

**Table S4** Type I error rate (and standard error) estimated from 250 simulations at genome-wide significance level 0.05. Five methods All, MBP, Indv, Seq and  $BIC_{\delta}$  were implemented for each of the five correlations between two traits.

Method	Correlation $\rho$				
	-0.9	-0.6	0	0.6	0.9
All	0.044 (0.013)	0.056 (0.015)	0.056 (0.015)	0.040 (0.012)	0.068 (0.016)
MBP	0.048 (0.014)	0.088 (0.018)	0.080 (0.017)	0.060 (0.015)	0.072 (0.016)
Indv	0.036 (0.012)	0.052 (0.014)	0.052 (0.014)	0.032 (0.011)	0.036 (0.012)
Seq	0.076 (0.017)	0.040 (0.012)	0.020 (0.009)	0.032 (0.011)	0.084 (0.018)
$BIC_{\delta}$	0.024 (0.010)	0.072 (0.016)	0.064 (0.015)	0.048 (0.014)	0.028 (0.010)