

Supplementary Table S2. Identified associated comorbidity disease genes from two different approaches (word2vec and statistical odds ratio) between MIMIC-IV 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-10-CM).

		ALS	W2V(TOP10)					
<i>Gene name</i>	<i>beta_diff</i>	<i>G12</i>	<i>J38</i>	<i>G23</i>	<i>Q02</i>	<i>G80</i>	<i>Q05</i>	<i>F72</i>
<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>DEAF1</i>	-0.071295549							
<i>ITGAX</i>	-0.051517017							
<i>KIF7</i>	-0.055397657							
<i>SEMA3E</i>	-0.098907746							
<i>SLC6A3</i>	-0.070583327							
<i>BHMT</i>	-0.061916558							
<i>DBT</i>	0.052108121							

		ALS	OR comorbidity				
<i>Gene name</i>	<i>beta_diff</i>	<i>G12</i>	<i>R13</i>	<i>R62</i>	<i>C82</i>	<i>E46</i>	<i>R47</i>
<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>DEAF1</i>	-0.071295549						
<i>ITGAX</i>	-0.051517017						
<i>KIF7</i>	-0.055397657						
<i>SEMA3E</i>	-0.098907746						
<i>SLC6A3</i>	-0.070583327						

<i>ZP3</i>	-0.060435033						
<i>MDN1</i>	0.056886275						
<i>EIF4A3</i>	-0.089896602						
<i>RIPK2</i>	-0.050872126						
<i>C1R</i>	-0.067458677						
<i>SORL1</i>	-0.090807461						