UNSUCCESSFUL IVF TREATMENTS, RECURRENT MOLAR PREGNANCIES AND/OR RECURRENT PREGNANCY LOSS PANEL[1] DG-4.2.0 (29 GENES)

Gene	*Twist X2 covered 10x*	*Twist X2 covered 20x*	*srWGS covered 10x*	*srWGS covered 15x*	*srWGS covered 20x*	*Associated Phenotype description and OMIM disease ID*
ASTL	100%	100%	100%	100%	99.5%	?Oocyte/zygote/embryo maturation arrest 11, 619643
BTG4	100%	100%	100%	100%	99.5%	Oocyte/zygote/embryo maturation arrest 8, 619009
C11orf80	92.2%	92.2%	100%	100%	99.2%	
CCNB3	100%	100%	99.2%	91.2%	71.5%	
CDC20	100%	100%	100%	100%	98.8%	Oocyte/zygote/embryo maturation arrest 14, 620276
FBXO43	100%	100%	100%	100%	99.6%	Spermatogenic failure 64, 619696;Oocyte/zygote/embryo maturation arrest 12, 619697
KHDC3L	100%	100%	100%	99.8%	99.2%	Hydatidiform mole, recurrent, 2, 614293

KPNA7	100%	100%	100%	100%	98.9%	Oocyte/zygote/embryo maturation arrest 17, 620319
LHCGR	100%	100%	100%	99.9%	99.1%	Leydig cell adenoma, somatic, with precocious puberty, 176410;Leydig cell hypoplasia with pseudohermaphroditism, 238320;Leydig cell hypoplasia with hypergonadotropic hypogonadism, 238320;Luteinizing hormone resistance, female, 238320;Precocious puberty, male, 176410
MEI1	100%	100%	100%	100%	99.3%	Hydatidiform mole, recurrent, 3, 618431
MOS	100%	100%	100%	99.4%	97.1%	Oocyte/zygote/embryo maturation arrest 20, 620383
NLRP2	100%	100%	100%	100%	99.1%	Oocyte/zygote/embryo maturation arrest 18, 620332
NLRP5	100%	100%	100%	100%	99.1%	Oocyte/zygote/embryo maturation arrest 19, 620333
NLRP7	100%	100%	100%	99.9%	99.2%	Hydatidiform mole, recurrent, 1, 231090
OOEP	100%	100%	100%	100%	99%	

PABPC1L	100%	100%	100%	99.8%	98.4%	
PADI6	100%	99.9%	99.4%	98.1%	95.7%	Oocyte/zygote/embryo maturation arrest 16, 617234
PANX1	100%	100%	100%	100%	99.3%	Oocyte/zygote/embryo maturation arrest 7, 618550
PATL2	100%	100%	100%	99.9%	99.3%	Oocyte/zygote/embryo maturation arrest 4, 617743
REC114	100%	100%	100%	99.9%	99.1%	Oocyte/zygote/embryo maturation arrest 10, 619176
TBPL2	100%	100%	100%	100%	99.3%	
TLE6	100%	100%	100%	100%	98.3%	Oocyte/zygote/embryo maturation arrest 15, 616814
TRIP13	100%	100%	100%	99.9%	99.1%	Oocyte/zygote/embryo maturation arrest 9, 619011;Mosaic variegated aneuploidy syndrome 3, 617598
TUBB8	100%	100%	100%	100%	99.7%	Oocyte/zygote/embryo maturation arrest 2, 616780
WEE2	100%	100%	100%	100%	99.5%	Oocyte/zygote/embryo maturation arrest 5, 617996
ZFP36L2	100%	100%	100%	99.7%	98.3%	Oocyte/zygote/embryo maturation arrest 13, 620154

ZP1	100%	100%	100%	99.9%	98.9%	Oocyte/zygote/embryo maturation arrest 1, 615774
ZP2	100%	100%	100%	100%	99.2%	Oocyte/zygote/embryo maturation arrest 6, 618353
ZP3	100%	100%	100%	100%	99.2%	Oocyte/zygote/embryo maturation arrest 3, 617712

Gene symbols used follow HGCN guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan 43(Database issue):D1079-85.
TWIST X2 covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x when analyzed by WES using TWIST X2 chemistry mapped against GRCh38.
TWIST X2 covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x when analyzed by WES using TWIST X2 chemistry mapped against GRCh38.
srWGS covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x when analyzed by WGS mapped against GRCh38.
srWGS covered 15x describes the percentage of a gene's coding sequence that is covered at least 15x when analyzed by WGS mapped against GRCh38.
srWGS covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x when analyzed by WGS mapped against GRCh38.
non-protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions : November 25th, 2024.
This list is accurate for panel version DG 4.2.0

Ad 1. Blank field signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors