Supplemental Table 2a

Annotation Cluster 1	**Enrichment Score**	**2.09**
Term	**p-value**	**Genes**
GO0006935~chemotaxis	0.002	ROBO1, S100A9, CCL9, CCL17, CCL6
GO0042330~taxis	0.002	ROBO1, S100A9, CCL9, CCL17, CCL6
GO0007610~behavior	0.010	ROBO1, S100A9, CCL9, ZIC1, APBB1, CCL17, CCL6
GO0007626~locomotory behavior	0.024	ROBO1, S100A9, CCL9, CCL17, CCL6
GO0006955~immune response	0.063	THEMIS, CCL9, CFI, LTB, CCL17, CCL6
Annotation Cluster 2	**Enrichment Score**	**1.99**
Term	**p-value**	**Genes**
GO0016477~cell migration	0.005	VAV3, TNS1, MDGA1, S100A9, ESR2, APBB1
GO0006928~cell motion	0.006	VAV3, TNS1, ROBO1, MDGA1, S100A9, ESR2, APBB1
GO0048870~cell motility	0.009	VAV3, TNS1, MDGA1, S100A9, ESR2, APBB1
GO0051674~localization of cell	0.009	VAV3, TNS1, MDGA1, S100A9, ESR2, APBB1
GO0001764~neuron migration	0.041	MDGA1, ESR2, APBB1
Annotation Cluster 3	**Enrichment Score**	**0.94**
Term	**p-value**	**Genes**
GO0030029~actin filament-based process	0.046	ACTA1, S100A9, CNN1, APBB1
GO0030036~actin cytoskeleton organization	0.174	ACTA1, S100A9, CNN1
GO0007010~cytoskeleton organization	0.186	ACTA1, S100A9, CNN1, TACC2

Supplemental Table 2b

Annotation Cluster 1	**Enrichment Score**	**12.61**
GO Term	**p-value**	**Genes**
0048232~male gamete generation	0.000	RAD51C, RNF17, SOX3, ADAD1, MAEL, GGT1, ZBTB16, SOHLH1, SOHLH2, TAF7L, STRA8, DDX25, OVOL1, PIWIL2, DAZL, SPATA5, TDRD1, CCNB1IP1, MSH4, TLE3, MORC1, HMGA1, REC8, CLGN, TEX15, SYCP3, TCFL5, D1PAS1, SPATA19, DMC1
0007283~spermato-genesis	0.000	RAD51C, RNF17, SOX3, ADAD1, MAEL, GGT1, ZBTB16, SOHLH1, SOHLH2, TAF7L, STRA8, DDX25, OVOL1, PIWIL2, DAZL, SPATA5, TDRD1, CCNB1IP1, MSH4, TLE3, MORC1, HMGA1, REC8, CLGN, TEX15, SYCP3, TCFL5, D1PAS1, SPATA19, DMC1
0019953~sexual reproduction	0.000	RAD51C, RNF17, SOX3, ADAD1, FIGLA, MAEL, ASZ1, GGT1, ZBTB16, SYCP2, SOHLH1, SOHLH2, TAF7L, ZPBP, STRA8, DDX25, OVOL1, PIWIL2, DAZL, DND1, SPATA5, TDRD1, CCNB1IP1, MSH4, TLE3, MORC1, HMGA1, REC8, TEX15, CLGN, TCFL5, SYCP3, D1PAS1, SPATA19, DMC1, TEX11
0007276~gamete generation	0.000	RAD51C, RNF17, SOX3, ADAD1, FIGLA, MAEL, ASZ1, GGT1, ZBTB16, SOHLH1, SOHLH2, TAF7L, STRA8, DDX25, OVOL1, PIWIL2, DAZL, DND1, SPATA5, TDRD1, CCNB1IP1, MSH4, TLE3, MORC1, HMGA1, REC8, CLGN, TEX15, TCFL5, SYCP3, D1PAS1, SPATA19, DMC1
0032504~multicellular organism reproduction	0.000	RAD51C, RNF17, SOX3, ADAD1, FIGLA, MAEL, ASZ1, GGT1, ZBTB16, SOHLH1, SOHLH2, TAF7L, STRA8, DDX25, OVOL1, PIWIL2, DAZL, CHRNA7, DND1, SPATA5, TDRD1, CCNB1IP1, FOXL2, MSH4, TLE3, MORC1, HMGA1, REC8, CLGN, TEX15, TCFL5, SYCP3, D1PAS1, SPATA19, DMC1
0048609~reproductive process in a multicellular organism	0.000	RAD51C, RNF17, SOX3, ADAD1, FIGLA, MAEL, ASZ1, GGT1, ZBTB16, SOHLH1, SOHLH2, TAF7L, STRA8, DDX25, OVOL1, PIWIL2, DAZL, CHRNA7, DND1, SPATA5, TDRD1, CCNB1IP1, FOXL2, MSH4, TLE3, MORC1, HMGA1, REC8, CLGN, TEX15, TCFL5, SYCP3, D1PAS1, SPATA19, DMC1
Annotation Cluster 2	**Enrichment Score**	**10.53**
GO Term	**p-value**	**Genes**
0007127~meiosis I	0.000	CCNB1IP1, RAD51C, MSH4, MAEL, CPEB1, SYCP1, RAD51, REC8, TEX15, STRA8, SYCP3, OVOL1, PIWIL2, DMC1, TEX11

