

Figure S2. Population structure and linkage disequilibrium analyses of the fiber flax and linseed groups (Portable Document Format file). (a) Bayesian clustering analysis (STRUCTURE K = 2) of fiber flax and linseed. (b) *ad-hoc* statistic ΔK [62] for K values ranging from 1 to 4. (c) Average genome-wide LD decay (r^2) against genetic distance (cM) within fiber and linseed flax groups. The black line represents the decay curve at the genome level of the two flax groups.