

*Supplementary data:*

**Genome-wide analyses as part of the international FTLD-TDP whole genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLD**

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## SUPPLEMENTARY DATA

### LEGEND ELECTRONIC DATA

**Online Resource 2. Variants identified in the known FTLD genes.** All rare variants identified via whole genome-sequencing in the known FTLD genes are presented and classified according to the ACMG guidelines.

**Online Resource 3. Gene-based association analysis with rare variants results.** Each gene is presented along with its total number of variants in FTLD-TDP patients (Total variant alleles patients), controls (Total variant alleles controls) and the number of variants included in the test (Number of markers in test). P values are presented with adjustment for sex and four PCs, and only adjusted for sex. Spreadsheet 1(Nominally sig LOF) represents the genes with LOF variants. Spreadsheet 2 (LOF3vs0) provides the genes carrying rare LOF in at least 3 FTLD-TDP patients and not in controls. Spreadsheet 3 (Nominally sig LOFandmissense) represents the genes with LOF variants and coding changes predicted to be pathogenic by SIFT and Polyphen2. Spreadsheet 4 (LOFmissense3vs0) provides the genes carrying rare LOF and missense predicted pathogenic by SIFT and Polyphen2 in at least 3 FTLD-TDPpatients and not in controls.

**Online Resource 4. Similarity analyses between the known FTLD genes and genes identified via burden tests.** Each gene is presented along with its prioritized rank, an overall p-value after FDR correction (Overall pValue) and the detail of each similarity queried by the ToppGene algorithm. Spreadsheet 1 (LOF) represents Toppgenes results for the genes with LOF variants in at least 3 FTLD-TDP patients and not in controls. Spreadsheet 2 (LOF and missense) represents Toppgenes results for the genes with LOF variants and coding changes predicted to be pathogenic by SIFT and Polyphen2 in at least 3 FTLD-TDP patients and not in controls.

**Supplementary Table 1. Overview of FTLD-TDP patients with genetic causes updated after whole genome sequencing.** The number of FTLD-TDP patients per site is presented and includes: patients without mutations, patients carrying mutations in the major FTLD-TDP genes (*GRN*, *C9ORF72*, *TBK1*) and patients carrying mutations in other genes (*OPTN*, *VCP*, *TARDBP*, *CHCHD10*, *SQSTM1*, *UBQLN2*, *hnRNPA1*, *hnRNPA2B1*, *CSF1R*, *FUS*, *CHMP2B*, *LRRK2*, and *TIA1*).

Site	Number of FTLD-TDP	Caucasian				
		Non mutation carriers	<i>GRN</i>	<i>C9ORF72</i>	<i>TBK1</i>	Other genes
Banner Sun Health Research Institute	29	20	6	3	0	0
Columbia University	25	20	2	3	0	0
Emory University	48	25	6	13	0	1
Erasmus University	93	63	5	22	0	2
German Center for Neurodegenerative Diseases	24	14	2	7	1	0
Indiana University	32	14	13	4	1	0
Karolinska University	44	18	4	20	1	1
King's College London	50	39	3	6	1	0
Ludwig-Maximilians-University Munich	40	15	4	16	2	3
Mayo Clinic Jacksonville/Rochester	207	125	27	51	2	2
Northwestern University	69	43	16	8	1	1
University College London	54	28	13	13	0	0
University of British Columbia	72	30	9	26	1	0
University of California San Diego	15	10	2	3	0	0
University of New South Wales	47	16	9	20	0	2
University of Pennsylvania	95	41	17	29	3	2
University of San Francisco	101	62	10	22	2	1
University of Toronto	18	11	1	5	0	1
University of Pittsburgh Medical Center	20	14	2	3	1	0
University Texas Southwestern Medical Center	41	27	5	9	0	0
Washington University School of Medicine	24	17	2	4	0	0
University of Western Ontario	6	2	0	2	1	0
<b>TOTAL</b>	<b>1154</b>	<b>654</b> (57.7%)	<b>158</b> (13.9%)	<b>289</b> (25.5%)	<b>17</b> (1.5%)	<b>16</b> (1.4%)

**Supplementary Table 2. Overview of FTLD-TDP patients and controls included in the discovery and replication stage after quality controls.**

