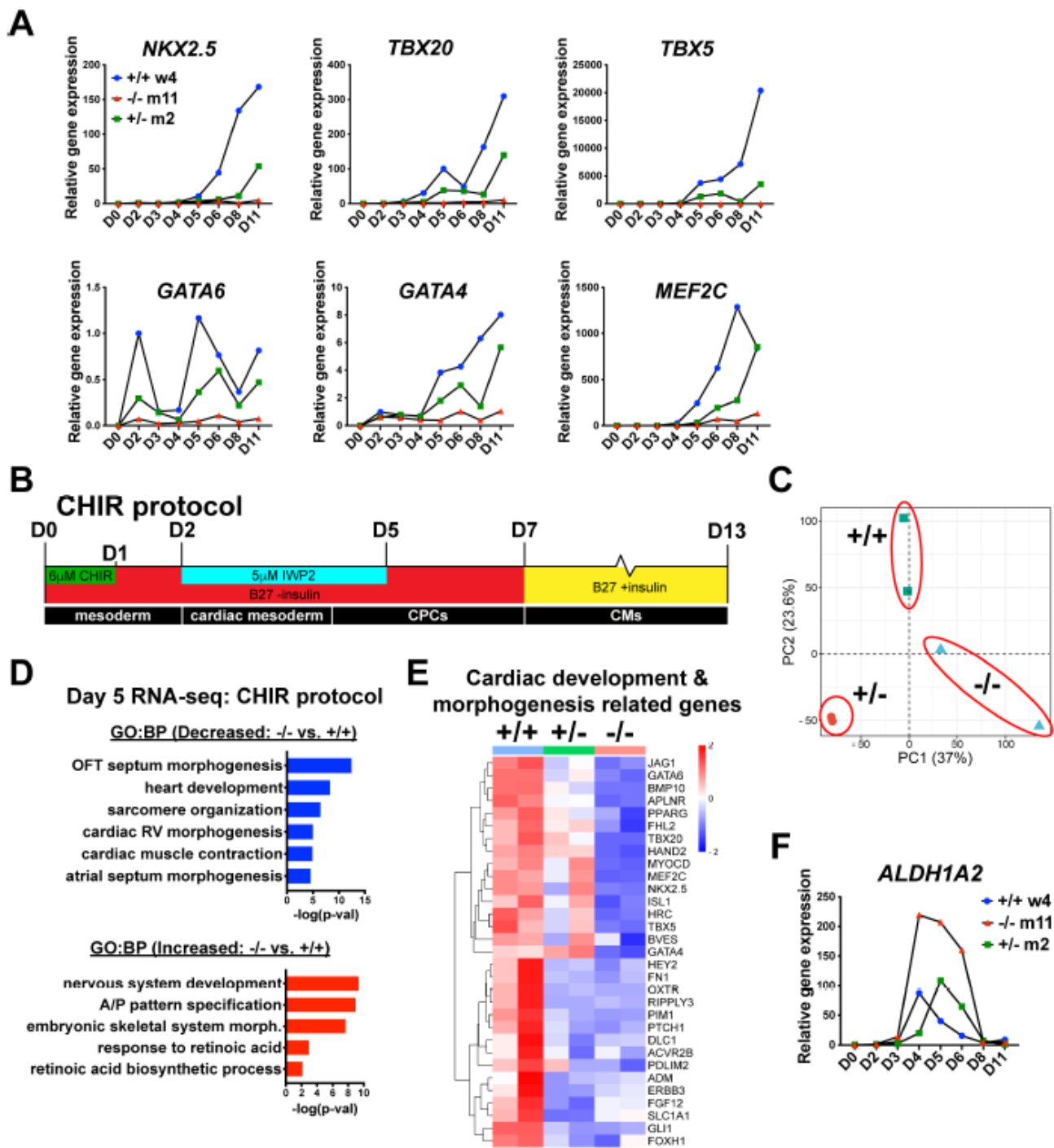
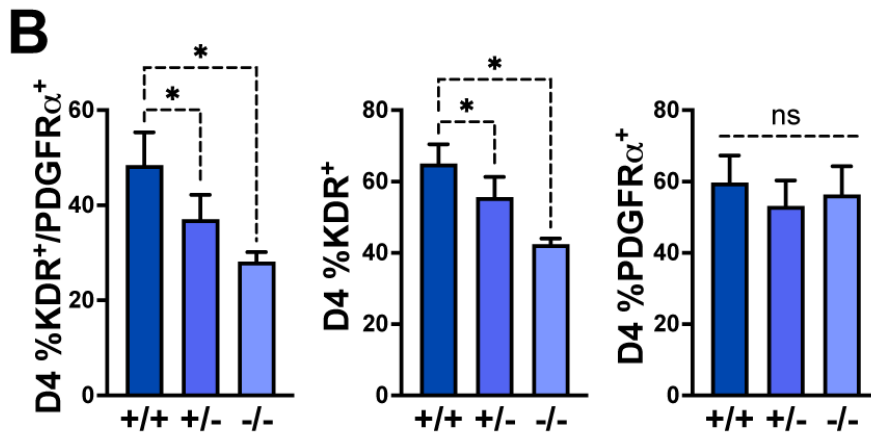
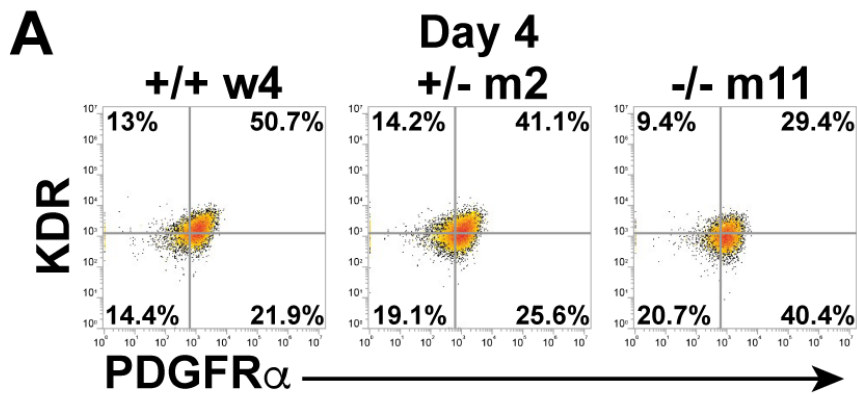


