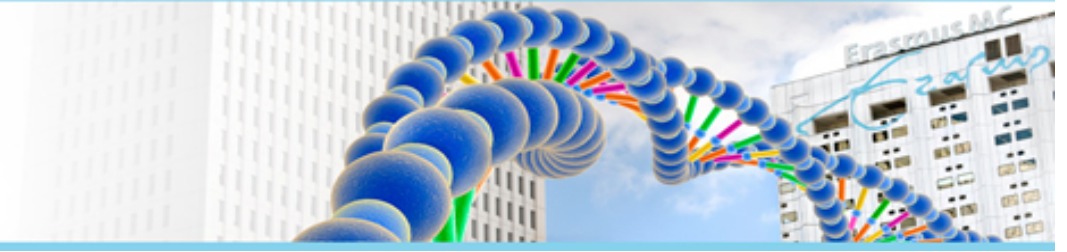


Whole Exome Sequencing

Gene package Skeletal Dysplasia, version 4, 30-9-2021



Technical information

DNA was enriched using Agilent SureSelect DNA + SureSelect OneSeq 300kb CNV Backbone + Human All Exon V7 capture and paired-end sequenced on the Illumina platform (outsourced). The aim is to obtain 10 Giga base pairs per exome with a mapped fraction of 0.99. The average coverage of the exome is ~50x. Duplicate and non-unique reads are excluded. Data are demultiplexed with bcl2fastq Conversion Software from Illumina. Reads are mapped to the genome using the BWA-MEM algorithm (reference: <http://bio-bwa.sourceforge.net/>). Sequence variant detection is performed by the Genome Analysis Toolkit HaplotypeCaller (reference: <http://www.broadinstitute.org/gatk/>). The detected sequence variants are filtered and annotated with Alissa Interpret software and classified with Alamut Visual. Copy variant detection is performed using the BAM multiscale reference method using depth of coverage analysis and dynamical bins in NexusClinical. The detected copy number variants are filtered and annotated with the NexusClinical software and classified using UCSC Genome Browser (NCBI37/hg19). It is not excluded that pathogenic variants are being missed using this technology. At this moment, there is not enough information about the sensitivity of this technique with respect to the detection of deletions and duplications of more than 5 nucleotides and of somatic mosaic mutations (all types of sequence changes).



Dept. Clinical Genetics

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
ABCC9	601439	100	100	99.81	97.71
ACAN	155760	93.08	92.50	91.57	88.85
ACP5	171640	100	100	100	100
ACTB	102630	100	100	100	99.59
ACVR1	102576	100	100	100	99.36
ADAMTS10	608990	100	100	99.74	94.21
ADAMTS17	607511	95.41	90.13	86.31	82.79
ADAMTSL2	612277	45.35	42.70	40.34	33.50
AGA	613228	100	100	100	97.37
AGPS	603051	95.91	95.91	95.22	90.86
ALG12	607144	100	100	100	100
ALG3	608750	100	100	99.33	95.82
ALG9	606941	99.91	99.91	98.32	90.50
ALMS1	606844	99.93	99.38	98.73	95.61
ALPL	171760	100	100	100	99.94
AMER1	300647	100	100	100	100
ANKH	605145	100	100	100	98.72
ANKRD11	611192	100	99.77	97.95	94.26
ANOS	608662	100	99.70	98.33	91.32