Site	Discovery		Replication	
	Number of FTLD-TDP patients	Number of controls	Number of FTLD-TDP patients	Number of controls
Banner Sun Health Research Institute	13	0	2	0
Columbia University	20	0	0	0
Emory University	25	0	2	0
Erasmus University	40	0	1	0
German Center for Neurodegenerative Diseases	10	0	0	0
Indiana University	13	0	1	13
Karolinska University	9	0	0	0
King's College London	39	0	1	0
Ludwig-Maximilians-University Munich	17	0	0	0
Mayo Clinic Jacksonville/Rochester	124	838	7	1288
Northwestern University	23	0	17	38
University College London	12	0	10	0
University of British Columbia	20	0	15	0
University of California San Diego	6	0	2	10
University of Manchester	0	0	30	0
University of New South Wales	14	0	7	0
University of Pennsylvania	29	0	0	0
University of San Francisco	44	0	20	304
University of Toronto	10	0	0	0
University of Pittsburgh Medical Center	14	0	0	0
University Texas Southwestern Medical Center	22	0	3	0
Washington University School of Medicine	10	0	1	0
University of Western Ontario	3	0	0	0
<b>TOTAL</b>	<b>517</b>	<b>838</b>	<b>119</b>	<b>1653</b>

**Supplementary Table 3. Candidate loci identified in genome-wide association analyses of the overall FTLD-TDP or FTLD-TDP pathological strata.**

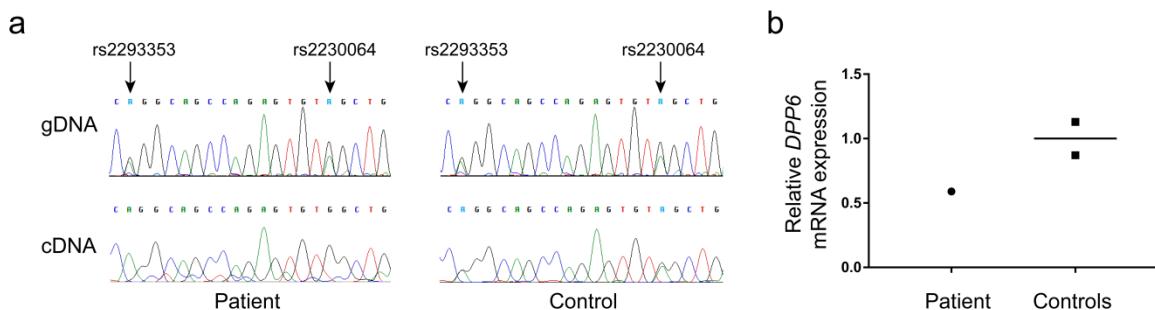
Each locus is presented with its most significant SNP along with its position, the closest gene (Locus Name), its minor allele frequency in controls and patients (MAF Controls/Patients), its odds ratio (OR) and pvalue.

