



**Supplementary Information for**

The genomes of ancient date palms germinated from 2,000-year-old seeds

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SI References

**Other supplementary materials for this manuscript include the following:**

Datasets S1 and S2

## Supplementary Information Text

**Sampling.** The seven ancient Judean date palm accessions originate from the germination of ancient date palm seeds collected during archaeological excavations of three sites in the Judean desert (1, 2). The seeds and seed shell fragments collected in the potting soil after germination were radiocarbon dated with ages ranging from the 4<sup>th</sup> century BCE to the 2<sup>nd</sup> century CE (Table 1). Full explanation on the provenance of the seeds, the germinating protocol and the radiocarbon dating may be found in Sallon *et al.* 2020, 2008 (1, 2). The genomes of the ancient Judean date palms were compared to whole genome re-sequencing data of 110 contemporary *Phoenix dactylifera* and other wild *Phoenix* species that we have previously published [Table S1] (3–5). Were included: 18 *P. theophrasti*, 8 *P. sylvestris*, 3 *P. atlantica*, 6 *P. canariensis*, 1 *P. reclinata*. We note that *P. atlantica* likely represents feral date palms rather than a distinct species (6).

**Library preparation and genome re-sequencing.** Genomic DNA was extracted from leaf tissue as explained in Sallon *et al.* 2020 (2). Libraries (2 x 100 paired-end) were constructed with Nextera library preparation protocols and sequenced on an Illumina HiSeq 2500 system according to the manufacturer's protocols.

**Read processing and genome alignment.** Reads were demultiplexed and those passing Illumina quality control filters were processed with Trimmomatic (7) v. 0.39 to remove contaminating adapter sequences. For adapter removal, we used the adapter and Nextera transposase sequence database included with Trimmomatic (v. 0.39) downloaded with the following setting ILLUMINACLIP:<adapter library>:2:30:10 and only reads pairs where both reads in a pair were 76 bp or longer following trimming were retained for subsequent steps.

We aligned reads to the reference genome from Hazzouri *et al.* 2019 (8). This genome is a PacBio/Illumina genome assembly from a male date palm from a fourth-generation backcross (BC4) with a female of the Barhee cultivar. Its size is ~772 Mb and it contains 18 primary contigs (49.9% of total length) along with 2,371 unplaced contigs. The nuclear and chloroplast genomes were combined to form a single modified reference sequence that was used in all subsequent steps.

Processed reads were aligned to this unmasked genome using bwa mem (9) v. 0.7.15-r1140. The bwa mem aligner was run with the -M option to mark supplementary reads (0x800 bitwise flag) as secondary (0x100). Sample alignments were processed with SamSort from Picard-tools (10) v. 2.8.2 to coordinate-sort the alignments. We used MarkDuplicates (Picard-tools) to flag duplicate read pairs. Processed alignments were summarized with samtools v. 1.9 (11) using the stats option.

**Variant calling and SNP filtering.** SNP-calling and genotyping was performed with the GATK v. 3.5-0-g36282e4 HaplotypeCaller (12) run in GVCF mode followed by joint-genotyping with GenotypeGVCFs. Reads were filtered from the HaplotypeCaller step to exclude those with a mapping quality <10 and to exclude those marked as secondary alignments. This approach yielded 47,035,054 variants across all 117 samples.

These variants were filtered using GATK v4.0.2.1. We restricted analysis to the non-repetitive fraction of the genome assembly by excluding SNPs in repetitive regions identified during the annotation of the genome assembly (8). Additional SNP filtering was conducted by applying hard filters to the raw variants. We excluded multi-allelic SNPs and SNPs within 6 bps of indel polymorphisms. For further filtering, thresholds were determined following Flowers *et al.* 2019 (4) from which most of our data come from. Flowers *et al.* 2019 (4) determined thresholds by considering GATK guidelines, considering the impact of thresholds on the transition:transversion ratio (13), and drawing on approaches of comparable re-sequencing studies of non-model organisms and their relatives. We tailored our filtering thresholds by filtering the raw call set to exclude SNPs with low (<585) and high depth (>2400) summed across samples. We also excluded SNPs meeting the following conditions: FS > 60.0, SOR > 3.0, QD < 8.0, MQ < 40.0, MQRankSum < - 3.0, ReadPosRankSum < -1.5, BaseQRankSum < -8.0. We filtered out genotypes having GQ < 20.0 and SNPs with a genotype call rate < 85%. This procedure yielded a filtered call set of 5,332,805 SNPs that served as the basis for subsequent analyses. Statistical analyses were conducted with the R Statistical Programming Language (14).

