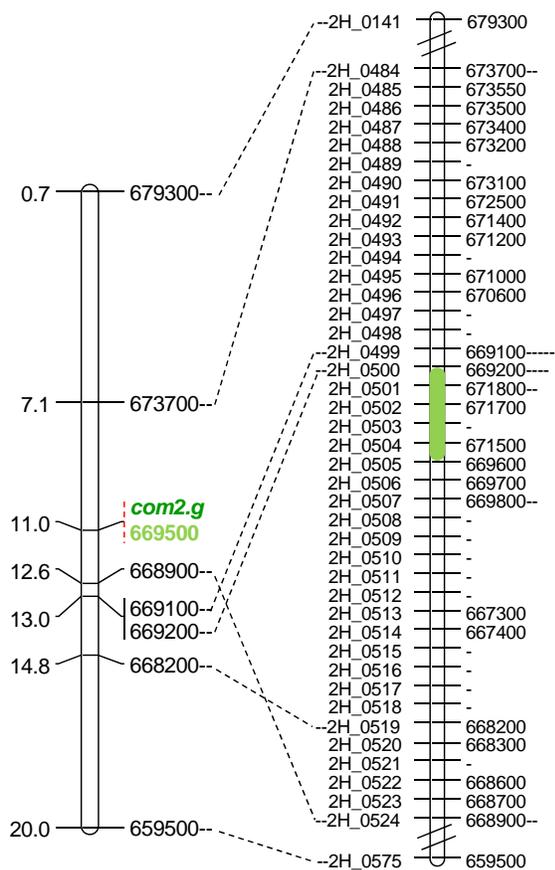


A. Barley; low resolution genetic map



B. Wheat; low resolution genetic map

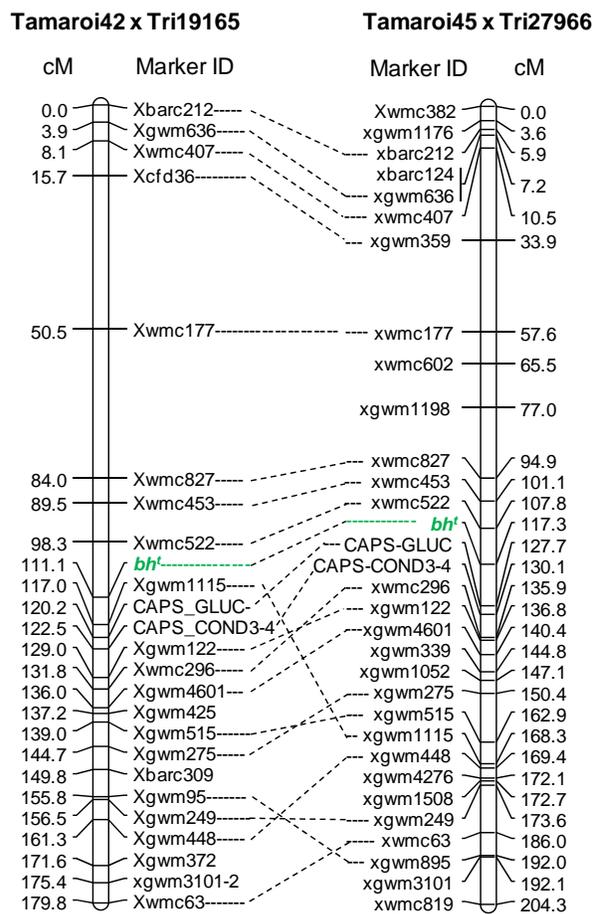


Figure S2 Low resolution linkage map of *com2.g* and *bh^t* locus in barley and tetraploid wheat. (A) Genetic linkage mapping of *com2.g* in barley. The genome zipper (GZ) model of barley chromosome 2H was considered as resource for marker development. Predicted order of rice genes along this barley chromosome is shown, all gene identifiers start originally with Os07g0. The virtual position for candidate gene ortholog (*Os07g0669500*) was not initially provided; a position (green area) was assumed for the *Os07g0669500* gene according to the gene identifier. Barley BW 192 (*com2.g*) and barley cv. Haruna Nijo were used as mutant and the wild type parents of the population, respectively. **(B)** Genetic linkage mapping of the *branched head^t* (*bh^t*) locus in two different tetraploid wheat F₂ mapping populations. Connected markers represent those used in both populations. cM stands for centiMorgan. Tetraploid wheat Tamaroi45 and Tamaroi42 were used as wild type while TRI 19165 and TRI 27966 were mutant parents of the corresponding population.