Supporting Information Legends

Figure S1. Dosage optimization curve for the development of CS-WGRH panel: For each radiation dose, a set of 10 spikes (~260 spikelets) from Altar (tetraploid wheat) were emasculated and pollinated with pollen from irradiated Chinese Spring spikes. Survival of the RH_1 was measured by successful germination. No viable seed was recovered with pollen radiation treatments above 15-Gy.

Figure S2. Development of CS-WGRH panel: Dehiscing spikes of the hexaploid wheat Chinese Spring were γ-irradiated with 15-Gy and used to pollinate previously emasculated spikes of the tetraploid wheat Altar 84. As pollen was completely mature at time of radiation treatment, each F_1 seed represents a unique RH event.

Figure S3. Distribution of RH lines among different marker retention bins: Blue bars represent distribution of the lines based on 27 SSR markers used to characterize the RH panel (115 lines) where black bars present distribution of lines based on all polymorphic SNP markers (38,404).

Figure S4. Number of markers mapped on D- genome chromosomes in recombination and WGRH maps: Comparison of marker numbers mapped on D- genome chromosomes in eight double-haploid mapping populations (Wang et al. 2014) and CS-WGRH panel (RH bins)

Supporting Table S1: Comparative mapping of chromosome arm 3BL.