Table S4. IPA Networks identified for genes affected in summer granulosa cells

ID	Molecules in Network	Score	Focus Molecules	Top Functions	Upstream regulators
N1	↓↓AKR1B10, ↑↑AKR1C1/AKR1C2, ↓ALAS1, ↑↑ALCAM, ↑↑ANXA4, Ap1, CD3, Cg, ERK1/2, ↑↑EZR, F Actin, ↓↓F2RL1, FSH, ↓↓GPX4, ↑↑H2AFY, ↓↓HMCN1, ↑↑HOPX, ↓↓MAFB, ↑↑MID1, ↑↑MT3, NFkB (complex), PI3K (family), Pkc(s), ↓↓PYGL, Ras homolog, ↑↑RORA, ↓↓SHISA2, ↑↑SLC20A1, ↓↓STC2, ↑↑TFG, ↑↑TFPI, Tgf beta, ↑↑TGFBR3, ↑↑TJP1, Vegf	49	23	Cellular Growth and Proliferation, Cancer, Gastrointestinal Disease	Vegf(M/5), Cg(M/5), PI3K (family)(M/3), ↓↓MAFB(M/2), hydrogen peroxide(5), TP53(4), TGFB1(7), EGF(4), OSM(4), FGF2(4), IL15(4), prostaglandin E2(4), dihydrotestosterone(4)
N2	ABCF2, ↑↑ACSL3, AGPAT2, ↑↑ALDH9A1, ANKRD26, ↑↑ANKRD28, ANKRD52, ↓C11orf58, CCND1, CTTNBP2NL, ↑DR1, ↓↓GALNT7, KIF14, ↓↓LYZ, ↑MARK1, ↑↑MDH1, ↓↓MT-ND2, MYO1G, NDUFS8, ODF2, PCNXL3, PPP6R1, ↑↑RBFOX1, RBM24, ↑↑RBMS3, STK33, ↓↓SVIL, TGS1, ↓↓TMEM219, ↓↓TMEM106B, UACA, UBC, ↑↑USP15, USP9Y, ↑↑VWF	34	17	Developmental Disorder, Hereditary Disorder, Metabolic Disease	CCND1(M/3), TP53(2), TGFB1(3), SYVN1(2), ERG(2), PPARG(2)
N3	↑↑ARID5B, ↓↓C8orf47, CEP120, CEP350, ↑↑COL14A1, ↑↑FAM13A, FANCB, GABRB2, ↑↑GPM6A, IGF2BP1, LETM1, ↓↓MRPL36, ↓↓MT-ATP8, ↓↓NAV1, ↑↑NPTN, NUP210, OPRD1, PACSIN1, PAM16, ↑↑PGAP1, POLD2, POLD3, POLG, POLH, ↑↑PRICKLE1, RAB34, RAPGEF2, REV1, ↑↑REV3L, ↓↓SLC26A2, ↓↓SPICE1, TCF7L1, ↑TMEM87A, UBC, ↓↓VAT1L	31	16	Cell Cycle, DNA Replication, Recombination, and Repair, Cellular Assembly and Organization	TCF7L1(M/1), TGFB1(2), RAF1(2)

N4	ABHD16A, ↑↑AUTS2, CCR6, CH25H, CLIC5, ↑↑CRIPT, ↑↑DNAJC1, DUSP7, GNA14, GNAQ, GRPR, HNF4A, IFNG, IL2, IL12 (family), IL23R, ↑↑KCTD12, ↑↑MLLT3, MLLT10, ↓↓MT-ND2, ↓↓MT-ND4L, NAA10, NDUFS4, ↑↑NEAT1, PPP6C, ↓↓PTGER3, PTPRE, ↑↑PTPRM, SRC, STAT1, TBC1D10A, Tcrd, TRIP11, Villin, ↑↑ZNF614	19	11	Hematological System Development and Function, Immune Cell Trafficking, Inflammatory Response	
N5	Akt, ↑↑ANGPTL1, APP, Calmodulin, CCSER2, Ck2, COL4A6, ↑CORO6, DIXDC1, DUSP7, ↑↑EID3, ELAVL4, ERK, ESR1, ICAM3, ↑↑INPP4A, ↓↓KCNAB1, MAGEH1, ↑↑MAP9, miR-101-3p (and other miRNAs w/seed ACAGUAC), ↓↓MYCN, phosphatidylinositol 3, 4-diphosphate, phosphatidylinositol-3, 4-bisphosphate 4-phosphatase, PPP6R2, ↑↑PRICKLE2, RGS5, RPL41, SH3BP5, SLC38A2, SUN1, ↓↓SUSD3, ↑↑SYNE1, WAC, ↑WDFY1, ZFAND5	18	11	Cellular Development, Cell Cycle, Nervous System Development and Function	miR-101-3p (and other miRNAs w/seed ACAGUAC)(M/1), Calmodulin(M/2), ELAVL4(M/1), HOXA10(2), GLI1(2), progesterone(2)

The numbers in parenthesis next to regulators' gene IDs in the last column signify how many molecules in those networks the regulators are affecting (e.g. Vegf regulates five molecules in Network 1). Letter (M/…) signifies that the regulators are also member of those networks, e.g. Vegf is also a member of network 1.
Symbols for regulators with increased (or decreased) expression and fold-change>=2 are preceded with ↑↑ (or ↓↓).
Symbols for genes with increased (or decreased) expression and fold-change<2 are preceded with ↑ (or ↓).