

Supplement 8: Screening of families with particularly complex *SYNE1* phenotypes for possible 2nd hits in other disease genes

Three *CA plus* patients, belonging to two different index families (family #13 and family #23), showed a particularly severe and complex multisystemic phenotype. This phenotype comprised of very early onset ataxia, spasticity, weakness and muscle wasting of all four limbs, mental retardation, dysphagia, pes cavus, respiratory dysfunction and a broad range of variable skeletal and soft-tissue abnormalities such as sacral cysts, pseudarthrosis clavicular, hyperlaxity of joints, achilles tendon contractures, kyphosis, scoliosis, cataract, hypertelorism.

Theoretically, such a more complex phenotype might be explained by a second hit in other disease gene, rather than by the observed truncating *SYNE1* mutations *per se*. We screened for additional disease mutations in the index patient of family #13 by whole exome sequencing (WES) and in the index patient of family #23 by a customized Nextera Rapid Custom kit (Illumina) gene panel containing 204 genes for ataxia (104 genes) and spastic paraplegia (100 genes), sequenced with a MiSeq (Illumina). Variants resulting from WES and panel sequencing, respectively, were filtered to produce two gene lists: one for single heterozygous variants ("dominant variants" = dominant list); one for two homozygous or compound heterozygous variants ("recessive variants" = recessive list). For each of the two lists, we filtered for non-synonymous heterozygous variants (for dominant list) or homozygous or compound heterozygous variants (for recessive list), passing strict in-house quality filters (for gem.app GATK quality index > 50 and genotype quality GQ > 30) and/or show a coverage of at least 20x, and that were absent or extremely rare in public databases (minor allele frequency in dbSNP137, NHLBI ESP6500, and ExAc < < 0.01% for dominant and < 0.5% for recessive list).

For the WES of index patient of family #13 several dominant and recessive variants passed these filter settings (see below). However, none of the variants in these genes could obviously explain the specific phenotypic features observed in this patient, except the two recessive

SYNE1 variants. Only one rare *OPA1* variant was identified, which was also observed in the affected brother; however, it was also present in healthy sibling as well as in the healthy mother, thus we do not think that this variant adds to the phenotype, in particular as none of the affected siblings showed typical signs of *OPA1/OPA1*- plus-disease such as e.g. optic atrophy, ptosis, external ophthalmoplegia, hypoakusis or sensorimotor peripheral neuropathy (Bonifert *et al.*, 2014).

For the 204 gene panel of the index patient of family #23, no recessive variants passed the filters, except the two *SYNE1* variants. For dominant genes, only one variant in the *PRNP* gene was identified. This 24-nt deletion, which eliminates one of the 4 tandem octapeptide repeats located in the PrP N-terminal region, likely presents a benign rare polymorphism. Deletion of these repeats has been reported as nonpathogenic (Palmer *et al.*, 1993), such deletion has been observed in 2/186 Italian controls (Salvatore *et al.*, 1994), and we observed such a deletion in another patient presenting with early-onset ataxia. As the case in the current index subject, also in this other patient neither parent was affected.

In summary, no obvious second hit in any other disease gene was detected in these patients. Thus, rather than explained by a second hit in another gene or by a different disease, the complex phenotype in these three subjects seems to present one end of the *SYNE1*-disease spectrum, which literally encompasses *all* of the *SYNE1*-associated phenotypic domains described in the main text, and includes also mental retardation and respiratory distress.

References:

Bonifert T, Karle KN, Tonagel F, Batra M, Wilhelm C, Theurer Y, et al. Pure and syndromic optic atrophy explained by deep intronic OPA1 mutations and an intralocus modifier. *Brain*. 2014;137(Pt 8):2164-77.

Palmer MS, Mahal SP, Campbell TA, Hill AF, Sidle KC, Laplanche JL, et al. Deletions in the prion protein gene are not associated with CJD. *Human molecular genetics*. 1993;2(5):541-4.

