WES MALE INFERTILITY DG 3.5

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACTL9	120.2	100.0	100.0	619258
ADAD2	127.4	100.0	100.0	No OMIM phenotype
ADCY10	136.4	100.0	100.0	-
ADGRG2	103.6	100.0	99.8	300985
AR	99.1	99.5	99.0	-
ARMC2	145.0	100.0	100.0	618433
AURKC	136.7	100.0	100.0	243060
BPY2	42.6	50.0	49.1	No OMIM phenotype
BPY2B	41.1	50.0	48.9	No OMIM phenotype
BPY2C	41.5	50.0	49.9	No OMIM phenotype
C14orf39	159.4	100.0	100.0	No OMIM phenotype
CATIP	126.0	100.0	100.0	-
CATSPER1	117.1	100.0	100.0	612997
CATSPER2	127.0	100.0	100.0	611102
CCDC155	121.5	100.0	100.0	No OMIM phenotype
CCDC39	154.2	100.0	100.0	613807
CCDC40	125.2	100.0	100.0	613808
CDC14A	138.0	100.0	100.0	608653
CDY1	58.3	50.0	50.0	No OMIM phenotype
CDY1B	57.3	50.0	49.9	No OMIM phenotype
CDY2A	58.7	50.0	50.0	No OMIM phenotype
CDY2B	59.7	50.0	50.0	No OMIM phenotype
CFAP43	151.3	100.0	100.0	617592
CFAP44	142.8	100.0	100.0	617593
CFAP58	128.2	100.0	100.0	619144

CFAP65	124.8	100.0	100.0	618664
CFAP69	152.9	100.0	100.0	617959
CFTR	166.7	100.0	100.0	277180
DAZ1	44.7	50.0	49.7	No OMIM phenotype
DAZ2	44.5	50.0	49.8	No OMIM phenotype
DAZ3	38.9	49.9	49.0	No OMIM phenotype
DAZ4	42.8	49.7	49.0	No OMIM phenotype
DCAF12L1	118.6	100.0	100.0	No OMIM phenotype
DDX3Y	36.9	50.0	50.0	No OMIM phenotype
DMC1	149.0	100.0	100.0	-
DMRT1	140.3	100.0	100.0	-
DNAAF2	149.8	100.0	100.0	612518
DNAAF4	147.4	100.0	100.0	615482
DNAAF5	123.0	100.0	99.9	614874
DNAH1	116.0	100.0	100.0	617576
DNAH17	118.5	100.0	100.0	618643
DNAH7	145.8	100.0	100.0	No OMIM phenotype
DNAH8	144.6	100.0	99.7	619095
DNAI1	123.2	100.0	100.0	244400
DNAI2	117.7	100.0	100.0	612444
DNAJB13	138.3	100.0	100.0	617091
DNHD1	124.4	100.0	100.0	619712
DPY19L2	144.8	100.0	100.0	613958
E2F1	118.9	100.0	99.8	-
EIF1AY	35.9	50.0	50.0	No OMIM phenotype
FANCA	134.3	100.0	100.0	-
FANCM	150.0	100.0	100.0	-
FKBP6	134.1	100.0	100.0	No OMIM phenotype
FSIP2	169.4	100.0	100.0	618153
GALNTL5	147.5	100.0	100.0	-

