Supplementary Figure 1: Functional Annotation of the *FKBP4* locus. Chromosomal coordinates (Chr12: 2,878,815-2,919,530 (GR37/hg19)) are shown across the top of the locus.

The coding region of *FKBP4* is shown by black vertical lines (exons, untranslated regions) and horizontal lines (introns), with direction of transcription shown by small arrows within introns. Genotyped SNPs that were significantly associated with PCOS are shown within rectangles, and SNPs with which they are in linkage disequilibrium (r^2>0.8) are marked with * in the corresponding color. Active chromatin sites are shown by DNase I hypersensitivity clusters (by greyscale with black indicating high chromatin availability). Transcription factor binding sites (TFBSs) are shown by greyscale, with black indicating high transcription factor occupancy. Chromatin states in six ENCODE cell lines (GM12878, Epstein-Barr virus transformed B-lymphocyte cell line from Caucasian (CEPH) subject from the International HapMap Project; H1-hESC, embryonic stem cell; K562, immortalized cell line produced from a female patient with chronic myelogenous leukemia; HeLa-S3, immortalized cell line derived from a patient with cervical cancer; HepG2, cell line derived from a male patient with liver carcinoma; HUVEC, human umbilical vein endothelial cells) are highlighted as follows: active enhancer (orange), poised enhancer (yellow), promoter/transcription start site (red), promoter flanking region (pink), insulator binding site (blue), transcribed (green), inactive chromatin (grey).

Supplementary Table 1

Power to detect association with PCOS: 354 cases, 161 controls, alpha=0.05

Risk allele frequency = 0.1			Risk allele frequency = 0.2			Risk allele frequency = 0.3		
Marker allele frequency	Relative risk	Power	Marker allele frequency	Relative risk	Power	Marker allele frequency	Relative risk	Power
0.1	1.5	0.43	0.2	1.5	0.53	0.3	1.5	0.51
	1.75	0.70		1.75	0.79		1.75	0.76
	2	0.87		2	0.93		2	0.90
	3	0.99		3	0.99		3	0.99
0.2	1.5	0.24	0.3	1.5	0.36	0.4	1.5	0.37
	1.75	0.43		1.75	0.60		1.75	0.59
	2	0.62		2	0.78		2	0.76
	3	0.96		3	0.99		3	0.98

Power to detect association with PCOS: 397 cases, 306 controls, alpha=0.05

Risk allele frequency = 0.1			Risk allele frequency = 0.2			Risk allele frequency = 0.3		
Marker allele frequency	Relative risk	Power	Marker allele frequency	Relative risk	Power	Marker allele frequency	Relative risk	Power
0.1	1.5	0.62	0.2	1.5	0.73	0.3	1.5	0.70
	1.75	0.89		1.75	0.94		1.75	0.92
	2	0.98		2	0.99		2	0.98
	3	0.99		3	0.99		3	0.99
0.2	1.5	0.36	0.3	1.5	0.52	0.4	1.5	0.53
	1.75	0.62		1.75	0.80		1.75	0.79
	2	0.82		2	0.94		2	0.92
	3	0.99		3	0.99		3	0.99

Supplementary Table 2: Frequency and position information for SNPs in the discovery cohort

