Supplemental Table 1A Details of DHS and ChIP measurements at endogenous GREs.

Internal Locus ID #	Gene Name description	Unique Internal locus description	DHS peak seq tag count - dex	DHS peak seq tag count + dex	DHS ratio DHS ratio +dex/-dex	GR ChIP + dex	GR ChIP + dex + E2	GR ChIP Ratio +dex+E2/+dex	ERpBox ChIP + E2	ERpBox ChIP + dex + E2	ERpBox ChIP Ratio +dex+E2/+E2
Preprogrammed sites											
1	Slc5a5	chr8_73809380	462	475	1.03	0.0001243	0.00023276	1.872566193	0.00093363	0.00069478	0.74
2	ND	chr7_112937750	34	37	1.09	0.0019598	0.00167482	0.854591125	0.00129272	0.00128267	0.99
3	Spp2/Glrp1	chr1_90306468	107	119	1.11	0.00152132	0.0014933	0.98158272	0.00372546	0.00272714	0.73
4	Tbl1xr1	chr3_22143881	114	155	1.36	0.00138335	0.000967	0.699023533	0.00076966	0.00112488	1.46
5	ND	chr6_28982040	41	66	1.61	0.00345054	0.00292163	0.846717549	0.00169957	0.00202999	1.19
***de novo* sites**											
6	Sys1/Sdc4	chr2_164146892	45	494	10.98	0.00959871	0.00992899	1.034408297	0.00789394	0.00941958	1.19
7	Tns1 Intron 4	chr1_73948020	2	42	21.00	0.00454624	0.0035061	0.771210164	0.00026992	0.00210237	7.79
8	Slc44a3 50kb Pr	chr3_121597000	9	224	24.89	0.00646772	0.00515919	0.797682902	0.0013308	0.00255533	1.92
9	Tsku	chr7_98267828	12	347	28.92	0.01080488	0.01104406	1.022136347	0.00491957	0.00935684	1.90
10	Rlbp1l1	chr4_9187915	1	43	43.00	0.00186196	0.0014597	0.783958934	0.00049665	0.00150721	3.03
11	Lcn2	chr2_32210200	1	55	55.00	0.00273052	0.00178083	0.6521947	0.00062448	0.00204808	3.28
12	Ggta1 Intron 1	chr2_35262340	1	57	57.00	0.00284432	0.00295558	1.039116842	0.00165691	0.00419515	2.53
13	Cugbp2 alt pr1 Intr	chr2_7160037	1	73	73.00	0.00102724	0.00125195	1.218755595	0.00036985	0.00075955	2.05
14	Rpl29	chr9_106271900	1	92	92.00	0.00225594	0.00197216	0.874207234	0.00132128	0.00162055	1.23
15	Slc25a33	chr4_148657510	2	199	99.50	0.00920885	0.00780574	0.847634561	0.00399993	0.00726651	1.82

