

# WES PREMATURE OVARIAN INSUFFICIENCY DG 3.2

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
AARS2	131.7	100.0	99.4	615889
BMP15	102.8	100.0	98.7	300510
CLPP	146.0	100.0	99.5	614129
CYP17A1	109.0	99.9	98.5	202110
CYP19A1	137.2	98.3	95.7	613546
EIF2B5	104.1	99.8	98.5	603896
ESR2	112.9	99.9	98.9	618187
FANCM	99.4	98.9	96.3	609644
FOXL2	72.5	99.4	94.7	110100;608996
FSHB	104.6	100.0	100.0	229070
FSHR	87.9	99.2	97.0	233300
GALT	160.1	100.0	99.6	230400
GDF9	144.2	100.0	100.0	618014
HFM1	54.5	95.4	89.8	615724
HSD17B4	114.3	95.3	92.8	233400
LARS2	123.2	100.0	100.0	615300
MCM8	113.6	99.9	98.8	612885
MCM9	132.6	99.9	99.0	616185
MSH4	85.0	98.8	96.5	-
NOBOX	95.3	99.3	96.6	611548
NR5A1	96.8	100.0	100.0	612964;612965;617480
PMM2	127.8	99.8	99.8	212065
POLG	113.2	99.9	98.8	157640
PSMC3IP	94.7	100.0	100.0	614324
SOHLH1	123.1	99.7	96.8	617690

STAG3	105.5	93.5	92.8	615723
TWNK	173.4	100.0	99.9	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.*

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