

Full name:	RASopathy - KUL
Provider:	Agilent
Laboratory:	<u>Centrum Menselijke Erfelijkheid - KUL</u>
Created:	03 Jul 2019 - 09:41
Changed:	22 Dec 2021 - 09:22

Related Diseases

- Cardiofaciocutaneous syndrome
- Costello syndrome
- Neurofibromatosis-Noonan syndrome
- Noonan syndrome
- Noonan syndrome with multiple lentigines
- Noonan syndrome-like disorder with loose anagen hair

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>A2ML1</u>	95.00	0	research gene + % of coding sequence represents the minimum CS1 interpretable range
<u>BRAF</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>CBL</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>HRAS</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>KRAS</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>LZTR1</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>MAP2K1</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>MAP2K2</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>MRAS</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>NRAS</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>PPP1CB</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>PTPN11</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>RAF1</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>RASA1</u>	95.00	0	research gene + % of coding sequence represents the minimum CS1 interpretable range
<u>RASA2</u>	95.00	0	research gene + % of coding sequence represents the minimum CS1 interpretable range
<u>RIT1</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>RRAS</u>	80.00	0	research gene + % of coding sequence represents the minimum CS1 interpretable range
<u>RRAS2</u>	95.00	0	research gene + % of coding sequence represents the minimum CS1 interpretable range
<u>SHOC2</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>SOS1</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range
<u>SOS2</u>	95.00	0	core gene + % of coding sequence represents the minimum CS1 interpretable range