

Supplementary Table S3. Identified associated comorbidity disease genes from two different approaches (word2vec and statistical odds ratio) between NHIRD and DNA methylation primary biomarkers from ALS epigenomic samples; the grey grid indicates genes in the DisGenet database that are annotated as being associated with the diseases (ICD-9-CM).

		ALS	W2V(TOP10)			
<i>Gene name</i>	<i>beta_diff</i>	335	359			
<i>MPZ</i>	-0.058103059					
<i>HOMER1</i>	0.0500659					
<i>MGLL</i>	-0.091682367					
<i>SOD3</i>	-0.052781241					
<i>CACNA1H</i>	-0.051671094					
<i>ERBB4</i>	-0.092216964					
<i>TBCD</i>	0.055823477					
<i>DPYSL2</i>	-0.054262751					
<i>ANGPT1</i>	-0.072167322					
<i>VCL</i>	-0.072211199					
		ALS	OR comorbidity			
<i>Gene name</i>	<i>beta_diff</i>	335	356	354	722	728
<i>MPZ</i>	-0.058103059					
<i>HOMER1</i>	0.0500659					
<i>MGLL</i>	-0.091682367					
<i>SOD3</i>	-0.052781241					
<i>CACNA1H</i>	-0.051671094					
<i>ERBB4</i>	-0.092216964					
<i>TBCD</i>	0.055823477					
<i>DPYSL2</i>	-0.054262751					
<i>ANGPT1</i>	-0.072167322					
<i>RHOBTB2</i>	-0.064946839					
<i>ADAMTS1</i>	-0.064411414					
<i>UNC5D</i>	-0.057662729					