Supplementary Table SVII **Oocyte enriched biological functions within genes belonging to modules significantly associated with patient traits.**

Module color (total genes) Trait (correlation, *P*-value)[a]	Function	Gene count	FDR[b]	Genes
Germinal vesicle oocytes				
Sky blue (70) age (0.66, 0.04)	Long term depression of hippocampal neurons	2	2.74E-02	CAMK2A, HTT
	Stress response of neurons	2	2.74E-02	HSD17B10, HTT
	Transport of mitochondrial membrane	2	2.74E-02	HTT, TMEM14C
	Concentration of GABA	2	2.74E-02	HTT, SLC6A11
	Elongation of cellular protrusions	3	2.74E-02	CAMK2A, HTT, ICAM2
	Branching of neurites	5	2.74E-02	CAMK2A, DLG5, HTT, PKP4, RND2
Cyan (231) maturation% (−0.77, 0.01), blastocyst% (−0.67, 0.03)	Proliferation of cells	76	1.18E-02	ACER3, AGGF1, AKIP1, ANP32A, ASPM, ATAD2, ATG5, ATRAID, BARD1, BCCIP, BCLAF1, BIRC6, BNIP3, CACYBP, CBX4, CDC25C, CDC42BPA, CDCA7, CDKN1B, CRY1, CSNK1G3, DCLRE1A, DKC1, DUSP6, EIF4E3, FN1, GRHL2, HPRT1, IDH1, KDM3A, KDM6A, KIDINS220, LAMA5, LGALS1, LPIN1, MAPK9, MELK, MLLT6, MSX2, MT2A, MYH7, NAA35, NFATC3, NOC3L, NOLC1, NSA2, PAG1, PAPSS2, PCNA, PLA2G10, PRKAR1A, PRMT6, PTPN2, RAE1, RBL1, RNF34, SART1, SAV1, SEMA3A, SMURF2, STOX1, STRAP, STX2, SUMO2, TCP1, TIPIN, TNFRSF11B, TOMIL1, TOP1MT, TOP2A, TRPC4, UHRF2, WASF2, XRN2, ZNF143, ZNRF3
	Maturation of connective tissue cells	5	2.14E-02	CDKN1B, LPIN1, MSX2, RBL1, TNFRSF11B
	Ubiquitination	13	2.84E-02	ATG5, BIRC6, CRY1, ERCC8, FBXO45, HPRT1, MAPK9, RNF34, SHPRH, SUMO2, TRIM59, UHRF2, ZNRF3
	Growth of heart	7	3.61E-02	AKIP1, CDKN1B, DUSP6, MAPK9, NFATC3, PRKAR1A, SAV1
	Cell cycle progression of cervical cancer cell lines	4	4.50E-02	CDC25C, CDKN1B, MMS22L, TCP1
Metaphase II oocytes				
Green (682) good quality blastocyst % (−0.72, 0.02)	Transcription of RNA	125	1.19E-06	ACVR1B, ACVR2B, AKT1, ARID4A, ASH1L, ATRX, BACH2, BID, BMPR1A, BPTF, BRD4, BRD7, C14orf166, CBY1, CD3EAP, CDC5L, CEP290, CIR1, CKS1B, CRTC2, CRY1, DAP, DCP1A, DHX36, DNMT3B, DVL2, E2F1, EHMT1, EID1, EIF2S1, ELK4, ELP4, ENY2, EP300, EPC1, ERN1, FN1, FNIP2, FOS, FST, GNAQ, GNB1, GSK3A, GTF2F2, GTF2H4, HBG2, HDAC6, HEXB, HMGB1, HNRNPA1, HNRNPAB, HNRNPC, HOXA7, HTT, IFNB1, IKZF4, KLF2, KMT2D, MAFG, MAP2K1, MAP2K3, MAP2K6, MAZ, MLLT1, MLXIP, MORF4L2, MXD4, NCOA6, NELFB, NFATC3, NFIB, NIPBL, NKAP, NR6A1, NUFIP1, OSR2, PABPN1, PICALM, PIK3R2, POLR2H, POU2F2, POU4F2, PPP1R12A, PRMT2, PSMD9, PTMS, PTPN11, PTTG1, RBBP7, RBBP8, RNASEK, RNF10, SALL2, SBNO2, SET, SLC30A9, SMAD2, SMAD4, SMARCA4, SPEN, STAT3, STRAP, SUMO1, TAB2, TAF3, TAF5, TAF6, TCEA1, TET3, THRA, THRB, TLR2, TNFAIP1, TOX2, TP53, TP53INP1, TRIP11, YLPM1, YY1, YY1AP1, ZBTB17, ZC3H8, ZNF395, ZNF462, ZNF76
	Formation of nuclear foci	11	4.68E-05	BACH2, BARD1, BRD4, DNMT3B, EP300, FAAP24, HTT, PALB2, SUMO1, TP53, YY1
	G2 phase	26	3.28E-04	AKT1, ATRX, CDC5L, CKS1B, E2F1, EIF3E, ELAVL1, EP300, FBXL7, MAD2L1, MAP2K1, MAP2K6, MBD4, MCM10, MDC1, NUMB, PTPN11, PTTG1, RBBP8, RPA1, SKP2, SMARCA4, TAF6, TAOK3, TP53, YY1AP1
	Size of embryo	31	5.03E-04	BMPR1A, BPTF, CHMP5, DNMT3B, EP300, ERN1, FN1, HTT, KLF2, LMNB2, MAD2L1, MORF4L1, MORF4L2, NF1, NFATC3, NR6A1, NUMB, PALB2, PICALM, POFUT1, PTPN11, PTTG1, REV3L, SMAD2, SMAD4, STAT3, TCEA1, TP53, UBR4, YY1, ZBTB17
	Processing of RNA	27	6.86E-04	BARD1, BRDT, BUD13, CDC40, CDC5L, CDK11B, ERN1, EXOSC3, EXOSC7, HNRNPA1, HNRNPC, HNRNPF, HTT, KHDRBS3, MTPAP, NOL8, NSRP1, NUFIP1, PABPC4, PABPN1, PPIG, PPIH, RBM11, RPL7, SNRPD1, SNRPD2, TRMT112