GAS8	114.8	100.0	100.0	616726
GCNA	135.1	100.0	100.0	No OMIM phenotype
HSF2	152.7	100.0	100.0	-
HSFY1	46.5	49.9	49.7	No OMIM phenotype
HSFY2	46.9	49.9	49.3	No OMIM phenotype
KDM5D	33.6	48.9	48.8	No OMIM phenotype
KLHL10	120.6	100.0	100.0	615081
LRRC6	157.3	100.0	100.0	614935
M1AP	127.5	100.0	100.0	619108
MAATS1	140.5	100.0	100.0	609910
MCM9	137.7	100.0	100.0	No OMIM phenotype
MEI1	124.0	100.0	100.0	-
MEIOB	144.9	100.0	100.0	617706
MLH3	146.5	100.0	100.0	-
MNS1	147.8	100.0	100.0	-
MSH4	143.0	100.0	100.0	No OMIM phenotype
MSH5	135.1	100.0	100.0	No OMIM phenotype
NR0B1	109.1	100.0	99.8	-
NR5A1	136.8	100.0	100.0	184757
PDHA2	160.6	100.0	100.0	619828
PIH1D3	113.2	100.0	100.0	300991
PIWIL2	127.8	100.0	100.0	No OMIM phenotype
PKD1	156.6	99.9	99.7	173900
PLCZ1	154.9	100.0	100.0	617214
PLK4	157.0	100.0	100.0	-
PMFBP1	132.4	100.0	100.0	618112
PNLDC1	135.8	100.0	100.0	-
PRY	41.3	50.0	50.0	No OMIM phenotype
PRY2	42.0	50.0	50.0	No OMIM phenotype
QRICH2	136.1	100.0	100.0	618341

RAD21L1	149.1	100.0	100.0	No OMIM phenotype
RBBP7	104.8	100.0	99.7	No OMIM phenotype
RBMY1A1	85.4	50.0	50.0	No OMIM phenotype
RBMY1B	71.7	50.0	49.9	No OMIM phenotype
RBMY1D	64.1	49.5	48.5	No OMIM phenotype
RBMY1E	66.1	50.0	49.7	No OMIM phenotype
RBMY1F	49.3	49.3	48.7	No OMIM phenotype
RBMY1J	51.7	49.6	49.5	No OMIM phenotype
RNF212	133.1	100.0	100.0	-
RPS4Y2	38.4	50.0	50.0	No OMIM phenotype
RSPH3	131.5	100.0	100.0	616481
RSPH9	127.1	100.0	100.0	612650
SEPTIN12	117.2	100.0	100.0	614822
SHOC1	152.6	100.0	100.0	No OMIM phenotype
SPAG6	144.7	100.0	100.0	-
SPATA16	147.7	100.0	100.0	102530
SPATA22	161.2	100.0	100.0	No OMIM phenotype
SPEF2	146.9	100.0	100.0	618751
SPINK2	144.6	96.8	96.8	-
SPO11	153.4	100.0	100.0	No OMIM phenotype
SRY	36.8	50.0	50.0	-
STAG3	125.1	100.0	100.0	-
SUN5	137.6	100.0	100.0	617187
SYCE1	163.9	100.0	100.0	616950
SYCP2	163.6	100.0	100.0	258150
SYCP3	162.1	100.0	100.0	270960
TAF4B	140.1	100.0	100.0	615841
TDRD9	135.7	100.0	100.0	-
TERB1	155.3	100.0	100.0	-
TERB2	153.1	100.0	100.0	-

TEX11	109.6	97.1	96.8	309120
TEX14	128.6	100.0	100.0	617707
TEX15	156.8	100.0	100.0	617960
TRIM71	120.5	100.0	100.0	No OMIM phenotype
TSGA10	150.2	100.0	100.0	617961
TTC29	143.0	99.6	99.2	618745
UBR2	144.8	100.0	99.9	-
USP26	113.2	100.0	100.0	-
USP9Y	36.4	49.9	49.6	No OMIM phenotype
WDR66	125.0	100.0	100.0	-
XKRY				No OMIM phenotype
XKRY2				No OMIM phenotype
XRCC2	154.7	100.0	100.0	617247
ZFX	123.2	100.0	100.0	No OMIM phenotype
ZMYND15	121.6	100.0	100.0	615842

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 is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.
Median Coverage describes the average number of reads seen across 50 exomes.
Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.
Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x.
Genes with no value for coverage are non protein coding genes.
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: September 1st, 2021.

Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors