

Supporting Information

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SI Materials and Methods

Table S1. Glucocorticoid responsive genes identified in C3H10T1/2 cells.

Glucocorticoid responsive genes identified in C3H10T1/2 cells. The genes found to be responsive to 1 μ M dex (1 μ M) in the microarray experiments are listed. Note: only the genes that were validated by qPCR as being dex responsive (at least 1.5-fold change compared to ethanol treated samples averaged over at least two independent experiments) after 1.5–2 hrs of treatment are shown. The relative fold dex-stimulated induction/repression are displayed. Of the genes found to be unresponsive to dex in the microarray experiments, 40 were randomly chosen for this study and listed in the table. Dex responsiveness of nine of these genes were examined by qPCR, and all nine were found to be unresponsive to dex after 1.5–2 hrs of treatment (less than 1.5-fold change compared to ethanol treated samples averaged over at least two independent experiments). The corresponding primers used for qPCR analysis of the respective genes are shown.

See Table on next page.

Dex-induced genes

GenBank accession no.	Gene	Fold induction, Dex/EtOH	Forward primer	Reverse primer
NM_011361.1	Sgk	4.9	cgctcgaacgggacaacat	gtccaccgtccgggtacac
NM_008630	Mt2	5.8	gcctgcgaatgcaacaat	actgtcggaaagcctctttg
NM_013602	Mt1	6.6	ctccgtagctccagcttcac	aggagcagcagctctcttg
NM_009516	Wee1	2.0	agtcgtatgtgctgtggtg	tctgtcactcctcgggaaag
NM_010559	IL6ra	3.1	gatgtttacgcgagtgaca	ttcgctgaagtcctgagat
NM_007679	Cebpd	7.6	ttcagcgctacattgactc	tgtggtgtgcttgaagagg
NM_019740	Foxo3a	2.3	ttcccatataccgccaaagag	tggatagtctgcatgggtga
NM_023324	Peli1	2.5	ttggtccctatgtccctctg	tgggactctgggaccagtaag
NM_199299	Phf15	2.9	actggaagttgaagcggaga	aaaagcttcaggcgctgata
NM_001024955	Pik3r1	2.0	gagcaaaagccaaggaaactg	gtgctggtggatccatttc
NM_010286	Tsc22d3	6.4	tggggcctagtaacaccaag	gagcacactggcatcacatc
NM_020507	Tob2	3.1	ttctcagcttagcaccact	aaggcaacaccaactgttc
NM_013642	Dusp1	11.9	cagctgctgcagtttgatgc	gggatggaacagggaaggt
NM_010638	Bteb1	2.4	gcagtgagctccacatttca	cgctagtgatggctgtgta
NM_010220	Fkbp5	10.6	aggccgtgattcagtcagg	gaacgactctgaggctttgg
NM_008587	Mertk	4.6	caaatgtatgcgcgtattgg	tgcaaacctgacttgacagc
NM_207205	Igfbp3	1.8	tcccagtggtgagctgtctg	tgatgtgggagctctctgtg
NM_010516	Cyr61	6.2	acgaggactgcagcaaaact	ggggtctgcttctgactgag
NM_022305	B4 galt1	1.5	ccaaatcacagtggacatcg	ccagtcactggcagagaca
NM_009743	Bcl2l1	1.7	ttcgggatggagtaaaactgg	tgcaatccgactaccaata
NM_130895	Adarb1	3.0	gataccgtgcagttccacct	gtagctgtcccttgccttg
NM_175638	Prkwnk4	2.3	tgccccatcttctcatcac	acctgagaagcactggagga
NM_198092	Usp2	6.3	gctgtttgaaaggcagcacaca	actctgggaaagggacagg
NM_009026	Rasd1	2.7	tggctatttgcggtatacaaa	gggtcaagctgctgttcttc
NM_011521	Sdc4	1.5	ctgatcctgctgctggtgta	ggaggaagcttcatgctgag
NM_001033453	Gm1024	5.3	agcagttgggtgggtacaagg	ctacgatggcgaatgaga
NM_011567	Tea4	3.9	caacttggaactccacgat	gaaagccgagaactccaact
NM_009228	Snta1	2.9	agctggagctcttctgggtca	gatgaaggaggggagagagg
NM_009061	Rgs2	13.6	acgaaaacccaagtttcct	cctgcatttagtgcaagcaa
NM_025367	Sphk1	2.9	tggggctatgacttggaaag	ccagggaaggtccctaagag
NM_173733	Suox	2.7	gaggaacacgtgtccagga	attggggctacagtgtctgg
NM_008638	Mthfd2	4.7	aggtcccaagcctttgagtt	gtaagggagtgccgttgaaa
NM_010070	Dok1	2.4	ttttctgccttgagatgct	tctcagcttccaccctcagt
NM_011817	Gadd45 g	8.2	tgcttggagaagctcagtt	tcaccaagtcgatcagacca
NM_013867	Bcar3	2.2	gatgccatgggagactctta	atggctgtctgcgtgtagtg
NM_008131	GluL	7.9	tagcaacctttgacccaag	actggtgccttctgtcagtg
NM_009504	Vdr	2.6	agattgcgcgcatcaccaagg	atctctcgcttacgcgtcac
NM_175445	Rassf2	1.8	cccacaatgtgtatgcttgc	gctgctgggaatttaaccaa
NM_013870	Smtn	2.0	tcaagcagatgtgtctggac	tcaaaagcctcagggaagaa
NM_144925	Tnrc6a	1.8	ttgaatcatgcaggccaata	ggaaagaaggaatccaagg
NM_013703	Vldlr	3.0	tcgggctttgttactggtc	agtagaggcggttttgaca
NM_010834	Mstn	>100	ctgtaaccttccaggacca	cgagtcagcccaaggtctc
NM_023377	Stard5	2.3	aagttccctctatgcccacct	aagaccacacagggacaaag
NM_033602	Peli2	1.5	ccagacggtagtgggtggagt	gtgatctgggcatcttcggt
NM_183187	Bc055107	9.9	gacgcacccaagagtggat	ggccaaggaaattctgtgtg
NM_173440	Nrip1	4.3	tgaggcagacgatactgacg	cctcgcaacttcttagcac
NM_009769	Klf5	3.6	cacgtacaccatgcgaagtc	ctcgacatctcagcttgctc
NM_144808	Slc39a14	2.5	cagaggcttttggcttcaac	gggtgctgcttttctgcttc
NM_008046	Fst	2.0	ctctcaagtggatgatttc	cattcgttgcggtaggtttt
NM_009627	Adm	8.8	ttcgcagttccgaaagaagt	tgtcgtctcatcagcgagtc
NM_181444	Rai3	2.0	gagtttgcagacgtcccaag	ggctctgttctccacacct
NM_009667	Ampd3	4.1	ctcccaatttgggtgcaact	gtggacagtcagggaacagg
NM_010295	Gclc	8.5	aacacagaccacccagag	tggcacattgatgacaacct
NM_009883	Cebpb	9.1	tggacaagctgagcgacgag	tgtgtcgtctccagggttg
NM_024406	Fabp4	4.1	tcacttggaaagacagctct	aagccactccactcttctt
NM_175175	Plekha2	4.7	ggcttggctcgtctttttg	ccaagttccatcagcattt
NM_020257	Clec2i	1.8	tgggtccacagtgctatcaa	acaccatgtggttgctcaga
NM_008871	serpine1	3.9	gtcttccgcaccaagagcag	gacaaaggctgtggagggaag
NM_011756	Zfp36	2.8	ccctctgcaactctggtctc	gaccaccggacactgaacct
NM_025404	Arfl4	9.7	tgctacctgcccgttttaagg	taggggacctttcagtcagg
NM_177710	Shh2	3.3	gcagccttttctcacttg	tgtgaagagggtctggagagt
NM_133919	Mlt2 h	2.9	agttggacaggaatcgtttg	caataagcagcgagaaacag
NM_007796	Ctla2a	2.5	agggctcagccagagtaaca	gagcctctcagcatcattc
NM_026232	Slc25a30	2.4	ggaagccctttgtgtatgga	ctcggaagttggcatcattt
NM_010276	Gem	4.5	cctgctacgtggatgtctca	aggactcgaaatcacatgg
AK150917	Ctla2b	2.7	caaatgtgctggaagctca	gcccttcagggtgtcagata
NM_133232	Pfkfb3	2.2	cttgaggaaaccttgagctg	cccagaagacatgtggacct
NM_178076	Mcf2l	3.3	gcagtagaccagcatgcaaa	actaagcaagcccaagcaaa

Dex-induced genes

GenBank accession no.	Gene	Fold induction, Dex/EtOH	Forward primer	Reverse primer
NM_145076	Trim24	1.7	gcctaagcagaatcctgtcg	tgctgaatatgctggagtcg
Dex-unresponsive genes		Fold change, Dex/EtOH		
NM_028408	Cnih3	1.1	gctggccttctacctctct	catctggtgctcctctagcc
NM_029949	Snapc3	0.8	gcacacaccacagtgaatcc	acgttccatcccgactacag
NM_172760	Elmo3	0.8	cgagagtccgcaagttagg	ttggtgcatgtctggagaag
NM_013663	Sfrs3	0.8	agatttgcaagggttcct	tgaaggacactggcatctg
NM_009004	Kif20a	0.7	cctgaagccctattgtcca	gtggacagctcctctcttg
NM_010158	Khdrbs3	1.4	attatgggcatggactcagc	gtctctgtagacgcccttcg
NM_023743	Eif4enif1	0.8	ccaaatggtttggctcagat	tgtcaccacaggtccaggta
NM_133987	Slc6a8	0.9	gttggagggaatccccatttt	aatcaccatggaggcatagc
NM_172665	Pdk1	0.8	ggtcagtgggataagcgaaa	gcttctggtcggagttcttg
NM_028047	1500002O20Rik			
NM_175506	Adams19			
NM_178713	Aldh8a1			
NM_009842	Cd151			
NM_007684	Cetn3			
NM_199068	Foxk1			
NM_010815	Grap2			
NM_008181	Gsta1			
NM_027927	Ints12			
NM_012057	Irf5			
NM_008477	Ktn1			
NM_177178	Lmbrd2			
NM_146365	Olfr1094			
NM_146416	Olfr290			
NM_146295	Olfr446			
NM_001011822	Olfr787			
NM_008768	Orm1			
NM_008771	P2rx1			
AF123502	Pole			
NM_008905	Ppfibp2			
NM_019651	Ptpn9			
NM_021888	Qtrt1			
NM_013649	Ryk			
NM_172537	Sema6d			
NM_021793	Tmem8			
XM_283286	Troap			
NM_028006	Tube1			
NM_054093	Ube3b			
NM_011910	Uts2			
NM_198246	Yars2			
NM_009544	Zfp105			
Dex-repressed genes		Fold repression, Dex/EtOH		
NM_031874	Rab3d	−1.5	atcaccacggcctactatcg	cttgttccccacgaggatta
NM_007678	Cebpa	−1.7	tggaacaagaacagcaacgag	tcactgggtcaactccagcac
NM_178357	Tieg2	−1.7	atgaccagtgtgatccgtca	caaacgctcctgtccttctc
NM_008390	Irf1	−3.5	tcttgccctctgagtgagt	gggactatgcttggcatgt
NM_011824	Grem1	−1.5	gacaaggctcagcacaatga	actcaagcactcctctcca
NM_178382	Flrt3	−2.7	accctcaatcgagagcaaga	acagtgacccgttctctatgc
NM_020581	Fiaf	−2.5	aagatgcacagcatcacagg	atggatgggaattggagc
NM_009621	Adams1	−2.5	gtgtccagccccgttatgt	cgagaacagggttagaaggtaatgc
NM_009062	Rgs4	−2.2	gctgggttggtctagagctg	tctgcccctcacctaagcagt
NM_176933	Dusp4	−2.8	gcatgtgtgtgcaggagtct	accctgcgtctgatggtaac
AK020467	9430052C07Rik	−4.6	ggagcaagactgtacttttctg	gacaacagcagcacgatttca
NM_011333	Ccl2	−2.4	agcaccagccaactctcact	cgtaactgcatctggctga
AK074068	A930021H16Rik	−2.0	agaggaatgaaggtggctca	gggtgaacatgtttgccacag
NM_008764	Tnfrsf11b	−1.6	gttcctgcacagcttcacaa	aaacagccagtgaccattc
NM_013654	Ccl7	−2.4	aagtgggtcgaggaggctat	agaaagaacagcggtgagga
NM_029682	1700095N21Rik	−2.0	tctgtcgtggctgactcta	tttggcacaccacatgagt
NM_010501	Ifit3	−1.7	gtgggtgattcttggcagtt	gacacactccggtgtcct

Glucocorticoid responsive genes identified in C3H10T1/2 cells. The genes found to be responsive to 1 μ M dex (1 μ M) in the microarray experiments are listed. Note: only the genes that were validated by qPCR as being dex responsive (at least 1.5-fold change compared to ethanol treated samples averaged over at least two independent experiments) after 1.5–2 hrs of treatment are shown. The relative fold dex-stimulated induction/repression are displayed. Of the genes found to be unresponsive to dex in the microarray experiments, 40 were randomly chosen for this study and listed in the table. Dex responsiveness of nine of these genes were examined by qPCR, and all nine were found to be unresponsive to dex after 1.5–2 hrs of treatment (less than 1.5-fold change compared to ethanol treated samples averaged over at least two independent experiments). The corresponding primers used for qPCR analysis of the respective genes are shown.

Table S2. Positional weight matrix generating GBSs

GGAACAGGCCGTACT	AGAACAGAATGTCCT
GGTACAAGAAGTACA	AGAACAGGGTGTCT
GGGACAGAGAGATCA	GGAACACGGCGTCCC
AGAACAGCGCGTTTC	AGGACAGGACGTCCC
AGGACATAGTGTCT	TGCACAGAGTGTCC
GGTACAGAATGTGTG	GGAACAGCATGTGCA
GGCACAGAATGACCA	AGTACAAACTGTACC
TGAACACAATGTGTC	AGTACAGGGCGTTCC
AGGACACTTTGTTC	GGGACACAGTGTCCA
GGCACAAGGTGATTG	AGAACAGAGTGTTC
AGCACATACTGAACC	GGAACAAACAGTCCT
GGCACAGGCTGTTTC	AGAACACAGTGACTT
TGTACAGCAAGTGCA	GGCACAGGGTGTTC
GGAACATCCTGTCTG	AGCACAAAGCGAGTG
GGGACAAGGAGTTCT	AGGACAGCCTGTCCT
GGGACAAGGAGTTCT	AGAACAACATGTCTT
AGAACATGCTGTCAT	TGGACAGACAGATCA
AGGACAGGACGTGCA	AGCACAGCATGTCCT
TGAACAGAATGTACC	TGCACAGACTGTGCT
GGAACAGAAAGTATT	AGCACAGAAAGTTCC
AGAACAGGGTGTTC	TGTACACAGTGTCCC
GGTACAGTTTGTTAC	GGCACATCGTGTCCA
GGTACAAACTGAGTG	GGTACAAACAGTACC
AGAACAGCGTGACCT	GGCACAAAGGTGTTC
TGGACACAGTGTCTT	GGTACAGAATGTTC
AGGACAGAGTGTCTG	AGAACATTGGGTTC
AGCACATACTGTATC	GGCACAGCGTGTGGC
GGTACAACCTGTATC	AGAACATTTGTCCG
AGCACATCGAGTTCA	AGAACATTTGGTGCT
GGTACAGAGTGTGAG	GGGACATCTGGTTCC
AGCACACTCAGTTTG	AGAACATTCTGTGAG
TGAACAAACTGTTTT	AGGACATGCTGGTCA
AGAACAGGATGTTTA	AGGACACTGTGGACA
GGGACAAACTGTGTT	AGGACAGTGTGGACA
GGTACAGAGTGATAT	AGGACATGGAGGTCT
AGTACAGGAAGTACA	TGAACACTCTGAAAT
GGTACAGACCGTTCT	GGAACAATGTGTGAG
AGAACACAATGTTCT	GGAACATTCTGATT
GGGACAAACTGTGTT	AGCACATCCTGAGGG
GGTACAGAGTGATAT	

Positional-weight matrix generating GBSs. The GBSs displayed were extracted from known GR-binding regions as described in *Materials and Methods*. These sequences were used to generate the GBS positional-weight matrix.