**Identifying DNA lesions associated with prolonged period of seed storage.** In order to identify whether some types of mutations are more prevalent in the ancient Judean date palms compared to the modern varieties, we profiled the mutation pattern of each singleton, where singletons are defined as alleles found at frequency of  $1/2N$ , where N is the sum of all date palm and wild relative samples. Using a custom Perl script, we identified singleton mutations in each accession, computed the number in each substitution class (G-to-C, A-to-C, etc.), and normalized it by the total number of singletons observed in the accession, in order to account for variation in diversity among accessions. We checked for normality within each group (modern and ancient) and for each of the six mutation classes using the *normality* function from the R package *dlookr*. Since some distributions are not normal, we used Wilcoxon rank sum tests to examine whether there is a significant difference among ancient germinated and present-day genomes in each of the six mutation type fractions (*wilcox.test* function in R).

We also examined small indels, as they could have been inserted during strand break repair at the onset of the germination process (15). We used a custom Perl script to identify, from the raw indel call set (5,341,932 indels called in all 117 *Phoenix* accessions), the singleton indels (i.e. mutations found in only one accession at a frequency  $1/2N$ , where N is the sum of all date palm and wild relative samples). We restricted our analysis to indels having the following features: QUAL  $\geq$  30, DP  $\geq$  5 and maximum missing data of 15%, and to indels found in the date palm accessions, that is a total of 99,567 indels. We tested whether there is a significant difference in small indel numbers using a multivariate Wilcoxon test implemented in the *mWilcoxonTest* function from the R package *DepthProc* v.2.1.3 (<https://www.rdocumentation.org/packages/DepthProc>).

**Population clustering and relatedness among samples.** Global patterns of individual ancestry and population structure were examined using maximum-likelihood-based clustering and principal component analysis (PCA). We estimated individual

ancestries on (i) all accessions, and (ii) date palms and *P. theophrasti* only using ADMIXTURE (16) v. 1.3.0. We used 53,845 randomly sampled SNPs and default parameters. The optimization method was a block relaxation algorithm and the termination criterion was to stop when the log-likelihood increases by less than  $\epsilon = 10^{-4}$  between iterations. We ran the PCA on date palms and *P. theophrasti* accessions using genotype calls with the PCAdapt (17–19) *R* package v. 4.3.3, using a subset of randomly sampled SNPs and further filtered out SNPs with minor allele frequencies below 5%, resulting in 24,689 SNPs.

We generated maximum-likelihood trees of *Phoenix* spp. accessions using RAXML-NG (20) v. 0.9.0 and a randomly downsampled SNP set including 1% of our full SNP set (53,845 SNPs). The VCF file was converted in PHYLIP format using the python script `vcf2phylip.py` (21). The command `raxml-ng -parse` was run to compress the PHYLIP format file into the binary format used by RAXML-NG. We then performed 20 maximum-likelihood tree searches using 10 random and 10 parsimony-based starting trees. The log likelihood of the 20 tree searches ranged between -1,909,270.82 and -1,908,426.36, and thus had low variability indicating that all runs converge toward the same likelihood maxima despite different starting trees. We picked the best-scoring topology and checked the robustness of the tree by performing 100 bootstrap replicates using the same software. We rooted the tree with *P. reclinata* and made the plot using the *R* package `treeio` (22). We repeated a similar tree inference after exclusion of the North African date palms from the alignment, leading to an alignment containing 97.79% of informative sites. As before, the log likelihood varies only slightly across the 20 searches, from -1,423,671.29 to 1,423,389.26 and we picked the best-scoring topology and performed bootstrap analysis with 100 replicates.

**Individual and population statistics.** We calculated for each date palm and *P. theophrasti* accession the level of heterozygosity using VCFtools v 0.1.14 (23) in non-overlapping sliding windows of 5 kb. We calculated the mean for each accession across each window and reported for each population the mean  $\pm$  standard error. We tested whether there was significant difference in heterozygosity among populations with Wilcoxon rank sum tests using `wilcox.test` function in *R* (14), after finding that distributions within each population are not normally distributed (using `shapiro.test` function).

Further, the level of polymorphism was calculated in each population or species using a custom perl script calculating the number of polymorphic sites in each group. We then identified private polymorphisms using a custom perl script that count each SNP segregating for an allele (“private allele”) that is restricted in its distribution to a particular focal population or species in our analysis. For this analysis, we removed admixed samples, as identified using the ADMIXTURE analysis, namely PDAC64, PTHE2, PTHE3, PTHE4, PTHE26, PTHE27, PSYL7 and PSYL44. We further identified private fixations as alleles observed at 100% frequency in the focal population or species, but not observed in the non-focal set.

**Admixture tests and ancestry proportions.** We tested for the presence and extent of admixture between *Phoenix* populations/species using the *R* package `admixr` (24) v.0.9.1.9000, which provides an implementation of ADMIXTOOLS (25). We used a

script available online to generate the input in EIGENSTRAT format from our VCF (<https://github.com/joanam/scripts/blob/master/convertVCFtoEigenstrat.sh>). We ran the tool using the full SNP set after filtering out regions associated with sex determination (see above). We focused on determining whether the Judean date palms show evidence of gene flow with *P. theophrasti* as evidenced in North African cultivars (4), or with *P. sylvestris*. Computing the below admixture statistics require the understanding of the relationships between populations and species. This phylogenetic tree shows that *P. theophrasti* is sister to the date palm (Fig. S6a), rather than *P. sylvestris* as previously reported (4). Nonetheless, we believe this pattern is driven by North African date palms being introgressed by *P. theophrasti*. To test this hypothesis, we generated a phylogenetic tree after excluding the North African samples. The resulting tree (Fig. S6b) shows that *P. theophrasti* is indeed an outgroup to both *P. dactylifera* and *P. sylvestris* in agreement with our previous report (4).