0007126~meiosis	0.000	CCNB1IP1, RAD51C, MSH4, MAEL, CPEB1, SYCP2, SYCP1, RAD51, SUV39H2, REC8, CLGN, TEX15, STRA8, SYCP3, OVOL1, PIWIL2, DMC1, TDRD1, TEX11, SMC1B
0051327~M phase of meiotic cell cycle	0.000	CCNB1IP1, RAD51C, MSH4, MAEL, CPEB1, SYCP2, SYCP1, RAD51, SUV39H2, REC8, CLGN, TEX15, STRA8, SYCP3, OVOL1, PIWIL2, DMC1, TDRD1, TEX11, SMC1B
0051321~meiotic cell cycle	0.000	CCNB1IP1, RAD51C, MSH4, MAEL, CPEB1, SYCP2, SYCP1, RAD51, SUV39H2, REC8, CLGN, TEX15, STRA8, SYCP3, OVOL1, PIWIL2, DMC1, TDRD1, TEX11, SMC1B
0000279~M phase	0.000	RAD51C, NEK3, MAEL, CPEB1, SYCP2, SYCP1, STRA8, OVOL1, PIWIL2, TDRD1, HELLS, CCNB1IP1, MSH4, RAD51, SUV39H2, FSD1, REC8, CLGN, TEX15, SYCP3, HORMAD1, HORMAD2, DMC1, SMC1B, TEX11
0022403~cell cycle phase	0.000	RAD51C, NEK3, MAEL, CPEB1, SYCP2, SYCP1, STRA8, OVOL1, PIWIL2, TDRD1, HELLS, CCNB1IP1, MSH4, RAD51, SUV39H2, FSD1, REC8, CLGN, TEX15, SYCP3, HORMAD1, HORMAD2, DMC1, SMC1B, TEX11
0022402~cell cycle process	0.000	RAD51C, NEK3, MAEL, CPEB1, SYCP2, SYCP1, UHMK1, CDKN2A, STRA8, OVOL1, PIWIL2, TDRD1, HELLS, CCNB1IP1, MSH4, RAD51, SUV39H2, FSD1, REC8, CLGN, TEX15, SYCP3, HORMAD1, HORMAD2, DMC1, TEX11, SMC1B
0007049~cell cycle	0.000	RAD51C, NEK3, MAEL, CPEB1, SYCP2, SYCP1, UHMK1, CDKN2A, STRA8, FANCI, OVOL1, PIWIL2, TDRD1, HELLS, CCNB1IP1, TRNP1, MSH4, SUV39H2, RAD51, FSD1, REC8, TEX15, CLGN, SYCP3, UBA3, HORMAD1, RBM38, HORMAD2, DMC1, TEX11, SMC1B
Annotation Cluster 3	**Enrichment Score**	**2.73**
GO Term	p-value	Genes
0007062~sister chromatid cohesion	0.001	RAD51C, SYCP3, STRA8, SMC1B
0045132~meiotic chromosome segregation	0.001	RAD51C, SYCP3, STRA8, TEX11
0007066~female meiosis sister chromatid cohesion	0.002	RAD51C, SYCP3, STRA8
0007143~female meiosis	0.003	RAD51C, SYCP3, STRA8, SYCP2
0051177~meiotic sister chromatid cohesion	0.004	RAD51C, SYCP3, STRA8

Annotation Cluster 4	**Enrichment Score**	**2.33**
GO Term	**p-value**	**Genes**
0010557~positive regulation of macromolecule biosynthetic process	0.001	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, LIN28A, ISL1, HMGA1, SHH, SALL4, OVOL2, KRT17, IRF6, PAX8, POU2F2, POU3F3, PIWIL2, DAZL, EAF2, NFIB
0031328~positive regulation of cellular biosynthetic process	0.002	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, LIN28A, ISL1, HMGA1, SHH, SALL4, OVOL2, KRT17, IRF6, PAX8, POU2F2, POU3F3, PIWIL2, DAZL, EAF2, NFIB
0009891~positive regulation of biosynthetic process	0.002	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, LIN28A, ISL1, HMGA1, SHH, SALL4, OVOL2, KRT17, IRF6, PAX8, POU2F2, POU3F3, PIWIL2, DAZL, EAF2, NFIB
0010604~positive regulation of macromolecule metabolic process	0.002	FGF8, HNF1B, HTATIP2, GLIS1, EHF, LIN28A, SHH, OVOL2, POU2F2, PAX8, POU3F3, PIWIL2, DAZL, UTF1, FOXL2, SIX2, GRHL3, RICTOR, ISL1, HMGA1, SALL4, KRT17, IRF6, EAF2, NFIB
0010628~positive regulation of gene expression	0.005	FOXL2, UTF1, HNF1B, FGF8, HTATIP2, GLIS1, SIX2, EHF, GRHL3, ISL1, HMGA1, SHH, SALL4, OVOL2, IRF6, PAX8, POU2F2, POU3F3, EAF2, NFIB
0045941~positive regulation of transcription	0.008	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, ISL1, HMGA1, SHH, SALL4, OVOL2, IRF6, PAX8, POU2F2, POU3F3, EAF2, NFIB
0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.017	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, ISL1, HMGA1, SHH, SALL4, OVOL2, IRF6, PAX8, POU2F2, POU3F3, EAF2, NFIB
0051173~positive regulation of nitrogen compound metabolic process	0.022	FOXL2, UTF1, HNF1B, HTATIP2, GLIS1, SIX2, EHF, GRHL3, ISL1, HMGA1, SHH, SALL4, OVOL2, IRF6, PAX8, POU2F2, POU3F3, EAF2, NFIB
Annotation Cluster 5	**Enrichment Score**	**2.21**
GO Term	**p-value**	**Genes**
0022602~ovulation cycle process	0.003	FOXL2, STRA8, MSH4, CHRNA7, DMC1, SOHLH1
0042698~ovulation cycle	0.003	FOXL2, STRA8, MSH4, CHRNA7, DMC1, SOHLH1
0001541~ovarian follicle development	0.004	FOXL2, STRA8, MSH4, DMC1, SOHLH1
0048511~rhythmic process	0.049	FOXL2, STRA8, MSH4, CHRNA7, DMC1, SOHLH1

Annotation Cluster 6	**Enrichment Score**	**2.13**
GO Term	**p-value**	**Genes**
0001541~ovarian follicle development	0.004	FOXL2, STRA8, MSH4, DMC1, SOHLH1
0008585~female gonad development	0.004	FOXL2, STRA8, MSH4, LHX8, DMC1, SOHLH1
0046545~development of primary female sexual characteristics	0.006	FOXL2, STRA8, MSH4, LHX8, DMC1, SOHLH1
0008406~gonad development	0.009	FOXL2, STRA8, MSH4, LHX8, DMC1, SOHLH1, TEX11
0046660~female sex differentiation	0.010	FOXL2, STRA8, MSH4, LHX8, DMC1, SOHLH1
0048608~reproductive structure development	0.017	FOXL2, STRA8, MSH4, LHX8, DMC1, SOHLH1, SHH, TEX11
Annotation Cluster 7	**Enrichment Score**	**1.99**
GO Term	**p-value**	**Genes**
0021795~cerebral cortex cell migration	0.004	DAB1, POU3F3, LHX6, RELN
0022029~telencephalon cell migration	0.005	DAB1, POU3F3, LHX6, RELN
0021885~forebrain cell migration	0.006	DAB1, POU3F3, LHX6, RELN
0021799~cerebral cortex radially oriented cell migration	0.011	DAB1, POU3F3, LHX6
0021543~pallium development	0.022	FGF8, DAB1, POU3F3, LHX6, RELN
0021987~cerebral cortex development	0.039	DAB1, POU3F3, LHX6, RELN
Annotation Cluster 8	**Enrichment Score**	**1.96**
GO Term	**p-value**	**Genes**
0044265~cellular macromolecule catabolic process	0.003	FOXL2, UCHL1, UBA6, HERC3, RFFL, OAS2, DNAHC12, LIN28A, PSMA8, PSMB9, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, STRA8, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
0009057~macromolecule catabolic process	0.007	FOXL2, UCHL1, UBA6, HERC3, RFFL, OAS2, DNAHC12, LIN28A, PSMA8, PSMB9, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, STRA8, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45