GBS identifier	Mismatch, bp	Mouse Feb 2006 (mm8),	Sequence of GBSs	ChIP (Dex/EtOH)
		Chromosome coordinates		
+GBS 1	0	chr2:164147136–164147150	AGGACAGTTTGTCCC	21.1
+GBS 2	0	chr2:128400941–128400955	AGAACAGGCTGTCTT	4.4
+GBS 3	0	chr13:102819770–102819784	AGAACAAAATGTACA	19.2
+GBS 4	0	chr15:81667054–81667068	AGGACATTGTGTCCA	11.6
+GBS 5	0	chr19:23202190–23202204	AGGACAAACTGTTCC	31.1
+GBS 6	0	chr8:97060665–97060679	AGGACAGCCTGTCTT	22.4
+GBS 7	0	chr4:10959827–10959841	AGAACAACAATGTATT	20.3
+GBS 8	1	chr15:81661712–81661726	GGCACAGGATGTCCC	24.7
+GBS 9	1	chr17:28243704–28243718	GGAACAGGCAGTGCC	20.7
+GBS 10	1	chr11:20961517–20961531	GGTACAGAAAGTGCT	15.3
+GBS 11	1	chr11:101047378–101047392	AGGACAAAGTGTTCA	17.7
+GBS 12	1	chr9:43837537–43837551	AGAACAAAATGTCCC	12.3
+GBS 13	1	chr9:43830085–43830099	AGGACAAGCTGTTCC	17.7
+GBS 14	1	chr2:152511910–152511924	GGGACACTGTGTTCC	16.1
+GBS 15	1	chr17:28243222–28243236	GGTACAGTGTGTTAC	15.4
+GBS 16	1	chr1:155663844–155663858	AGAACAATATGTTCC	20.0
+GBS 17	1	chr11:51717800–51717814	AGTACACTCTGTTCT	18.3
+GBS 18	2	chr10:21694418–21694432	AGTACACTCTGTTCA	4.1
+GBS 19	2	chr10:76884709–76884723	AGAACATTCTGTCCT	21.4
+GBS 20	2	chr11:101046391–101046405	GGCACACTGTGTCCA	14.5
+GBS 21	2	chr11:59777200–59777214	GGAACAGTATGTACC	4.9
+GBS 22	2	chr6:82993665–82993679	AGTACAGGGAGTTCC	45.1
+GBS 23	2	chr4:11907250–11907264	AGGACATTCTGTACC	5.6
+GBS 24	2	chr17:28215926–28215940	GGAACAGTCAGTTCT	3
+GBS 25	2	chr10:128075663–128075677	GGCACAGTGTGTCCT	6.3
+GBS 26	2	chr14:7103641–7103655	TGGACATGGTGTTCT	12.1
+GBS 27	3	chr10:21683118–21683132	AGAACAGAATGTTCT	23.4
+GBS 28	3	chr7:109908279–109908293	AGTACATTTTGTACT	21.2
+GBS 29	3	chr8:97078693–97078707	GGAACACAATGTCTT	8.7
+GBS 30	3	chr17:28212542–28212556	GGGACAGGGTGTACA	4.5
+GBS 31	3	chr17:26262929–26262943	GGAACAGAATGTTCA	17.4
+GBS 32	3	chr4:41038353–41038367	AGAACAGTCTGTACT	3.2
+GBS 33	3	chr8:97060562–97060576	AGGACACGGTGTTTA	22.4
+GBS 34	4	chr16:15803412–15803426	GGAACAAAATGTCCA	3.5
+GBS 35	4	chr11:116350355–116350369	GGGACAAAATGTTTC	7.4
+GBS 36	4	chr2:154094475–154094489	AGTACACAGAGTTCC	6.6
+GBS 37	4	chr3:101516409–101516423	GGAACAGAACGTTCT	6.6
+GBS 38	4	chr3:101527211–101527225	AGCACAGATTGTTCC	9.2
+GBS 39	4	chr3:89998667–89998681	AGGACAGTGTGTTTT	9.7
+GBS 40	5	chr4:11899855–11899869	AGCACAGAGTGTTC	25.1
+GBS 41	5	chr8:97068124–97068138	GGGACATGATGTTCC	9.0
+GBS 42	5	chr8:97078800–97078814	AGAACAGGGTGATTG	13.2
+GBS 43	5	chr17:28241492–28241506	AGAACACAGTGTCCC	3.9
+GBS 44	5	chr8:97060824–97060838	GGTACATGGTGTTTC	22.4
+GBS 45	6	chr1:145759784–145759798	AGAACAGGGAGTACA	7.0
+GBS 46	6	chr10:128075253–128075267	AGCACAGAACGTCCC	4.8
+GBS 47	>6	chrX:135859919–135859933	AGAACACTGTGTGCT	3.5
+GBS 48	>6	chr14:69071730–69071744	AGGACAGCCTGTCCA	2.5
+GBS 49	>6	chr6:128267383–128267397	AGTACAGACTGTCCC	2.9
+GBS 50	>6	chr6:83268255–83268269	AGGACACTTGTTCT	6.8
+NBS 1	1	chr4:11889612–11889626	AGTACAAACTGTTCA	1.3
+NBS 2	1	chr15:97759398–97759412	AGCACAGCGTGTTAT	1.2
+NBS 3	1	chr10:41963309–41963323	GGGACAAAGTGAGCC	0.7
+NBS 4	2	chr1:155659337–155659351	GGAACAGGCTGTTCT	0.7
+NBS 5	2	chr4:41065960–41065974	AGCACAGGCTGTTTG	1.3
+NBS 6	2	chr8:12905870–12905884	AGAACAGAGTGTCTT	1.5
+NBS 7	2	chr3:101520657–101520671	AGAACAAACAGTTCT	1.2
+NBS 8	2	chr11:116351825–116351839	AGGACAGACTGAGCA	1.3
+NBS 9	3	chr13:51852465–51852479	AGAACAAACTGTTTA	0.

GBS identifier	Mismatch, bp	Mouse Feb 2006 (mm8), Chromosome coordinates	Sequence of GBSs	ChIP (Dex/EtOH)
+NBS 14	3	chr14:47055485–47055499	GGAACAAGCTGTACT	1.1
+NBS 15	3	chr13:51860406–51860420	AGAACAACTGAGCT	1.2
+NBS 16	3	chr15:81678080–81678094	AGAACAGGCTGTAG	0.8
+NBS 17	3	chr13:102802613–102802627	AGAACAAAATGTGTC	1.1
+NBS 18	3	chr11:116352030–116352044	GGAACAAGGTGTGTG	1.3
+NBS 19	3	chr1:53014283–53014297	TGAACAGAGTGATTT	0.7
+NBS 20	3	chr5:104094589–104094603	AGAACAGAGTGTGAT	0.9
+NBS 21	3	chr3:89995879–89995893	GGGACAGATTGTCTC	1.6
+NBS 22	4	chr7:122999632–122999646	AGGACAGAGTGACTC	0.9
+NBS 23	4	chr13:115599835–115599849	AGAACAACGTGTATC	1.1
+NBS 24	4	chr3:101503816–101503830	AGCACATGCTGTCTC	1.0
+NBS 25	4	chr1:145793113–145793127	AGGACAAAGTGTTC	1.3
+NBS 26	4	chr11:101092520–101092534	AGAACAGAGTGTTC	1.2
+NBS 27	4	chr4:11913868–11913882	GGCACAGTATGTCCT	1.7
+NBS 28	4	chr7:110583516–110583530	GGAACAGGCTGACCC	1.0
+NBS 29	4	chr6:83297769–83297783	GGCACAAGCTGTCTT	0.9
+NBS 30	4	chr3:122397212–122397226	GGCACAGGCTGGTCT	0.6
+NBS 31	5	chr11:59800223–59800237	GGTACAGACTGTGCG	1.3
+NBS 32	5	chr4:11890964–11890978	TGGACAGAATGTCTT	0.9
+NBS 33	5	chr14:69107438–69107452	GGAACAAAGTGATTT	1.0
+NBS 34	5	chr11:21000700–21000714	AGTACAACCTGTACT	1.5
+NBS 35	5	chr2:128392278–128392292	GGCACACAGTGTCCC	0.7
+NBS 36	5	chr4:41063531–41063545	AGAACAGAGTGATTG	1.0
+NBS 37	5	chr14:98170324–98170338	GGCACAGACTGAGCT	0.7
+NBS 38	5	chr8:97063821–97063835	GGCACAATGTGTCCA	1.6
+NBS 39	5	chr16:15775335–15775349	AGGACAAGCTGTATT	0.8
+NBS 40	5	chr13:51860641–51860655	GGAACAAGGTGTCCC	1.2
+NBS 41	5	chr3:10221919–10221933	AGAACAACTGTCAT	0.7
+NBS 42	6	chr2:11397863–11397877	AGAACATACCGTTCT	1.0
+NBS 43	6	chr13:115585291–115585305	GGGACAGAAAGTACT	1.1
+NBS 44	6	chr7:110414748–110414762	AGGACAGGATGTATA	0.8
+NBS 45	6	chr7:122943446–122943460	GGAACAGGCTGTGTC	0.7
+NBS 46	6	chr13:102798755–102798769	GGGACAGGCTGAACT	1.6
+NBS 47	6	chr7:83517077–83517091	GGGACAAGGTGTCTT	1.0
+NBS 48	>6	chr17:26259587–26259601	AGAACAAGCTGTGCT	1.4
+NBS 49	>6	chr11:51713295–51713309	AGAACAGGCTGACCT	0.9
+NBS 50	>6	chr10:41942528–41942542	AGGACAGACAGATCT	0.6
+NBS 51	>6	chr8:97053899–97053913	AGAACAGTCAGTGCT	0.6
+NBS 52	>6	chr2:131750046–131750060	AGAACAGCCAGTGCC	1.0
+NBS 53	>6	chr2:128373638–128373652	AGGACAGAGTGGGCT	1.2
+NBS 54	>6	chr2:152529152–152529166	AGCACATGCTGTTTT	0.9
+NBS 55	>6	chr9:43834330–43834344	AGGACAGTGTGTCTC	0.9
+NBS 56	>6	chr9:43808132–43808146	AGGACAGCCTGAGCT	0.7
+NBS 57	>6	chr11:59773054–59773068	AGCACAGGGAGTTCA	1.0
+NBS 58	>6	chr10:76885372–76885386	AGGACAGAGTGTCTC	1.7
+NBS 59	>6	chr10:76832988–76833002	GGTACATAATGTACT	1.0
+NBS 60	>6	chr10:76890077–76890091	GGGACACAGTGTTC	0.7
+NBS 61	>6	chr4:11641976–11641990	GGGACAGACAGTTTC	0.9
+NBS 62	>6	chr5:137327677–137327691	GGGACAGAGTGTAC	0.6
+NBS 63	>6	chr4:10902731–10902745	AGAACAGTCAGTGCT	1.3
+NBS 64	>6	chr7:110553382–110553396	AGTACAGAGAGTACA	0.7
+NBS 65	>6	chr7:110398200–110398214	AGAACAGTCTGTATT	0.8
+NBS 66	>6	chr13:115547863–115547877	GGGACAGTGTGTGTG	0.7
+NBS 67	>6	chr14:69096205–69096219	AGAACAGAATGTCTC	0.7
+NBS 68	>6	chr7:122994132–122994146	AGAACAGCATGTACA	0.7
+NBS 69	>6	chr10:128083130–128083144	AGAACAGTATGTACT	1.0
+NBS 70	>6	chr5:137329538–137329552	AGCACAGGCTGATCT	1.0
+NBS 71	>6	chr14:98210760–98210774	AGGACAGACTGACCC	1.1
+NBS 72	>6	chr15:97716171–97716185	AGAACACGGTGTGCA	0.8
+NBS 73	>6	chr13:51882431–51882445	GGAACAAGATGTGCC	0.7
+NBS 74	>6	chr14:74492403–74492417	GGCACAGACTGTGAC	1.3
+NBS 75	>6	chr11:77023417–77023431	AGGACAAAATGTTTT	1.0
+NBS 76	>6	chrX:135884296–135884310	AGTACAGAAAGTGCT	1.0
+NBS 77	>6	chr11:21003610–21003624	AGTACAGACTGTCTC	1.1

