



Figure S7 Hotspot size significance profile derived with the *NL*-method for simulated example 2. For each genomic location (i.e., x-axis position) this figure shows the hotspot sizes at which the hotspot was significant, that is, at which the hotspot locus had more traits mapping to it with a LOD score higher than the threshold on the right, than expected by chance. The scale in the left shows the range of spurious hotspot sizes investigated by our approach. The scale in the right shows the respective LOD thresholds associated with the spurious hotspot sizes in the left. The range is from 7.66, the conservative empirical LOD threshold associated with a spurious “hotspot of size 1”, to 3.65, the single trait empirical threshold, associated with a spurious hotspot of size 19. All permutation thresholds were computed targeting $\text{GWER} \leq 0.05$, for $n = 1, \dots, 19$. Note that this figure does not show the actual size of the hotspots. For instance, at the single trait LOD threshold of 3.65 this plot indicates that more traits mapped to the middle regions of chromosomes 5, 7 and 15 than what would be expected by chance (19 traits), but do not show the actual hotspot sizes (50, 464 and 220, respectively, as depicted in Figure 4a).