HGNC approved gene symbol	OMIM gene ID	% covered $\geq 10x$	% covered $\geq 20x$	% covered $\geq 30x$	% covered $\geq 50x$
ARSB	611542	100	100	98.12	84.71
ARSL	300180	100	100	99.83	90.82
B3GALT6	615291	79.89	76.12	72.74	70.01
B3GAT3	606374	100	100	100	95.97
B4GALT7	604327	98.64	93.64	93.64	85.79
BMP1	112264	100	100	99.82	95.41
BMPER	608699	100	99.15	98.00	93.50
BMPR1B	603248	100	100	99.45	95.46
BPNT2	614010	100	100	100	99.11
BRAF	164757	95.04	94.33	93.05	87.97
BTK	300300	100	100	100	97.97
CA2	611492	100	100	100	100
CANT1	613165	100	100	100	98.50
CBL	165360	100	100	100	99.36
CCDC134	618788	100	100	100	94.67
CCDC8	614145	100	100	99.69	96.39
CCN6	603400	100	100	98.97	93.98
CDC45	603465	100	100	100	98.94
CDC6	602627	100	100	100	99.11
CDKN1C	600856	82.09	66.60	58.55	48.84
CDT1	605525	99.67	92.79	88.36	76.25
CEP120	613446	100	100	99.84	96.58
CFAP410	603191	100	100	98.79	83.09
CHST3	603799	100	100	100	100
CLCN5	300008	100	100	99.52	92.85
CLCN7	602727	100	100	99.90	94.44
COG1	606973	100	100	100	97.97
COL10A1	120110	100	100	99.18	97.24
COL11A1	120280	100	99.17	97.37	87.82
COL11A2	120290	100	100	98.35	87.06
COL1A1	120150	100	100	99.00	92.15
COL1A2	120160	100	99.09	96.75	86.41
COL2A1	120140	100	100	99.72	94.32
COL9A1	120210	100	100	97.67	84.62
COL9A2	120260	100	96.12	88.64	64.54
COL9A3	120270	100	99.22	95.30	79.74
COLEC11	612502	100	100	99.10	93.47
COMP	600310	98.62	92.78	92.72	85.48
CREB3L1	616215	99.94	97.66	93.07	78.85
CREBBP	600140	100	99.23	97.31	92.60

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
CRTAP	605497	100	100	100	98.66
CSGALNACT1	616615	100	100	100	100
CTSA	613111	100	99.83	99.83	94.72
CTSK	601105	100	100	100	100
CUL7	609577	100	100	99.99	99.41
CYP26B1	605207	100	100	100	95.05
CYP27B1	609506	100	100	100	96.92
DDR2	191311	100	100	100	100
DHCR24	606418	100	100	100	97.63
DLL3	602768	100	98.61	88.43	65.34
DLX3	600525	100	100	100	96.15
DMP1	600980	100	100	100	98.54
DONSON	611428	98.37	93.78	87.07	76.08
DPM1	603503	100	100	100	98.96
DVL1	601365	100	95.79	91.17	78.57
DYM	607461	100	100	100	98.23
DYNC2H1	603297	99.09	98.62	96.54	89.35
DYNC2I1	615462	99.65	95.06	86.63	76.05
DYNC2I2	613363	100	100	97.93	83.59
DYNLT2B	617353	100	100	100	100
EBP	300205	100	100	100	91.30
EIF2AK3	604032	100	97.98	94.32	90.79
ENPP1	173335	92.64	91.71	89.21	86.14
EVC	604831	94.29	94.26	93.76	88.41
EVC2	607261	100	99.98	99.01	94.63
EXT1	608177	100	100	100	99.29
EXT2	608210	100	100	100	99.76
EXTL3	605744	100	100	100	100
FAM111A	615292	100	100	100	98.85
FAM20C	611061	100	97.18	91.01	76.72
FBN1	134797	100	100	100	99.50
FERMT3	607901	100	98.55	95.07	89.17
FGD1	300546	100	97.33	93.32	77.63
FGF23	605380	100	100	100	100
FGF8	600483	93.90	87.44	87.21	69.01
FGF9	600921	100	100	100	98.54
FGFR1	136350	100	100	100	98.89
FGFR2	176943	100	100	99.89	98.47
FGFR3	134934	100	99.64	98.10	91.14
FIG4	609390	100	100	100	99.32