Continued

Supplementary Table SVII *Continued*

Module color (total genes) Trait (correlation, *P*-value)[a]	Function	Gene count	FDR[b]	Genes
	Organismal death	133	2.14E-03	ABCA5, ACVR1B, ACVR2B, AKAP9, AKT1, ARF6, ARID4A, ATP1A1, B4GALT1, BARD1, BID, BIRC6, BMPR1A, BPTF, CAPRIN1, CBY1, CHMP5, CKS1B, CR2, DCLRE1C, DHX36, DNMT3B, DVL2, E2F1, EEF2K, EHMT1, EIF2AK3, EIF2S1, EIF4A1, ELAVL1, ENAH, EP300, ERN1, F9, FAT1, FN1, FOS, FST, FTO, GCH1, GJC1, GNA11, GNAQ, GNB1, GNPAT, GPNMB, GRID2, HEXB, HMGB1, HNRNPA1, HNRNPAB, HNRNPC, HOXA7, HRH2, HTR2C, HTR7, HTT, ICA1, IFNB1, INCENP, KIF2A, KLF2, KMT2B, KMT2C, LAMC1, LAMP1, LIN7C, LMNB2, MAD2L1, MAFG, MAP2K1, MAP2K3, MBD5, MCM10, MKI67, MLLT1, MORF4L1, MORF4L2, MUT, NEDD4L, NELFB, NF1, NFATC3, NFIB, NIPBL, NOA1, NR6A1, NUMB, PALB2, PHC2, PICALM, POFUT1, POU2F2, PPIA, PPIG, PPP1R12A, PRMT1, PTPN11, PTPRN2, PTTG1, RASA3, RBBP8, RCE1, REV3L, RHEBL1, RPGRIP1L, RTN4, SALL2, SBNO2, SC5D, SH3GL1, SIAH2, SMAD2, SMAD4, SMARCA4, SPEN, STAT3, SYCP2, TAB2, TCEA1, THRA, THRB, TJP2, TLR2, TP53, TP53INP1, UBR4, UPF2, USE1, USP25, USP8, YY1, ZBTB17
	Abnormal morphology of embryonic tissue	40	3.47E-03	ACVR1B, ACVR2B, BIRC6, BMPR1A, BPTF, CHMP5, DVL2, EP300, ERN1, FN1, GNA11, GNAQ, HTT, INCENP, KLF2, KMT2B, LAMC1, MAD2L1, MAP2K1, MCM10, NF1, NFATC3, NOA1, NR6A1, NUMB, OFD1, PALB2, PHC2, PICALM, POFUT1, PTPN11, REV3L, RPGRIP1L, SALL2, SMAD2, SMAD4, STAT3, TP53, UBR4, ZBTB17
	Arrest in proliferation of cells	20	3.49E-03	AKT1, E2F1, EP300, FOS, IFNB1, MAP2K3, MAP2K6, MAZ, NUMB, PHF1, PRMT1, PTTG1, SKP2, SMAD2, SMAD4, SMARCA4, STAT3, THRA, TP53, ZBTB17