Salvatore M, Genuardi M, Petraroli R, Masullo C, D'Alessandro M, Pocchiari M. Polymorphisms of the prion protein gene in Italian patients with Creutzfeldt-Jakob disease. *Human genetics*. 1994;94(4):375-9.

recessive variant list of the index patient of family #13

										number of families with							
chr	pos	ref	genotype	gene	transcript	mutation type	cDNA	protein notation	EVS6500 allele counts	variant in	phastcons	GERP	Mutation			dbSNP_ID	
										GENESIS			_Taster	Poly_Phen	SNP		
2	231678762	A	W	CAB39	NM_001130849.1	splice-acceptor			A=13006	42	0.943	5.370					
2	231678763	G	K	CAB39	NM_001130849.1	splice-acceptor			G=13006	47	0.998	5.370					
10	106214246	TGG	TGG/T	CCDC147	NM_001008723.1	frameshift				1	0.999	5.470					
10	106214253	G	K	CCDC147	NM_001008723.1	stop-gained	c.2584G>T	p.G862X	G=13006	1	1.000	5.470	D		D		
4	1388570	G	S	CRIPAK	NM_175918.3	missense	c.271G>C	p.D91H	G=13006	14	0.000	-1.880	N	0.004	T	28561739	
4	1388497	TCACA	TCACA/T	CRIPAK	NM_175918.3	frameshift				10	0.002	0.631				55954740	
4	1388559	TCA	TCA/T	CRIPAK	NM_175918.3	frameshift				14	0.000	-0.171				201311249	
7	74212352	A	G	GTF2IRD2	NM_173537.3	missense	c.1499T>C	p.L500S	A=12764	32	0.009	1.740	N	0.000	T	200619072	
2	90414097	G	R	LOC101060017	XM_003959983.1	missense	c.160G>A	p.R54C		29	0.351						
2	90414093	C	Y	LOC101060017	XM_003959983.1	missense	c.164C>T	p.G55D		11	0.353						
15	102303356	G	R	LOC101927594	XM_005255005.1	missense	c.688G>A	p.A230T		35	0.617	1.390					
15	102304462	C	S	LOC101927594	XM_005255005.1	missense	c.1794C>G	p.H598Q		1	0.979	0.415					
22	20715097	C	S	LOC101927859	XM_005261896.1	missense	c.2630C>G	p.T877R		9	0.020						
22	20714877	C	Y	LOC101927859	XM_005261896.1	missense	c.2410C>T	p.P804S		14	0.006						
22	20715133	G	R	LOC101927859	XM_005261896.1	missense	c.2666G>A	p.R889Q		20	0.018					111437983	
12	40904643	A	R	MUC19	XM_003846356.2	missense	c.19595A>G	p.N6533D		44	0.000	-3.270				77925138	
12	40922977	A	M	MUC19	XM_003846356.2	splice-acceptor				21	0.395	0.753				78062154	
3	195510615	G	R	MUC4	XM_005269329.1	missense	c.2264C>T	p.P755L	G=3402	29	0.168						
3	195515390	G	S	MUC4	NM_018406.6	missense	c.3061C>G	p.H1021D	G=4562	19	0.000	-1.390	N	0.001		200400545	
3	195506386	G	S	MUC4	NM_018406.6	missense	c.12065C>G	p.P4022R	G=3908	4	0.001		N	0.988			
3	195508613	A	R	MUC4	NM_018406.6	missense	c.9838T>C	p.S3280P	A=4352	45	0.006	-1.600	N	0.001			
3	195508188	G	S	MUC4	NM_018406.6	missense	c.10263C>G	p.H3421Q	G=4534	47	0.005	-1.790	N	0.010		372617756	
3	195515353	T	K	MUC4	NM_018406.6	missense	c.3098A>C	p.E1033A	T=4564	47	0.000	-2.010	N	0.002		13065435	
3	195508622	C	S	MUC4	NM_018406.6	missense	c.9829G>C	p.D3277H	C=4318	22	0.010	-2.050	N	0.010			
3	195508599	G	R	MUC4	XM_005269323.1	missense	c.728C>T	p.P243L	G=4390	15	0.001	-0.846				201939860	
3	195508558	A	R	MUC4	NM_018406.6	missense	c.9893T>C	p.L3298P	A=4476	48	0.005		N	0.000		201559646	
3	195507637	T	W	MUC4	NM_018406.6	missense	c.10814A>T	p.D3605V	T=3146	48	0.001	-2.030	N	0.004			
3	195508639	G	K	MUC4	NM_018406.6	missense	c.9812C>A	p.S3271Y	G=4176	3	0.004	-0.120	N	0.932			
3	195506867	G	S	MUC4	NM_018406.6	missense	c.11584C>G	p.P3862A	G=3992	23	0.004		N	0.001			
3	195506922	G	R	MUC4	XM_005269323.1	missense	c.2405C>T	p.S802L	G=3024	30	0.098						
3	195510279	G	R	MUC4	XM_005269329.1	missense	c.2600C>T	p.P867L	G=1842	18	0.003	-1.380					
3	195510471	G	R	MUC4	XM_005269329.1	missense	c.2408C>T	p.P803L	G=868	10	0.003	-1.380				202095630	
3	195508700	C	Y	MUC4	NM_018406.6	missense	c.9751G>A	p.V3251I	C=3484	45	0.003	1.030	N	0.978		201890853	
3	195510375	G	R	MUC4	XM_005269329.1	missense	c.2504C>T	p.P835L	G=3404	49	0.007	-1.380					
16	22546105	C	Y	NPIP85	NM_001135865.1	missense	c.1801C>T	p.P601S	C=310	22			N		T	200797153	
16	22546050	G	G/GATA	NPIP85	NM_001135865.1	coding				30							
3	40503520	ACTGCTC	ACTGCTGCT	RPL14	NM_001034996.2	codingComplex				13	0.188					147295890	
6	152551729	G	R	SYNE1	NM_033071.3	stop-gained	c.20935C>T	p.R6979X	G=13006	1	0.000	1.140	A		T		