0051603~proteolysis involved in cellular protein catabolic process	0.013	UCHL1, UBA6, HERC3, RFFL, DNAHC12, PSMA8, PSMB9, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
0044257~cellular protein catabolic process	0.014	UCHL1, UBA6, HERC3, RFFL, DNAHC12, PSMA8, PSMB9, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
0043632~modification-dependent macromolecule catabolic process	0.016	UCHL1, UBA6, HERC3, RFFL, DNAHC12, PSMA8, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
0019941~modification-dependent protein catabolic process	0.016	UCHL1, UBA6, HERC3, RFFL, DNAHC12, PSMA8, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
0030163~protein catabolic process	0.019	UCHL1, UBA6, HERC3, RFFL, DNAHC12, PSMA8, PSMB9, ATE1, ZYG11B, ASB9, UBE2E3, ARIH1, USP18, SIAH1B, RNF128, UBA3, USP12, USP37, FBXO15, USP45
Annotation Cluster 9	**Enrichment Score**	**1.91**
GO Term	**p-value**	**Genes**
0010605~negative regulation of macromolecule metabolic process	0.002	SATB1, GTPBP4, SPINK12, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, LIN28A, SHH, ZBTB42, SALL4, CDKN2A, OVOL2, STRA8, RNF128, OVOL1, PIWIL2, POU3F3, TDRD1, HELLS
0010629~negative regulation of gene expression	0.010	SATB1, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, LIN28A, SHH, ZBTB42, SALL4, OVOL2, OVOL1, POU3F3, PIWIL2, TDRD1, HELLS
0045892~negative regulation of transcription, DNA-dependent	0.010	SATB1, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, OVOL1, POU3F3, HELLS
0051253~negative regulation of RNA metabolic process	0.011	SATB1, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, OVOL1, POU3F3, HELLS
0010558~negative regulation of macromolecule biosynthetic process	0.012	SATB1, GTPBP4, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, STRA8, RNF128, OVOL1, POU3F3, HELLS
0031327~negative regulation of cellular biosynthetic process	0.015	SATB1, GTPBP4, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, STRA8, RNF128, OVOL1, POU3F3, HELLS

0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.016	SATB1, GTPBP4, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, STRA8, OVOL1, POU3F3, HELLS
0009890~negative regulation of biosynthetic process	0.016	SATB1, GTPBP4, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, STRA8, RNF128, OVOL1, POU3F3, HELLS
0051172~negative regulation of nitrogen compound metabolic process	0.017	SATB1, GTPBP4, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, STRA8, OVOL1, POU3F3, HELLS
0000122~negative regulation of transcription from RNA polymerase II promoter	0.020	SATB1, HMX1, SALL4, GABPA, GLIS1, OVOL1, MAEL, POU3F3, CBX2, SHH, ZBTB42
0016481~negative regulation of transcription	0.041	SATB1, HMX1, GLIS1, GABPA, MAEL, CBX2, ZBTB16, SHH, ZBTB42, SALL4, OVOL2, OVOL1, POU3F3, HELLS
Annotation Cluster 10	**Enrichment Score**	**1.90**
GO Term	**p-value**	**Genes**
0030539~male genitalia development	0.003	FGF8, TEX15, SYCP2, SHH
0046546~development of primary male sexual characteristics	0.022	FGF8, TEX15, SYCP2, SHH, TEX11
0046661~male sex differentiation	0.028	FGF8, TEX15, SYCP2, SHH, TEX11
Annotation Cluster 11	**Enrichment Score**	**1.86**
GO Term	**p-value**	**Genes**
0034587~piRNA metabolic process	0.004	MAEL, PIWIL2, TDRD1
0043046~DNA methylation during gametogenesis	0.011	MAEL, PIWIL2, TDRD1
0006306~DNA methylation	0.011	MAEL, PIWIL2, TDRD1, HELLS
0006305~DNA alkylation	0.011	MAEL, PIWIL2, TDRD1, HELLS
0006304~DNA modification	0.012	MAEL, PIWIL2, TDRD1, HELLS
0016458~gene silencing	0.028	MAEL, PIWIL2, LIN28A, TDRD1, HELLS

