

HGNC approved gene symbol	Transcript	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x	% covered >50x
<i>ARID1A</i> **	NM_006015.4	603024	183	98	97	97	96
<i>ARID1B</i> **	NM_020732.3	614556	182	100	98	96	94
<i>PHF6</i>	NM_001015877	300414	141	100	100	100	100
<i>SMARCA2</i>	NM_003070.4	600014	133	97	97	97	97
<i>SMARCA4</i> **	NM_001128849.1	603254	121	100	100	100	100
<i>SMARCB1</i> **	NM_003073.3	601607	136	100	100	100	100
<i>SMARCC2</i>	NM_003075	601734	0	0	0	0	0
<i>SMARCE1</i> **	NM_003079.4	603111	139	100	100	100	100

* Coffin-Siris / Nicolaides-Baraitser syndrome

** Core genes (if necessary additional Sanger sequencing will be performed for 100% coverage)

MLPA for *ARID1A* and *ARID1B* is included in the genepanel CSS