Whole Exome Sequencing
Gene package Aneurysm, version 6, 30-9-2019

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, 608232	189980	141	100	100	100
ACTA2	Aortic aneurysm, familial thoracic 6, 611788 Moyamoya disease 5, 614042 Multisystemic smooth muscle dysfunction syndrome, 613834	102620	167	100	100	100
BGN	Meester-Loeys syndrome, 300989 Spondyloepimetaphyseal dysplasia, 300106	301870	87	100	100	98
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	130	100	100	100

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 Osteogenesis imperfecta, type II, 166210 Osteogenesis imperfecta, type III, 259420 Osteogenesis imperfecta, type IV, 166220 {Osteoporosis, postmenopausal}, 166710	120160	70	100	100	97
COL3A1	Ehlers-Danlos syndrome, vascular type, 130050 Polymicrogyria with or without vascular-type EDS, 618343	120180	122	100	100	100
COL5A1	Ehlers-Danlos syndrome, classic type, 1, 130000	120215	136	100	100	98
COL5A2	Ehlers-Danlos syndrome, classic type, 2, 130010	120190	65	100	100	94
DCHS1	Mitral valve prolapse 2, 607829 Van Maldergem syndrome 1, 601390	603057	128	100	100	100
EFEMP2	Cutis laxa, type IB, 614437	604633	103	100	100	100
ELN	Cutis laxa, 123700 Supravalvar aortic stenosis, 185500	130160	85	100	100	98
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	186	100	100	100
FBN2	Contractural arachnodactyly, congenital, 121050 Macular degeneration, early-onset, 616118	612570	74	100	100	97
FLNA	Cardiac valvular dysplasia, 314400 Congenital short bowel syndrome, 300048 ?FG syndrome 2, 300321 Frontometaphyseal dysplasia 1, 305620 Heterotopia, periventricular, 1, 300049 Intestinal pseudoobstruction, neuronal, 300048 Melnick-Needles syndrome, 309350 Otopalatodigital syndrome, type I, 311300 Otopalatodigital syndrome, type II, 304120 Terminal osseous dysplasia, 300244	300017	110	100	100	100
FOXE3	Anterior segment dysgenesis 2, multiple subtypes, 610256 {Aortic aneurysm, familial thoracic 11, susceptibility to}, 617349 Cataract 34, multiple types, 612968	601094	74	87	79	74

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GATA5	Congenital heart defects, multiple types, 5, 617912	611496	78	100	99	95
HCN4	Brugada syndrome 8, 613123 Sick sinus syndrome 2, 163800	605206	103	100	100	99
LMOD1	No OMIM phenotype	602715	128	100	100	100
LOX	Aortic aneurysm, familial thoracic 10, 617168	153455	119	100	100	100
LTBP3	Dental anomalies and short stature, 601216 Geleophysic dysplasia 3, 617809	602090	130	100	99	96
MAT2A	No OMIM phenotype	601468	83	100	100	96
MFAP5	Aortic aneurysm, familial thoracic 9, 616166	601103	50	100	100	92
MYH11	Aortic aneurysm, familial thoracic 4, 132900	160745	136	100	100	99
MYLK	Aortic aneurysm, familial thoracic 7, 613780	600922	121	100	100	99
NOTCH1	Adams-Oliver syndrome 5, 616028 Aortic valve disease 1, 109730	190198	117	100	99	98
PLOD1	Ehlers-Danlos syndrome, kyphoscoliotic type, 1, 225400	153454	100	100	100	99
PRKG1	Aortic aneurysm, familial thoracic 8, 615436	176894	69	100	100	98
ROBO4	Aortic valve disease 8, 618496	607528	91	100	100	98
SKI	Shprintzen-Goldberg syndrome, 182212	164780	123	100	100	99
SLC2A10	Arterial tortuosity syndrome, 208050	606145	125	100	100	100
SMAD2	No OMIM phenotype	601366	69	100	100	97
SMAD3	Loeys-Dietz syndrome 3, 613795	603109	188	100	100	100
SMAD4	Juvenile polyposis/hereditary hemorrhagic telangiectasia syndrome, 175050 Myhre syndrome, 139210 Pancreatic cancer, somatic, 260350 Polyposis, juvenile intestinal, 174900	600993	79	100	100	98
SMAD6	Aortic valve disease 2, 614823 {Craniosynostosis 7, susceptibility to}, 617439	602931	165	100	97	87
TGFB2	Loeys-Dietz syndrome 4, 614816	190220	88	100	100	98
TGFB3	Arrhythmogenic right ventricular dysplasia 1, 107970 Loeys-Dietz syndrome 5, 615582	190230	104	100	100	100
TGFBR1	Loeys-Dietz syndrome 1, 609192 {Multiple self-healing squamous epithelioma, susceptibility to}, 132800	190181	171	94	93	93
TGFBR2	Colorectal cancer, hereditary nonpolyposis, type 6, 614331 Esophageal cancer, somatic, 133239 Loeys-Dietz syndrome 2, 610168	190182	210	100	100	100
TLN1	No OMIM phenotype	186745	100	100	100	100

- Gene symbols according HGCN
- OMIM release used: 8-9-2019
- "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

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x	% covered >30x

- 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
- The statistics above are based on a set of 100 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