

WES HYPOGONADOTROPIC HYPOGONADISM (KALLMANN)

DG 3.2

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ADCY3	128.7	100.0	99.0	617885
ANOS1	81.6	89.8	88.3	308700
AXL	162.9	100.0	98.9	No OMIM phenotype
CCDC141	121.5	99.8	99.5	-
CHD7	137.1	100.0	99.2	612370
DCC	124.0	100.0	100.0	157600
DUSP6	150.2	100.0	100.0	615269
FEZF1	152.5	100.0	100.0	616030
FGF17	153.9	100.0	100.0	615270
FGF8	123.7	97.1	87.2	612702
FGFR1	128.6	100.0	99.3	147950
FLRT3	171.7	100.0	100.0	615271
FSHB	104.6	100.0	100.0	229070
GNRH1	85.2	99.5	89.5	614841
GNRHR	133.1	100.0	100.0	138850
HESX1	60.2	99.3	97.3	182230
HS6ST1	59.3	93.6	86.7	614880
IGSF10	190.5	100.0	99.9	-
IL17RD	130.2	99.9	99.0	615267
KISS1	74.1	100.0	98.2	614842
KISS1R	109.1	100.0	99.6	614837
KLB	205.0	100.0	99.9	-

LEP	172.5	100.0	99.6	614962
LEPR	113.2	94.1	92.3	614963
LHB	21.7	91.7	42.8	228300
LHX3	85.9	96.6	96.2	221750
NR0B1	120.6	99.9	99.2	300200
NSMF	97.3	96.9	95.5	614838
PCSK1	147.3	99.9	99.4	600955
PLXNA1	190.3	100.0	99.9	-
POLG	113.2	99.9	98.8	157640
PROK2	106.6	99.9	98.9	610628
PROKR2	228.0	100.0	100.0	244200
PROP1	97.0	91.0	80.2	262600
SEMA3A	163.6	100.0	99.7	614897
SEMA3E	137.7	99.1	98.9	214800
SOX10	69.2	99.9	97.2	-
SOX2	194.7	100.0	99.8	206900
SPRY4	155.9	100.0	100.0	615266
TAC3	69.3	99.9	93.6	614839
TACR3	140.8	100.0	100.0	614840
TCF12	136.8	99.9	99.7	615314
WDR11	121.8	98.2	96.5	614858

Gene symbols used follow HGNC 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.