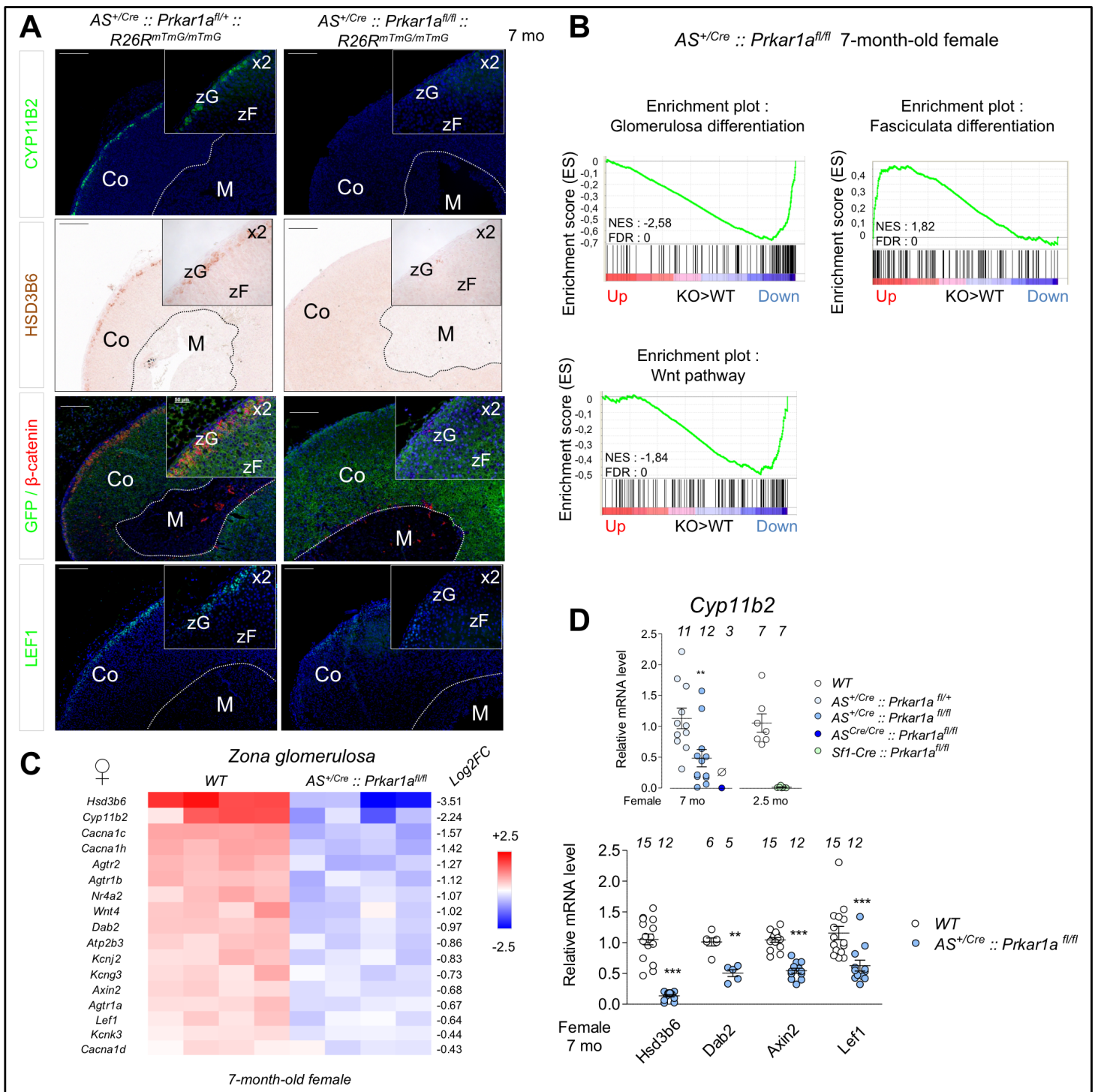
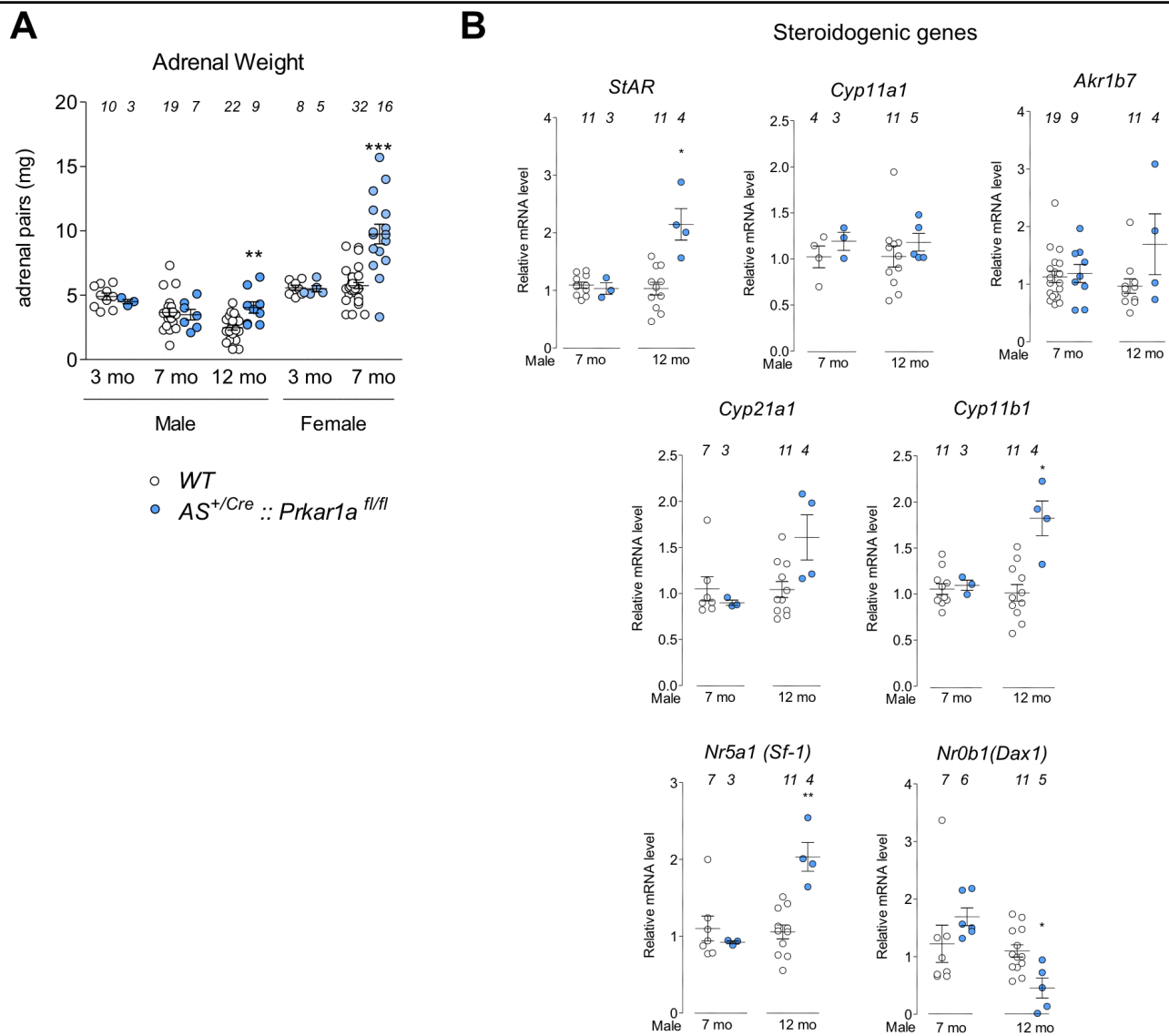
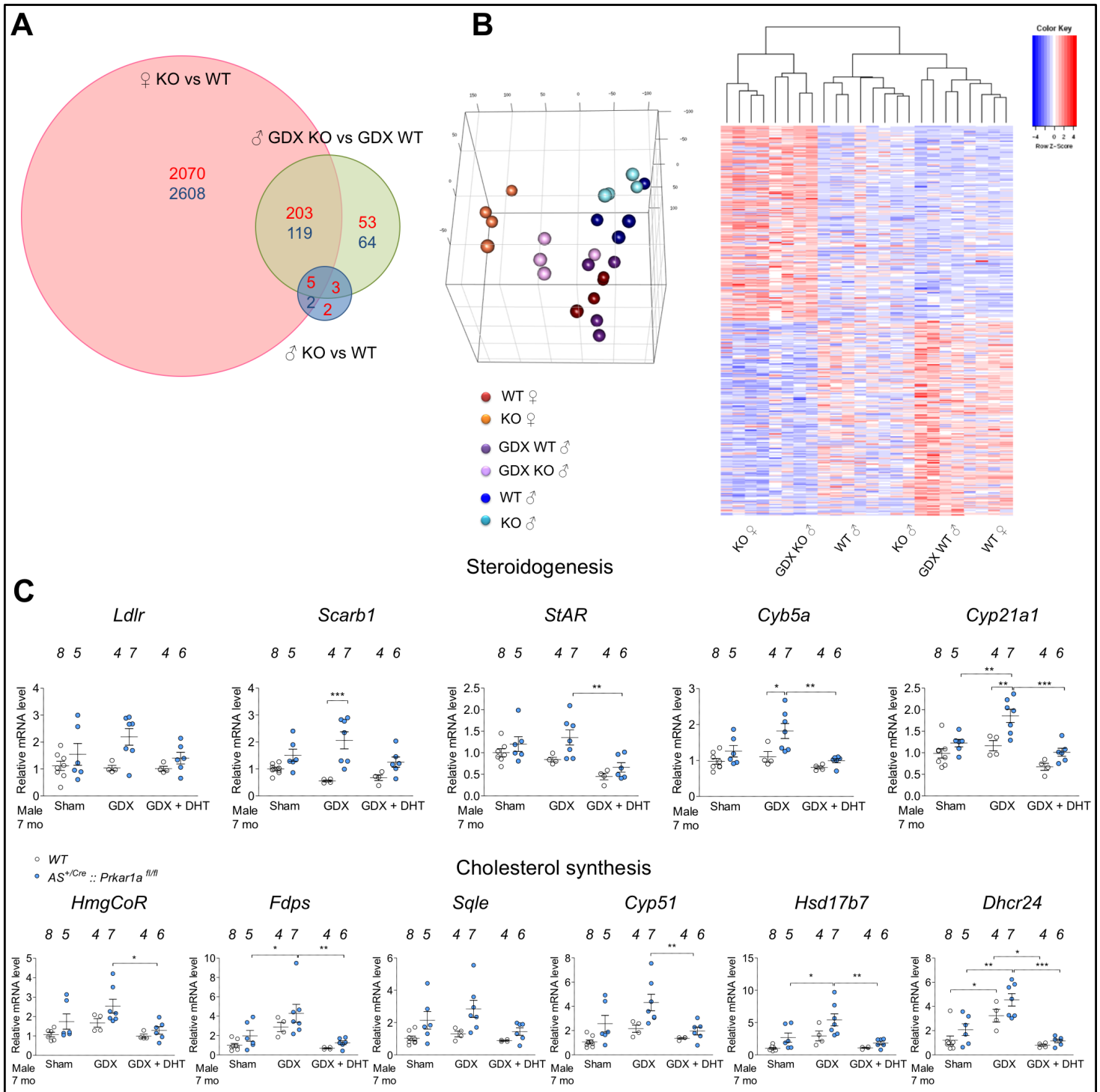




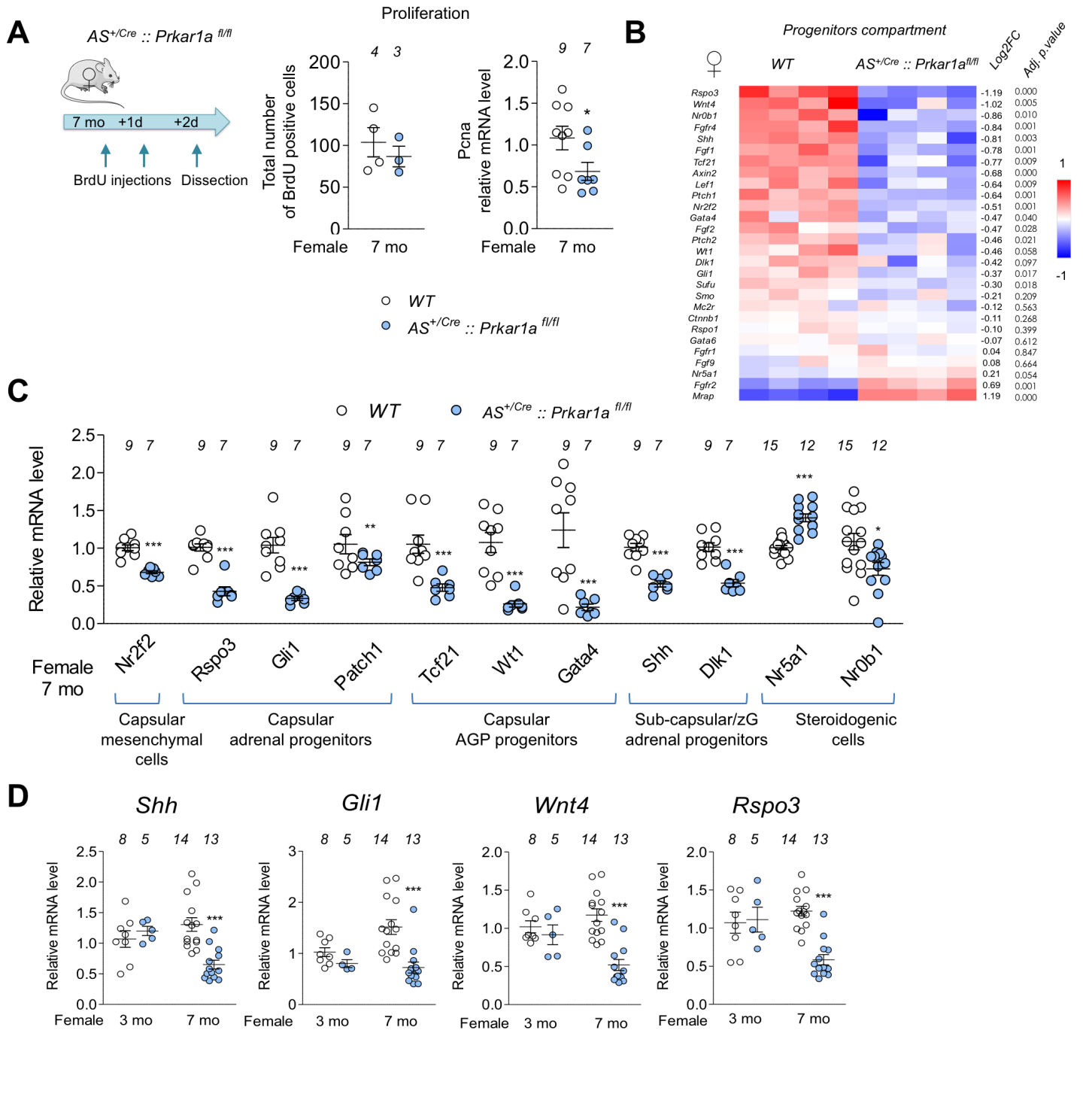
Supplemental Figure S1. Post-natal PKA activation in the adult cortex leads to increased zF differentiation and attenuates zG differentiation through antagonism with WNT/ β -catenin signalling. (A) Immunofluorescent and immunostaining analyses show important loss of zG markers CYP11B2, HSD3B6, β -catenin and LEF1 and complete recombination attested by GFP, in 7-month-old *AS^{+/Cre}::Prkar1a^{fl/fl}* females. zG=zona Glomerulosa, zF=zona Fasciculata, Co= Cortex, M=Medulla. Scale bars: 200 μ m. The black or white dots represent the border between the cortex and the medulla. (B) Gene set enrichment analyses (GSEA) were performed using signatures gene sets of zG differentiation, zF differentiation and WNT pathway by comparing gene expression data from WT and *AS^{+/Cre}::Prkar1a^{fl/fl}* female adrenals. Normalized enrichment score (NES) and false discovery rates (FDR) are shown on plots. (C) Colour-coded heatmap shows expression of the 17 genes linked to zG identity that are significantly deregulated in the transcriptome of mutant adrenals (adjusted p-value 