

Supplementary Figure Legends

Supplementary Figure 1.

Pie charts from the current ChIP-seq experiment and data from ENCODE in A549 cells subjected to GR ChIP-seq demonstrating similar enrichment in several key pathways of interest.

Supplementary Figure 2

Primer-specific qPCR for genes in the angiogenesis, cadherin and inflammation by cytokine/chemokine pathways identified in the top 1,000 peaks of the glucocorticoid receptor (GR) ChIP-seq dataset was performed both in vitro and in vivo. In vitro, RNA from control siRNA- or GR siRNA-treated mouse lung endothelial cells (MLECs) was isolated. (A) In vitro angiogenesis (B) In vitro cadherin (C) In vitro inflammation by cytokine/chemokine. In vivo, double knock-out (DKO) (n=6) or Apo E KO mice (n=3) were fed with high-fat diet for 3 weeks. Whole aortas were dissected for RNA isolation and qPCR. (D) In vivo angiogenesis (E) In vivo cadherin (F) In vivo inflammation by cytokine/chemokine. Data represent 3 separate experiments. Unpaired t test was used for each primer set. *p < 0.05. .

Supplementary Figure 3

Control or glucocorticoid receptor (GR) siRNA MLECs were treated with either Wnt3a 100 ng/ml or Wnt 5a 150 ng/ml for 4 hours and mRNA expression of the

inflammatory genes (A) IL-6 and (B) TNF- α was measured. Data represent 3 separate experiments. Unpaired t test was used for each primer set. *p<0.05.

Supplementary Figure 4

Mouse endothelial cells (MLECs) were treated with (A) LRP5 siRNA (25 nM) alone or with dexamethasone (DEX) 100 nm for 1 hour and qPCR for the expression of axin2 and sox17 was performed. (B) Cells were treated with LRP6 siRNA (25 nM) alone or with dexamethasone (DEX) 100 nm for 1 hour and qPCR for the expression of axin2 and sox17 was performed. Unpaired t test was used for each primer set. N=3 separate experiments. *p<0.05.

Supplementary Figure 5

Genomic DNA sequence of the mouse *frzb* gene. Exons are highlighted in red and the motif is highlighted in yellow in intron 5.

Supplementary Figure 6

(A) Mouse endothelial cells (MLECs) were treated with either control or CTCF siRNA (25 nM). Effective down regulation of CTCF mRNA expression is shown.

(B) qPCR for *frzb* in CTCF knockdown cells shows significantly reduced expression compared to that in control cells. Expression of axin 2 mRNA (C) and sox 17 mRNA (D) in control and GR siRNA treated endothelial cells that were either unstimulated or treated with Sfrp3 200 ng/ml for 4 hours is shown. Data represent 3 separate experiments. Unpaired t test was used for each primer set

in (A) and (B); one way ANOVA with Tukey's post-test was used to analyze data in (C) and (D). *p<0.05.

Supplementary Figure 7

Luciferase constructs for (A) known GRE and (B) experimental motif.

Supplementary Figure 8

Plasma (A) cholesterol and (B) triglyceride measurements in *Apoe* -/- and double knock-out (DKO) mice fed a high-fat diet for 12-weeks. Unpaired t test was used for analysis. N=6/group.

Supplementary Table 1

List of genes that resulted when the top 1000 peaks were queried using the classic glucocorticoid response element (GRE) as a seed sequence.

Supplementary Table 2

List of genes that resulted when the top 1000 peaks were queried for any *de novo* motifs.

Supplementary Table 3

List of genes that resulted that resulted when the top 1000 peaks were queried for both the classic glucocorticoid response element (GRE) and *de novo* motifs.

Supplementary Table 4

Identity of the top 10 most enriched ENCODE transcription factors within \pm 500 base pairs of the transcriptional start site (TSS)/5' end for 65 genes possessing both a glucocorticoid response element (GRE) and novel motif

Supplementary Table 5

Genes identified from the top 1000 peaks with binding sites within \pm 1kb from the transcriptional start site (TSS).

Supplementary Table 6

Identity of the top 10 enriched ENCODE transcription factors within \pm 500 base pairs of the transcriptional start site (TSS)/5' end for 29 genes with peak binding sites within \pm 1kb from the TSS.

Supplementary Table 7

Genes identified from RNA-seq as significantly down regulated in the absence of the glucocorticoid receptor (GR).

Supplementary Table 8

Genes identified from RNA-seq as significantly up regulated in the absence of the glucocorticoid receptor (GR).

Supplementary Table 9

Genes in the Wnt signaling pathway with peaks in close proximity to the transcriptional start site (TSS).



