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## Supplemental information

## PPT1 regulation of HSP90α

## depalmitoylation participates

## in the pathogenesis of hyperandrogenism

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Figure S1 The DHEA-induced mouse model displayed hyperandrogenism phenotypes, related to Figure 1. (A) Timeline of DHEA treatment of mice. (B) Representative hematoxylineosin (H&E)-stained sections from the ovaries of the control and DHEA groups. Scale bar: 200  $\mu$ m. The asterisk (\*) represents the corpus luteum, and the pound sign (#) represents the ovary vacuoles. (C) Number of cystic follicles in the control and DHEA groups. (D) Representative estrous cycles. (E) Weight (n=7 mice per group). (F) Ovary weight (n=7 mice per group). (G) Testosterone levels (n=7 mice per group). (H) Estradiol levels (n=7 mice per group). (I) LH levels (n=7 mice per group). (J) FSH levels (n=7 mice per group). (K) LH/FSH (n=7 mice per group). For (C, E-K), *P* values were determined by two-tailed Student's *t* test, and data are presented as the mean values ± SD.



**Figure S2 HSP90α equal protein expression between WT and mutants after plasmids transfection and DHT treatment, related to Figure 4.** (A) Immunoblot analysis showing *m*HSP90α protein level in HEK293T cells transfected with Flag-tagged *m*HSP90α-WT or *m*HSP90α-C598, 599S treated with methanol or DHT (100 nM) for 24 hours. (B) Immunoblot analysis showing *m*HSP90α-C598, 599S treated with methanol or DHT (100 nM) for 24 hours. (B) Immunoblot analysis showing *m*HSP90α-C598, 599S treated with methanol or DHT (100 nM) for 24 hours. (C) Immunoblot analysis showing *m*HSP90α-C597, 598S treated with methanol or DHT (100 nM) for 24 hours. (C) Immunoblot analysis showing *m*HSP90α-C597, 598S treated with methanol or DHT (10 nM) for 24 hours. (D) Immunoblot analysis showing *h*HSP90α protein level in LnCaP cells transfected with Flag-tagged *h*HSP90α-WT or *h*HSP90α-C597, 598S treated with methanol or DHT (10 nM) for 24 hours.



Figure S3 Dipyridamole treatment protects against a DHEA-induced poor-quality oocyte phenotype, related to Figure 7. (A) Timeline of dipyridamole treatment in hyperandrogenism phenotype or control mice. (B) Germinal vesicle breakdown (GVBD) percentage (n=4 mice per group). (C and D) The first polar body extrusion (PBE) rate (n=4 mice per group). For (B and D), *P* values were determined by Student's *t* test, and the data are presented as the mean values  $\pm$  SEMs.

Table S1 increased level of S-painitoyiation proteins, related to Figure 5.				
Gene	Full name			
DYH5	Dynein heavy chain 5			
CAC1E	Voltage-dependent R-type calcium channel subunit alpha-1E			
SEPT7	Septin-7			
H12	Histone H1.2			
KPYM	Pyruvate kinase PKM			
STOM	Erythrocyte band 7 integral membrane protein			
DAD1	Dolichyl-diphosphooligosaccharideprotein glycosyltransferase subunit			
RANT	GTP-binding nuclear protein Ran,			
1433Z	14-3-3 protein zeta/delta			
CO6A2	Collagen alpha-2(VI) chain			
TNR6A	Trinucleotide repeat-containing gene 6A protein			
LTBP1	Latent-transforming growth factor beta-binding protein 1			
FIBB	Fibrinogen beta chain			
ZDHC1	Palmitoyltransferase ZDHHC1			
NB5R3	NADH-cytochrome b5 reductase 3			

Table S1 Increased level of S-palmitoylation proteins, related to Figure 3.

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Gene	Full name
TITIN	Titin
DPYL3	Dihydropyrimidinase-related protein 3
PRDX6	Peroxiredoxin-6
CD151	CD151 antigen
PDIA4	Protein disulfide-isomerase A4
CO3A1	Collagen alpha-1(III) chain
MDHM	Malate dehydrogenase
GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2
GPX1	Glutathione peroxidase 1
AT1B2	Sodium/potassium-transporting ATPase subunit beta-2
HSP72	Heat shock-related 70 kDa protein 2
ENOG	Gamma-enolase
3BHS1	3 beta-hydroxysteroid dehydrogenase/Delta 54-isomerase type 1
GRP75	Stress-70 protein
CHD1	Chromodomain-helicase-DNA-binding protein 1
H15	Histone H1.5
HSP90A	Heat shock protein 90, alpha (Cytosolic), class A member 1
CDN1B	Cyclin-dependent kinase inhibitor 1B
ASPX	Acrosomal protein SP-10
RHG39	Rho GTPase-activating protein 39
RS8	40S ribosomal protein S8
RAP1B	Ras-related protein Rap-1b
UB2L3	Ubiquitin-conjugating enzyme E2 L3
1433T	14-3-3 protein theta
TERA	Transitional endoplasmic reticulum ATPase
PGBM	Basement membrane-specific heparan sulfate proteoglycan core protein
SPB6	Serpin B6
ADRO	NADPH:adrenodoxin oxidoreductase
ZYX	Zyxin
HUMMR	Protein MGARP
THIKA	3-ketoacyl-CoA thiolase A
MCCA	Methylcrotonoyl-CoA carboxylase subunit alpha
RRBP1	Ribosome-binding protein 1
ACBG1	Long-chain-fatty-acidCoA ligase ACSBG1
UQCC2	Ubiquinol-cytochrome-c reductase complex assembly factor 2
CRIP2	Cysteine-rich protein 2
AL9A1	4-trimethylaminobutyraldehyde dehydrogenase
K1C17	Keratin, type I cytoskeletal 17
PEPL	Periplakin
INSRR	Insulin receptor-related protein
ASAH1	Acid ceramidase
SAE2	SUMO-activating enzyme subunit 2

Table S2 Decreased level of S-palmitoylation proteins, related to Figure 3.

r COS, felateu to Figure 5.					
	Control (n=5)	ovarian	<i>P</i> value		
		hyperandrogenism in			
		PCOS (n=5)			
Age (year)	26.5±2.26	24.0±1.79	0.059		
Body Mass Index	21.3±1.71	24.0±4.33	0.189		
FSH (IU/L)	8.05±1.94	4.79±1.22	0.006		
LH (IU/L)	9.3±3.20	16.8±6.25	0.033		
LH/FSH	1.2±0.33	$3.4 \pm 0.48$	< 0.0001		
Estradiol (nmol/L)	$0.22{\pm}0.088$	$0.185 {\pm} 0.056$	0.449		
Testosterone (nmol/L)	4.35±0.78	4.94±1.39	0.387		
Dehydroepiandrosterone (nmol/L)	4.12±0.82	7.83±1.78	0.001		

 Table S3.
 Clinical characteristics in women with or without ovarian hyperandrogenism in

 PCOS
 related to Figure 5

FSH, follicle-stimulating hormone; LH, luteinizing hormone; P value were analyzed by two-tailed Student's *t*-test (for two groups).