0.05). (D) Decreased expressions of *Cyp11b2*, *Hsd3b6*, *Dab2*, *Axin2* and *Lef1* were confirmed by qPCR in adrenals of 7-month-old wild-type (WT) or *AS^{+/Cre}::Prkar1a^{fl/fl}* (for *Cyp11b2*) and *AS^{+/Cre}::Prkar1a^{fl/fl}* females. *Cyp11b2* expression is decreased in *AS^{+/Cre}::Prkar1a^{fl/fl}* adrenals whereas it is almost undetectable in *Sf1-Cre::Prkar1a^{fl/fl}* adrenals (upper panel). Lines in dot plots represent the mean relative quantification of gene expression (relative to the control counterparts) $\pm$ se. $\emptyset$ = under detection threshold. Statistical analyses were conducted by Student's t-test. * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001. Number of samples is indicated above dot plots.



Supplemental Figure S2. Mutant phenotype is delayed in DAdKO males. (A) Delayed adrenal growth phenotype in mutant males. Compared to age-matched wild-type (WT), mutant ($AS^{+/Cre}::Prkar1a^{fl/fl}$) adrenal weight increases at 12 months in males while at 7 in females. Lines in dot plots represent the mean of pairs adrenal weight $\pm$ se. **(B)** Induction of steroidogenic genes in mutant males that declared Cushing's syndrome. QPCR analysis shows that *Star*, *Cyp11b1* and *Nr5a1* expression is