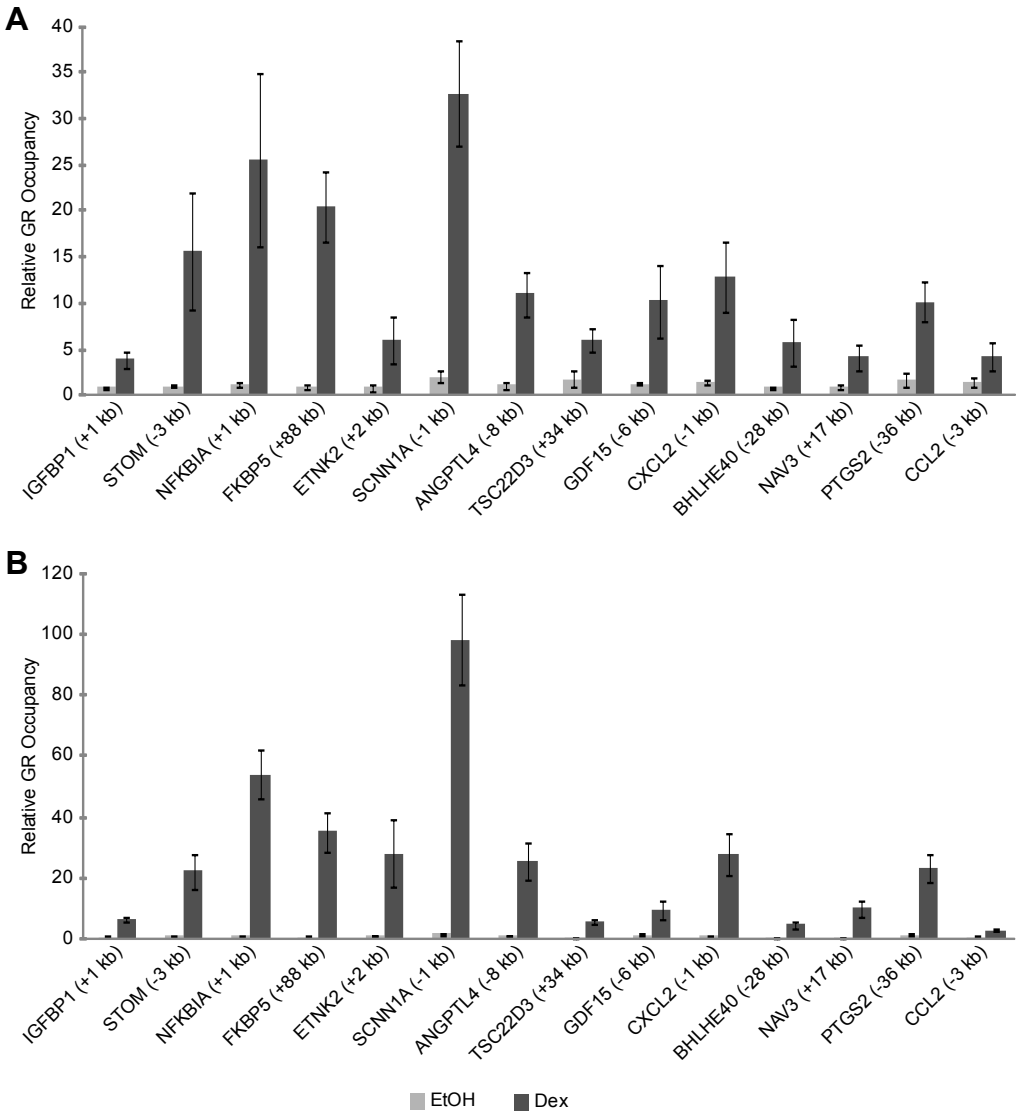

FIG. S1. Similar patterns of GR occupancy following 30 min (A) or 4 h (B) dex treatment. Cells were treated with EtOH or 100 nm dex. ChIP data is displayed as enrichment of GBRs near the corresponding gene relative to IgG ± SEM (n ≥ 3). The location of the GBR relative to the TSS is indicated.