6	152542097	G	K	SYNE1	NM_033071.3	stop-gained	c.21528C>A	p.Y7176X	G=13006	1	0.967	2.630	A		T
1	152084873	C	Y	TCHH	NM_007113.3	missense	c.820G>A	p.E274K	C=12670	1	0.000	0.974	N	0.000	T
1	152084872	T	W	TCHH	NM_007113.3	missense	c.821A>T	p.E274V	T=12676	1	0.000	0.112	N	0.004	T
22	20715133	G	R	USP41	XM_005261896.1	missense	c.2666G>A	p.R889Q		20	0.018				
22	20714877	C	Y	USP41	XM_005261896.1	missense	c.2410C>T	p.P804S		14	0.006				
22	20710358	C	Y	USP41	XM_005261895.1	missense	c.1967C>T	p.T656M		44	0.009	1.050			
22	20715097	C	S	USP41	XM_005261896.1	missense	c.2630C>G	p.T877R		9	0.020				

111437983

dominant variant list of the index patient of family #13

chr	pos	ref	genotype	gene	transcript	mutation type	cDNA	protein notation	EVS6500 allele counts	number of families with variant in		phastcons	GERP	Mutation_Taster		SNP	dbSNP_ID
										GENESIS				er	Poly_Phen		
19	1231208	CCCT	CCCT/C	C19ORF26	NM_152769.2	coding				2		0,614	2,78				
11	1997500	G	G/GTCC	LOC101927645	XM_005253275.1	coding				23		0,034	0,904				
11	1997500	G	G/GTCC	MRPL23	XM_005253275.1	coding				23		0,034	0,904				
16	22546050	G	G/GATA	NPIPB5	NM_001135865.1	coding				30							
16	87637893	CCTGCTGCTG	CCTGCTGCTG/C	JPH3	NM_001271604.2	codingComplex				35		0,017	3				193922903
4	5527115	AT	AT/A	C4ORF6	NM_005750.2	frameshift				43		0,05	-0,451				75708175
10	1,06E+08	TGG	TGG/T	CCDC147	NM_001008723.1	frameshift				1		0,999	5,47				
1	86965571	CTT	CTT/C	CLCA1	NM_001285.3	frameshift				1		0,999	2,06				
4	1388497	TCACA	TCACA/T	CRIPAK	NM_175918.3	frameshift				10		0,002	0,631				55954740
4	1388559	TCA	TCA/T	CRIPAK	NM_175918.3	frameshift				14		0	-0,171				201311249
6	12290903	C	C/CT	EDN1	NM_001168319.1	frameshift				39		0,808	3,28				372164724
11	62369890	A	A/AAGGGC	EML3	XM_005273876.1	frameshift				14		0,009	-0,317				113521256
1	65272918	A	A/AT	RAVER2	NM_018211.3	frameshift				1		0,069	2,69				
14	38679763	CGCTCTGAGCCCG	CGCTCTGAGCC	SSTR1	NM_001049.2	frameshift				9		0,774					375891291
15	90611145	C	C/CG	ZNF710	NM_198526.2	frameshift				7		0,068	4,02				
5	80626692	T	Y	ACOT12	NM_130767.2	missense	c.1459A>G	p.R487G	T=13006	1		0,899	4,55	D	1		D
1	1,97E+08	G	K	CRB1	NM_001193640.1	missense	c.2708G>T	p.G903V	G=13004	1		1	4,53	D	1		T
