Evaluation Only. Created with Aspose.PDF. Copyright 2002-2025 Aspose Pty Ltd.

# UNSUCCESSFUL IVF TREATMENTS, RECURRENT MOLAR PREGNANCIES AND/OR RECURRENT PREGNANCY LOSS PANEL[1] DG-5.1.0 (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% | 99.7% | ?Oocyte/zygote/embryo maturation arrest 11, 619643 |
| BTG4 | 100% | 100% | 100% | 99.9% | 99.8% | Oocyte/zygote/embryo maturation arrest 8, 619009 |
| CCNB3 | 100% | 100% | 99.5% | 92.1% | 73.8% | |
| CCNP | 100% | 100% | 100% | 100% | 99.4% | |
| CDC20 | 100% | 100% | 100% | 100% | 99.6% | Oocyte/zygote/embryo maturation arrest 14, 620276 |
| CDC23 | 100% | 100% | 100% | 100% | 99.8% | |
| CENPH | 100% | 100% | 100% | 100% | 99.6% | |
| CHEK1 | 100% | 100% | 100% | 99.9% | 99.7% | Oocyte/zygote/embryo maturation arrest 21, 620610 |
| CIP2A | 100% | 100% | 100% | 99.9% | 99.5% | |
| COX15 | 100% | 100% | 100% | 100% | 99.4% | Mitochondrial complex IV deficiency, nuclear type 6, 615119 |
| DDOST | 100% | 100% | 100% | 99.9% | 99.2% | Congenital disorder of glycosylation, type Ir, 614507 |
| DLGAP5 | 99.9% | 99.2% | 100% | 99.9% | 99.5% | |
| FBXO43 | 100% | 100% | 100% | 100% | 99.9% | Spermatogenic failure 64, 619696;Oocyte/zygote/embryo maturation arrest 12, 619697 |

Evaluation Only. Created with Aspose.PDF. Copyright 2002-2025 Aspose Pty Ltd.

| | | | | | | |
|---|---|---|---|---|---|---|
| HAUS6 | 92.1% | 92.1% | 100% | 100% | 99.9% | |
| HFM1 | 100% | 100% | 100% | 100% | 99.7% | Premature ovarian failure 9, 615724 |
| HORMAD2 | 100% | 100% | 100% | 100% | 99.4% | |
| INCENP | 100% | 100% | 100% | 100% | 99.7% | |
| KHDC3L | 100% | 100% | 100% | 100% | 99.8% | Hydatidiform mole, recurrent, 2, 614293 |
| KIF11 | 100% | 100% | 100% | 100% | 99.8% | Microcephaly with or without chorioretinopathy, lymphedema, or impaired intellectual development, 152950 |
| KIF18A | 100% | 100% | 100% | 100% | 99.9% | |
| KPNA7 | 100% | 100% | 100% | 100% | 99.3% | Oocyte/zygote/embryo maturation arrest 17, 620319 |
| LHCGR | 100% | 100% | 100% | 100% | 99.7% | 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% | 99.1% | |
| MAD2L1BP | 86.6% | 86.6% | 100% | 100% | 99.5% | |
| MEI1 | 100% | 100% | 100% | 100% | 99.6% | Hydatidiform mole, recurrent, 3, 618431 |
| MEI4 | 100% | 100% | 100% | 100% | 99.9% | |

Evaluation Only. Created with Aspose.PDF. Copyright 2002-2025 Aspose Pty Ltd.

| | | | | | | |
|---|---|---|---|---|---|---|
| MLH3 | 100% | 100% | 100% | 99.9% | 99.2% | {Endometrial cancer, susceptibility to}, 608089;Colorectal cancer, somatic, 114500;Colorectal cancer, hereditary nonpolyposis, type 7, 614385 |
| MOS | 100% | 100% | 99.9% | 99.8% | 98.3% | Oocyte/zygote/embryo maturation arrest 20, 620383 |
| NLRP14 | 100% | 100% | 100% | 100% | 99.9% | |
| NLRP2 | 100% | 100% | 100% | 100% | 99.3% | Oocyte/zygote/embryo maturation arrest 18, 620332 |
| NLRP5 | 100% | 100% | 100% | 100% | 99.6% | Oocyte/zygote/embryo maturation arrest 19, 620333 |
| NLRP7 | 100% | 100% | 100% | 100% | 99.3% | ?Ooxyte/zygote/embryo maturation arrest 25, 621471;Hydatidiform mole, recurrent, 1, 231090 |
| OOEP | 100% | 100% | 100% | 99.9% | 99.2% | |
| PABPC1L | 100% | 100% | 100% | 99.9% | 99.5% | Oocyte/zygote/embryo maturation arrest 22, 621093 |
| PADI6 | 100% | 100% | 100% | 99.9% | 99.1% | Oocyte/zygote/embryo maturation arrest 16, 617234 |
| PANX1 | 100% | 100% | 100% | 100% | 99.5% | Oocyte/zygote/embryo maturation arrest 7, 618550 |
| PATL2 | 100% | 100% | 100% | 100% | 99.8% | Oocyte/zygote/embryo maturation arrest 4, 617743 |
| REC114 | 100% | 100% | 100% | 100% | 100% | Oocyte/zygote/embryo maturation arrest 10, 619176 |
| RGS12 | 100% | 100% | 100% | 100% | 99.5% | |
| RNF212B | 100% | 100% | 100% | 99.9% | 99.6% | |
| SPDYC | 100% | 100% | 100% | 99.9% | 99.2% | |

Evaluation Only. Created with Aspose.PDF. Copyright 2002-2025 Aspose Pty Ltd.

| | | | | | | |
|---|---|---|---|---|---|---|
| SPRY4 | 100% | 100% | 100% | 100% | 99.4% | 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% | 99.4% | Oocyte/zygote/embryo maturation arrest 15, 616814 |
| TOP6BL | 89.2% | 89.1% | 100% | 100% | 99.7% | Hydatidiform mole, recurrent, 4, 618432 |
| TRIP13 | 100% | 100% | 100% | 100% | 99.7% | Oocyte/zygote/embryo maturation arrest 9, 619011;Mosaic variegated aneuploidy syndrome 3, 617598 |
| TUBA1C | 100% | 100% | 100% | 99.9% | 99.3% | 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% | 99.5% | Oocyte/zygote/embryo maturation arrest 2, 616780 |
| WEE2 | 100% | 100% | 100% | 100% | 99.8% | Oocyte/zygote/embryo maturation arrest 5, 617996 |
| ZFP36L2 | 100% | 100% | 100% | 99.7% | 98.5% | Oocyte/zygote/embryo maturation arrest 13, 620154 |
| ZP1 | 100% | 100% | 100% | 100% | 99.4% | Oocyte/zygote/embryo maturation arrest 1, 615774 |

Evaluation Only. Created with Aspose.PDF. Copyright 2002-2025 Aspose Pty Ltd.

| | | | | | | |
|---|---|---|---|---|---|---|
| ZP2 | 100% | 100% | 100% | 100% | 99.8% | Oocyte/zygote/embryo maturation arrest 6, 618353 |
| ZP3 | 100% | 100% | 100% | 99.8% | 98.8% | 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*