

# WES OROFACIAL CLEFTING DG 3.1

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
ACTB	74.3	99.7	96.1	243310
ACTG1	121.5	100.0	100.0	614583
ALX1	169.2	99.7	97.1	613456
ALX3	124.9	77.9	73.3	136760
AMER1	108.0	99.9	98.5	300373
AMMECR1	94.4	100.0	99.1	300990
ANKRD11	118.7	96.1	93.5	148050
ARHGAP29	168.5	99.5	98.0	-
ARHGAP31	161.2	99.9	98.8	100300
ASXL1	145.8	99.8	99.3	605039
B3GALT6	43.1	75.7	69.7	615349
B3GLCT	116.4	99.6	96.3	261540
B4GALT7	122.2	99.8	97.4	130070
B9D2	97.6	100.0	100.0	614175
BCOR	117.1	99.6	97.4	300166
BMP2	178.0	100.0	100.0	617877
BMPER	148.8	100.0	99.8	608022
C2CD3	140.4	95.8	95.6	615948
CC2D2A	131.6	98.5	96.5	612284
CDC45	162.6	99.8	98.5	617063
CDH1	126.7	99.2	99.1	137215
CDKN1C	66.8	88.0	77.8	614732
CHD7	158.7	100.0	99.5	214800
CHRNA3	149.9	100.0	100.0	253290;265000
CHST14	147.4	99.9	98.9	601776

CILK1	133.5	99.9	98.7	612651
COL11A1	113.4	96.2	92.8	604841;154780
COL11A2	127.0	100.0	99.7	184840;215150
COL2A1	125.9	100.0	99.7	108300
COL9A1	159.8	100.0	99.2	614134
COLEC10	140.4	100.0	100.0	248340
COLEC11	178.1	100.0	100.0	265050
CPLANE1	148.8	99.7	98.4	277170
CTCF	150.1	100.0	99.3	615502
CTNND1	150.1	100.0	100.0	617681
DDX3X	76.6	81.2	78.9	300958
DDX59	172.0	100.0	100.0	174300
DHCR7	152.1	100.0	100.0	270400
DHODH	112.7	100.0	100.0	263750
DLL4	178.9	100.0	99.2	616589
DOCK6	122.2	99.3	98.9	614219
DVL1	137.3	97.2	95.0	616331
DVL3	192.3	100.0	100.0	616894
DYNC2H1	122.7	98.8	95.5	613091
DYNC2LI1	121.3	99.7	97.6	617088
EBP	73.3	99.7	95.8	302960
EDN1	166.4	100.0	100.0	615706
EDNRA	196.2	100.0	100.0	616367
EFNB1	142.1	100.0	100.0	304110
EFTUD2	123.9	100.0	99.8	610536
EIF2S3	91.9	95.4	89.1	300148
EIF4A3	106.3	100.0	99.5	268305
EOGT	125.8	79.4	78.4	615297
EPG5	137.8	99.5	98.5	242840
ESCO2	139.5	98.7	95.2	268300

EYA1	145.7	99.9	99.7	113650
FAM20C	132.4	100.0	100.0	259775
FGD1	91.2	97.3	92.8	305400
FGF8	127.7	98.2	88.9	612702
FGFR1	137.7	100.0	99.9	615465
FGFR2	134.1	97.7	97.1	101400
FLNA	138.5	100.0	99.9	311300
FLNB	140.5	99.5	98.8	150250
FOXC2	99.8	100.0	96.7	153400
FOXE1	42.5	96.9	78.5	241850
FRAS1	140.3	100.0	99.4	219000
FTO	115.2	83.8	83.7	612938
GDF6	116.8	100.0	99.9	118100
GJA1	187.7	100.0	100.0	164200
GLI2	155.7	99.1	97.4	610829;615849
GLI3	140.8	98.5	98.0	146510
GNAI3	108.8	99.3	95.2	602483
GNB1	183.7	100.0	100.0	616973
GPC3	90.4	99.1	94.7	312870
GRHL3	156.5	100.0	100.0	606713
HDAC8	106.0	86.5	85.1	300882
HYLS1	183.5	100.0	100.0	236680
IFT140	124.5	99.8	98.8	266920
IFT172	107.8	99.9	99.1	615630
IFT57	147.3	99.9	99.1	617927
IFT80	78.3	97.6	88.2	611263
IMPAD1	157.7	100.0	100.0	614078
INTU	141.9	99.7	98.1	617926
IRF6	91.7	99.6	95.9	119500;119300
KANSL1	179.7	99.9	99.2	610443

