

	<b>± 0Kb</b>	<b>± 20Kb</b>	<b>± 50Kb</b>
Coverage of genic regions	36.1%	49.2%	58.9%
Estimated $h_{G_g}^2$	0.0637	0.0889	0.0996
SE	0.0060	0.0066	0.0069
Estimated $h_{G_i}^2$	0.0655	0.0445	0.0341
SE	0.0068	0.0059	0.0052
Expected $h_{G_g}^2$	0.047	0.066	0.079
Expected $h_{G_i}^2$	0.083	0.068	0.055
Goodness of fit test p-value	1.6E-04	1.3E-07	5.4E-07

Note: The SE of averaged estimate was calculated as  $SE = \frac{1}{t} \sqrt{\sum_{i=1} S_i^2}$ , where  $S_i$  is the standard error of the estimate for each trait and  $t$  is the effective number of independent traits with  $t = 34.0$ , which was calculated by matrix spectral decomposition of the phenotypic correlation matrix [1].

## Reference

1. Li J, Ji L (2005) Adjusting multiple testing in multilocus analyses using the eigenvalues of a correlation matrix. *Heredity* (Edinb) 95: 221-227.