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
FKBP10	607063	100	99.59	98.23	92.39
FLNA	300017	99.98	98.83	97.47	92.13
FLNB	603381	100	100	99.93	98.27
FN1	135600	100	100	100	98.89
FUCA1	612280	100	100	100	99.84
FZD2	600667	99.42	97.20	95.69	92.77
GALNS	612222	100	100	99.46	86.86
GALNT3	601756	100	100	100	98.79
GDF3	606522	100	100	100	99.20
GDF5	601146	100	100	100	99.68
GDF6	601147	100	100	99.07	74.80
GH1	139250	100	100	100	100
GHR	600946	100	100	100	98.55
GHRH	139190	100	100	100	92.08
GHRHR	139191	100	99.08	95.65	82.80
GHSR	601898	100	100	100	100
GJA1	121014	100	100	100	100
GLB1	611458	100	100	100	98.35
GLI2	165230	100	98.72	96.47	88.37
GLI3	165240	100	100	100	99.98
GMNN	602842	100	96.85	86.21	70.82
GNAS	139320	100	100	100	98.21
GNPAT	602744	100	100	99.79	95.83
GNPTAB	607840	100	100	99.81	98.21
GNPTG	607838	100	97.00	93.66	93.66
GNS	607664	100	98.09	96.36	93.21
GORAB	607983	100	100	100	95.83
GPC6	604404	100	100	100	98.24
GPX4	138322	100	98.52	94.89	89.25
GUSB	611499	100	100	100	98.65
HDAC4	605314	99.74	95.85	94.63	84.31
HES7	608059	91.30	73.64	63.83	35.26
HESX1	601802	100	100	93.54	82.44
HGSNAT	610453	94.18	93.95	91.93	84.15
HMGA2	600698	70.15	59.31	45.68	29.85
HOXA13	142959	83.39	77.70	73.96	67.07
HPGD	601688	100	100	100	97.39
HRAS	190020	100	100	100	100
HSPA9	600548	100	100	99.73	97.50
HSPG2	142461	99.45	99.27	98.26	92.79

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
HYLS1	610693	100	100	100	98.91
IDH2	147650	100	97.56	91.43	91.43
IDS	300823	100	99.97	95.71	84.45
IDUA	252800	99.58	89.68	81.91	70.12
IFITM5	614757	100	100	100	100
IFT122	606045	100	100	99.92	96.77
IFT140	614620	100	100	99.50	94.87
IFT172	607386	100	100	99.99	98.15
IFT43	614068	100	100	100	98.88
IFT80	611177	100	100	97.60	87.68
IGF1	147440	100	100	100	96.47
IGF1R	147370	100	100	98.94	96.84
IGF2	147470	100	100	100	98.35
IGFALS	601489	100	100	100	99.72
IGFBP3	146732	100	100	100	79.25
IGSF1	300137	100	100	100	97.83
IHH	600726	100	100	98.14	93.62
IKBKB	603258	100	100	99.63	95.13
IKBKG	300248	38.62	26.61	25.50	20.50
IL2RG	308380	100	100	100	95.50
INPPL1	600829	98.29	95.34	95.15	90.85
KDELR2	609024	100	100	98.17	78.12
KIAA0753	617112	100	100	100	98.24
KIF22	603213	100	100	99.47	96.73
KIF7	611254	99.84	96.33	91.96	81.11
KMT2A	159555	99.92	99.22	98.31	95.93
KRAS	190070	100	100	100	100
LBR	600024	100	100	99.57	94.18
LEMD3	607844	100	100	99.50	94.34
LFNG	602576	100	100	100	93.46
LHX3	600577	100	98.60	93.59	80.84
LHX4	602146	100	100	100	94.03
LIFR	151443	100	98.67	94.27	86.12
LMX1B	602575	100	97.57	91.29	84.22
LONP1	605490	100	98.80	96.85	90.50
LRP4	604270	100	100	99.78	97.85
LRP5	603506	97.91	97.91	97.46	94.32
LRRK1	610986	100	99.43	98.18	93.51
LTBP2	602091	100	98.58	95.78	88.07
LTBP3	602090	99.90	98.83	94.23	80.91

