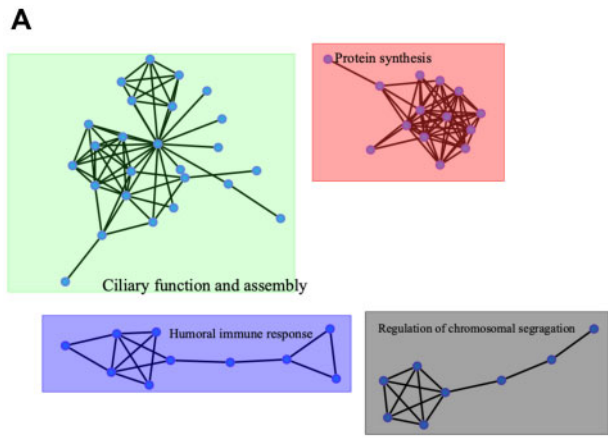


human reproduction SUPPLEMENTARY DATA



B GSEA leading edge analysis

Gene	Pathway Count	Log2 Fold Change	FDR Adj. p Value
DNAH5	7	-0.7948286	0.0435408
LRRC6	6	-0.8887169	0.02652041
HYDIN	5	-0.8073503	0.01389937
RPL22	3	-0.4615764	0.0191597
RPL29	3	-0.3939145	0.0050124
ARMC2	3	-0.7467087	0.04711549
LRGUK	3	-0.9003781	0.03034573
WDR34	3	-0.6553714	0.00775826
HLA-DRB5	2	-0.8312272	0.00744005
MRPS2	2	-0.423432	0.04146957
SPEF1	2	-0.9388008	0.02666659
TCTEX1D4	2	-0.9656942	0.02029424
FOXJ1	2	-0.8627706	0.04388163
NDUFAB1	1	-0.2715718	0.01851209
CCNO	1	-0.9100443	0.02187927
NEK2	1	-0.7824038	0.0424908

Supplementary Figure S3. (A) Cytoscape pathway clustering analysis of pathways identified by GSEA with P -value <0.005 and false discovery rate (FDR) q -value <0.1 . **(B)** GSEA leading edge analysis of enrichment score driving genes over-represented in pathways with FWER P -value <0.05 .