SNP ID	Position	Locus Name	MAF Controls/ Patients	All FTLD-TDP vs controls		FTLD-TDP type A vs controls		FTLD-TDP type B vs controls		FTLD-TDP type C vs controls	
				OR	pvalue	OR	pvalue	OR	pvalue	OR	pvalue
rs59810358	chr1:25055747	<i>MIR4425</i>	0.15/0.17	1.38	4.94e-03	1.29	1.43e-01	1.12	5.01e-01	2.09	9.42e-06
rs200527740	chr1:61764008	<i>INADL</i>	0.07/0.08	1.42	2.64e-02	0.93	7.87e-01	1.04	8.77e-01	2.73	2.70e-06
rs138835186	chr1:173334272	<i>LOC100506023</i>	0.00/0.01	4.58	1.38e-03	1.74	4.45e-01	2.61	1.54e-01	11.21	3.89e-06
rs61831315	chr1:186126654	<i>HMCN1</i>	0.05/0.04	0.31	4.28e-06	0.26	2.44e-03	0.33	3.70e-03	0.22	2.18e-03
rs6676599	chr1:206711310	<i>MAPKAPK2</i>	0.19/0.21	1.41	1.09e-03	2.01	6.98e-06	1.31	7.05e-02	1.10	5.70e-01
rs472856	chr1:214936242	<i>KCNK2</i>	0.21/0.23	1.29	1.14e-02	1.01	9.65e-01	1.86	7.10e-06	1.09	5.95e-01
rs34447323	chr1:232974879	<i>NTPCR</i>	0.06/0.07	1.43	2.76e-02	2.59	8.18e-06	1.20	4.56e-01	0.80	4.85e-01
.	chr1:245753541	<i>SMYD3</i>	0.07/0.09	1.54	3.32e-03	1.59	3.62e-02	0.99	9.59e-01	2.40	7.29e-06
rs2003298	chr2:10946024	<i>KCNF1</i>	0.33/0.35	1.23	2.17e-02	0.99	9.38e-01	1.77	6.75e-06	1.05	7.21e-01
rs4325802	chr2:48717394	<i>LHCGR; STON1-GTF2A1L</i>	0.08/0.09	1.49	8.06e-03	1.23	3.87e-01	1.38	1.46e-01	2.64	6.19e-06
rs76291845	chr2:111131781	<i>BCL2L11</i>	0.01/0.01	2.78	3.61e-03	5.83	8.39e-06	1.29	6.41e-01	0.87	8.41e-01
rs143339003	chr2:142622395	<i>KYNU</i>	0.01/0.02	2.26	1.20e-02	5.09	6.80e-06	1.00	9.97e-01	0.33	2.85e-01
rs78370899	chr2:214695123	<i>BARD1</i>	0.00/0.01	6.38	1.19e-04	10.93	7.80e-06	2.41	2.57e-01	3.87	8.36e-02
rs11712238	chr3:82726692	<i>GBE1</i>	0.12/0.13	1.44	3.35e-03	1.43	4.96e-02	1.10	6.12e-01	2.25	3.49e-06
rs34572606	chr3:104580495	<i>ALCAM</i>	0.09/0.10	1.44	7.37e-03	0.83	4.38e-01	2.48	8.86e-08	1.16	5.25e-01
rs13098438	chr3:107115462	<i>LINC00882</i>	0.02/0.03	2.18	1.59e-03	1.64	2.06e-01	3.87	6.47e-06	0.87	7.81e-01
rs397957892	chr3:140089009	<i>CLSTN2</i>	0.09/0.10	1.43	6.68e-03	2.29	2.03e-06	1.14	5.30e-01	1.10	6.85e-01
rs114146294	chr3:162019418	<i>LINC01192</i>	0.02/0.02	2.43	1.79e-03	2.36	2.64e-02	0.82	7.13e-01	4.89	6.69e-06
rs138512547	chr3:194634939	<i>TMEM44</i>	0.02/0.03	2.01	4.47e-03	0.77	6.22e-01	1.50	2.79e-01	4.10	1.88e-06
rs9818987	chr3:194681701	<i>FAM43A</i>	0.36/0.33	0.66	8.49e-06	0.64	2.00e-03	0.67	3.04e-03	0.66	6.00e-03
rs7683451	chr4:22370936	<i>ADGRA3</i>	0.25/0.27	1.36	1.13e-03	0.93	6.22e-01	1.86	3.59e-06	1.34	5.18e-02
rs62319305	chr4:129302471	<i>C4orf33</i>	0.02/0.03	1.75	2.45e-02	0.99	9.83e-01	1.27	5.44e-01	4.06	8.39e-06
rs78753485	chr4:135810669	<i>LINC00613</i>	0.01/0.02	3.85	1.37e-04	2.29	1.36e-01	6.76	1.26e-06	2.35	1.28e-01

