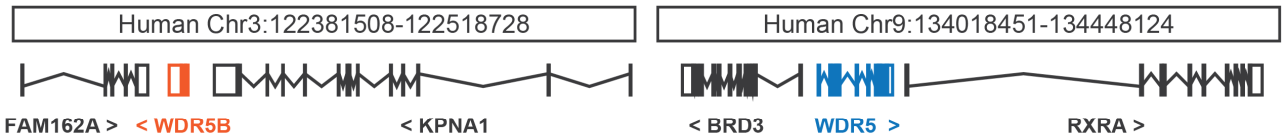
Figure S1

A



B

		Species	WDR5B locus						WDR5 locus						Location and Genome Version	
			Upstream				Downstream		Upstream				Downstream		WDR5B locus	WDR5 locus
			FAM162A		WDR5B		KPNA1		BRD3		WDR5		RXRA			
Mammals	Primates	Chimpanzee (Pan troglodytes)	✓	99.4%	✓	99.7%	✓	99.8%	✓	99.7%	✓	100.0%	✓	100.0%	Chromosome 3 (mPanTro3-v1.1)	Chromosome 9 (mPanTro3-v1.1)
		Gorilla (Gorilla gorilla gorilla)	✓	99.4%	✓	99.1%	✓	99.8%	✓	99.6%	✓	100.0%	✓	99.8%	Chromosome 3 (mGorGor1-v1.1-0.2)	Chromosome 9 (mGorGor1-v1.1-0.2)
		Orangutan (Pongo abelii)	✓	94.8%	✓	99.1%	✓	99.8%	✓	99.6%	✓	100.0%	✓	99.8%	Chromosome 3 (mPonAbe1-v1.1)	Chromosome 9 (mPonAbe1-v1.1)
		Gibbon (Nomascus leucogenys)	✓	97.4%	✓	98.8%	✓	99.8%	✓	99.3%	✓	100.0%	✓	100.0%	Chromosome 21 (Asia_NLE_v1)	Chromosome 8 (Asia_NLE_v1)
		Rhesus Macaque (Macaca mulatta)	✓	88.3%	✓	97.3%	✓	99.8%	✓	99.0%	✓	100.0%	✓	100.0%	Chromosome 2 (Mmul_10)	Chromosome 15 (Mmul_10)
	Artiodactyla, Perissodactyla, and Carnivora	Pig (Sus scrofa)	✓	83.9%	✓	91.8%	✓	99.4%	✓	92.6%	✓	99.1%	✓	97.5%	Chromosome 13 (Sscrofa11.1)	Chromosome 1 (Sscrofa11.1)
		Giant panda (Ailuropoda melanoleuca)	✓	81.0%	✓	91.8%	✓	72.7%	✓	94.3%	✓	100.0%	✓	98.2%	Chromosome 1 (ASM200744v2)	Chromosome 7 (ASM200744v2)
		Sheep (Ovis aries)	✓	82.6%	✓	91.5%	✓	99.4%	✓	92.6%	✓	99.7%	✓	97.3%	Chromosome 1 (ARS-UI_Ramb_v2.0)	Chromosome 3 (ARS-UI_Ramb_v2.0)
		Dolphin (Tursiops truncatus)	✓	83.9%	✓	91.2%	✓	99.1%	✓	93.5%	✓	99.7%	✓	97.2%	Chromosome 4 (mTurTru1.mat.Y)	Chromosome 6 (mTurTru1.mat.Y)
		Horse (Equus caballus)	✓	88.4%	✓	91.2%	✓	99.1%	✓	94.2%	✓	100.0%	✓	99.2%	Chromosome 19 (EquCab3.0)	Chromosome 25 (EquCab3.0)
		Donkey (Equus asinus)	✓	87.1%	✓	91.2%	✓	99.1%	✓	94.3%	✓	99.7%	✓	99.5%	Chromosome 5 (ASM1607732v2)	Chromosome 10 (ASM1607732v2)
		Cow (Bos taurus)	✓	84.0%	✓	91.2%	✓	99.3%	✓	92.0%	✓	100.0%	✓	97.5%	Chromosome 1 (ARS-UCD1.2)	Chromosome 11 (ARS-UCD1.2)
		Hippo (Hippopotamus amphibius kiboko)	✓	81.3%	✓	91.2%	✓	99.4%	✓	94.4%	✓	100.0%	✓	96.4%	Chromosome 10 (mHipAmp2.hap2)	Chromosome 2 (mHipAmp2.hap2)
		Dog (Canis lupus familiaris)	✓	80.6%	✓	91.2%	✓	99.4%	✓	94.4%	✓	100.0%	✓	97.9%	Chromosome 33 (ROS_Cfam_1.0)	Chromosome 9 (ROS_Cfam_1.0)
		Cat (Felis catus)	✓	84.0%	✓	90.6%	✓	99.4%	✓	92.8%	✓	100.0%	✓	99.2%	Chromosome C2 (F.catus_Fca126_mat1.0)	Chromosome D4 (F.catus_Fca126_mat1.0)
	Rodents and lagomorphs	Hamster (Mesocricetus auratus)	✓	81.3%	✓	86.3%	✓	98.5%	✓	95.6%	✓	100.0%	✓	97.9%	NW_024429192 Unplaced Scaffold (BCM_Maur_2.0)	NW_024429189 Unplaced Scaffold (BCM_Maur_2.0)
		Guinea Pig (Cavia porcellus)	✓	74.2%	✓	85.2%	✓	99.1%	✓	95.2%	✓	100.0%	✓	98.6%	NT_176332 Unplaced Scaffold (Cavpor3.0)	NT_176401 Unplaced Scaffold (Cavpor3.0)
		Rat (Rattus norvegicus)	✓	80.6%	✓	84.5%	✓	98.8%	✓	95.2%	✓	100.0%	✓	98.7%	Chromosome 11 (mRatBN7.2)	Chromosome 3 (mRatBN7.2)
		Mouse (Mus musculus)	✓	78.7%	✓	83.3%	✓	97.8%	✓	94.4%	✓	100.0%	✓	97.4%	Chromosome 16 (GRCm39 C57BL/6J)	Chromosome 2 (GRCm39 C57BL/6J)
		American Pika (Ochotona princeps)	✓	78.7%	✓	81.9%	✓	99.4%	✓	92.1%	✓	98.2%	✓	94.4%	Chromosome 3 (mOchPri1.hap1)	Chromosome 14 (mOchPri1.hap1)
	Monotremes and marsupials	Echidna (Tachyglossus aculeatus)	✓	70.8%		---	✓	92.0%	✓	91.3%	✓	97.9%	✓	96.8%	Chromosome 16 (mTacAcu1.pri)	Chromosome 4 (mTacAcu1.pri)
		Platypus (Ornithorhynchus anatinus)	✓	75.3%		---	✓	92.4%	✓	91.5%	✓	97.6%	✓	98.3%	Chromosome 16 (mOrnAna1.pri.v4)	Chromosome 4 (mOrnAna1.pri.v4)
		Possum (Monodelphis domestica)	✓	64.2%		---	✓	97.0%	✓	91.3%	✓	97.3%	✓	97.8%	Chromosome 4 (mMonDom1.pri)	Chromosome 1 (mMonDom1.pri)
		Tasmanian devil (Sarcophilus harrisii)	✓	65.2%		---	✓	97.3%	✓	91.3%	✓	97.3%	✓	96.4%	Chromosome 3 (mSarHar1.11)	Chromosome 2 (mSarHar1.11)
Birds, reptiles, and amphibians		Common toad (Bufo bufo)	✓	53.3%		---	✓	92.0%	✓	73.2%	✓	97.3%	✓	85.9%	Chromosome 3 (aBufBuf1.1)	Chromosome 8 (aBufBuf1.1)
		Komodo dragon (Varanus komodoensis)	✓	48.3%		---	✓	95.2%	✓	85.7%	✓	97.3%	✓	92.1%	NW_025336223 Unplaced Scaffold (ASM479886v1)	NW_025336442 Unplaced Scaffold (ASM479886v1)
		Chicken (Gallus gallus)	✓	54.7%		---	✓	95.7%	✓	91.2%	✓	97.0%	✓	96.4%	Chromosome 1 (bGalGal1.mat.broiler.GRCg7b)	Chromosome 17 (bGalGal1.mat.broiler.GRCg7b)
		Turkey (Meleagris gallopavo)	✓	53.6%		---	✓	96.1%	✓	90.7%	✓	97.0%	✓	96.4%	Chromosome 1 (Turkey_5.1)	Chromosome 19 (Turkey_5.1)
		Peregrine falcon (Falco peregrinus)	✓	55.0%		---	✓	96.3%	✓	91.2%	✓	97.0%	✓	95.1%	Chromosome 6 (bFalPer1.pri)	Chromosome 1 (bFalPer1.pri)
		Ostrich (Struthio camelus australis)	✓	56.9%		---	✓	96.3%	✓	91.4%	✓	97.0%	✓	96.4%	NW_009271951.1 Unplaced Scaffold (ASM69896v1)	NW_009270502.1 Unplaced Scaffold (ASM69896v1)
		Zebra finch (Taeniopygia guttata)	✓	49.3%		---	✓	95.7%	✓	92.2%	✓	97.0%	✓	94.6%	Chromosome 1 (bTaeGut1.4.pri)	Chromosome 17 (bTaeGut1.4.pri)
		Clawed frog (Xenopus tropicalis)	✓	60.2%		---	✓	94.1%	✓	74.6%	✓	97.0%	✓	85.2%	Chromosome 2 (UCB_Xtro_10.0)	Chromosome 8 (UCB_Xtro_10.0)
		Painted turtle (Chrysemys picta bellii)	✓	59.6%		---	✓	95.9%	✓	90.2%	✓	96.7%	✓	95.9%	NW_024885710 Unplaced Scaffold (Chrysemys_picta_BioNano-3.0.4)	Chromosome 20 (Chrysemys_picta_BioNano-3.0.4)
		Garter snake (Thamnophis elegans)	✓	29.8%		---	✓	94.4%	✓	86.4%	✓	96.7%	✓	91.7%	Chromosome 3 (rThaEle1.pri)	Chromosome 16 (rThaEle1.pri)
Fish		Spotted gar (Lepisosteus oculatus)	✓	45.3%		---	✓	86.0%	✓	84.8%	✓	96.1%	✓	89.3%	Chromosome LG3 (LepOcu1)	Chromosome LG21 (LepOcu1)
		Piranha (Pygocentrus nattereri)	✓	51.5%		---	✓	84.7%	✓	74.4%	✓	95.8%	✓	89.2%	Chromosome 24 (fPygNat1.pri)	Chromosome 16 (fPygNat1.pri)
		Zebrafish (Danio rerio)	✓	49.5%		---	✓	84.6%	✓	75.0%	✓	95.8%	✓	89.1%	Chromosome 24 (GRCz11)	Chromosome 21 (GRCz11)
		Atlantic herring (Clupea harengus)	✓	49.1%		---	✓	82.5%	✓	72.6%	✓	95.5%	✓	82.6%	Chromosome 17 (Ch_v2.0.2)	Chromosome 12 (Ch_v2.0.2)
		Great white shark (Carcharodon carcharias)	✓	51.6%		---	✓	87.4%	✓	72.5%	✓	94.6%	✓	89.7%	Chromosome 18 (sCarCar2.pri)	Chromosome 8 (sCarCar2.pri)
		Pufferfish (Takifugu rubripes)	✓	47.0%		---	✓	83.4%	✓	71.0%	✓	94.3%	✓	84.3%	Chromosome 10 (fTakRub1.2)	Chromosome 6 (fTakRub1.2)