Primers for qPCR analysis of ChIP experiments

internal locus ID num	unique internal locus description	primer sequence	primer direction	ChIP amplicon genomic coordinates (Mouse Feb 2006 Build)
1	chr8_73809380	CCCACCTGGCTTGGGATTGTCAGTA	For	chr8:73809333+73809520
		TCCCGAGGTGCCCAACTTGA	Rev	
2	chr7_112937750	GCTTTCTCCCCGTCTCCAGGCTGACATGTA	For	chr7:112937902+112938059
		CCCAAACCCGTCATTTTAGGAAAGCTGTTG	Rev	
3	chr1_90306468	TTGCAGAATGTCAAGCAACATCTTCAGG	For	chr1:90306579+90306741
		GGAGCCCCAGTTAATGACTGACTTG	Rev	
4	chr3_22143881	ATGCCCTCCTTAAATCAGTTCTCTGTG	For	chr3:22143981+22144156
		TGAAATGCAGTCATGAATACTGGGG	Rev	
5	chr6_28982040	CGAATTCTGATACCTGACACTAGGCCCACA	For	chr6:28982390+28982530
		TGTTTCAACTACCCTGTGCCAAAGAATCGA	Rev	
6	chr2_164146892	TGTCCTTATATGCTTGTAGTTAGGCCCC	For	chr2:164147064+164147193
		TCAAACTTTGGGTCAGAGGCAGAAG	Rev	
7	chr1_73948020	CCTGCCTCATGGTCCCTAAACCCT	For	chr1:73947956+73948057
		GGTCATCTGTGCTAAGCTGCTGCC	Rev	
8	chr3_121597000	ATCCCCCAACCCAGCCGTGATGTCTA	For	chr3:121597010+121597136
		GCTCAGAGCCATAGGCTTAGAGCCAAC	Rev	
9	chr7_98267828	TTCAACCCTCACTTCAAAGAAATGGATG	For	chr7:98267760+98267908
		CATTGATTTGAGACATGGACAGGTTCC	Rev	
10	chr4_9187915	TCCTGTAAAGGGACTTACTCATTGTATGTTTATG	For	chr4:9187989+9188104
		CATAATCCATAACTGTCTGTTCCCAAGAACA	Rev	
11	chr2_32210200 Lc	TCACCCTGTGCCAGGACCAA	For	chr2:32210236-32210338
		TGGGGAAGGGTGAGCAAGCT	Rev	
12	chr2_35262340	AACCCATAAAGTACTTAGGGAACAGCAGCT	For	chr2:35262280+35262404
		CAACACTGCAGGCTCTCCTGTAGATGTAG	Rev	
13	chr2_7160037	TAACTGTTACTACCATTGAAGGAATGATAAGAGGG	For	chr2:7160050+7160248
		CAAACAAACTCCTGTGCTTCAATATTTCCAT	Rev	
14	chr9_106271900	CGTCTTGCCTTTGAAGACATTGGACTAA	For	chr9:106271825+106271941
		TTACCAGGCCCAGCTCATGTTACAGT	Rev	
15	chr4_148657510	GAGTCTGACTCATTGTTTTGGTTTTCCC	For	chr4:148657472+148657557
		CCCCCACCCAGCAAACAAGATTT	Rev	

Supplemental Table 1B Additional examples: Assisted loading of ERpBox at endogenous GREs

Site #	Chromosome	DHS Site Start Position	DHS Site Stop Position	DHS peak seq tag count - dex	DHS peak seq tag count + dex	DHS ratio +dex/-dex	ERpBox ChIP Ratio +dex+E2/+E2
1	chr1	40378480	40378630	1	151	151.0	11.4
2	chr1	162016140	162016290	3	108	36.0	3.6
3	chr1	165400640	165400790	4	245	61.3	2.1
4	chr1	194433820	194433970	5	173	34.6	9.1
5	chr2	148804460	148804610	5	135	27.0	12.5
6	chr2	167448760	167448910	9	257	28.6	6.7
7	chr6	13011760	13011910	5	226	45.2	3.3
8	chr6	38765040	38765190	5	100	20.0	6.3
9	chr6	99141020	99141170	2	92	46.0	5.6
10	chr7	114368900	114369050	1	66	66.0	3.9
11	chr7	122838140	122838290	2	92	46.0	3.2
12	chr7	128581280	128581430	4	99	24.8	3.3
13	chr8	8401900	8402050	1	50	50.0	2.4
14	chr8	123215100	123215250	2	134	67.0	6.0
15	chr10	21694340	21694490	0	138	Inf	11.9
16	chr10	95203500	95203650	3	147	49.0	7.2
17	chr11	50497260	50497410	2	117	58.5	3.9
18	chr11	120818440	120818590	3	127	42.3	8.4
19	chr13	20235980	20236130	1	77	77.0	2.5
20	chr13	42585420	42585570	2	118	59.0	2.1
21	chr13	79161940	79162090	1	50	50.0	3.3
22	chr14	7103580	7103730	4	96	24.0	8.7
23	chr15	37128860	37129010	1	50	50.0	3.6
24	chr17	26240280	26240430	6	185	30.8	9.3
25	chr18	66372000	66372150	1	133	133.0	7.5
26	chrX	135859840	135859990	3	132	44.0	8.7