rs201446533	chr4:159457218	<i>RAPGEF2</i>	0.06/0.06	1.53	1.32e-02	1.15	6.17e-01	0.87	6.28e-01	2.74	4.57e-06
rs61707463	chr4:169787358	<i>C4orf27; LOC100506085</i>	0.02/0.03	3.58	1.60e-06	3.08	3.01e-03	4.38	6.42e-06	2.79	1.02e-02
rs11132244	chr4:184422579	<i>IRF2</i>	0.30/0.27	0.64	9.17e-06	0.56	3.39e-04	0.72	2.16e-02	0.67	1.25e-02
rs149734180	chr5:24135712	<i>C5orf17</i>	0.02/0.02	1.98	1.43e-02	4.21	7.77e-06	0.59	3.31e-01	1.21	6.85e-01
rs35422123	chr5:34517139	<i>RAI14</i>	0.02/0.03	2.36	2.44e-04	1.00	9.91e-01	4.00	9.64e-07	2.21	2.73e-02
rs35122968	chr6:32714422	<i>HLA-DQA2</i>	0.06/0.08	2.07	2.33e-06	1.65	3.28e-02	2.50	9.68e-06	2.28	4.34e-04
rs34422230	chr6:32809218	<i>HLA-DOB</i>	0.03/0.05	2.31	3.80e-05	2.00	1.71e-02	3.34	1.86e-06	1.87	5.37e-02
rs116655107	chr6:44178162	<i>CAPN11</i>	0.02/0.03	2.45	1.16e-04	4.13	2.28e-06	1.40	3.44e-01	1.89	7.98e-02
rs148211665	chr6:49401592	<i>MUT</i>	0.01/0.02	3.26	7.26e-04	6.33	4.27e-06	2.68	6.31e-02	1.45	5.83e-01
rs2781832	chr6:74582646	<i>LOC101928516</i>	0.02/0.03	2.33	8.70e-04	1.46	3.51e-01	1.49	2.89e-01	4.51	2.97e-06
rs11751521	chr6:166505657	<i>RPS6KA2</i>	0.02/0.03	2.51	1.39e-04	2.84	1.13e-03	3.79	6.94e-06	1.13	7.83e-01
rs6463679	chr7:7305371	<i>LOC101927354</i>	0.34/0.37	1.49	4.39e-06	1.43	6.27e-03	1.45	2.69e-03	1.62	3.25e-04
rs10231788	chr7:47912542	<i>PKD1L1</i>	0.38/0.37	0.75	1.70e-03	0.52	7.68e-06	0.77	4.47e-02	0.97	8.37e-01
rs2465481	chr7:80134858	<i>GNAII</i>	0.45/0.47	1.18	5.69e-02	1.94	2.72e-06	1.02	8.96e-01	1.05	7.49e-01
rs117924488	chr7:87788671	<i>RUNDC3B</i>	0.00/0.01	3.52	4.09e-03	0.38	4.10e-01	9.16	1.42e-06	1.89	3.68e-01
rs10267171	chr7:110723284	<i>IMMP2L</i>	0.19/0.21	1.61	6.53e-06	1.68	7.23e-04	1.73	2.33e-04	1.45	2.67e-02
rs118113626	chr7:154194746	<i>DPP6</i>	0.05/0.07	2.48	4.88e-08	2.80	5.93e-06	2.42	5.79e-05	2.17	1.63e-03
rs4726389	chr7:154225769	<i>DPP6</i>	0.05/0.07	2.45	4.63e-08	2.55	5.42e-05	2.65	5.52e-06	2.09	2.96e-03
rs10109928	chr8:10459514	<i>LINCR-0001</i>	0.03/0.04	2.32	1.88e-04	1.20	6.55e-01	2.56	1.25e-03	3.89	7.64e-06
rs537967198	chr8:13856936	<i>SGCZ</i>	0.02/0.03	2.60	1.44e-04	4.57	2.87e-06	2.59	4.62e-03	1.42	4.58e-01
rs34441160	chr8:95289791	<i>C8orf37-ASI</i>	0.07/0.08	1.63	1.13e-03	1.08	7.61e-01	2.36	9.13e-06	1.36	1.81e-01
rs6468704	chr8:99982161	<i>RGS22</i>	0.18/0.20	1.45	5.50e-04	1.12	4.74e-01	2.03	1.87e-06	1.30	1.14e-01
rs2597335	chr8:132411836	<i>KCNQ3</i>	0.36/0.34	0.78	8.21e-03	0.88	3.77e-01	0.97	8.05e-01	0.48	7.57e-06
rs150427844	chr8:139148204	<i>COL22A1</i>	0.00/0.01	3.66	5.97e-03	1.19	8.48e-01	2.02	3.08e-01	11.50	4.53e-06
rs560900477	chr8:142388515	<i>TSNARE1</i>	0.01/0.02	2.31	6.06e-03	5.24	3.43e-06	0.73	6.26e-01	1.24	7.04e-01
rs143407351	chr9:87397602	<i>DAPK1</i>	0.01/0.02	2.72	2.93e-04	1.63	2.88e-01	4.32	5.52e-06	2.19	6.88e-02
rs553772563	chr9:118093612	<i>TLR4</i>	0.00/0.01	7.19	1.22e-04	18.17	1.19e-06	2.25	3.50e-01	6.59	6.10e-03
rs35323587	chr9:135084306	<i>OLFMI</i>	0.12/0.15	1.78	1.50e-06	1.88	2.27e-04	1.74	9.47e-04	1.81	9.83e-04
rs10762302	chr10:69619172	<i>C10orf35</i>	0.40/0.38	0.83	3.74e-02	0.93	6.14e-01	1.03	8.44e-01	0.49	5.36e-06
rs846611	chr10:76791758	<i>KCNMA1</i>	0.04/0.05	1.87	8.84e-04	1.57	1.19e-01	1.22	4.94e-01	3.01	8.81e-06
rs61870346	chr10:125065282	<i>CTBP2</i>	0.02/0.03	2.63	3.64e-05	1.65	1.75e-01	3.83	3.29e-06	1.50	3.16e-01
rs60078451	chr11:1457322	<i>BRSK2</i>	0.05/0.07	1.92	1.46e-04	1.07	8.24e-01	2.75	5.77e-06	2.02	5.25e-03
rs78934618	chr11:2215067	<i>ASCL2</i>	0.02/0.03	2.18	1.67e-03	1.29	5.68e-01	1.97	5.39e-02	4.15	5.27e-06
rs117197016	chr11:87490779	<i>TMEM135</i>	0.01/0.01	2.24	2.39e-02	0.47	3.49e-01	0.51	3.78e-01	6.07	4.49e-06
rs112301159	chr11:94786566	<i>AMOTL1</i>	0.00/0.01	4.44	5.09e-03	2.47	3.28e-01	2.00	4.16e-01	13.35	7.35e-06