Figure S1. WDR5B is conserved among eutherian mammals. (**A**) Schematic illustrations of the human WDR5B and WDR5 genomic loci including the nearest annotated upstream and downstream protein coding genes. Arrows indicate the direction of transcription, and vertical bars indicate exons. Distances between genes are not to scale. (**B**) A table of 40 vertebrates indicates the maximum protein sequence identity (%) compared to the human Refseq homolog for each protein as determined by NCBI blastp searches against databases of all annotated proteins for each organism. As expected, collinearity of the WDR5 locus is well conserved in all vertebrate species examined. While collinearity of the genes upstream and downstream of human WDR5B (FAM162A and KPNA1) is also conserved among all vertebrate genomes examined, a gene corresponding to WDR5B is only annotated in the 20 eutherian mammals. Check marks and dashes denote the presence or absence, respectively, of a blastp hit in the expected collinear order for each organism and protein. Chromosome or genomic scaffold locations as well as genome versions for each locus are indicated in the rightmost columns.

Figure S2

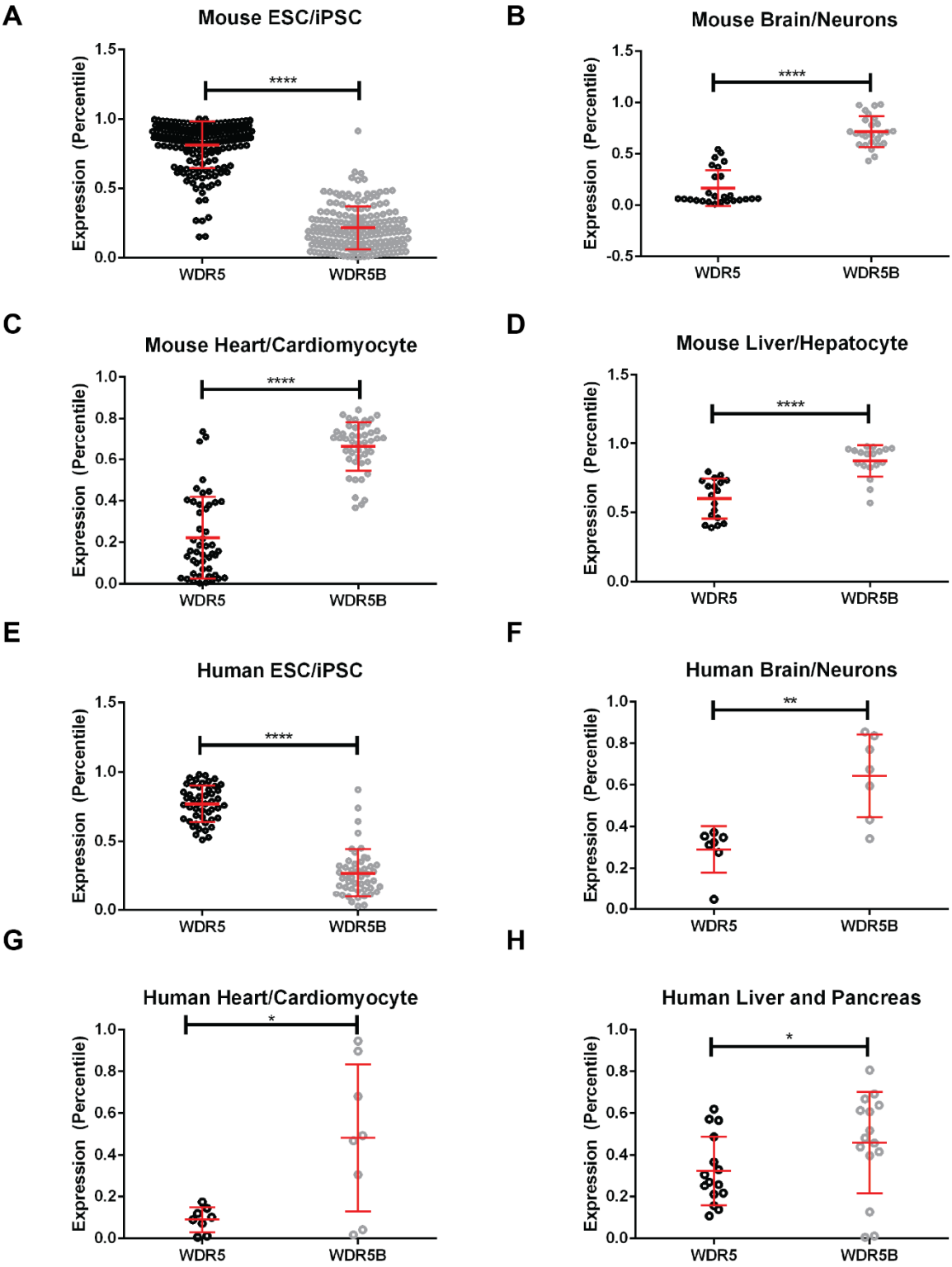
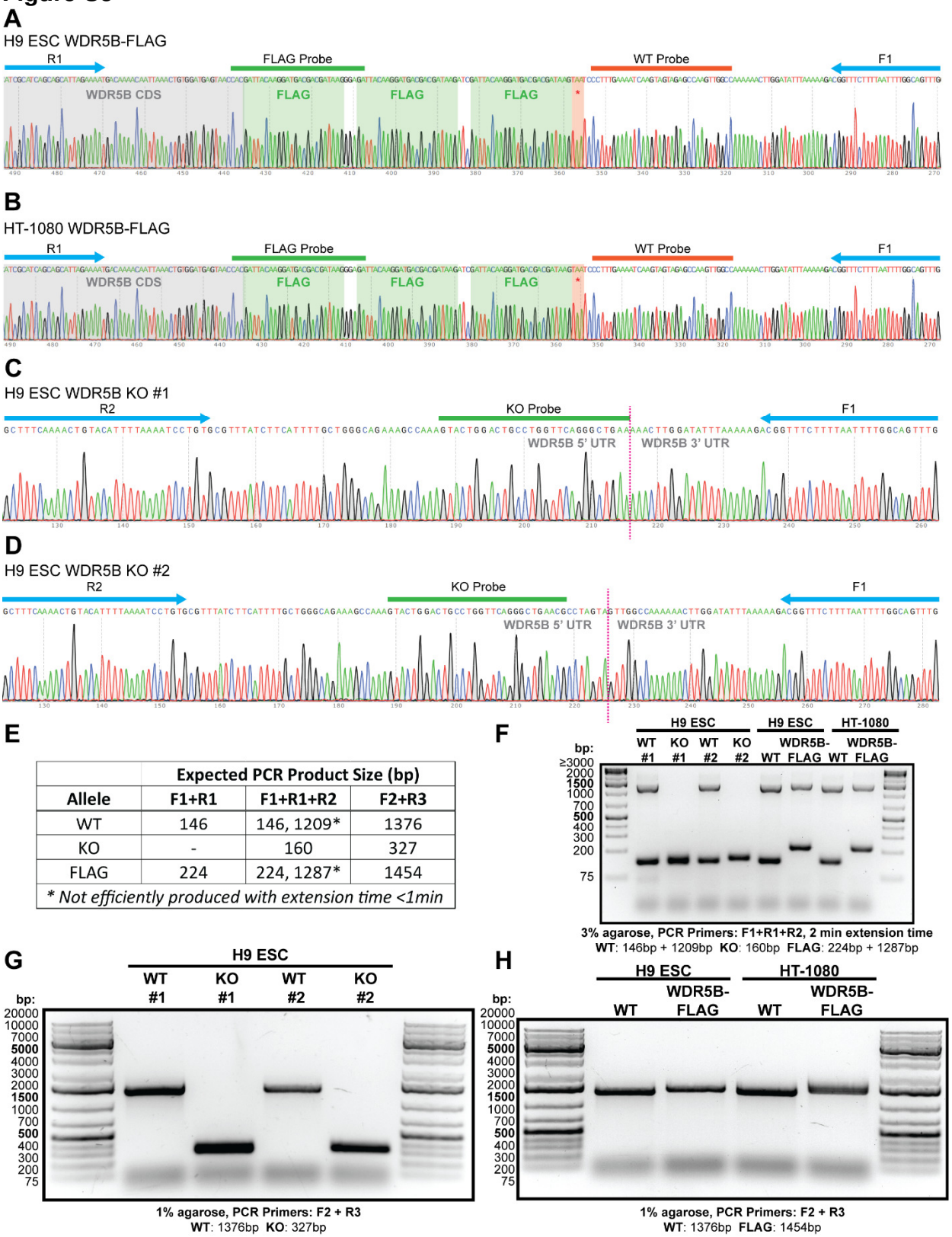

A
Mouse ESC/iPSC
Expression (Percentile)
****
WDR5
WDR5B
B
Mouse Brain/Neurons
Expression (Percentile)
****
WDR5
WDR5B
C
Mouse Heart/Cardiomyocyte
Expression (Percentile)
****
WDR5
WDR5B
D
Mouse Liver/Hepatocyte
Expression (Percentile)
****
WDR5
WDR5B
E
Human ESC/iPSC
Expression (Percentile)
****
WDR5
WDR5B
F
Human Brain/Neurons
Expression (Percentile)
**
WDR5
WDR5B
G
Human Heart/Cardiomyocyte
Expression (Percentile)
*
WDR5
WDR5B
H
Human Liver and Pancreas
Expression (Percentile)
*
WDR5
WDR5B

