WES NOONAN SYNDROME / RASOPATHY DG 3.3

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
BRAF	185.7	100.0	100.0	613706
CBL	208.8	100.0	100.0	613563
CDC42	131.4	100.0	100.0	616737
HRAS	270.5	100.0	100.0	218040
KRAS	171.7	100.0	100.0	609942
LZTR1	167.2	100.0	100.0	616564;605275
MAP2K1	189.1	100.0	100.0	615279
MAP2K2	233.3	100.0	100.0	615280
MAPK1	169.0	100.0	100.0	619087
MRAS	174.5	100.0	100.0	618499
NRAS	198.9	100.0	100.0	613224
PPP1CB	149.0	100.0	100.0	617506
PTPN11	196.6	100.0	100.0	163950
RAF1	193.0	100.0	100.0	611553
RIT1	181.4	100.0	100.0	615355
RRAS	141.5	100.0	100.0	No OMIM phenotype
RRAS2	131.0	100.0	100.0	618624
RREB1	210.5	100.0	100.0	-
SHOC2	146.4	100.0	100.0	607721
SOS1	137.5	100.0	100.0	610733
SOS2	147.3	100.0	100.0	616559
SPRED1	168.9	100.0	100.0	611431
SPRED2	219.2	100.0	100.0	No OMIM phenotype

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.