SNP	Coordinates	Location in gene	Alleles[a]	Overall MAF[b]	PCOS MAF	Control MAF
FKBP4	chr12:2,794,953-2,805,423					
rs7973927	2,745,644	5' near gene	G/A	0.26	0.26	0.28
rs4238008	2,763,663	5' near gene	A/G	0.23	0.23	0.26
rs11062351	2,772,597	5' near gene	G/A	0.4	0.38	0.42
rs10848704	2,773,378	5' near gene	G/A	0.21	0.21	0.21
rs4765709	2,774,471	5' near gene	G/A	0.36	0.34	0.39
rs4075718	2,775,142	5' near gene	A/G	0.21	0.2	0.21
rs4409904	2,776,963	5' near gene	A/G	0.14	0.12	0.18
rs4073426	2,777,133	5' near gene	A/G	0.18	0.18	0.18
rs2968909	2,788,698	5' near gene	G/C	0.17	0.16	0.2
rs3759411	2,792,404	5' near gene	G/A	0.13	0.12	0.14
rs11062360	2,805,002	3' UTR[c]	G/A	0.07	0.07	0.08
ST13	chr22:40,824,535-40,857,022					
rs13054099	40,819,668	3' near gene	G/A	0.25	0.25	0.25
rs6002171	40,827,855	Intron 10	A/G	0.05	0.05	0.07
rs5750998	40,833,145	Intron 7	A/G	0.05	0.04	0.07
rs7290793	40,855,008	Intron 1	A/G	0.08	0.07	0.09
rs138351	40,866,848	5' near gene	A/G	0.22	0.22	0.23
rs138354	40,876,139	5' near gene	A/G	0.46	0.48	0.45

rs1005402	40,895,726	5’ near gene	A/G	0.47	0.47	0.47
HSPA8	chr11:123,057,489-123,062,335					
rs7123232	123,056,237	3’ near gene	A/G	0.16	0.16	0.17
rs12575564	123,065,958	5’ near gene	A/G	0.14	0.14	0.15
rs11218950	123,072,200	5’ near gene	A/G	0.05	0.05	0.06
rs11218954	123,075,352	5’ near gene	G/A	0.21	0.2	0.23
rs7113273	123,092,192	5’ near gene	G/A	0.28	0.27	0.28
rs11218981	123,100,750	5’ near gene	A/G	0.12	0.12	0.11
rs7933576	123,105,745	5’ near gene	A/G	0.1	0.1	0.09
STUB1	chr16:680,276-682,799					
rs2076142	650,970	5’ near gene	A/G	0.22	0.22	0.21
rs3752490	667,828	5’near gene	A/C	0.35	0.34	0.37
rs11557858	669,592	5’ near gene	A/G	0.13	0.12	0.16
rs1045763	674,084	5’ near gene	A/G	0.06	0.06	0.06
rs3830140	675,335	5’near gene	A/G	0.09	0.09	0.08
rs6597	681,725	Intron 3	C/A	0.16	0.16	0.16
STIP1		chr11:64,186,115-64,204,543				
rs7112960	64,139,607	5’ near gene	G/A	0.35	0.36	0.34
rs1123251	64,150,129	5’ near gene	C/A	0.5	0.5	0.49
rs11603212	64,160,338	5’ near gene	G/A	0.17	0.18	0.16
rs4980508	64,174,262	5’ near gene	C/A	0.5	0.5	0.49
rs1011219	64,205,924	3’ near gene	A/G	0.16	0.16	0.17
HSPA1A	chr6:31,815,464-31,817,946					

rs707928	31,774,813	5'near gene	G/A	0.35	0.33	0.38
rs2736426	31,777,507	5' near gene	G/A	0.45	0.44	0.47
rs480092	31,797,122	5'near gene	G/A	0.18	0.17	0.22
rs2075800	31,810,169	5' near gene	A/G	0.33	0.36	0.28
rs2075799	31,810,752	5' near gene	A/G	0.09	0.1	0.07
PTGES3	chr12:56,663,343-56,688,300					
rs17444799	56,670,615	Intron 4	A/G	0.06	0.06	0.07
rs2926743	56,720,316	5' near gene	A/G	0.28	0.29	0.23
rs11171952	56,722,877	5' near gene	A/G	0.08	0.08	0.09
rs2035081	56,732,095	5' near gene	A/G	0.37	0.38	0.33
BAG1	chr9:33,252,477-33,264,761					
rs3758270	33,263,676	Intron 1	G/A	0.06	0.07	0.05
rs844239	33,270,481	5' near gene	A/G	0.24	0.24	0.21
rs831275	33,282,673	5' near gene	A/G	0.15	0.15	0.15

