UNSUCCESSFUL IVF TREATMENTS, RECURRENT MOLAR PREGNANCIES AND/OR RECURRENT PREGNANCY LOSS PANEL[1] DG-5.0.0 (56 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%	99.8%	?Oocyte/zygote/embryo maturation arrest 11, 619643
BTG4	100%	100%	100%	100%	99.7%	Oocyte/zygote/embryo maturation arrest 8, 619009
CCNB3	100%	100%	99.1%	90.1%	71.3%	
CCNP	100%	100%	100%	100%	99.2%	
CDC20	100%	100%	100%	100%	99.6%	Oocyte/zygote/embryo maturation arrest 14, 620276
CDC23	100%	100%	100%	100%	99.9%	
CENPH	100%	100%	100%	100%	99.9%	
CHEK1	100%	100%	100%	100%	99.8%	Oocyte/zygote/embryo maturation arrest 21, 620610
CIP2A	100%	100%	100%	100%	99.6%	
COX15	100%	100%	100%	100%	99.4%	Mitochondrial complex IV deficiency, nuclear type 6, 615119
DDOST	100%	100%	100%	100%	99.2%	Congenital disorder of glycosylation, type Ir, 614507
DLGAP5	100%	99.9%	100%	100%	99.8%	
FBXO43	100%	100%	100%	100%	99.9%	Spermatogenic failure 64, 619696;Oocyte/zygote/embryo maturation arrest 12, 619697

HAUS6	92.1%	92.1%	100%	100%	99.7%	
HFM1	100%	100%	100%	100%	99.8%	Premature ovarian failure 9, 615724
HORMAD2	100%	100%	100%	99.9%	99.6%	
INCENP	100%	100%	100%	100%	99.3%	
KHDC3L	100%	100%	100%	100%	99.6%	Hydatidiform mole, recurrent, 2, 614293
KIF11	100%	100%	100%	100%	99.5%	Microcephaly with or without chorioretinopathy, lymphedema, or impaired intellectual development, 152950
KIF18A	100%	100%	100%	100%	99.8%	
KPNA7	100%	100%	100%	100%	99.3%	Oocyte/zygote/embryo maturation arrest 17, 620319
LHCGR	100%	100%	100%	100%	99.9%	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
LHX8	92.5%	92.5%	100%	100%	99.4%	
MAD2L1BP	86.7%	86.6%	100%	100%	99.3%	
MEI1	100%	100%	100%	100%	99.8%	Hydatidiform mole, recurrent, 3, 618431
MEI4	100%	100%	100%	100%	99.8%	

MLH3	100%	100%	99.8%	99.5%	99%	{Endometrial cancer, susceptibility to}, 608089;Colorectal cancer, somatic, 114500;Colorectal cancer, hereditary nonpolyposis, type 7, 614385
MOS	100%	100%	100%	99.6%	97.9%	Oocyte/zygote/embryo maturation arrest 20, 620383
NLRP14	100%	100%	100%	100%	99.8%	
NLRP2	100%	100%	100%	99.9%	99.3%	Oocyte/zygote/embryo maturation arrest 18, 620332
NLRP5	100%	100%	100%	99.4%	98.3%	Oocyte/zygote/embryo maturation arrest 19, 620333
NLRP7	100%	100%	100%	100%	99.5%	Hydatidiform mole, recurrent, 1, 231090
OOEP	100%	100%	100%	100%	99.9%	
PABPC1L	100%	100%	100%	100%	99.4%	Oocyte/zygote/embryo maturation arrest 22, 621093
PADI6	100%	100%	100%	99.9%	98.9%	Oocyte/zygote/embryo maturation arrest 16, 617234
PANX1	100%	100%	100%	100%	99.7%	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%	100%	99.7%	Oocyte/zygote/embryo maturation arrest 10, 619176
RGS12	100%	100%	100%	99.9%	99.6%	
RNF212B	100%	100%	100%	100%	99.4%	
SPDYC	100%	100%	100%	100%	99%	

SPRY4	100%	100%	100%	100%	99.7%	Hypogonadotropic hypogonadism 17 with or without anosmia, 615266
TACC3	100%	100%	100%	100%	99.6%	
TBPL2	100%	100%	100%	100%	99.9%	
TLE6	100%	100%	100%	100%	99.1%	Oocyte/zygote/embryo maturation arrest 15, 616814
TOP6BL	89.2%	89.2%	100%	99.9%	99.4%	Hydatidiform mole, recurrent, 4, 618432
TRIP13	100%	100%	100%	100%	99.8%	Oocyte/zygote/embryo maturation arrest 9, 619011;Mosaic variegated aneuploidy syndrome 3, 617598
TUBA1C	100%	100%	100%	100%	99.5%	Oocyte/zygote/embryo maturation arrest 24, 621232
TUBA4A	100%	100%	100%	100%	99.6%	Oocyte/zygote/embryo maturation arrest 23, 621231;Spastic ataxia 11, autosomal dominant, 621226;Frontotemporal dementia and/or amyotrophic lateral sclerosis 9, 616208;Congenital myopathy 26, 621225
TUBB8	100%	100%	100%	100%	99.4%	Oocyte/zygote/embryo maturation arrest 2, 616780
WEE2	100%	100%	100%	100%	99.9%	Oocyte/zygote/embryo maturation arrest 5, 617996
ZFP36L2	100%	100%	100%	100%	98.9%	Oocyte/zygote/embryo maturation arrest 13, 620154
ZP1	100%	100%	100%	100%	99.6%	Oocyte/zygote/embryo maturation arrest 1, 615774

ZP2	100%	100%	100%	100%	99.7%	Oocyte/zygote/embryo maturation arrest 6, 618353
ZP3	100%	100%	99.9%	99.5%	98.1%	Oocyte/zygote/embryo maturation arrest 3, 617712
ZP4	100%	100%	100%	100%	99.4%	

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 5.0.0
Ad 1. Blank field signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors