

**Supplementary Table 1: List of 228 Peaks Bound by Scl in HPC-7.** All peaks are listed by chromosome number, start and end position in the mouse genome (build mm8 UCSC).

<i>peak co-ordinates</i>					
<i>chromosome</i>	<i>start</i>	<i>end</i>			
chr1	36217883	36218310	chr3	60873148	60873467
chr1	37176855	37177719	chr3	84546889	84547259
chr1	39678938	39679296	chr3	87987224	87987679
chr1	52667246	52667539	chr3	105936522	105936905
chr1	87415945	87416506	chr3	133276751	133277030
chr1	87419855	87420298	chr3	146636349	146636644
chr1	87422296	87423221	chr4	11648559	11648907
chr1	87423348	87424602	chr4	114593681	114593997
chr1	90066018	90066887	chr4	115347251	115347630
chr1	132953797	132954150	chr4	115347251	115347630
chr1	133923080	133923470	chr4	131348859	131349177
chr1	134611718	134612102	chr4	133766857	133767240
chr1	134611718	134612102	chr4	133874110	133874414
chr1	153777852	153778204	chr4	135449817	135450435
chr1	167159634	167160056	chr4	140088638	140088940
chr1	172347345	172347867	chr4	149305247	149305556
chr1	173367656	173368571	chr5	3676149	3676577
chr1	173387910	173388480	chr5	36914820	36915190
chr1	173394728	173395214	chr5	107999436	107999796
chr1	173395273	173396241	chr5	121496809	121497138
chr1	173396289	173396906	chr5	121496809	121497138
chr1	173397861	173398278	chr5	122913213	122913541
chr1	174363415	174363756	chr5	130456245	130456523
chr1	182687471	182687791	chr5	135998017	135998409
chr1	183208997	183209369	chr5	139986549	139986882
chr2	4350421	4350781	chr5	140029468	140029853
chr2	20406816	20407210	chr5	140461206	140461548
chr2	21881796	21882149	chr5	147968258	147968610
chr2	27525358	27525676	chr6	51689928	51690275
chr2	28419979	28420490	chr6	72319116	72319461
chr2	28421256	28421632	chr6	84848861	84849194
chr2	46192993	46193358	chr6	88082347	88082834
chr2	62419686	62420027	chr6	90583747	90584121
chr2	90360861	90361188	chr6	91587941	91588257
chr2	101837959	101838305	chr6	125439092	125439419
chr2	116690353	116690684	chr6	142788575	142788864
chr2	127019895	127020350	chr7	4233275	4233610
chr2	162920552	162920931	chr7	34865266	34865690
chr2	164132281	164132661	chr7	37888783	37889742
chr2	172677935	172678330	chr7	45392855	45393237
chr3	51832385	51832686	chr7	75485579	75485864
			chr7	80368737	80369140
			chr7	110795332	110795656
			chr7	144302389	144302764

chr8	70642103	70642533	chr10	59972770	59973083
chr8	71535701	71536060	chr10	66259848	66260193
chr8	73214923	73215238	chr10	80080924	80081733
chr8	75197298	75197656	chr10	80581073	80581493
chr8	75657418	75657757	chr10	80581604	80582057
chr8	87590032	87590384	chr10	117467906	117468299
chr8	87591588	87591922	chr10	120089189	120089593
chr8	87620765	87621220	chr11	3092820	3093905
chr8	91169786	91170125	chr11	3097508	3098610
chr8	97853954	97854321	chr11	16904936	16905278
chr8	97874237	97874853	chr11	20131167	20131478
chr8	98045213	98045554	chr11	30066220	30066522
chr8	108498536	108498830	chr11	62746088	62746400
chr8	108512305	108512718	chr11	74393342	74393667
chr8	108616531	108616924	chr11	78588117	78588431
chr8	113815682	113816048	chr11	87961863	87962219
chr8	114482385	114482925	chr11	102286089	102286479
chr8	117629179	117629471	chr11	104427671	104428032
chr8	117765541	117765994	chr12	12522508	12522848
chr8	120429724	120430075	chr12	17626683	17627070
chr8	120434303	120434880	chr12	55084434	55084758
chr8	123116808	123117132	chr12	81697062	81697410
chr8	123180030	123180377	chr12	112392847	112393211
chr8	123220706	123221020	chr12	113047022	113047301
chr8	123255938	123256344	chr13	13330724	13331160
chr8	123257731	123258097	chr13	20191008	20191336
chr8	123361523	123361846	chr13	37516876	37517328
chr8	123373000	123373352	chr13	40920031	40920368
chr8	125170759	125171143	chr13	43202756	43203139
chr8	125195419	125195796	chr13	43204082	43204573
chr8	125207681	125208311	chr13	44512695	44513098
chr8	125585165	125585505	chr13	51750439	51750814
chr8	125586701	125587190	chr13	102803338	102803574
chr8	125606517	125606821	chr13	109436497	109436889
chr9	13368466	13369107	chr13	109768163	109768503
chr9	32305818	32306221	chr13	111028537	111028843
chr9	37303884	37304235	chr14	53660017	53660430
chr9	45025152	45025644	chr14	53731953	53732487
chr9	57219369	57219686	chr14	71857566	71857904
chr9	57303945	57304255	chr14	75303440	75303730
chr9	61464157	61464509	chr15	10712221	10712650
chr9	74803298	74803600	chr15	27441658	27441978
chr9	96459315	96459622	chr15	37147625	37148016
chr9	98991653	98991944	chr15	63477954	63478273
chr9	107840737	107841098	chr15	66980833	66981169
chr9	110510759	110511056	chr15	78398932	78399253
chrX	165333297	165333719	chr15	94306940	94307228
chr10	19504831	19505138	chr15	103086426	103086762
chr10	19508200	19508510	chr15	103167377	103167715
chr10	19825174	19825443	chr16	10590336	10590662
chr10	20744133	20744573	chr16	91255546	91255826
chr10	20917952	20918325	chr16	92690471	92690780
chr10	40141221	40141539	chr16	93018031	93018356
chr10	41745745	41746041	chr16	93036086	93036405

