**Table S3** Hierarchical analysis of genetic variance among *P. tremuloides* SNPs within genetic clusters (*F*clust/total), within subpopulations by cluster (*F*pop/clust), and within individual trees relative to populations (*F*ind/pop) and the total variance (*F*ind/total). Ranges given in parentheses are 95% confidence intervals.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | ***F*clust/total** | ***F*pop/clust** | ***F*pop/total** | ***F*ind/total** |
| **Overall** | 0.092 (CIs: 0.090–0.094) | 0.089 (CIs: 0.088–0.091) | 0.173 (CIs: 0.170–0.176) | 0.326 (CIs: 0.319–0.333) |

Results are shown for hierarchical *F*-statistics (Yang 1998) as computed in hierfstat (Goudet 2005) based on 100 bootstrap pseudoreplicates.