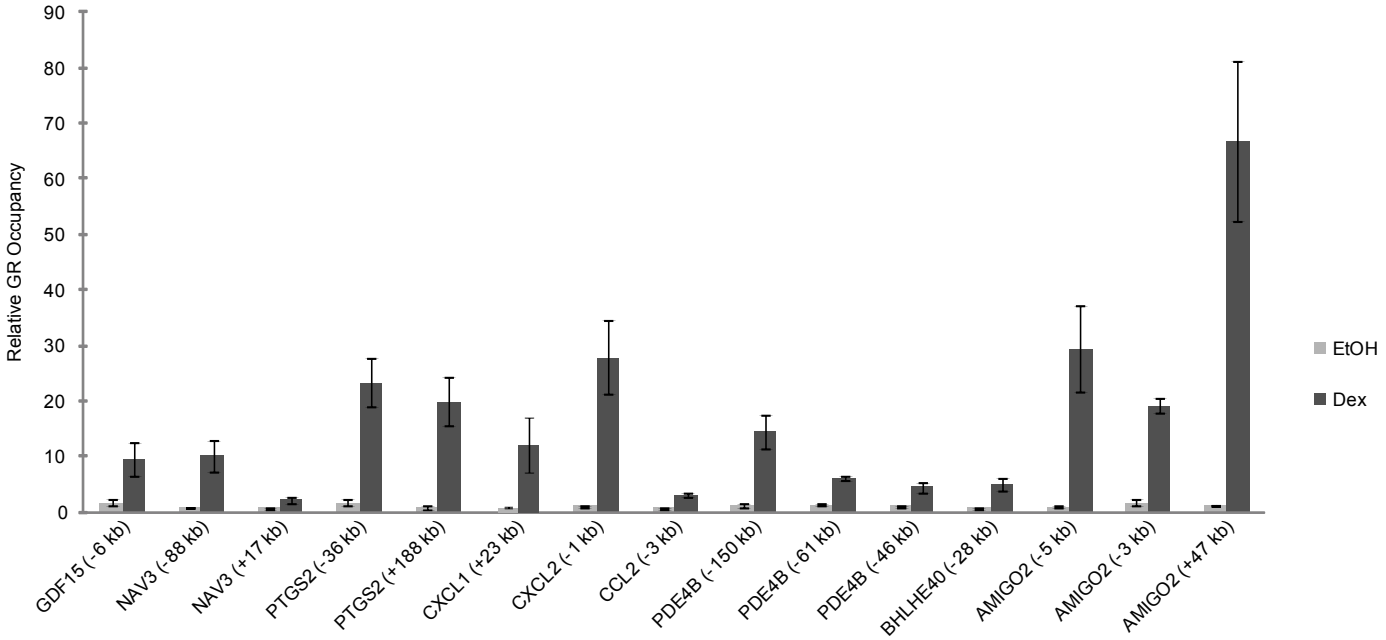

FIG. S2. GR occupancy at all verified GBRs of repressed genes. Cells were treated with EtOH or 100 nM dex for 4 hours. ChIP data is displayed as enrichment of GBRs near the corresponding gene relative to IgG ± SEM (n = 4). The location of the GBR relative to the TSS is indicated.