chr16	95547971	95548359	chr17	84684884	84685280
chr16	95966120	95966569	chr17	85782513	85782830
chr17	6129463	6129806	chr17	87882877	87883249
chr17	23459192	23459428	chr18	35975373	35975751
chr17	25733277	25733729	chr18	38051826	38052170
chr17	29586834	29587234	chr18	50153492	50154147
chr17	30952693	30953216	chr18	55027902	55028212
chr17	33320032	33320359	chr18	55232377	55232772
chr17	40270218	40270498	chr18	61884284	61884629
chr17	44117547	44117986	chr18	68355593	68355909
chr17	44135340	44135667	chr18	75786036	75786374
chr17	47058626	47058939	chr19	10131228	10131580
chr17	56447267	56447705	chr19	34910807	34911124
chr17	56975570	56975890	chr19	37500737	37501129
chr17	70393764	70394116	chr19	40866735	40867049
chr17	83870345	83870853	chr19	46508200	46508662
chr17	83898536	83899216	chr19	46941502	46941835
chr17	84024743	84025193			
chr17	84069656	84069945			

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**Supplementary Table 2: Motif discovery.** Over-represented motifs (z-score  $\geq 2.0$  relative to background set of sequences; see materials and methods). Over-represented motifs were determined by searching i) an in-house library of 54 consensus motifs, ii) the JASPAR Core library (138 matrices) and iii) a subset of the TRANSFAC release 10.4 library (506 matrices of human and mouse origin out of a total of 816 matrices).

	Motif	Motif instances in 228 Scl-bound regions	Mean instances in background set	St. Dev.	Z-score	Description	Class
<b>Consensus sites 11 out of 54</b>	EBOX.MyoD	990	559.24	31.61	13.63	EBOX.MyoD	bHLH
	GATA	558	300.09	21.6	11.94	GATA	GATA
	EBOX.1	617	403.45	21.87	9.77	EBOX.1	bHLH
	AML1	158	73.07	10.14	8.38	AML1	Runt
	MEIS1	177	102.95	10.23	7.24	MEIS1	Meis
	MYB	300	192.89	15.2	7.05	MYB	MYB
	ETS.EIk-1	513	373.29	21.88	6.39	ETS.EIk-1	ETS
	NBOX	229	166.42	13.17	4.75	NBOX	bHLH
	ETS.1	1746	1554.27	45.78	4.19	ETS.1	ETS
	IKAROS	851	726.94	30.53	4.06	IKAROS	
	IROQUOIS	39	20.73	4.57	3.99	IROQUOIS	
<b>Jaspar Core 12 out of 138</b>	MA0055	157	75.97	12.34	6.56	Myf,bHLH	bHLH
	MA0099	42	16.91	4.7	5.34	Fos,bZIP	
	MA0002	29	11.88	3.42	5.01	RUNX1,RUNT	Runt
	MA0091	41	17.56	5.04	4.65	TAL1-TCF3,bHLH	bHLH
	MA0136	45	24.39	4.95	4.16	ELF5,ETS	ETS
	MA0125	18	8.01	2.83	3.53	Nobox,HOMEO	
	MA0081	58	35.16	6.5	3.52	SPIB,ETS	ETS
	MA0048	93	58.4	10.07	3.44	NHLH1,bHLH	E-box
	MA0100	22	10.7	3.48	3.25	Myb,TRP-CLUSTER	MYB
	MA0109	13	5.63	2.4	3.07	RUSH1-alfa,ZN-FINGER, GATA	GATA
	MA0062	55	35.6	6.36	3.05	GABPA,ETS	ETS
	MA0126	18	9.36	3.07	2.81	ovo,ZN-FINGER, C2H2	

**TRANSFAC**  
**96 out of**  
**506**

M00789	79	9	3.02	23.16	GATA	GATA
M00462	70	9.62	3.09	19.57	GATA-6	GATA
M00128	83	18.28	4.46	14.51	GATA-1 (GATA-binding factor 1)	GATA
M00346	65	13.34	3.78	13.67	GATA-1 (GATA-binding factor 1)	GATA
M00278	54	10.04	3.25	13.51	Lmo2 complex (complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 2)	GATA
M00971	173	64.37	8.25	13.16	Ets	ETS
M00203	59	13.24	3.58	12.79	GATA-X (GATA binding site)	GATA
M00339	155	57.33	7.65	12.77	c-Ets-1 (c-ETS-1 binding site)	ETS
M00126	43	8.59	2.96	11.62	GATA-1 (GATA-binding factor 1)	GATA
M00771	133	52.84	7.46	10.75	ETS	ETS
M00658	144	59.9	7.96	10.57	PU.1	ETS
M00340	103	38.01	6.21	10.47	c-Ets-2 (c-Ets-2 binding sites)	ETS
M00722	69	21.67	5.12	9.25	core-binding factor	Runt
M00769	70	25.43	5.01	8.89	AML	Runt
M00955	59	20.19	4.4	8.82	GR (high affinity binding site for glucocorticoid receptor)	
M00175	111	46.04	8.04	8.08	AP-4 (activator protein 4)	
M00176	115	49.44	8.2	8	AP-4 (activator protein 4)	
M00984	60	22.4	4.72	7.97	PEBP	
M00644	150	64.99	10.86	7.83	LBP-1	
M00032	80	32.03	6.29	7.62	c-Ets-1(p54) (c-Ets-1(p54))	ETS

M00957	61	23.59	5	7.49	PR (is recognized by progesterone receptor)	
M00712	130	62.97	9.03	7.42	myogenin	bHLH
M00927	105	47.23	7.8	7.41	AP-4	
M00007	66	27.27	5.29	7.32	Elk-1 (Elk-1)	ETS
M00921	70	30.28	5.57	7.13	GR (half-site matrix)	
M00531	110	58.83	7.65	6.69	NERF1a (new ets-related factor 1a)	ETS
M00066	61	26.17	5.41	6.43	Tal-1alpha:E47 (Tal-1alpha:E47 heterodimer)	bHLH
M00065	55	23.35	5.02	6.3	Tal-1beta:E47 (Tal-1beta:E47 heterodimer)	bHLH
M00517	58	25.18	5.36	6.13	AP-1	
M00184	86	44.79	6.99	5.89	MyoD (myoblast determining factor)	bHLH
M00199	62	24.36	6.49	5.8	AP-1 (AP-1 binding site)	
M00993	83	42.95	6.91	5.79	TAL1	bHLH
M00698	111	60.55	8.71	5.79	HEB	bHLH
M00418	44	19.16	4.31	5.76	TGIF (TGIF (5'TG3' interacting factor))	
M00773	37	14.8	3.89	5.71	MYB	MYB
M00070	48	21.72	4.81	5.46	Tal-1beta:ITF-2 (Tal-1beta:ITF-2 heterodimer)	bHLH
M00011	14	3.56	1.94	5.38	Evi-1 (ectopic viral integration site 1 encoded factor)	
M00804	95	55.09	7.43	5.37	E2A	bHLH
M00277	95	52.95	8.04	5.23	Lmo2 complex (complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-1, half-site 1)	bHLH
M00983	61	33.39	5.8	4.76	MAF	
M00913	32	13.72	3.91	4.67	MYB	MYB

M00001	56	30.64	5.49	4.62	MyoD (myoblast determination gene product)	bHLH
M00821	50	26.11	5.17	4.62	Nrf2 (heterodimer containing Nrf2)	
M00419	47	23.93	5.03	4.59	MEIS1 (Meis-1 (myeloid ecotropic viral integration site 1))	Meis
M00532	43	21.99	4.62	4.55	RP58 (58 KDA repressor protein)	
M00678	58	32.02	5.76	4.51	Tel-2	ETS
M00037	49	25.62	5.36	4.36	NF-E2 (NF-E2 p45)	
M00079	28	12.65	3.56	4.31	Evi-1 (ectopic viral integration site 1 encoded factor)	
M00183	28	12.97	3.49	4.3	c-Myb (c-Myb)	MYB
M00731	29	13.1	3.7	4.3	Osf2	
M00500	65	38.27	6.3	4.24	STAT6 (signal transducer and activator of transcription 6)	
M00746	73	45.93	7.13	3.8	ELF-1	ETS
M00925	36	18.98	4.55	3.74	AP-1	
M00495	34	17.13	4.54	3.71	Bach1 (BTB and CNC homolog 1)	
M00490	33	17.66	4.18	3.66	Bach2 (BTB and CNC homolog 2)	
M01043	43	25.05	4.94	3.63	NKX25	
M00693	74	48.13	7.22	3.58	E12	bHLH
M00214	39	22.11	4.77	3.55	SEF-1 (SEF1 binding site)	
M00174	40	22.6	4.91	3.54	AP-1 (activator protein 1)	
M00926	36	19.73	4.6	3.54	AP-1	
M00975	25	12.28	3.71	3.43	RFX	

M01081	31	16.8	4.26	3.34	Zec (zinc finger protein expressed in embryonal cells and certain adult organs)	
M00155	48	29.89	5.45	3.32	ARP-1 (COUP-TF2) (apolipoprotein AI regulatory protein 1)	
M00954	35	21.01	4.52	3.09	PR (high affinity binding sites for progesterone receptor)	
M00071	46	28.97	5.65	3.01	E47 (E47)	bHLH
M00188	38	23.3	5	2.94	AP-1 (activator protein 1)	
M00284	26	14.51	3.95	2.91	TCF11:MafG (TCF11:MafG heterodimers)	
M00929	96	70.85	8.68	2.9	MyoD	bHLH
M00481	30	16.64	4.65	2.88	AR (androgen receptor)	
M01119	44	28.51	5.5	2.82	KAISO	
M01029	24	13.49	4.01	2.62	TFE	
M00002	78	57.55	7.84	2.61	E47 (E47)	bHLH
M00077	31	19.14	4.56	2.6	GATA-3 (GATA-binding factor 3)	GATA
M00493	33	20.85	4.69	2.59	STAT5A (signal transducer and activator of transcription 5a)	
M00648	68	50.11	7	2.56	MAF	
M01109	47	32.26	5.79	2.55	SZF1-1	
M01082	21	12.31	3.5	2.49	BRCA1:USF2 (BRCA1 containing protein complex with USF2)	
M00005	74	54.95	7.7	2.48	AP-4 (activator protein 4)	

M00221	39	26.52	5.11	2.44	SREBP-1 (sterol regulatory element- binding protein 1)	
M00793	32	20.47	4.78	2.41	YY1	
M00415	28	17.61	4.33	2.4	AREB6 (AREB6 (Atp1a1 regulatory element binding factor 6))	
M00492	37	24.75	5.12	2.39	STAT1 (signal transducer and activator of transcription 1)	
M00123	23	13.96	3.8	2.38	c-Myc:Max (c- Myc:Max heterodimer)	bHLH
M00437	13	6.05	2.97	2.34	CHX10	
M00997	40	27.22	5.48	2.33	DEC	
M00137	12	6.17	2.52	2.31	Oct-1 (octamer factor 1)	
M00416	17	9.06	3.44	2.31	Cart-1 (Cart-1 (cartilage homeoprotein 1))	
M00205	31	20.48	4.6	2.29	GR (Glucocorticoid response element)	
M00069	36	24.45	5.08	2.27	YY1 (Yin and Yang 1)	
M00973	62	46.04	7.18	2.22	E2A	bHLH
M00173	32	21.36	4.79	2.22	AP-1 (activator protein 1)	
M00484	12	6.48	2.55	2.17	Ncx	
M00468	50	36.91	6.05	2.16	AP-2rep (AP-2 repressor)	
M00632	46	33.37	5.91	2.14	GATA-4	GATA
M00004	31	20.88	4.74	2.13	c-Myb (c-Myb)	MYB
M00078	30	19.03	5.33	2.06	Evi-1 (ectopic viral integration site 1 encoded factor)	
M00651	25	16.55	4.19	2.02	NF- $\mu$ E1	

**Supplementary Table 3: List of 228 Peaks and Associated Genes.** Peaks were analysed to determine if they were within a promoter region, intronic or between two flanking genes (see materials and methods). Peak co-ordinate, gene name and Ensembl ID are shown.

<i>peak co-ordinates</i>			<i>gene name</i>	<i>Ensembl ID</i>
<i>chromosome</i>	<i>start</i>	<i>end</i>		
chr1	36217883	36218310	LincR	ENSMUSG00000047180
chr1	37176855	37177719	Cnga3	ENSMUSG00000026114
chr1	39678938	39679296	Creg2	ENSMUSG00000050967
chr1	39678938	39679296	Map4k4	ENSMUSG00000026074
chr1	52667246	52667539	2210010L05Rik	ENSMUSG00000041439
chr1	87415945	87416506	Sp110	ENSMUSG00000070034
chr1	87419855	87420298	Sp110	ENSMUSG00000070034
chr1	87422296	87423221	Sp110	ENSMUSG00000070034
chr1	87423348	87424602	Sp110	ENSMUSG00000070034
chr1	90066018	90066887	Ugt1a1	ENSMUSG00000054545
chr1	90066018	90066887	Hjurp	ENSMUSG00000044783
chr1	132953797	132954150	Mapkapk2	ENSMUSG00000016528
chr1	132953797	132954150	Dyrk3	ENSMUSG00000016526
chr1	133923080	133923470	Mfsd4	ENSMUSG00000059149
chr1	133923080	133923470	Pctk3	ENSMUSG00000026437
chr1	134611718	134612102	Nfasc	ENSMUSG00000026442
chr1	134611718	134612102	Lrrn2	ENSMUSG00000026443
chr1	153777852	153778204	1700025G04Rik	ENSMUSG00000032666
chr1	167159634	167160056	Gpr161	ENSMUSG00000040836
chr1	167159634	167160056	lqwd1	ENSMUSG00000026571
chr1	172347345	172347867	Nos1ap	ENSMUSG00000038473
chr1	173367656	173368571	Itln1	ENSMUSG00000038209
chr1	173387910	173388480	Itln1	ENSMUSG00000038209
chr1	173387910	173388480	Cd244	ENSMUSG00000004709
chr1	173394728	173395214	Cd244	ENSMUSG00000004709
chr1	173395273	173396241	Cd244	ENSMUSG00000004709
chr1	173396289	173396906	Cd244	ENSMUSG00000004709
chr1	173397861	173398278	Cd244	ENSMUSG00000004709
chr1	174363415	174363756	Ccdc19	ENSMUSG00000026546
chr1	182687471	182687791	BC031781	ENSMUSG00000038806
chr1	183208997	183209369	Cnih3	ENSMUSG00000026514
chr2	4350421	4350781	Frmd4a	ENSMUSG00000026657
chr2	20406816	20407210	Etl4	ENSMUSG00000036617
chr2	21881796	21882149	Gpr158	ENSMUSG00000045967
chr2	21881796	21882149	Myo3a	ENSMUSG00000025716
chr2	27525358	27525676	Rxra	ENSMUSG00000015846
chr2	28419979	28420490	Gtf3c5	ENSMUSG00000026816
chr2	28419979	28420490	Gfi1b	ENSMUSG00000026815
chr2	28421256	28421632	Gtf3c5	ENSMUSG00000026816
chr2	28421256	28421632	Gfi1b	ENSMUSG00000026815

chr2	46192993	46193358	Zeb2	ENSMUSG00000026872
chr2	46192993	46193358	Acvr2a	ENSMUSG00000052155
chr2	62419686	62420027	Ifih1	ENSMUSG00000026896
chr2	90360861	90361188	Ptprj	ENSMUSG00000025314
chr2	101837959	101838305	Ldlrad3	ENSMUSG00000048058
chr2	116690353	116690684	Tmco5	ENSMUSG00000027355
chr2	116690353	116690684	Spred1	ENSMUSG00000027351
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chr2	162920552	162920931	Tox2	ENSMUSG00000074607
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chr3	87987224	87987679	Prcc	ENSMUSG00000004895
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chr3	133276751	133277030	Ppa2	ENSMUSG00000028013
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chr4	149305247	149305556	Rere	ENSMUSG00000039852
chr5	3676149	3676577	4930511M11Rik	ENSMUSG00000014529
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chr5	36914820	36915190	D5Erttd579e	ENSMUSG00000029190
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chr5	121496809	121497138	Rpl6	ENSMUSG00000029614
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chr5	122913213	122913541	P2rx7	ENSMUSG00000029468
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chr5	139986549	139986882	Micall2	ENSMUSG00000036718
chr5	140029468	140029853	Ints1	ENSMUSG00000029547
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chr5	140461206	140461548	Mad11l	ENSMUSG00000029554
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chr6	88082347	88082834	Gata2	ENSMUSG00000015053
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chr6	91587941	91588257	Lsm3	ENSMUSG00000034192
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chr6	142788575	142788864	St8sia1	ENSMUSG00000030283
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chr8	98045213	98045554	Kifc3	ENSMUSG000000031788
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chr8	123180030	123180377	1700120B06Rik	ENSMUSG00000042269
chr8	123180030	123180377	Gse1	ENSMUSG00000031822
chr8	123220706	123221020	1700120B06Rik	ENSMUSG00000042269
chr8	123220706	123221020	Gse1	ENSMUSG00000031822
chr8	123255938	123256344	1700120B06Rik	ENSMUSG00000042269
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chr8	123257731	123258097	Gse1	ENSMUSG00000031822
chr8	123361523	123361846	1700120B06Rik	ENSMUSG00000042269
chr8	123361523	123361846	Gse1	ENSMUSG00000031822
chr8	123373000	123373352	1700120B06Rik	ENSMUSG00000042269
chr8	123373000	123373352	Gse1	ENSMUSG00000031822
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chr8	125195419	125195796	Zfpm1	ENSMUSG00000049577
chr8	125207681	125208311	Zfpm1	ENSMUSG00000049577
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chr9	37303884	37304235	Spa17	ENSMUSG00000001948
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chr9	57303945	57304255	Rpp25	ENSMUSG00000062309
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chr9	98991653	98991944	Pik3cb	ENSMUSG00000032462
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chr10	20744133	20744573	Ahi1	ENSMUSG00000019986
chr10	20917952	20918325	Myb	ENSMUSG00000019982
chr10	20917952	20918325	Hbs1l	ENSMUSG00000019977
chr10	40141221	40141539	Cdc2l6	ENSMUSG00000038481
chr10	41745745	41746041	Tdg	ENSMUSG00000051559
chr10	41745745	41746041	Foxo3	ENSMUSG00000075216
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chr10	80080924	80081733	Mobkl2a	ENSMUSG00000003348
chr10	80581073	80581493	Eef2	ENSMUSG00000034994
chr10	80581604	80582057	Eef2	ENSMUSG00000034994
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chr10	117467906	117468299	Mdm1	ENSMUSG00000020212
chr10	120089189	120089593	Hmga2	ENSMUSG00000056758
chr10	120089189	120089593	(AK156853)	ENSMUSG00000074675
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chr11	16904936	16905278	Plek	ENSMUSG00000020120
chr11	20131167	20131478	Cep68	ENSMUSG00000044066
chr11	30066220	30066522	Spnb2	ENSMUSG00000020315
chr11	62746088	62746400	Fam18b	ENSMUSG00000014177
chr11	62746088	62746400	Cdrt4	ENSMUSG00000042200
chr11	74393342	74393667	Garnl4	ENSMUSG00000038807
chr11	78588117	78588431	1810009O10Rik	ENSMUSG00000049489
chr11	78588117	78588431	1810012P15Rik	ENSMUSG00000072640
chr11	87961863	87962219	Cuedc1	ENSMUSG00000018378
chr11	102286089	102286479	Itga2b (CD41)	ENSMUSG00000034664
chr11	104427671	104428032	Itgb3 (CD61)	ENSMUSG00000020689
chr12	12522508	12522848	D12Erttd553e	ENSMUSG00000020589
chr12	12522508	12522848	Mycn	ENSMUSG00000037169
chr12	17626683	17627070	Odc1	ENSMUSG00000011179
chr12	17626683	17627070	Hpcal1	ENSMUSG00000071379
chr12	55084434	55084758	Npas3	ENSMUSG00000021010
chr12	55084434	55084758	Egln3	ENSMUSG00000035105
chr12	81697062	81697410	Gm1568	ENSMUSG00000062961
chr12	81697062	81697410	4933426M11Rik	ENSMUSG00000021133
chr12	112392847	112393211	Ppp1r13b	ENSMUSG00000021285
chr12	112392847	112393211	2010107E04Rik	ENSMUSG00000021290
chr12	113047022	113047301	Inf2	ENSMUSG00000037679
chr13	13330724	13331160	Nid1	ENSMUSG00000005397
chr13	13330724	13331160	Lyst	ENSMUSG00000019726
chr13	20191008	20191336	Elmo1	ENSMUSG00000041112
chr13	37516876	37517328	Ly86	ENSMUSG00000021423