induced while *Nr0b1* repressor expression is decreased in adrenals of $AS^{+/Cre}::Prkar1a^{fl/fl}$ male mice. Lines in dot plots represent the mean relative quantification of gene expression (relative to the control counterparts) for the different genotypes $\pm$ se. Statistical analyses were conducted by Student's t-test. * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001. Number of samples is indicated above dot plots.



Supplemental Figure S3. Gonadectomy induces molecular phenotype in DAdKO males. (A) Venn diagram of adrenal genes differentially expressed (adjusted p-value <0.05) between *AS^{+/-}Cre::Prkar1a^{fl/fl}* (KO) and wild-type (WT) 7-month-old mice being either females, males or gonadectomised males (GDX). Among the 5007 genes differentially regulated in mutant females, 2278 are up-regulated and 2729 are down-regulated. In contrast, only 12 genes are regulated (10 up-regulated and 2 down-regulated) in mutant males. Importantly, 449 genes are differentially regulated in mutant gonadectomised males, and there is a significant overlap of 332 genes with those differentially expressed in mutant females. (B) Principal component 3D projection of transcriptome coloured by sample type. The variability of the data set along principal component 1 is 19.9 %, along principal component 2 is 8.94 % and along principal component 3 is 7 %. Note the clustering representation of individual mice, clusters by sex and genotype. The first three components are represented by the axes of the plot and capture the most variance of the data. Unsupervised expression heatmap of the 200 most up-/downregulated genes, demonstrates that profiles of mutant female and gonadectomized mutant males gather in the same cluster (C) qPCR analysis of genes involved in steroidogenic pathway (*Ldlr*, *Scarb1*, *Star*, *Cyb5a* and *Cyp21a1*) and cholesterol synthesis (*Hmgcr*, *Fdps*, *Sqle*, *Cyp51*, *Hsd17b7* and *Dhcr24*) shows expression patterns globally sensitive to androgens. Sham-operated (Sham), gonadectomised (GDX) and gonadectomised supplemented by DHT (GDX + DHT) from 7-month-old wild-type (WT) and *AS^{+/-}Cre::Prkar1a^{fl/fl}* male mice. Lines in dot plots represent the mean quantification relative to sham wild-type (WT) gene expression $\pm$ se. Statistical analyses were conducted by ANOVA followed by Bonferroni's multiple comparison post-hoc test. * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001. Number of samples is indicated above dot plots.



