

**Supplementary Table 1 TUBA4A nonsynonymous variants identified in Chinese ALS patients and controls.**

<b>Genomic coordinate (GRCh37/hg19)</b>	<b>Amino acid change</b>	<b>Variant</b>	<b>Exon</b>	<b>FALS</b>	<b>SALS</b>	<b>Contr ols</b>	<b>dbSNP /novel</b>	<b>ExAC (MAF)</b>	<b>GnomAD (MAF)</b>	<b>PolyPhe n-2</b>	<b>SIFT Score</b>	<b>Mutation Taster</b>
chr2:220116831A>G	p.I42T	c.125T>C	2	0/113	1/610	3/1005	rs201865832	16/121360	49/277204	0.006(B)	0.35(T)	DC
chr2:220115720A>G	p.I234T	c.701T>C	4	0/113	1/610	0/1005	Novel	0	0	0.365(B)	0.01(D)	DC
chr2:220115274C>T	p.A383T	c.1147G>A	4	0/113	1/610	0/1005	rs368743618	1/121398	2/246252	0.915(P)	0.00(D)	DC
chr2:220115243_220115244insG	p.H393Pfs* 19	c.1177_1178insC	4	1/113	0/610	0/1005	Novel	0	0	-	-	DC

Note: ExAC, Exome Aggregation Consortium database; GnomAD, Genome Aggregation Database; MAF, Minor Allele Frequency; B, Benign; P, Probably Damaging; T, Tolerated; D, Deleterious; DC, Disease causing.

**Supplementary Table2: Synonymous variants of TUBA4A gene detected in Chinese ALS patients and controls**

<b>Genomic coordinate (GRCh37/hg19)</b>	<b>Amino acid change</b>	<b>Variant</b>	<b>Exon</b>	<b>FALS</b>	<b>SALS</b>	<b>Control</b>	<b>dbSNP /novel</b>	<b>ExAC (MAF)</b>	<b>GnomAD (MAF)</b>	<b>AASsites Prediction</b>
chr2:220116737 C>T	p.T73T	c.219G>A	2	1/113	0/610	1/1005	rs567717225	14/120748	26/277150	unlikely
chr2:220116407 C>T	p.Q85Q	c.255G>A	3	0/113	1/610	0/1005	rs763842483	1/121122	1/246112	unlikely
chr2:220116338 A>G	p.Y108Y	c.324T>C	3	0/113	4/610	8/1005	rs199579096	27/121364	65/277266	unlikely
chr2:220116010 C>T	p.V137V	c.411G>A	4	0/113	0/610	1/1005	novel	0	0	unlikely
chr2:220115854 C>T	p.L189L	c.567G>A	4	0/113	1/610	0/1005	novel	0	0	unlikely
chr2:220115320 G>A	p.D367D	c.1101C>T	4	0/113	1/610	0/1005	novel	0	0	unlikely