

# WES DYSKERATOSIS CONGENITA AND APLASTIC ANEMIA

## DG 3.6

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACD	120.5	100.0	100.0	616553
CTC1	120.1	100.0	100.0	612199
DKC1	105.8	100.0	100.0	305000
GRHL2	131.5	100.0	100.0	616029
LIG4	156.5	100.0	100.0	606593
NHP2	118.6	100.0	100.0	613987
NOP10	131.5	100.0	100.0	224230
NPM1	143.1	100.0	100.0	-
PARN	132.6	97.0	95.9	616353
POT1	156.3	100.0	100.0	615848
RPA1	129.5	100.0	100.0	619767
RTEL1	126.6	100.0	100.0	615190
TERC				127550;614743
TERT	156.5	100.0	100.0	615134;614742;613989
TINF2	124.5	100.0	100.0	268130;613990
USB1	132.2	100.0	100.0	604173
WRAP53	132.0	100.0	100.0	613988

Gene symbols used follow HGNC 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.*

[EAS.GenProductCoverage.pdf.footer.ad01](#)