GBS identifier	Mismatch, bp	Mouse Feb 2006 (mm8), Chromosome coordinates	Sequence of GBSs	ChIP (Dex/EtOH)
+NBS 78	>6	chr17:26258968–26258982	GGGACAGAGAGTGTC	1.0
+NBS 79	>6	chr2:128413051–128413065	AGAACAGAGTGTTAC	0.8
+NBS 80	>6	chr7:83491672–83491686	GGCAGAGACTGTCTT	0.9
+NBS 81	>6	chr14:47050065–47050079	AGAACAGGCTGTAA	0.4
+NBS 82	>6	chr6:37809902–37809916	AGAACAAAATGTAA	0.8
+NBS 83	>6	chr19:27295442–27295456	AGAACAGGGAGTTCA	1.1
+NBS 84	>6	chr11:116345419–116345433	GGAACACCATGTCCT	1.5
+NBS 85	>6	chr2:131746215–131746229	GGCAGAGAGTGAAC	1.2
+NBS 86	>6	chr9:77553727–77553741	AGAACAGCCAGTGCT	1.1
+NBS 87	>6	chr13:102806388–102806402	AGGACAGAGTGTCCT	1.0
+NBS 88	>6	chr15:81699982–81699996	GGCAGAGGCTGTTCC	0.8
+NBS 89	>6	chr2:128391007–128391021	GGGACAGCCTGTCTG	1.5
+NBS 90	>6	chr3:101497686–101497700	AGCAGAGGCTGTGCA	1.4
+NBS 91	>6	chr13:115594267–115594281	GGTACATGTTGTCCT	0.9
+NBS 92	>6	chr2:167403175–167403189	AGAACACCTTGTTCA	1.6
+NBS 93	>6	chr13:115558386–115558400	AGTACATAAAGTTCT	1.3
+NBS 94	>6	chr2:167363486–167363500	GGGACAGTATGTTCC	1.4
+NBS 95	>6	chr7:28077961–28077975	GGGACAGAGAGTTCA	1.5
+NBS 96	>6	chr6:128844559–128844573	AGGACAGAAAAGTACA	1.1
+NBS 97	>6	chr6:37789325–37789339	TGAACAGAAAAGTTCA	1.3
+NBS 98	>6	chr7:109945194–109945208	TGGACAAAAGTGTTCA	1.2
+NBS 99	>6	chr7:109922546–109922560	AGAACAGCCAGTGCT	1.2
+NBS 100	>6	chr3:89979974–89979988	GGTACAAGATGTTTT	1.1
+NBS 101	>6	chr11:21010976–21010990	AGAACAGGTTGTCCT	1.3
+NBS 102	>6	chrX:135890429–135890443	AGAACAGCCAGTGCT	1.1
+NBS 103	>6	chr7:28097274–28097288	GGAACAGGAAGTCCA	0.9
+NBS 104	>6	chr10:128073022–128073036	GGTACAGAGTGAGTT	1.3
+NBS 105	>6	chr11:116380780–116380794	AGAACAACTGTCCC	1.1
+NBS 106	>6	chr11:116379077–116379091	AGCAGAGGCTGATCT	0.9
+NBS 107	>6	chr14:98211187–98211201	AGGACAGGGTGTAT	1.1
+NBS 108	>6	chr16:76237617–76237631	AGAACAGGAAGTCTT	1.0
+NBS 109	>6	chr16:76268786–76268800	GGAACATCCAGTTCT	0.9
+NBS 110	>6	chr11:116366257–116366271	GGCAGAAAAGTGTCCT	1.2
+NBS 111	>6	chr1:53028975–53028989	GGCAGATGCTGTTCA	1.0
+NBS 112	>6	chr1:52994676–52994690	AGTACAGTGTGTACC	1.1
+NBS 113	>6	chr8:12934329–12934343	AGCACAAAAGTGCCC	0.7
+NBS 114	>6	chr2:11405981–11405995	AGCAGAGCCTGTTCT	0.6
+NBS 115	>6	chr2:11420060–11420074	GGAACAGAGCGTGCT	1.0
+NBS 116	>6	chr3:10180480–10180494	AGGACAGCCTGATCT	0.8
+NBS 117	>6	chr1:155647330–155647344	AGAACAGCATGTTTC	1.3
+NBS 118	>6	chr1:155689027–155689041	TGTACAGAGAGTTCA	0.8
+NBS 119	>6	chr15:97748177–97748191	AGTACAGAACGTTCC	1.9
GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
+GBS 1	Sdc4	12745	TGGGGAATGATGTAAGTGACC	CACACTGCCAAGTCTGTGGT
+GBS 2	Mertk	10503	ACGGGCTCAGCTAGCTGAA	ACCAGCCACCAGATACAAGC
+GBS 3	Pik3r1	26866	GGGTTGAACAGGAAGTGATAGC	GCGGTTGAAAAAGGAGTTGA
+GBS 4	Tob2	18527	AGAACAAGCCCTTTGCTCAG	TCACAGCTTGGCTGACTGAC
+GBS 5	Bteb1	6662	TGATGAAACGTGAGCGCTAT	GTGAGAAGGGCTGTGTTTCC
+GBS 6	Mt2	1248	GGGAAAGGACACGGTGTTTA	GCTGTCCTCGCAGCTCTTAG
+GBS 7	Plekhf2	25120	TGCTCTGCATTGTGTCATCA	TTGCTTCGCTGCTTTTAC
+GBS 8	Tob2	23869	CTGGCCAAGGTCTGAGAGTT	CTGCTATTTCCAGCCTCTGC
+GBS 9	Fkbp5	30027	TCCTAAGAGGTGGGAACACG	ACCAAAGGGACAGGGTCTTT
+GBS 10	Peli1	29810	CTAGTGTGCATGGAGGCTGA	GGGCTCTTACAAGCAAGCTG
+GBS 11	Prkwnk4	29323	AGTCAGACCCCTCCCTGAAT	AGCAACAGAGAGGCTTCCAG
+GBS 12	Usp2	19375	GAAAGGTCACTCCTGGGACA	AGGCCAGGCCAGATATTCTT
+GBS 13	Usp2	11923	CCTAGAGCCAGAGAGCCAGA	GTGCTCAGTGGGAACAGCTT
+GBS 14	Bcl2l1	11213	ATGAGGCTGGGCTCCTAAGT	CACACATGTGCCTTTGTCC
+GBS 15	Fkbp5	29545	TCCTAAGAGGTGGGAACACG	ACCAAAGGGACAGGGTCTTT
+GBS 16	Glul	1681	GGGAGAGGCAGTTGTTTCA	GGATAGCTGGAGAGGGGAACA
+GBS 17	Phf15	16896	TCACTCAGATCTCGGTCCAA	CCAGCCCTACCAGAACAGAG
+GBS 18	Sgk	10307	TGGCAAGCAGAAGATGATGT	CCCTTGGTCTACCCCTTCA
+GBS 19	Adarb1	22720	TCAACTCTGGGCTCTTTGCT	ATCGAGACTGGAGTGCTGT
+GBS 20	Prkwnk4	30310	AGCCACCCTCTCTCTCTGT	GGCTCCAATTTAAGAGCAA

