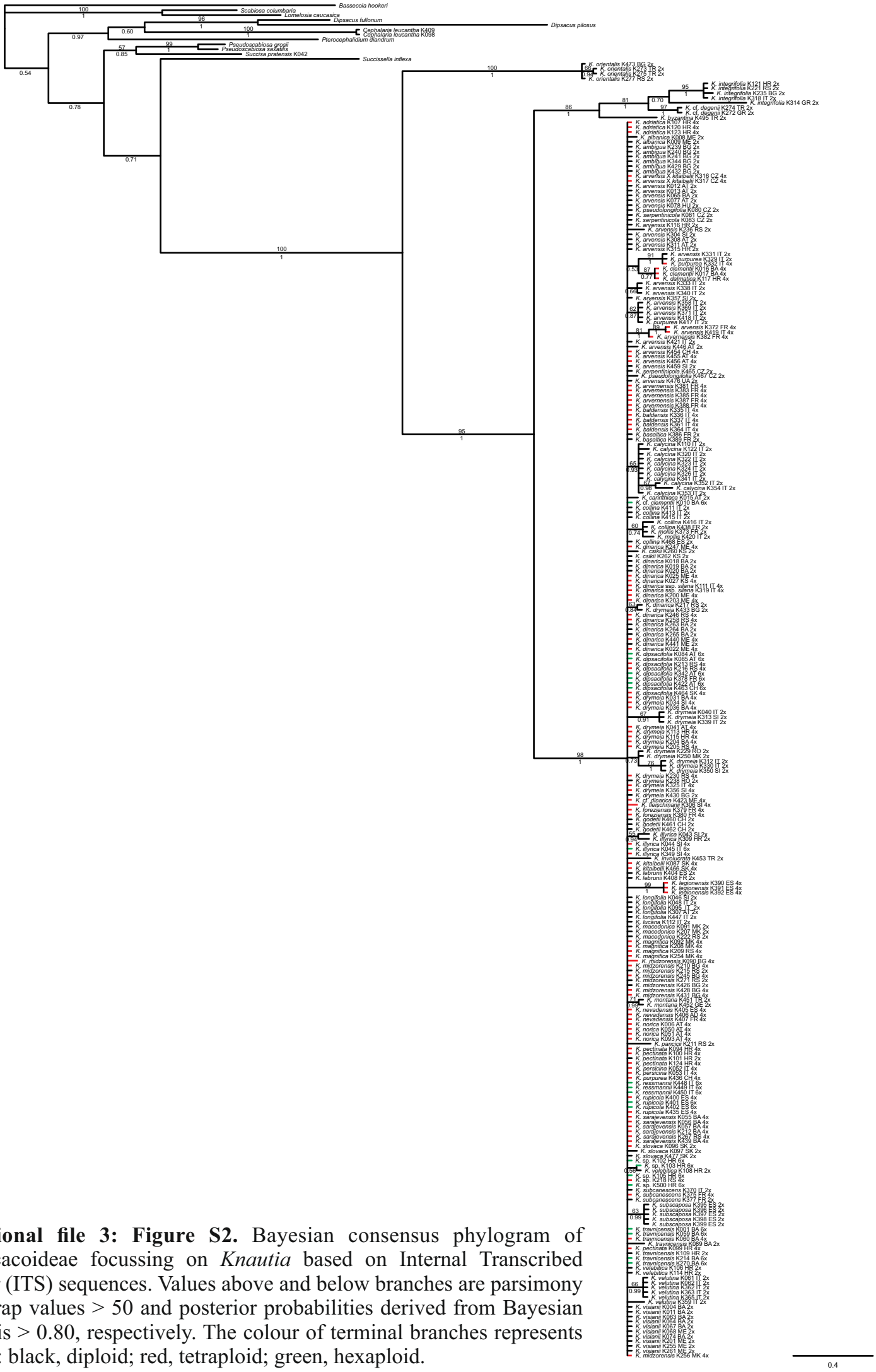

Additional file 3: Figure S2. Bayesian consensus phylogram of Dipsacacoideae focussing on *Knautia* based on Internal Transcribed Spacer (ITS) sequences. Values above and below branches are parsimony bootstrap values > 50 and posterior probabilities derived from Bayesian analysis > 0.80, respectively. The colour of terminal branches represents ploidy: black, diploid; red, tetraploid; green, hexaploid.