

Table S1. Genomic loci present on the 44K genomic tiling array

Gene	ID	Chromosome	Strand	TSS	TES	Coverage	Category
Gli	NM_010296	10	-	127066524	127078216	150001	Positive
Ptch1	NM_008957	13	-	60894523	60948510	150001	Positive
Ptch2	NM_008958	4	+	116055261	116073736	148978	Positive
Hhip	NM_020259	8	-	79185727	79272113	150001	Positive
Foxa2	NM_010446	2	-	147499859	147503905	150001	Positive
Nkx6-1	NM_144955	5	-	100679979	100685482	149959	Positive
Nkx2-2	NM_010919	2	-	146640088	146643295	150001	Positive
Hox D cluster		2	n/a	74133959	74195987	62029	Positive
Nkx2-1_Nkx2-9_Pax9		12	n/a	53197523	53497991	300469	Positive
Neurog2	NM_009718	3	+	126516140	126518624	50001	Positive
Ascl1	NM_008553	10	-	87463687	87466041	50001	Positive
Nkx6-2	NM_183248	7	-	133975237	133978657	49826	Positive
Ntn1	NM_008744	11	-	67938664	68111778	50001	Positive
Hsd11b2	NM_008289	8	+	104814482	104819145	50001	Positive
Ccnd1	NM_007631	7	-	139343751	139352397	50001	Positive
Cthrc1	AK003674	15	+	38976515	38986748	50001	Positive
3110038L01Rik	NM_026524	X	+	8956434	8958633	50001	Positive
Rab34	NM_033475	11	+	77914493	77917846	50001	Positive
Foxd1	NM_008242	13	+	94542754	94545191	50001	Positive
Foxf2	NM_010225	13	+	31105401	31111024	50001	Positive
Foxc2	NM_013519	8	+	120472104	120474411	50001	Positive
-	NM_177863	4	-	81884119	82007294	50001	Positive
AI504062	AI504062	5	+	3536607	3537009	56001	Positive
Sall1	NM_021390	8	-	88313728	88327923	50001	Positive
Shh	NM_009170	5	-	26906865	26917112	50001	Positive
Foxf1a	NM_010426	8	+	120439995	120442399	50001	Positive
Cspg2	AK034871	13	-	85826083	85857173	50001	Positive
Leprel1	NM_173379	16	-	24747134	24892594	50001	Positive
9430010M06Rik	AK020409	9	-	24616095	24617172	50001	Positive
Rhoe	NM_028810	2	-	51062603	51081273	50001	Positive
2310037P21Rik	NM_001002267	9	-	123277459	123278318	50001	Positive
Colec11	BC000078	12	-	25160227	25182803	50001	Positive
3110070M22Rik	NM_026084	Un_random	+	19413072	19414122	50001	Positive
Tpd52l1	NM_009413	10	-	31372578	31486119	50001	Positive
Ncor2	NM_011424	5	-	124178459	124340350	50001	Positive
Galt	NM_016658	4	+	41894196	41897373	50001	Positive
3230401I01Rik	NM_026140	7	-	115916679	115944921	50001	Positive
Homer2	NM_011983	7	-	75417865	75514933	50001	Positive
Ccl27	NM_011336	4	-	41908172	41908905	50001	Positive
Nkx2-5	NM_008700	17	-	24633727	24636672	50001	Positive
Nkx3-1	NM_010921	14	+	63724262	63728228	50001	Positive
Gdf1	NM_008107	8	+	69476431	69485066	50001	Positive
-	BB344065	X	+	118149099	118149801	0	Positive
Gpsm1	NM_153410	2	+	26247702	26280397	50001	Positive
Ccnd2	NM_009829	6	-	127802646	127824339	50001	Positive
Cdk2ap1	NM_013812	5	-	123516784	123525971	47196	Positive
Cdk6	NM_009873	5	+	3350317	3528230	50001	Positive
Arl4	NM_007487	12	-	36632029	36636075	50001	Positive
Fbn2	NM_010181	18	-	58225408	58424955	50001	Positive
Slit3	AF144629	11	+	34915546	35502170	50001	Positive
Foxc1	NM_008592	13	+	31286268	31290256	50001	Positive
Nsg2	NM_008741	11	+	31895253	31953996	50001	Positive
Hoxa11	NM_010450	6	-	52386167	52389779	50001	Positive
Hoxd11	NM_008273	2	+	74380142	74381886	50001	Positive
Hoxd13	NM_008275	2	+	74366059	74367884	50001	Positive
Hoxa13	NM_008264	6	-	52403288	52404984	50001	Positive

Foxa1	NM_008259	12	-	54272108	54277598	50001	Positive
Myf5	NM_008656	10	-	107369978	107373204	50001	Positive
Vtn	NM_011707	11	+	78224945	78227982	50001	Positive
Pitx1	NM_011097	13	-	54441613	54447983	50001	Positive
Hlx	NM_008250	1	-	184225321	184230785	50001	Positive
Hand2	NM_010402	8	+	56361191	56363149	50001	Positive
Cdh5	NM_009868	8	+	103396382	103438830	50001	Positive
Csnk2a1	NM_007788	2	+	151683883	151738781	50001	Positive
Jag1	NM_013822	2	-	136595317	136630150	50001	Positive
Hey1	NM_010423	3	-	8650291	8653917	50001	Positive
Meox2	NM_008584	12	+	33709011	33783546	50001	Positive
Pou3f1	NM_011141	4	+	123684765	123686282	50001	Positive
Angptl6	NM_145154	9	-	20751107	20756927	49924	Positive
Ror1	NM_013845	4	+	99054696	99401450	50001	Negative
-	BM211445	6	-	49390692	49391335	50001	Negative
-	BB759978	1	-	78388625	78389095	50001	Negative
Igfbp2	NM_008342	1	+	73126184	73154145	50001	Negative
Irx3	NM_008393	8	-	91085099	91087946	50001	Negative
Msx1	NM_010835	5	-	36327005	36330969	49989	Negative
Msx2	NM_013601	13	-	52026240	52031427	50001	Negative
Snai2	NM_011415	16	+	13416441	13419962	50001	Negative
Crabp1	NM_013496	9	+	54882658	54891162	50001	Negative
Crabp2	NM_007759	3	+	87692354	87697104	50001	Negative
Fap	NM_007986	2	-	62356345	62429421	50001	Negative
Irx2	NM_010574	13	+	68682462	68687568	50001	Negative
Ptn	NM_008973	6	-	36850202	36945899	50001	Negative
Irx5	NM_018826	8	+	91644914	91648572	50001	Negative
5031439A09Rik	NM_026582	3	+	158855550	158939401	50001	Negative
Flrt3	NM_178382	2	-	140172058	140185326	50001	Negative
6330404E20Rik	NM_028707	18	+	36188770	36238339	50001	Negative
6720477E09Rik	NM_178660	9	-	116564518	117239065	50001	Negative
Paip1	NM_145457	13_random	+	16918866	16946076	50001	Negative
Gsn	NM_146120	2	+	35214602	35240054	49986	Negative
MGC57096	NM_183191	3	-	63364164	63519393	50001	Negative
-	BE685845	7	+	122858915	122859376	50001	Negative
Fabp7	NM_021272	10	+	58050984	58054546	49901	Negative
Cbx1	NM_007622	11	+	96610246	96629727	50001	Negative
Dcc	NM_007831	18	-	71491611	72583420	50001	Negative
Dlgh1	NM_007862	16	+	30473410	30682713	50001	Negative
Efna5	NM_207654	17	-	60297718	60574961	50001	Negative
Lhx2	NM_010710	2	+	38283470	38301890	50001	Negative
Ndrp1	NM_010884	15	-	66953527	66993844	50001	Negative
Nfil3	NM_017373	13	-	51530723	51544552	50001	Negative
Prrx1	NM_011127	1	-	163163407	163227993	50001	Negative
Prdx2	NM_011563	8	+	84237800	84242986	50001	Negative
Zic2	NM_009574	14	+	117045015	117049406	50001	Negative
Taf7	NM_011901	18	-	37865744	37867869	50001	Negative
Axl	NM_009465	7	-	20922057	20953324	50001	Negative
Zic5	NM_022987	14	-	117028709	117035238	50001	Negative
2410012A13Rik	NM_023396	2	-	54009632	54011091	50001	Negative
BC030477	NM_177618	11	+	71476361	71515302	50001	Negative
-	BB534113	16	-	51367678	51368359	50001	Negative
Egr2	NM_010118	10	+	67591672	67595978	50001	Negative
Sfrp2	NM_009144	3	+	83502189	83510183	49997	Negative
Spry2	NM_011897	14	-	100435328	100439630	49984	Negative
Zfh4	NM_030708	3	+	5216397	5389233	50001	Negative
Boc	NM_172506	16	-	43368375	43441912	50001	Negative
Pde2a	NM_001008548	7	+	95527997	95619102	50001	Negative