Figure S2. Expression levels of WDR5 and WDR5B are inversely correlated in NCBI Gene Expression Omnibus (GEO) transcriptome datasets curated by StemMapper. (**A**) Compared to all other tissues, Mouse ESC and iPSC samples ranked in the 81st percentile for WDR5 expression and in the 22nd percentile for WDR5B expression (n=177 mouse ESC and iPSC transcriptomes). (**B**) Mouse brain and other neural samples had a mean rank of 17th percentile for WDR5 expression and 72nd percentile for WDR5B expression (n=26 mouse neural transcriptomes). (**C**) Mouse heart and cardiomyocyte samples had a mean rank of 22nd percentile for WDR5 expression and 66th percentile for WDR5B expression (n=47 mouse heart and cardiomyocyte transcriptomes). (**D**) Mouse liver and hepatocyte samples had a mean rank of 60th percentile for WDR5 expression and 87th percentile for WDR5B expression (n=18 mouse liver and hepatocyte transcriptomes). (**E**) Similar results were observed for human transcriptomes, where human ESC and iPSC samples ranked in the 77th percentile for WDR5 expression and in the 27th percentile for WDR5B expression (n=48 human ESC and iPSC transcriptomes). (**F**) Human brain and other neural samples had a mean rank of 29th percentile for WDR5 expression and 64th percentile for WDR5B expression (n=7 human neural transcriptomes). (**G**) Human heart and cardiomyocyte samples had a mean rank of 9th percentile for WDR5 expression and 48th percentile for WDR5B expression (n=8 human heart and cardiomyocyte transcriptomes). (**D**) Human liver and pancreas samples had a mean rank of 32nd percentile for WDR5 expression and 46th percentile for WDR5B expression (n=15 human liver and pancreas transcriptomes). All statistical analyses were conducted using the Kolmogorov-Smirnov test since some groups had unequal variance. Asterisks indicate significance as follows: **** ($p< 0.0001$), ** ($p<0.01$), * ($p<0.05$). Error bars are ±S.D.

Figure S3



E

	Expected PCR Product Size (bp)		
Allele	**F1+R1**	**F1+R1+R2**	**F2+R3**
WT	146	146, 1209*	1376
KO	-	160	327
FLAG	224	224, 1287*	1454
** Not efficiently produced with extension time <1min*			

3% agarose, PCR Primers: F1+R1+R2, 2 min extension time
WT: 146bp + 1209bp **KO**: 160bp **FLAG**: 224bp + 1287bp

1% agarose, PCR Primers: F2 + R3
WT: 1376bp **KO**: 327bp

1% agarose, PCR Primers: F2 + R3
WT: 1376bp **FLAG**: 1454bp

Figure S3. Verification of CRISPR-Cas9 genome editing. (**A**) Annotated Sanger sequencing traces for 3XFLAG-tagged WDR5B amplified from the gDNA of the H9 ESC WDR5B-FLAG clonal cell line. (**B**) Annotated Sanger sequencing traces for 3XFLAG-tagged WDR5B amplified from the gDNA of the HT-1080 WDR5B-FLAG clonal cell line. (**C**) Annotated Sanger sequencing traces for the WDR5B-null locus amplified from the gDNA of the H9 ESC WDR5B KO #1 clonal cell line. (**D**) Annotated Sanger sequencing traces for the WDR5B-null locus amplified from the gDNA of the H9 ESC WDR5B KO #2 clonal cell line. For annotated sequencing results, shaded regions and text within the traces indicate sequence features, annotations above the sequence indicate primer or probe binding sites, and dotted vertical lines indicate sites of non-homologous end joining (NHEJ). (**E**) Table of expected PCR product sizes in base pairs (bp) for each combination of alleles and primers. PCR products >1000 bp are not efficiently produced in the presence of shorter amplicons unless PCR extension time exceeds 1 min. (**F**) Primers F1, R1, and R2 produced PCR products of the expected sizes from the gDNA of H9 ESC and HT-1080 wild type and CRISPR-Cas9 edited cell lines. (**G**) Primers F2 and R3, which flank the CRISPR-Cas9 edited region, produced PCR products of the expected sizes from the gDNA of H9 ESC wild type and WDR5B-null clones. (**H**) Primers F2 and R3 also produced PCR products of the expected sizes from the gDNA of H9 ESC and HT-1080 WDR5B-FLAG clones.

