

Whole Exome Sequencing

Gene package Neurodegeneration, version 6.1, 25-2-2021



Technical information

DNA was enriched using the Agilent SureSelectXT Human All Exon V7 capture kit and paired-end sequenced on the Illumina platform (outsourced). Sequencing data are demultiplexed with bcl2fastq2 Conversion Software from Illumina. Illumina DRAGEN Bio-IT Platform is used for read mapping to the hg19 genome and sequence variant detection. The detected sequence variants are annotated and filtered with Alissa Interpret software and classified with Alamut Visual. Copy number 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 annotated and filtered with the NexusClinical software and classified using UCSC Genome Browser (NCBI37/hg19). Additionally, MPLA analysis was performed for APP (SALSA P170 Recessive Ataxias probemix; MRC Holland) and for several (fragments of) Parkinson genes (SALSA P051/P052 Parkinson probemix). For ATN1, C9orf72 and TBP a repeat expansion test was performed. The sensitivity to detect variants using this technology is not 100%; pathogenic variants could be missed. 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 (active link to omim.org)	% covered $\geq 10x$	% covered $\geq 20x$	% covered $\geq 30x$	% covered $\geq 50x$
AAAS	605378	100	100	100	99.95
AARS2	612035	100	99.82	98.91	93.03
ABCD1	300371	100	95.42	90.51	80.47
ADPRS	610624	100	100	98.10	92.97
AGTPBP1	606830	99.43	96.22	93.39	89.09
ALS2	606352	100	100	99.86	96.30
AMPD2	102771	100	99.89	97.72	87.37
ANG	105850	100	100	100	100
ANXA11	602572	100	100	99.53	92.53
APP	104760	100	99.94	98.50	94.18
ARHGEF28	612790	100	99.80	97.46	93.01
ARSA	607574	100	100	100	100
ATG7	608760	100	100	99.64	97.83
ATP13A2	610513	100	99.76	97.60	83.45
ATP1A3	182350	100	100	99.45	94.42
ATP6AP2	300556	100	100	99.59	93.78
ATP7B	606882	100	100	99.51	96.63
AUH	600529	100	100	100	100
C19orf12	614297	100	100	100	100
C9orf72	614260	100	100	100	100

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CACNA1A	601011	100	99.17	95.07	79.63
CAV1	601047	100	100	98.32	91.67
CBS	613381	100	100	100	100
CHCHD10	615903	92.41	85.29	78.46	62.43
CHCHD2	616244	100	100	100	91.78
CHMP2B	609512	100	100	90.18	80.17
CISD2	611507	88.49	76.99	76.99	76.99
CLCN2	600570	100	100	100	96.25
CLN3	607042	100	98.64	91.76	88.17
CLN5	608102	93.14	93.14	88.00	73.62
CLN6	606725	100	100	100	96.55
CLN8	607837	100	100	100	100
CNP	123830	99.55	98.29	98.29	95.68
COASY	609855	100	100	98.69	92.60
COL4A1	120130	99.39	97.25	93.74	85.37
COL4A2	120090	100	99.79	98.72	91.61
COQ4	612898	100	93.69	80.43	63.74
CP	117700	99.05	99.05	99.05	98.77
CRAT	600184	100	98.24	95.86	90.14
CSF1R	164770	100	99.58	97.75	90.20
CST3	604312	100	98.09	91.97	83.73
CTSA	613111	100	99.85	99.59	92.57
CTSD	116840	100	93.79	93.79	90.47
CTSF	603539	95.77	88.58	86.39	83.35
CYP27A1	606530	100	100	100	100
DARS2	610956	100	100	100	97.36
DCAF17	612515	100	100	100	96.52
DCTN1	601143	100	99.35	98.33	91.75
DNAJC13	614334	100	100	99.96	98.65
DNAJC5	611203	100	100	98.81	82.05
DNAJC6	608375	100	100	100	97.28
DNMT1	126375	100	99.85	98.71	94.39
DPYSL5	608383	100	100	99.79	96.14
EIF2AK2	176871	100	100	99.74	95.75
EIF2B1	606686	100	100	100	97.53
EIF2B2	606454	100	100	99.55	96.74
EIF2B3	606273	100	100	100	100
EIF2B4	606687	100	98.64	95.06	90.52
EIF2B5	603945	100	98.27	96.72	91.34
EIF4G1	600495	100	99.30	98.58	93.78
ERBB4	600543	100	100	100	99.21
EXOSC3	606489	100	100	100	100
FA2H	611026	100	96.58	89.53	72.53

