Whole-exome sequencing identifies a novel *de novo* mutation in *DYNC1H1* in epileptic encephalopathies

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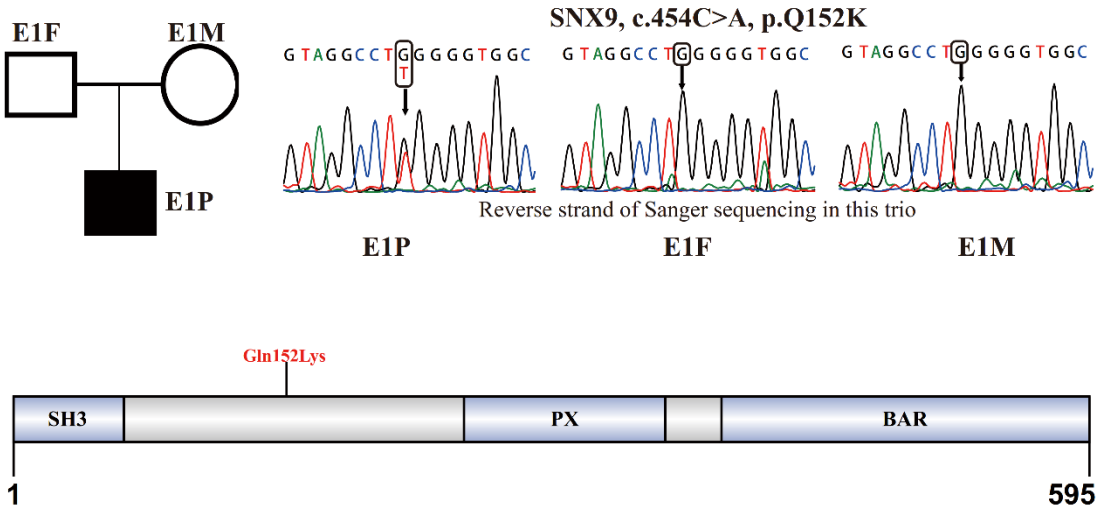
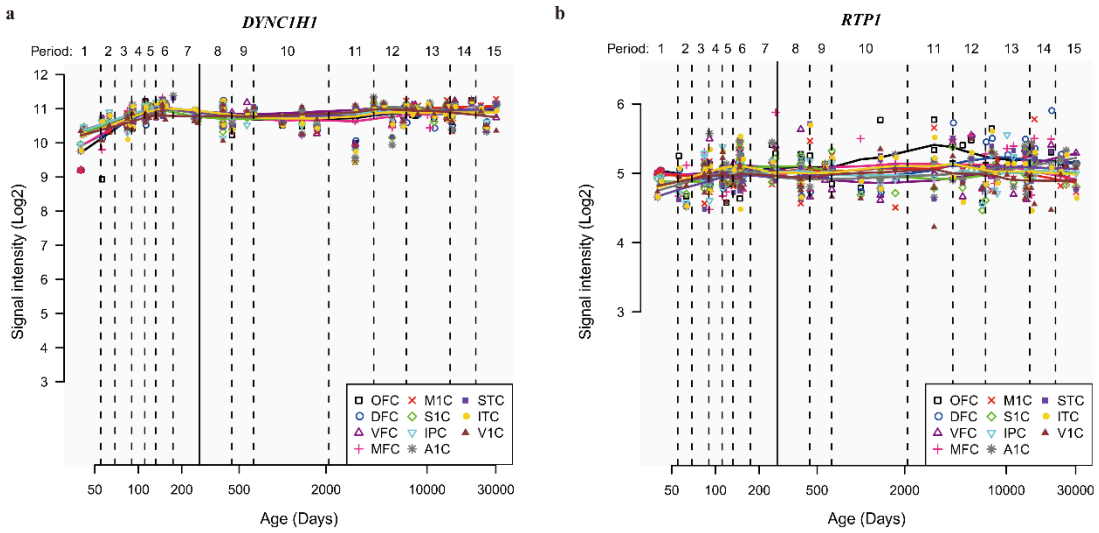