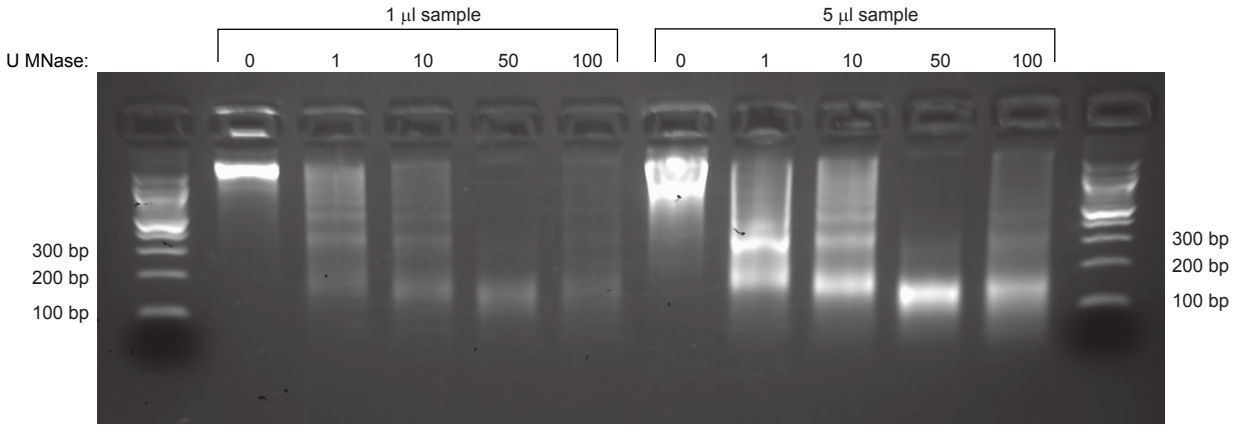

FIG. S3. MNase titration to achieve mononucleosome-sized DNA fragments. After adjusting nuclear suspensions to 3 mM $CaCl_2$, the sample was split into five 200 µl reactions, which were digested with a titration from 0 to 100 U MNase for 10 min at 37°C. After eluting purified DNA, 1 or 5 µl was run on a 2.5% agarose gel. Digestion to mononucleosome-sized DNA fragments was achieved with 50 U MNase.

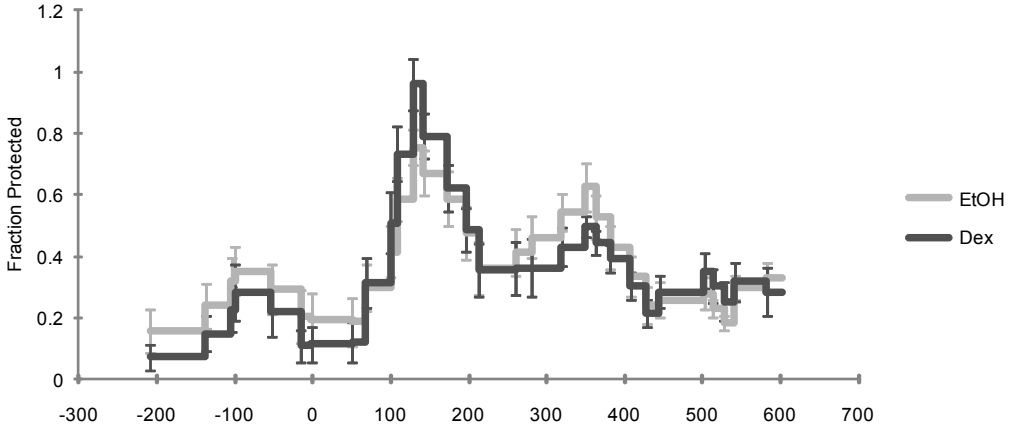

FIG. S4. Housekeeping gene RPL19 shows no chromatin changes upon hormone treatment, as a negative control for the MNase assay. Cells were treated with EtOH or 100 nM dex for 10 min. Data is displayed as fraction of MNase protection by calculating a fold difference between MNase-treated and untreated samples (y-axis), plotted against the location relative to the TSS (x-axis) ± SEM (n = 3).

