WES NOONAN SYNDROME / RASOPATHY DG 2.18

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
BRAF	83.8	95.6	85.1	613706
CBL	152.5	97.3	97.1	613563
HRAS	177.9	100.0	100.0	218040
KRAS	84.3	99.5	96.9	609942
LZTR1	136.8	100.0	99.9	616564
MAP2K1	111.1	99.8	97.1	615279
MAP2K2	123.0	98.5	95.1	615280
NRAS	185.6	100.0	100.0	613224
PPP1CB	127.9	99.9	99.3	617506
PTPN11	100.3	99.1	93.7	163950
RAF1	125.8	100.0	100.0	611553
RIT1	178.7	100.0	100.0	615355
SHOC2	164.2	99.9	99.4	607721
SOS1	123.6	99.8	98.4	610733
SOS2	123.5	100.0	99.2	616559
SPRED1	171.2	100.0	98.9	611431

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.
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 10x describes the percentage of a gene's coding sequence that is covered at least 20x.
Genes with Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.

Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors