Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease

Do, Tung, Dorfman, Kiefer, Drabant, Francke, Mountain, Goldman, Tanner, Langston, Wojcicki, Eriksson

Internal

1	**0.024**			
10	**0.000**	**0.000**		
100	**0.000**	**0.000**	**0.026**	
1000	**0.001**	**0.004**	0.075	0.308
	0.05	1	10	100

External

1	**0.025**			
10	**0.009**	0.120		
100	**0.022**	0.179	0.452	
1000	**0.010**	0.081	0.205	0.182
	0.05	1	10	100

Table S3. Internal and external cross-validation AUC difference test for sparse logistic regression models. Rows and columns of each table correspond to models being compared, and are labeled using the theoretical upper bound on $E[FP]$ of the model for that particular row or column. Elements of the tables are one-sided p-value tests for the alternative hypothesis that the row model has a higher AUC than the column model. One-sided comparisons significant at the 0.05 level are indicated in bold.