WES PREMATURE OVARIAN INSUFFICIENCY DG 3.4

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
AARS2	191.4	100.0	100.0	615889
BMP15	161.6	100.0	100.0	300510
CLPP	190.0	100.0	100.0	614129
CYP17A1	177.3	100.0	100.0	202110
CYP19A1	172.7	100.0	100.0	613546
EIF2B5	167.3	100.0	100.0	603896
ERAL1	171.6	100.0	100.0	617565
ESR2	191.2	100.0	100.0	618187
FANCM	152.5	100.0	100.0	609644
FOXL2	198.3	100.0	100.0	110100;608996
FSHB	159.2	100.0	100.0	229070
FSHR	189.6	100.0	100.0	233300
GALT	182.2	100.0	100.0	230400
GDF9	200.3	100.0	100.0	618014
HARS2	154.5	100.0	100.0	614926
HFM1	134.4	100.0	100.0	615724
HSD17B4	137.6	96.6	96.6	233400
LARS2	171.4	100.0	100.0	615300
MCM8	154.1	94.4	94.4	612885
MCM9	186.3	100.0	100.0	616185
MSH4	128.9	100.0	100.0	-
NOBOX	160.2	100.0	100.0	611548
NR5A1	225.9	100.0	100.0	612964;612965;617480
PMM2	144.9	100.0	100.0	212065
POLG	195.1	100.0	100.0	157640

PSMC3IP	160.4	100.0	100.0	614324
REC8	181.4	100.0	100.0	No OMIM phenotype
SOHLH1	199.6	100.0	100.0	617690
STAG3	157.2	100.0	100.0	615723
TWNK	197.1	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.