Figure S4

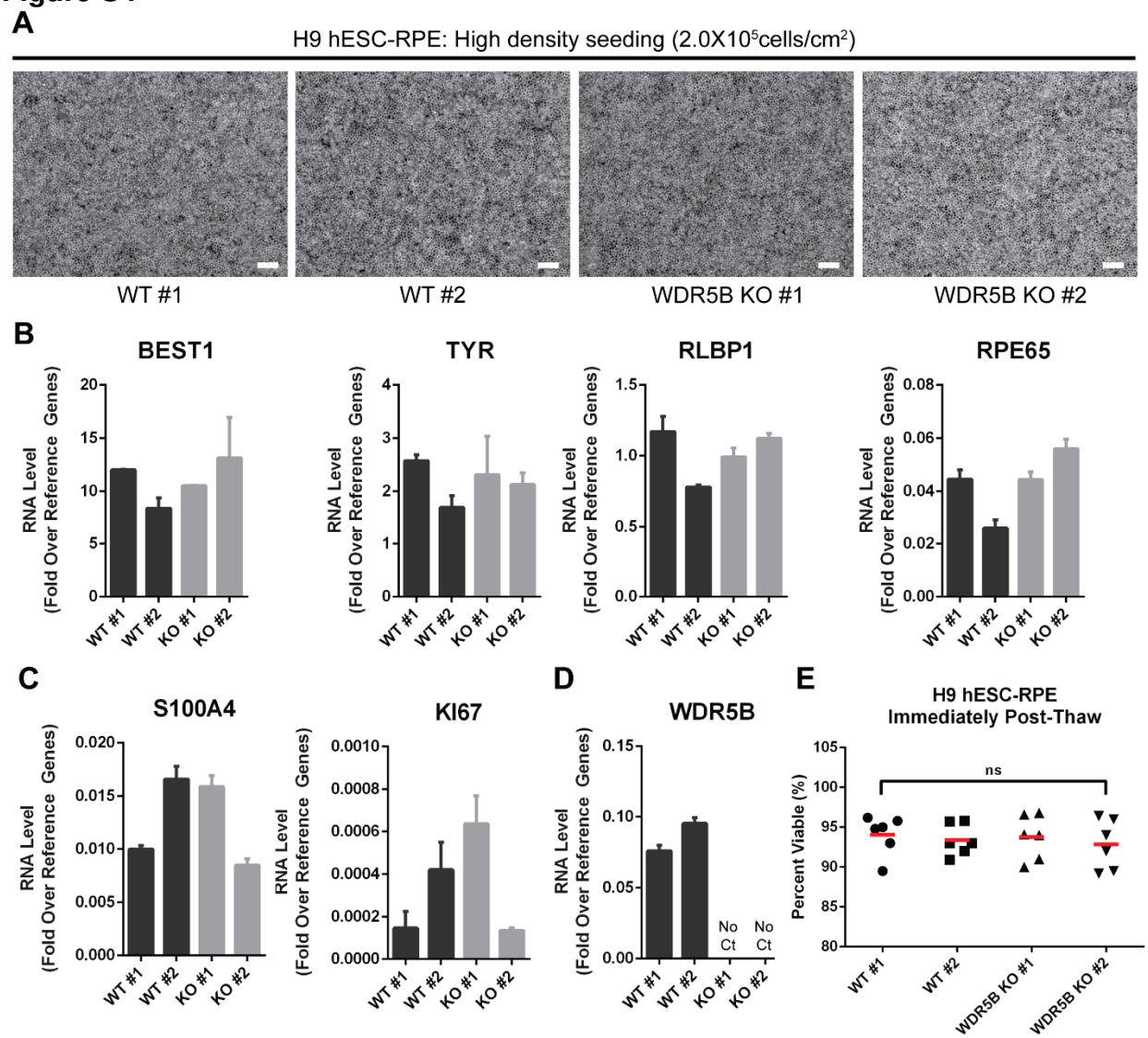

A
H9 hESC-RPE: High density seeding (2.0X10⁵cells/cm²)
WT #1
WT #2
WDR5B KO #1
WDR5B KO #2
B
BEST1
TYR
RLBP1
RPE65
RNA Level (Fold Over Reference Genes)
WT #1
WT #2
KO #1
KO #2
C
S100A4
KI67
D
WDR5B
No Ct
No Ct
E
H9 hESC-RPE Immediately Post-Thaw
Percent Viable (%)
ns
WDR5B KO #1
WDR5B KO #2

Figure S4. WDR5B knockout hESC-RPE exhibit normal RPE morphology and expression of RPE marker genes when seeded at high density. (**A**) Both wild type and WDR5B null hESC-RPE lines exhibit similar cobblestone RPE morphology when seeded at confluence ($2.0X10^5$ cells/cm^2, images captured on day 54 post-seeding). Scale bars: 100 µm. (**B**) Expression of the RPE marker genes BEST1, TYR, RLBP1, and RPE65 did not significantly differ by genotype when cells were seeded at high density (n=3 experimental replicates). (**C**) Levels of epithelial-to-mesenchymal transition (S100A4) and cell proliferation (MKI67) markers were also not significantly different by genotype in cells seeded at high density (**D**) WDR5B mRNA was detected in both wild type clones while no amplification (No Ct) was observed in either knockout clone (n=3 experimental replicates for all RT-qPCR). (**E**) Immediately upon thaw of cryopreserved stocks, no significant differences in viability among RPE lines were observed (n=6 replicates from three independent thaws). Red bars indicate group means. Statistical analyses were conducted by univariate ANOVA with Tukey's post-hoc (ns, not significant). Error bars are ±S.D.

Table S1: Oligonucleotide sequences

ID	Sequence (5' to 3') or Catalog Number	Assay
WDR5B Forward	GCTCGTTGATGACGATAACCCTCCTGTCT	RT-qPCR
WDR5B Reverse	GGCACCTGCCTCTGCTATAATCCCATAGTT	RT-qPCR
WDR5 Forward	CCCGAACGGCAAATACATCCTG	RT-qPCR
WDR5 Reverse	TTCTTGTGGCCAGTGTACGTCTTC	RT-qPCR
EIF2B2 Forward	CACTCTGGCACTGGCAGCAAA	RT-qPCR
EIF2B2 Reverse	GGACTTCTTCAGGAGCCACAAACTTATGA	RT-qPCR
UBE2R2 Forward	CCCCTATTCACCACCTACCTTCAGAT	RT-qPCR
UBE2R2 Reverse	CTACAGGCGGATGAAGAATCGAAATGC	RT-qPCR
EIF2B2	Hs00204540_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
UBE2R2	Hs00215107_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
RPE65	Hs01071462_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
S100A4	Hs00243202_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
BEST1	Hs00188249_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
RLBP1	Hs00165632_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
TYR	Hs00165976_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
MKI67	Hs01032443_m1 (Thermo Fisher Scientific)	Taqman RT-qPCR
PUM1 Forward	TATGAAGGGACAATCTGCTC	CUT&RUN -qPCR
PUM1 Reverse	AATCCATCTTCATCCTACCG	CUT&RUN -qPCR
RPS6 Forward	GAGACCCTTCTCCACCTAAA	CUT&RUN -qPCR
RPS6 Reverse	CGAGTGTTAGACTGGGTTTG	CUT&RUN -qPCR
RPL26 Forward	GGTCTGGAAATTCCGTGAAGACTTT	CUT&RUN -qPCR