Supplemental Figure 1: CRISPR gene editing and characterization of mutant GATA6 hESC and iPSC lines. (A) GATA6 CRISPR targeting scheme using H1 iCas9 hESCs was described in Shi et al. (Ref. 20). Two CRISPR gRNAs were used targeting the C-terminal zinc finger domain (GATA6-Cr1 and Cr2 gRNA target sequence in green, red indicates the PAM). (B) Table describing H1-GATA6-hESC clonal lines, genotype designation, and gRNA used in gene editing. Predicted protein describes mutant alleles according to the Human Genome Variation Society (HGVS) guidelines, fs indicates frameshift mutation. (C) Western blots from GATA6^{+/+}, GATA6^{+/-}, and GATA6^{-/-} protein lysates at day 2 or 5 of cardiac differentiation probed for GATA6 with β-actin used as a loading control. (D) Immunofluorescence for the sarcomere marker α-Actinin and co-stained with DAPI on day 23 lactate-purified CMs. (E) Schematic for CRISPR-based correction of the GATA6 c.1071delG iPSC mutant allele to WT sequence (GATA6^{corr/+}). A pair of gRNAs flanking the G deletion site were used for targeting with Nickase-Cas9 and a WT repair template to allow for homology directed repair (HDR) of the mutant allele. A single base substitution of G to A (indicated by brown) was used in the WT repair template to induce a silent mutation in the gRNA 2 recognition sequence to prevent additional Cas9 activity after HDR. (F) Table describing the GATA6 iPSC clonal lines. The GATA6 c.1071delG mutant allele is indicated as the protein V358Cfs (according to HGVS guidelines). (G) Immunofluorescence for the pluripotency markers NANOG or SOX2 on

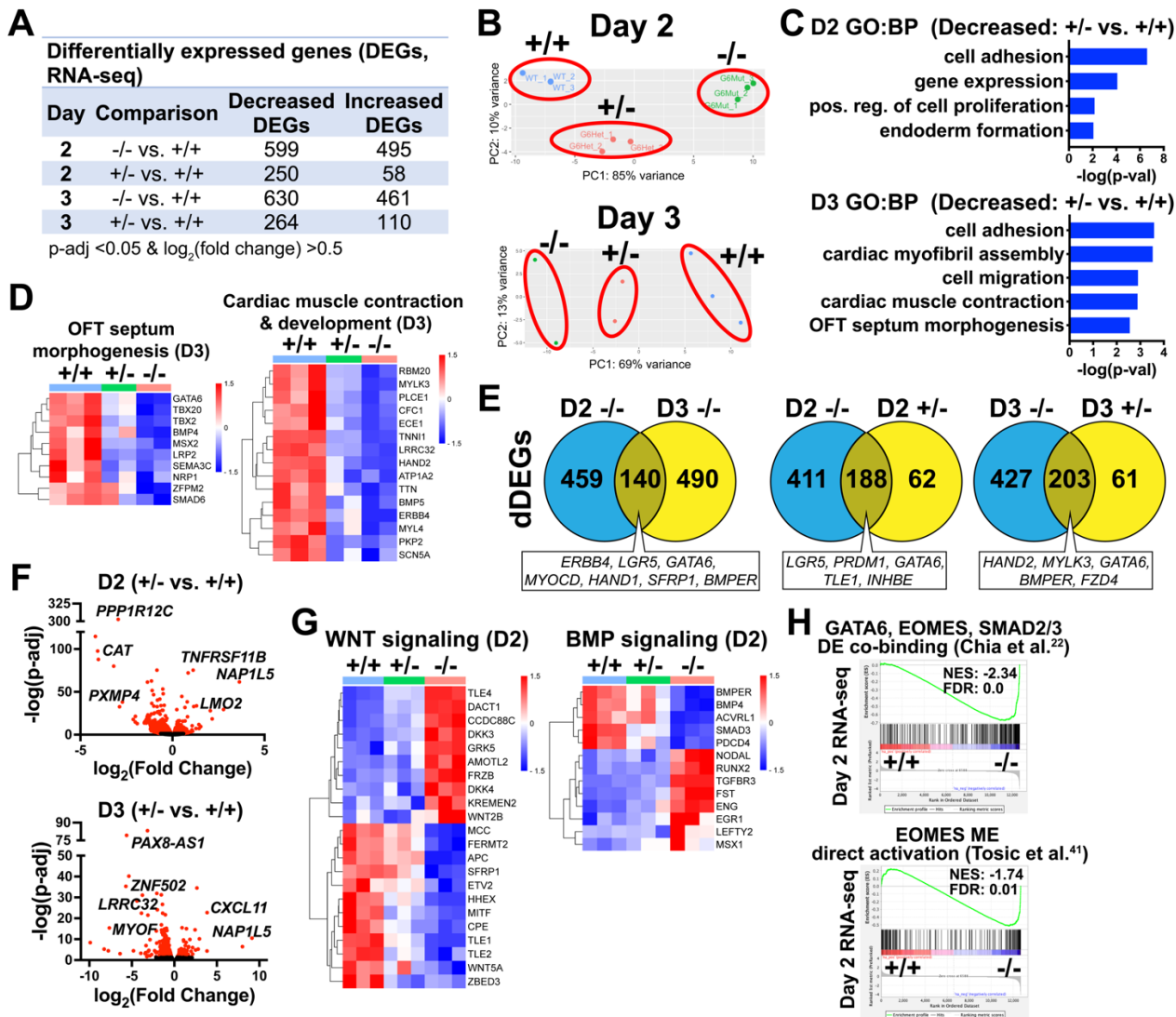
GATA6^{corr/+} or *GATA6*^{1071delG/+} iPSC colonies. **(H)** Flow cytometry quantification for %cTnT⁺ CMs following cardiac directed differentiation for days 13 to 16 of *GATA6*^{corr/+} or *GATA6*^{1071delG/+} iPSCs. Data represents the mean ± SEM, dots represent independent biological replicates. Significance defined as **p<0.01 using the two-tailed Student's T-test. **(I)** Immunofluorescence for cTnT and co-stained with DAPI on day 23 lactate-purified iPSC-CMs. **(J)** Representative karyogram for *GATA6*^{corr/+} iPSCs. **(K)** Western blots from *GATA6*^{corr/+} or *GATA6*^{1071delG/+} protein lysates at day 5 of cardiac differentiation probed for GATA6 with β-actin used as a loading control.



