Human Genomics

CORRECTION

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Correction: Comprehensive genetic screening of early-onset dementia patients in an Austrian cohort-suggesting new disease-contributing genes

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Following publication of the original article [1], the authors reported an error in Table 1. The correct Table 1 has been provided in this Correction.

The original article [1] has been corrected.

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†Sara Silvaieh and Theresa König have contributed equally to this work.

The original article can be found online at https://doi.org/10.1186/s40246-023-00499-z.

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Table 1 Basic clinical and genetic characteristics of all 60 EOD patients

ID	Diagnosis	AAO (years)	Sex	FH	APOE	Gene	Variant	Position	Transcript	CADD	ClinVar	Significance for disease
EOD-1	**AD**	**54**	**f**	**3**	**E2/E3**	***PSEN1***	**c.356C > T; p.T119I**	**chr14:73640291-73640291**	**NM_000021.3**	**24.4**	**LP**	**Relevant for diagnosis**
EOD-2	**bvFTD**	**44**	**f**	**1**	**E4/E3**	***MAPT***	**c.1907C > T; p.P636L**	**chr17:44087755-44087755**	**NM_001123066.3**	**34.0**	**P**	**Relevant for diagnosis**
						TREM2	c.184G > A; p.R62C	chr6:41129208-41129208	NM_001271821.1	25.5	n.r	Risk modifier
						APOE						Risk modifier
EOD-3	AD	45	f	2	E3/E3							
EOD-4	AD	51	f	4	E4/E3	*APOE*						Risk modifier
EOD-5	nfPPA	58	f	2	E3/E2							
EOD-6	AD	56	f	3	E3/E3							
EOD-7	AD/PCA	56	f	4	E3/E3							
EOD-8	bvFTD	56	m	4	E3/E3	*BACE1*	c.1427T > C; p.M476T	chr11:117160361-117160361	NM_012104.3	26.4	n.r	Unknown
						VPS13C	c.9757A > G; p.S3253G	chr15:62173781-62173781	NM_020821.2	29.5	n.r	Unknown
EOD-9	AD	55	f	3,5	E4/E3	*APOE*						Risk modifier
EOD-10	AD	58	f	3,5	E3/E3							
EOD-11	AD	63	m	4	E3/E3							
EOD-12	mixed dementia (AD + VD)	55	m	3,5	E4/E3	*APOE*						Risk modifier
EOD-13	AD	61	m	4,5	E3/E3							
EOD-14	AD/lpPPA	61	m	4	E4/E3	*APOE*						Risk modifier
						VPS13C	c.4300C > T; p.V1434I	chr15:62244179-62244179	NM_020821.2	24.8	n.r	Unknown
EOD-15	nfPPA	64	m	2	E3/E3	*DCTN1*	c.2218C > T; p.E740K	chr2:74594514-74594514	NM_004082.4	24.0	n.r	Unknown
EOD-16	AD	56	f	4	E3/E3							
EOD-17	AD (PD)	60	m	1	E4/E3	*APOE*						Risk modifier
						MAPK8IP3	g.chr16:1816528 A > G; c.2817-2A > G	chr16:1816528-1816528	NM_015133.3	22.3	n.r	Unknown
EOD-18[a]	**AD**	**47**	**m**	**4**	**E3/E3**	***APP***	**g. chr.21:(?_26958019)-(27852747_?)dup**				**P**	**Relevant for diagnosis**
						ABCA7	c.2914C > T; p.P972S	chr19:1051537-1051537	NM_019112.3	25.3	n.r	Potential risk modifier

Table 1 (continued)

ID	Diagnosis	AAO (years)	Sex	FH	APOE	Gene	Variant	Position	Transcript	CADD	ClinVar	Significance for disease
EOD-19	**AD**	**51**	**m**	**1**	**E3/E3**	***APP***	**g. chr.21:(?_27253981)-(27542937_?)dup**				**P**	**Relevant for diagnosis**
EOD-19 (2)[b]	**AD**	**47**	**m**	**1**	**E3/E3**	***APP***	**g. chr.21:(?_27253981)-(27542937_?)dup**				**P**	**Relevant for diagnosis**
EOD-20	AD	57	m	4,5	E3/E3	*LRRK2*	c.7397T > A; p.L2466H	chr12:40760814-40760814	NM_198578.3	25.7	VUS	Unknown
EOD-21	**CAA**	**54**	**m**	**3,5**	**E4/E4**	***APOE***						**Relevant for diagnosis**
EOD-22	**AD**	**49**	**m**	**4**	**E4/E4**	***APOE***						**Relevant for diagnosis**
EOD-23	**AD**	**36**	**f**	**1**	**E3/E3**	***PSEN1***	**c.617G > A; p.G206D**	**chr14:73659420-73659420**	**NM_000021.3**	**31.0**	**P**	**Relevant for diagnosis**
EOD-24	**AD**	**53**	**m**	**3,5**	**E4/E4**	***APOE***						**Relevant for diagnosis**
EOD-25	**AD**	**51**	**f**	**3,5**	**E4/E4**	***APOE***						**Relevant for diagnosis**
EOD-26	AD	56	f	4	E3/E3	*DCTN1*	c.2980G > C; p.P994A	chr2:74590268-74590268	NM_023019.3	17.3	VUS	Unknown
						MAPK8IP3	c.2087G > A; p.R696H	chr16:1814180-1814180	NM_015133.3	31.0	n.r	Unknown
EOD-27	AD	57	f	4	E4/E3	*APOE*						Risk modifier
EOD-28	AD	54	m	4	E3/E3							
EOD-29	AD	54	m	4	E3/E3							
EOD-30	AD	64	m	4	E3/E3							
EOD-31	mixed dementia (AD + VD)	58	m	3,5	E3/E3							
EOD-32	FTD/svPPA	61	m	4	E3/E3							
EOD-33	AD	62	f	4,5	E4/E3	*APOE*						Risk modifier
						DCTN1	c.521G > A; p.S174L	chr2:74598788-74598788	NM_004082.4	24.4	VUS	Unknown
EOD-34	AD	59	f	2	E4/E3	*APOE*						Risk modifier
EOD-35	AD	55	m	3,5	E4/E3	*APOE*						Risk modifier
EOD-36[c]	AD	64	m	2	E4/E3	*TREM2*	c.140G > A; p.R47H	chr6:41129252-41129252	NM_018965.3	9.7	LB	Risk modifier
						APOE						Risk modifier
EOD-37	AD	52	f	3,5	E3/E3	*LRRK2*	c.7397T > A; p.L2466H	chr12:40760814-40760814	NM_198578.3	25.7	VUS	Unknown
EOD-38	AD	52	f	3,5	E4/E3	*APOE*						Risk modifier