rs148048968	chr12:15166523	<i>RERG</i>	0.22/0.19	0.59	7.35e-06	0.49	2.45e-04	0.58	1.43e-03	0.74	1.05e-01
rs11064952	chr12:119894382	<i>CIT</i>	0.01/0.02	3.39	1.81e-04	3.26	1.50e-02	6.25	1.88e-06	2.72	5.26e-02
rs76586200	chr12:130670602	<i>STX2</i>	0.01/0.01	3.28	1.78e-03	6.75	9.24e-06	2.78	6.68e-02	1.47	5.66e-01
rs79079778	chr13:32665173	<i>PDS5B</i>	0.00/0.01	4.09	2.22e-03	0.85	8.84e-01	10.63	8.16e-07	0.92	9.41e-01
.	chr13:75544760	<i>COMM6D</i>	0.01/0.01	2.32	2.79e-02	1.88	2.91e-01	na	na	7.15	6.04e-06
rs56232509	chr14:32354422	<i>AKAP6</i>	0.08/0.09	1.58	2.00e-03	0.95	8.49e-01	2.42	3.63e-06	1.52	7.09e-02
rs1198035	chr14:81972701	<i>LINC01467</i>	0.30/0.32	1.48	2.81e-05	1.87	7.69e-06	1.53	1.41e-03	1.27	1.08e-01
rs147183330	chr14:87538376	<i>GALC</i>	0.02/0.04	2.46	1.11e-04	3.96	2.80e-06	1.92	4.39e-02	1.92	6.44e-02
rs145502725	chr15:25138308	<i>PWAR1</i>	0.01/0.01	4.98	1.70e-04	3.95	2.93e-02	2.50	1.53e-01	8.72	8.16e-06
rs4240777	chr15:85946519	<i>MIR548AP</i>	0.31/0.35	1.51	4.97e-06	1.45	6.22e-03	1.47	2.30e-03	1.52	3.14e-03
rs6496125	chr15:95592748	<i>LINC00924</i>	0.09/0.10	1.55	1.55e-03	1.26	2.84e-01	1.29	2.06e-01	2.66	2.27e-07
rs117434909	chr16:15716617	<i>MYH11;NDE1</i>	0.02/0.02	2.42	2.62e-03	4.92	7.85e-06	1.07	9.04e-01	2.16	9.29e-02
rs79805801	chr16:79600738	<i>MAF</i>	0.01/0.01	4.30	2.95e-04	3.04	5.09e-02	8.30	3.21e-06	2.46	1.91e-01
rs16940783	chr16:86303304	<i>LOC146513</i>	0.07/0.08	1.59	2.34e-03	1.23	3.85e-01	1.47	7.52e-02	2.59	9.73e-06
rs200162587	chr17:2713612	<i>CLUH</i>	0.03/0.04	2.23	1.67e-04	1.82	5.43e-02	3.31	6.78e-06	2.01	2.40e-02
rs708383	chr17:44360386	<i>FAM171A2</i>	0.37/0.39	1.27	5.38e-03	1.97	1.69e-07	0.99	9.32e-01	0.94	6.80e-01
rs1032914	chr18:77787710	<i>LINC01029</i>	0.38/0.39	1.26	7.48e-03	1.24	1.10e-01	0.98	8.95e-01	1.86	8.78e-06
rs118107613	chr19:3020644	<i>MIR1268A</i>	0.02/0.02	2.04	1.62e-02	0.73	6.22e-01	1.50	3.63e-01	4.85	5.62e-06
rs3952538	chr19:15878713	<i>CYP4F2</i>	0.01/0.02	5.29	7.71e-06	5.39	1.21e-03	4.46	2.78e-03	8.88	3.85e-06
rs12973192	chr19:17642430	<i>UNC13A</i>	0.37/0.40	1.48	3.44e-06	1.35	1.90e-02	1.95	4.67e-08	1.10	4.94e-01
rs35471514	chr19:55544212	<i>SBK3</i>	0.03/0.03	1.96	3.00e-03	3.69	3.21e-06	1.22	5.80e-01	1.17	6.89e-01
rs117883823	chr20:37186204	<i>RPN2</i>	0.01/0.02	2.28	1.27e-02	0.55	4.39e-01	1.94	1.61e-01	5.61	6.73e-06
rs6072689	chr20:42341450	<i>PTPRT</i>	0.31/0.28	0.67	4.41e-05	0.77	7.38e-02	0.49	3.45e-06	0.73	4.15e-02
rs56290045	chr20:60462610	<i>LOC101928048</i>	0.02/0.02	2.53	7.39e-04	1.74	1.99e-01	1.47	3.74e-01	5.66	1.94e-07