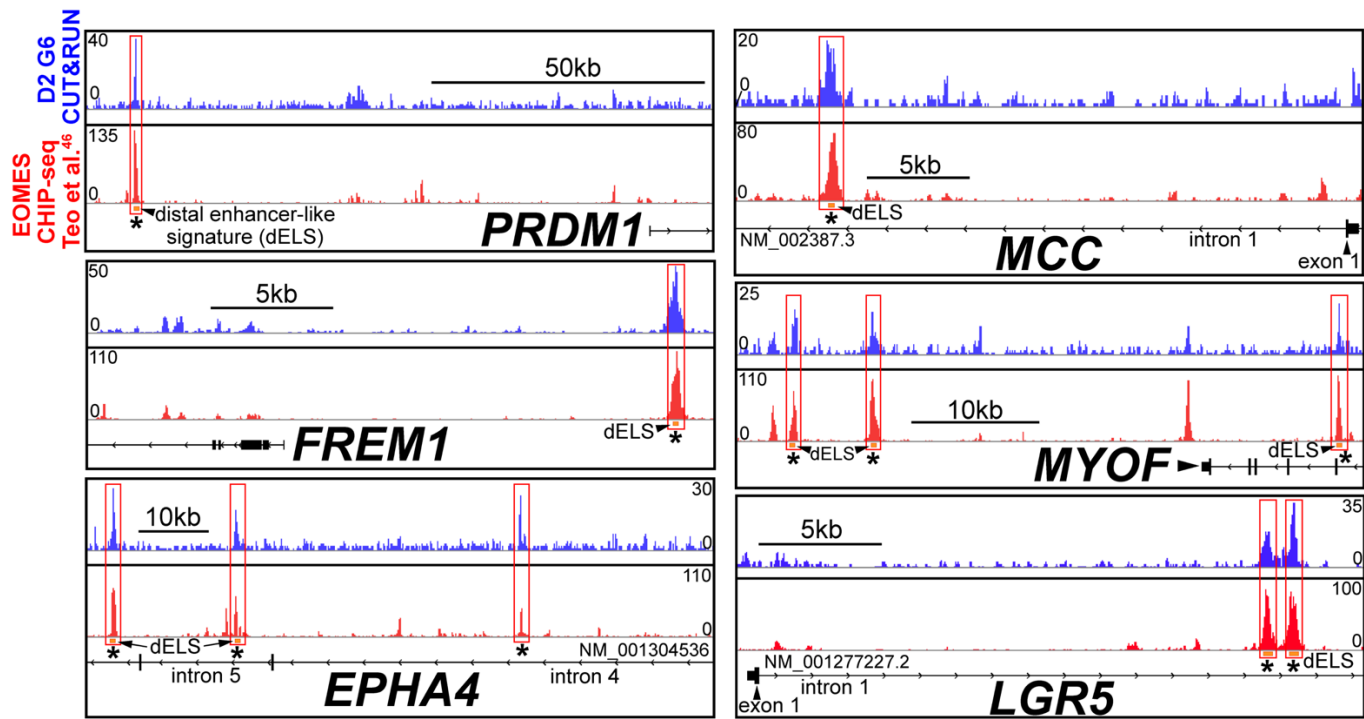
Supplemental Figure 2: CPC marker gene transcriptional analysis of GATA6 WT or mutant hESCs. (A) RT-qPCR time course for CPC markers (and GATA6) in differentiating $GATA6^{+/+}$, $GATA6^{+/-}$, and $GATA6^{-/-}$ hESCs (normalized to day 2 WT gene expression levels). **(B)** Schematic for *in vitro* CM directed differentiation CHIR protocol. **(C)** Principal component analysis (PCA) for comparisons of day 5 bulk RNA-seq from $GATA6^{+/+}$, $GATA6^{+/-}$, and $GATA6^{-/-}$ hESCs using the CHIR protocol (n=2). **(D)** Gene ontology (GO) analysis for biological process (BP) using differentially expressed genes (DEGs) from day 5 RNA-seq comparing $GATA6^{-/-}$ to WT. **(E)** Heatmap for cardiac development related genes from day 5 RNA-seq. Color gradient indicates relative gene expression level. **(F)** RT-qPCR time course for *ALDH1A2* transcript levels in differentiating $GATA6^{+/+}$, $GATA6^{+/-}$, and $GATA6^{-/-}$ hESCs using the cytokine-based protocol.



