**Table S3** Statistics of the markers used in the phylogenetic analysis of 50 species of Annona. For each marker, the number of species with information, the number of characters aligned in base pairs (bp), the percentage of conserved characters and the evolutionary substitution model are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | *rbc*L | *trn*L | *mat*K | *Ndh*f | *psb*A-*trn*H |
| Number of species | 47 | 36 | 33 | 19 | 26 |
| Alignment length (sc) | 470 | 232 | 880 | 445 | 172 |
| Preserved characters (%) | 91.1 | 75.9 | 84 | 84.3 | 65.1 |
| Substitution model | K80+I | HKY+I | TPM1uF+G | HKY+I | HKY+G |