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
+GBS 21	Rsd1	3930	GTGCTATCTCAGCCCTGACC	AGGAGCTGAGGGAAAGAAGG
+GBS 22	Dok1	5456	GTCCTCCTTCTGTGCTCGAC	GGCTGAGGGAGAGTGTGTTC
+GBS 23	Gm1024	13683	GGCATCCAGAGGAGAAAGACT	CTTTGAAGCCCAGGAACATC
+GBS 24	Fkbp5	2249	CCCTTCTAGGCCCTGTGTCTG	AAGGTGGATTTGGTGGTCAG
+GBS 25	Suox	111	CTGAGAGTGCATGGTCCAAA	TGTACCTTTCCATCCCCACT
+GBS 26	Bc055107	109	GCACTTTTGACTCCCATTT	GCTTGGACATGGTGTCTGA
+GBS 27	Sgk	993	GGCAGTGCAATGCAATCTT	GTGAGGAGGTGGCGAGTTAG
+GBS 28	Wee1	4957	GGAGAGAACTGGAGATTTGACTTC	TAAAATTGCATGCTCCTCCA
+GBS 29	Mt1	10337	GCCATTGCTCCTTGTTAACT	GCTGCACGTAAATGACTGG
+GBS 30	Fkbp5	1135	CCGCATGCAGAATTTACTGA	GCGTTGGAAGGTACAGATCG
+GBS 31	Dusp1	26868	GGCTTTGAGTCACTTCCTG	CTGGTCCACTTTCCCACTA
+GBS 32	B4	4316	ACCCTAAAGCAGAGGGTGCT	ACCTTCACCCATTTGTGCAT
	galt1			
+GBS 33	Mt2	1351	GGGAAAGGACACGGTGTITA	GCTGTCCTCGCAGCTCTTAG
+GBS 34	Cebpδ	2548	CCTTCCCAAGGACGCTCT	AGGAAAGCTGCAGCTTATGA
+GBS 35	Sphk1	918	TCTTCCCCAAGAAATGATG	CACAGGTTGTCTGGGAGTGA
+GBS 36	Snta1	5047	TGACCTCAGCAGCTTTGCTA	CCTTTCCCTCGAAGCTCTGTG
+GBS 37	Igsf3	9032	TTGCAGTCTTTGTCCACAC	GAACGTTCTGTACGGTTCCA
+GBS 38	Igsf3	19834	TCACTGGTGGAGTTGCTCAG	CAGGAGCCAGCATCTTAGGT
+GBS 39	Il6ra	422	GAGAGCCAGTGGCATAAAGG	GGTGTCTGGTCCCAGTGTT
+GBS 40	Gm1024	6288	TGGTTTCAGGGAACCTCTGG	GTGACAGCCAGCAGCAAAT
+GBS 41	Mt1	232	TCAGGAACTCCAGGAAAGGA	TATTACGGCCTATCGTGCT
+GBS 42	Mt1	10444	CGTGCAGCCTTTCTTTTTC	ACGCCAAAAGCATTCAATTT
+GBS 43	Fkbp5	27815	AGAAAAAGCTGCCAGACA	CAGATGGAGCAGAGACACCA
+GBS 44	Mt2	1089	GGGAAAGGACACGGTGTITA	GCTGTCTCGCAGCTCTTAG
+GBS 45	Rgs2	6583	TGGTGCTACTTGGAGAACAGG	CATGTGTAATAATTCCATGTAGCTT
+GBS 46	Suox	299	GGGGTTGACTTGACTCTGGA	TTCCAATTGCAAACCTGGTGA
+GBS 47	Tsc22d3	29612	GGGACAGTGATTCACCCAAC	TTTCTCTGGCCTGTTGGTC
+GBS 48	Slc39a14	14774	TTTTGTTCCCATACGCACA	TGTCATCCACTCCCTCTTCC
+GBS 49	Tead	30692	AACAAAGCTGGTGCACATCC	TGGTACCAGGTTCAATGAAGG
+GBS 50	Mthfd2	15007	CAGGCTGTGACCAAGTTCACT	GGCCTTGAATTCCTGATCCT
+NBS 1	Gm1024	3955	TGCAGTACAACTGTTCAAGCAT	AATGGTGATTGGGCAGGTAG
+NBS 2	Vdr	23068	AAACCATGGCTTGAATTTCTG	AGATCCAACCACATCCTTCC
+NBS 3	Foxo3a	1848	CTGTGCCCCCTATCCTTGAA	CTGTCTCTATGCCGACCTGAT
+NBS 4	Glul	2826	GGTGGAATTTAGGGGAGA	CTTAAGTGGCTTGCCCTCTG
+NBS 5	B4	23291	GCAGCCCTTGACAAAAACAT	AGCCTGTGCTGTCAAGGAAG
	galt1			
+NBS 6	Mcf2l	10065	TACTCTCTGGCACCAGCTC	CTCACCTCACTGCAGGAACA
+NBS 7	Igsf3	13280	GACCCGCTATAGGGGAGAAAG	GGGAGTTTCACGGGGACTAT
+NBS 8	Sphk1	2388	CTGCGGCTCTATTCTGTGCT	GCCCACTGTGAAACGAATCT
+NBS 9	Gadd45	6726	ATCACCTGCAACCACATC	CCAAGGACAAGATCATCACG
	g			
+NBS 10	Bcar3	13481	GGAGAACCATTCTGGCATA	AAGTGGTCTGGGAAATGTCG
+NBS 11	Mcf2l	13639	ACATGTTTGAGGTTGGCACA	CACACGCTGGTCTTCACACT
+NBS 12	Sgk	3901	GCACTTCGATCCCGAGTTTA	GCTTCTGCTGCTTCTTCAC
+NBS 13	Sgk	5656	TCAATAATGTTCCCTGTGTTGA	CATATTTGTTAAAAGAATTACCTGTCA
+NBS 14	Peli2	12594	TCCCCAGTACAGCTTGTTCC	AAAGCCTTGAACCGGAATCT
+NBS 15	Gadd45	1215	TGCCTTGGAGAAGCTCAGTT	TCACCAAGTCGATCAGACCA
	g			
+NBS 16	Tob2	7501	AGGGCTGGTTGGGATACTG	CAGCAGCAGCTTTGATGTGT
+NBS 17	Pik3r1	9709	GCGTGATTGGCTACTTCCTC	ATGTGTCGAGGGTGGGAAGAC
+NBS 18	Sphk1	2593	TGCCTTCTCATTGGAGCTGTG	GATGCATAACACCAGCCTCA
+NBS 19	Mstn	7969	CCACTCCAAATCACTCTGTTCA	AGGCCAAAACCGCATAAAC
+NBS 20	Mlt2	1135	GGGGGTGAATCACACTCTGT	TGTCCTCTGGCTCCCTCTTA
	h			
+NBS 21	Il6ra	3210	ATGCCAGTCAGATGGGGTAG	AATGTGGCCAAAAGCAAATC
+NBS 22	Tnrc6a	28694	GTGGAGGGACAATGACATCC	GGGAATGGCCTATGGTGAGT
+NBS 23	Fst	20371	CCACCAAAGCATCTCAAAT	GCCCAAATTTCACTCTGTC
+NBS 24	Igsf3	3561	CAGGTAGCTGGCCTAGCAC	GGGATGGTGAAGGAGGATT
+NBS 25	Rgs2	26746	GCCCTGAAAGAGTTGCAAGA	AAGCCATGCATTGCAGAAC
+NBS 26	Prkwnk4	15819	GAACCTTCGGCAGAAGTGAG	ACTTCCGACAAGTGCTGAG
+NBS 27	Gm1024	20301	ATGACAGCTGCTCTCTGCT	GGTTCTCTCTCGGATCTTC
+NBS 28	Ampd3	19735	GCATCCTGGCTCTGCTATGT	ACAACCTTGGCTCTGAGTG
+NBS 29	Mthfd2	14507	GGGCCCCATCTTCTGTCTA	ATCTGCTTCAGAGCCAGCAC
+NBS 30	Bcar3	14637	GTCCTCTTGAAGCCCTGTG	CAGAAGCCAGGTCATCATCA

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
+NBS 31	Rasd1	19093	ACCCACAGGGTCATTTCAGG	TCATTCATACCCGCACAGTC
+NBS 32	Gm1024	2603	TGACAGATTGTGTCTCTTTTG	AAACAAATCTCTCTTGGGTAGTC
+NBS 33	Slc39a14	20934	GCCCCAAATGATTCAAACAC	CAAAGTGATTTACCCCTGAGC
+NBS 34	Peli1	9373	GGAGAACAATTGCTATGCAAAA	GCTGAACCATCTGGTCATCTC
+NBS 35	Mertk	1840	CGTGTTTCAGGAGTCCCAGT	GGACACTGTGTGCCCTTAT
+NBS 36	B4	20862	ATCCTGCCACACCCACATAC	ACTCATGTGTGGCCCCTAAG
	galt1			
+NBS 37	Klf5	11510	GCGGAAACATATACGCACCT	CACAATCAGCCACCGTAGAA
+NBS 38	Mt1	4535	TGCAGCGTGGAGACTAAATG	GCTCTGTGGAAGAGGGAAAAA
+NBS 39	Cebpd	25529	GTCCGACAGGCAGAGAGAAC	TCACCCAGTTCTCAGGTGTG
+NBS 40	Gadd45	1450	GAGGCTGCTAGCACAGGAAG	CTTTCAGTGGAAGGCTGCTT
	g			
+NBS 41	Fabp4	30833	TCAGCCAGGATTTGAAACT	ACCTCCCTGACGGATCCTAT
+NBS 42	Pfkfb3	22057	CTCTGCTGATTCTGCTCAA	GAGTGCCTGTGTTCAAGTGG
+NBS 43	Fst	5827	AAAATGCCAGCATGTGAATG	GCAAATGCTGGGTTTGTITT
+NBS 44	Adm	4098	ACAGTTCAAAACAAAACCTCCAA	TGGCACTTCAATGTCTTCCTC
+NBS 45	Tnrc6a	27492	CACCTTCAGGATGGGAGAAA	CGCACACCATAAAAAAGCTCA
+NBS 46	Pik3r1	5851	GGACAGGCTGAACTCAAAGG	ATCACTGGGACGATGAGGAG
+NBS 47	Stard5	8875	AAGTCCCTCTATGGCCACCT	AAGACCCACACAGGGACAAG
+NBS 48	Dusp1	23526	CTGAAGTCACACAGCCAGGA	CTTCCCCCTCCATCTTTTT
+NBS 49	Phf15	12391	AATGCACGTATGGCCAGTCT	GGTTCAGAACAGCAGCTA
+NBS 50	Foxo3a	22629	GGCAGTTCAAAGGTCAAAGC	TTGGAGAAAGGTTTGCTGCT
+NBS 51	Mt2	8014	GATCTGATGCCCTCTTCTGG	AGTCCCCCTCTTTAGTGCT
+NBS 52	Rassf2	28795	GGCTGTTGTGGGGCTTAGTA	CCCATGGAGGTTAGGAGACA
+NBS 53	Mertk	16800	GCTCTGGCCAGCTAGCTTTA	GGGCATAGCCATTTACAGGA
+NBS 54	Bcl2l1	6029	AGCTGTGTGCACCTTCCTT	GTGGACATGCAGCACTGAAC
+NBS 55	Usp2	16168	GGGTGAAATGCTTGTGTGTG	GACTGGCCAGGACCTTGTA
+NBS 56	Usp2	10030	TAGGCAGCACATTTGCTCAG	GCCTGACTCTGCCTTCTGAC
+NBS 57	Rasd1	8076	TCCCTTCCTGTCTCACTGCT	GGCTCTCCTGTACCCACAAG
+NBS 58	Adarb1	23383	CTGTGAGCCCTTCTGGAGTC	GGAGCACTGTAAAGGCTTGC
+NBS 59	Adarb1	29001	TGGGTTTGGGTTCTAGATGG	TGTCACATCAAAGCCAGGAG
+NBS 60	Adarb1	28088	ACCACCTTTCATCCCACCAG	GTGCCATCAGGGAATCTCAA
+NBS 61	Gem	10372	GACAGTTCCTCCCTGCCATTA	ATTTGACCCCAATCCTTCC
+NBS 62	Serpine1	29209	CATTTGAACCCACAATGCAA	AATGTGCAGCTTCCTGGAGT
+NBS 63	Plekhf2	31976	TGAAGCTTTAACGGCCTCAG	TGGGTCTGTGTCTCAGGCTA
+NBS 64	Ampd3	10399	GCCCCCAATCAATAGGACTT	GCGTCTCCTTGGTCTGAGAG
+NBS 65	Adm	20646	AAGCCAGGTATGGTGGTGAA	TCCCTGGCTGTATTGGAAC
+NBS 66	Fst	31601	CCACTCTTGAAATGGCTTC	AGGGGACTGGCTAGATGGTT
+NBS 67	Slc39a14	9701	TCCCAGATGAGTGTGCTCAG	CAGGGTTTTGCTCTGTAGCC
+NBS 68	Tnrc6a	23194	TATCACCGAACCACGACTCA	CTCCTGCTGTGAGCAGACAC
+NBS 69	Suox	7578	CCTCCTGAATGGCAGGATTA	TCTGTGTGCACCTAGCCACT
+NBS 70	Serpine1	27348	GTGCACTCTAAGGCTGACC	GGGAAGCAGTGAGGACTCTG
+NBS 71	Klf5	28926	TGCCTCTTGGCTACTTGAT	ATGCTAGCTTGGGCGATTTA
+NBS 72	Vdr	20159	AGCCAGTGCTTCACCAGAAT	CTCTTCCCTTCTGCACACC
+NBS 73	Gadd45	23240	GAAGGGGTAGAGGCTTGGAC	CAGGGCTTCAGGTACCATA
	g			
+NBS 74	Slc25a30	28789	GGGATTAAAGGCATGAGCAA	ACCCACTACCCAATGCTTGA
+NBS 75	Ssh2	9203	GCCTGAAATCTTTTTGCCAAT	TGGCTTCTTGAAAGGCAGAT
+NBS 76	Tsc22d3	5235	CACTAAGTGACTGCGGGACA	CATGAGAGAAAAGGCCTGAG
+NBS 77	Peli1	12283	AGTGACACAGAGTGCTCAAG	CATGGAATCTTGAAGCCAGAA
+NBS 78	Dusp1	22907	TCCCTTGTAGACACTCTCTG	GTGGGAGGGGACTCATAGTG
+NBS 79	Mertk	22613	GGGCTCAGTGATTCCAGTA	CCCTGGGAGACACAGTAAGG
+NBS 80	Stard5	16530	CAGTCTGTGCCAGCTTTCAG	GAGTGCCTGGCCTTTTAGC
+NBS 81	Peli2	7174	CCTTAGCTCTGCCCTTCTT	CACAGAGCACGAGGTGTTGT
+NBS 82	Trim24	9483	AGCCCCGTGTATCCTGCTA	GCCCAGTGGTTTTGTGTTTT
+NBS 83	Vldlr	10913	ACTTCTGCTGAGCCATCTC	ATGTGATGCATGGCTGTCTC
+NBS 84	Sphk1	4018	TCTTGTGAGGCGTGCTGTG	ACATGGTGTTCCAATGCTGA
+NBS 85	Rassf2	24964	ATTACAGGCCGCTTCTCATGC	CCTCCATTTGCATTTTGCTT
+NBS 86	Gclc	13233	GTGGGCCTCTTCTCACTGAC	CCAGCACTGGCTGTTCTTTT
+NBS 87	Pik3r1	13484	CACCTGGCAAGCAGTTTGTA	TTACCACAGCTCTTGCGTTG
+NBS 88	Tob2	14401	GCAAGCTTGGGTTTAAGCAG	CCTTGTCTACCTTGAGGAA
+NBS 89	Mertk	569	TTGCTTGGAGGCTAGGTGTC	CAGGCTGTCCCTACAAAGGA
+NBS 90	Igsf3	9691	CACATCCAGCTTCGAGATCA	GGTTCTCCAGGGTATGCTCA
+NBS 91	Fst	14803	CACCGACCCCTTCTCTAAT	CCCAGTTTCAACCCTGACAT
+NBS 92	Cebpb	23055	TGTGCTGGTGGTCAGCTAAG	TGCTCTTTGTGTGCCATTA

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
+NBS 93	Fst	21078	TTGGTTTCCAAAATGGCTGT	ATTTTCATCCCCACGTGAAC
+NBS 94	Cebpb	16634	CCTCCCATTCGAGTCCAC	AGACCTCGCTTTCATTTTG
+NBS 95	Zfp36	10027	GGAAGGGGGGTGTTGTAAT	GAACTCTGTGCCCCCTTC
+NBS 96	Clec2l	8674	CAGCTCAGGGCTAATCTGCT	TGCCCTTAAATCTGCCTGA
+NBS 97	Trim24	11094	TCCATAAGGCTGGGTGTCTC	CTTGCCCTGTAGCACACCT
+NBS 98	Wee1	31958	AAGTGAGGCAGGAAGATCA	TGCTAAACGAAGCACACAGG
+NBS 99	Wee1	9310	CAGAAGCCCTGAAACTGGAG	TGGCTCAGCAGTTTTAAAGCA
+NBS 100	Il6ra	19115	CTGCAGCTGAAGAGCGACTA	TGAGATGTCCATGGTGTGCTG
+NBS 101	Peli1	19649	ATATGGGAGGGAGGGTGAAA	GGCACAGAGGGCAAGTTAAG
+NBS 102	Tsc22d3	898	TCCTCTGGAGAACAGCCAGT	AGGCCAGCCTGAGCTATGTA
+NBS 103	Zfp36	9286	GAGGTGGAACAGGAAGTCCA	ACCACTGCGAAGTCTCAACC
+NBS 104	Suox	2530	GGACAACCAGGGCTACACAG	TGTGTGTGGTGTGTGGAATG
+NBS 105	Sphk1	31343	GGAGCAAGCCAGTACAGTCC	TGAGCAGAGCACCTGCACATT
+NBS 106	Sphk1	29640	CGGGGTTTAACTCCCAAAAT	CGCTGTTTTTGAAATTGGAT
+NBS 107	Klf5	29353	CTTCTCCCACGTTGTCAGGT	TTTGTTGGTTGGTTGGTTT
+NBS 108	Nrip1	18112	GTCCCCACCCATAGACACAC	CCAGTCGAATCCCTTTGCTA
+NBS 109	Nrip1	13057	AATGGTGTGTGGAAGGGAAG	CCACTGCCAGACACATTTCa
+NBS 110	Sphk1	16820	GCTTCACTCAACTGCCTTC	AGCTCAAGGCTCTCGTCAAG
+NBS 111	Mstn	22661	AAGCAGCAGGGTTCACATTCT	GCCCAGAAGGGAAGGTGTAT
+NBS 112	Mstn	11638	GCCCGACACTCTGTCTAAGG	TGTCAAGAAAGGCAAAAGCA
+NBS 113	Mcf2l	18394	GCCAGTCTCTGAACCACCAT	CACGAATGGTCAAAGGGATT
+NBS 114	Pfkfb3	13939	AACTGGGACCTTTGCCTTT	CCATCCAGCTGTTCAAGTTT
+NBS 115	Pfkfb3	140	CCAATGTGGTTCGTTGACAG	GGCTTGTAAGGCTGAACCTGG
+NBS 116	Fabp4	10606	TCAAGGATAGGTGGGGACTG	GGCGAATTTTCTAGGCACTG
+NBS 117	Glul	14833	ACCATGACAACAGGGCTAGG	AGCCTCTCAGTCCCCAACT
+NBS 118	Glul	26864	CAGGGATGCAGAGTTTGACA	CCAACATACAATGGCAAGGA
+NBS 119	Vdr	11847	GGGCAAAAACCTTGCTCAA	TTCAATTGGTGTGCCAGA

ChIP of GR in C3H10T1/2 cells at dex-induced genes. All GBs found at dex-induced genes and examined by ChIP followed by qPCR analysis are displayed. NBSs represent those GBs that were not occupied by GR in C3H10T1/2 cells. The chromosome coordinate, the relative fold dex-induced GR occupancy, and the sequences of the GBs are listed. The distance of the GBs relative to the transcriptional start site (TSS) of the corresponding genes are shown. The qPCR primer sequences are also displayed. Note that within the set of GBs occupied by GR, no obvious correlation was observed between the level of conservation versus the degree of receptor occupancy as measured by ChIP signal at the GR-occupied GBs.

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
rNBS 8	Aldh8a1	29050	GAAAGCCTGCAGCCATGTA	GCCAGAGCTGTAAGCCAAGT
rNBS 9	Grap2	28775	CTTCCTTCAGCTCCAGATG	GGGGTGATGAGAGGAAGTGA
rNBS 10	Irf5	9472	TTGATGCAGAGCTCATCTG	TTCTCTCGGGGTTTGACATC
rNBS 11	Orm1	19957	GAGGTCTGGAAAGCTTG TG	TGGCATGGAAACTTCAATCA
rNBS 12	Ryk	13430	GGAAGAACACTGCGAAAAGC	TCCCATGACTTGTGCTTCA
rNBS 13	Yars2	10469	TAATGCACAGGGCAGTGTA	CAAACAAAACCTCTTTTCAGTTT
rNBS 14	Cetn3	3969	CTGTGCGCTGTGACTTTTGT	TGGACTTCATGTCCCATCT
rNBS 15	Grap2	29711	AAGCAAAATGCTTCCCAAGA	GCATGTGTCCCTTGTCTGTG
rNBS 16	Ktn1	290	CTCCAATGAATGTGGCAGAA	TTTTCCTGGGATCTTTGAT
rNBS 17	Grap2	18075	AGCCATTGACAGCACCAATA	CTCAGCTCTGGTCTTTCTCCA
rNBS 18	Troap	7523	CAGAACTAAAGCCCCAGTG	CTGTCCCCGACAGCTAGG
rNBS 19	Elmo3	10141	TAAGATCACGGAGGCCACTC	CTTGATCTCAGTGGCTGCAA
rNBS 20	Ptpn9	22614	CTGATGTGCCACTCTACA	ATCACACTGTCCACAACCA
rNBS 21	Foxk1	1953	AGGAAGTGCTGTGCCTCAGT	CCTGGGAATAATGGGAGCTT
rNBS 22	Ints12	18218	CATCTGGTTGCACATTCTG	GAAGAAGCTGGGTGCAAACT
rNBS 23	Tmem8	30269	GCACAGGGTGTCCATTTTCT	AGCAATTTCACTGGGGTTA
rNBS 24	Elmo3	25589	CAGATTCTGAAGGCCAGAA	GGAACAGACTGACCCTCTG
rNBS 25	Sema6d	6881	GGGGGAGGAAAGACAGACAT	GAGCCAGGAGCAGGTACAAG
rNBS 26	Pole	3882	TTGCTCATCACTTGCCACTC	GACCTTTCTCGCTGCAATGT
rNBS 27	Grap2	28289	TGCAGGAAGACTTCTCAGGAA	TTTTGACCAGGACGGTCTGT
rNBS 28	Ppfibp2	3648	CTGGCAGGTTTTGCTTCTGT	TGAGCCATTCTTCTTGAGC
rNBS 29	Ppfibp2	11695	GGCTCTGGTAGCTGAGAGA	GAAACGGAGTGCAGGCTTAG
rNBS 30	Uts2	7490	ACAGCAGGAACACGTGTCAG	TTTTTCTGGACCGCAGTTCT
rNBS 31	Aldh8a1	19570	ACAGAAGGTATGGGGCACAG	AACAATGTGTGCTGGGATCA
rNBS 32	Ppfibp2	6265	CTCTCCAGGGTAAAGCTGTCA	TGGGACACCTTGTTCA GTCA
rNBS 33	Zfp105	27886	GCGGACTTCTGACGTAGACC	CACCAGAATCCTCCCTTCAA
rNBS 34	Lmbrd2	13742	TGCAGAAAAAGTGACCTCATTG	TTAGGAAACTTCAGGGGACT
rNBS 35	Ppfibp2	9558	GTGGGCTGATGCTCTAAAGG	ACTCTGGGTCTGGAGAGCA
rNBS 36	Yars2	18050	GAGGGATCTGATTTTCCGAAG	GAGGATGAAGGATGCTGGAA
rNBS 37	Yars2	17908	GAGGGATCTGATTTTCCGAAG	GAGGATGAAGGATGCTGGAA
rNBS 38	Adamts19	7005	CGTAGATGGCTTGGAGAACAG	GCCCATGATGGAATTGTCTC
rNBS 39	Ryk	22231	ATCTGCAGCCATTCAAGGTCT	CTGTGGTGGGAGAGACATCC
rNBS 40	Cnih3	8409	GCATCGAAATAGGATGCACA	TTAGCCTTGCCACTCCAGTT
rNBS 41	Troap	21083	GACACATGGCTCTCAGCAAA	GGCTGGTGTCTGACCTTTGT
rNBS 42	Olfr446	7766	GCAGAAGACTCTTGCCCTGT	AAGGATTTCTTCCCAAGGAT
rNBS 43	P2rx1	2507	CTCTTCCATGCACAAGCAAA	TGGCCCTATAAAGTGGATGC
rNBS 44	Sema6d	9257	CTGCTTTTCTGTGTGCAAG	TTTCATGCAATCATGCAGGT
rNBS 45	Snapc3	16262	TCAGTTGGGGAAAGCTGATTT	TCTGTTCA TTCCACCATGA
rNBS 46	Ints12	13052	TCTTGCTTAGGGATGGTGCT	CACAACCTGCAGTCACTTGG
rNBS 47	Tmem8	13570	AGATATCTGCCTGCCTCTGC	ACAGTGGACCTGGGATGGTA
rNBS 48	Olfr787	31555	CTGTGGCCAGATAGGCATT	GGGAAGGAATTAAGGGGAGA
rNBS 49	Adamts19	11661	GCCATTCCACAAGCCTTAAA	ATCAGTCGGAATCTGCTCGT

ChIP of GR in C3H10T1/2 cells at dex-unreponsive genes. The table is displayed as indicated in Table S4.

GBS identifier	Mismatch, bp	Mouse Feb 2006 (mm8) Chromosome coordinates	Sequence of GBSs	ChIP (Dex/EtOH)
-NBS 1	1	chr2:113566773–113566787	AGCACAGGCTGAGCT	1.4
-NBS 2	1	chr17:33381772–33381786	AGAACAAAAATGTTCT	1.9
-NBS 3	1	chr16:85668398–85668412	TGAACACAGTGTTTA	1.4
-NBS 4	1	chr17:33419255–33419269	AGGACAGCCAGTGCC	0.9
-NBS 5	2	chr11:53627644–53627658	AGGACAGGCTGAGCT	1.1
-NBS 6	3	chr16:85683741–85683755	GGAACATGGTGATCA	1.8
-NBS 7	4	chr19:34639193–34639207	AGAACAGTGAGTTTA	1.5
-NBS 8	5	chr1:171602766–171602780	AGGACAGGATGATCA	1.5
-NBS 9	5	chr19:34639163–34639177	AGGACAGGGTGTTTA	0.5
-NBS 10	6	chr2:113558275–113558289	GGAACAGCCAGTCCA	1.4
-NBS 11	6	chr15:54112238–54112252	TGAACACTGTGTGCT	0.9
-NBS 12	6	chr9:21679854–21679868	GGTACACCTGTTC	1.9
-NBS 13	6	chr11:53617327–53617341	AGAACAGGCTGTGTG	1.0
-NBS 14	6	chr19:34619336–34619350	AGCACATTGTGTTCC	1.7
-NBS 15	>6	chr2:140379805–140379819	AGAACAAAGTGTTC	1.6
-NBS 16	>6	chr16:85715383–85715397	GGGACAAAGTGAAC	1.4
-NBS 17	>6	chr12:25212705–25212719	AGTACATGGTGATCC	0.7
-NBS 18	>6	chr9:21680879–21680893	AGCACAAGGTGTCCA	0.9
-NBS 19	>6	chr12:25259555–25259569	GGAACATCTGTGCT	0.9
-NBS 20	>6	chr7:34796141–34796155	AGTACATGCTGTGCT	1.1
-NBS 21	>6	chr7:34818835–34818849	AGCACAGCCAGTGCT	1.1
-NBS 22	>6	chr7:34842851–34842865	GGAACAGGGTGTGTA	1.2
-NBS 23	>6	chr1:171559249–171559263	AGAACAGCGTGATCA	0.6
-NBS 24	>6	chr2:140381328–140381342	GGGACACAATGTGCA	0.9
-NBS 25	>6	chr11:81837798–81837812	AGAACAGAAAGTGCC	1.4
-NBS 26	>6	chr11:81855390–81855404	GGGACAGGCTGTCTG	0.7
-NBS 27	>6	chr11:81855390–81855404	GGGACAGGCTGTCTG	0.9
-NBS 28	>6	chr11:81837798–81837812	AGAACAGAAAGTGCC	0.5
-NBS 29	>6	chr11:53612814–53612828	AGGACAAGGTGTTCC	1.5
-NBS 30	>6	chr5:139981116–139981130	AGAACAGAGAGTGTC	1.1
-NBS 31	>6	chr5:140009174–140009188	AGCACAGCCTGTGCC	1.1
-NBS 32	>6	chrX:49287573–49287587	AGAACAGACTGTGCT	1.2
-NBS 33	>6	chrX:49278384–49278398	AGAACAGGCTGAGCA	0.8
-NBS 34	>6	chr19:34248392–34248406	TGCACAGACTGTGTT	0.7
-NBS 35	>6	chr9:21669685–21669699	AGAACAGTCAGTGCT	1.0
-NBS 36	>6	chr9:21696342–21696356	AGGACAGCCTGAGCT	1.1
-NBS 37	>6	chr7:34821618–34821632	AGGACAAAAATGTCTT	1.7
-NBS 38	>6	chr7:34857457–34857471	AGGACATGCTGTTTG	1.1
-NBS 39	>6	chr12:25259977–25259991	AGAACAGTCAGTGCT	1.0
-NBS 40	>6	chr11:53597350–53597364	AGAACAGTCAGTCCT	1.1
-NBS 41	>6	chr2:113542322–113542336	AGGACAAAGAGTTTT	1.4
-NBS 42	>6	chr2:113568635–113568649	AGAACAGTCAGTGCT	1.1
-NBS 43	>6	chr2:113551639–113551653	AGAACAGAAAGTGTT	0.9
-NBS 44	>6	chr2:113576556–113576570	AGCACAGGAAGTCCT	1.0
-NBS 45	>6	chr17:33369357–33369371	AGAACAGAATGTGAT	0.6
-NBS 46	>6	chr2:113560456–113560470	GGAACAGTGTGTGTG	1.2
-NBS 47	>6	chr17:33415229–33415243	AGGACAGCCAGTGCT	1.0
-NBS 48	>6	chr17:33415109–33415123	AGGACAGCCTGAGCT	1.0
-NBS 49	>6	chr17:33379629–33379643	AGAACAGCCAGTGCA	1.0
-NBS 50	>6	chr4:36264491–36264505	GGAACAGATTGTTTT	0.9
-NBS 51	>6	chrX:49311863–49311877	AGGACAGTCAGTTCT	1.6
-NBS 52	>6	chr11:81865889–81865903	AGGACATCCAGTTCT	1.1
-NBS 53	>6	chr19:34667299–34667313	AGAACAATGTGTCCT	1.1
-NBS 54	>6	chr19:34625936–34625950	AGGACAGGCAGTTCT	1.0
-NBS 55	>6	chr19:34618582–34618596	AGCACACAAAGTTCC	1.5
-NBS 56	>6	chr15:54116271–54116285	AGGACAAATTGTGCT	1.2
-NBS 57	>6	chr11:81865889–81865903	AGGACATCCAGTTCT	0.7
-NBS 58	>6	chr7:34807445–34807459	TGAACAGTGAGTTCT	1.6
-NBS 59	>6	chr5:139958553–139958567	TGGACACAGTGTTTC	0.7