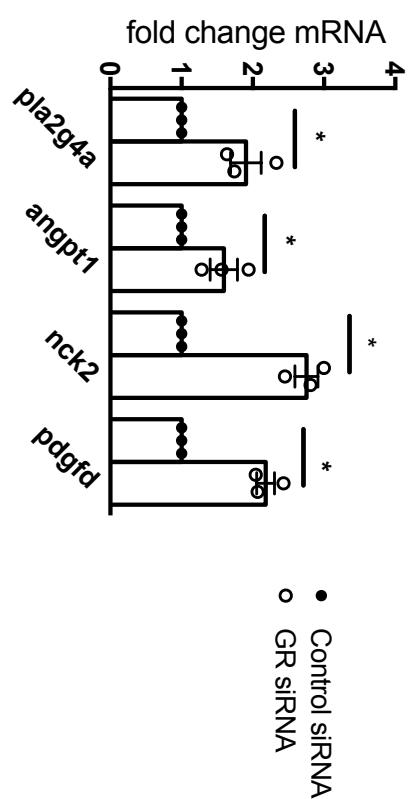
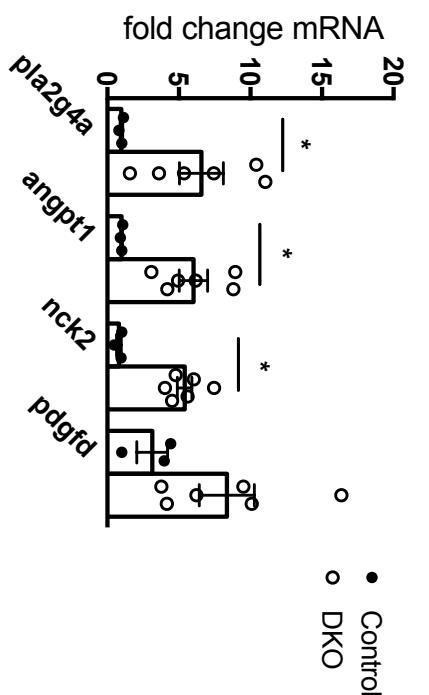
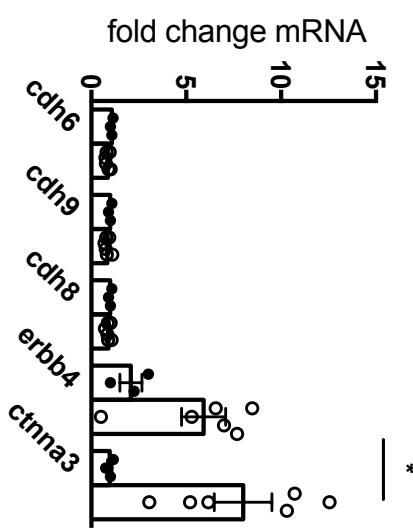
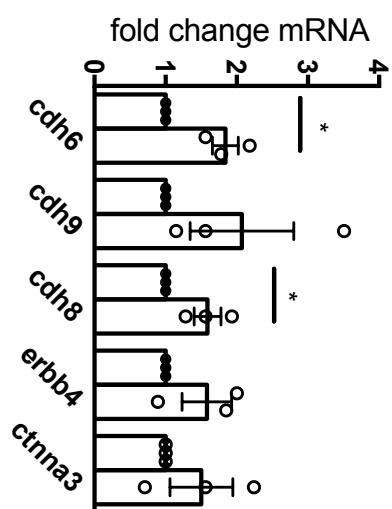
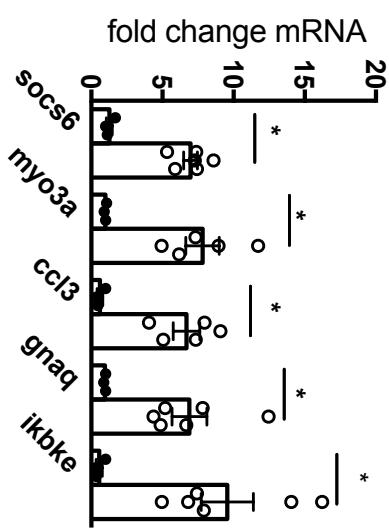
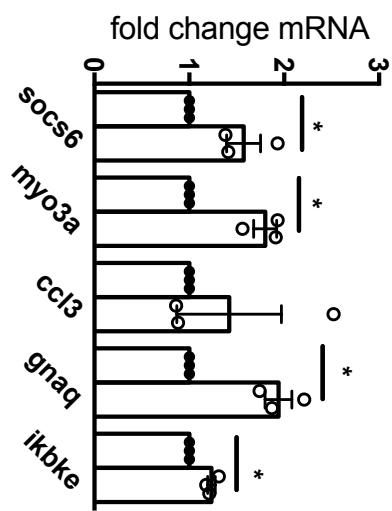
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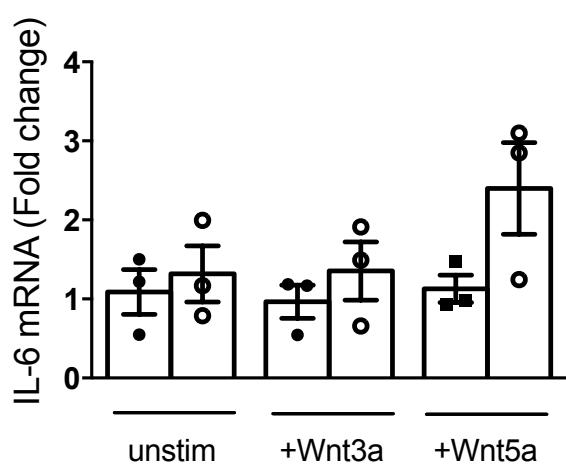
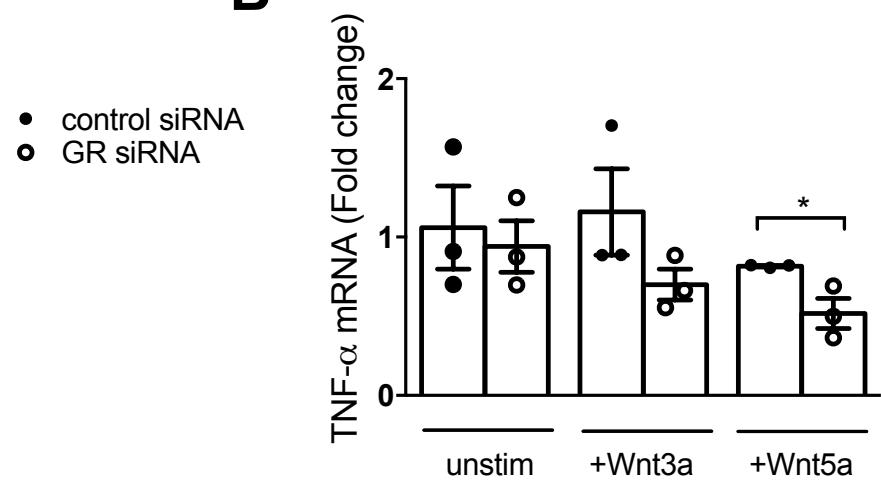


