

WES OROFACIAL CLEFTING DG 3.4

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ACTB	292.9	100.0	100.0	243310
ACTG1	270.4	100.0	100.0	614583
ALX1	184.4	100.0	100.0	613456
ALX3	186.7	100.0	100.0	136760
AMER1	237.8	100.0	100.0	300373
AMMECR1	155.9	100.0	100.0	300990
ANKRD11	202.6	100.0	100.0	148050
ARHGAP29	160.8	100.0	100.0	-
ARHGAP31	200.2	100.0	100.0	100300
ASXL1	224.7	99.9	99.9	605039
B3GALT6	231.8	99.8	98.8	615349
B3GLCT	149.7	100.0	100.0	261540
B4GALT7	162.3	100.0	100.0	130070
B9D2	201.8	100.0	100.0	614175
BCOR	211.7	100.0	100.0	300166
BMP2	196.6	100.0	100.0	617877
BMPER	173.4	100.0	100.0	608022
C2CD3	168.1	95.9	95.9	615948
CC2D2A	156.9	97.1	97.1	612284
CDC45	174.4	100.0	100.0	617063
CDH1	184.9	97.8	97.8	137215
CDKN1C	232.6	100.0	100.0	614732
CHD7	185.7	100.0	100.0	214800
CHRNA	188.0	100.0	100.0	253290;265000
CHST14	217.4	100.0	100.0	601776

CILK1	165.5	100.0	100.0	612651
COL11A1	149.2	100.0	100.0	604841;154780
COL11A2	274.6	100.0	100.0	184840;215150
COL2A1	179.8	100.0	100.0	108300
COL9A1	162.2	100.0	100.0	614134
COLEC10	168.5	100.0	100.0	248340
COLEC11	215.7	100.0	100.0	265050
CPLANE1	155.0	100.0	100.0	277170
CTCF	192.1	100.0	100.0	615502
CTNND1	177.0	100.0	100.0	617681
DDX3X	142.8	99.2	97.6	300958
DDX59	169.2	100.0	100.0	174300
DHCR7	189.2	100.0	100.0	270400
DHODH	177.3	100.0	100.0	263750
DLL4	213.0	100.0	100.0	616589
DOCK6	189.5	100.0	100.0	614219
DVL1	239.2	100.0	100.0	616331
DVL3	211.6	100.0	100.0	616894
DYNC2H1	143.7	100.0	100.0	613091
DYNC2LI1	137.7	100.0	100.0	617088
EBP	181.5	100.0	100.0	302960
EDN1	144.4	100.0	100.0	615706
EDNRA	178.0	100.0	100.0	616367
EFNB1	195.6	100.0	100.0	304110
EFTUD2	150.3	100.0	100.0	610536
EIF2S3	161.4	100.0	100.0	300148
EIF4A3	161.4	100.0	100.0	268305
EOGT	116.6	94.3	90.6	615297
EPG5	167.5	100.0	100.0	242840
ESCO2	142.7	100.0	100.0	268300

EYA1	161.7	100.0	100.0	113650
FAM20C	200.0	100.0	100.0	259775
FGD1	196.6	100.0	100.0	305400
FGF8	200.6	100.0	100.0	612702
FGFR1	214.8	100.0	100.0	615465
FGFR2	193.1	100.0	100.0	101400
FLNA	208.6	100.0	100.0	311300
FLNB	178.2	100.0	100.0	150250
FOXC2	222.2	100.0	100.0	153400
FOXE1	206.3	100.0	100.0	241850
FRAS1	171.0	100.0	100.0	219000
FTO	163.6	94.2	94.2	612938
GDF6	189.1	100.0	100.0	118100
GJA1	216.3	100.0	100.0	164200
GLI2	235.0	100.0	100.0	610829;615849
GLI3	207.6	100.0	100.0	146510
GNAI3	147.1	100.0	100.0	602483
GNB1	158.6	100.0	100.0	616973
GPC3	175.9	100.0	99.9	312870
GRHL3	164.8	100.0	100.0	606713
HDAC8	140.7	96.6	96.0	300882
HYLS1	197.0	100.0	100.0	236680
IFT140	196.6	100.0	100.0	266920
IFT172	164.7	100.0	100.0	615630
IFT57	158.6	100.0	100.0	617927
IFT80	150.1	100.0	100.0	611263
IMPAD1	201.7	100.0	100.0	614078
INTU	150.0	100.0	100.0	617926
IRF6	187.9	100.0	100.0	119500;119300
KANSL1	306.9	100.0	100.0	610443