Supplemental Table 1B Primers for qPCR analysis of ChIP experiments

Internal Locus ID #	Unique internal locus description	Primer sequence	Primer direction	ChIP amplicon genomic coordinates Mouse Feb 2006 Build
1	chr1_40378446	GTCACCTCCCTTTCCAGTGAACCAT	For	chr1:40378446+40378568
		GCGAAAGTTGCCAAATACAGAACAG	Rev	
2	chr1_162016160	CCTTCACTCTGCAACCACACAAAA	For	chr1:162016160+162016259
		TGGAGGGTTTGATTCTGACTCAGTG	Rev	
3	chr1_165400589	GAAAAAATGTCCCTGGATTCCTTCA	For	chr1:165400589+165400731
		ATATCTGTGGTTGCCTTGTCAGGAC	Rev	
4	chr1_194433844	AGTCTCCCAGGCACACAATGTTCT	For	chr1:194433844+194433944
		CCACAGCAGCACAAAAGGTGTTATT	Rev	
5	chr2_148804463	ATGTTTACAGTGTGTCCCTTCTGCC	For	chr2:148804463+148804547
		AATATGCACAGTTGCTCCCATTGTT	Rev	
6	chr2_167448768	CCCCAGGGTTGGTGCGTTCTAT	For	chr2:167448768+167448874
		CCCAGATAGGGTGACAGCCACA	Rev	
7	chr6_13011895	TGTTTTCTTTCTTCCCCTTCTACCC	For	chr6:13011895+13012032
		GGAAGCTCAGGATACAGGAAACCAG	Rev	
8	chr6_38765085	TTACTCATGGTATGCTCTCAAGCCC	For	chr6:38765085+38765191
		GGTACTCTGGGTGTGTAAGCAACGT	Rev	
9	chr6_99141032	CTTGCTCAACTAAGGGATGATGCA	For	chr6:99141032+99141146
		TTGTCATGCTGACCACATCCATG	Rev	
10	chr7_114369031	GACCATTTGTCATGGCTATTGCTGA	For	chr7:114368852-114369221
		GGTGCCCAAGGATACAACTAAGACC	Rev	
11	chr7_122838106	CTTGTCTTTGTCAGAGGTGGGAAGA	For	chr7:122838106+122838251
		GCAATGAGTTCAATTTCCTGGTGTC	Rev	
12	chr7_128581278	AAGTCAGGTGTCTTTGGCAAGGC	For	chr7:128581278+128581459
		CAAACCAGTTAGGTTCAAAGGGCAT	Rev	
13	chr8_8402017	TATAGAACACAAGCAAGCTGCTGGC	For	chr8:8402017+8402101
		AGCCACTCAGCACAATGCAGTG	Rev	
14	chr8_123215110	AATGACAATACCAGGACACAGTGGC	For	chr8:123215110+123215258
		CAGTTGCCAGGTCGCACATTG	Rev	
15	chr10_21694338	TCCTTTCTTCTGTGTCCTCTGTCCG	For	chr10:21694338+21694456
		GCCTGTCTGCATTTATGCCTTCTAC	Rev	
16	chr10_95203537	GCAGGAGGGAAAGGCATGACTT	For	chr10:95203537+95203682
		CCCAAAATGAGACTGCCAGGAA	Rev	
17	chr11_50497316	CCTCCCTGCATCTTTCAACACTGTC	For	chr11:50497316+50497438
		ATCTGGGCCTAGCTGGAGACACT	Rev	
18	chr11_120818481	GGACCAGCGAACCCTTGCTT	For	chr11:120818481+120818575
		TGGTCTGGGTTGGCACAGTCCT	Rev	
19	chr13_20235879	AGCACTGTAGAGCACAGAACAGGCA	For	chr13:20235879-20236248
		CCCAGTGTGTCCCGAGTCACTATT	Rev	
20	chr13_42585368	AAAGGGGCGAGGAGTGGAATT	For	chr13:42585368+42585527
		TTCTTTCTTGGATGAGAACAGGCTG	Rev	
21	chr13_79161815	TCATAAACAAACAGGCTGCAATGTG	For	chr13:79161815+79161937
		TGGACTTGGCAAGGAATGTGGTT	Rev	
22	chr14:7103601	ACCGTTATTTCACTTGGTGAGTGGC	For	chr14:7103601+7103710
		TGCCTCATCAGTCTGACAGAACATG	Rev	
23	chr15_37128871	GTCATTTCAGGGAGTTGGTCTGTTC	For	chr15:37128871+37128984
		CAGTCAACCCACAGGTTCAAGGTA	Rev	
24	chr17_26240311	GCAACTTGTCCAAAGTCACACTGTG	For	chr17:26240311+26240415
		GGAGCACTGACCCCTAAAGATAAGC	Rev	
25	chr18_66371979	ACTGAGCCAAGTTCAACACCTCTCA	For	chr18:66371979+66372135
		CCGTGTTCTACTGGTGTAGGACTGG	Rev	
26	chrX_135859793	ACCTTCCTAGTCTGATTCCCACAGG	For	chrX:135859793+135859906
		GCAAACATTCTGAGTTGGGTGAATC	Rev	