WES PREMATURE OVARIAN INSUFFICIENCY DG 3.5

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
AARS2	124.6	100.0	100.0	615889
BMP15	111.0	100.0	100.0	300510
CLPP	112.2	100.0	100.0	614129
CYP17A1	124.2	100.0	100.0	202110
CYP19A1	149.0	100.0	99.9	613546
EIF2B5	132.6	100.0	100.0	603896
ERAL1	120.6	100.0	100.0	617565
ESR2	150.5	100.0	100.0	618187
FANCM	150.0	100.0	100.0	609644
FOXL2	123.1	100.0	100.0	110100;608996
FSHB	132.8	98.7	98.0	229070
FSHR	149.3	100.0	99.9	233300
GALT	130.4	100.0	100.0	230400
GDF9	148.4	100.0	100.0	618014
HARS2	140.0	100.0	100.0	614926
HFM1	158.9	100.0	100.0	615724
HSD17B4	142.8	96.6	96.6	233400
LARS2	127.2	100.0	100.0	615300
MCM8	137.7	94.4	94.4	612885
MCM9	137.7	100.0	100.0	616185
MSH4	143.0	100.0	100.0	-
NOBOX	115.6	100.0	100.0	611548
NR5A1	136.8	100.0	100.0	612964;612965;617480
PMM2	145.7	100.0	100.0	212065
POLG	138.3	100.0	100.0	157640

PSMC3IP	120.2	100.0	100.0	614324
SOHLH1	131.4	100.0	100.0	617690
SPATA22	161.2	100.0	100.0	No OMIM phenotype
SPIDR	119.5	100.0	100.0	619665
STAG3	125.1	100.0	100.0	615723
TWNK	117.5	100.0	100.0	616138

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