Cart1	NM_172553	10	-	102921768	102942802	50001	Negative
Efemp1	NM_146015	11	+	28762563	28821523	50001	Negative
Cpeb2	NM_175937	5	+	41990144	42042375	50001	Negative
Pbx3	NM_016768	2	-	34104071	34304198	50001	Negative
Tcfap2a	NM_011547	13	-	40277825	40296013	50001	Negative
Twist1	NM_011658	12	+	30570330	30572488	50001	Negative
Cntnap2	NM_025771	6	+	47445151	47500249	50001	Negative
Sox10	BC023356	15	-	79206196	79215611	50001	Negative
Gas1	NM_008086	13	-	58831933	58834893	150001	Negative
Zic1	NM_009573	9	-	91251442	91256620	150001	Negative
Zic3	NM_009575	X	+	52785357	52790617	150001	Negative
Gli3	NM_008130	13	+	14911831	15175564	150001	Negative
Pax6	NM_013627	2	+	105381207	105401822	150001	Negative
Cdon	NM_021339	9	+	35364530	35416802	150001	Negative
Pax7	NM_011039	4	-	138619342	138714229	150001	Negative

Genes were tiled over the range defined by the above coordinates. Coverage refers to the distance tiled (not including regions that were masked for repeats). Positive genes were upregulated by Hh signaling in transcriptional profiling studies, whereas negative genes were downregulated (combinations of genes in the HoxD cluster and Nkx2.1_Nkx2.9_Pax9 refer to additional loci that contained extensive tiling throughout the region).

Table S2. Summary statistics of Gli1 ChIP peaks

Rank	Gene	Peak	Chr	Start	End	Size of region	Center	T-Stat	FDR	Fold change
1	Ptch1	Peak 2	13	60949397	60950371	974	60949566	5.507	0	16.0503
2	Nkx2-2	Peak 1	2	146644626	146645570	944	146645242	5.144	0	12.8085
3	Ptch1	Peak 3	13	60951377	60952953	1576	60952201	4.8769	0	11.2259
4	Nkx2-9	Peak 1	12	53347310	53348354	1044	53347899	4.7249	0	6.9036
5	Ptch1	Peak 5	13	60956284	60956777	493	60956284	4.2212	0	7.1708
6	Nkx2-9	Peak 2	12	53340519	53341015	496	53340862	4.1573	0	4.1739
7	Rab34	Peak 1	11	77915220	77915560	340	77915220	4.0735	0	9.0651
8	Ptch2	Peak 1	4	116057320	116057946	626	116057561	3.9081	0	5.5392
9	Ptch1	Peak 1	13	60945578	60945972	394	60945972	3.8484	0	7.9795
10	Nkx2.1	Peak 1	12	53245748	53246351	603	53246120	3.7201	0	4.0266
11	Gli1	Peak 1	10	127076571	127078099	1528	127076975	3.4976	0	4.6198
12	Hhip	Peak 1	8	79270092	79270492	400	79270240	3.4535	0	4.9558
13	Foxa2	Peak 1	2	147493701	147494245	544	147493953	3.4405	0	3.1634
14	Ptch2	Peak 2	4	116054385	116054954	569	116054597	3.3145	0	3.9994
15	Cart1	Peak 1	10	102925949	102926177	228	102926042	3.116	0	3.559
16	Ptch1	Peak 4	13	60953950	60955072	1122	60954831	3.0549	0	3.8567
17	Prdx2	Peak 1	8	84215218	84215559	341	84215273	3.0089	0	4.0679
18	Cart1	Peak 2	10	102938208	102938208	0	102938208	2.9954	0	3.2221
19	Ptch1	Peak 6	13	61010241	61010714	473	61010369	2.9851	0	3.3462
20	Hhip	Peak 2	8	79268419	79268867	448	79268732	2.9702	0	4.4496
21	Flrt3	Peak 1	2	140191468	140191692	224	140191623	2.8017	0	3.5177
22	Pax9	Peak 1	12	53443055	53443311	256	53443186	2.7947	0	2.9971
23	Ncor2	Peak 1	5	124340743	124341009	266	124340909	2.7832	0.0435	3.5798
24	Zic3	Peak 1	20	52789693	52789967	274	52789693	2.6971	0.0769	2.6119
25	Hand2	Peak 1	8	56373391	56373692	301	56373552	2.6907	0.0769	2.7515
26	Cart1		10	102963671	102964187	516	102963911	2.6876	0.0769	4.6047
27	Twist1		12	30577542	30577932	390	30577763	2.6562	0.1034	4.3133
28	Nkx2-9		12	53333143	53333408	265	53333313	2.6414	0.1034	3.5581
29	Myf5		10	107361999	107362096	97	107362096	2.6329	0.1034	3.9894
30	Ptn		6	36849581	36849581	0	36849581	2.5351	0.1667	3.5856
31	Ncor2		5	124356413	124356633	220	124356540	2.4556	0.1818	3.1064
32	Nkx2.1		12	53220111	53220111	0	53220111	2.3832	0.1818	2.9039
33	Foxa2		2	147497880	147498001	121	147497880	2.3664	0.1818	3.2767
34	Pax9		12	53399381	53399596	215	53399475	2.3388	0.1842	3.3657
35	Ncor2		5	124346282	124346436	154	124346375	2.3308	0.1842	2.9774
36	Ptch1		13	60955660	60955823	163	60955660	2.3207	0.1842	3.6777
37	Foxf2		13	31129412	31129501	89	31129501	2.3084	0.1842	2.8392
38	Mid1ip1		20	8973477	8973606	129	8973606	2.3043	0.1842	3.3893
39	Nkx6-1		5	100666378	100666493	115	100666493	2.2766	0.2051	3.4918
40	Ptch1		13	60946669	60946815	146	60946815	2.237	0.2128	2.8874
41	Angpt16		9	20734531	20734687	156	20734531	2.222	0.2128	3.4968
42	Foxc1		13	31302115	31302268	153	31302268	2.2081	0.2128	2.8619
43	5031439A09Rik		3	158868339	158868516	177	158868516	2.2043	0.2128	2.9474
44	Fabp7		10	58049170	58049170	0	58049170	2.2036	0.2128	2.8
45	Dlgh1		16	30486849	30487046	197	30486849	2.1944	0.2128	2.7407
46	Hhip		8	79267697	79267697	0	79267697	2.1859	0.2128	2.5583
47	Pbx3		2	34297540	34297625	85	34297625	2.1846	0.2128	2.1798

Peaks were defined and ranked using TileMap. Using an FDR cut-off of $\leq 25\%$, there are a total of 47 peaks. Chromosomal coordinates (Build 34) showing the boundary coordinates for peaks. The size of the region is measured by subtracting these values. In the instances where the region has a size of zero, there is only one probe that is significantly enriched. The T-statistic gives the value for the highest peak probe in the region. FDR, false discovery rate.

Table S3. Enrichment of Gli-binding motif in candidate regions

Peak Rank	n1/n2	r1	FDR(1/r1)	n3/n4	r2/r3
1-10	13/10820	5.33	19%	10/5328	7.73/17.34
11-20	11/9579	5.09	20%	8/4740	6.95/15.66
21-30	5/ 6280	3.53	28%	3/2720	4.54/8.96
31-40	4/ 4959	3.58	28%	1/1594	2.58/3.78
41-50	1/ 4919	0.9	100%	0/1826	0.00/0.00
51-60	2/ 4159	2.13	47%	2/1241	6.64/9.02
Control	1264/5608267	1		299/1231633	1.00/1.00

The Gli consensus motif TGGGTGGTC, with a tolerance for 1 bp mismatch was mapped to statistically ranked peak regions. Peaks were grouped into bins of size 10. The number of Gli sites (n_1) and the total number of surveyed non-repeat base pairs (n_2) were counted for each bin as well as control regions (i.e. all regions tiled in the array). $r_1 = (n_1/n_2)_{\text{target}} / (n_1/n_2)_{\text{control}}$ measures the Gli enrichment level for each bin. $\text{FDR} = 1/r_1$ measures the false discovery rate of Gli-binding sites as predicted by consensus. Sites that reside within the top 10% of most-conserved regions of the genome are defined as conserved binding sites. n_3 and n_4 are the number of conserved Gli consensus sites and the total number of conserved base pairs in each bin, respectively. $r_2 = (n_3/n_4)_{\text{target}} / (n_3/n_4)_{\text{control}}$ measures the extent to which Gli sites are enriched in conserved regions, and $r_3 = (n_3/n_2)_{\text{target}} / (n_3/n_2)_{\text{control}}$ measures the combined gain we can obtain using both binding-sequence specificity and cross-species conservation information. The level of Gli enrichment (r_1 , r_2 and r_3) is reduced in lower-scoring regions

Table S4. Validation with qPCR on unamplified ChIPs showing enrichment values, primers and coordinates

Primer	Locus	Peak	$\Delta\Delta C(T)$	St. dev.	Fold enrichment	Amplicon coordinates	Forward primer	Reverse primer
807808	Ptch1	Peak1	4.91	0.8	30.0	13:60945711-60945972	TTATAAAGCAGGTCCCCAAC	ACGCATGTTTGCAAAGTAGA
727728	Nkx2.2	Peak1	4.87	0.6	29.2	2:146645052-146645290	CGGGTTTCTAGAGCCTTGTG	GACAAAGGCTCCAACAGGA
801802	Rab34	Peak1	4.81	0.6	28.1	11:77915199-77915431	CAAAAGCTCCATTCTCACAA	AGGAAACTGGGAGAACATCA
793794	Nkx2.9	Peak1	4.01	0.7	16.2	12:53347646-53347851	GAGTCTTAAATCGGGGATGA	GAGACAATTTTCTGCCATC
731732	Gli1	Peak1	3.65	0.6	12.5	10:127077945-127078145	GGACAAAGAGACCTGGGACA	AGGAGATGCTCTGACGCCTA
803804	Nkx2.1	Peak1	3.18	0.6	9.1	12:53245985-53246192	AATTGCTTAGGGTTCAGGTG	TTTGTGAAGGCCTGTAGAA
879880	Gli1	Peak1	2.85	0.7	7.2	10:127076806-127076959	ATCCTGAAAGCAGGCAGTAG	AGGAATCCAAGGTGCTCTCT
713714	FoxA2	Peak1	2.68	0.6	6.4	2:147493520-147493736	GGGGCCAGTCTAGATCTTC	CACACCACAAAACACAGCA
777778	Hhip1	Peak1	2.48	0.8	5.6	8:79,270,322-79,270,491	CGCAGGAGCTGTTTACATGA	AAGCCTGCAGTTGCAAGGT
799800	Ptch2	Peak1	2.47	0.7	5.6	4:116057694-116057895	GGTAGTCCCTGCAGTTATG	TCAGCTCTCAACTCCATCAA
729730	Gli1	Peak1	2.24	0.6	4.7	10:127077694-127077964	CCACAGGTCAGGAGTCCAAT	TGTCCCAGGTCTCTTTGTCC
855856	Hand2	Peak1	1.45	0.8	2.7	8:56373405-56373599	TTGGCTCTGTACTTTGTCTCA	TAGAGGCTCCAGTCTTTTG
7918792	Prdx2	Peak1	0.44	0.6	1.4	8:84215391-84215629	TGAACACCCTGAATGAAATG	TAGTAATGCCTTCCCCTCTG
833834	Ptch2	Peak2	5.59	0.6	48.3	4:116054701-116054867	ACTTACACTTGGCCAACGAC	CGGATCCGTTGCTAGGTA
805806	Nkx2.9	Peak2	5.24	0.6	37.7	12:53340854-53341077	CTACCAAGCGTGCCTAAAGT	TTTATCCCAGGGAGCTAAAG
711712	Ptch1	Peak2	5.09	0.6	34.0	13:60949317-60949518	GAAGTATTGCATGCGAGAGG	CTGTCAGATGGCTTGGGTTT
841842	Hhip1	Peak2	3.15	0.7	8.9	8:79268572-79268810	TAAAAGGGCCACACTTGAAAA	AATTGCTGCAGACCTTAAAT
795796	Ptch1	Peak3	5.50	0.6	45.3	13:60952107-60952356	CCAGGCTCTCTAACAAGC	ACAACATTATCGTCTGGAAT
831832	Ptch1	Peak4	3.17	0.8	9.0	13:60954689-60954893	GAAGGACTCTGGGTGACAAC	TTGGCTCCAGTACTTCAACA
797798	Ptch1	Peak5	6.02	0.7	65.0	13:60956197-60956431	ACAAAAGGAACGGAAAGTGT	AGCACGTTCTCCAGTTTAC
829830	Ptch1	Peak6	1.48	0.6	2.8	13:61010364-61010604	GCAGGGTAATGGGATTTATG	GTCTTCTGAAAGCCAAAA
<u>825826</u>	Negative control	Neg Ctrl	1.32	0.7	2.5	7:133989909-133990158	CAAGCTCCAGCCATTAAGTT	GGTACTCAGTGTGCTTGCTG
<u>861862</u>	Ptch1 locus Gli b.s. (-)	Neg Ctrl	2.28	0.6	4.8	13:60946932-60947110	GGTAGTCCCTGCAGTTATG	TCAGCTCTCAACTCCATCAA
<u>863864</u>	Ptch1 locus Gli b.s. (-)	Neg Ctrl	1.09	0.7	2.1	13:60953479-60953701	GGGCTTGACTCTTTCACAT	ACTGTAAGCTCCTGGGTCTG
<u>867868</u>	Nkx2.2 locus Gli b.s. (-)	Neg Ctrl	0.75	0.6	1.7	2:146647208-146647417	ATCCAAGCTCTGAGTTGAGG	AAGTGCCAAACAGGTCTCTC
<u>859860</u>	Ptch1 locus Gli b.s. (-)	Neg Ctrl	0.67	0.7	1.6	13:60942920-60943069	TCACCCTATCTTGAAAGC	GTTGGGGAAATCAGTGAAAG
<u>689690</u>	B-actin	Neg Ctrl	0.44	2.8	1.4	5:141969468-141969691	AGAAGGACTCCTATGTGGGTGA	ACTGACCTGGGTCACTTTTC
<u>865866</u>	Ptch1 locus Gli b.s. (-)	Neg Ctrl	0.16	0.7	1.1	13:60958637-60958864	TTCTTTGGAGCTCAATTTCC	GTTTTCCCGATTTTAAAGT
<u>811812</u>	Negative control region 2	Neg Ctrl	0.00	0.7	1.0	13:51535150-51535387	CTGGCCTCCATACACACATA	AGTCAGCAGGATCCACACTT
<u>827828</u>	Negative control region 10	Neg Ctrl	-0.14	0.7	0.9	15:66979588-66979802	AGAGGTATGGCAGAGGTGAG	CTTGGTGAGTCTTTGGGAAC
<u>869870</u>	Nkx2-1 locus Gli b.s. (-)	Neg Ctrl	-0.36	0.6	0.8	12:53255352-53255521	ATTTCTTTTCTGGGAGGTC	TAGGAGCTGGGTTTAAAGGTG
<u>875876</u>	Hhip1 locus Gli b.s. (-)	Neg Ctrl	-0.51	0.8	0.7	8:79272744-79272928	TGAGTTCGTTGGAGACTTT	AGTCTGGGTGTACAGGTGTT
<u>691692</u>	Rosa26	Neg Ctrl	-0.54	0.7	0.7	6:113638429-113638553	CACCACAAATCGAGGCTGTA	CCTGACGGGAGAGGTGATAG
<u>809810</u>	Negative control region 1	Neg Ctrl	-1.04	1.2	0.5	10:127016990-127017237	AAGCCAGATGTGATGTAGCA	TTATGGAAGGACAGACAGCA

All enrichment values are determined using primer pair 811-812 for baseline values. Negative controls (see 'Peak' column) fall into several categories: (i) loci referred to by name only are random loci that are not affected by Hh signalling; (ii) loci referred to as negative control refer to random tiled regions of the genome that were not enriched in the chip; (iii) loci containing 'Gli b.s.' contain a Gli site with no more than two deviations from consensus. This final class consists of Gli-like motifs that were adjacent to positive peak regions but which showed no ChIP enrichment in the microarray data set.

Table S5. The 365 probe-sets exhibiting maximal differences in transcriptional profiling studies of EBs treated with retinoic acid and Hh agonist versus retinoic acid only

Rank	Probeset_id	Score	FDR	Gene	Gene ID	Accession
1	1422284_at	-1.80E+01	0.00E+00	Nkx2-9	18094	NM_008701
2	1451342_at	-1.42E+01	0.00E+00	Spon1	233744	NM_145584
3	1455907_x_at	-1.37E+01	0.00E+00	Phox2b	18935	NM_008888
4	1416286_at	-1.20E+01	0.00E+00	Rgs4	19736	NM_009062
5	1418054_at	-1.14E+01	0.00E+00	Neurod4	11923	NM_007501
6	1422833_at	-1.07E+01	1.25E-02	Foxa2	15376	NM_010446
7	1436694_s_at	-1.06E+01	1.25E-02	Neurod4	11923	NM_007501
8	1422720_at	-1.04E+01	1.25E-02	Isl1	16392	NM_021459
9	1450723_at	-9.60E+00	2.00E-02	Isl1	16392	NM_021459
10	1458536_at	-9.07E+00	2.00E-02	Ccni	12453	NM_017367
11	1428741_at	-8.99E+00	2.08E-02	Elavl4	15572	NM_010488
12	1425828_at	-8.82E+00	2.08E-02	Nkx6-1	18096	NM_144955
13	1416287_at	-8.38E+00	4.23E-02	Rgs4	19736	NM_009062
14	1452894_at	-8.24E+00	4.29E-02	Elavl4	15572	NM_010488
15	1450258_a_at	-7.77E+00	5.33E-02	Elavl4	15572	NM_010488
16	1419549_at	-7.47E+00	5.58E-02	Arg1	11846	NM_007482
17	1445047_at	-7.39E+00	5.58E-02	C79246	96891	--
18	1448475_at	-7.21E+00	5.58E-02	Olfml3	99543	NM_133859
19	1416232_at	-7.17E+00	5.58E-02	Olig2	50913	NM_016967
20	1426255_at	-7.16E+00	5.58E-02	Nefl	18039	NM_010910
21	1415885_at	-7.11E+00	5.58E-02	Chgb	12653	NM_007694
22	1433906_at	-7.07E+00	5.58E-02	4933402J24Rik	74438	NM_028940
23	1436319_at	-6.94E+00	5.58E-02	Sulf1	240725	NM_172294
24	1422520_at	-6.85E+00	5.58E-02	Nef3	18040	NM_008691
25	1440056_at	-6.79E+00	5.58E-02	--	--	--
26	1423977_at	-6.79E+00	5.58E-02	4930453N24Rik	67609	XM_148353
27	1458140_at	-6.75E+00	5.93E-02	Slit2	20563	NM_178804
28	1460000_at	-6.68E+00	6.25E-02	D830007B15Rik	330096	XM_485619
29	1459852_x_at	-6.54E+00	6.71E-02	Trib2	217410	NM_144551
30	1447709_at	-6.44E+00	6.71E-02	Epb4.1l3	13823	NM_013813
31	1425412_at	-6.34E+00	6.71E-02	Cias1	216799	NM_145827
32	1416149_at	-6.31E+00	6.71E-02	Olig1	50914	NM_016968
33	1423281_at	-6.25E+00	6.71E-02	Stmn2	20257	NM_025285
34	1460181_at	-6.24E+00	6.71E-02	Stmn3	20262	NM_009133
35	1454672_at	-6.19E+00	6.71E-02	--	--	--
36	1452842_at	-6.07E+00	7.22E-02	Hspb9	75482	--
37	1459524_at	-5.99E+00	7.57E-02	Mcc	328949	XM_140309
38	1436359_at	-5.94E+00	7.89E-02	Ret	19713	NM_009050
39	1451990_at	-5.89E+00	8.26E-02	Mapre2	212307	NM_153058
40	1455865_at	-5.86E+00	8.26E-02	Insm1	53626	NM_016889
41	1438989_s_at	-5.86E+00	8.26E-02	B130021B11Rik	320860	--
42	1418620_at	-5.83E+00	8.26E-02	Phox2a	11859	NM_008887
43	1438200_at	-5.81E+00	8.26E-02	Sulf1	240725	NM_172294
44	1415999_at	-5.60E+00	1.05E-01	Hey1	15213	NM_010423
45	1457403_at	-5.48E+00	1.16E-01	--	--	--
46	1436287_at	-5.46E+00	1.18E-01	--	--	--
47	1416313_at	-5.42E+00	1.18E-01	Mllt11	56772	NM_019914
48	1425078_x_at	-5.42E+00	1.18E-01	5830484A20Rik /// LOC546062	109032 /// 546062	NM_175397 /// XM_620658
49	1423537_at	-5.39E+00	1.22E-01	Gap43	14432	NM_008083
50	1421399_at	-5.36E+00	1.23E-01	Insm1	53626	NM_016889
51	1458229_at	-5.23E+00	1.40E-01	Robo2	268902	NM_175549
52	1449468_at	-5.21E+00	1.40E-01	St6galnac5	26938	NM_012028
53	1442710_at	-5.15E+00	1.53E-01	Pdlim5	56376	NM_019808 /// NM_019809 ///

54	1450492_at	-5.11E+00	1.57E-01	Cngb3	30952	NM_022554
55	1459941_at	-5.09E+00	1.57E-01	4933402J24Rik	74438	NM_013927
56	1438258_at	-5.04E+00	1.57E-01	Vldlr	22359	NM_028940
57	1454660_at	-5.02E+00	1.57E-01	1100001E04Rik	75404	NM_013703
58	1453916_at	-5.01E+00	1.57E-01	4933431K23Rik	74475	XM_135854
59	1426864_a_at	-5.00E+00	1.57E-01	Ncam1	17967	--
60	1425928_at	-4.99E+00	1.57E-01	Xkr6	219149	NM_010875
61	1442180_at	-4.93E+00	1.57E-01	Dleu7	239133	NM_173393
62	1437558_at	-4.92E+00	1.57E-01	B130021B11Rik	320860	NM_173419
63	1456002_at	-4.92E+00	1.57E-01	Xpa	22590	--
64	1458275_at	-4.91E+00	1.57E-01	2310045A20Rik	231238	NM_011728
65	1450683_at	-4.89E+00	1.57E-01	Tagln3	56370	NM_172710
66	1454245_at	-4.88E+00	1.57E-01	Csmd3	239420	NM_019754
67	1445279_at	-4.88E+00	1.57E-01	BC034902	228642	XM_139502
68	1440839_x_at	-4.87E+00	1.57E-01	1700065I16Rik	78462	NM_177654
69	1460083_at	-4.84E+00	1.58E-01	Adam10	11487	--
70	1437191_at	-4.84E+00	1.58E-01	BC050789	213234	NM_007399
71	1421958_at	-4.83E+00	1.58E-01	L1cam	16728	NM_172515
72	1422232_at	-4.78E+00	1.63E-01	Phox2b	18935	NM_008478
73	1437467_at	-4.77E+00	1.63E-01	Alcam	11658	NM_008888
74	1448628_at	-4.71E+00	1.73E-01	Scg3	20255	NM_009655
75	1435396_at	-4.68E+00	1.74E-01	C85317	97823	NM_009130
76	1455123_at	-4.68E+00	1.74E-01	St18	240690	--
77	1421359_at	-4.67E+00	1.74E-01	Ret	19713	NM_173868
78	1459249_at	-4.64E+00	1.80E-01	Tdrd3	219249	NM_009050
79	1452123_s_at	-4.62E+00	1.82E-01	Frmd4b	232288	NM_172605
80	1436931_at	-4.60E+00	1.82E-01	Rfx4	71137	NM_145148
81	1418415_at	-4.59E+00	1.82E-01	Hoxb5	15413	NM_001024918 ///
82	1446144_at	-4.58E+00	1.82E-01	Pex2	58869	NM_027689
83	1426865_a_at	-4.56E+00	1.83E-01	Ncam1	17967	NM_008268
84	1420484_a_at	-4.54E+00	1.86E-01	Vtn	22370	NM_021483
85	1448289_at	-4.53E+00	1.89E-01	Crmp1	12933	NM_010875
86	1418452_at	-4.51E+00	1.92E-01	Gng2	14702	NM_011707
87	1452010_at	-4.49E+00	1.94E-01	Chrna3	110834	NM_007765
88	1427867_at	-4.48E+00	1.97E-01	Myh1	17879	NM_010315
89	1440005_at	-4.46E+00	1.98E-01	C730009D12	328974	NM_145129
90	1442893_at	-4.45E+00	2.00E-01	Lrrtm1	74342	XM_354615
91	1457146_at	-4.39E+00	2.17E-01	Dock4	238130	--
92	1459613_at	-4.37E+00	2.17E-01	--	--	NM_028880
93	1435165_at	-4.37E+00	2.17E-01	Cntn2	21367	NM_172803
94	1441163_at	-4.36E+00	2.17E-01	Med12l	329650	NM_011531 ///
95	1457399_at	-4.34E+00	2.20E-01	--	--	NM_177129
96	1452357_at	-4.33E+00	2.20E-01	Gp1bb /// Sept5	14724 ///	NM_001001999 ///
97	1448759_at	-4.31E+00	2.27E-01	Il2rb	16185	NM_010327 ///
98	1450661_x_at	-4.29E+00	2.27E-01	Nfic	18029	NM_213614
99	1431045_at	-4.29E+00	2.27E-01	D12Ertd553e	76820	NM_008368
100	1447586_at	-4.28E+00	2.27E-01	Cspg2	13003	NM_008688
101	1418105_at	-4.28E+00	2.27E-01	Stmn4	56471	NM_029758
102	1418451_at	-4.28E+00	2.27E-01	Gng2	14702	XM_488510
103	1436557_at	-4.27E+00	2.27E-01	Kb36	223915	NM_019675
104	1418877_at	-4.26E+00	2.27E-01	Foxd1	15229	NM_010315
105	1423506_a_at	-4.25E+00	2.28E-01	Nnat	18111	NM_212485
106	1422839_at	-4.25E+00	2.28E-01	Neurog2	11924	NM_008242
						NM_010923 ///
						NM_180960
						NM_009718

107	1435195_at	-4.24E+00	2.28E-01	D930046M13Rik	104880	--
108	1452399_at	-4.22E+00	2.28E-01	Rgs6	50779	NM_015812
109	1439789_at	-4.22E+00	2.28E-01	--	--	--
110	1459929_at	-4.22E+00	2.28E-01	C80731	243905	XM_145503
111	1442553_at	-4.20E+00	2.29E-01	Mapre2	212307	NM_153058
112	1422401_at	-4.20E+00	2.29E-01	Sprr3	20766	NM_011478
113	1442675_at	-4.19E+00	2.29E-01	2300006M17Rik	69466	--
114	1433551_at	-4.18E+00	2.29E-01	AI427515	270097	NM_173016
115	1453300_at	-4.17E+00	2.29E-01	Slc35d2	70484	NM_001001321
116	1436148_at	-4.17E+00	2.29E-01	--	--	--
117	1416646_at	-4.16E+00	2.30E-01	Afp	11576	NM_007423
118	1432516_at	-4.15E+00	2.30E-01	4930447F04Rik	74862	XM_135902
119	1458306_at	-4.15E+00	2.30E-01	F630022B06Rik	239827	NM_172822
120	1447929_at	-4.09E+00	2.53E-01	Ssh3	245857	NM_198113
121	1442257_at	-4.08E+00	2.53E-01	--	--	--
122	1426215_at	-4.06E+00	2.59E-01	Ddc	13195	NM_016672
123	1425111_at	-4.05E+00	2.59E-01	Sorcs3	66673	NM_025696
124	1448944_at	-4.04E+00	2.59E-01	Nrp1	18186	NM_008737
125	1428157_at	-4.03E+00	2.59E-01	Gng2	14702	NM_010315
126	1438036_x_at	-4.02E+00	2.59E-01	AW061290	381110	NM_201361
127	1435941_at	-4.02E+00	2.59E-01	Rhbdl4	246104	NM_139228
128	1454110_at	-4.01E+00	2.59E-01	4930408K08Rik	76865	--
129	1440256_at	-4.01E+00	2.59E-01	Rgs9bp	243923	NM_145840
130	1455027_at	-4.00E+00	2.62E-01	D5Bwg0860e	52822	NM_027530
131	1456121_at	-4.00E+00	2.63E-01	Lrriq2	74201	NM_028815
132	1455447_at	-3.99E+00	2.63E-01	D430019H16Rik	268595	--
133	1455033_at	-3.97E+00	2.69E-01	B430201A12Rik	329739	XM_283903
134	1442230_at	-3.96E+00	2.69E-01	--	--	--
135	1453351_at	-3.95E+00	2.70E-01	Tbx20	57246	NM_020496 ///
						NM_194263
136	1448233_at	-3.93E+00	2.75E-01	Prnp	19122	NM_011170
137	1417280_at	-3.92E+00	2.76E-01	Slc17a1	20504	NM_009198
138	1445737_at	-3.91E+00	2.76E-01	1700057H21Rik	73375	--
139	1418055_at	-3.90E+00	2.78E-01	Neurod4	11923	NM_007501
140	1431556_at	-3.89E+00	2.78E-01	4930435M08Rik	74651	--
141	1444080_at	-3.89E+00	2.78E-01	E430014L09Rik	320937	--
142	1420662_at	-3.87E+00	2.82E-01	4933439F18Rik	66771	NM_025757
143	1417988_at	-3.86E+00	2.82E-01	Resp18	19711	NM_009049
144	1454449_at	-3.86E+00	2.82E-01	Rabepk	227746	NM_145522
145	1415978_at	-3.85E+00	2.82E-01	Tubb3	22152	NM_023279
146	1454974_at	-3.84E+00	2.82E-01	Ntn1	18208	NM_008744
147	1440422_at	-3.84E+00	2.82E-01	Htr1f	15557	NM_008310
148	1424403_a_at	-3.84E+00	2.82E-01	D5Bwg0860e	52822	NM_027530
149	1458793_at	-3.82E+00	2.90E-01	--	--	--
150	1424719_a_at	-3.82E+00	2.90E-01	Mapt	17762	NM_010838
151	1428156_at	-3.81E+00	2.93E-01	Gng2	14702	NM_010315
152	1448991_a_at	-3.81E+00	2.93E-01	Ina	226180	NM_146100
153	1455266_at	-3.80E+00	2.94E-01	Kif5c	16574	NM_008449
154	1434670_at	-3.79E+00	2.94E-01	Kif5a	16572	NM_008447
155	1430222_at	-3.78E+00	2.94E-01	9130007G19Rik	74550	--
156	1442613_at	-3.78E+00	2.94E-01	Spon1	233744	NM_145584
157	1416301_a_at	-3.76E+00	2.94E-01	Ebf1	13591	NM_007897
158	1443086_at	-3.76E+00	2.94E-01	Alcam	11658	NM_009655
159	1443855_at	-3.76E+00	2.94E-01	Kcnc1	16502	NM_008421
160	1435323_a_at	-3.76E+00	2.94E-01	Oact1	218121	NM_153546
161	1431484_at	-3.75E+00	2.96E-01	2010007L08Rik	70114	--
162	1450779_at	-3.73E+00	3.03E-01	Fabp7	12140	NM_021272
163	1459760_at	-3.71E+00	3.13E-01	Ndufs4	17993	NM_010887

