**Supplemental Material**

**Figure S1** Pedigree network of the pear cultivars a) ‘Roi Charles de Wurttemberg’; b) ‘Clapp Favorite’; c) ‘Kieffer’; d) Coscia (note that ‘Coscia Tardive’ and ‘Coscia’ are swapped at the NCGR); e) ‘Nijisseiki’; and f) ‘Hau Kai’. A species-based colour-coding is used, as shown in the legends

**Table S1** Sample list. For each sample genotyped, this table reports accession ID, best array (generated at Affymetrix and composed by the plate barcode and well), sample name, heterozygosity rate, samples status (if it failed or passed genotyping), failure mode if applicable (where QC CR = Quality Control Call Rate, and dQC = dish QC), taxon, plant name, origin, group (according to Table 2), ploidy, genotyping panel, notes and/or known pedigree as from the NCGR website (<https://www.ars.usda.gov/ARSUserFiles/20721500/catalogs/pyrcult.html>)

**Table S2** Duplicated samples. For each sample that was identical to at least another sample, this table reports accession ID, sample name, best array (generated at Affymetrix and composed by the plate barcode and well), taxon, plant name, duplicate group number, and relative notes

**Table S3** Inferred parentage of each accessions. For each unique genotype, this table reports accession ID, sample name, taxon, plant name, estimated year of origin, inferred parent 1 and 2 (sample name and plant name), relative reference for estimated origin and known parentage, and relative notes

**Table S4** Subpopulation memberships and proposed re-classification. For each unique genotype, this table reports accession ID, sample name, taxon, plant name, eigenvalues (EV) for principal components 1 through 4, subpopulation as from principal component analysis, subpopulation as from structure analysis at K = 2, subpopulations as from hierarchical structure analysis, subpopulation as from discriminant analysis of principal components (only for the Occidental group), and proposed taxon

**Files S1-S5** Input files for interactive pedigree visualization in Helium. File S1 is the pedigree file for all accessions; File S2 is the pedigree file only for the Occidental accessions, and File S3 the relative species file for colour-coding; File S4 is the pedigree file only for the Oriental accessions, and File S5 the relative species file for colour-coding