Supplementary table 3 Candidate pathogenic gene identified in patients of this study.

Gene	RefSeq ID	Chr	Position	dbSNP ID	Function	Amino Acid Alteration
SYCP2L	NM_001040274	6	10894170	rs119621 5011	frameshift deletion	c.150_151del: p.Ser52Profs*7
SYCP2L	NM_001040274	6	10912986	rs189836 527	missense variant	c. 999A>G: p.Ile333Met

1000G	GO-ESP	gnomAD	Polyphen-2	Mutation Taster	CADD	MGI
NA	NA	0.00001	-	Disease causing	22.9	Early reproductive senescence;
0.0001	NA	0.00005	Probably damaging	polymorp hism	24.7	Decreased oocyte number; Decreased primary ovarian follicle number

Note: CADD score: amino acid substitution is predicted damaging if the score is >20. NA: not available.