

Full name:	Short Stature (46 genes) - IPG
Version number:	Version 3
Laboratory:	<u>Centre de Génétique-Institut de Pathologie et de Génétique (IPG)</u>
Created:	04 Jul 2019 - 10:43
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Related Diseases

- 16q24.3 microdeletion syndrome
- 3M syndrome
- Aarskog-Scott syndrome
- Achondroplasia
- Acromesomelic dysplasia, Maroteaux type
- Autosomal dominant Robinow syndrome
- Autosomal recessive Robinow syndrome
- Camptodactyly-tall stature-scoliosis-hearing loss syndrome
- Coffin-Lowry syndrome
- Combined pituitary hormone deficiencies, genetic forms
- Costello syndrome
- Crouzon syndrome-acanthosis nigricans syndrome
- Familial osteochondritis dissecans
- Floating-Harbor syndrome
- Growth delay due to insulin-like growth factor I resistance
- Growth delay due to insulin-like growth factor type 1 deficiency
- Hypochondroplasia
- Hypothyroidism due to deficient transcription factors involved in pituitary development or function
- Isolated growth hormone deficiency type IB
- Isolated growth hormone deficiency type II
- KBG syndrome
- Kabuki syndrome
- Langer mesomelic dysplasia

- [Laron syndrome](#)
- [Laron syndrome with immunodeficiency](#)
- [Léri-Weill dyschondrosteosis](#)
- [Muenke syndrome](#)
- [Mulibrey nanism](#)
- [Noonan syndrome](#)
- [Noonan syndrome with multiple lentigines](#)
- [Noonan syndrome-like disorder with juvenile myelomonocytic leukemia](#)
- [Noonan syndrome-like disorder with loose anagen hair](#)
- [Rubinstein-Taybi syndrome due to 16p13.3 microdeletion](#)
- [Rubinstein-Taybi syndrome due to CREBBP mutations](#)
- [Rubinstein-Taybi syndrome due to EP300 haploinsufficiency](#)
- [SHORT syndrome](#)
- [SHOX-related short stature](#)
- [Saethre-Chotzen syndrome](#)
- [Severe achondroplasia-developmental delay-acanthosis nigricans syndrome](#)
- [Short stature due to GHSR deficiency](#)
- [Short stature due to growth hormone qualitative anomaly](#)
- [Short stature due to isolated growth hormone deficiency with X-linked hypogammaglobulinemia](#)
- [Short stature due to partial GHR deficiency](#)
- [Short stature due to primary acid-labile subunit deficiency](#)
- [Short stature-advanced bone age-early-onset osteoarthritis syndrome](#)
- [Silver-Russell syndrome due to a point mutation](#)
- [Smith-Lemli-Opitz syndrome](#)
- [Spondyloepimetaphyseal dysplasia, aggrecan type](#)
- [Spondyloepiphyseal dysplasia, Kimberley type](#)
- [Symptomatic form of Coffin-Lowry syndrome in female carriers](#)
- [Tall stature-long halluces-multiple extra-epiphyses syndrome](#)
- [Thanatophoric dysplasia type 1](#)
- [Thanatophoric dysplasia type 2](#)

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ACAN	90.00	1	NM_001369268.1

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ANKRD11</u>	100.00	1	NM_013275.6
<u>BRAF</u>	100.00	1	NM_001354609.2
<u>BTK</u>	100.00	1	NM_000061.3
<u>CBL</u>	100.00	1	NM_005188.4
<u>CCDC8</u>	100.00	1	NM_032040.5
<u>CREBBP</u>	100.00	1	NM_004380.3
<u>CUL7</u>	100.00	1	NM_014780.5
<u>DHCR7</u>	100.00	1	NM_001360.3
<u>DVL1</u>	100.00	1	NM_001330311.2
<u>EP300</u>	100.00	1	NM_001429.4
<u>FGD1</u>	100.00	1	NM_004463.3
<u>FGFR3</u>	100.00	1	NM_001163213.1
<u>GH1</u>	100.00	1	NM_000515.5
<u>GHR</u>	100.00	1	NM_000163.5
<u>GHRHR</u>	100.00	1	NM_000823.4
<u>GHSR</u>	100.00	1	NM_198407.2
<u>HRAS</u>	100.00	1	NM_005343.4
<u>IGF1</u>	100.00	1	NM_000618.5
<u>IGF1R</u>	100.00	1	NM_000875.5
<u>IGF2</u>	100.00	1	NM_000612.6

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>IGFALS</u>	100.00	1	NM_004970.3
<u>KDM6A</u>	100.00	1	NM_001291415.2
<u>KMT2D</u>	100.00	1	NM_003482.3
<u>KRAS</u>	100.00	1	NM_033360.4
<u>NPPC</u>	100.00	1	NM_024409.4
<u>NPR2</u>	100.00	1	NM_003995.3
<u>NPR3</u>	100.00	1	NM_001204375.2
<u>NRAS</u>	100.00	1	NM_002524.5
<u>OBSL1</u>	100.00	1	NM_015311.3
<u>PIK3R1</u>	100.00	1	NM_181523.3
<u>POU1F1</u>	100.00	1	NM_000306.4
<u>PTPN11</u>	100.00	1	NM_002834.5
<u>RAF1</u>	100.00	1	NM_001354689.3
<u>RASA2</u>	100.00	1	NM_006506.5
<u>RIT1</u>	100.00	1	NM_006912.6
<u>ROR2</u>	100.00	1	NM_004560.4
<u>RPS6KA3</u>	100.00	1	NM_004586.3
<u>SHOC2</u>	100.00	1	NM_007373.4
<u>SHOX</u>	100.00	1	NM_000451.3
<u>SOS1</u>	100.00	1	NM_005633.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SOX3</u>	100.00	1	NM_005634.2
<u>SRCAP</u>	100.00	1	NM_006662.3
<u>STAT5B</u>	100.00	1	NM_012448.4
<u>TRIM37</u>	100.00	1	NM_015294.6
<u>WNT5A</u>	100.00	1	NM_003392.4