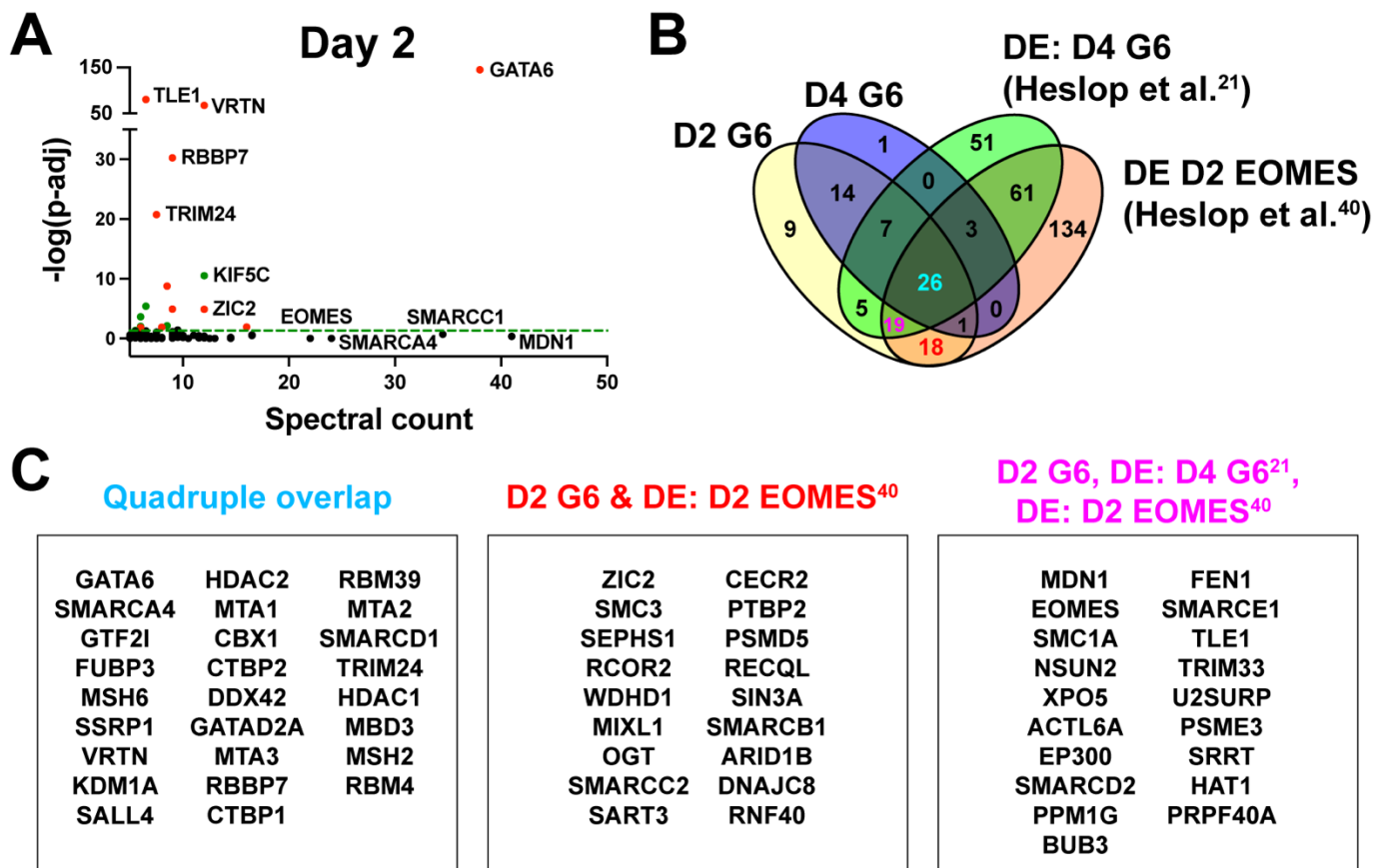
Supplemental Figure 3: KDR and PDGFR α cardiac mesoderm analysis at day 4. (A) Representative flow cytometry plots at day 4 of cardiac differentiation analyzing the % KDR and PDGFR α double-positive cells (%K⁺P⁺) from GATA6^{+/+}, GATA6^{+/-}, or GATA6^{-/-} hESCs. (B) Quantification of day 4 flow cytometry data for %K⁺P⁺ double-positive, %KDR⁺ single positive, or %PDGFR α ⁺ single positive cells (n=6). Data represent the mean \pm SEM, with statistical significance indicated as *p<0.05 and ns indicating not significant by one-way repeated measures ANOVA with Holm-Šidák's multiple comparison test.