chr13	37516876	37517328	Rreb1	ENSMUSG00000039087
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chr13	43202756	43203139	Tbc1d7	ENSMUSG00000021368
chr13	43202756	43203139	Gfod1	ENSMUSG00000051335
chr13	43204082	43204573	Tbc1d7	ENSMUSG00000021368
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chr13	44512695	44513098	Cd83	ENSMUSG00000015396
chr13	44512695	44513098	Jarid2	ENSMUSG00000038518
chr13	51750439	51750814	Sema4d	ENSMUSG00000021451
chr13	102803338	102803574	Pik3r1	ENSMUSG00000041417
chr13	109436497	109436889	Depdc1b	ENSMUSG00000021697
chr13	109768163	109768503	Depdc1b	ENSMUSG00000021697
chr13	109768163	109768503	Pde4d	ENSMUSG00000021699
chr13	111028537	111028843	Pde4d	ENSMUSG00000021699
chr14	53660017	53660430	1700123O20Rik	ENSMUSG00000040822
chr14	53660017	53660430	Cebpe	ENSMUSG00000052435
chr14	53731953	53732487	Slc7a8	ENSMUSG00000022180
chr14	71857566	71857904	Cysltr2	ENSMUSG00000033470
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chr14	75303440	75303730	9030625A04Rik	ENSMUSG00000044350
chr15	10712221	10712650	Rai14	ENSMUSG00000022246
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chr15	27441658	27441978	Ank	ENSMUSG00000022265
chr15	37147625	37148016	Zfp706	ENSMUSG00000062397
chr15	37147625	37148016	Grhl2	ENSMUSG00000022286
chr15	63477954	63478273	Pvt1	ENSMUSG00000072566
chr15	63477954	63478273	Gsdmc1	ENSMUSG00000079025
chr15	66980833	66981169	St3gal1	ENSMUSG00000013846
chr15	66980833	66981169	Zfat1	ENSMUSG00000022335
chr15	78398932	78399253	Rac2	ENSMUSG00000033220
chr15	94306940	94307228	Adamts20	ENSMUSG00000022449
chr15	94306940	94307228	Pus7l	ENSMUSG00000033356
chr15	103086426	103086762	Nfe2	ENSMUSG00000058794
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chr15	103167377	103167715	Zfp385	ENSMUSG00000000552
chr16	10590336	10590662	Clec16a	ENSMUSG00000068663
chr16	91255546	91255826	Olig1	ENSMUSG00000046160
chr16	91255546	91255826	ifnar2	ENSMUSG00000022971
chr16	92690471	92690780	Runx1	ENSMUSG00000022952
chr16	93018031	93018356	Runx1	ENSMUSG00000022952
chr16	93018031	93018356	Setd4	ENSMUSG00000022948
chr16	93036086	93036405	Runx1	ENSMUSG00000022952
chr16	93036086	93036405	Setd4	ENSMUSG00000022948
chr16	95547971	95548359	Erg	ENSMUSG00000040732
chr16	95966120	95966569	Ets2	ENSMUSG00000022895
chr16	95966120	95966569	Psmg1	ENSMUSG00000022913
chr17	6129463	6129806	Tulp4	ENSMUSG00000034377
chr17	23459192	23459428	Pkmyt1	ENSMUSG00000023908

