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### Correction

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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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**Correction to:** Human Genomics (2023) 17:55  
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The original article [1] has been corrected.

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.

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<sup>†</sup>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
							c.184G>A; p.R62C	chr6:41129208-41129208	NM_001271821.1	25.5	n.r	Risk modifier
												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/PPA	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
							c.975T>G; p.S3253G	chr15:62173781-62173781	NM_020821.2	29.5	n.r	Unknown
EOD-9	AD	55	f	3,5	E4/E3	APOE						
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						
EOD-13	AD	61	m	4,5	E3/E3							
EOD-14	AD/PPA	61	m	4	E4/E3	APOE						
EOD-15	nfPPA	64	m	2	E3/E3	DCTN1	c.4300C>T; p.V1434I	chr15:62244179-62244179	NM_020821.2	24.8	n.r	Unknown
							c.2218C>T; p.E740K	chr27:4594514-74594514	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						
EOD-18 <sup>a</sup>	AD	47	m	4	E3/E3	APP	g.chr21:(?_26958019)- (27852747_?)dup	NM_015133.3	22.3	n.r	P	Relevant for diagnosis
							c.2914C>T; p.P972S	chr19:1051537-1051537	NM_019112.3	25.3	n.r	Potential risk modifier

**Table 1** (continued)

D	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) <sup>b</sup>	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	chr12:40766814- 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
EOD-27	AD											Risk modifier
EOD-28	AD	57	f	4	E4/E3	APOE						Risk modifier
EOD-29	AD	54	m	4	E3/E3							Risk modifier
EOD-30	AD	54	m	4	E3/E3							Risk modifier
EOD-31	mixed dementia (AD+VD)	64	m	4	E3/E3							Risk modifier
EOD-32	FTD/svPPA	58	m	3,5	E3/E3							Risk modifier
EOD-33	AD	61	m	4	E3/E3	APOE						Risk modifier
EOD-34	AD	62	f	4,5	E4/E3	DCTN1	c.521G>A; p.S174L	chr2:74598788- 74598788	NM_004082.4	24.4	VUS	Unknown
EOD-35	AD	59	f	2	E4/E3	APOE						Risk modifier
EOD-36 <sup>c</sup>	AD	55	m	3,5	E4/E3	APOE						Risk modifier
EOD-37	AD	64	m	2	E4/E3	TREM2	c.140G>A; p.R47H	chr6:41129252- 41129252	NM_018965.3	9.7	LB	Risk modifier
EOD-38	AD	52	f	3,5	E3/E3	LRRK2	c.7397T>A; p.L2466H	chr12:40766814- 40760814	NM_198578.3	25.7	VUS	Unknown
EOD-39	AD	52	f	3,5	E4/E3	APOE						Risk modifier

**Table 1** (continued)

ID	Diagnosis	AAO (years)	Sex	FH	APP	Gene	Variant	Position	Transcript	CADD	ClinVar	Significance for disease	
EOD-39	AD	63	f	3	E4/E3	<i>APOE</i>						Risk modifier	
EOD-40	AD	55	f	4	E4/E3	<i>APOE</i>						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	<i>VPS13C</i>	c.3148A>G; p.I1050V	chr15:62256964-62256964	NM_020821.2	0.001	VUS	Unknown	
EOD-44	AD/pPPA	58	f	3,5	E3/E3	<i>SORL1</i>	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	<i>SORL1</i>	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/nPPA+ALS	58	m	4	E3/E3	<i>TBK1</i>	c.986T>C; p.L276P	chr12:64875636-64875636	NM_013254.3	n.r	Potential risk modifier		
EOD-50	FTD (bvFTD+nPPA)	55	f	3,5	E4/E3	<i>PGRN</i>	c.328C>T; p.R110*	chr15:62212307-62212307	NM_020821.2	n.r	Unknown		
							<b>chr17:42427098-42427098</b>		<b>NM_002087.3</b>	<b>29.4</b>	<b>P</b>	<b>Relevant for diagnosis</b>	
EOD-51	FTD/SvPPA	62	f	4	E3/E3	<i>APOE</i>						Risk modifier	
EOD-52	AD	57	m	4	E4/E3	<i>APOE</i>						Risk modifier	
EOD-53	<b>AD</b>	<b>57</b>	<b>m</b>	<b>4</b>	<b>E4/E4</b>	<b>APOE</b>	<i>LRRK2</i>	c.7377G>A; p.M2459I	chr12:40758839-40758839	NM_198578.3	17.7	n.r	Unknown
EOD-54	AD	59	m	1	E4/E3	<i>APOE</i>							
EOD-55	AD	49	m	4	E3/E3								
EOD-56	AD	61	m	3,5	E3/E3								
EOD-57	AD/pPPA	57	f	4	E3/E3	<i>DCTN1</i>	c.823C>T; p.R141C	chr2:74598126-74598126	NM_004082.3	29.3	VUS	Unknown	
EOD-58	AD+VD	64	f	3	E3/E3								
EOD-59	bvFTD	52	m	4	E4/E3	<i>APOE</i>							
EOD-60	<b>AD</b>	<b>49</b>	<b>f</b>	<b>3</b>	<b>E3/E3</b>	<b>APP</b>	<b>c.2092G&gt;A; p.Y586I</b>	<b>chr21:27264096</b>	<b>NM_201413.3</b>	<b>28.2</b>	<b>P</b>	<b>Relevant for diagnosis</b>	

**a.** EOD-18: The APP duplication was confirmed to be 'de novo'. Both parents did not show this duplication**b.** EOD-19 (2) is the brother of EOD-19. 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. Silvaeih 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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