

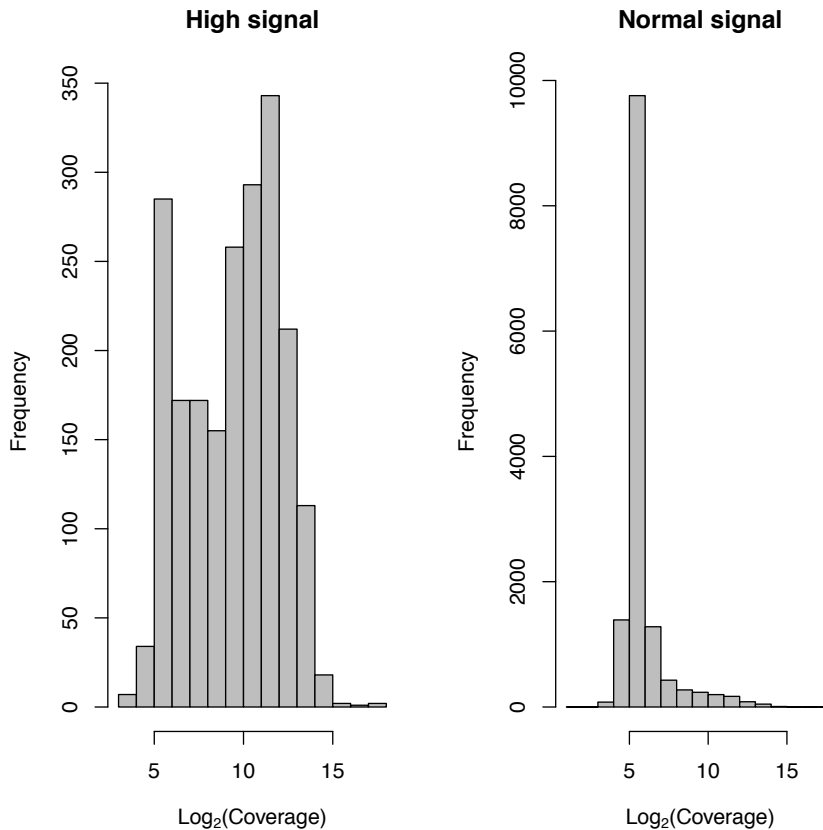


Fig. S2. Genome sequencing coverage for genes with normal and high aCGH signal intensities .

Coverage in the *Littorina* genome sequencing was calculated for 2,067 genome contigs identified by aCGH as multiple-copy ("High signal") and for 13,956 contig identified by aCGH as single-copy ("Normal signal"). Coverage is given at log₂ scale, i.e. 5 corresponds to x32, 10 to x1024 and 15 to x32,768 times coverage. Median coverage for single-copy genes was x50 (5.64 at log₂ scale). For multiple-copy genes it was x880 (9.8 at log₂ scale, or 18 copies). Expected genome sequencing coverage was x67.