

Table S2. Pairwise phenotype overlap. The significance is measures based on a whole genome comprised of 25,000 genes. ↓ the observed overlap is less than expected.

	degeneration	abnormal foliation	abnormal vermis	absent cerebellum	small cerebellum	ataxia
gene count	39	56	24	10	70	172
abnormal foliation	1					
expected	0.087					
<i>p</i> -value	0.003					
abnormal vermis	2	11				
expected	0.037	0.054				
<i>p</i> -value	7×10^{-6}	2×10^{-11}				
absent cerebellum	0 [↓]	2	3			
expected	0.016	0.022	0.010			
<i>p</i> -value	0.985	1×10^{-6}	2×10^{-10}			
small cerebellum	8	37	13	2		
expected	0.109	0.157	0.067	0.028		
<i>p</i> -value	$<10^{-12}$	2×10^{-12}	4×10^{-11}	2×10^{-6}		
ataxia	28	22	12	2	36	
expected	0.268	0.385	0.165	0.069	0.482	
<i>p</i> -value	$<10^{-12}$	2×10^{-11}	5×10^{-11}	4×10^{-5}	4×10^{-11}	