



Additional file 9. Pattern of linkage disequilibrium (LD) decay calculated genome-wide (black-dashed line) and for each chromosome separately (colored lines) in a MAGIC population of common bean. The pairwise measures of LD were calculated in sliding windows of 100 markers and corrected for kinship relationships in the population (r_v^2). Each line corresponds to a locally estimated scatterplot smoothing (LOESS) regression on the LD measures.