**Supplementary Figure 1. mRNA expression of *DPP6* in the LOF mutation carrier.** **a)** *DPP6* complementary DNA (cDNA) and genomic DNA (gDNA) was used as template to perform PCR and sequencing analysis of a fragment containing the LOF mutation c.1345+1G>T and two known common variants: rs2293353 and rs2230064 in the FTLD-TDP patient carrying the *DPP6* splice site mutation and a control. Based on gDNA sequencing, both our carrier and the selected control are heterozygous for rs2293353 and rs2230064. At the cDNA level, sequence chromatograms show the absence of the rare alleles of rs2293353 and rs2230064 in the *DPP6* LOF mutation carrier, suggesting degradation of the mutant allele by nonsense mediated decay. **b)** Relative mRNA expression of *DPP6* in cortex is presented after normalization to *GAPDH* and *MAP2*. The patient carrying the LOF mutation has reduced expression of *DPP6* mRNA as compared to two pathologically normal controls.



**Supplementary Figure 2. TBK1 immunity related pathway and LOF variants identified in FTLD-TDP.** The TBK1 pathway is shown along with the number of LOF variants identified through WGS in patients (red) and in controls (blue). LOF variants were identified in *TBK1*, *TRIM21*, *IRF3*, *IRF7*, *IRF8*, DHX58 and *NOD2*. Following activation through the detection of DNA/RNA viruses, viral proteins or LPS, by different sensors, adaptor proteins are recruited (TRIF, MAVS, STING) to activate TBK1. Activated TBK1 then phosphorylates IRF3/8/7 triggering their nuclear translocation and activation of IFN gene expression. NEMO can also be activated triggering the NF $\kappa$ B pathway (p50/p65).