RPL26 Reverse	GTCTGGGTAGTGTCGTTTCCTAGAG	CUT&RUN -qPCR
Negative Control Forward	AGGGCTATAAATTTACCTTTAAGTTCAGCT	CUT&RUN -qPCR
Negative Control Reverse	CCCCTCTGTTGAAAGCACAATACTT	CUT&RUN -qPCR
Nucleosome Forward	CGTATCGCGCGCATAATA	qPCR
Nucleosome Reverse	CGCGTAACGACGTACC	qPCR
Nucleosome Probe	/56-FAM/ TCTAGCACC/ZEN/GCTTAAACGCACGTA /3IABkFQ/	qPCR
WDR5B-3XFLAG HDR Template	C*T*C*ATCGCATCAGCAGCATTAGAAAATGACAAAAC AATTAAACTGTGGATGAGTAACCACGATTACAAGGAT GACGACGATAAGGGAGATTACAAGGATGACGACGAT AAGATCGATTACAAGGATGACGACGATAAGTAATCC CTTTGAAAATCAAGTAGTAGAGCCAAGTTGGCCAAA AAACTTGGATATTTAAA*A*A*G	Knock-in HDR template
CD.Cas9.TFZZ6738.AD	/ALTR1/rUrUrGrArUrUrUrUrCrArArArGrGrGrArUrUrArGrGrUrUrUrUrArGrArGrCrUrArUrGrCrU/ALTR2/	Knock-in crRNA
CD.Cas9.PVWS8678.AA	/ALTR1/rUrCrCrArArGrUrUrArGrCrArGrGrUrGrUrArCrUrGrUrUrUrUrArGrArGrCrUrArUrGrCrU/ALTR2/	Knockout crRNA #1
CD.Cas9.DJVX5152.AA	/ALTR1/rArUrCrArArGrUrArGrUrArGrArGrCrCrArArGrUrGrUrUrUrUrArGrArGrCrUrArUrGrCrU/ALTR2/	Knockout crRNA #2
F1	CAAACTGCCAAAATTAAAAGAAACCGT	Knockout and Knock-in genotyping primer
R1	ATCGCATCAGCAGCATTAGAAAAT	Knockout and Knock-in genotyping primer
R2	GCTTTCAAAACTGTACATTTTAAAATCCTGTG	Knockout genotyping primer
WDR5B-FLAG Probe	/56-FAM/ CACGATTACAAGGATGACGACGATAAGGGAGA /3IABkFQ/	Knock-in genotyping probe
WDR5B-WT-Probe	/5HEX/ CCTTTGAAAATCAAGTAGTAGAGCCAAGTTGGCC /3IABkFQ/	Knockout and Knock-in

		genotyping probe
WDR5B-KO-Probe	/56-FAM/ CGTTCAGCC/ZEN/CTGAACCAGGCAGTCCAGTAC /3IABkFQ/	Knockout genotyping probe
R3	CATCATACCGGTGAAGTCCAAGCCGTGCTGCTG	Cloning
F2	GATTGGTAGTCAGAAGCTGAATTCTAGATGTGC	Cloning
WDR5-FLAG Cloning XhoI Forward	CATCATCTCGAGGCCACCATGGCGACGGAGGAGAAGAAGC	Cloning
WDR5-FLAG Cloning NotI Reverse	TACTACGCGGCCGCTTACTTATCGTCGTCATCCTTGTAATCGCAGTCACTCTTCCACAGTTTAATTGTTTTGTC	Cloning
WDR5B-3XFLAG Cloning XhoI Forward	CATCATCTCGAGGCCACCATGGCAACCAAGGAGTCAAGAGAC	Cloning
WDR5B-3XFLAG Cloning XbaI Reverse	CATCATTCTAGATTACTTATCGTCGTCATCCTTGTAATCGATCTTATCG	Cloning
PLVX 2A Cloning XhoI Forward	CATCATCTCGAGGGAGATAGCGGATC	Cloning
PLVX 2A Cloning AgeI Reverse	GTAGTAACCGGTGGATGTGGAATGTGT	Cloning
WDR5B-NLUC-HA XbaI Forward	CATCATTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCAACCAAGGAGTCAAGAGAC	Cloning
WDR5B-NLUC-HA XhoI Reverse	CATCATCTCGAGGTGGTTACTCATCCACAGTTTAATTGTTTTGTC	Cloning
WDR5-NLUC-HA XbaI Forward	CATCATTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCGACGGAGGAGAAGAAG	Cloning
WDR5-NLUC-HA XhoI Reverse	CATCATCTCGAGGCAGTCACTCTTCCACAGTTTAATTGTTTTG	Cloning