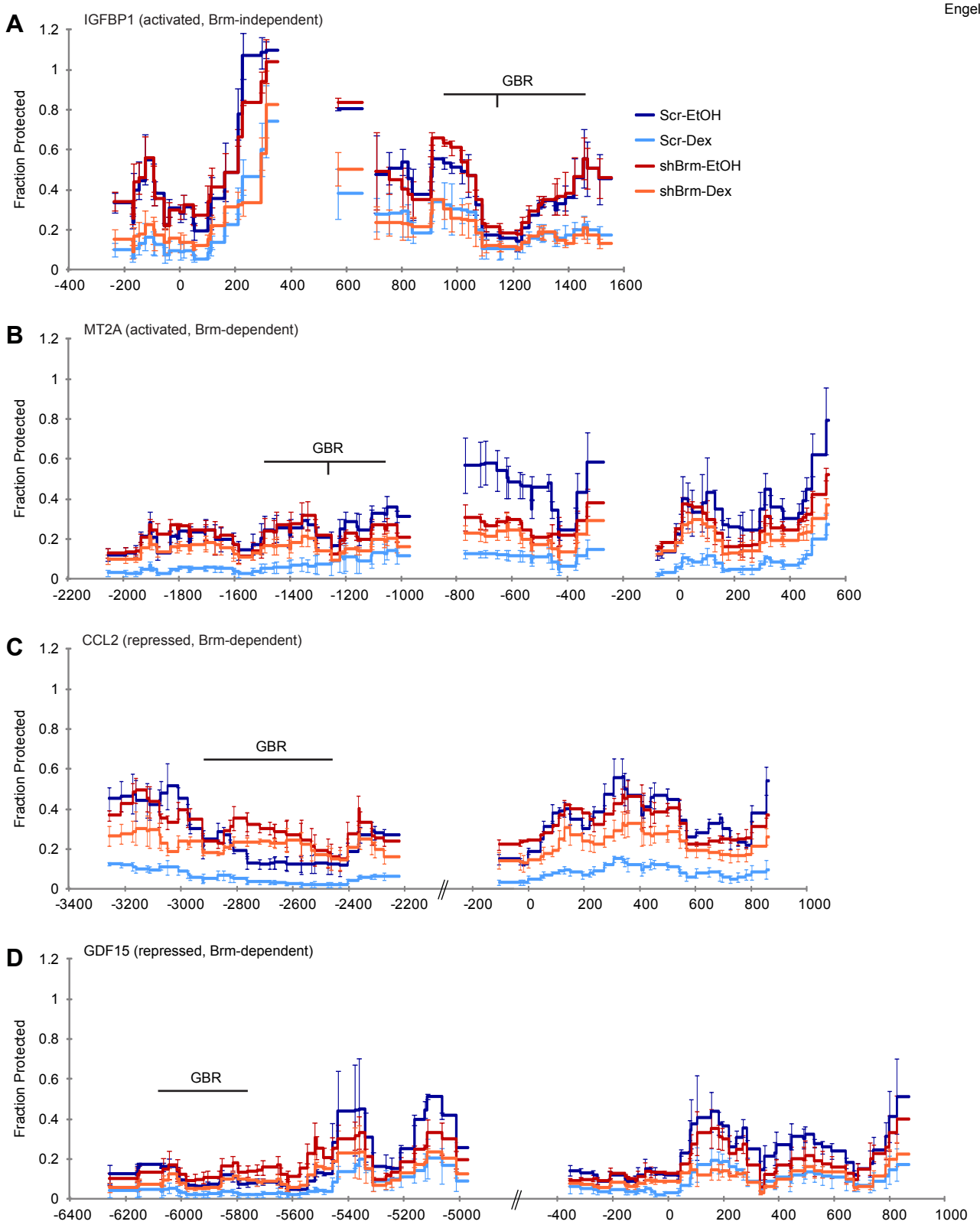

FIG. S5. MNase assay showing fraction protected with error bars at IGFBP1 (A), MT2A (B), CCL2 (C), and GDF15 (D). Cells were treated with EtOH or 100 nM dex for 10 min. Data is displayed as fraction of MNase protection by calculating a fold difference between MNase-treated and untreated samples (y-axis), plotted against the location relative to the TSS (x-axis) ± SEM (n = 3). The horizontal line with GBR written above it represents the region of GR binding, and the vertical line shows the location of the canonical GR binding motif. The motif is not present at CCL2 or GDF15.

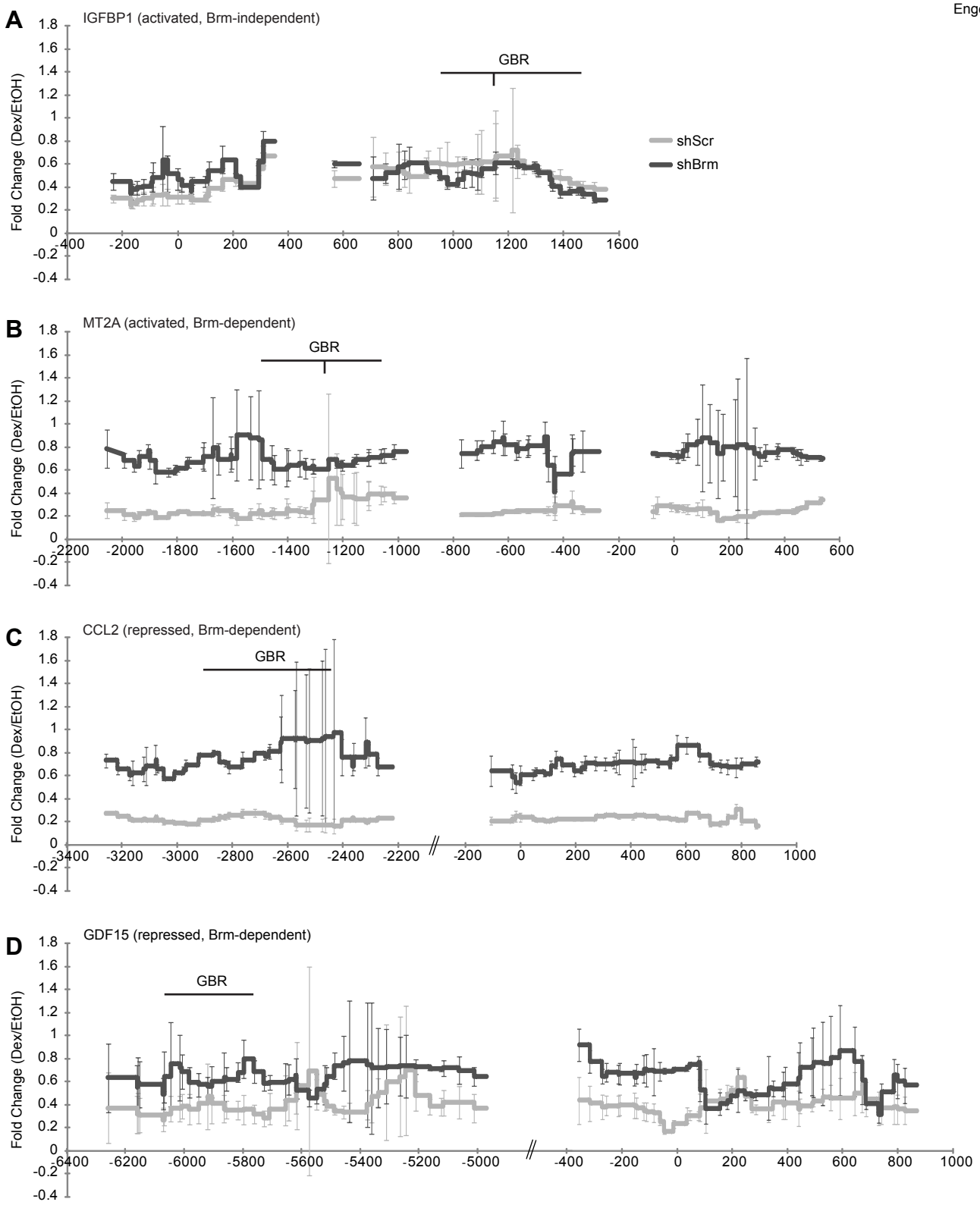

FIG. S6. Fold change of MNase protection with error propagation at IGFBP1 (A), MT2A (B), CCL2 (C), and GDF15 (D). Data is displayed as the fold difference between dex- and EtOH-treated MNase samples (y-axis), plotted against the location relative to the TSS (x-axis) ± variance (n = 3). The horizontal line with GBR written above it represents the region of GR binding, and the vertical line shows the location of the canonical GR binding motif. The motif is not present at CCL2 or GDF15.

