

HGNC approved gene symbol	Transcript	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x	% covered >50x	
<i>ACAN</i> **	NM_013227	155760	291	87	87	86	86	
<i>COMP</i>	NM_000095	600310	140	100	100	100	98	
<i>FGFR3</i> **	NM_000142	134934	216	100	100	99	97	
<i>GH1</i> **	NM_000515	139250	258	100	100	100	100	
<i>GHR</i> **	NM_000163	600946	319	100	100	100	100	
<i>GHRH</i> **	NM_021081	139190	90	100	100	98	98	
<i>GHRHR</i> **	NM_000823	139191	140	100	100	100	100	
<i>GHSR</i> **	NM_198407	601898	391	100	100	100	100	
<i>HMGA2</i>	NM_003483	600698	174	100	94	79	66	
<i>IGF1</i> **	NM_000618	147440	107	100	100	100	100	
<i>IGF1R</i> **	NM_000875	147370	142	100	100	100	99	
<i>IGFALS</i> **	NM_004970	601489	Sanger sequencing is performed					
<i>IGFBP3</i> **	NM_001013398	146732	Sanger sequencing is performed					
<i>IHH</i>	NM_002181	600726	261	100	100	100	100	
<i>NPR2</i> **	NM_003995	607072	284	100	100	100	100	
<i>PAPSS2</i> **	NM_001015880	603005	170	100	100	100	100	
<i>PTPN11</i>	NM_002834	176876	195	100	100	99	99	
<i>SHOX</i> **	NM_000451	312865	Sanger sequencing is performed					
<i>STAT5B</i> **	NM_012448	604260	141	100	100	100	99	

\* See also exome sequencing for the larger panel

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

For some genes Sanger sequencing is performed

MLPA for SHOX is included in the gene panel Growth Disorders