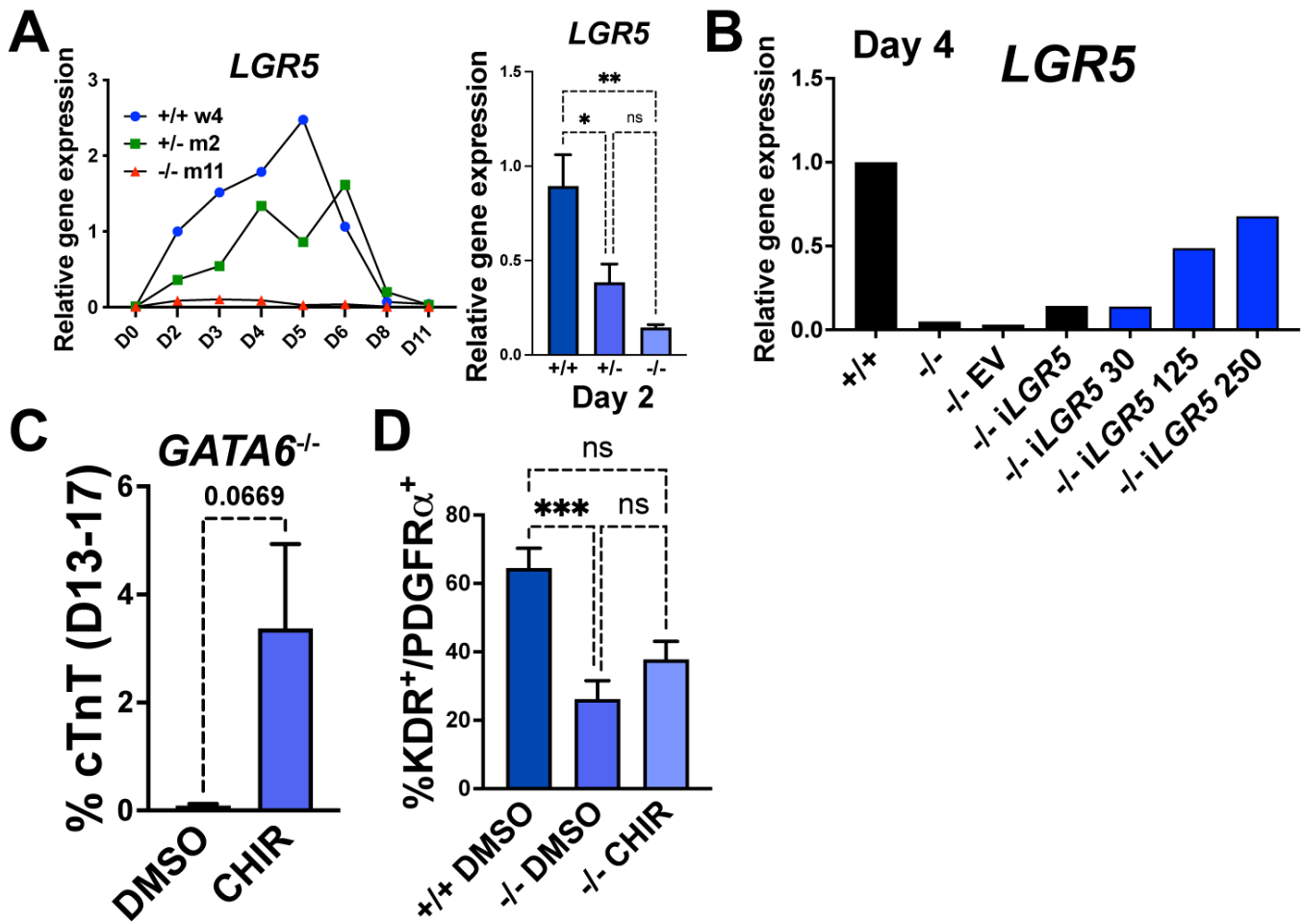
Supplemental Figure 4: RNA-seq analysis following cardiac differentiation at day 2 or day 3. (A) Number of DEGs identified when comparing GATA6^{+/+} and GATA6^{-/-} samples to GATA6^{+/+} controls from day 2 and 3 RNA-seq data. **(B)** PCA analysis for GATA6^{+/+}, GATA6^{+/-}, and GATA6^{-/-} profiles from day 2 or day 3 RNA-seq. Data is representative of at least 2 independent biological replicates per sample. **(C)** Day 2 and 3 GO (BP) analysis using dDEGs identified comparing GATA6^{+/+} to WT samples. **(D)** Heatmaps for OFT septum morphogenesis and cardiac development related genes from day 3 RNA-seq. Color gradient indicates relative gene expression levels. **(E)** Venn diagram comparisons of dDEGs (relative to WT) identified by day 2 or day 3 RNA-seq of GATA6^{+/+} and GATA6^{-/-} samples. **(F)** Volcano plots for day 2 or 3 GATA6^{+/+} sample RNA-seq gene expression data relative to WT. Dots represent genes, red indicates p-adj < 0.05 and black indicates p-adj > 0.05. **(G)** Heatmaps for WNT and BMP related genes from day 2 RNA-seq. **(H)** Gene set enrichment analysis (GSEA) analysis of day 2 RNA-seq gene expression data (GATA6^{-/-} relative to WT) using the GATA6, EOMES, and SMAD2/3 co-binding during hESC-DE differentiation dataset from Chia et al. (Ref. 22) and EOMES ME direct activation dataset from Tosic et al. (Ref. 41). NES indicates normalized enrichment score; FDR indicates false discovery rate.



Supplemental Figure 5: GATA6 CUT&RUN peaks overlap with previously published EOMES CHIP-seq peaks. Human genome browser representations of GATA6 CUT&RUN data at day 2 of cardiac differentiation (blue tracks) and EOMES CHIP-seq identified genes at day 2 of hESC-DE differentiation from Teo et al. (Ref. 46) (red tracks). Orange rectangles represent approximate location for distal enhancer-like signatures (dELS) via the ENCODE Project (indicated by black arrows). Asterisks indicate significant GATA6 binding peaks ($p < 0.003$ relative to IgG controls) and significant EOMES binding peaks as defined by Teo et al. (Ref. 46).



Supplemental Figure 6: Extended GATA6-RIME analysis. (A) Graph depicts GATA6-RIME enriched proteins (spectral count) identified at day 2 of cardiac differentiation and their corresponding day 2 RNA-seq gene expression level significance (p-adj, *GATA6*^{-/-} relative to WT). Dots indicate genes, black indicates p-adj>0.05, red indicates decreased expression level (p-adj<0.05), green indicates increased expression level (p-adj<0.5). (B) Venn diagram comparisons for GATA6-RIME enriched proteins from day 2 (D2 G6) and day 4 (D4 G6) of cardiac differentiation from the present study with day 4 GATA6-RIME (DE: D4 G6) or day 2 EOMES-RIME (DE: D2 EOMES) enriched proteins reported during hESC-DE differentiation from Heslop et al. (Ref. 21 and Ref. 39). (C) Proteins identified in the Venn diagram comparisons of RIME data described in (B).