KAT6A	175.7	100.0	99.8	616268
KCNJ2	183.9	100.0	100.0	170390
KCNK9	153.1	97.3	97.3	612292
KDM6A	114.8	96.1	88.7	300867
KIAA0586	143.8	97.3	93.1	616546
KIF7	100.0	93.6	90.6	200990
KIFBP	176.1	96.1	96.1	609460
KMT2D	142.1	100.0	99.4	147920
MAP3K7	144.4	100.0	99.6	617137
MAPRE2	184.9	100.0	99.3	616734
MASP1	146.6	100.0	99.9	257920
MBTPS2	133.0	100.0	99.0	308205
MED25	151.9	100.0	99.8	616449
MEIS2	149.4	100.0	100.0	600987
MID1	159.2	99.8	98.7	300000
MKS1	104.7	99.8	97.9	249000
MSX1	96.5	96.9	89.3	608874;106600
MYMK	141.0	100.0	100.0	254940
NECTIN1	135.3	100.0	99.9	225060
NEDD4L	116.7	72.0	71.5	617201
NEK1	141.3	99.8	98.0	263520
NIPBL	142.8	98.9	97.0	122470
NOTCH1	121.7	99.2	97.2	616028
OFD1	61.2	88.0	73.7	311200
ORC1	110.6	100.0	99.4	224690
PAX3	114.5	100.0	99.9	193500
PGM1	147.7	94.2	94.2	614921
PHF8	90.9	99.7	96.8	300263
PHGDH	116.1	99.9	98.8	256520
PIEZO2	121.6	100.0	99.5	114300

PIGN	117.3	93.8	91.5	614080
PIGV	145.1	100.0	100.0	239300
PLCB4	117.7	99.9	98.8	614669
POLR1A	124.0	100.0	99.4	616462
POLR1C	102.8	90.5	87.0	248390
POLR1D	210.1	91.6	91.6	613717
POMT1	150.5	99.3	97.5	236670
PORCN	121.0	100.0	99.1	305600
PQBP1	137.8	100.0	100.0	309500
PROKR2	228.4	100.0	100.0	244200
PRRX1	110.0	100.0	99.7	202650
PTCH1	127.2	99.2	97.6	610828
PTCH2	118.2	99.9	99.0	109400
RBM10	121.7	99.5	97.1	311900
RIPK4	144.6	100.0	99.9	263650
ROR2	168.7	100.0	99.9	268310
RPGRIP1L	155.5	96.7	95.7	611561
RPL11	111.0	100.0	100.0	612562
RPL26	42.3	97.2	84.4	614900
RPL5	42.2	86.2	70.0	612561
RPS19	92.9	100.0	99.6	105650
RPS26	92.6	95.7	84.9	613309
RPS28	57.7	100.0	94.8	606164
RUNX2	113.5	72.2	72.2	119600
SALL4	136.9	98.6	96.7	-
SATB2	126.5	99.7	97.4	612313
SCARF2	74.5	95.4	86.2	600920
SEC23A	154.5	99.7	98.2	607812
SEMA3E	158.1	99.2	98.9	214800
SEPTIN9	154.2	100.0	99.9	162100

SF3B4	69.4	99.9	97.3	154400
SHH	128.7	100.0	99.5	142945
SIX1	137.0	100.0	99.2	608389
SIX3	154.3	99.9	98.6	157170
SIX5	67.0	95.4	88.2	610896
SKI	101.8	99.3	94.9	182212
SLC26A2	234.0	100.0	100.0	222600
SMAD3	144.4	99.9	99.0	613795
SMAD4	127.2	100.0	99.9	139210
SMC1A	102.0	100.0	98.7	300590
SMC3	91.6	95.2	91.0	610759
SMCHD1	116.5	99.5	96.3	603457
SMS	80.6	91.5	78.5	309583
SNRPB	93.2	100.0	99.3	117650
SON	126.1	98.8	94.9	617140
SOX9	161.0	100.0	98.6	114290
SPECC1L	135.8	96.0	95.7	145410
STAC3	132.6	100.0	100.0	255995
STAMPB	118.1	100.0	99.4	614261
TAPT1	111.4	91.7	86.9	616897
TBX1	89.7	87.0	77.5	192430;188400
TBX15	113.0	100.0	99.9	260660
TBX2	132.9	99.9	97.5	618223
TBX22	142.6	99.2	95.7	303400
TCOF1	123.4	99.7	98.6	154500
TCTN3	136.4	100.0	100.0	258860
TFAP2A	119.1	99.4	94.3	113620
TGDS	108.6	99.4	96.8	616145
TGFB3	160.1	100.0	100.0	615582
TGFBR1	181.8	93.7	93.6	609192

TGFB2	171.6	100.0	100.0	610168
TGIF1	160.4	100.0	100.0	142946
TMCO1	86.2	88.0	87.4	213980
TMEM216	114.4	99.9	98.1	603194
TP63	188.5	100.0	100.0	603543;106260;618149;129400;103285;604292
TRIM37	141.7	98.6	98.1	253250
TUBB	125.1	97.3	93.9	156610
TWIST1	96.4	100.0	98.9	101400;617746
TXNL4A	104.3	100.0	99.4	608572
USP9X	109.6	98.2	92.9	300968
WASHC5	164.8	100.0	99.8	220210
WDR35	172.4	99.8	98.9	613610;614091
WNT4	200.3	99.1	94.8	611812
WNT5A	127.0	100.0	100.0	180700
XYLT1	148.0	97.4	89.6	615777
ZEB2	158.7	99.9	99.1	235730
ZIC2	110.1	100.0	98.7	609637
ZIC3	129.6	100.0	99.9	314390
ZMPSTE24	155.1	100.0	99.9	275210
ZSWIM6	142.4	95.5	91.9	603671

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 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