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
LZTR1	600574	100	100	100	98.72
MAN2B1	609458	100	99.90	97.81	88.61
MANBA	609489	100	100	99.97	99.16
MAP2K1	176872	100	100	100	98.21
MAP2K2	601263	100	100	98.06	86.80
MAP3K7	602614	100	100	99.17	97.17
MATN3	602109	90.82	85.63	84.98	84.98
MBTPS2	300294	100	99.80	96.51	91.78
MEOX1	600147	100	100	100	87.41
MESD	607783	100	100	100	99.41
MESP2	605195	100	98.09	95.45	83.23
MGP	154870	100	91.94	89.05	89.05
MMP13	600108	100	100	100	100
MMP14	600754	100	100	99.51	93.42
MMP2	120360	100	100	98.77	91.07
MMP9	120361	100	100	99.85	94.06
MTAP	156540	100	100	100	100
MYH3	160720	100	99.91	98.94	96.08
MYO18B	607295	100	99.93	98.98	93.36
NAGLU	609701	100	94.55	91.12	82.97
NANS	605202	100	100	100	97.28
NBAS	608025	100	100	99.93	97.07
NEK1	604588	100	98.90	97.43	90.88
NEK9	609798	100	100	99.11	95.77
NEU1	608272	100	100	100	99.71
NIN	608684	100	100	99.22	96.48
NIPBL	608667	100	99.98	99.38	96.10
NKX3-2	602183	100	100	97.83	85.23
NOTCH2	600275	99.88	98.85	98.47	95.83
NPPA	108780	100	100	100	100
NPPB	600295	100	100	98.59	68.61
NPPC	600296	100	100	92.22	62.20
NPR1	108960	100	99.92	97.05	86.97
NPR2	108961	100	100	100	99.69
NPR3	108962	100	100	100	100
NRAS	164790	100	100	100	99.85
OBSL1	610991	100	100	99.42	94.70
OFD1	300170	100	99.66	98.24	86.94
ORC1	601902	100	100	100	99.40
ORC4	603056	100	100	99.94	90.85

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
ORC6	607213	100	100	100	94.92
OSTM1	607649	100	95.94	82.58	65.29
OTX2	600037	100	100	100	100
P3H1	610339	100	100	100	100
P4HA1	176710	100	100	100	94.90
P4HB	176790	100	99.14	95.56	82.37
PAM16	614336	100	100	96.95	95.16
PAPPA	176385	95.25	93.79	91.82	90.05
PAPPA2	619485	100	100	100	98.22
PAPSS2	603005	100	100	100	96.03
PCNT	605925	100	99.96	99.08	93.59
PCYT1A	123695	100	100	100	99.64
PDE4D	600129	100	100	100	100
PEX5	600414	100	100	100	95.40
PEX7	601757	100	100	98.16	87.17
PHEX	300550	100	100	100	96.19
PHGDH	606879	100	100	100	96.57
PHYH	602026	100	89.33	89.33	80.90
PIK3CA	171834	100	100	100	98.85
PIK3R1	171833	100	100	100	98.58
PIK3R3	606076	100	100	100	95.95
PITX1	602149	99.20	92.71	84.78	76.00
PITX2	601542	100	97.48	93.41	85.17
PLEKHM1	611466	99.28	97.99	96.81	90.73
PLK4	605031	100	100	100	97.35
PLOD2	601865	96.30	91.47	91.02	86.20
PLOD3	603066	100	96.13	94.04	80.47
PLS3	300131	100	100	100	97.90
POC1A	614783	100	100	100	97.36
POP1	602486	100	100	100	97.51
POR	124015	96.93	96.93	96.93	96.73
POU1F1	173110	100	91.84	91.79	87.61
PIIB	123841	100	100	100	100
PRKAR1A	188830	100	100	100	100
PROKR2	607123	100	100	100	100
PROP1	601538	100	100	96.61	74.66
PSAT1	610936	100	100	100	95.58
PTDSS1	612792	100	100	100	99.11
PTH1R	168468	100	100	99.90	95.31
PTPN11	176876	98.37	98.37	98.37	98.37

