Supplementary Table SVI Oocyte enriched canonical pathways within genes belonging to modules significantly associated with patient traits.

Module color (total genes) Trait (correlation, *P*-value)[a]	Canonical pathway	Gene count	FDR[b]	Genes
Germinal vesicle oocytes				
Sky blue (70) age (0.66, 0.04)	Superpathway of Inositol Phosphate Compounds	4	1.55E-02	ACP1, IGBP1, MTMR7, STYXL1
Metaphase II oocytes				
Green (682) good quality blastocyst% (−0.72, 0.02)	Glucocorticoid Receptor Signaling	22	2.14E-03	AKT1, BRD7, EP300, FOS, GTF2F2, GTF2H4, HMGB1, KRT36, MAP2K1, NFATC3, PIK3R2, POLR2H, POU2F2, PPP3CC, SMAD2, SMAD4, SMARCA4, STAT3, SUMO1, TAF3, TAF5, TAF6
	Role of PKR in Interferon Induction and Antiviral Response	8	2.14E-03	AKT1, BID, EIF2S1, IFNB1, MAP2K3, MAP2K6, TAB2, TP53
	Hereditary Breast Cancer Signaling	13	7.59E-03	AKT1, BARD1, BRD7, E2F1, EP300, FAAP24, HDAC6, PALB2, PIK3R2, POLR2H, RPA1, SMARCA4, TP53
	TGF-β Signaling	10	1.35E-02	ACVR1B, ACVR2B, BMPR1A, EP300, FOS, MAP2K1, MAP2K3, MAP2K6, SMAD2, SMAD4
	Role of BRCA1 in DNA Damage Response	9	1.91E-02	BARD1, BRD7, E2F1, FAAP24, MDC1, RBBP8, RPA1, SMARCA4, TP53
	ERK5 Signaling	8	1.91E-02	AKT1, ELK4, EP300, FOS, GNAQ, PTPN11, RPS6KA6, WNK1
	B Cell Receptor Signaling	14	1.91E-02	AKT1, EP300, GSK3A, MAP2K1, MAP2K3, MAP2K6, MAP3K9, MAP3K13, NFATC3, PAG1, PIK3R2, POU2F2, PPP3CC, PTPN11
	Neurotrophin/TRK Signaling	8	2.24E-02	AKT1, EP300, FOS, MAP2K1, MAP2K3, MAP2K6, PIK3R2, PTPN11
	CD27 Signaling in Lymphocytes	7	2.24E-02	BID, FOS, MAP2K1, MAP2K3, MAP2K6, MAP3K9, MAP3K13
	RANK Signaling in Osteoclasts	9	2.75E-02	AKT1, FOS, MAP2K1, MAP2K6, MAP3K9, MAP3K13, PIK3R2, PPP3CC, TAB2
	Mouse Embryonic Stem Cell Pluripotency	9	4.27E-02	AKT1, BMPR1A, DVL2, MAP2K1, PIK3R2, PTPN11, SMAD4, STAT3, TP53
Turquoise (2, 604) good quality blastocyst% (0.76, 0.01)	Mitochondrial Dysfunction	52	2.45E-10	ACO1, ACO2, AIFM1, ATP5A1, ATP5B, ATP5E, ATP5F1, ATP5G1, ATP5H, ATP5I, ATP5L, ATP5O, ATP5S, ATPAF1, ATPAF2, CASP3, COX10, COX17, COX7B, CPT1C, CYB5R3, FIS1, HSD17B10, MAPK10, NDUFA1, NDUFA2, NDUFA3, NDUFA7, NDUFA8, NDUFA9, NDUFA10, NDUFA12, NDUFAF2, NDUFB3, NDUFB7, NDUFS2, NDUFS5, NDUFS6, NDUFS7, NDUFS8, NDUFV1, NDUFV2, PARK7, PDHA1, PINK1, PSEN1, PSEN2, SDHA, SOD2, UCP2, UQCRC1, VDAC3
	Oxidative Phosphorylation	34	6.31E-07	ATP5A1, ATP5B, ATP5E, ATP5F1, ATP5G1, ATP5H, ATP5I, ATP5L, ATP5O, ATP5S, ATPAF1, ATPAF2, COX10, COX17, COX7B, NDUFA1, NDUFA2, NDUFA3, NDUFA7, NDUFA8, NDUFA9, NDUFA10, NDUFA12, NDUFB3, NDUFB7, NDUFS2, NDUFS5, NDUFS6, NDUFS7, NDUFS8, NDUFV1, NDUFV2, SDHA, UQCRC1
	tRNA Charging	16	1.17E-04	AARS, CARS, DARS2, FARS2, HARS, LARS, LARS2, MARS, NARS, PARS2, RARS, SARS, TARS, TARS2, VARS, WARS
	phagosome maturation	29	1.55E-03	ATP6V0A1, ATP6V0D1, ATP6V0E1, ATP6V0E2, ATP6V1A, ATP6V1B2, ATP6V1C1, ATP6V1D, ATP6V1E1, ATP6V1G1, ATP6V1H, DYNC1I2, DYNC1LI1, DYNLL1, DYNLRB1, DYNLT1, M6PR, NSF, PIK3C3, RAB5B, RAB7A, TUBA1A, TUBA1B, TUBA1C, TUBA4A, VPS39, VPS41, VPS33B, VTI1A
	Cell Cycle Control of Chromosomal Replication	11	4.37E-03	CDK2, CDK5, MCM3, MCM4, MCM5, MCM6, MCM7, ORC2, ORC4, ORC5, RPA2

