

**Supp. Table 1.** Number of identified genome-wide significant loci.

Trait	20 kb						100 kb			
	G	S	SP	B*	V**	L	G	S	SP	L
PR	2	2	2	2	2	1	2	2	2	1
QRS	1	0	0	0	0	0	1	0	0	1
QT	3	2	2	3	2	1	3	2	2	1

Results are reported for 20 kb and 100 kb flanking transcription boundaries. G: GWIS, S: minSNP, SP: minSNP-P, B: BIMBAM, V: VEGAS, L: LASSO. \*BIMBAM was only tested for 20 kb. \*\*VEGAS is hard-coded to use  $\pm 50$  kb.