WES HYPOGONADOTROPIC HYPOGONADISM (KALLMANN) DG 3.1

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ADCY3	130.7	100.0	99.1	617885
ANOS1	97.2	89.8	88.9	308700
AXL	171.7	100.0	99.7	No OMIM phenotype
CCDC141	143.7	100.0	99.5	-
CHD7	158.7	100.0	99.5	612370
DCC	147.1	100.0	100.0	157600
DUSP6	157.9	100.0	100.0	615269
FEZF1	172.6	100.0	99.9	616030
FGF17	150.4	100.0	100.0	615270
FGF8	127.7	98.2	88.9	612702
FGFR1	137.7	100.0	99.9	147950
FLRT3	199.1	100.0	100.0	615271
FSHB	115.6	100.0	100.0	229070
GNRH1	100.9	100.0	93.7	614841
GNRHR	156.3	100.0	100.0	138850
HESX1	80.5	99.7	97.3	182230
HS6ST1	54.3	92.9	84.5	614880
IGSF10	220.0	100.0	100.0	-
IL17RD	145.4	99.9	99.1	615267
KISS1	62.5	100.0	98.3	614842
KISS1R	109.4	100.0	99.5	614837
KLB	225.5	100.0	99.9	-

LEP	198.4	99.9	97.3	614962
LEPR	128.3	94.3	92.6	614963
LHB	21.0	90.4	38.9	228300
LHX3	86.2	96.6	96.5	221750
NR0B1	132.2	100.0	99.5	300200
NSMF	105.0	96.1	95.6	614838
PCSK1	175.2	100.0	99.5	600955
PLXNA1	177.0	100.0	99.6	-
POLG	111.5	100.0	99.3	157640
PROK2	136.2	99.9	98.5	610628
PROKR2	228.4	100.0	100.0	244200
PROP1	98.8	92.6	82.6	262600
SEMA3A	196.5	100.0	99.9	614897
SOX10	70.3	99.9	97.9	-
SOX2	207.1	100.0	100.0	206900
SPRY4	153.2	100.0	100.0	615266
TAC3	79.3	100.0	99.6	614839
TACR3	150.3	100.0	100.0	614840
TCF12	155.4	100.0	99.9	615314
WDR11	139.6	98.0	96.5	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.
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 10x 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