8	1,13E+08	G	R	CSMD3	NM_052900.2	missense	c.5750C>T	p.T1917M	G=12990	1		1	5,64	D	1		T
7	21847510	G	K	DNAH11	NM_001277115.1	missense	c.10175G>T	p.R3392L	G=12016	1		1	6,02	D	1		D
6	87994407	C	S	GJB7	NM_198568.2	missense	c.224G>C	p.R75T	C=13006	1		1	3,96	D	1		D
12	85449613	G	S	LRRIQ1	NM_001079910.1	missense	c.1042G>C	p.E348Q	G=12876	1		0,052	4,38	N	1		201413710
13	30077146	A	R	MTUS2	NM_001033602.2	missense	c.3943A>G	p.N1315D	A=12358	1		0,978	4,63	D	1		201810554
18	31538262	C	Y	NOL4	NM_001198546.1	missense	c.1177G>A	p.D393N	C=13006	1		0,64	5,39	D	1		D
12	1,33E+08	A	M	PXMP2	NM_018663.1	missense	c.566A>C	p.Y189S	A=13006	3		1	3,9	D	1		T
1	1,7E+08	A	R	SELP	NM_003005.3	missense	c.395T>C	p.V132A	A=13006	2		1	5,79	D	1		D
21	46945835	C	M	SLC19A1	NM_001205206.1	missense	c.1189G>T	p.A397S	C=13006	1		1	4,51	D	1		D
15	65916494	C	Y	SLC24A1	NM_004727.2	missense	c.76C>T	p.L26F	C=12094	1		0,966	2,09	N	1		D
10	98155732	G	K	TLL2	NM_012465.3	missense	c.1430C>A	p.S477Y	G=13006	1		1	5,37	D	1		D
8	1,46E+08	G	S	TONSL	NM_013432.4	missense	c.1802C>G	p.P601R	G=13006	1		0,989	4,73	D	1		D
3	47456620	G	R	SCAP	NM_012235.2	missense	c.3107C>T	p.T1036I	G=13000	1		0,986	5,26	D	0,083		D
15	71704139	A	W	THSD4	NM_024817.2	missense	c.1129A>T	p.I377F	G=1/A=12813	1		1	5,47	D	0,2		371755466
17	37899218	G	R	GRB7	NM_001030002.2	missense	c.374G>A	p.R125H	G=13006	2		0,969	4,77	D	0,557		200112951
3	36898518	T	W	TRANK1	NM_014831.2	missense	c.2563A>T	p.M855L	T=12254	1		1	5,51	D	0,615		T
1	87033135	A	R	CLCA4	NM_012128.3	missense	c.983A>G	p.Q328R	A=12212	1		1	5,87	N	0,732		183460731
1	20678651	G	R	VWASB1	NM_001039500.2	missense	c.3127G>A	p.D1043N	G=4566	1		0,911	3,45	D	0,742		200924861
3	1,93E+08	A	R	OPA1	NM_015560.2	missense	c.635A>G	p.K212R	A=12998	1		1	5,42	D	0,787		D
1	17085078	T	Y	MST1L	NM_001271733.1	missense	c.1397A>G	p.Q466R		44		0			0,82		T
10	70998810	T	Y	HKDC1	NM_025130.3	missense	c.508T>C	p.S170P	T=13006	1		0,991	4,92	D	0,828		D
3	1,96E+08	G	K	MUC4	NM_018406.6	missense	c.9812C>A	p.S3271Y	G=4176	3		0,004	-0,12	N	0,932		
19	9073383	G	R	MUC16	NM_024690.2	missense	c.14063C>T	p.A4688V	G=12132	1		0	-1,33		0,938		D
8	77617526	G	R	ZFHx4	NM_024721.4	missense	c.1203G>A	p.M401I	G=11962	1		1	5,38	D	0,962		T
3	1,25E+08	G	K	ITGB5	NM_002213.3	missense	c.391C>A	p.R131S	G=13006	1		0,982	5,15	D	0,975		D