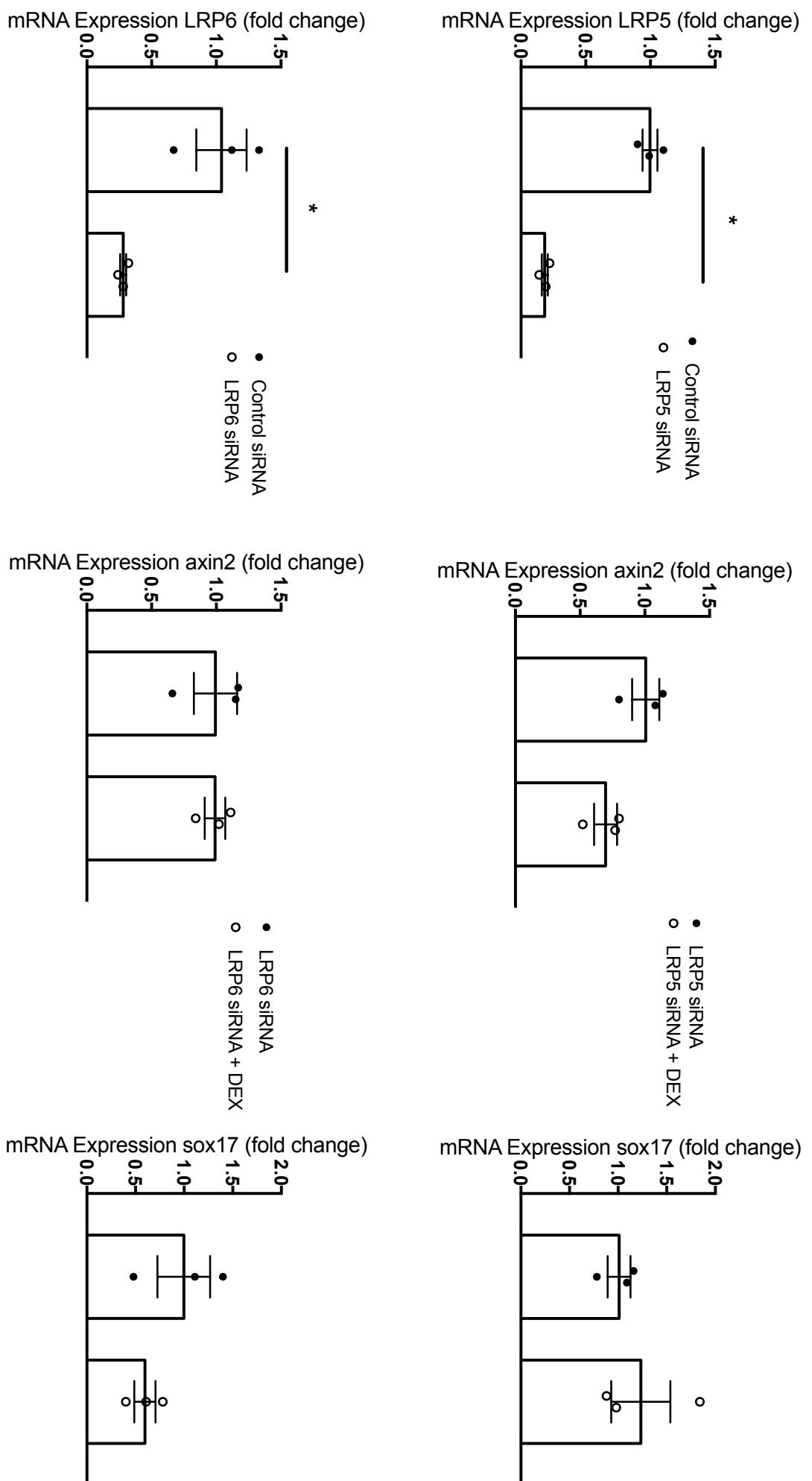
A549

Total Genes:	708	1626
Pathway Hits	279	633

1. Wnt signaling
2. Inflammation by chemokine/cytokine
3. Cadherin signaling
4. Angiogenesis

A**D****E****B****F****C**

A**B**

A**B**

Supplementary Figure 3

FRZB genomic DNA with exons highlighted in RED and the detected motif in YELLOW