KAT6A	207.7	100.0	100.0	616268
KCNJ2	214.4	100.0	100.0	170390
KCNK9	206.6	97.3	97.3	612292
KDM6A	167.6	100.0	100.0	300867
KIAA0586	144.7	95.8	95.8	616546
KIF7	196.2	100.0	100.0	200990
KIFBP	188.3	96.1	96.1	609460
KMT2D	227.9	100.0	100.0	147920
MAP3K7	153.1	100.0	100.0	617137
MAPRE2	167.4	100.0	100.0	616734
MASP1	190.9	100.0	100.0	257920
MBTPS2	147.0	100.0	100.0	308205
MED25	201.0	100.0	100.0	616449
MEIS2	189.5	100.0	100.0	600987
MID1	181.9	100.0	100.0	300000
MKS1	157.2	100.0	100.0	249000
MSX1	242.7	100.0	100.0	608874;106600
MYMK	183.2	100.0	100.0	254940
NECTIN1	208.1	100.0	100.0	225060
NEDD4L	183.3	100.0	100.0	617201
NEK1	142.5	100.0	100.0	263520
NIPBL	156.1	100.0	100.0	122470
NOTCH1	259.6	100.0	100.0	616028
OFD1	130.4	100.0	100.0	311200
ORC1	160.6	100.0	100.0	224690
PAX3	207.8	100.0	100.0	193500
PGM1	157.8	94.2	94.2	614921
PHF8	174.2	100.0	100.0	300263
PHGDH	190.3	100.0	100.0	256520
PIEZO2	173.1	100.0	100.0	114300

PIGN	143.2	98.8	98.8	614080
PIGV	188.8	100.0	100.0	239300
PLCB4	151.2	100.0	100.0	614669
POLR1A	173.3	100.0	100.0	616462
POLR1C	139.8	83.0	82.8	248390
POLR1D	176.7	100.0	100.0	613717
POMT1	166.5	100.0	100.0	236670
PORCN	175.9	100.0	100.0	305600
PQBP1	183.4	100.0	100.0	309500
PROKR2	211.7	100.0	100.0	244200
PRRX1	213.1	100.0	100.0	202650
PTCH1	215.7	100.0	100.0	610828
PTCH2	211.3	100.0	100.0	109400
RBM10	198.5	100.0	100.0	311900
RIPK4	239.3	100.0	100.0	263650
ROR2	209.3	97.0	97.0	268310
RPGRIP1L	154.2	100.0	99.8	611561
RPL11	150.9	100.0	100.0	612562
RPL26	157.0	100.0	100.0	614900
RPL5	152.4	100.0	100.0	612561
RPS19	167.2	100.0	100.0	105650
RPS26	156.1	100.0	100.0	613309
RPS28	187.0	100.0	100.0	606164
RUNX2	210.1	100.0	100.0	119600
SALL4	209.8	100.0	100.0	-
SATB2	193.6	100.0	100.0	612313
SCARF2	218.6	100.0	100.0	600920
SEC23A	149.5	100.0	100.0	607812
SEMA3E	161.7	100.0	100.0	214800
SEPTIN9	227.8	100.0	100.0	162100

SF3B4	187.0	100.0	100.0	154400
SHH	230.9	100.0	100.0	142945
SIX1	215.6	100.0	100.0	608389
SIX3	235.5	100.0	100.0	157170
SIX5	227.7	100.0	100.0	610896
SKI	184.5	100.0	100.0	182212
SLC10A7	149.5	100.0	100.0	618363
SLC26A2	188.6	100.0	100.0	222600
SMAD3	199.2	100.0	100.0	613795
SMAD4	189.0	100.0	100.0	139210
SMC1A	164.8	100.0	100.0	300590
SMC3	142.5	100.0	100.0	610759
SMCHD1	139.6	100.0	100.0	603457
SMS	139.8	100.0	100.0	309583
SNRPB	189.8	100.0	100.0	117650
SON	202.0	100.0	100.0	617140
SOX9	258.7	100.0	100.0	114290
SPECC1L	163.7	97.8	96.2	145410
STAC3	165.6	100.0	100.0	255995
STAMBP	167.8	100.0	100.0	614261
TAPT1	135.3	100.0	100.0	616897
TBX1	158.0	98.1	95.9	192430;188400
TBX15	187.2	100.0	100.0	260660
TBX2	215.6	100.0	100.0	618223
TBX22	201.1	100.0	100.0	303400
TCOF1	188.3	100.0	100.0	154500
TCTN3	169.8	100.0	100.0	258860
TFAP2A	192.5	100.0	100.0	113620
TGDS	136.1	100.0	100.0	616145
TGFB3	181.1	100.0	100.0	615582

TGFBR1	161.3	100.0	99.9	609192
TGFBR2	218.2	100.0	100.0	610168
TGIF1	212.8	100.0	100.0	142946
TMCO1	137.2	88.0	88.0	213980
TMEM216	168.9	100.0	100.0	603194
TP63	184.0	100.0	100.0	603543;106260;618149;129400;103285;604292
TRIM37	141.8	98.7	98.7	253250
TUBB	318.7	100.0	99.8	156610
TWIST1	189.8	100.0	100.0	101400;617746
TXNL4A	199.3	100.0	100.0	608572
USP9X	148.6	100.0	100.0	300968
WASHC5	145.5	100.0	100.0	220210
WDR35	151.2	100.0	100.0	613610;614091
WNT4	199.3	100.0	99.8	611812
WNT5A	219.5	100.0	100.0	180700
XYLT1	186.4	100.0	99.7	615777
ZEB2	179.1	97.4	97.4	235730
ZIC2	212.2	100.0	100.0	609637
ZIC3	217.2	100.0	100.0	314390
ZMPSTE24	139.3	100.0	100.0	275210
ZSWIM6	156.2	97.6	96.3	603671

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.