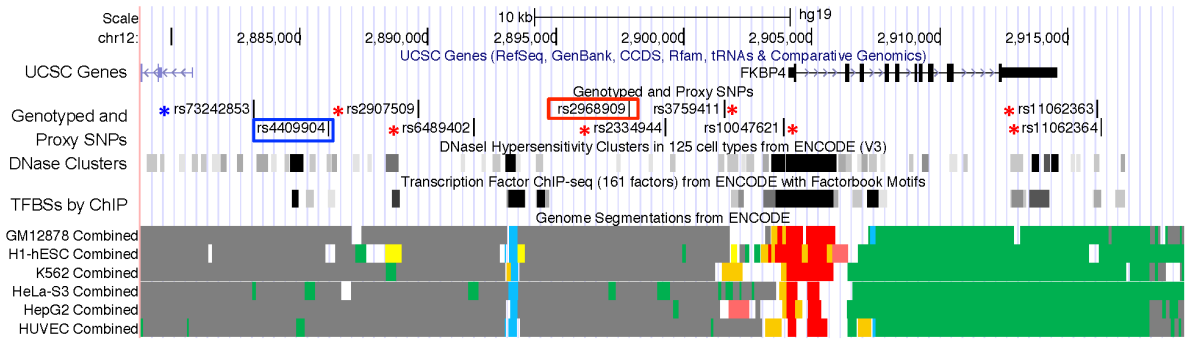
[a]Alleles are listed as minor/major, [b]MAF = minor allele frequency, [c]UTR = untranslated region
Coordinates are from the UCSC Genome Browser on human Dec. 2013 (GRCh38/hg38) assembly.

Supplementary Table 3: Association of *FKBP4* variants with quantitative traits in women with PCOS

SNP	Trait	Beta	SE	P value
Discovery cohort				
rs2968909	Total testosterone	-0.433	1.691	0.80
rs2968909	DHEAS	-3.686	2.532	0.15
rs2968909	Insulin	-11.060	4.450	0.013
rs2968909	HOMA-IR	-7.585	4.759	0.11
rs2968909	HOMA-%B	-7.937	4.975	0.11
rs2968909	Glucose	-18.640	7.937	0.019
rs2968909	BMI	-0.005	0.028	0.87
rs4409904	Total testosterone	1.445	1.901	0.45
rs4409904	DHEAS	2.576	2.848	0.37
rs4409904	Insulin	-5.507	5.021	0.27
rs4409904	HOMA-IR	-3.879	5.351	0.47
rs4409904	HOMA-%B	-4.087	5.594	0.47
rs4409904	Glucose	-11.120	8.940	0.21
rs4409904	BMI	0.011	0.032	0.73
Replication cohort				
rs2968909	Total testosterone	0.240	0.589	0.68
rs2968909	DHEAS	0.241	2.155	0.91
rs2968909	Insulin	4.102	3.481	0.24
rs2968909	HOMA-IR	6.427	3.885	0.099
rs2968909	HOMA-%B	6.736	4.050	0.097

rs2968909	Glucose	4.386	5.082	0.39
rs2968909	BMI	-0.074	0.026	0.0043
rs4409904	Total testosterone	0.332	0.702	0.64
rs4409904	DHEAS	0.814	2.688	0.76
rs4409904	Insulin	1.073	4.175	0.80
rs4409904	HOMA-IR	1.000	4.691	0.83
rs4409904	HOMA-%B	1.022	4.891	0.83
rs4409904	Glucose	1.857	6.029	0.76
rs4409904	BMI	-0.030	0.032	0.36

Associations above are adjusted for age, BMI, and recruitment site, except for BMI where adjustment was for age and site. Testosterone and DHEAS were square root transformed and BMI, insulin, HOMA-IR, and HOMA-%B were log transformed. SE = standard error; DHEAS = dehydroepiandrosterone sulfate.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K562 Combined
HeLa-S3 Combined
HepG2 Combined
HUVEC Combined