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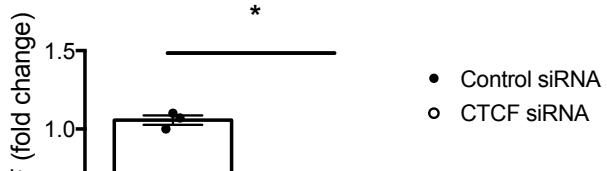
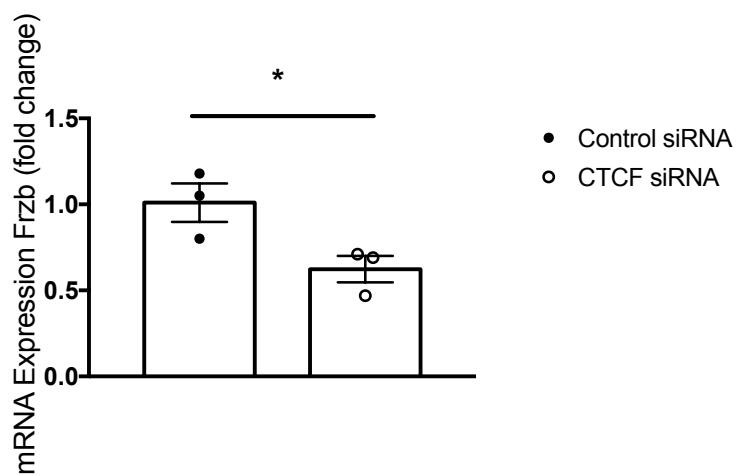
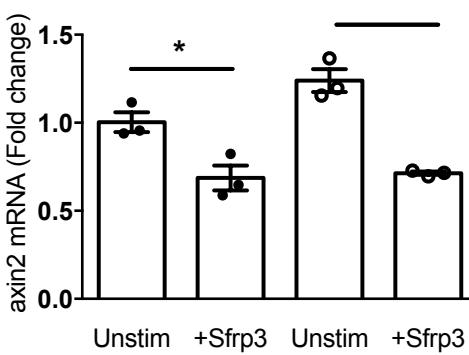
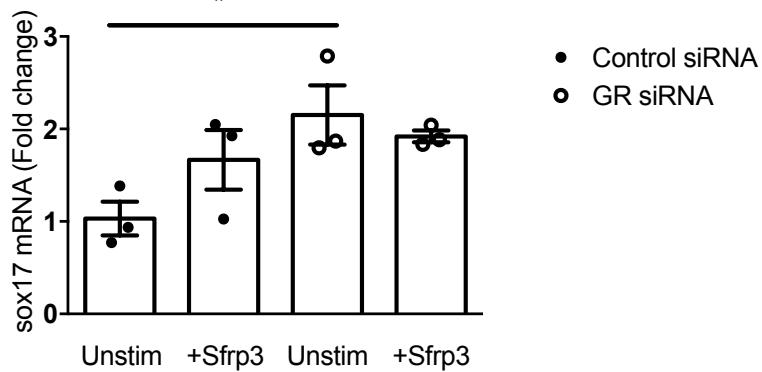
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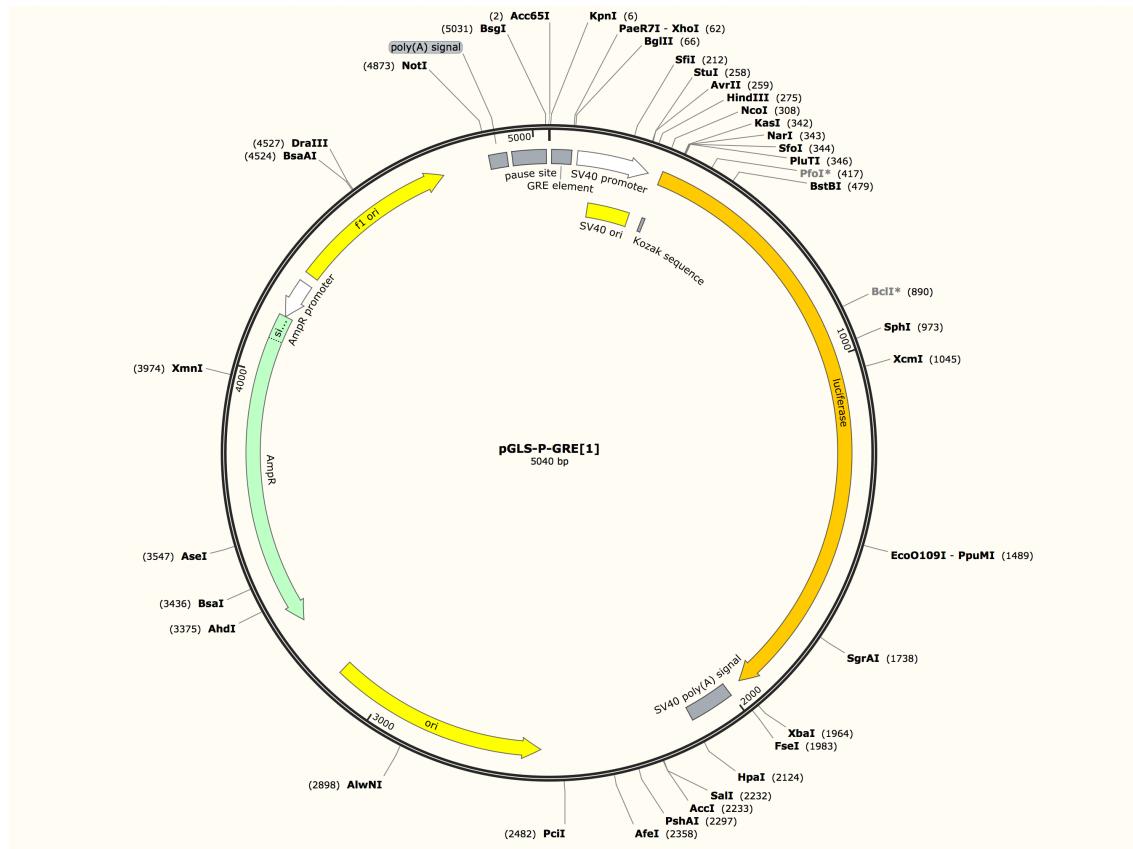
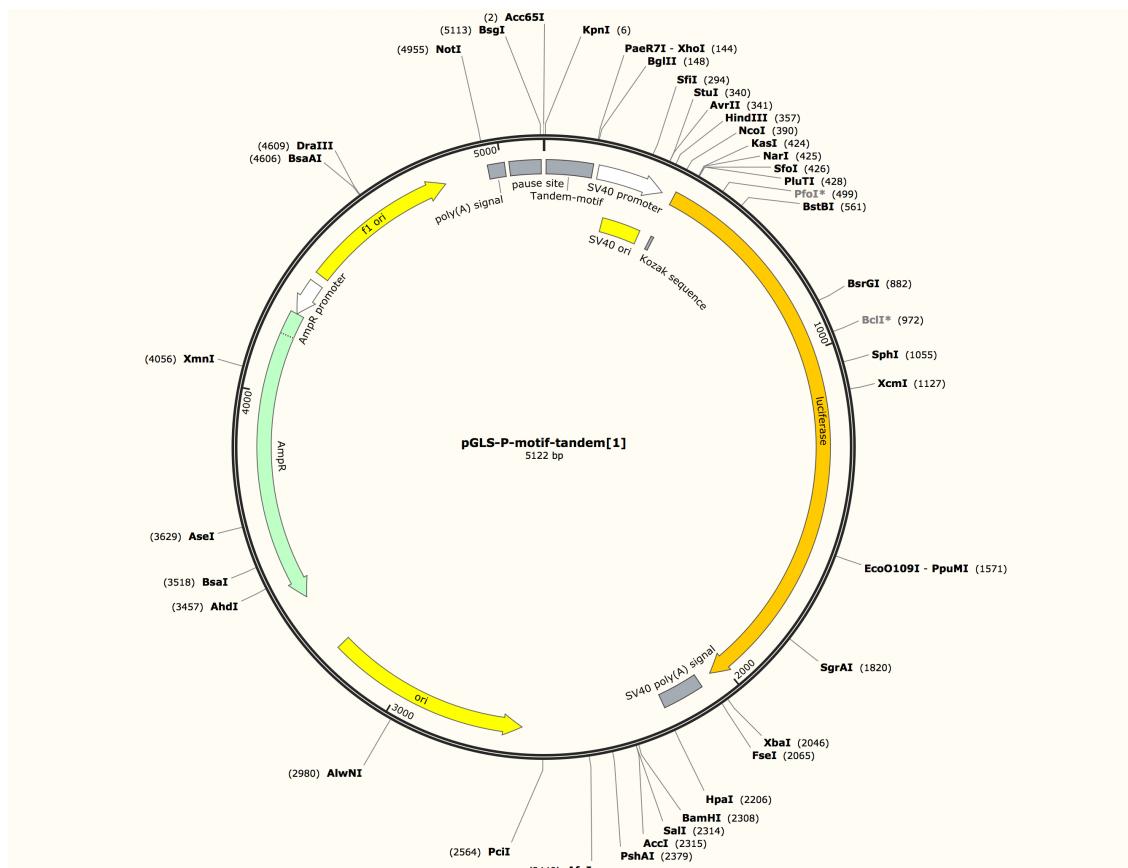
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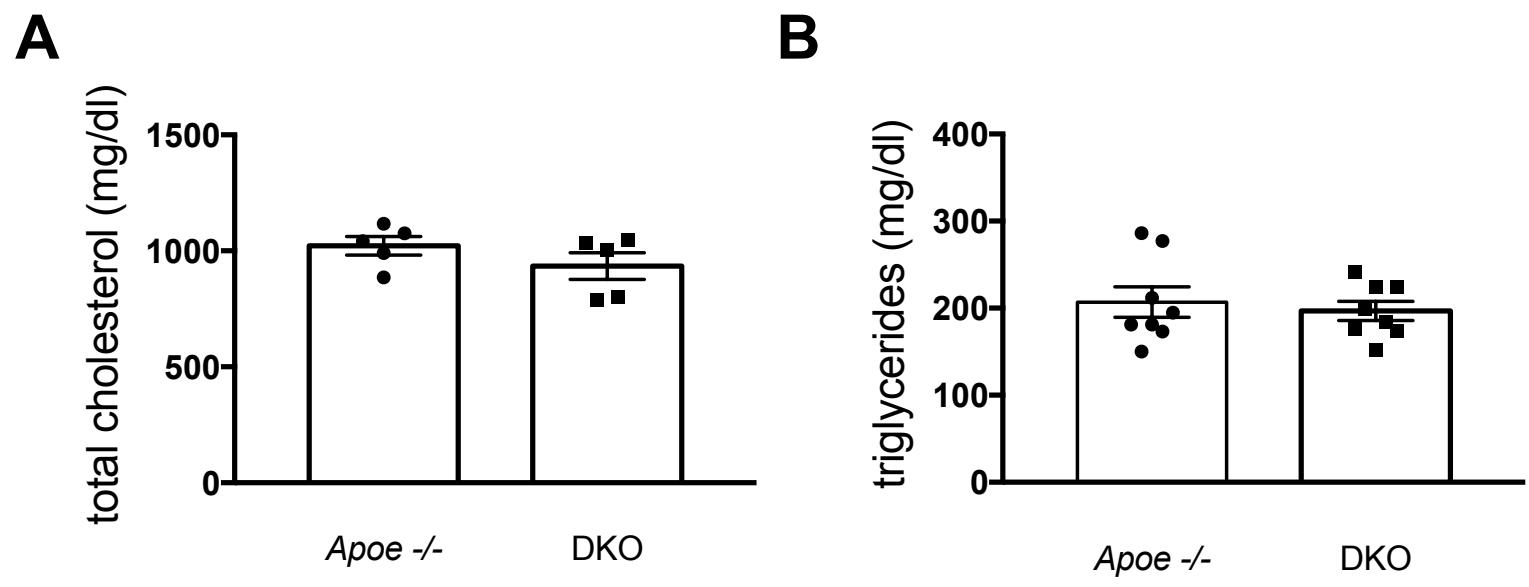
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cagcacagcagcaaaacagtcgtgtgcacggtaatgatgatcatgcatttcatttcatttcatttcatt
catggatccatgatgttagtgcatttcatttcatttcatttcatttcatttcatttcatt
ggtagggacaatccctgttccatctgttgcatttcatttcatttcatttcatttcatt
gctctgcattactgcctctgcatttcatttcatttcatttcatttcatttcatt
ggtttatgttagtgcatttcatttcatttcatttcatttcatttcatttcatt
cagacttttagtgcatttcatttcatttcatttcatttcatttcatt
gtacgcatacttcatttcatttcatttcatttcatttcatttcatt
tgtagttgcatttcatttcatttcatttcatttcatttcatttcatt