Supplementary figure 1. *De novo* mutations identified in *SNX9*. The *SNX9* variant (c.454C>A, p.Q152K) of trio E1 were confirmed using Sanger sequencing and Schematic representation of the SNX9 protein



Supplementary figure 2. Expression analysis of *DYNC1H1* and *RTP1* in 11 areas of the neocortex (NCX). OFC, orbital prefrontal cortex; DFC, dorsolateral prefrontal cortex; VFC, ventrolateral prefrontal cortex; MFC, medial prefrontal cortex; M1C, primary motor cortex; S1C, primary somatosensory cortex; IPC, posterior inferior parietal cortex; A1C, primary auditory cortex; STC, posterior superior temporal cortex; ITC, inferior temporal cortex; V1C, primary visual cortex.

Supplemental Table 1. Summary of whole-exome sequencing data

Sample	Clean data (Gb)	Initial bases on target (Mb)	Alignment rate (%)	Base covered on target(Mb)	Fraction of effective bases on target (%)	Average sequencing depth	4× coverage (%)	10× coverage (%)	20× coverage (%)
E1F	3.18	50.34	99.48	49.06	56.60	61.38	96.00	92.40	83.90
E1M	4.24	50.34	99.61	49.07	57.20	84.35	96.40	94.00	88.70
E1P	3.09	50.34	99.51	49.03	57.40	61.77	95.90	92.10	83.50
E2F	2.12	50.34	99.48	48.69	56.20	41.01	93.60	86.00	71.30
E2M	3.72	50.34	99.45	48.68	55.30	63.43	95.20	91.10	82.70
E2P	3.47	50.34	99.49	49.19	55.70	66.51	96.20	93.00	85.30
E3F	3.92	50.34	99.55	48.98	58.00	77.36	95.90	92.70	86.10
E3M	3.43	50.34	99.52	48.94	56.20	65.95	95.70	92.20	84.30
E3P	4.72	50.34	99.58	48.99	56.70	86.45	96.10	93.30	87.80
E4F	3.79	50.34	99.51	48.98	55.90	69.27	96.00	92.70	85.50
E4M	4.30	50.34	99.43	48.77	55.70	72.83	95.60	92.40	85.60
E4P	3.76	50.34	99.42	48.66	55.70	63.76	95.20	91.20	83.00
Mean	3.78	50.34	99.51	48.93	56.38	70.25	95.72	92.15	84.56
SD	0.67	0.00	0.06	0.18	0.79	12.33	0.72	1.93	4.19

Supplemental Table 2. The evaluation of the tolerance of genes with de novo mutation in this study

Trio	Gene	Probability of HI	RVIS	RVIS Percentile	Z score for missense from ExAC
E1	*SNX9*	0.143	-0.13	43.91%	1.31
E2	*RTP1*	0.736	0.06	58.84%	0.76
E3	*DYNC1H1*	0.436	-6.01	4.13%	13.88

Not: HI, haploinsufficiency; RVIS, residual variation intolerance score; Lower RVIS percentiles and higher Z scores correspond to higher constraint

Supplemental Table 3. PCR information for the validation of de novo mutation in this study

Trio	Gene	Mutation	Primers (5'→ 3')	Length(bp)
E1	*SNX9*	c.454C >A, p.Q152K	Forword: CAACTGGGACACTGCCTTCG Reverse: CTTCCCTGTCTCTCCCACTCAG	110
E2	*RTP1*	c.323T>A, p.I108N	Forword: AGTGCACCAAGCGCATTTT Reverse: GGCCCAACCACGGAATCTTA	858
E3	*DYNC1H1*	c.10174A>G, p.M3392V	Forword: TCAGTCACTGGGGCAATGAG Reverse: AAGAGGTCACCTTTCACACGG	279