164	1440264_at	-3.70E+00	3.16E-01	--	--	--
165	1443723_at	-3.70E+00	3.16E-01	Trpm3	226025	NM_177341
166	1448250_at	-3.70E+00	3.16E-01	9030425E11Rik	71566	NM_133733
167	1450397_at	-3.69E+00	3.16E-01	Mtap1b	17755	NM_008634
168	1459840_s_at	-3.69E+00	3.16E-01	Ccdc28b	66264	NM_025455
169	1438607_at	-3.68E+00	3.16E-01	Zdhhc19	245308	NM_199309
170	1446300_at	-3.68E+00	3.16E-01	--	--	--
171	1429816_at	-3.68E+00	3.16E-01	Armc3	70882	XM_130012 /// XM_622876
172	1441118_at	-3.67E+00	3.17E-01	BC017647	216971	NM_145430
173	1432591_at	-3.66E+00	3.25E-01	Pappa	18491	NM_021362
174	1422586_at	-3.64E+00	3.31E-01	Ecel1	13599	NM_021306
175	1440991_at	-3.63E+00	3.36E-01	Plekhg1	213783	XM_136911
176	1417625_s_at	-3.63E+00	3.37E-01	Cmkor1	12778	NM_007722
177	1448099_at	-3.62E+00	3.37E-01	--	432995	XM_488763
178	1433776_at	-3.62E+00	3.37E-01	Lhfp	108927	NM_175386
179	1459186_at	-3.61E+00	3.39E-01	C80165	97726	--
180	1419524_at	-3.61E+00	3.39E-01	Tph1	21990	NM_009414
181	1435321_at	-3.60E+00	3.40E-01	3732412D22Rik	77569	NM_001001980
182	1435404_at	-3.60E+00	3.40E-01	Disp2	214240	NM_170593
183	1446237_at	-3.59E+00	3.45E-01	Akap9	100986	NM_194462
184	1442347_at	-3.59E+00	3.45E-01	Lrp8	16975	NM_053073
185	1415844_at	-3.57E+00	3.52E-01	Syt4	20983	NM_009308
186	1438042_at	-3.56E+00	3.52E-01	Shox2	20429	NM_013665
187	1435142_at	-3.56E+00	3.52E-01	Sft2d2	108735	NM_145512
188	1459702_at	-3.54E+00	3.55E-01	--	--	--
189	1457762_at	-3.54E+00	3.55E-01	Ttc15	217449	NM_178811
190	1423713_at	-3.54E+00	3.55E-01	Abcb8	74610	NM_029020
191	1456198_at	-3.54E+00	3.55E-01	1810007D17Rik	69055	--
192	1439795_at	-3.54E+00	3.57E-01	Gpr64	237175	NM_178712
193	1455037_at	-3.53E+00	3.57E-01	Plxna2	18845	NM_008882
194	1435408_at	-3.53E+00	3.57E-01	--	--	--
195	1419672_at	-3.52E+00	3.59E-01	Spock1	20745	NM_009262
196	1423280_at	-3.52E+00	3.59E-01	Stmn2	20257	NM_025285
197	1456206_at	-3.52E+00	3.59E-01	1810020C19Rik	69113	XM_130317
198	1439286_at	-3.51E+00	3.59E-01	Grik2	14806	NM_010349
199	1438169_a_at	-3.51E+00	3.60E-01	Frmd4b	232288	NM_145148
200	1445215_at	-3.50E+00	3.60E-01	2600003E23Rik	70292	NM_027373
201	1416713_at	-3.50E+00	3.60E-01	2700055K07Rik	67971	NM_026481
202	1442428_at	-3.46E+00	3.78E-01	--	--	--
203	1446324_at	-3.45E+00	3.79E-01	--	--	--
204	1439663_at	-3.45E+00	3.79E-01	Ptch1	19206	NM_008957
205	1457260_at	-3.45E+00	3.79E-01	--	--	--
206	1423274_at	-3.43E+00	3.84E-01	Ddx26	18130	NM_008715
207	1418178_at	-3.43E+00	3.84E-01	Ina	226180	NM_146100
208	1445227_at	-3.43E+00	3.84E-01	Tnfsf13	69583	NM_023517
209	1419420_at	-3.42E+00	3.86E-01	St6galnac5	26938	NM_012028
210	1428136_at	-3.41E+00	3.88E-01	Sfrp1	20377	NM_013834
211	1441764_at	-3.40E+00	3.88E-01	Prdm10	382066	XM_356146
212	1429474_at	-3.40E+00	3.88E-01	Zadh1	77219	NM_029880
213	1421851_at	-3.40E+00	3.88E-01	Mtap1b	17755	NM_008634
214	1429019_s_at	-3.40E+00	3.88E-01	Pon2	330260	NM_183308
215	1421739_a_at	-3.40E+00	3.88E-01	Matk	17179	NM_010768
216	1434502_x_at	-3.40E+00	3.88E-01	Slc4a1	20533	NM_011403
217	1450686_at	-3.39E+00	3.88E-01	Pon2	330260	NM_183308
218	1444212_at	-3.38E+00	3.90E-01	Hip2	53323	NM_016786
219	1442638_at	-3.38E+00	3.90E-01	--	--	--
220	1437086_at	-3.37E+00	3.93E-01	Ascl1	17172	NM_008553

221	1443809_at	-3.36E+00	3.93E-01	Ptn	19242	NM_008973
222	1443372_at	-3.36E+00	3.93E-01	Chat	12647	NM_009891
223	1416359_at	-3.36E+00	3.97E-01	Snag1	170625	NM_130796
224	1454507_at	-3.35E+00	4.00E-01	8430432A02Rik	71524	--
225	1417871_at	-3.35E+00	4.01E-01	Hsd17b7	15490	NM_010476
226	1441440_at	-3.34E+00	4.01E-01	Apg4c	242557	NM_175029
227	1426442_at	-3.34E+00	4.01E-01	Gpm6a	234267	NM_153581
228	1455090_at	-3.34E+00	4.03E-01	Angptl2	26360	NM_011923
229	1450164_at	-3.33E+00	4.03E-01	Ascl1	17172	NM_008553
230	1457600_x_at	-3.33E+00	4.03E-01	--	--	--
231	1423091_a_at	-3.33E+00	4.03E-01	Gpm6b	14758	NM_023122
232	1434828_at	-3.32E+00	4.03E-01	B430201A12Rik	329739	XM_283903
233	1442269_at	-3.32E+00	4.03E-01	Seh1l	72124	NM_028112
234	1455874_at	-3.32E+00	4.03E-01	1810059G22Rik	67706	NM_026325
235	1429978_at	-3.32E+00	4.03E-01	5830467E07Rik	76107	--
236	1426551_at	-3.32E+00	4.03E-01	Sidt1	320007	NM_198034
237	1459355_at	-3.31E+00	4.03E-01	Tgfb3	21814	NM_011578
238	1448961_at	-3.31E+00	4.03E-01	Plscr2	18828	NM_008880
239	1426045_at	-3.31E+00	4.03E-01	Kng1	16644	NM_023125
240	1424402_at	-3.31E+00	4.03E-01	D5Bwg0860e	52822	NM_027530
241	1450438_at	-3.30E+00	4.04E-01	Ncam1	17967	NM_010875
242	1419009_at	-3.30E+00	4.08E-01	Actl7a	11470	NM_009611
243	1459028_at	-3.29E+00	4.11E-01	3830408P06Rik	70683	XM_125867
244	1421712_at	-3.28E+00	4.11E-01	Sele	20339	NM_011345
245	1456551_at	-3.27E+00	4.17E-01	--	--	--
246	1447389_at	-3.26E+00	4.20E-01	Al662168	102573	--
247	1441017_at	-3.26E+00	4.20E-01	Zcchc14	142682	NM_080855
248	1446355_at	-3.26E+00	4.20E-01	9530085L11Rik	320362	--
249	1445672_at	-3.26E+00	4.20E-01	--	--	--
250	1448895_a_at	-3.25E+00	4.26E-01	Ctnna2	12386	NM_009819 ///
						NM_145732
251	1425784_a_at	-3.24E+00	4.27E-01	Olfm1	56177	NM_019498
252	1417381_at	-3.24E+00	4.29E-01	C1qa	12259	NM_007572
253	1432873_at	-3.24E+00	4.29E-01	4932702M13Rik	74418	--
254	1442619_at	-3.23E+00	4.30E-01	Klf15	66277	NM_023184
255	1453926_at	-3.23E+00	4.30E-01	Rad54l	19366	NM_009015
256	1440525_at	-3.22E+00	4.30E-01	Acvr2b	11481	NM_007397
257	1429651_at	-3.22E+00	4.30E-01	Phactr3	74189	NM_001007154 ///
						NM_028806
258	1423287_at	-3.22E+00	4.30E-01	Cbln1	12404	NM_019626
259	1449757_x_at	-3.22E+00	4.30E-01	Dntt	21673	NM_009345
260	1457979_at	-3.22E+00	4.30E-01	--	--	--
261	1447497_at	-3.21E+00	4.30E-01	Rab21	216344	NM_024454
262	1440402_at	-3.21E+00	4.30E-01	4831426l19Rik	212073	NM_172500
263	1436815_x_at	-3.20E+00	4.31E-01	--	--	--
264	1445168_at	-3.20E+00	4.31E-01	--	--	--
265	1436470_at	-3.20E+00	4.31E-01	Rims2	116838	NM_053271
266	1421946_at	-3.19E+00	4.33E-01	Crp	12944	NM_007768
267	1421898_a_at	-3.18E+00	4.33E-01	Mr1	15064	NM_008209
268	1420432_at	-3.18E+00	4.33E-01	Tas1r1	110326	NM_031867
269	1460383_at	-3.18E+00	4.33E-01	Gnao1	14681	NM_010308
270	1421605_a_at	-3.18E+00	4.33E-01	Aqp9	64008	NM_022026
271	1440304_at	-3.18E+00	4.33E-01	BB214985	100485	--
272	1452537_at	-3.17E+00	4.33E-01	Igk-V1	16081	--
273	1449925_at	-3.16E+00	4.33E-01	Cxcr3	12766	NM_009910
274	1419746_at	-3.16E+00	4.33E-01	Arhgap23	58996	NM_021493
275	1458519_at	-3.16E+00	4.33E-01	--	--	--
276	1440820_x_at	-3.16E+00	4.33E-01	Tmco2	69469	--
277	1457008_at	-3.16E+00	4.33E-01	Chrn4	108015	NM_148944

