WES DISORDERS OF SEX DEVELOPMENT DG 2.15

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
AKR1C2	179.5	96.3	89.6	614279
AMH	42.1	92.8	74.2	261550
AMHR2	158.0	100.0	99.5	261550
AR	85.3	93.8	88.3	300068
ARX	29.1	75.8	59.5	300215
ATF3	138.1	99.8	98.7	-
ATRX	82.6	98.2	92.2	309580;301040
B9D1	115.3	92.1	91.4	614209
CBX2	96.6	99.9	98.4	613080
CEP41	83.5	97.7	89.6	614464
CYB5A	133.5	100.0	100.0	250790
CYP11A1	123.9	99.6	97.7	613743
CYP11B1	175.9	100.0	100.0	202010
CYP17A1	135.0	100.0	99.7	202110
CYP19A1	160.6	99.1	97.3	613546
CYP21A2	93.8	95.8	86.6	201910
DHCR7	158.3	100.0	100.0	270400
DHH	117.7	100.0	100.0	233420
DMRT1	99.4	99.3	92.4	154230
DMRT2	154.3	98.4	90.6	-
DYNC2H1	90.5	96.6	87.0	613091
FAM58A	73.2	82.8	78.8	300707
FGFR2	140.1	97.4	96.4	101200
FOXL2	39.5	92.8	71.0	110100;608996
FRAS1	147.8	100.0	99.7	219000

FREM2	182.4	100.0	99.5	219000
GATA4	87.4	68.6	60.7	615542
GRIP1	130.8	100.0	99.9	219000
HOXA13	49.0	69.2	61.7	140000
HSD17B3	156.4	100.0	100.0	264300
HSD3B2	189.2	100.0	100.0	201810
LHCGR	154.5	95.4	92.8	238320
MAMLD1	131.4	99.9	98.3	300758
MAP3K1	166.0	92.9	89.2	613762
MKKS	208.5	83.2	83.1	236700
NEK1	103.2	98.1	93.0	263520
NR0B1	119.3	99.9	98.6	300018;300200
NR3C1	137.4	100.0	99.8	615962
NR5A1	79.9	100.0	98.3	612965
POR	167.7	99.9	98.7	201750
RIPK4	163.3	100.0	99.6	263650
ROR2	165.9	99.4	98.0	268310
RSPO1	109.7	100.0	100.0	610644
SOX3	37.7	86.4	71.5	300833
SOX9	134.0	97.8	93.8	114290
SRCAP	153.9	99.8	99.1	136140
SRD5A2	77.6	100.0	96.4	264600
SRY	46.1	50.0	50.0	400044;400045
STAR	124.0	100.0	100.0	201710
TCTN3	127.6	100.0	99.8	614815
TOE1	165.1	100.0	100.0	614969
TSPYL1	141.5	100.0	99.4	608800
WDR60	114.2	99.1	96.3	615503
WNT4	263.1	93.4	92.7	611812
WT1	76.5	91.8	81.4	194080;136680

ZFPM2	196.3	100.0	99.6	616067

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