

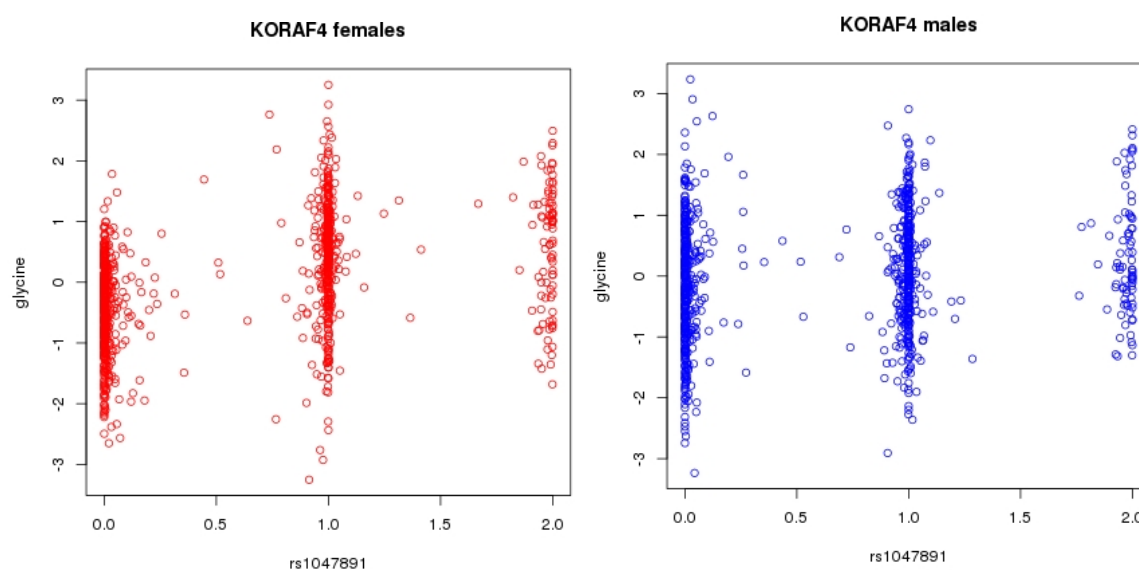
## Supplementary material 8: Sex-specific genome-wide association study

This supplementary text contains detailed statistics and plots for the genome-wide significant hit.

### Genome-wide significant differences

Metabolite	SNP	chr	pos	info	MAF (f/m)	females			males			p-val $\beta$ diff	count (f/m)
						$\beta$	SE	p-val	$\beta$	SE	p-val		
glycine	rs1047891	2	211540507	0.95	0.32/0.32	0.09	0.006	1.8E-45	0.03	0.005	1.3E-06	7.2E-14	872/823
glycine	rs715	2	211543055	1.00	0.31/0.31	0.08	0.006	1.6E-43	0.02	0.005	3.7E-06	1.5E-13	872/823

**Explanations:** chr = chromosome, pos = chromosomal position, info = imputation quality, MAF = major allele frequency,  $\beta$  = effect size from additive genetic model, SE = standard error



**Figure:** Associations between glycine and rs1047891 stratified by females and males. Note that genotypes on the x-axis can have non-integer values due to the imputation process.