Supplemental Figure S4. Adrenal cortex stem/progenitor cells depletion/recruitment is stimulated by PKA activation. (A) Experimental setup of cell proliferation study: mice received BrdU injections during 2 consecutive days and were dissected one day later. Total number of positive cells per cortex section was counted and is not significantly altered or tends to decrease in mutants. According to qPCR analysis of *Pcna* transcripts, cell proliferation is rather decreased in mutants. Lines in dot plots represent the mean relative quantification of gene expression $\pm$ se. (B) Colour-coded heatmap shows expression data of genes involved in progenitors compartment and significantly deregulated (adjusted p-value 0.05). (C) qPCR analysis of capsular and subcapsular markers of stem/progenitor cell niche shows overall downregulation in mutant adrenals from 7-month-old females while steroidogenic capacities are enhanced. AGP, adrenogonadal primordium. (D) Time-dependent changes in the expression of capsular (*Rspo3* and *Gli1*), subcapsular (*Shh*) stem/progenitor cell markers and *Wnt4*, analysed by qPCR in DAdKO adrenals of 3- and 7-month-old females. Lines in dot plots represent the mean relative quantification of gene expression (relative to the control counterparts, white bars) $\pm$ se. Statistical analyses were conducted by one-way ANOVA followed by Bonferroni's multiple comparison post-hoc test. * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001. Number of samples is indicated above dot plots.

Supplemental Table S1. Immunohistological and western blot conditions

Immunohistochemistry and immunofluorescence			
	Dilution	Origin	Epitope retrieval
3bHSD	1/3,000	kind gift of M. Thomas	25 min. boiling in Vector Retrieval Solution (H330, Vector Labs)
CYTB5	1/500	kind gift of A.C. Conley	
CYP11A1	1/200	Santa Cruz sc-18043	
CYP21	1/600	Sigma-Aldrich HPA048979	
b-catenin	1/500	BD biosciences 610153	
CYP11B2	1/100	kind gift of C. Gomez-Sanchez	
GFP	1/1,000	Abcam ab5450	
20aHSD	1/20,000	kind gift of Y. Weinstein	25 min. in TE (Tris10mM 1mM pH 9.0)
HDS3B6	1/500	kind gift of H. Okamura	
Lef1	1/200	Abcam ab137872	None
CYP17	1/500	kind gift of A.C. Conley	

Western Blot			
	Dilution	Origin	Blocking
CYP17	1/4,000	kind gift of A.C. Conley	Milk 10%
CYTB5	1/2,500	kind gift of A.C. Conley	
GAPDH	1/1,000	Novus NB30021	

Supplemental Table S2. Sequences of the primers used for RTqPCR

Target	Forward	Reverse
<i>eGFP</i>	5'-GAAGCAGCAGCACTTCTTCAAG-3'	5'-AAGTCGATGCCCTTCAGCTC-3'
mm <i>Actin</i>	5'-TCATCACTATTGGCAACGAGC-3'	5'-AGTTTCATGGATGCCACAGG-3'
mm <i>Akr1b7</i>	5'-GGCTGCCATTCTCAGCTTCAACAG-3'	5'-GCAAGTGGACCTCAGTATTCCTCG-3'
mm <i>Akr1c18 (20aHSD)</i>	5'-GGCTTTGGCACCTATGCAAC-3'	5'-TGGGTCTGACCAACTCTGGA-3'
mm <i>Axin2</i>	5'-TGGGGAGTAAGAAACAGCTCC-3'	5'-CCAGCTCCAGTTTCAGTTTCTC-3'