NLUC-HA XhoI Forward	CATCATCTCGAGGGCAGCAGCGGCATGGTCTTCACACTCGAAGATTTCGTTG	Cloning
NLUC-HA BamHI Reverse	CATCATGGATCCTTAAGCGTAATCTGGAACATCGTATGGGTAC	Cloning
NLUC-HA NdeI Forward	CATCATCATATGGTCTTCACACTCGAAGATTTCGTTGG	Cloning
NLUC-HA BlpI Reverse	CATCATGCTCAGCTTAAGCGTAATCTGGAACATCGTATGGGTAC	Cloning
WDR5-FLAG Template	CATCATCTCGAGGCCACCATGGCGACGGAGGAGAAGAAGCCCGAGACCGAGGCCGCCAGAGCACAGCCAACCCCTTCGTCATCCGCCACTCAGAGCAAGCCTACACCTGTGAAGCCAAACTATGCTCTAAAGTTCACCCTTGCTGGCCACACCAAAGCAGTGTCCTCCGTGAAATTCAGCCCGAATGGAGAGTGGCTGGCAAGTTCATCTGCTGATAAACTTATTAAAATTTGGGGCGCGTATGATGGGAAATTTGAGAAAACCATATCTGGTCACAAGCTGGGAATATCCGATGTAGCCTGGTCGTCAGATTCTAACCTTCTTGTTTCTGCCTCAGATGACAAAACCTTGAAGATATGGGACGTGAGCTCGGGCAAGTGTCTGAAAACCCTGAAGGGACACAGTAATTATGTCTTTTGCTGCAACTTCAATCCCCAGTCCAACCTTATTGTCTCAGGATCCTTTGACGAAAGCGTGAGGATATGGGATGTGAAAACAGGGAAGTGCCTCAAGACTTTGCCAGCTCACTCGGATCCAGTCTCGGCCGTTCATTTTAATCGTGATGGATCCTTGATAGTTTCAAGTAGCTATGATGGTCTCTGTCGCATCTGGGACACCGCCTCAGGCCAGTGCCTGAAGACGCTCATCGATGACGACAACCCCCCCGTGTCTTTTGTGAAGTTCTCCCCGAACGGCAAATACATCCTGGCCGCCACGCTGGACAACACTCTGAAGCTCTGGGACTACAGCAAGGGGAAGTGCCTGAAGACGTACACTGGCCACAAGAATGAGAAATACTGCATATTTGCCAATTTCTCTGTTACTGGTGGGAAGTGGATTGTGTCTGGCTCAGAGGATAACCTTGTTTACATCTGGAACCTTCAGACGAAAGAGATTGTACAGAAACTACAAGGCCACACAGATGTCGTGATCTCAACAGCTTGTCACCCAACAGAAAACATCATCGCCTCTGCTGCGCTAGAAAATGACAAAACAATTAAACTGTGGAAGAGTGACTGCGATTACAAGGATGACGACGATAAGTAAGACTCTAGATAATTCTAC	Cloning
PLVXpuro P2A T2A Template	CATCATCTCGAGGGAGATAGCGGATCCGGCAGCGGCGCCACAAACTTCTCTCTGCTAAAGCAAGCAGGTGATGTTGAAGAAAACCCAGGGCCTGAATTCGCTGGAAAGCGCGGCCGCGGCTCCGGCGAGGGCAGGGGAAGT	Cloning

	CTTCTAACATGCGGGGACGTGGAGGAAAATCCCGG CCCACCCGGGGGAGCATCCGGACTCTAGATAATTCT ACCGGGTAGGGGAGGCGCTTTTCCCAAGGCAGTCT GGAGCATGCGCTTTAGCAGCCCCGCTGGGCACTTG GCGCTACACAAGTGGCCTCTGGCCTCGCACACATTC CACATCCACCGGTTACTAC	
NLUC-HA Template	ATGGTCTTCACACTCGAAGATTTCGTTGGGGACTGG CGACAGACAGCCGGCTACAACCTGGACCAAGTCCTT GAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTC GGGGTGTCCGTAACTCCGATCCAAAGGATTGTCCTG AGCGGTGAAAATGGGCTGAAGATCGACATCCATGTC ATCATCCCGTATGAAGGTCTGAGCGGCGACCAAATG GGCCAGATCGAAAAAATTTTTAAGGTGGTGTACCCT GTGGATGATCATCACTTTAAGGTGATCCTGCACTAT GGCACACTGGTAATCGACGGGGTTACGCCGAACAT GATCGACTATTTCGGACGGCCGTATGAAGGCATCGC CGTGTTCGACGGCAAAAAGATCACTGTAACAGGGAC CCTGTGGAACGGCAACAAAATTATCGACGAGCGCCT GATCAACCCCGACGGCTCCCTGCTGTTCCGAGTAAC CATCAACGGAGTGACCGGCTGGCGGCTGTGCGAAC GCATTCTGGCGTACCCATACGATGTTCCAGATTACG CTTAA	Cloning
Control shRNA	CAACAAGATGAAGAGCACCAA (Sigma Aldrich #SHC002)	shRNA
WDR5B shRNA #1	CCTTATAATCTCGGGATCTTT (Sigma Aldrich #TRCN0000117883)	shRNA
WDR5B shRNA #2	GCAACTTTGGACAACACTCTT (Sigma Aldrich #TRCN0000117884)	shRNA

Modification Notes:
***** Indicates a phosphorothioate bond
r Indicates an RNA base
ALTR1 and ALTR2 Indicate crRNA-tracrRNA hybridization sequences
/**56-FAM**/ indicates a 5' 6-FAM (fluorescein) fluorophore
/**5HEX**/ indicates a 5’ hexachlorofluorescein fluorophore
/**ZEN**/ indicates the IDT ZEN internal fluorescence quencher
/**3IABkFQ**/ indicates the IDT 3' Iowa Black FQ fluorescence quencher