11	1780845	T	Y	CTSD	NM_001909.4	missense	c.253A>G	p.I85V	T=13000	1	0,989	4,2	D	0,976	D	
3	1,96E+08	C	Y	MUC4	NM_018406.6	missense	c.9751G>A	p.V3251I	C=3484	45	0,003	1,03	N	0,978		201890853
16	77325275	C	S	ADAMTS18	NM_199355.2	missense	c.3290G>C	p.R1097P	T=4/C=12992	1	0,962	5,8	D	0,979	T	150975249
1	1,45E+08	A	R	NBPF10	NM_001039703.5	missense	c.8729A>G	p.D2910G		28	0,105	1,17	N	0,98	D	
17	76886725	A	R	LOC100653515	NM_001243540.1	missense	c.1861T>C	p.C621R		1	0	-0,302	N	0,981	D	
17	76886725	A	R	TIMP2	NM_001243540.1	missense	c.1861T>C	p.C621R		1	0	-0,302	N	0,981	D	
1	2,01E+08	G	K	KIF14	NM_014875.2	missense	c.1800C>A	p.N600K	G=13006	1	0,484	4,33	D	0,985	D	
3	1,96E+08	G	S	MUC4	NM_018406.6	missense	c.12065C>G	p.P4022R	G=3908	4	0,001		N	0,988		
12	46322435	C	M	SCAF11	NM_004719.2	missense	c.1049G>T	p.G350V	C=13006	1	0,93	3,94	D	0,989	D	
21	45971309	G	S	KRTAP10-2	NM_198693.2	missense	c.33C>G	p.S11R	A=44/G=12962	10	0,006	0,091	N	0,993	D	180855850
21	45971309	G	S	TSPEAR	NM_198693.2	missense	c.33C>G	p.S11R	A=44/G=12962	10	0,006	0,091	N	0,993	D	180855850
1	55066959	G	R	ACOT11	NM_015547.3	missense	c.902G>A	p.C301Y	G=13006	1	0,971	4,03	D	0,994	T	
2	1,07E+08	C	Y	RGPD3	NM_001144013.1	missense	c.4054G>A	p.E1352K	C=4534	23	1	2,35	D	0,998	D	199689380
9	1,39E+08	A	R	SNAPC4	NM_003086.2	missense	c.575T>C	p.L192P	A=13006	1	0,92	4,8	D	0,998	D	
3	1,3E+08	G	R	COL6A6	NM_001102608.1	missense	c.2890G>A	p.D964N	G=12256	1	0,937	4,82	D	0,999	T	
17	648633	G	R	GEMIN4	NM_015721.2	missense	c.2650C>T	p.L884F	G=12444	1	0,998	5,83	D	0,999	D	
1	1,49E+08	A	M	NBPF15	NM_001170755.2	missense	c.1430A>C	p.D477A	A=2550	16	0	-1,03	N	0,999	D	200054103
2	2,19E+08	G	R	PNKD	NM_015488.4	missense	c.646G>A	p.V216M	G=13006	1	0,997	3,89	D	0,999	D	
2	3756146	C	Y	DCDC2C	XM_001127882.4	missense	c.295C>T	p.H99Y		8	0,999	3,59	N		D	191299579
22	20710358	C	Y	FAM230A	XM_005261895.1	missense	c.1967C>T	p.T656M		44	0,009	1,05				
1	16865918	G	R	LOC100133301	XM_001721533.2	missense	c.358G>A	p.E120K		4	0,023					185495452
2	90414097	G	R	LOC101060017	XM_003959983.1	missense	c.160G>A	p.R54C		29	0,351					
2	90414093	C	Y	LOC101060017	XM_003959983.1	missense	c.164C>T	p.G55D		11	0,353					
15	1,02E+08	G	R	LOC101927594	XM_005255005.1	missense	c.688G>A	p.A230T		35	0,617	1,39				
15	1,02E+08	C	S	LOC101927594	XM_005255005.1	missense	c.1794C>G	p.H598Q		1	0,979	0,415				
15	83013643	G	R	LOC101927601	XM_005272450.1	missense	c.709G>A	p.R237C		11	0	-2,02				
15	1,02E+08	C	S	LOC101927662	XM_005255007.1	missense	c.1024C>G	p.R342G		41	0,969	1,4				
22	20715097	C	S	LOC101927859	XM_005261896.1	missense	c.2630C>G	p.T877R		9	0,02					
22	20714877	C	Y	LOC101927859	XM_005261896.1	missense	c.2410C>T	p.P804S		14	0,006					
22	20715133	G	R	LOC101927859	XM_005261896.1	missense	c.2666G>A	p.R889Q		20	0,018					111437983
12	40904643	A	R	MUC19	XM_003846356.2	missense	c.19595A>G	p.N6533D		44	0	-3,27				77925138
3	1,96E+08	G	R	MUC4	XM_005269329.1	missense	c.2264C>T	p.P755L	G=3402	29	0,168					
3	1,96E+08	G	R	MUC4	XM_005269323.1	missense	c.728C>T	p.P243L	G=4390	15	0,001	-0,846				201939860
3	1,96E+08	G	R	MUC4	XM_005269329.1	missense	c.2504C>T	p.P835L	G=3404	49	0,007	-1,38				
3	1,96E+08	G	R	MUC4	XM_005269323.1	missense	c.2405C>T	p.S802L	G=3024	30	0,098					
3	1,96E+08	G	R	MUC4	XM_005269329.1	missense	c.2600C>T	p.P867L	G=1842	18	0,003	-1,38				
3	1,96E+08	G	R	MUC4	XM_005269329.1	missense	c.2408C>T	p.P803L	G=868	10	0,003	-1,38				202095630
14	20181373	G	K	OR11H2	NM_001197287.1	missense	c.703C>A	p.L235I		1	0,95	1,26				
2	1,31E+08	A	W	POTEJ	NM_001277083.1	missense	c.2021A>T	p.D674V		14	0,212	0,736	D		D	199811130
22	20714877	C	Y	USP41	XM_005261896.1	missense	c.2410C>T	p.P804S		14	0,006					
22	20715133	G	R	USP41	XM_005261896.1	missense	c.2666G>A	p.R889Q		20	0,018					111437983
22	20710358	C	Y	USP41	XM_005261895.1	missense	c.1967C>T	p.T656M		44	0,009	1,05				
22	20715097	C	S	USP41	XM_005261896.1	missense	c.2630C>G	p.T877R		9	0,02					
15	91025331	C	Y	IQGAP1	NM_003870.3	missense-near-splice	c.3469C>T	p.P1157S	C=12992	1	1	6,04	D	1.000	T	
5	1053464	A	R	SLC12A7	NM_006598.2	missense-near-splice	c.3160T>C	p.Y1054H	A=13006	1	1	3,88	D	0.105		
11	1,26E+08	T	K	KIRREL3	NM_001161707.1	missense-near-splice	c.743A>C	p.H248P	T=12462	2	0,998	5,48	D	0.997	D	
5	34925330	G	R	BRIX1	NM_018321.3	splice-acceptor			G=12994	5	0,998	5,57	D			
2	2,32E+08	A	W	CAB39	NM_001130849.1	splice-acceptor			A=13006	42	0,943	5,37				

