WES HYPOGONADOTROPIC HYPOGONADISM (KALLMANN)

DG 3.4

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ADCY3	178.8	100.0	100.0	617885
ANOS1	166.7	100.0	100.0	308700
AXL	191.2	100.0	100.0	No OMIM phenotype
CCDC141	156.3	100.0	100.0	-
CHD7	185.7	100.0	100.0	612370
CNGA2	181.7	100.0	100.0	No OMIM phenotype
DCC	175.2	100.0	100.0	157600
DUSP6	205.3	100.0	100.0	615269
FEZF1	235.0	100.0	100.0	616030
FGF17	206.9	100.0	100.0	615270
FGF8	200.6	100.0	100.0	612702
FGFR1	214.8	100.0	100.0	147950
FLRT3	191.9	100.0	100.0	615271
FSHB	159.2	100.0	100.0	229070
GNRH1	168.3	100.0	100.0	614841
GNRHR	183.2	100.0	100.0	138850
HESX1	156.6	100.0	100.0	182230
HS6ST1	225.5	100.0	100.0	614880
IGSF10	196.5	100.0	100.0	-
IL17RD	173.0	100.0	100.0	615267
KISS1	222.3	100.0	100.0	614842
KISS1R	235.7	100.0	100.0	614837

KLB	215.9	100.0	100.0	-
LEP	177.2	100.0	100.0	614962
LEPR	148.5	94.6	94.6	614963
LHB	352.7	100.0	100.0	228300
LHX3	215.5	100.0	100.0	221750
NR0B1	233.8	100.0	100.0	300200
NSMF	194.9	100.0	100.0	614838
PCSK1	177.5	100.0	100.0	600955
PLXNA1	242.4	100.0	100.0	-
POLG	195.1	100.0	100.0	157640
PROK2	152.9	100.0	100.0	610628
PROKR2	211.7	100.0	100.0	244200
PROP1	260.4	100.0	100.0	262600
SEMA3A	163.1	100.0	100.0	614897
SEMA3E	161.7	100.0	100.0	214800
SOX10	254.5	100.0	100.0	-
SOX2	323.4	100.0	100.0	206900
SPRY4	231.0	100.0	100.0	615266
TAC3	135.9	100.0	100.0	614839
TACR3	211.1	100.0	100.0	614840
TCF12	165.0	100.0	100.0	615314
WDR11	159.1	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