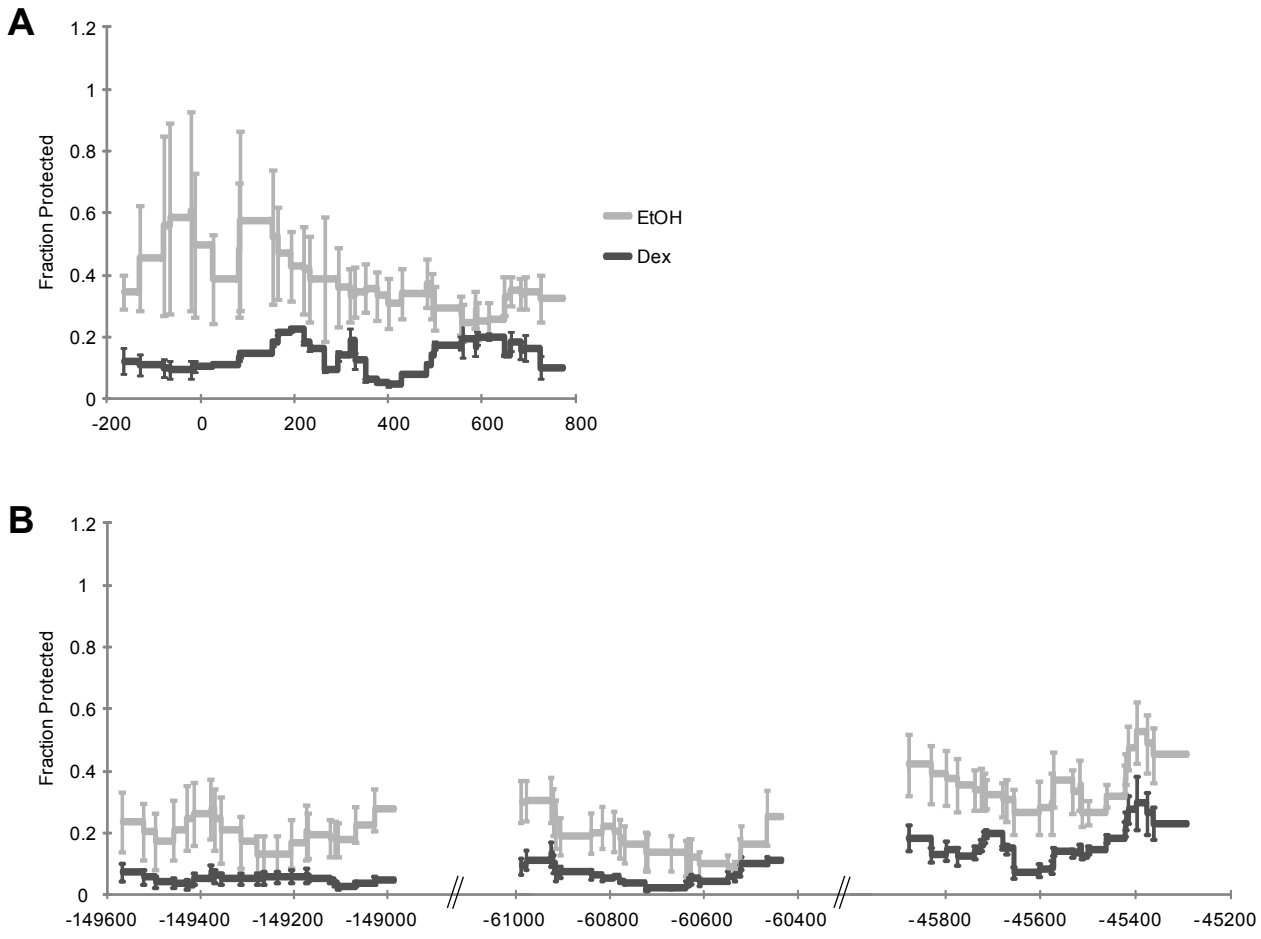

FIG. S7. Chromatin becomes more accessible upon dex treatment at another GR-regulated gene. (A-B) MNase assay showing fraction protected around PDE4B TSS (A) and GBR regions (B). Cells were treated with EtOH or 100 nM dex for 10 min. Data is displayed as fraction of MNase protection by calculating a fold difference between MNase-treated and untreated samples (y-axis), plotted against the location relative to the TSS (x-axis) ± SEM (n = 3).

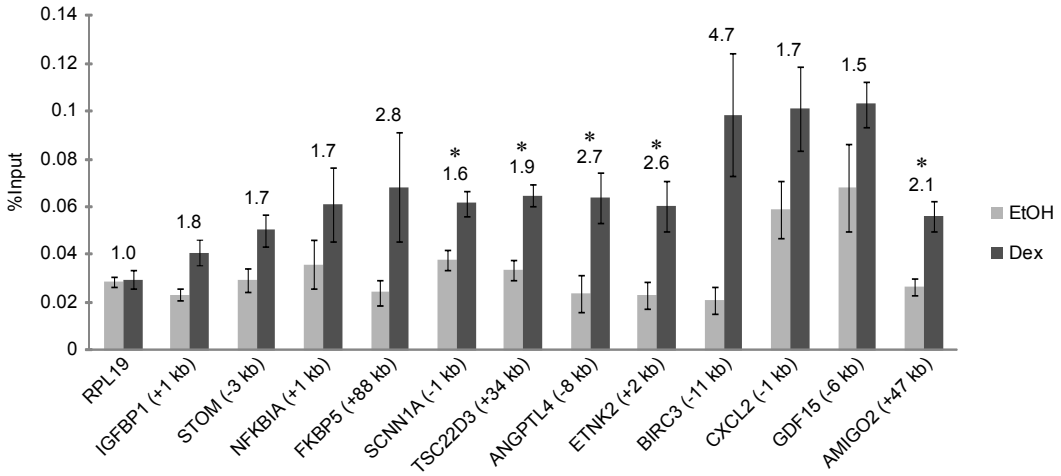

FIG. S8. Brg1 occupies a subset of GBRs in a dex-stimulated manner. Cells were treated with EtOH or 100 nM dex for 2 hours. Data is displayed as enrichment of GBRs near the corresponding gene normalized to input samples ± SEM (n = 3). The location of the GBR relative to the TSS is indicated. Fold change is displayed above the bar graphs. *, $P \leq 0.05$ by Welch's t-test.

Table S1. Primers used for qPCR analysis of cDNA sequences

Gene Symbol:	Gene ID:	Forward Primer:	Reverse Primer:
AMIGO2	347902	catgcccctgcaagtgtaaa	tcaggggttccaaaaacacc
ANGPTL4	51129	tcagcatctgcaaagccagt	tctccccaacctggaacag
BHLHE40	100172646	tgaaggccatttcactagcag	gtagaagggcaggcagaaag
BIRC3	330	gacaggagttcatccgtcaag	ttccacggcagcattaatc
CCL2	6347	gctcatagcagccaccttca	cttggccacaatggtcttga
CXCL1	2919	cagaccctgcagggaattc	tggctatgacttcggtttgg
CXCL2	2920	gcagggaattcacctcaaga	gacaagctttctgcccattc
ETNK2	55224	ctactgcaccttccagaatgg	ccgttggcgtggatagtatg
FKBP5	2289	aggctgcaagactgcagatc	cttgcccattgctttattgg
GDF15	9518	ctcattcaaaagaccgacacc	agtggaaggaccaggactgc
IGFBP1	3484	tcacagcagacagtgtgagac	agacccagggatcctcttc
MT2A	4502	gcaaatgcaaagagtgcaaa	atccaggtttgtggaagtcg
NAV3	89795	ttccaacgtcagcagcaagt	gatttgggggaacctgacaa
NFKBIA	4792	cacctccactccatcctgaag	atcagcacccaaggacacc
PDE4B	5142	tcatgcttttctttattcacctca	gcacaaatgtgcatgaccaa
PTGS2	5743	cgcaaacgctttatgctgaa	ggcttccagtaggcaggaga
RPL19	6143	atcgatcgccacatgtatca	gcgtgcttccttggtcttag
SCNN1A	6337	aacggtctgtccctgatgct	ttggtgcagtcgccataatc
SMARCA2 (Brm)	6595	tttatgcggatggacatgga	tagccactgcttctccgtga
SMARCA4 (Brg1)	6597	aggtccggcagaagaaatca	gtgaggttgggtgggttagg
STOM	2040	cagacactgaccaccattgc	ttcatgcttggaaggctagc
TSC22D3	1831	agatcgaacaggccatggat	ttacaccgcagaaccaccag