Table 1 (continued)

ID	Diagnosis	AAO (years)	Sex	FH	APOE	Gene	Variant	Position	Transcript	CADD	ClinVar	Significance for disease
EOD-39	AD	63	f	3	E4/E3	*APOE*						Risk modifier
EOD-40	AD	55	f	4	E4/E3	*APOE*						Risk modifier
EOD-41	AD	58	m	3,5	E3/E3							
EOD-42	AD	39	m	4	E3/E2							
EOD-43	AD	63	m	4	E3/E3	*VPS13C*	c.3148A > G; p.I1050V	chr15:62256964-62256964	NM_020821.2	0.001	VUS	Unknown
EOD-44	AD/lpPPA	58	f	3,5	E3/E3	*SORL1*	c.3014T > G; p.M1005R	chr11:121430331-121430331	NM_003105.5	27.9	n.r	Potential risk modifier
EOD-45	AD	65	m	4	E3/E3							
EOD-46	CBS + AD	51	f	3,5	E3/E3	*SORL1*	c.4606G > A; p.G1536S	chr11:121474988-121474988	NM_003105.5	25.2	B	Risk modifier
EOD-47	AD	54	f	4	E3/E3							
EOD-48	bvFTD	57	m	4	E3/E3							
EOD-49	FTD/nfPPA + ALS	58	m	4	E3/E3	*TBK1*	c.986T > C; p.L276P	chr12:64875636-64875636	NM_013254.3		n.r	Potential risk modifier
						VPS13C	c.7436T > C; p.I2429T	chr15:62212307-62212307	NM_020821.2		n.r	Unknown
EOD-50	**FTD (bvFTD + nfPPA)**	**55**	**f**	**3,5**	**E4/E3**	***PGRN***	**c.328C > T; p.R110***	**chr17:42427098-42427098**	**NM_002087.3**	**29.4**	**P**	**Relevant for diagnosis**
						APOE						Risk modifier
EOD-51	FTD/svPPA	62	f	4	E3/E3							
EOD-52	AD	57	m	4	E4/E3	*APOE*						Risk modifier
EOD-53	**AD**	**57**	**m**	**4**	**E4/E4**	***APOE***						**Relevant for diagnosis**
						LRRK2	c.7377G > A; p.M2459I	chr12:40758839-40758839	NM_198578.3	17.7	n.r	Unknown
EOD-54	AD	59	m	1	E4/E3	*APOE*						Risk modifier
EOD-55	AD	49	m	4	E3/E3							
EOD-56	AD	61	m	3,5	E3/E3							
EOD-57	AD/lpPPA	57	f	4	E3/E3							
EOD-58	AD + VD	64	f	3	E3/E3	*DCTN1*	c.823C > T; p.R141C	chr2:74598126-74598126	NM_004082.3	29.3	VUS	Unknown
EOD-59	bvFTD	52	m	4	E4/E3	*APOE*						Risk modifier
EOD-60	**AD**	**49**	**f**	**3**	**E3/E3**	***APP***	**c.2092G > A; p.V586I**	**chr21:27264096**	**NM_201413.3**	**28.2**	**P**	**Relevant for diagnosis**

a, EOD-18: The APP duplication of was confirmed to be 'de novo'. Both parents did not show this duplication

b, EOD-19 (2) is the brother of EOD19. He was also affected by AD and carrier of the same duplication. EOD 19 (2) was not included in the analyses of AAO and FH

c, EOD-36: ClinVar assessment of TREM2 p.R47H of LB (likely benign) refers to Nasu-Hakola disease. However, p.R47H is an established risk variant for dementia (Ref. 15)

Reference

1. Silvaieh S, König T, Wurm R, et al. Comprehensive genetic screening of early-onset dementia patients in an Austrian cohort-suggesting new disease-contributing genes. Hum Genom. 2023;17:55. https://doi.org/10.1186/s40246-023-00499-z.

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