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
RAB33B	605950	100	100	100	100
RAF1	164760	100	100	99.87	97.21
RASGRP2	605577	100	100	99.11	91.54
RBM8A	605313	100	100	100	97.51
RBPJ	147183	100	100	98.87	96.74
RIPPLY2	609891	100	100	100	91.59
RIT1	609591	100	100	100	100
RMRP	157660	No coverage data			
RNU4ATAC	601428	No coverage data			
ROR2	602337	100	100	99.40	95.61
RPGRIP1L	610937	99.64	97.81	94.99	91.37
RPL10	312173	100	100	100	100
RSPRY1	616585	100	100	100	100
RUNX2	600211	100	100	100	100
SBDS	607444	100	100	100	100
SCARF2	613619	97.24	89.06	76.92	61.10
SCUBE3	614708	100	99.97	98.48	96.55
SEC24D	607186	100	100	99.45	96.65
SERPINF1	172860	100	100	100	99.22
SERPINH1	600943	100	100	100	100
SGMS2	611574	100	100	100	100
SGSH	605270	93.52	93.52	93.52	93.52
SH3PXD2B	613293	100	98.76	96.11	88.47
SHOC2	602775	100	100	100	98.74
SHOX	312865	100	100	94.67	73.05
SHOX2	602504	100	99.49	98.31	82.41
SLC10A7	611459	100	100	100	74.35
SLC17A5	604322	93.58	93.58	93.58	91.22
SLC25A24	608744	100	100	99.82	92.80
SLC26A2	606718	100	100	100	100
SLC29A3	612373	100	97.60	97.60	97.60
SLC34A3	609826	100	99.31	98.33	90.40
SLC35D1	610804	100	99.73	97.59	87.93
SLC39A13	608735	100	100	100	97.99
SLCO2A1	601460	100	100	98.55	88.57
SLCO5A1	613543	100	100	99.28	95.87
SMAD4	600993	100	100	100	99.36
SMARCAL1	606622	100	100	100	97.91
SNRPB	182282	100	100	98.49	86.51
SNX10	614780	100	100	100	100

HGNC approved gene symbol	OMIM gene ID	% covered ≥10x	% covered ≥20x	% covered ≥30x	% covered ≥50x
SOS1	182530	100	98.47	97.56	94.16
SOS2	601247	99.48	98.09	95.96	88.50
SOST	605740	100	100	100	100
SOX2	184429	100	100	99.23	93.41
SOX3	313430	100	99.04	90.83	63.55
SOX9	608160	100	97.48	94.83	87.05
SP7	606633	100	100	100	94.45
SPARC	182120	100	100	100	97.13
SPINK5	605010	100	99.14	96.90	84.44
SPR	182125	100	100	97.33	81.97
SRCAP	611421	100	100	99.70	96.68
STAT3	102582	100	100	100	96.39
STAT5B	604260	100	99.49	97.08	89.89
SULF1	610012	100	100	99.33	95.62
SUMF1	607939	100	100	100	100
TAPT1	612758	95.71	88.94	83.17	77.21
TBCE	604934	100	100	99.18	95.59
TBX15	604127	100	100	99.44	97.61
TBX4	601719	100	97.27	93.49	86.54
TBX6	602427	100	100	100	91.11
TBXAS1	274180	100	100	100	100
TCIRG1	604592	100	99.23	95.33	87.67
TCTN2	613846	100	100	100	96.98
TCTN3	613847	100	100	100	98.86
TENT5A	611357	100	100	100	100
TGFB1	190180	100	100	100	99.39
TMEM165	614726	100	100	100	96.98
TMEM216	613277	100	100	100	100
TMEM231	614949	100	100	100	97.47
TMEM38B	611236	100	100	100	100
TNFRSF11A	603499	90.20	90.20	88.03	82.66
TNFRSF11B	602643	100	100	100	100
TNFSF11	602642	100	100	100	100
TRAPPC2	300202	100	100	100	81.35
TRIP11	604505	100	99.29	97.00	88.46
TRPS1	604386	100	100	100	100
TRPV4	605427	100	100	99.98	95.90
TTC21B	612014	100	100	100	99.26
VDR	601769	100	98.33	93.88	80.91
WDR19	608151	100	100	99.54	96.20

HGNC approved gene symbol	OMIM gene ID	% covered $\geq 10x$	% covered $\geq 20x$	% covered $\geq 30x$	% covered $\geq 50x$
WDR35	613602	100	99.48	97.81	95.83
WNT1	164820	100	100	100	95.59
WNT5A	164975	100	100	97.90	96.09
XRCC4	194363	100	100	100	93.77
XYLT1	608124	98.57	94.72	91.00	86.04
XYLT2	608125	94.49	94.49	94.49	92.50
ZBTB16	176797	100	100	100	100
ZMPSTE24	606480	100	100	100	99.85

- OMIM release used: 23-9-2021

- The statistics above are based on a set of 150 samples

- % Covered 10x , 20x, 30x and 50x describes the percentage of a gene's coding sequence ($\pm 10bp$ flanking introns) that is covered at least 10x, 20x, 30x or 50x