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
-NBS 1	Grem1	7288	AACCAGCCCTAAGTGCACAG	GCTGACGAGACTCACAGCAC

GBS identifier	Gene	Position from TSS	Forward primer	Reverse primer
-NBS 2	Fiaf	6500	GGAATACGATGTCCGAGGAA	GCACAGCTCACAGCATTCTT
-NBS 3	Adamts1	23897	ATGCCCTCTATGCATCGTTT	GGGAATACCAGAATGGCTTG
-NBS 4	Fiaf	30983	TTTCTCGTCTCTGTTGCTTT	AATTGCCAGGGGAAAAACTGA
-NBS 5	Irf1	14143	CAAGAACTGGGAGCAAGAGG	ACTGGACCACAGGTGGGATA
-NBS 6	Adamts1	8554	CACCAGGATACGACTGTTGG	GATCAGGGTCCCATGAGATG
-NBS 7	Ifit3	10358	AATGCCATTTTCACCTGGAAC	TGCACATGGTGGCTTTAAACT
-NBS 8	Rgs4	18471	GACAAGGAGCCTTGAAGCAC	AGCAACAGAGAAGCAAAGCA
-NBS 9	Ifit3	10388	TTGGATGAGTTTGAGGACAGG	TGCAGTGTCTGCTCATTTAG
-NBS 10	Grem1	1210	AGACCAGAGAGCCCCCTAAG	GACTGGCTGTTCCCTCTCTG
-NBS 11	Tnfrsf11b	3671	CCTGAACACTGTGTGCTTCC	TTGTCCGGGTTTCAGCTATC
-NBS 12	Rab3d	11331	AGGGTTTTGGAGCTGAGAT	TCACGTCTGAGCTGGAACAG
-NBS 13	Irf1	3826	CCCTCACACAGCCTGTTCTT	TCACTGCCCACTTACCTAC
-NBS 14	Ifit3	30215	AAACCTACCTGTGCAGGAAAA	CCAGGTCTCTGGAAGAACA
-NBS 15	Flrt3	16895	GCCATTCTCTTTCTCCTTGA	AAGCTCTGCCAGGTGTG
-NBS 16	Adamts1	23088	CTCAGGGTGTGCACAGATGA	ATAGGAGCGCTGGGAAGACAA
-NBS 17	Tieg2	27648	GCTCTGTCAGTGCAGATGGA	CTCATTAGCAGCCATGCAGA
-NBS 18	Rab3d	12356	GCTACTGCCTCCCAAGTGTC	CCTAAGATTTGGTCCCAGCA
-NBS 19	Tieg2	19202	ACTCTGACACCTGCACGTA	CACGAGGCTCGAAAACTAGG
-NBS 20	Cebpa	31922	CAGGCTGGCTTTGAACTCTC	GTTGCGATGCCTAGCACAACA
-NBS 21	Cebpa	9228	CGAGAGCGGCATGAGTAGAT	GGTTGGTGAGATGGCTCAGT
-NBS 22	Cebpa	14788	TCACTCACACCCACTCTTCTCAGT	CAAAGCCCAGCAGCAATCTACA
-NBS 23	Rgs4	25046	TGGCATCACTGGCTACTCAC	ATGGTGCGAGAGATGGGAGAG
-NBS 24	Flrt3	18418	GTTTGGGACACAATGTGCAG	TTGCTCCTTCCAACAACCTGA
-NBS 25	Ccl2	13974	CCCCACCTCTACCACAGAGA	CCACAGCTTCAAGGCACTTT
-NBS 26	Ccl2	3618	GGAGCTAAAGGGATCTGCAA	AATGGGCCTCTCTTCCAGT
-NBS 27	Ccl7	6519	AAGGAAGTGGGGCACAAATA	GCAAGGATGGAGGAACCTCAG
-NBS 28	Ccl7	24111	CCCCACCTCTACCACAGAGA	CCACAGCTTCAAGGCACTTT
-NBS 29	Irf1	687	GTGTTCCCCCATCACTTCAG	TTGGAAATACGGGGCAGTAG
-NBS 30	A930021H16Rik	7542	CCTGCAGTTCTCTTGCAATTG	TCAGGACGTGTGTGTGTGTG
-NBS 31	A930021H16Rik	20516	GTCTCCCTGACCCACACACT	TTGACTGTGACAGGCCCATA
-NBS 32	9430052C07Rik	10330	CTGGCTACGCAAACAGTTCA	CTGTGCTTAAGCCTGAGACG
-NBS 33	9430052C07Rik	19519	CCTTGTGGGTGAGACCATCT	GACTGGAACTCAGGCAGTCTC
-NBS 34	1700095N21Rik	9875	GCATCTCTGACACCAATGCTA	CTTCTGCGAGCTTGAAAAAT
-NBS 35	Rab3d	1162	TGGCTCAGCAGTTAAGAGCA	CTGTCTTCAGGCACACCAGA
-NBS 36	Rab3d	27819	AAGCTCAGGCTGTCTTGAA	AGGGCACTGATGGGACATAG
-NBS 37	Cebpa	6445	CAGAGCCAGGGTAGCTTTTG	GCCTTGGAAGGAGGAGAAAA
-NBS 38	Cebpa	29394	GTTGCCCAGGCTCTGTAGTC	TGCTGTTTGCTCCACCAAG
-NBS 39	Tieg2	19624	ACACCTGTATATCCCAGCA	ATGGTTGTGAGCCCAATGT
-NBS 40	Irf1	16151	AAACCTACCTGTGCGAGAAAA	CCAGGTCTCTGGAAGAACA
-NBS 41	Grem1	17163	TGTGTCCCAAAGAGTTTGATGA	TCCTCCCTTCCAGATCAAAA
-NBS 42	Grem1	9150	AGGACCCAGGTTCAATTTCC	GGTGTTTTGCCTTCATGGAT
-NBS 43	Grem1	7846	GGGCAATAGAACACCCAGAA	GTTGAAAAGTGGGGTCTGGA
-NBS 44	Grem1	17071	TTCCAGACCAGTGCTTACCA	TCCATGGAGACGAGGACTTC
-NBS 45	Fiaf	18915	AAGGTCACTCTCTGCCACAT	AGCCACCATGTGTTGCTACTGA
-NBS 46	Grem1	971	ACACAGCAGATACCCAAAC	GGGCTTCGGGACTATAACT
-NBS 47	Fiaf	26957	GGCTGTCTTGAACTCACTC	TGGTGTGTGCACACCTTAAT
-NBS 48	Fiaf	26837	TCATAACTCCAAATGGGTTAAAGT	GCCAGCCTGGTCTACAGAGT
-NBS 49	Fiaf	8643	GGGTTCAAGTCTCAGGACCA	ATCAAACATGGCTCCTCTGC
-NBS 50	Dusp4	11636	TCCACCTCACACCAATCAGA	GCTTAAAAATCCCACCAGCAA
-NBS 51	9430052C07Rik	13960	TGTGGAGCAATTGGCAGTTG	TGCAATTGGGAATAATTGAGG
-NBS 52	Ccl2	14117	ATGTTCCAAAGCACCAAAGC	GATGCAGACAGAAGCAACCA
-NBS 53	Ifit3	17748	CCTCTTCTTCTCCCTGGAC	GAGTGGGAAATCAAGCATGG
-NBS 54	Ifit3	23615	GCCTGGAGCAAATAACAGGA	AGAACTGCCTGTCTTCAGC
-NBS 55	Ifit3	30969	CCTTGATGGAGAGGTGCAAT	GGCTGTCTTTGATTGGTGTG
-NBS 56	Tnfrsf11b	7704	GCTTGATCTGGAGGTGGGTA	GGTAGGAAGGCATGCTGGTA
-NBS 57	Ccl7	3980	ATGTTCCAAAGCACCAAAGC	GATGCAGACAGAAGCAACCA
-NBS 58	Cebpa	20618	CCCAGTGTGGTTGAACAGTG	CCACCAAATATGGCACCTTC
-NBS 59	A930021H16Rik	30105	CTGTAGGCACAGCCAGGAAG	GCCTGCAGACCAACCTAATC

ChIP of GR in C3H10T1/2 cells at dex-repressed genes. Primers used for qPCR analysis of ChIP samples targeted against GR of GB5s found at genes repressed by dex are shown. All GB5s identified at GR repressed genes are shown. The table is displayed as indicated in Table S3.