Supplemental Figure 7: Extended data for iLGR5 and early CHIR treatment. (A) RT-qPCR time course for relative *LGR5* expression in differentiating *GATA6*^{+/+}, *GATA6*^{+/-}, and *GATA6*^{-/-} hESCs normalized to day 2 WT gene expression level (on left). Day 2 RT-qPCR quantification for relative *LGR5* expression level normalized to WT (on right, n=6). (B) Day 4 RT-qPCR for relative *LGR5* expression level (normalized to WT) in iLGR5 or EV transduced *GATA6*^{-/-} hESCs treated with or without varying concentrations of DOX (30, 125, and 250 indicate ng/mL concentrations of DOX). (C) %cTnT⁺ CMs from days 13 to 17 of cardiac differentiation quantified by flow cytometry in *GATA6*^{-/-} cells treated with CHIR (3μM) or vehicle (n≥8). (D) Flow cytometry quantification for %K⁺P⁺ double-positive cells at day 5 of cardiac differentiation from *GATA6*^{-/-} hESCs treated with CHIR and vehicle treated *GATA6*^{+/+} or *GATA6*^{-/-} hESCs controls (n≥3). Data represents the mean ± SEM, significance indicated by *p<0.05, **p<0.01, ***p<0.001, by two-tailed Student's t-test (C) or one-way ANOVA with Tukey's multiple comparisons test (A, D).

Supplemental Table 1: GATA6-RIME Enriched Proteins

99 common elements in Day_2_G6_R1 and Day_2_G6_R2		
Gene Name	Protein Name	Spectral Count (Avg)
MDN1	Midasin	41
GATA6	Transcription factor GATA-6	38
SMARCC1	SWI/SNF complex subunit SMARCC1	34.5
SMARCA4	Transcription activator BRG1	24
EOMES	Eomesodermin homolog	22
KLC3	Kinesin light chain 3	16.5
MRPL15	39S ribosomal protein L15 mitochondrial	16.5
DZIP3	E3 ubiquitin-protein ligase DZIP3	16
DNM2	Dynamin-2	14.5
GTF2I	General transcription factor II-I	14.5
FUBP3	Far upstream element-binding protein 3	13
KIF5B	Kinesin-1 heavy chain	13
MSH6	DNA mismatch repair protein Msh6	12.5
SSRP1	FACT complex subunit SSRP1	12.5
ARID1A	AT-rich interactive domain-containing protein 1A	12
GADD45GIP1	Growth arrest and DNA damage-inducible proteins-interacting protein 1	12
KIF5C	Kinesin heavy chain isoform 5C	12
VRTN	Vertnin	12
ZIC2	Zinc finger protein ZIC 2	12
KDM1A	Lysine-specific histone demethylase 1A	11.5
SALL4	Sal-like protein 4	11.5
TOP2B	DNA topoisomerase 2 (Fragment)	11.5
HDAC2	Histone deacetylase 2	11
MRPL44	39S ribosomal protein L44 mitochondrial	10.5
ELAVL1	ELAV-like protein 1	10
MTA1	Metastasis-associated protein MTA1	10
SMC1A	Structural maintenance of chromosomes protein	10
CBX1	Chromobox protein homolog 1	9.5
PYCR2	Pyroline-5-carboxylate reductase 2	9.5
SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	9.5
SMC3	Structural maintenance of chromosomes protein 3	9.5
CTBP2	C-terminal-binding protein 2	9
ODX42	ATP-dependent RNA helicase DDX42	9
GATAD2A	Transcriptional repressor p66-alpha	9
MTA3	Metastasis-associated protein MTA3	9
NSUN2	tRNA (cytosine(34)-C(5))-methyltransferase	9
RBBP7	Histone-binding protein RBBP7	9
SF1	Splicing factor 1	9
SMU1	WD40 repeat-containing protein SMU1	9
XPO5	Exportin-5	9
ACTL6A	Actin-like protein 6A	8.5
SEPHS1	Selenide water dikinase 1	8.5
CTBP1	C-terminal-binding protein 1	8
EP300	Histone acetyltransferase p300	8
RBM39	RNA-binding protein 39	8
RCOR2	REST corepressor 2	8
SMARCD2	SMARCD2 protein	8
DAZAP1	DAZ-associated protein 1	7.5
HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	7.5
MRPL4	39S ribosomal protein L4 mitochondrial (Fragment)	7.5
MTA2	Metastasis-associated protein MTA2	7.5
SMARCD1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	7.5
TRIM24	Transcription intermediary factor 1-alpha	7.5
WDHD1	WD repeat and HMG-box DNA-binding protein 1	7.5
HDAC1	Histone deacetylase 1	7
MIXL1	Homeobox protein MIXL1	7
OGT	UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase 110 kDa subunit	7
PPM1G	Protein phosphatase 1G	7
SMARCC2	SWI/SNF complex subunit SMARCC2	7
XRN2	5'-3' exonuclease 2	7
BUB3	Mitotic checkpoint protein BUB3 (Fragment)	6.5
DUT	DUTP pyrophosphatase isoform CRA_c	6.5
FEN1	Flap endonuclease 1	6.5
MBD3	Methyl-CpG-binding domain protein 3	6.5
MSH2	DNA mismatch repair protein Msh2	6.5
RBM4	RNA-binding protein 4	6.5
SART3	Squamous cell carcinoma antigen recognized by T-cells 3	6.5
SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment)	6.5
SNX9	Sorting nexin-9	6.5
THRAP3	Thyroid hormone receptor-associated protein 3	6.5
TLE1	Transducin-like enhancer protein 1	6.5
TRIM33	E3 ubiquitin-protein ligase TRIM33 (Fragment)	6.5
U2SURP	U2 snRNP-associated SURP motif-containing protein	6.5
CECR2	Cat eye syndrome critical region protein 2	6
MRPL38	39S ribosomal protein L38 mitochondrial	6
MRPL47	39S ribosomal protein L47 mitochondrial	6
PSME3	Proteasome activator complex subunit 3	6
PTBP2	Polypyrimidine tract-binding protein 2	6
SRRT	Serrate RNA effector molecule homolog	6
USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	6
DDX46	Probable ATP-dependent RNA helicase DDX46	5.5
HAT1	Histone acetyltransferase type B catalytic subunit	5.5
HINT1	Histidine triad nucleotide-binding protein 1	5.5
MRPL13	39S ribosomal protein L13 mitochondrial	5.5
MRPL20	39S ribosomal protein L20 mitochondrial	5.5
MRPL50	39S ribosomal protein L50 mitochondrial	5.5
MSI1	RNA-binding protein Musashi homolog 1	5.5
PSMD5	26S proteasome non-ATPase regulatory subunit 5	5.5
RECQL	ATP-dependent DNA helicase Q1	5.5
SIN3A	Paired amphipathic helix protein Sin3a	5.5
SMARCB1	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily b member 1 isoform CRA_c	5.5
SNRNP70	U1 small nuclear ribonucleoprotein 70 kDa	5.5
ARID1B	AT-rich interactive domain-containing protein 1B	5
DNAJC8	DnaJ homolog subfamily C member 8	5
MRPL43	39S ribosomal protein L43 mitochondrial (Fragment)	5
MRPL49	39S ribosomal protein L49 mitochondrial	5
MSI2	RNA-binding protein Musashi homolog 2	5
PRPF40A	Pre-mRNA-processing factor 40 homolog A	5
RNF40	E3 ubiquitin-protein ligase BRE1B	5
RNF40	E3 ubiquitin-protein ligase BRE1B	5

52 common elements in Day_4_G6_R1 and Day_4_G6_R2		
Gene Name	Protein Name	Spectral Count (Avg)
DNM2	Dynamin-2	24.5
GATA6	Transcription factor GATA-6	24
SMARCC1	SWI/SNF complex subunit SMARCC1	24
PYCR2	Pyrroline-5-carboxylate reductase 2	23.5
DZIP3	E3 ubiquitin-protein ligase DZIP3	21.5
SMARCA4	Transcription activator BRG1	18.5
FUBP3	Far upstream element-binding protein 3	15.5
MRPL15	39S ribosomal protein L15 mitochondrial	13
MRPL44	39S ribosomal protein L44 mitochondrial	13
SNX9	Sorting nexin-9	12
GADD45GIP1	Growth arrest and DNA damage-inducible proteins-interacting protein 1	11.5
SSRP1	FACT complex subunit SSRP1	11.5
KIF5B	Kinesin-1 heavy chain	10.5
MSH6	DNA mismatch repair protein Msh6	9.5
SALL4	Sal-like protein 4	9.5
VRTN	Vertnin	9.5
GTF2I	General transcription factor II-I	9
TRIM24	Transcription intermediary factor 1-alpha	9
ELAVL1	ELAV-like protein 1	8.5
KDM1A	Lysine-specific histone demethylase 1A	8.5
SMU1	WD40 repeat-containing protein SMU1	8.5
HDAC2	Histone deacetylase 2	8
MSI2	RNA-binding protein Musashi homolog 2	7.5
MTA1	Metastasis-associated protein MTA1	7.5
RBBP7	Histone-binding protein RBBP7	7.5
SMARCD1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1	7.5
CBX1	Chromobox protein homolog 1	7
CTBP1	C-terminal-binding protein 1	7
DDX42	ATP-dependent RNA helicase DDX42	7
KLC3	Kinesin light chain 3	7
MSH2	DNA mismatch repair protein Msh2	7
MSI1	RNA-binding protein Musashi homolog 1	7
MTA3	Metastasis-associated protein MTA3	7
SF1	Splicing factor 1	7
TAF15	TATA-binding protein-associated factor 2N	7
CTBP2	C-terminal-binding protein 2	6.5
RBM39	RNA-binding protein 39	6.5
SNRPN	Small nuclear ribonucleoprotein-associated protein N (Fragment)	6.5
TIAL1	Nucleolysin TIAR	6.5
GATAD2A	Transcriptional repressor p66-alpha	6
MRPL47	39S ribosomal protein L47 mitochondrial	6
MTA2	Metastasis-associated protein MTA2	6
RBM4	RNA-binding protein 4	6
TOP2B	DNA topoisomerase 2 (Fragment)	6
USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	6
ARID1A	AT-rich interactive domain-containing protein 1A	5.5
HDAC1	Histone deacetylase 1	5.5
HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	5.5
MRPL4	39S ribosomal protein L4 mitochondrial (Fragment)	5.5
ADAR	Double-stranded RNA-specific adenosine deaminase	5
MBD3	Methyl-CpG-binding domain protein 3	5
MRPL49	39S ribosomal protein L49 mitochondrial	5

Supplemental Table 2: Cell lines, primer sequences, and antibodies used.

Cell Lines

Name	Source	Notes
H1-GATA6-hESCs	Parent line: WiCell Research Institute, H1 (WA01), NIHhESC-10-0043	Male
GATA6 c.1071delG iPSCs	Yu et al., 2014 (Ref: 15)	Male
293T	ATCC: human embryonic kidney cells, CRL-11268	
CF1 Mouse Embryonic Fibroblasts, irradiated	MTI Global Stem: CF-1 MEF 2M IRR	

gRNAs sequences

Name	Sequence 5' to 3'	Cell line used	Notes
G6-Cr1	GGCGTTTCTGCGCCATAAGG	H1-GATA6-hESCs	
G6-Cr2	TTATGGCGCAGAAACGCCG	H1-GATA6-hESCs	
gRNA 1 - F	caccgCACAGCCTGCAGAGCCGCGC	GATA6 c.1071delG iPSCs	gRNA target sequence capitalized
gRNA 1 - R	aaacGCGCGGCTCTGCAGGCTGTGc	GATA6 c.1071delG iPSCs	gRNA target sequence capitalized
gRNA 2 - F	caccgGTGCAGCACGGGTCTCGAA	GATA6 c.1071delG iPSCs	gRNA target sequence capitalized
gRNA 2 - R	aaacTTGAGACCCCGTGTGCAC	GATA6 c.1071delG iPSCs	gRNA target sequence capitalized

