WES HYPOGONADOTROPIC HYPOGONADISM (KALLMANN)

DG 3.6

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ADCY3	120.5	100.0	100.0	617885
ANOS1	102.3	100.0	99.8	308700
ARHGAP35	131.0	100.0	100.0	No OMIM phenotype
AXL	113.7	100.0	100.0	No OMIM phenotype
CCDC141	135.1	99.5	98.9	-
CHD7	133.9	100.0	100.0	612370
CNGA2	91.9	99.9	99.7	No OMIM phenotype
DCC	142.6	100.0	100.0	157600
DUSP6	124.9	100.0	100.0	615269
FEZF1	148.4	100.0	100.0	616030
FGF17	132.6	100.0	100.0	615270
FGF8	128.5	100.0	100.0	612702
FGFR1	125.7	100.0	100.0	147950
FLRT3	148.6	100.0	99.7	615271
FSHB	132.8	98.7	98.0	229070
GNRH1	149.4	100.0	100.0	614841
GNRHR	153.8	100.0	100.0	138850
HESX1	152.7	100.0	100.0	182230
HS6ST1	143.6	100.0	100.0	614880
IGSF10	148.1	100.0	100.0	-
IL17RD	125.0	100.0	100.0	615267
KISS1	191.5	100.0	100.0	614842

KISS1R	158.7	100.0	100.0	614837
KLB	135.6	100.0	100.0	-
LEP	116.6	100.0	100.0	614962
LEPR	144.9	94.6	94.6	614963
LHB	232.2	100.0	100.0	228300
LHX3	146.3	100.0	100.0	221750
NOS1	118.1	100.0	100.0	No OMIM phenotype
NR0B1	109.1	100.0	99.8	300200
NSMF	135.1	100.0	100.0	614838
PCSK1	132.5	100.0	100.0	600955
PLXNA1	137.3	100.0	100.0	-
POLG	138.3	100.0	100.0	157640
PROK2	143.5	100.0	100.0	610628
PROKR2	155.8	100.0	100.0	244200
PROP1	131.4	100.0	100.0	262600
SEMA3A	148.2	100.0	100.0	614897
SEMA3E	144.5	100.0	100.0	214800
SOX10	142.9	100.0	100.0	-
SOX2	135.3	100.0	100.0	206900
SPRY4	114.1	100.0	100.0	615266
TAC3	134.6	100.0	100.0	614839
TACR3	141.0	100.0	99.8	614840
TCF12	138.9	100.0	100.0	615314
TENM1	104.9	99.9	99.5	301700
WDR11	143.8	100.0	100.0	614858

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.
TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.
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 20x describes the percentage of a gene's coding sequence that is covered at least 20x.
Genes with no value for coverage are non protein coding genes.

Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.
OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.

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