mm <i>Cyb5a</i>	5'-ACGGATGCACGAGAAGTCTC-3'	5'-GGATCAGCCAGTTGGTCCAC-3'
mm <i>Cyp11a1(v1)</i>	5'-GGTTTGGGGCAGAGACACTC-3'	5'-AGCCTTTGACCAGCACTGAG-3'
mm <i>Cyp11b1</i>	5'-GCAGAGATGATGCTCCTGCTT-3'	5'-GAGAGGGCAATGTGTATCAGAA-3'
mm <i>Cyp11b2</i>	5'-ATGCTGAGAAGTTGCACCAAG-3'	5'-ATTCTGCCCCATTTAGCAAG-3'
mm <i>Cyp17a1</i>	5'-TGGAGGCCACTATCCGAGAA-3'	5'-CACATGTGTGCTCTCGGGA-3'
mm <i>Cyp21a1</i>	5'-GCTGTGGCTTTCTGCTTCTAC-3'	5'-GGCCCAGCTTGAGGTCTAACT-3'
mm <i>Cyp51</i>	5'-GCCTATGTGCCATTTGGAGC-3'	5'-GGGTTTTCTGGGGTGTGGAT-3'
mm <i>Dab2</i>	5'-CCTGCATCTTCTGATCCCCAC-3'	5'-CATGTTTCTGGCTGTCTGCTT-3'
mm <i>Dhcr24</i>	5'-CGCTCTCGCTCATCTTCGAT-3'	5'-TGCCCTGTTCTCTCCATTCC-3'
mm <i>Dlk1</i>	5'-CTCCTGCGCGTCTCTTGTCTC-3'	5'-CTGCAGACATTGTCAGCCTCGCAG-3'
mm <i>Fdps</i>	5'-TCTTGGACCCCGGGAATC-3'	5'-TGTAGGAAACCAAGCCACCTC-3'
mm <i>Frzb</i>	5'-GTGTACGACCGCGCGTGTG-3'	5'-CTGCTTGCCCCTCTCGAGTGTG-3'
mm <i>Gata4</i>	5'-AACCAGAAAACGGAAGCCCA-3'	5'-TTGATGGGGCGCATCTCTTC-3'
mm <i>Gli1</i>	5'-CCTGGTGGCTTTTCATCACTCTCG-3'	5'-CACAGGGCTGGACTCCATAGG-3'
mm <i>HmgcoR</i>	5'-AGCAGAGCTACGTTTGTGCTC-3'	5'-ATTAGTCTGTGGCTCGATGG-3'
mm <i>Hsd17b7</i>	5'-ATGCGCTCACTGTGACACC-3'	5'-TCCAGCTCCAGTAAGACCTCA-3'
mm <i>Hsd3b1</i>	5'-ATGGTCTGCCTGGGAATGAC-3'	5'-ACTGCAGGAGGTGAGAGCT-3'
mm <i>Hsd3b6</i>	5'-CATCCTTCCACAGTTCTAGC-3'	5'-TGGTGTGAGATTAATGTACT-3'
mm <i>Ldlr</i>	5'-GGAGGCCGTGTACGCCGATG-3'	5'-CGGCCCTGGCAGTTCTGTGG-3'
mm <i>Lef1</i>	5'-GACGAGCACTTTCTCCGGG-3'	5'-TGGGGTGATCTGTCCAACGC-3'
mm <i>Nr0b1 (Dax-1)</i>	5'-GGTCCAGGCCATCAAGAGTTT-3'	5'-CCGGATGTGCTCAGTAAGGAT-3'
mm <i>Nr2f2</i>	5'-GAGCGAGCTGTTCTGTGAA-3'	5'-ACTTGCTCTTGAAGATCCG-3'
mm <i>Nr5a1(Sf-1)</i>	5'-TGCAGAATGCCGACCAG-3'	5'-TGGCGGTAGATGTGGTC-3'
mm <i>Patch1</i>	5'-CCATACACCAGCCACAGCTTCG-3'	5'-GGAGGCTGGAGTCTGAGAACTG-3'
mm <i>Pcna</i>	5'-CCTGTGCAAAGAATGGGGTG-3'	5'-AGACAGTGGAGTGGCTTTTGT-3'
mm <i>Pik3c2g</i>	5'-CCATTTGTGGACCCAGGTGA-3'	5'-GGGTCAAGTGCATTTTGAACA-3'
mm <i>Tcf21</i>	5'-CAGATCCTGGCCAACGACAAGTACG-3'	5'-CATTCTCTGTTTGGCGCCACC-3'
mm <i>Prkar1a</i>	5'-CGGGAATGCGAGCTCTATGT-3'	5'-CTCGAGTCAGTACGGATGCC-3'
mm <i>Hspo3</i>	5'-TCATTTTGAACTTTATGGAATACATTG-3'	5'-CAGCCATTGTAATCTGAACACG-3'
mm <i>Shh</i>	5'-GCGGCAGATATGAAGGGAAGATC-3'	5'-GTTTCATCACAGAGATGGCCAAGGC-3'
mm <i>Sqle</i>	5'-TCTCAGAATGGTCTGCTGCC-3'	5'-ACCAGTAAGAGGGTGCCTCA-3'
mm <i>Scarb1</i>	5'-CCTTCGTGGAGAACCAGCAGCC-3'	5'-CCCATGGTGACCAGCGCCAA-3'
mm <i>Sreb12</i>	5'-AGCTGGGCGATGGATGAGAG-3'	5'-TCAGGGAAGTCTCCCACTTGA-3'
mm <i>StAH</i>	5'-TCGCTACGTTCAAGCTGTGT-3'	5'-ACGTCGAAGTTGACCCATCC-3'
mm <i>Sult1e1</i>	5'-AAAGGGAATTTATAGGAGACTGGAAGAA-3'	5'-TGCTGCTTGTAGTGCTCATCA-3'
mm <i>Wnt4</i>	5'-CCCTGTCTTTGGGAAGGTGGTG-3'	5'-CACCTGCTGAAGAGATGGCGTATAC-3'
mm <i>Wt1</i>	5'-CGGCGCAGTTCCCCAACCATTC-3'	5'-GCACGGAGTACTGCTGCTCGC-3'

Supplemental Table S3. Lists of genes used in gene set enrichment analyses (GSEA)

Cholesterol	Glomerulosa				Fasciculata				Wnt		