0040029~regulation of gene expression, epigenetic	0.054	MAEL, PIWIL2, LIN28A, TDRD1, HELLS
Annotation Cluster 12	**Enrichment Score**	**1.74**
GO Term	**p-value**	**Genes**
0001701~in utero embryonic development	0.009	CCNB1IP1, HNF1B, KIF3A, GABPA, SPINT1, CX43, CDH1, ASCL2, FOXF1A, SALL4, OVOL2, COL4A3BP, KRT8
0043009~chordate embryonic development	0.025	CCNB1IP1, FGF8, HNF1B, KIF3A, GABPA, CX43, SPINT1, SIX2, CDH1, SHH, ASCL2, FOXF1A, SALL4, OVOL2, COL4A3BP, KRT8
0009792~embryonic development ending in birth or egg hatching	0.027	CCNB1IP1, FGF8, HNF1B, KIF3A, GABPA, CX43, SPINT1, SIX2, CDH1, SHH, ASCL2, FOXF1A, SALL4, OVOL2, COL4A3BP, KRT8
Annotation Cluster 13	**Enrichment Score**	**1.69**
GO Term	**p-value**	**Genes**
0051674~localization of cell	0.013	ASZ1, CX43, ISL1, SHH, TAF7L, DAB1, OVOL2, POU3F3, CHRNA7, TNN, LHX6, RELN, MESP1
0048870~cell motility	0.013	ASZ1, CX43, ISL1, SHH, TAF7L, DAB1, OVOL2, POU3F3, CHRNA7, TNN, LHX6, RELN, MESP1
0016477~cell migration	0.025	DAB1, OVOL2, ASZ1, CX43, POU3F3, LHX6, RELN, TNN, ISL1, MESP1, SHH
0006928~cell motion	0.037	ASZ1, CX43, ISL1, SHH, TAF7L, DAB1, OVOL2, LHX2, POU3F3, RELN, CHRNA7, TNN, LHX6, MESP1
Annotation Cluster 14	**Enrichment Score**	**1.51**
GO Term	**p-value**	**Genes**
0043414~biopolymer methylation	0.015	SATB1, MAEL, PIWIL2, TDRD1, HELLS, SUV39H2
0032259~methylation	0.022	SATB1, MAEL, PIWIL2, TDRD1, HELLS, SUV39H2
0006730~one-carbon metabolic process	0.090	SATB1, MAEL, PIWIL2, TDRD1, HELLS, SUV39H2
Annotation Cluster 15	**Enrichment Score**	**1.36**
GO Term	**p-value**	**Genes**
0045727~positive regulation of translation	0.003	KRT17, PIWIL2, DAZL, LIN28A
0032270~positive regulation of cellular protein metabolic process	0.146	KRT17, PIWIL2, DAZL, RICTOR, LIN28A

0051247~positive regulation of protein metabolic process	0.181	KRT17, PIWIL2, DAZL, RICTOR, LIN28A
Annotation Cluster 16	**Enrichment Score**	**1.25**
GO Term	**p-value**	**Genes**
0045109~inGO Termediate filament organization	0.028	KRT17, KRT14, SHH
0045104~inGO Termediate filament cytoskeleton organization	0.073	KRT17, KRT14, SHH
0045103~inGO Termediate filament-based process	0.091	KRT17, KRT14, SHH