4	UTF1-Hs00747497_g1	10.3484	8.686739	8.821062
2	4	Xist-Hs01079824_m1	16.72187	14.674978	15.391283
2	4	ZFP42-Hs00399279_m1	7.9675903	7.7949123	8.215143
3	1	DNMT3B-Hs00171876_m1	3.341051	2.8118992	3.4344406
3	1	GABRB3-Hs00241459_m1	5.7876015	5.55616	6.124378
3	1	GDF3-Hs00220998_m1	8.000185	8.764572	8.626259
3	1	Nanog*-Hs02387400_g1	5.576128	5.2050285	5.790201
3	1	POU5F1-Hs00742896_s1	8.05052	8.464413	9.603638
3	1	SOX2-Hs00602736_s1	7.8542194	7.332653	8.205547
3	1	TDGF1-Hs02339499_g1	5.6434975	4.420849	5.379223
3	2	DNMT3B-Hs00171876_m1	3.5921621	2.599556	2.8742895
3	2	GABRB3-Hs00241459_m1	6.299575	5.906332	6.1623297
3	2	GDF3-Hs00220998_m1	10.190074	8.483831	10.446088
3	2	Nanog*-Hs02387400_g1	4.7901087	4.0627728	4.749528
3	2	POU5F1-Hs00742896_s1	8.936715	7.200144	7.886258
3	2	SOX2-Hs00602736_s1	9.174354	8.185217	8.606576
3	2	TDGF1-Hs02339499_g1	4.64828	3.569746	4.5931063
3	3	DNMT3B-Hs00171876_m1	3.0816536	2.6902542	2.8365698
3	3	GABRB3-Hs00241459_m1	5.7696285	5.4866886	5.96947
3	3	GDF3-Hs00220998_m1	7.7536163	7.6233673	8.324746
3	3	Nanog*-Hs02387400_g1	4.4519367	3.744646	4.7848177
3	3	POU5F1-Hs00742896_s1	7.995735	7.2315655	8.282138
3	3	SOX2-Hs00602736_s1	8.558119	7.463463	8.282256

3	3 TDGF1-Hs02339499_g1	4.7641716	3.751852	4.7028074
3	4 DNMT3B-Hs00171876_m1	3.0967789	2.5322514	3.2662983
3	4 GABRB3-Hs00241459_m1	5.542631	6.0078754	5.830179
3	4 GDF3-Hs00220998_m1	6.894331	7.6703453	7.08477
3	4 Nanog*-Hs02387400_g1	5.127327	4.9505405	5.1373844
3	4 POU5F1-Hs00742896_s1	8.818459	8.54051	8.477934
3	4 SOX2-Hs00602736_s1	8.672863	7.8711433	8.179039
3	4 TDGF1-Hs02339499_g1	4.588274	4.420809	4.8527813