Continued

Supplementary Table SVI *Continued*

Module color (total genes) Trait (correlation, *P*-value)[a]	Canonical pathway	Gene count	FDR[b]	Genes
	N-acetylglucosamine Degradation II	4	1.02E-02	AMDHD2, GNPDA1, GNPDA2, NAGK
	Nucleotide Excision Repair Pathway	12	1.02E-02	CCNH, ERCC1, ERCC3, GTF2H1, GTF2H5, MNAT1, POLR2B, POLR2E, POLR2I, POLR2J, POLR2L, RPA2
	Acetyl-CoA Biosynthesis I (Pyruvate Dehydrogenase Complex)	5	1.38E-02	DBT, DLAT, DLD, PDHA1, PDHB
	Valine Degradation I	8	1.38E-02	ABAT, BCKDHA, DBT, DLD, ECHS1, HADHB, HIBADH, HIBCH
	Assembly of RNA Polymerase II Complex	14	2.29E-02	CCNH, ERCC3, GTF2E1, GTF2E2, GTF2H1, GTF2H5, MNAT1, POLR2B, POLR2E, POLR2I, POLR2J, POLR2L, TAF9, TAF9B
	CDP-diacylglycerol Biosynthesis I	7	3.16E-02	ABHD5, AGPAT2, AGPAT3, CDS2, GPAT3, GPAT4, LPCAT4
	Germ Cell-Sertoli Cell Junction Signaling	30	4.37E-02	ACTG2, CDC42, CDH1, CDH2, CFL1, CFL2, CTNND1, DIRAS3, EPN1, GSN, ITGA3, JUP, LIMK1, LIMK2, MAP3K2, MAP3K7, MAPK10, MTMR2, PAK1, PIK3C3, PIK3CD, PIK3R4, PLS1, RHOC, RHOG, SORBS1, TUBA1A, TUBA1B, TUBA1C, TUBA4A
Red (582) fertilization% (−0.68, 0.03)	Tight Junction Signaling	14	1.17E-02	CLDN6, CSTF3, CTNNA1, EPB41, GOSR2, MYH7, MYL4, NAPG, NUDT21, OCLN, PPP2CB, PRKAR1A, SAFB, YKT6

Canonical pathway enrichment analysis was conducted using IPA.
Gene modules within the respective stages contain unique genes.
[a]Physical traits significantly (*P* < 0.05) correlated with respective gene modules.
[b]Benjamini-Hochberg multiple testing correction *P*-value (FDR).