Primer sequences

Name	Sequence 5' to 3'	Application
G6-iPSC-F	GCCCTACTCGCCCTACG	PCR genotyping
G6-iPSC-R	CACCCGACGAGAAAGTCCT	PCR genotyping
LGR5-cloning-F	TTCGTACGTACTTCGGGCACCATGGA	Full Length LGR5 PCR (using day 2 cDNA). Includes BsiWI site.
LGR5-cloning-R	GGCAATTGTAGAGACATGGGACAAATGCC	Full Length LGR5 PCR (using day 2 cDNA). Includes MfeI site.
LGR5-seq1	GAAAGAAATGCTTTGATGGG	LGR5 Sanger sequencing primer 1
LGR5-seq2	ATGCATTTTCCACTTTGCCA	LGR5 Sanger sequencing primer 2
LGR5-seq3	CTGGTGGGAAATGGGGTTG	LGR5 Sanger sequencing primer 3
CS-TRE-F	ATTTTCGGGTTTATTACAGG	Lentiviral vector Sanger sequencing primer
CS-TRE-R	GGAAAGGAGCTGACAGGT	Lentiviral vector Sanger sequencing primer
HPRT-F	ACCAAGTCAACAGGGGACATAA	RT-qPCR
HPRT-R	CTTCGTGGGGTCTTTTCACC	RT-qPCR
NKX2.5-F	AGCCGAAAAGAAAGAGCTGTGCG	RT-qPCR
NKX2.5-R	GACCTGCGCCTGCGAGAAGAG	RT-qPCR
TBX20-F	GGCGACGGAGAACACAATCAA	RT-qPCR
TBX20-R	CTGGGCACAGGACACTTC	RT-qPCR
TBX5-F	AGCAGTGACTTCTACCAGAAC	RT-qPCR
TBX5-R	TGACATTCTGTGCAGCTCCAT	RT-qPCR
GATA6-F	CTGCGGGCTCTACAGCAAG	RT-qPCR
GATA6-R	GTTGGCACAGGACAATCCAAG	RT-qPCR
GATA4-F	AAAGAGGGGATCCAAACCAG	RT-qPCR
GATA4-R	TTGCTGGAGTTGCTGGAAG	RT-qPCR
MEF2C-F	CTGGTGTAACACATCGACCTC	RT-qPCR
MEF2C-R	GATTGCCATACCCGTTCCCT	RT-qPCR
ALDH1A2-F	GGAGTCCCTTTGACCCCACT	RT-qPCR
ALDH1A2-R	CCCTTTCGGGCCAGTCCTTTGC	RT-qPCR
LGR5-F	GTTTCCCGCAAGACGTAAC	RT-qPCR
LGR5-R	CAGCGTCTTCACTCTCTACC	RT-qPCR
T-F	ACCCAGTTCATAGCGGTGAC	RT-qPCR
T-R	CCATTGGGAGTACCCAGGTT	RT-qPCR
EOMES-F	CTGCCCACTACAATGTGTTG	RT-qPCR
EOMES-R	GCGCCTTTGTTATTGGTGAGTTT	RT-qPCR

Antibodies

Antibody	Source	Application
mouse monoclonal α -Actinin	Sigma-Aldrich A7811	immunocytochemistry 1:200
rabbit polyclonal NANOG	Cell Signaling Technology 3850	immunocytochemistry 1:250
rabbit polyclonal SOX2	Invitrogen 48-1400	immunocytochemistry 1:100
mouse monoclonal cardiac troponin T	Invitrogen MA5-12960	immunocytochemistry 1:200, flow cytometry 1:500
rabbit monoclonal GATA6	Cell Signaling Technology 5851	western blotting 1:1000
mouse monoclonal β -actin	Sigma-Aldrich A1978	western blotting 1:50000
mouse monoclonal anti-human KDR PE conjugated	R&D Systems FAB357P-100	flow cytometry 10 μ L per million cells
mouse monoclonal anti-human PDGFR α PE conjugated	R&D Systems FAB1264A	flow cytometry 10 μ L per million cells
goat polyclonal anti-human/mouse Brachyury PE-conjugated	R&D Systems IC2085P	flow cytometry 1:40
rabbit polyclonal SMAD2/3	Cell Signaling Technology 3102	western blotting 1:500
rabbit monoclonal Phospho-SMAD2 (Ser465/467)/SMAD3 (Ser423/425) (D27F4)	Cell Signaling Technology 8828	western blotting 1:500
rabbit monoclonal Phospho-SMAD1 (Ser463/465)/ SMAD5 (Ser463/465)/ SMAD9 (Ser465/467) (D5B10)	Cell Signaling Technology 13820	western blotting 1:500
rabbit monoclonal non-phospho (Active) β -Catenin (Ser33/37/Thr41) (D13A1)	Cell Signaling Technology 8814	western blotting 1:1000
rabbit polyclonal β -Catenin	Cell Signaling Technology 9562	western blotting 1:1000
rabbit monoclonal SMARCC1/BAF155 (D7F8S)	Cell Signaling Technology 11956	western blotting 1:1000
rabbit polyclonal TBR2 / Eomes	Abcam ab23345	western blotting 1:500
goat anti-mouse IgG1 Alexa Fluor™ 488	Invitrogen A-21121	immunocytochemistry 1:500
goat anti-rabbit Alexa Fluor™ 488	Invitrogen A-11008	immunocytochemistry 1:1000
goat anti-mouse Alexa Fluor™ 488	Invitrogen A-10667	immunocytochemistry 1:500
goat anti-mouse Alexa Fluor™ 647	Invitrogen A-21236	flow cytometry 1:400
goat anti-rabbit HRP	Bio-Rad 1706515	western blotting 1:2000 - 1:10000
goat anti-mouse HRP	Bio-Rad 1706516	western blotting 1:2000 - 1:10000
mouse monoclonal IgG1 APC-conjugated	R&D Systems IC002A	flow cytometry 10 μ L per million cells
mouse monoclonal IgG1 PE-conjugated	R&D Systems IC002P	flow cytometry 10 μ L per million cells
goat polyclonal IgG PE-conjugated	R&D Systems IC108P	flow cytometry 1:40