

# WES HYPOGONADOTROPIC HYPOGONADISM (KALLMANN)

## DG 2.15

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
ADCY3	130.4	99.8	98.4	-
ANOS1	90.3	89.4	87.6	308700
CCDC141	111.9	99.9	98.0	-
CHD7	150.7	99.9	98.9	612370
DCC	138.5	100.0	99.9	157600
DUSP6	175.9	100.0	99.9	615269
FEZF1	158.8	99.9	99.3	616030
FGF17	138.6	100.0	100.0	615270
FGF8	111.4	90.2	79.7	612702
FGFR1	148.0	99.7	98.3	147950
FLRT3	225.7	100.0	100.0	615271
FSHB	149.1	100.0	100.0	229070
GNRH1	86.7	99.5	91.5	614841
GNRHR	161.9	100.0	100.0	138850
HESX1	57.6	99.2	92.6	182230
HS6ST1	75.3	94.8	85.0	614880
IGSF10	246.8	100.0	99.9	-
IL17RD	135.6	99.3	97.7	615267
KISS1	41.4	98.5	91.2	614842
KISS1R	106.4	99.5	95.3	614837
KLB	213.4	100.0	100.0	-
LEP	188.8	100.0	99.6	614962

LEPR	109.6	93.8	90.2	614963
LHB	29.0	97.2	73.2	228300
NR0B1	119.3	99.9	98.6	300200
NSMF	78.4	95.7	95.2	614838
PCSK1	147.2	100.0	99.0	600955
PROK2	105.6	98.4	91.9	610628
PROKR2	331.8	100.0	100.0	244200
PROP1	76.5	91.6	84.3	262600
SEMA3A	182.0	100.0	100.0	614897
SOX10	65.8	98.2	91.3	-
SPRY4	138.7	100.0	100.0	615266
TAC3	80.5	99.1	91.1	614839
TACR3	180.3	100.0	100.0	614840
TCF12	150.3	100.0	99.8	615314
WDR11	130.6	96.9	96.4	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.*

*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 Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.*

*OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.*

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