A**B****C****D**

A**B**



Supplementary Table 1: Genes from the top 1000 peaks with a classic GRE

NEGR1-IT1	MYEOV	DDR2	GRM5	CHEK2P2
EMBP1	PARP11	CSF3R	CNTN5	CHEK2P2
RASAL2	CTDSP2	ANK3	PCF11	KIAA1024
SLC25A33	LINC00374	LOC100499489	USP47	SNORD115-31
LOC100499489	RPL23AP87	ACTR3BP5	LOC105369423	FLJ26245
LOC646813	ZNF507	LINC00839	EMSY	ANKRD26P1
WNT11	NKPD1	SLC16A9	TRIM48	LOC102723692
OR10W1	KLF9	NEUROG3	LOC646813	KCNJ2
CHRNA10	LINC01474	SGMS1	LOC105369443	POLG2
OR4C46	LHX8	TMEM72	HOXC13	SNORA111
MPEG1	ANKRD20A12P	MIR4490	SLC2A3	C19orf33
OR5AN1	EMBP1	TYR	LMO3	TNFSF14
KDM4E	ROR1-AS1	DNHD1	MIR3169	KCNJ3
MARK2	MEF2D	LOC100996455	LOC101927780	PTPN4
LOC102724784	FAM69A	DEPDC7	GPHN	MYLK-AS2
PPIC	KIFC1	LZTS1-AS1	NUTM2G	SPANXN2
ARHGAP26-IT1	MEI4	RALYL	MIR651	BRDTP1
RFPL4B	AGK	CDCA2	ARX	DANT2

Supplementary Table 2: Genes from the top 1000 peaks with a de novo motif

MIR4459	LHX8	TMEM72	HOXC13	SNORA11	NUTM2G
OR4C46	ANKRD20A12P	MIR4490	SLC2A3	C19orf33	MIR651
FAM66C	EMBP1	TYR	LMO3	TNFSF14	ARX
GLI1	ROR1-AS1	DNHD1	MIR3169	KCNJ3	SPANXN2
MON2	MEF2D	LOC100996455	LOC101927780	PTPN4	BRDTP1
MTHFS	FAM69A	DEPDC7	GPHN	MYLK-AS2	DANT2
CYFIP1	DDR2	GRM5	CHEK2P2	PPIC	
B4GALT4	CSF3R	CNTN5	CHEK2P2	ARHGAP26-IT1	
PAPSS1	ANK3	PCF11	KIAA1024	RFPL4B	
ZNF608	LOC100499489	USP47	SNORD115-31	KIFC1	
TBX18	ACTR3BP5	LOC105369423	FLJ26245	MEI4	
LOC105373156	LINC00839	EMSY	ANKRD26P1	AGK	
PLXDC2	SLC16A9	TRIM48	LOC102723692	LZTS1-AS1	
OR51L1	NEUROG3	LOC646813	KCNJ2	RALYL	
OR4A16	SGMS1	LOC105369443	POLG2	CDCA2	

Supplementary Table 3: Genes possessing both a GRE and a de novo motif

LHX8	TMEM72	HOXC13	C19orf33	MIR651
ANKRD20A12P	MIR4490	SLC2A3	TNFSF14	ARX
EMBP1	TYR	LMO3	KCNJ3	SPANXN2
ROR1-AS1	DNHD1	MIR3169	PTPN4	BRDTP1
MEF2D	LOC100996455	LOC101927780	MYLK-AS2	DANT2
FAM69A	DEPDC7	GPHN	PPIC	
DDR2	GRM5	CHEK2P2	ARHGAP26-IT1	
CSF3R	CNTN5	KIAA1024	RFPL4B	
ANK3	PCF11	SNORD115-31	KIFC1	
LOC100499489	USP47	FLJ26245	MEI4	
ACTR3BP5	LOC105369423	ANKRD26P1	AGK	
LINC00839	EMSY	LOC102723692	LZTS1-AS1	
SLC16A9	TRIM48	KCNJ2	RALYL	
NEUROG3	LOC646813	POLG2	CDCA2	
SGMS1	LOC105369443	SNORA111	NUTM2G	

Supplementary Table 4. Top 10 most enriched transcription factors within \pm 500 base pairs of the TSS/5' end for 65 genes possessing both motifs.

Transcription Factor	# genes with factor	# genes observed	Q value
CTCF	9919	49	1.79e-17
p300	6918	36	1.17e-11
Pol2	19191	54	2.844e-9
TBP	10622	38	1.056e-7
HCFC1	11217	39	1.067e-7
Mxi1	9375	35	1.88e-7
NELF ϵ	10103	35	1.274e-6
UBF	5258	24	1.764e-6
GCN5	7291	28	4.654e-6
SIN3A	9393	32	7.317e-6

Supplementary Table 5: Genes identified from the top 1000 peaks with binding sites within \pm 1kb from the TSS.

Hnrnpu	Mir132
Sfpq	Srsf2
Ifi27l2a	Ralgps2
Ccm2	Oifr1434
Umps	Fzd5
Awat2	AA465934
Ywhae	Taar5
Pik3r6	Fbxl20
Mab21l2	Rasl10a
Afmid	Fbxo5
Smyd3	Ifi47
Myog	Eef1b2
Gm11981	Mir6950
Shroom1	Elk4
Ahr	

Supplementary Table 6. Top most enriched transcription factors within \pm 500 base pairs of the TSS/5' end with ChIP peak binding with \pm 1 kb from the TSS

Transcription Factor	# genes with Factor	# genes observed	Q value
CTCF	6944	22	4.457e-12
p300	5053	16	7.817e-8
Pol2	16854	25	1.758e-7
NELF ϵ	10103	20	5.777e-7
E2F4	2303	10	2.068e-6
ZNF	6652	16	2.068e-6
COREST	3857	11	3.509e-5
HCFC1	10255	17	1.108e-4
c-Myc	5228	17	1.108e-4
BHLHE40	6205	13	1.199e-4

Supplementary Table 7: Genes down-regulated in the absence of GR

Chuk	Fkbp5	Lyve1	Per1	Tcn2	Bean1	Ankrd1
Mgat4a	Fry	Map3k6	Pi15	Tgoln1	Cdc42ep4	Galnt3
Rcan1	Glipr2	Masp1	Plat	Thrsp	Cntn1	Hhipl1
Ap1s1	Gm12505	Mctp2	Pomp	Tmem252	Man2a1	Igfbp3
Arl4a	Gpihbp1	Mpp3	Prkacb	Tmem260	Pcdh20	Klk8
Atoh8	Gpr182	Mum1l1	Pttg1ip	Trp53i11	Rhou	Pdlm1
Cebpb	H19	Mxd1	Rab15	Trp53inp1	Shroom2	Rn45s
Clca1	Hif3a	Mxd4	Rcan2	Tsc22d3	Atp6v0c	Asph
Cnot6	Ifit1	N4bp2l1	Rgcc	Ttyh1	Clec14a	Jazf1
Crispld1	Igfbp5	Ndufc2	Rpn2	Ucp2	Gpx3	
Ctla2b	Inhbb	Nr3c1	Rsad2	Wdr92	Hspe1	
Ctnnbip1	Itgb3	Olfr1033	Sema3a	Wipf1	Tmem30a	
Ednrb	Kat2b	Ormdl3	Sema7a	Wnt9b	Tmx3	
Fabp5	Kbtbd11	Osbp2	Sepp1	Zbtb16	Ndufs5	
Fam63b	Kit	Ostm1	Serinc3	Zhx1	Ctla2a	
Fgfr3	Lcn2	Pak3	Slc40a1	Ace	Kctd12b	
Fkbp14	Lrg1	Pde4c	Spsb1	Alg10b	Amigo2	

Supplementary Table 8: Genes upregulated in the absence of GR

Col5a3	Ddc	Lpl	Tfcp2l1	Atxn1	Elovl4
Fbn1	Deptor	Ltbp1	Tgfb2	Fbxl5	Fam20a
Fgd3	Dram1	Ndrg4	Tgfb3	Jarid2	Htra3
Nppc	Ehd3	Nov	Thbs2	Mmp2	Msi2
Abca1	Emilin2	Nrp1	Tmem132a	Piezo2	Nuak1
Afap1l2	Ephx1	Pde1b	Tmem37	Prodh	Ptp4a3
Angptl4	Fam189a2	S100a4	Tpbg	Arl4c	Pvrl1
Anxa6	Fam213a	Scd1	Txnrd3	Megf6	
Aplnr	Flrt3	Sema3d	Vegfc	Ank2	
Btg1	Gad2	Serpinb9b	Cst6	Cyp1b1	
Ccdc80	Gap43	Sertad4	Dnm3	Htra1	
Ckb	Gfra1	Slc12a8	Eln	Pcolce2	
Col5a1	Gja4	Slc6a6	Eltd1	Sdc1	
Col8a1	Itga4	Smpdl3b	Gpr176	Slc14a1	
Cxcl12	Itga7	Sprr2b	Kcnn4	Tmem40	
Cyp51	Itih5	St14	Tbxa2r	Armcx4	
Dcn	L1cam	Sybu	Atp6v0c-ps2	Cd24a	

Supplementary Table 9. Genes in the Wnt signaling pathway with GR binding sites within 5 kB of TSS (upper panel) and GR binding sites between 5-10 kb from TSS (lower panel)

Gene symbol	Gene name
Tbl1xr1	F-box-like/WD repeat-containing protein TLB1XR1
Lrp5	Low-density lipoprotein receptor-related protein 5
Ppp2r5a	Serine/threonine-protein phosphatase 2A
Arid1a	AT-rich interactive domain containing protein 1A
Mycl	Protein L-myc
Tcf7l2	Transcription factor 7-like 2
Smad5	Mothers against decapentaplegic homolog 5
Dact1	Dapper homolog 1
Csnk1e	Casein kinase I isoform epsilon
Plcg2	Phospholipase C, gamma 2
Gng2	Guanine nucleotide protein subunit gamma 2
Nkd2	Protein naked cuticle homolog 2
Adssl1	Adenylosuccinate synthetase isozyme 1
Ugdh	UDP-glucose 6-dehydrogenase
Hdac3	Histone deacetylase 3
Wnt5b	Protein Wnt 5b