chr17	25733277	25733729	Rab11fip3	ENSMUSG00000037098
chr17	29586834	29587234	Mdga1	ENSMUSG00000043557
chr17	30952693	30953216	Ubash3a	ENSMUSG00000042345
chr17	33320032	33320359	March2	ENSMUSG00000059208
chr17	40270218	40270498	Crisp2	ENSMUSG00000023930
chr17	40270218	40270498	Rhag	ENSMUSG00000023926
chr17	44117547	44117986	Runx2	ENSMUSG00000039153
chr17	44135340	44135667	Runx2	ENSMUSG00000039153
chr17	47058626	47058939	Ccnd3	ENSMUSG00000034165
chr17	56447267	56447705	Nrtn	ENSMUSG00000039481
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chr17	56975570	56975890	Vav1	ENSMUSG00000034116
chr17	70393764	70394116	Dlgap1	ENSMUSG00000003279
chr17	83870345	83870853	Haa0	ENSMUSG00000000673
chr17	83870345	83870853	Zfp36l2	ENSMUSG00000045817
chr17	83898536	83899216	Haa0	ENSMUSG00000000673
chr17	83898536	83899216	Zfp36l2	ENSMUSG00000045817
chr17	84024743	84025193	Haa0	ENSMUSG00000000673
chr17	84024743	84025193	Zfp36l2	ENSMUSG00000045817
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chr17	84069656	84069945	Zfp36l2	ENSMUSG00000045817
chr17	84684884	84685280	Lrrprc	ENSMUSG00000024120
chr17	85782513	85782830	Six2	ENSMUSG00000024134
chr17	85782513	85782830	Srbd1	ENSMUSG00000024135
chr17	87882877	87883249	Msh6	ENSMUSG00000005370
chr18	35975373	35975751	Cxxc5	ENSMUSG00000046668
chr18	38051826	38052170	Diap1	ENSMUSG00000024456
chr18	50153492	50154147	Tnfaip8	ENSMUSG00000062210
chr18	55027902	55028212	Zfp608	ENSMUSG00000052713
chr18	55232377	55232772	Zfp608	ENSMUSG00000052713
chr18	55232377	55232772	Gramd3	ENSMUSG00000001700
chr18	61884284	61884629	Afap1l1	ENSMUSG00000033032
chr18	68355593	68355909	D18Ert653e	ENSMUSG00000024544
chr18	75786036	75786374	Gm672	ENSMUSG00000052928
chr19	10131228	10131580	Fads2	ENSMUSG00000024665
chr19	34910807	34911124	Pank1	ENSMUSG00000033610
chr19	37500737	37501129	Hhex	ENSMUSG00000024986
chr19	40866735	40867049	Entpd1	ENSMUSG00000048120
chr19	40866735	40867049	Ccnj	ENSMUSG00000025010
chr19	46508200	46508662	Sufu	ENSMUSG00000025231
chr19	46941502	46941835	Nt5c2	ENSMUSG00000025041

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**Supplementary Table 4: Primer Sequences Used for Quantitative Real Time PCR and Cloning.** Primers were designed using Primer3.

**Real-time PCR**

Primer name	Sequence 5'-3'
Cbfa2t3h_F:	GCCGCTCGCTTTATAATCAG
Cbfa2t3h_R:	GACCCACAGACTTGCCCTTCT
CEBPe_F:	GTGTCATGGTCACCCTAGCC
CEBPe_R:	CGAGCTTATCTCCCAAGTGC
c-Myb_F:	ATGTGACTACTGCCCTTTTC
c-Myb_R:	GTGACAGAGACCCTTGATAA
Gfi1b_F:	GCTATTTCTGCCAAGGGTGA
Gfi1b_R:	GGGGTCTGAGGACCATGATA
Klf2_F:	TCCTTGGCCTGATATTTTGG
Klf2_R:	GCTTCTGAGGGATGTGAAAA
Mafk_F:	CTGCTGTGGTCTAACTGCC
Mafk_R:	ATACAGGGAGCCACAGAGC
Nfe2_F:	TCACACCAGTAGGCAATCCA
Nfe2_R:	GTGGCTAGAGGTGGAACCAG
Tox2_F:	CTGTCTCTCCAACCACAGCA
Tox2_R:	CAGAGGGATGATAGGGCAAAA
Zfp1_F:	AGATAGATGTGCCGTGCTGA
Zfp1_R:	CCCTCTCCCACGTTTGAAGT
Runx2_F:	TGCCTCCTCCCCAACTCT
Runx2_R:	CATCTTCAACCTCCAAAACC
Runx1_+23kb_F:	AAGCTGCCCACGTTATCAGT
Runx1_+23kb_R:	CAGATGGAGGCATCCTGTTT
Runx1_+31kb_F:	GCCACAGAGAGGATGTGGAC
Runx1_+31kb_R:	AGCACCTGCCAAGAGACATC

**Cloning**

Cbfa2t3h_F:	TTGGGATCCAGTCGAGCTATTGATGGTTGC
Cbfa2t3h_R:	CCGCAGCTGGGCAGCACAGACTGTCAGAA
CEBPe_F:	GGGGGATCCCCGCCAACACCTAGTGTCAT
CEBPe_R:	GTGCAGCTGGCCTTTATCTCCGAGTGCAG
c-Myb_F:	GCCGGATCCGCACACAGTCCTGCAGCTT
c-Myb_R:	ATTCAGCTGTCATACACCCACCATGTTGAT
Erg_F:	AATGGATCCAACGGTTGGACAGAACTTGC
Erg_R:	TCGCAGCTGGCAACAGGGCTGAAATGTG
Gfi1b_F:	AATGGATCCCTTAGGAACAACACCAGTTTGG
Gfi1b_R:	AGACAGCTGGGCTTTCCAGGACTCTGTA

Klf2\_F: GCAGGATCCACGGGACTCCGAATACAGTG  
Klf2\_R: TGGGTCGACGCTTCTGAGGGATGTGGAAA  
Mafk\_F: TCTGGATCCTCCAGTAGATCCTAACCCAGTGA  
Mafk\_R: AGTGTCGACAGGGATGCAGGGTGTGTG  
Nfe2\_F: TTTGGATCCTCCACATGTAAACTGGAACACA  
Nfe2\_R: GTGCAGCTGACCAGCAGCATCAGGTCAA  
Tox2\_F: CGGGGATCCGTCCCTAACAGGGGCAA  
Tox2\_R: GCACAGCTGCAGAGGGATGATAGGGCAA  
Zfp1\_F: CAGGGATCCGAGGGGAAGCAGGCTGAG  
Zfp1\_R: GGGCAGCTGCCCTTCGCAGGTGACAAAC  
Runx2\_F: TCAGGATCCGCCTTTTCTAATGTCTCTTGCAG  
Runx2\_R: CAGGTCGACGATCAAAATTCCATCCCACAG

**Supplementary Table 5: Summary of F0 transgenic embryo analysis.** Shown is the total number of transgenic embryos generated for each construct together with the staining patterns observed. FL = fetal liver. Absence of fetal liver expression was confirmed in three SV-LacZ control embryos using histological sections.

