Whole Exome Sequencing
Gene package Aneurysm, version 5, 18-2-2019

Technical information
DNA was enriched using Agilent SureSelect Clinical Research Exome V2 capture and paired-end sequenced on the Illumina platform (outsourced). The aim is to obtain 8.1 Giga base pairs per exome with a mapped fraction of 0.99. The average coverage of the exome is ~50x. Duplicate 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/). Variant detection is performed by the Genome Analysis Toolkit HaplotypeCaller (reference: http://www.broadinstitute.org/gatk/). The detected variants are filtered and annotated with Cartagenia software and classified with Alamut Visual. It is not excluded that pathogenic mutations 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).

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HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x
ABL1	Congenital heart defects and skeletal malformations syndrome, 617602 Leukemia, Philadelphia chromosome-positive, resistant to imatinib	189980	129	100	100	99
ACTA2	Aortic aneurysm, familial thoracic 6, 611788 Moyamoya disease 5, 614042 Multisystemic smooth muscle dysfunction syndrome, 613834	102620	163	100	100	100
BGN	Meester-Loeys syndrome, 300989 Spondyloepimetaphyseal dysplasia, X-linked, 300106	301870	78	100	100	97
COL1A1	{Bone mineral density variation QTL, osteoporosis}, 166710 Caffey disease, 114000 Ehlers-Danlos syndrome, arthrochalasia type, 1, 130060 Osteogenesis imperfecta, type I, 166200 Osteogenesis imperfecta, type II, 166210 Osteogenesis imperfecta, type III, 259420 Osteogenesis imperfecta, type IV, 166220	120150	120	100	100	99

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x
COL1A2	Ehlers-Danlos syndrome, arthrochalasia type, 2, 617821 Ehlers-Danlos syndrome, cardiac valvular type, 225320 imperfecta, type III, 259420 Osteogenesis imperfecta, type II, 166210 Osteogenesis imperfecta, type IV, 166220 {Osteoporosis, postmenopausal}, 166710	120160	62	100	99	94
COL3A1	Ehlers-Danlos syndrome, vascular type, 130050	120180	110	100	100	99
COL5A1	Ehlers-Danlos syndrome, classic type, 1, 130000	120215	130	100	100	98
COL5A2	Ehlers-Danlos syndrome, classic type, 2, 130010	120190	56	100	99	88
DCHS1	Mitral valve prolapse 2, 607829 Van Maldergem syndrome 1, 601390	603057	118	100	100	100
EFEMP2	Cutis laxa, autosomal recessive, type IB, 614437	604633	97	100	100	100
ELN	Cutis laxa, autosomal dominant, 123700 Supravalvar aortic stenosis, 185500	130160	81	100	100	97
FBN1	Acromicric dysplasia, 102370 Ectopia lentis, familial, 129600 Geleophysic dysplasia 2, 614185 MASS syndrome, 604308 Marfan lipodystrophy syndrome, 616914 Marfan syndrome, 154700 Stiff skin syndrome, 184900 Weill-Marchesani syndrome 2, dominant, 608328	134797	175	100	100	100
FBN2	Contractural arachnodactyly, congenital, 121050 Macular degeneration, early-onset, 616118	612570	66	100	99	94
FLNA	Cardiac valvular dysplasia, 314400 Congenital short bowel syndrome, 300048 ?FG syndrome 2, 300321 Frontometaphyseal dysplasia 1, 305620 Heterotopia, periventricular, 300049 Intestinal pseudoobstruction, neuronal, 300048 Melnick-Needles syndrome, 309350 Otopalatodigital syndrome, type I, 311300 Otopalatodigital syndrome, type II, 304120 Terminal osseous dysplasia, 300244	300017	98	100	100	99
FOXE3	Anterior segment dysgenesis 2, multiple subtypes, 610256 {Aortic aneurysm, familial thoracic 11, susceptibility to}, 617349 Cataract 34, multiple types, 612968	601094	60	88	78	70
GATA5	Congenital heart defects, multiple types, 5, 617912	611496	77	100	99	96

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x
HCN4	Brugada syndrome 8, 613123 Sick sinus syndrome 2, 163800	605206	102	100	100	98
LMOD1	No OMIM phenotype	602715	109	100	100	100
LOX	Aortic aneurysm, familial thoracic 10, 617168	153455	125	100	100	100
LTBP3	Dental anomalies and short stature, 601216 Geleophysic dysplasia 3, 617809	602090	125	100	99	96
MAT2A	No OMIM phenotype	601468	71	100	100	91
MFAP5	Aortic aneurysm, familial thoracic 9, 616166	601103	42	100	96	81
MYH11	Aortic aneurysm, familial thoracic 4, 132900	160745	128	100	100	96
MYLK	Aortic aneurysm, familial thoracic 7, 613780	600922	114	100	100	99
NOTCH1	Adams-Oliver syndrome 5, 616028 Aortic valve disease 1, 109730	190198	114	100	100	98
PLOD1	Ehlers-Danlos syndrome, kyphoscoliotic type, 1, 225400	153454	98	100	100	99
PRKG1	Aortic aneurysm, familial thoracic 8, 615436	176894	56	100	100	93
ROBO4	No OMIM phenotype	607528	85	100	100	96
SKI	Shprintzen-Goldberg syndrome, 182212	164780	118	100	100	99
SLC2A10	Arterial tortuosity syndrome, 208050	606145	117	100	100	100
SMAD2	No OMIM phenotype	601366	59	100	99	93
SMAD3	Loeys-Dietz syndrome 3, 613795	603109	177	100	100	100
SMAD4	Juvenile polyposis/hereditary hemorrhagic telangiectasia syndrome, 175050 Myhre syndrome, 139210 Pancreatic cancer, somatic, 260350 Polyposis, juvenile intestinal, 174900	600993	69	100	100	96
SMAD6	Aortic valve disease 2, 614823 {Craniosynostosis 7, susceptibility to}, 617439	602931	153	100	100	92
TGFB2	Loeys-Dietz syndrome 4, 614816	190220	74	100	100	96
TGFB3	Arrhythmogenic right ventricular dysplasia 1, 107970 Loeys-Dietz syndrome 5, 615582	190230	96	100	100	100
TGFBR1	Loeys-Dietz syndrome 1, 609192 {Multiple self-healing squamous epithelioma, susceptibility to}, 132800	190181	161	96	93	93
TGFBR2	Colorectal cancer, hereditary nonpolyposis, type 6, 614331 Esophageal cancer, somatic, 133239 Loeys-Dietz syndrome 2, 610168	190182	200	100	100	100

- Gene symbols according HGCN
- OMIM release used: 4-7-2018
- "No OMIM phenotypes" indicates a gene without a current OMIM association
- OMIM phenotypes between "[ ]", indicate "nondiseases," mainly genetic variations that lead to apparently abnormal laboratory test values
- OMIM phenotypes between "{}", indicate risk factors
- OMIM phenotypes with a question mark, "?", before the disease name indicates an unconfirmed or possibly spurious mapping

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- The statistics above are based on a set of 95 samples
- Median depth is the median of the mean sequence depth over the protein coding exons (±10bp flanking introns) of the longest transcript
- % Covered 10x , 20x and 30 x describes the percentage of a gene's coding sequence (±10bp flanking introns) that is covered at least 10x, 20x or 30x