

Table S3. Pairwise phenotype overlap. The significance is measures based on a ataxia sub-network comprising 172 genes. ↓ the observed overlap is less than expected.

	degeneration	abnormal foliation	abnormal vermis	absent cerebellum	small cerebellum
gene count	28	22	12	2	36
abnormal foliation	1↓				
expected	3.581				
<i>p</i> -value	0.090				
abnormal vermis	1↓	8			
expected	1.953	1.535			
<i>p</i> -value	0.387	3×10^{-7}			
absent cerebellum	0↓	1	1		
expected	0.326	0.256	0.140		
<i>p</i> -value	0.700	0.016	0.004		
small cerebellum	7	18	10	1	
expected	5.860	4.605	2.512	0.419	
<i>p</i> -value	0.200	1×10^{-12}	9×10^{-8}	0.043	