2	2,32E+08	G	K	CAB39	NM_001130849.1	splice-acceptor			G=13006	47	0,998	5,37			
19	33579038	A	W	GPATCH1	NM_018025.2	splice-acceptor			A=12992	36	0,973	5,28			
9	1,3E+08	A	R	LRSAM1	NM_001005373.3	splice-acceptor			A=13006	1	1	5,46	D		
12	40922977	A	M	MUC19	XM_003846356.2	splice-acceptor				21	0,395	0,753			78062154
4	1,29E+08	A	W	PLK4	NM_001190799.1	splice-acceptor			A=13002	20	0,938	5	D		
1	16856	A	R	WASH7P	NR_024540.1	splice-donor				10	0,081	0,906			200205172
10	1,06E+08	G	K	CCDC147	NM_001008723.1	stop-gained	c.2584G>T	p.G862X	G=13006	1	1	5,47	D	D	
14	55615330	G	R	DLGAP5	NM_001146015.1	stop-gained	c.2491C>T	p.R831X		6	0,013	-0,311	N	T	181931242
1	26359737	C	M	EXTL1	NM_004455.2	stop-gained	c.1449C>A	p.Y483X	C=13006	1	0,794	1,02	A	T	
7	1,01E+08	C	Y	MUC12	NM_001164462.1	stop-gained	c.9415C>T	p.R3139X	C=4540	19	0	-1,72	A	T	
17	18872403	C	M	SLC5A10	NM_001042450.2	stop-gained	c.492C>A	p.C164X	C=13006	2	1	2,74	D	T	
6	1,53E+08	G	K	SYNE1	NM_033071.3	stop-gained	c.21528C>A	p.Y7176X	G=13006	1	0,967	2,63	A	T	
6	1,53E+08	G	R	SYNE1	NM_033071.3	stop-gained	c.20935C>T	p.R6979X	G=13006	1	0	1,14	A	T	