acat1	Cyp11b2	LOC294942	Cacnb3	Nbl1	LOC363306	Cdh9_predicted	RGD1562991_predicted	Nf2	vsnl1	rspo3	chd8
acat2	Rgs4	Ampd3	Ssg1	Sat2_predicted	Ddah1	Prlr	Baalc	RGD1566239_predicted	wnt1	rspo4	tgfb11
hmgcs1	Smoc2_predicted	RGD1305645_predicted	Pdia5	LOC366505	LOC498373	Gm2a	Acaa2	LOC687579	wnt2	lgr4	bcr
hmgcr	Mia1	Jub	Prkra	Gclc	Cidea_predicted	Tekt1	RGD1311827	Tmem192	wnt2b	lgr5	hint1
mvk	Dlk1	Sept8_predicted	Fkbp9	Fkbp7_predicted	Hpx	C4-2	Sdhb_predicted	LOC297110	wnt3	lgr6	dixc1
pmvk	Sstr2	Rcan2	Sphk1	Evl	Hamp	Spink4	Card9	LOC684872	wnt3a	notum	psen1
mvd	Cadps	Abcg1	Snx1	Ahtcf1_predicted	RGD1562717_predicted	Olah	Tbc1d15	Slc22a6	wnt4	wif1	sufu
fdps	LOC311772	Col1a2	Serpinb9	Cygb	Cyp4f4	LOC498722	RGD1311444_predicted	Nrbf2	wnt5a	znrf3	ppp2r5b
fdft1	Igsf1	Gpha2	Arhgap24	Vtn	Serpina11	Nubpl_predicted	RGD1561530_predicted	Abhd2_predicted	wnt5b	rnf43	ppp2r5c
sqle	LOC362564	RGD1561041_predicted	Ivns1abp_predicted	LOC682869	LOC501497	Retsat	Lyplal1_predicted	RGD1561113_predicted	wnt6	apcdd1	frat1
lss	Gpc3	Hoxa7_mapped	Bzw2	Cdca1_predicted	Fabp6	Il18	Mst1	Mdm2_predicted	wnt7a	birc5	pak4
cyp51	Cpxm2_predicted	RGD1562562_predicted	Cpb1	Sav1_predicted	Nkx6-2_predicted	Sod3	Gsdmdc1_predicted	Lmo4	wnt7b	wisp1	ano4
tm7sf2	Atp10a	Epb4.1i3	Cyrr1	Heph	RGD1560609_predicted	LOC498736	Ydjc	Wbp5_predicted	wnt8a	wisp2	dab2
lbr	Postn_predicted	Pgf	Irak1bp1_predicted	Galm	Frzb	Atp6v1g1_predicted	LOC682174	Pkn1	wnt8b	btrc	
nsdh1	Boc_predicted	Sparc1	Slc7a6_predicted	Kbtbd9_predicted	LOC363060	Fads2	Dph5	Ccbl1	wnt9a	birc5	
msmo1	RGD1566317_predicted	Ckap4_predicted	Sncg	Mrps14_predicted	Ephb6	Tnni3	Trb3	Cib1	wnt10a	crebbp	
hsd17b7	Ndn	LOC501633	Fxyd1	Pfkf	Fbxo17	Ass	Tir3	Baiap2	wnt10b	ep300	
ebp	Dpt_predicted	Bok	Gls	Cryab	Rab33a_predicted	Pafah1b3	04-sept	Mmaa_predicted	wnt11	dact1	
sc5d	Kcnn2	Npr2	Adam33_predicted	Hhex	Gmpr	Phgdh	Maged2	wnt16	disc1		
dchr7	Rbp1	Spon1	Scn4b	RGD1560062_predicted	Vnn1	Pex16	Mlf1_predicted	Ctnnb1	fzd1	sost	
dhcr24	Wfdc1	Plod2	Stf6galnac2	Ublcp1	Hsd11b2	Pldx2_predicted	Ddt	RGD1563250_predicted	fzd2	dach1	
scap	Acy3	Atp2c1	Ptprr	Metrn	Mtla	Gdap2	RGD1559673_predicted	Gpi	fzd3	nkd1	
sreb2	RGD1307506_predicted	Chst1	Rom1	Rab28	Macro1	LOC316507	Apoc1	Chchd6_predicted	fzd4	nkd2	
sreb1	Ptgis	Sl3gal6	Myo1b	Sema7a_predicted	Edg4_predicted	Myom2	Dnajd1_predicted	LOC360800	fzd5	pias2	
insig1	Reck_predicted	LOC497723	Bcar3_predicted	Ndr4	Dchr7	Cebpb	Pgd	Lipa	fzd6	wif1	
insig2	RGD1564008_predicted	Stk39	LOC56764	Inpp5a_predicted	LOC681153	Kcnh1	Mvd	RGD1562178_predicted	fzd7	ezh2	
lipe	Nr0b1	Lum	Arhgef2	Stx6	Arlh1	Zfp533_predicted	Echs1	LOC293589	fzd8	podn	
plin1	Fmod	RGD1564914_predicted	Hexb	Ubqln2_predicted	F11r	Slc25a1	RGD1562658_predicted	Rsaf1_predicted	fzd9	nr3c1	
osbp11	Pde2a	RGD1564451_predicted	Nid67	LOC501223	Comtd1_predicted	LOC499675	Ptkp	Tnfp1_predicted	fzd10	dact3	