Table S2. Primers used for qPCR analysis of ChIP samples

GBR Symbol:	Forward Primer:	Reverse Primer:
AMIGO2 (-5 kb)	ccctgggttttgtttcttca	gaagtagcaatgggactgacg
AMIGO2 (-3 kb)	gggtgtggtcatgtgagtgt	cagggctagaactcctgtga
AMIGO2 (+47 kb)	cacagcctctttcacaacca	ggaaccagtgaggaatggaa
ANGPTL4 (-8 kb)	tctgccctgcaatgtacaag	ccaagagcaggacctcaaac
BHLHE40 (-28 kb)	tctccgtgcagtctctcctc	cgttgggagggacattaataag
BIRC3 (-11 kb)	accccaaatgaatggtgaaa	agggtacgcggagtacagag
CCL2 (-3 kb)	acttctctcacgccagcact	tagctgtctgcctcccactt
CXCL1 (+23 kb)	tcacttcagctatttcccaca	aacaaactgggcctattcaca
CXCL2 (-1 kb)	tagggcaagaactgcagcat	ccaggaaggagacaaaagctc
ETNK2 (+2 kb)	agtgaatgggatttggcagt	aaggggtagagcagagcaca
FKBP5 (+88 kb)	taaccacatcaagcgagctg	gcatggtttaggggttcttg
GDF15 (-6 kb)	tgtgcctcttccaaatctcc	cccaatctcccaaaatctcc
HSP70	tctggagagttctgagcagg	cccttctgagccaatcaccg
IGFBP1 (+1 kb)	ctcatctggactgcttgcac	cagagaatccgcaggaaatc
MT2A (-1 kb)	gacgattcggctgagctaga	agggccttagatcgtcaacc
NAV3 (-88 kb)	tggcactattgggagtccag	gggtcacgtgatgttttaagc
NAV3 (+17 kb)	atgtcttgccacctggattc	acaacaggaagcaccctctg
NFKBIA (+1 kb)	ccatggtcagtgccttttct	gccaggaacactcagctcat
PDE4B (-150 kb)	agggtgtctagtaaacctgcaca	aaggctataacagccacctcttt
PDE4B (-61 kb)	ctgaacagttgagtccgttcc	gcatgattccaactttcaagg
PDE4B (-46 kb)	ggcagaaacatagcctgtgg	gtttgttttggggaatgtgg
PTGS2 (-36 kb)	acacaatgctgtgtatttccat	gaagctggcttcaaagttaatg
PTGS2 (+188 kb)	ttgccaatgtgatccgaata	cccaaatcctttgtctcacc
RPL19	ctttcttgcttggcacacc	gatcacctctctcggcagtc
SCNN1A (-1 kb)	aggccaggaatgtgtaatcg	caccttcagtgcctgctttc
STOM (-3 kb)	gaacaggctccagtgtgtga	agtgactgcacaagctgcac
TSC22D3 (+34 kb)	gtgcctggagaccaactcat	acccttgatgctgagcaagt

Table S3. Primers used for qPCR analysis of MNase samples.

Primer Name:	Forward Primer:	Reverse Primer:
CCL2 #1	gggctctattctacctggagc	ccgtagctctgcactcacc
CCL2 #2	gtgggggttgtctagaaagg	cccacctagtgcaggctc
CCL2 #3	ttgaaggctgagtgaaggg	ggctcccaccaacttctg
CCL2 #4	actaggtggggagggacaag	tctctggaaagatctgaagcc
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CCL2 #7	gcagaggatcttagtggtggg	ggggcctcctctctatcaac
CCL2 #8	ccaagaggagcttttccattc	ctatggggaaaatgagggtc
CCL2 #9	acagcatcagagcattgacc	gggttggactctcgcttg
CCL2 #10	attttccccatagcccctc	gggaacatctcggcacaag
CCL2 #11	ccaggtttgtgccagagc	ctgcattccagatactgggc
CCL2 #12	ccagtatctggaatgcaggc	gaagttcccagatcccgtag
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CCL2 #19	gtgaacactcagccagcaaag	tctgataaagccacaatccag
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CCL2 #29	cagctgtgaaccccaaatc	ggagtaactgcgctgagtgtg
CCL2 #30	aaccccaaatccagctcc	ctgatccccaaactctgctg
CCL2 #31	gcttccagcagagtttggg	agattctgggtctccagcg
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MT2A #34	actctagccgcctcttcagc	atccccagcctcttaccg
MT2A #35	cggtaagaggctggggatg	cagagaaagaaagaggggtcag
MT2A #36	gcaatttctgacccctctttc	aacctagaatggagagaaagatacc
MT2A #37	ggagttgctccttcccaaag	agatctccttaacggtaaaaaggg
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