Whole Exome Sequencing
Gene package Aneurysm, version 2, 8-7-2016

Technical information
After DNA was enriched using Agilent Sureselect Clinical Research Exome (CRE) Capture, samples were run on the Illumina Hiseq platform. The aim is to obtain 50 million total reads per exome with a mapped fraction >0.98. The average coverage of the exome is ~50x. Data are demultiplexed by Illumina software bcl2fastq. Reads are mapped to the genome using BWA (reference: http://bio-bwa.sourceforge.net/). Variant detection is performed by Genome Analysis Toolkit (reference: http://www.broadinstitute.org/gatk/). Analysis is performed in Cartagenia using The Variant Calling File (VCF) followed by filtering. 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).

Erasmus MC
University Medical Center Rotterdam

Dept. Clinical Genetics

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x
ACTA2	Aortic aneurysm, familial thoracic 6, 611788 Multisystemic smooth muscle dysfunction syndrome, 613834 Moyamoya disease 5, 614042	102620	96	100	100
BGN	No OMIM phenotype	301870	63	100	100
COL3A1	Ehlers-Danlos syndrome, type IV, 130050	120180	63	99	93
COL5A1	Ehlers-Danlos syndrome, classic type, 130000	120215	77	99	97
EFEMP2	Cutis laxa, autosomal recessive, type IB, 614437	604633	82	100	100
ELN	Supravalvar aortic stenosis, 185500 Cutis laxa, AD, 123700	130160	65	100	99
FBN1	Marfan syndrome, 154700 Ectopia lentis, familial, 129600 MASS syndrome, 604308 Weill-Marchesani syndrome 2, dominant, 608328 Aortic aneurysm, ascending, and dissection Stiff skin syndrome, 184900 Acromicric dysplasia, 102370 Geleophysic dysplasia 2, 614185	134797	86	100	100
FBN2	Contractural arachnodactyly, congenital, 121050 Macular degeneration, early-onset, 616118	612570	90	100	98

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x
FLNA	Heterotopia, periventricular, 300049 Otopalatodigital syndrome, type I, 311300 Otopalatodigital syndrome, type II, 304120 Intestinal pseudoobstruction, neuronal, 300048 Melnick-Needles syndrome, 309350 Frontometaphyseal dysplasia, 305620 Heterotopia, periventricular, ED variant, 300537 FG syndrome 2, 300321 Cardiac valvular dysplasia, X-linked, 314400 Terminal osseous dysplasia, 300244 Congenital short bowel syndrome, 300048	300017	55	100	99
FOXE3	Anterior segment mesenchymal dysgenesis, 107250 Aphakia, congenital primary, 610256	601094	40	73	58
GATA5	No OMIM phenotype	611496	54	100	100
LOX	No OMIM phenotype	153455	87	100	100
MAT2A	No OMIM phenotype	601468	37	93	74
MATR3	Amyotrophic lateral sclerosis 21, 606070	164015	56	91	80
MFAP5	Aortic aneurysm, familial thoracic 9, 616166	601103	38	95	80
MTHFR	Homocystinuria due to MTHFR deficiency, 236250 {Schizophrenia, susceptibility to}, 181500 {Vascular disease, susceptibility to} {Neural tube defects, susceptibility to}, 601634 {Thromboembolism, susceptibility to}, 188050	607093	94	100	100
MYH11	Aortic aneurysm, familial thoracic 4, 132900	160745	90	100	100
MYLK	Aortic aneurysm, familial thoracic 7, 613780	600922	102	100	100
NOTCH1	Aortic valve disease 1, 109730 Adams-Oliver syndrome 5, 616028	190198	86	100	99
PLOD1	Ehlers-Danlos syndrome, type VI, 225400	153454	88	100	98
PRKG1	Aortic aneurysm, familial thoracic 8, 615436	176894	46	97	82
SKI	Shprintzen-Goldberg syndrome, 182212	164780	55	99	97
SLC2A10	Arterial tortuosity syndrome, 208050	606145	95	100	100
SMAD2	No OMIM phenotype	601366	94	100	96
SMAD3	Loeys-Dietz syndrome 3, 613795	603109	93	100	100
SMAD4	Pancreatic cancer, somatic, 260350 Juvenile polyposis/hereditary hemorrhagic telangiectasia syndrome, 175050 Myhre syndrome, 139210 Polyposis, juvenile intestinal, 174900	600993	76	100	98
TGFB2	Loeys-Dietz syndrome 4, 614816	190220	107	100	100

HGNC approved gene symbol	Phenotype description including OMIM phenotype ID(s)	OMIM gene ID	median depth	% covered >10x	% covered >20x
TGFB3	Arrhythmogenic right ventricular dysplasia 1, 107970 Loeys-Dietz syndrome 5, 615582	190230	96	100	100
TGFBR1	Loeys-Dietz syndrome 1, 609192 {Multiple self-healing squamous epithelioma, susceptibility to}, 132800	190181	111	93	93
TGFBR2	Colorectal cancer, hereditary nonpolyposis, type 6, 614331 Esophageal cancer, somatic, 133239 Loeys-Dietz syndrome 2, 610168	190182	100	100	100

- Gene symbols according HGCN
- OMIM release used: 17-3-2016
- "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.
- The statistics above are based on a set of 50 samples
- Median depth is the median of the mean sequence depth over the protein coding exons of the transcript
- % 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