278	1427866_x_at	-3.16E+00	4.33E-01	Hbb	15127	XM_489729
279	1432006_at	-3.16E+00	4.33E-01	Ap2a2	11772	NM_007459
280	1428048_at	-3.15E+00	4.33E-01	BC027582	269472	--
281	1420190_at	-3.15E+00	4.33E-01	--	--	--
282	1440973_at	-3.15E+00	4.33E-01	LOC552874	552874	--
283	1450288_at	-3.15E+00	4.33E-01	Cdh6	12563	NM_007666
284	1443044_at	-3.15E+00	4.33E-01	A830091E24	414271	--
285	1445687_at	-3.14E+00	4.33E-01	--	380732	XM_354645
286	1421104_at	-3.14E+00	4.33E-01	Mpa2 /// LOC547126	17472 /// 547126	NM_008620 /// XM_621976
287	1431732_at	-3.14E+00	4.33E-01	Spag16	66722	NM_025728 /// NM_029160
288	1447619_at	-3.14E+00	4.33E-01	Rtn3	20168	NM_001003930 /// NM_001003933 /// NM_001003934 /// NM_053076
289	1436188_a_at	-3.14E+00	4.33E-01	Ndrp4	234593	NM_145602
290	1427157_at	-3.13E+00	4.33E-01	E030025D05Rik	216613	NM_181577
291	1431698_at	-3.13E+00	4.33E-01	Ubash3a	328795	NM_177823
292	1424029_at	-3.13E+00	4.33E-01	Tspsyl4	72480	NM_030203
293	1425395_at	-3.13E+00	4.33E-01	Adam26a	13525	NM_010085
294	1459357_at	-3.13E+00	4.33E-01	Nfasc	269116	NM_182716
295	1445096_at	-3.12E+00	4.39E-01	--	--	--
296	1458061_at	-3.11E+00	4.43E-01	C130033P17Rik	402769	--
297	1440148_at	-3.10E+00	4.44E-01	Gpr6	140741	NM_199058
298	1425833_a_at	-3.10E+00	4.45E-01	Hpca	15444	NM_010471
299	1420543_at	-3.10E+00	4.45E-01	ORF28	246738	NM_138664
300	1433965_at	-3.09E+00	4.45E-01	Atp8a1	11980	NM_009727
301	1427667_s_at	-3.09E+00	4.49E-01	Tcrb-J /// LOC330294 /// LOC333791	21580 /// 330294 /// 333791	XM_284182 /// XM_289900
302	1420618_at	-3.08E+00	4.50E-01	Cpeb4	67579	NM_026252
303	1444428_at	-3.08E+00	4.50E-01	--	--	--
304	1452072_at	-3.08E+00	4.50E-01	Myct1	68632	NM_026793
305	1456536_at	-3.08E+00	4.50E-01	Thap6	381650	--
306	1431684_at	-3.07E+00	4.50E-01	4933402J24Rik	74438	NM_028940
307	1456562_x_at	-3.07E+00	4.50E-01	KIAA0415	231855	NM_172725
308	1436178_at	-3.07E+00	4.50E-01	Leprel1	210530	NM_173379
309	1457289_at	-3.07E+00	4.50E-01	Nr2e1	21907	NM_152229
310	1436025_at	-3.07E+00	4.50E-01	A430106J12Rik	108686	NM_176841
311	1443005_at	-3.07E+00	4.50E-01	Zfhx1a	21417	NM_011546
312	1445580_at	-3.06E+00	4.50E-01	Matn2	17181	NM_016762
313	1431091_at	-3.06E+00	4.50E-01	Pygo1	72135	XM_134865
314	1421483_at	-3.05E+00	4.55E-01	Lhx4	16872	NM_010712
315	1444145_at	-3.05E+00	4.55E-01	--	--	--
316	1455701_at	-3.05E+00	4.55E-01	Snx26	233071	NM_178252
317	1446525_at	-3.05E+00	4.55E-01	Gpc3	14734	NM_016697
318	1435113_x_at	-3.05E+00	4.55E-01	Stmn3	20262	NM_009133
319	1439018_at	-3.04E+00	4.58E-01	--	--	--
320	1422606_at	-3.04E+00	4.59E-01	C1qtnf3	81799	NM_030888
321	1454903_at	-3.04E+00	4.59E-01	Ngfr	18053	NM_033217
322	1445331_at	-3.03E+00	4.59E-01	--	--	--
323	1448748_at	-3.03E+00	4.59E-01	Plek	56193	NM_019549
324	1430511_at	-3.03E+00	4.59E-01	1500037O19Rik	70254	--
325	1417803_at	-3.03E+00	4.59E-01	1110032A04Rik	66183	NM_133675
326	1446327_at	-3.03E+00	4.59E-01	--	--	--
327	1448785_at	-3.02E+00	4.59E-01	Cbfa2t1h	12395	NM_009822
328	1458673_at	-3.02E+00	4.59E-01	1700093J21Rik	74296	XM_484572 /// XM_622717
329	1444784_at	-3.02E+00	4.59E-01	4930564K09Rik	78212	--

330	1428902_at	-3.01E+00	4.59E-01	Chst11	58250	NM_021439
331	1453969_at	-3.01E+00	4.59E-01	MGI:1920494	73244	NM_028477
332	1458643_at	-3.01E+00	4.59E-01	Dtx1	14357	NM_008052
333	1440363_at	-3.00E+00	4.65E-01	--	--	--
334	1454719_at	-3.00E+00	4.65E-01	5730411O18Rik	279766	NM_177370
335	1443347_at	-3.00E+00	4.65E-01	--	--	--
336	1427845_at	-2.99E+00	4.68E-01	Fgfr4	14186	NM_008011
337	1444608_at	-2.99E+00	4.70E-01	Ankrd17	81702	NM_030886 /// NM_198010 NM_011196
338	1450344_a_at	-2.98E+00	4.72E-01	Ptger3	19218	
339	1439912_at	-2.97E+00	4.76E-01	9430098F02Rik	103793	--
340	1425905_at	-2.97E+00	4.76E-01	--	--	--
341	1452644_at	-2.97E+00	4.76E-01	Mbd3l2	234988	NM_144934
342	1420582_at	-2.97E+00	4.76E-01	Cd209e	170780	NM_130905
343	1433770_at	-2.97E+00	4.76E-01	Dpysl2	12934	NM_009955
344	1444778_at	-2.96E+00	4.76E-01	Sept3	24050	NM_011889
345	1432169_at	-2.96E+00	4.76E-01	4930523O13Rik	74726	--
346	1459250_at	-2.96E+00	4.76E-01	MGI:2153084	228911	NM_080455
347	1444423_at	-2.96E+00	4.76E-01	--	--	--
348	1416992_at	-2.96E+00	4.76E-01	Mfng	17305	NM_008595
349	1435280_at	-2.95E+00	4.80E-01	AI452195	105178	--
350	1440396_at	-2.95E+00	4.81E-01	Mpp6	56524	NM_019939
351	1442615_at	-2.95E+00	4.82E-01	Adk	11534	NM_134079
352	1447857_at	-2.94E+00	4.87E-01	D230005D02Rik	239188	NM_172813
353	1448812_at	-2.94E+00	4.87E-01	Hpcal1	53602	NM_016677
354	1439557_s_at	-2.93E+00	4.91E-01	Ldb2	16826	NM_010698
355	1449637_at	-2.93E+00	4.91E-01	Cdh4	12561	NM_009867
356	1445816_at	-2.93E+00	4.91E-01	--	--	--
357	1452467_at	-2.93E+00	4.91E-01	Mmab	77697	NM_029956
358	1432518_at	-2.92E+00	4.91E-01	4930430J20Rik	78109	--
359	1441628_at	-2.92E+00	4.91E-01	Diap3	56419	NM_019670
360	1438772_at	-2.92E+00	4.91E-01	Zfp367	238673	NM_175494
361	1440302_at	-2.92E+00	4.93E-01	Slc25a3	18674	NM_133668
362	1441831_x_at	-2.91E+00	4.96E-01	Clcn5	12728	NM_016691
363	1449874_at	-2.91E+00	4.96E-01	Ly96	17087	NM_016923
364	1446155_at	-2.91E+00	4.97E-01	--	--	--
365	1452751_at	-2.90E+00	5.00E-01	Ebf3	13593	NM_010096