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FBXO7	605648	100	98.28	91.87	91.87
FIG4	609390	100	100	100	99.50
FOLR1	136430	100	100	100	100
FTL	134790	100	100	95.12	84.71
FUS	137070	100	100	99.84	96.09
GALC	606890	99.96	99.96	99.96	97.95
GBE1	607839	100	100	100	99.38
GCDH	608801	100	100	100	96.94
GEMIN5	607005	100	100	99.76	98.25
GFAP	137780	100	99.81	96.10	81.56
GLA	300644	100	100	100	98.28
GRN	138945	100	100	100	97.18
GSN	137350	100	98.34	94.75	86.19
HEXA	606869	100	100	100	98.79
HEXB	606873	100	97.84	95.71	90.79
HNRNPA1	164017	100	100	100	100
HNRNPA2B1	600124	100	100	100	98.63
HPDL	618994	100	100	100	100
HTRA1	602194	90.80	87.87	86.45	84.48
HTRA2	606441	100	100	100	99.54
ISCA2	615317	100	100	100	100
ITM2B	603904	100	100	99.95	96.73
JAM2	606870	100	96.95	90.99	89.86
KARS1	601421	100	100	100	99.05
KCTD7	611725	100	100	100	98.73
LMNB1	150340	100	100	98.89	93.02
LRP10	609921	100	99.32	96.80	89.43
LRRK2	609007	100	99.70	98.95	96.98
MAPT	157140	95.53	92.66	89.69	79.70
MATR3	164015	100	100	100	97.96
MECR	608205	99.10	92.73	86.22	82.27
MED20	612915	100	100	100	99.30
MFSD8	611124	100	100	100	97.84
MMACHC	609831	100	100	100	95.30
MTHFR	607093	100	100	99.74	95.92
MTR	156570	100	100	99.44	97.37
MYORG	618255	100	100	100	99.68
NARS1	108410	100	100	100	95.63
NKX6-2	605955	100	95.01	89.17	78.00
NOTCH3	600276	99.58	95.67	92.96	85.47
NOVA2	601991	93.25	86.50	80.59	67.77
NPC1	607623	100	99.98	98.96	97.40
NPC2	601015	100	100	100	100

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NRROS	615322	100	99.88	97.76	91.23
OPTN	602432	100	100	97.51	79.26
PAH	612349	100	100	100	100
PANK2	606157	100	100	100	99.69
PARK7	602533	100	100	100	98.11
PDGFB	190040	100	100	100	96.14
PDGFRB	173410	100	100	99.40	94.76
PFN1	176610	95.71	83.88	77.79	69.81
PINK1	608309	98.53	95.03	90.78	77.59
PLA2G6	603604	100	100	99.56	94.14
POLG	174763	100	100	98.60	90.96
POU4F1	601632	78.68	75.21	72.21	67.46
PPIL1	601301	100	99.83	98.27	96.02
PPP1R21	618159	100	100	100	98.62
PPT1	600722	100	100	100	96.71
PRKAR1B	176911	100	100	99.03	91.36
PRKN	602544	100	99.08	97.31	93.27
PRKRA	603424	100	100	100	100
PRNP	176640	100	100	100	100
PSAP	176801	100	100	100	95.51
PSEN1	104311	100	100	100	98.72
PSEN2	600759	100	98.28	94.53	83.29
PSENER	607632	100	100	98.35	89.94
PTRHD1	617342	100	100	100	100
QARS1	603727	100	100	100	97.99
RARS2	611524	100	100	100	98.90
REPS1	614825	100	100	100	99.14
RNU7-1	617876	No coverage data			
SCN1A	182389	100	100	100	99.91
SDHA	600857	100	97.10	96.38	94.50
SDHAF1	612848	100	100	100	86.16
SEMA6B	608873	99.36	89.71	80.97	70.89
SEPSECS	613009	100	100	100	99.65
SERPINI1	602445	100	100	100	98.38
SETX	608465	100	100	100	99.74
SIGMAR1	601978	100	100	100	99.73
SLC17A5	604322	93.58	93.58	93.58	92.55
SLC20A2	158378	100	100	100	94.67
SLC33A1	603690	100	100	100	99.18
SLC39A14	608736	97.92	97.92	97.03	91.16
SLC44A1	606105	97.56	97.56	97.56	92.41
SLC5A6	604024	100	100	100	97.96
SLC6A3	126455	100	99.86	98.69	92.78

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SMPD1	607608	100	100	100	98.58
SNCA	163890	100	100	100	98.27
SNCB	602569	100	100	97.31	74.20
SNORD118	616663	No coverage data			
SOD1	147450	100	100	100	100
SORL1	602005	100	99.69	99.29	95.93
SPG11	610844	100	100	99.85	97.72
SPR	182125	100	100	99.05	88.20
SPTBN1	182790	100	100	99.60	97.26
SQSTM1	601530	100	100	100	97.43
STUB1	607207	100	100	100	100
SUMF1	607939	100	100	100	100
SYNJ1	604297	99.84	97.11	94.83	92.88
TAF1	313650	100	99.95	99.77	97.63
TANGO2	616830	100	100	99.95	96.86
TARDBP	605078	100	100	100	100
TBC1D23	617687	100	100	99.62	97.13
TBCD	604649	99.13	96.29	93.82	86.91
TBK1	604834	99.69	97.68	97.68	95.59
TBP	600075	100	100	100	100
TH	191290	100	98.04	94.21	86.67
TOE1	613931	100	100	100	100
TPP1	607998	100	98.87	96.77	93.28
TREM2	605086	100	100	100	97.91
TREX1	606609	100	100	100	100
TSEN2	608753	86.99	86.99	86.99	86.79
TTR	176300	100	100	100	100
TUBA4A	191110	100	100	100	99.05
TYMP	131222	100	100	97.96	83.49
TYROBP	604142	100	100	91.57	69.48
UBQLN2	300264	100	100	100	100
UCHL1	191342	100	97.35	82.45	77.62
UQCRC1	191328	100	100	100	98.21
VAPB	605704	100	100	100	97.53
VCP	601023	100	100	99.67	98.66
VPS13A	605978	100	99.76	98.64	93.61
VPS13C	608879	99.07	98.02	97.41	94.36
VPS35	601501	100	100	100	99.16
VPS41	605485	100	100	99.00	97.55
VPS4A	609982	100	99.48	97.26	93.79
VPS53	615850	100	100	100	98.67
WDR45	300526	100	100	100	98.36
XPR1	605237	100	100	100	99.25

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- OMIM release used: 23-9-2021
- The statistics above are based on a set of 104 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