sec22b	Dab2	Ckb	Csac	LOC499856	Amid_predicted	RGD1311132_predicted	Hac2	Arpp19	sfrp1	ptk7	
sec23p	Sdc2	Gja4	Ccl19_predicted	Tmem204	Rhbg	Appbp2	Blvr6_predicted	Nduf57	sfrp2	nedd4l	
ralgs2	LOC363153	Jag1	RGD1307119	Igf2p2	Cyp1b1	Gstm1	Hspb1	Arndc1	frzb	senp2	
golga5	Pde9a	LOC311171	LOC497828	Cand2	Mmd2_predicted	Admr	LOC503418	Ivd	sfrp4	wis	
arfgap1	Agr1b	Slc7a1	Myh10	Sf3b1	Capn8	Msh5	LOC679271	LOC498674	sfrp5	kl	
atg16l1	Nfatc4	Plac9_predicted	Nde1	Cdc98	Dmd	RGD1561422_predicted	LOC292780	LOC293589	dv1	cpe	
nck1	Ccnd1	Scopdh	Tegt	Mmp23	LOC301506	RGD1306952	Anxa5	Exosc5_predicted	dv2	arntl	
arfgf2	Agtr1a	Rarres2	Rpl15	Tspan2	RGD1306364	Snappc1_predicted	LOC498228	LOC499812	dv3	ndrg1	
gpr107	Scarf2_predicted	LOC363181	Tjp1_predicted	LOC499004	MGC116197	Gja1	Pdyn	Usf1	hnf1a	tnks	
plekhf2	Mxra8	Dync1i1	Egr1	Snd1	LOC302210	Gml_predicted	Lox	Nsmce2	tcf3	amer2	
tbc1d10b	Gstm5	LOC497767	Kns2	Dab2ip	Anub1	Lonp1	Bckdha	RGD1307789	tcf4	amer1	
rin2	Cpxm1_predicted	Sfrp2	Adcy3	Cacna1d	Olr472_predicted	Vegfc	Chchd5_predicted	Mfge8	lef1	nfatc2	
als2	Fbln1_predicted	Serping1	RGD1563226_predicted	Ppt1	RGD1565105_predicted	MGC95152	RGD1309410_predicted	RGD1309562_predicted	lrp5	vax2	
dennd1a	Dmpk_predicted	Ptafr	Dlgap1	Rarb	LOC363408	Jun	LOC499465	RGD1565407_predicted	lrp6	slit2	
rmdn2	LOC367314	Dusp6	Nphp1_predicted	Rtn4	Csrp2	RGD1561445_predicted	Pkn2	Cbr1	apc	faf1	
clip1	Bhlhb3	Abr_predicted	Smarca5_predicted	Cxcl16	Gadd45g	Mthfd1	Cdc50	Mboat5	apc2	pmt1	
clip2	Ces3	Ldhb	Svs5	Fundc1	RGD1560183_predicted	Elf4ebp1	LOC683578	Gpx4	ctnnb1	smurf2	
ckap5	Tagln	Wee1	Tpm1	Altn	Kif22	Rit1_predicted	Tbc1d20	RGD1308750_predicted	axin1	sostdc1	
nav1	Pfn2	Ltbp1	Stim1_predicted	Slc25a4	Tas1r1	Rnaseh2a	Gaa	LOC692000	axin2	kremen2	
slain2	Col6a1_predicted	LOC679974	Nkd1_predicted	RGD1561255_predicted	Stom	Agpat3_predicted	Np_mapped	RGD1309313	dkk1	kremen1	
arhgap21	Col6a3_predicted	Galnt4_predicted	Pole4_predicted	Rshl2_predicted	RGD1560394_predicted	LOC681180	LOC497693	Trap1	dkk2	cyld	
arhgap17	LOC311984	Ftn1	Inpp4a	Itm2c	Litaf	RGD1310348_predicted	Slc25a16	Anxa4	dkk3	btik	
plekhg3	Flna_predicted	RGD1563167_predicted	Igf2p7	Pdia4	Tsn	LOC501045	Gm	RGD1563438_predicted	dkk4	cdc73	
arhgef17	Adcy4	Tm4sf1_predicted	RGD1562920_predicted	Gtf2h1_predicted	Slk19	04-sept	Pold4	Serpina6	gsk3a	dact3	
arhgef2	Cxcl12	Galnt14	Cpz	Ltv1	Dblif	Rarsl_predicted	Pcy2	Pomc	gsk3b	wt1	
arhgap23	Esm1	Numb_predicted	Slit3	Tada1l	Farp1_predicted	RGD1309385_predicted	Hexa	RGD1560964_predicted	porcn	aluba	
arhgef11	Myh11	Btg2	Vsnl1	LOC499677	Dhcr24	Cth	Susd5_predicted	Thop1	wis	grb10	
pi4kb	Loxl1	Hspa4l_predicted	Atp2a2	P18srp	MGC112790	Hes6	Acaa1		rspo1	prickle1	
mxipl	Tmem14a_predicted	Arhgap9	Cacna1c		Slc6a8	LOC683385	Prdx5		rspo2	qskip	
dhhd2	G0s2	Atp1b2	RGD1305288		RGD1304982_predicted	RGD1564762_predicted	Fdps		rspo2	en1	