	Cell death of tumor cell lines	90	7.08E-03	ACVR1B, ACVR2B, AIMP2, AKAP1, AKT1, ATP1A1, BACH2, BARD1, BID, BIRC6, BRD4, CHMP5, CNOT11, CRTC2, DNAJC15, DVL2, E2F1, EEF2K, EHMT1, EIF2AK3, EIF2S1, ELAVL1, EP300, ERN1, FAHD2A, FN1, FOS, FST, GNA11, HDAC6, HNRNPA1, HNRNPC, HOXA7, HTT, IFNB1, INCENP, INIP, KLF2, KSR1, LAMP1, MAD2L1, MAP2K1, MAP2K3, MAP2K6, MAP3K9, MCM10, MDC1, NAA30, NAA35, NF1, NFIB, NUMB, OAZ1, ODC1, PARP16, PCBP2, PCDH15, PHF1, PPIA, PRMT1, PTPN11, PTPN13, PTTG1, RASSF3, RNF13, RPA1, RTN4, SALL2, SAR1A, SIAH2, SKP2, SMAD2, SMAD4, ST3GAL1, STAT3, SUMO1, TAF6, TAOK3, THRA, TLR2, TM2D1, TMEM69, TMSB10/TMSB4X, TOLLIP, TP53, TPD52, UHRF2, VPS28, YY1, ZMYM3
	Size of animal	17	7.65E-03	AKT1, BIRC6, CAPRIN1, CKS1B, DNMT3B, FOS, FST, LAMC1, LMNB2, MAP2K1, MORF4L1, NFIB, PHC2, REV3L, SMAD2, THRA, TP53
	Arrest in G2 phase of fibroblasts	5	1.10E-02	MAP2K6, MBD4, PTPN11, SMARCA4, TP53
	Morphology of thyroid gland	6	1.12E-02	ABCA5, E2F1, FN1, SMAD2, THRA, THRB
	Quantity of spermine	3	1.12E-02	HTT, OAZ1, ODC1
Dark red (134) maturation% (0.72, 0.02)	Swelling of colorectal cancer cell lines	2	3.87E-02	FA2H, RAP1GAP
Turquoise (2604) good quality blastocyst% (0.76, 0.01)	Organization of organelle	114	2.74E-03	ACP2, AFG3L2, ARL2, ATG7, AURKA, BAZ2A, BBS4, BCS1L, BLZF1, CCDC13, CDC25B, CDC42, CDH1, CFL1, CFL2, CHCHD3, CHMP1A, CHMP2A, CHMP2B, CHMP7, CLN6, CLTC, CNP, COG4, COX10, CSF1R, CTC1, CTDNEP1, DAXX, DES, DMRTC2, DNAJA3, DNAJB6, DNM1L, DOPEY2, DPYSL2, ERCC1, FIG4, FIS1, FSD1, GAA, GAK, GBF1, GNPTAB, GORASP1, GPI, GSN, HAUS8, HMGCL, HPS4, HPS5, IFT20, IGSF9, JUP, KIF4A, LAMTOR1, LIMK1, LIMK2, LRRTM4, LTBP2, MBP, MFSD8, MTFR2, MUL1, MYH9, NCK2, NDEL1, NFASC, NLGN1, NPLOC4, NSFL1C, NUMA1, OBSL1, PAFAH1B1, PARK7, PARP1, PARP11, PES1, PEX1, PEX11 A, PEX11B, PEX12, PEX16, PEX2, PHB, PIK3C3, PIN1, PINK1, PLK1, PPP1R9A, PPP1R9B, RAB3A, RAB43, RAB5B, RAB8A, RAD51D, RBBP4, RHOC, RRN3, SLC9A6, SOD1, SOD2, SPTBN5, STX17, SUN1, TMEM11, TRPV4, TSC1, TSC2, USO1, VCPIP1, VPS33B, VPS4A, VPS54
	Quantity of lysophospholipids	11	3.40E-03	ABCB4, AGPAT2, CD36, F2, LIPG, PDCD6IP, PLA2G6, PLPP2, PON1, SIRT6, SLC27A4