<b>Construct</b>	<b>number of transgenics</b>	<b>number of stained embryos</b>	<b>FL</b>	<b>neuronal</b>
Cbfa2t3h -22kb	8	6	3	5
Cebpe +6kb	2	1	1	1
c-myb -68kb	7	2	0	2
Erg +85kb	4	2	2	1
Gfi1b +16kb	6	3	3	0
Klf2 -51kb	3	3	2	0
Mafk -22kb	10	5	2	1
Nfe2 -7.8kb	6	4	4	2
Runx2 +160kb	4	1	1	0
Tox2 +4kb	5	3	2	1
Zfp1 +2.7kb	4	4	2	4
SvLacZ control	21	2	0	1

**Supplementary Table 6: Presence of GATA Binding Motifs and Binding Events within the Nuclear Targets of Scl.** All peaks are listed by chromosome number, start and end position in the mouse genome (build mm8). The table lists the number of identified GATA motifs in all Scl bound regions localised to loci containing genes with “transcriptional regulation” annotation. Rows highlighted in grey indicate loci that contain at least one peak shown to have a Gata2 binding event with a false discovery rate (FDR) of less than 0.0009 (rounded down to 0); other FDRs are listed in the table.

Gene	Chr	Start	End	Gata sites	FDR
<b>rxra</b>	chr2	27525358	27525676	2	0
<b>Gfi1b</b>	chr2	28419979	28420490	3	0
<b>gtf3c5</b>	chr2	28419979	28420490	3	0
	chr2	28421256	28421632	2	0
<b>zeb2</b>	chr2	46192993	46193358	1	0.0641
<b>maml3</b>	chr3	51832385	51832686	1	0
<b>scl</b>	chr4	114593681	114593997	2	0
<b>e2f2</b>	chr4	135449817	135450435	1	0
<b>Rere</b>	chr4	149305247	149305556	2	>0.0641
<b>mafk</b>	chr5	140029468	140029853	No GATA	No peak
<b>gata2</b>	chr6	88082347	88082834	2	0
<b>cebpa</b>	chr7	34865266	34865690	2	0
<b>klf2</b>	chr8	75197298	75197656	4	0
<b>lyl1</b>	chr8	87590032	87590384	1	>0.0641
	chr8	87591588	87591922	2	0
<b>nfix</b>	chr8	87620765	87621220	3	0
<b>ctcf</b>	chr8	108512305	108512718	2	>0.0641
<b>zfp1</b>	chr8	125170759	125171143	4	0
	chr8	125195419	125195796	6	0
	chr8	125207681	125208311	4	0.0009
<b>cbfa2t3</b>	chr8	125585165	125585505	2	0.008
	chr8	125586701	125587190	2	0
	chr8	125606517	125606821	4	<0.0641
<b>maml2</b>	chr9	13368466	13369107	2	0.0641
<b>ets1</b>	chr9	32305818	32306221	3	0
<b>fli-1</b>	chr9	32305818	32306221	3	0
<b>tle3</b>	chr9	61464157	61464509	3	0.0001
<b>myb</b>	chr10	20917952	20918325	3	0
<b>hmg2</b>	chr10	120089189	120089593	1	0.0001
<b>mycn</b>	chr12	12522508	12522848	3	0.0009
<b>rreb1</b>	chr13	37516876	37517328	3	0
<b>jarid2</b>	chr13	44512695	44513098	4	0.008
<b>cebpe</b>	chr14	53660017	53660430	4	0
<b>rai14</b>	chr15	10712221	10712650	3	0.0641
<b>zfp706</b>	chr15	37147625	37148016	1	0
<b>grhl2</b>	chr15	37147625	37148016	1	0
<b>zfat</b>	chr15	66980833	66981169	4	0
<b>Nfe2</b>	chr15	103086426	103086762	3	0
<b>zfp385</b>	chr15	103167377	103167715	2	0.2835
<b>runx1</b>	chr16	92690471	92690780	1	0
	chr16	93018031	93018356	3	0.0641
	chr16	93036086	93036405	5	0.0009
<b>erg</b>	chr16	95547971	95548359	2	0
<b>ets2</b>	chr16	95966120	95966569	2	0
<b>runx2</b>	chr17	44117547	44117986	1	0
	chr17	44135340	44135667	1	0
<b>Zfp3612</b>	chr17	83870345	83870853	3	0
	chr17	83898536	83899216	4	<0.0641
	chr17	84024743	84025193	1	0
	chr17	84069656	84069945	1	No peak
<b>hhex</b>	chr19	37500737	37501129	4	0
<b>sufu</b>	chr19	46508200	46508662	2	0