Title refers to the gene title, Probeset_id refers to the Affymetrix probe ID. The score refers to the PowerExpress value that incorporates both fold-change and *P*-value. FDR indicates the false discovery rate, and the gene ID is given in the final column.

Table S6. The top-20 predicted enhancer elements using EEL

Rank	Gene	Coordinates	qPCR
1	<u>Ptch1</u>	chr13:60949059-60949576	+
2	BC017647	chr11:77879370-77881080	
3	Kif5a	chr10:127004002-127004301	
4	<u>Ptch1</u>	chr13:60956203-60957612	+
5	Ntn1	chr11:68031783-68031998	
6	Ngfr	chr11:95396268-95396731	
7	4831426119Rik	chr12:100377810-100377958	+
8	Abcb8	chr5:22884482-22884701	
9	Olfm1	chr2:28152536-28152588	
10	<u>Nkx2-9</u>	chr12:53347501-53347755	+
11	2600003E23Rik	chr5:34368835-34369174	
12	Phox2a	chr7:95939471-95939679	
13	Rad54l	chr4:115033946-115035434	
14	Hoxb2	chr11:96176306-96176394	
15	Nkx2-9	chr12:53332902-53334901	
16	Snx26	chr7:25981542-25982431	
17	1810059G22Rik	chr19:7999574-8001182	
18	<u>Nkx2-9</u>	chr12:53340887-53341102	+
19	<u>Foxa2</u>	chr2:147493732-147495645	+
20	Mtap1b	chr13:95603717-95603819	

Enhancers also identified by location analysis are underlined. Conditions were performed as described (Hallikas et al., 2006) ($\lambda=2$, $\mu=0.12$, $\nu=200$, $\xi=200$, module length ≤ 2000 , Gli score ≥ 25) except that we required EEL score ≥ 100 instead of ≥ 500 , and the predictions were ranked by combined Gli score instead of by total EEL score. We chose our current criteria since they resulted in the inclusion of validated enhancers in Ptch1 and Nkx2-9 into the top 20 predictions. Enhancers were tested by qPCR on LMP-PCR amplified CHIP tissue.

Table S7. Genome-wide screen of Gli target genes in mouse using MCA

Rank	Gene	Rank	Gene	Rank	Gene
1	Zswim2	18	1700011F03Rik	35	Ntn4
2	Ppp3ca	19	Gpc3	36	Cntnap2
3	Lrfr5	20	Utrn	37	Nol4
4	Ncam1	21	Nfia	38	Camk2g
5	Hhip	22	Gpc5	39	<u>Nkx2-9</u>
6	<u>Ptch1</u>	23	Eda	40	Ntrk2
7	A2bp1	24	1700108E19Rik	41	Ahd1
8	Stk32a	25	2810426N06Rik	42	1700022L09Rik
9	Odz2	26	Arid5b	43	Foxf1a
10	Bcas3	27	Adamts2	44	BC052066
11	Srisnf2l	28	Tex264	45	Pitpnb
12	Mapk4	29	Xlr3a	46	Ndr3
13	Ntng2	30	Prkag1	47	Sh2d1b
14	Opcm1	31	Dcbl1	48	Ank2
15	Reln	32	Gopc	49	Mar1
16	Grm3	33	Nrf1	50	Prkce
17	Ctnna2	34	<u>Robo2</u>	51	Atp5h

Genes are ranked by combined Gli-binding affinity. The neural targets that were subsequently validated by qPCR are denoted by bold, underlined text.

Table S8. Top-20 Gli enhancers identified by MCA present in the pool of EB genes upregulated by Hh treatment

Rank	MCA	Coordinates	qPCR
1	Ncam1	chr9:49835328-49835543	
2	Ebf3	chr7:131683012-131684612	
3	<u>Nkx2-9</u>	chr12:53347461-53347776	+
4	<u>Ptch1</u>	chr13:60948913-60949595	+
5	Gpm6b	chrX:159911226-159911457	
6	Gpc3	chrX:47041532-47041785	
7	Robo2	chr16:73388698-73389494	+
8	Gpc3	chrX:47086023-47086378	+
9	Ret	chr6:118619345-118619637	+
10	Neurog2	chr3:126511586-126512041	
11	Ebf1	chr11:44728066-44728630	
12	Ctnna2	chr6:77576792-77577343	
13	<u>Ptch1</u>	chr13:60951919-60952536	+
14	Ctnna2	chr6:77525938-77526505	
15	<u>Ptch1</u>	chr13:60955950-60956548	+
16	<u>Nkx2-9</u>	chr12:53340885-53341147	+
17	Ascl1	chr10:87473182-87474379	
18	Hoxb	chr11:96102714-96103772	
19	Trpm3	chr19:21679064-21679850	
20	<u>FoxA2</u>	chr2:147493773-147494127	+

Note that the Gpc3 enhancers predicted here differ from a validated enhancer present in the mesenchyme ventral to the neural tube. This target, identified in a previous study using EEL (Hallikas et al., 2006), is not present as a top-20 target in Table S6 because it is sorted based on Gli score instead of total EEL score.

Table S9. Summary of qPCR-validated Gli-binding regions and procedures that identified sites

Gene	Coordinates	Identification
FoxA2 – peak1	chr2:147493701-147494245	ChIP-on-chip, MCA, EEL
Gli1 – peak1	chr 10:127076571-127078504	ChIP-on-chip
Gpc3	chr X:47086023-47086378	MCA
Hhip – peak1	chr 8:79270092-79270492	ChIP-on-chip
Hhip – peak2	chr 8:79268419-79268867	ChIP-on-chip
Nkx 2-1 – peak1	chr 12:53245748-53246351	ChIP-on-chip
Nkx2-2 – peak1	chr 2:146644626-146645570	ChIP-on-chip
Nkx2-9 – peak1	chr 12:53340519-53341015	ChIP-on-chip, MCA, EEL
Nkx2-9 – peak2	chr 12:53347310-53348354	ChIP-on-chip, MCA, EEL
Ptch1 – peak1	chr 13:60945578-60945972	ChIP-on-chip
Ptch1 – peak2	chr 13:60949397-60950371	ChIP-on-chip, MCA, EEL
Ptch1 – peak3	chr 13:60951377-60952953	ChIP-on-chip, MCA
Ptch1 – peak4	chr 13:60953950-60955072	ChIP-on-chip
Ptch1 – peak5	chr 1360956284-60956777	ChIP-on-chip, MCA, EEL
Ptch2 – peak1	chr 4:116057320-116057946	ChIP-on-chip
Ptch2 – peak2	chr 4:116054385-116054954	ChIP-on-chip
Rab34 – peak1	chr 11:77915220-77915560	ChIP-on-chip
Ret	chr 6:118619345-118619637	MCA
Robo2	chr 16:73388698-73389494	MCA
4831426119Rik	chr 12:100377810-100377958	EEL

All Gli1-binding sites identified in this study that showed enrichment in additional qPCR-based ChIP assays are listed along with the identification methods that identified each site (see results). When more than one method identified overlapping coordinates, the values refer to the ChIP-on-chip coordinates defined in Table 1 (other coordinates refer to Tables S6 and S8). Note that several sites were identified only by the EEL or MCA algorithms; in all cases, these regions were not present on the custom tiling array.