Continued

Supplementary Table SVII *Continued*

Module color (total genes) Trait (correlation, *P*-value)[a]	**Function**	**Gene count**	**FDR**[b]	**Genes**
	Cell death of cervical cancer cell lines	77	3.40E-03	ABCB7, ACD, AIFM1, ATG7, AURKB, BAD, BBS4, BIRC5, BOK, BUB1, BUB1B, CASP2, CASP3, CCAR2, CCND2, CDK1, CHTOP, CLK3, CSF1R, CTSB, DAP3, DAXX, DCC, DCLRE1B, DDIT3, DIABLO, DNAJA3, DNM1L, EIF4G2, EZR, FASTKD2, FLNB, GORASP1, HAUS8, IMMT, IRGM, KIF11, KIF14, LATS2, LCMT1, LYPLA2, MADD, MCRS1, NCOA4, NEK6, NUDCD3, OGFOD1, PAK1, PARP1, PDCD6IP, PIK3C3, PINK1, PLK1, PPP1R10, PSEN1, PSEN2, PTMA, RALB, RICTOR, RINT1, SMPD3, SOD1, SOD2, SRCAP, SRSF1, STYXL1, TCP1, TDGF1, TMEM214, TOP2A, TRAF2, TRAP1, TSC2, TUBA1A, TXNRD1, UCHL1, UCP2
	Quantity of mitotic spindle	9	7.95E-03	AURKA, AURKB, FLII, KIF11, KIF2C, KIF4A, NUDCD3, PAK1, PLK1
	Quantity of lysophosphatidic acid	10	8.24E-03	ABCB4, AGPAT2, CD36, F2, LIPG, PLA2G6, PLPP2, PON1, SIRT6, SLC27 A4
	Homologous recombination	31	1.01E-02	CDK2, CHCHD3, COPS7A, DDA1, FBXO18, HJURP, IK, KAT5, LRRC40, MAEL, MEPCE, PARP1, PRPF8, PSMC3IP, RAD51, RAD51D, RAD54B, RELN, RFC2, RPA2, SART1, SF3A3, SF3B2, SF3B5, SIRT6, SNRPA1, SNU13, SRCAP, SUN1, SYCP3, ZMYND8
	Transport of protein	63	1.43E-02	ACD, ADAR, AP1G1, AP1M1, AP2A1, AP2M1, AP3S2, AP4B1, ARCN1, ARF3, ASPSCR1, ATG14, BLZF1, CDK5, CFL1, CHCHD4, COG7, CRY2, CTSA, DNAJA4, DYNLT1, GGA1, IPO13, IPO9, JUP, KLC2, KPNA2, M6PR, MBP, MYH9, NDEL1, NSF, NUP214, NUP62, PEX1, PEX16, POLA2, PPP1R10, PSEN1, PSEN2, RAB11A, RAB7A, RAB8A, RBM22, RPAIN, SCAMP2, SCAMP3, SCFD1, SELK, SNX1, SNX13, SNX4, SOD1, STRADA, TIMM23, TSC2, USO1, VPS33B, VPS39, VPS41, WWP2, XPO6, ZP3
	Clathrin mediated endocytosis	19	1.84E-02	AP2A1, AP2B1, AP2M1, AP2S1, ASB1, ATP6V0D1, ATP6V0E1, ATP6V1B2, ATP6V1D, ATP6V1E1, CDC42, CLTC, DLL1, EPN1, GAK, KAT5, NAA60, SART1, SRSF3
	Metabolism of purine nucleotide	23	4.00E-02	ADSL, AMPD2, AMPD3, ATP5A1, ATP5B, ATP5F1, ATP5G1, ATP5H, ATP5L, ATP5O, BAD, COASY, CTNS, IDH3B, LHB, MDH1, PANK3, PDE1C, PGD, PPCDC, SHC1, SLC25A25, SLC27A4
Red (582) fertilization% (−0.68, 0.03)	Repair of DNA	27	2.07E-05	APP, ATF2, BCLAF1, ERCC4, ERCC5, ERCC6, EXOG, GSTP1, HSPA1A/HSPA1B, MLH1, NAE1, NHEJ1, NRAS, POLG, POLH, POLK, RAD50, RIF1, RNF168, RNF2, SLX4, SMARCC2, SMC1A, TMEM161A, UIMC1, USP3, UVSSA
	Cell death of fibroblasts	23	2.44E-04	APP, ATF2, EIF2AK2, EIF4E, EMD, EPHX1, GAB1, GPX4, IKBKG, MAPK14, MAPK8, MEN1, MLH1, NEK1, NRAS, OPA1, POLK, PPP1R15A, RB1CC1, SLK, STK3, STK4, TCEB3
	Movement of organelle	10	4.18E-03	APP, DNAH5, EMD, HAP1, KIF1C, MYO5A, MYO6, RAB6A, RSPH9, SYNE2
	Light sensitivity of skin	3	1.22E-02	ERCC6, POLH, TROVE2
	Orientation of Golgi apparatus	4	1.22E-02	ARFGEF1, DCTN1, SLK, STRN
	Damage of chromosomes	7	3.15E-02	ERCC4, HSPA1A/HSPA1B, MCM9, MCPH1, NHEJ1, POLH, SLX4
	Abnormal morphology of mitral valve	4	3.28E-02	ADAM15, ADAM17, ADAM9, TLL1

Biological function 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).