We calculated Patterson's  $D$  (25, 26) also known as the ABBA-BABA test. The implementation of the test in *admixr* requires a rooted and asymmetric four population tree in the form  $((W, X), Y), Z$ , where  $Z$  is an outgroup to a clade formed by  $W, X$  and  $Y$ , and  $Y$  is an outgroup to a clade formed by  $W$  and  $X$ . The test is used to evaluate if the data is inconsistent with the null hypothesis that the tree is correct and that there is no gene flow between  $Y$  and either  $W$  or  $X$ . It is based on comparing the proportions of BABA and ABBA sites patterns observed in the data.  $D$  is calculated as follow:  $D = (nBABA - nABBA) / (nBABA + nABBA)$ . We also calculated the  $f_4$ -statistic, which is very similar to  $D$  except that the denominator is the total number of sites (25). Gene flow between populations  $W$  and  $Y$  leads to an increase of shared alleles between populations resulting in an elevated number of BABA sites and thus a positive  $D$ -statistic and a positive  $f_4$ -statistic. Here, we tested for gene flow between both North African and Judean date palms individually (test sample) and two wild relative species, namely *P. theophrasti* and *P. sylvestris*. We conducted the tests separately including either *P. reclinata* or *P. canariensis* as the outgroup, following our tree reconstruction (Fig. S6b). We therefore estimated the  $D$ -statistics using the following tree:  $(((\text{test sample}, \text{West Asian date palms}), P. theophrasti \text{ or } P. sylvestris), P. reclinata \text{ or } P. canariensis)$ . We used all samples together for each population/species and after removing admixed samples, as identified using the ADMIXTURE analysis (PDAC64, PTHE2, PTHE3, PTHE4, PTHE26, PTHE27, PSYL7 and PSYL44). Significance was tested with block jackknife with each linkage groups and unplaced contigs treated as a separate block. The standard error of the statistics was used to calculate a standard score ( $Z$ -score = statistics / standard error), and we used an absolute  $Z$ -score  $>2$  to assess statistically significant results.

The  $f_3$ -statistic, also known as the three-population statistic, was used to test whether sample  $C$  is a mixture of two populations  $A$  and  $B$  (25). It measures the covariance of the difference in allele frequencies between populations  $C$  and  $A$  and populations  $C$  and  $B$  across genomic loci. If  $f_3$  is negative,  $C$  may be admixed between  $A$  and  $B$ ; a positive  $f_3$  is uninformative. Here, we tested whether each individual sample from the ancient Judean and the North African populations are a mixture of West Asian date palms and *P. theophrasti* i.e. we estimated the  $f_3$ -statistics as  $f_3(\text{test sample}; \text{West Asian date palms}; P. theophrasti)$ . We used all samples together for these two populations and after removing admixed samples, as identified using the ADMIXTURE analysis (PDAC64, PTHE2, PTHE3, PTHE4, PTHE 26 and PTHE27). Significance was

tested with block jackknife with each linkage groups and unplaced contigs treated as a separate block. The standard error of the statistics was used to calculate a standard score (Z-score = statistics / standard error), and we used an absolute Z-score >2 to assess statistically significant results.

To infer the proportion of ancestry in the North African and ancient Judean date palms from West Asian date palms and *P. theophrasti*, we calculated the  $f_4$ -ratio statistics, as described in Patterson *et al.* 2012 (25). More precisely, we defined the following tree (((A,B), C), O). The  $f_4$ -ratio is  $f_4(A,O;X,C)/f_4(A,O;B,C)$ , where X is the test sample, A is a sister species, namely *P. sylvestris*, B and C are the mixing populations, namely West Asian date palms and *P. theophrasti*, respectively, and O is the outgroup, that is *P. reclinata* or *P. canariensis*. We used all samples together for each population/species and after removing admixed samples, as identified using the ADMIXTURE analysis (PDAC64, PTHE2, PTHE3, PTHE4, PTHE26, PTHE27, PSYL7 and PSYL44). The resulting alpha value corresponds to the ancestry proportion of B in X, and by extension 1-alpha provides the proportion of C in X, therefore the proportion of *P. theophrasti* in the test sample X. Negative values are uninformative. Significance was tested with block jackknife with each linkage groups and unplaced contigs treated as a separate block. The standard error of the statistics was used to calculate a standard score (Z-score = statistics / standard error), and we used an absolute Z-score >2 to assess statistically significant results. We tested whether the most ancient Judean date palms show a different *P. theophrasti* introgression fraction than the most recent ones with a Wilcoxon rank sum test using the *wilcox.test* function.

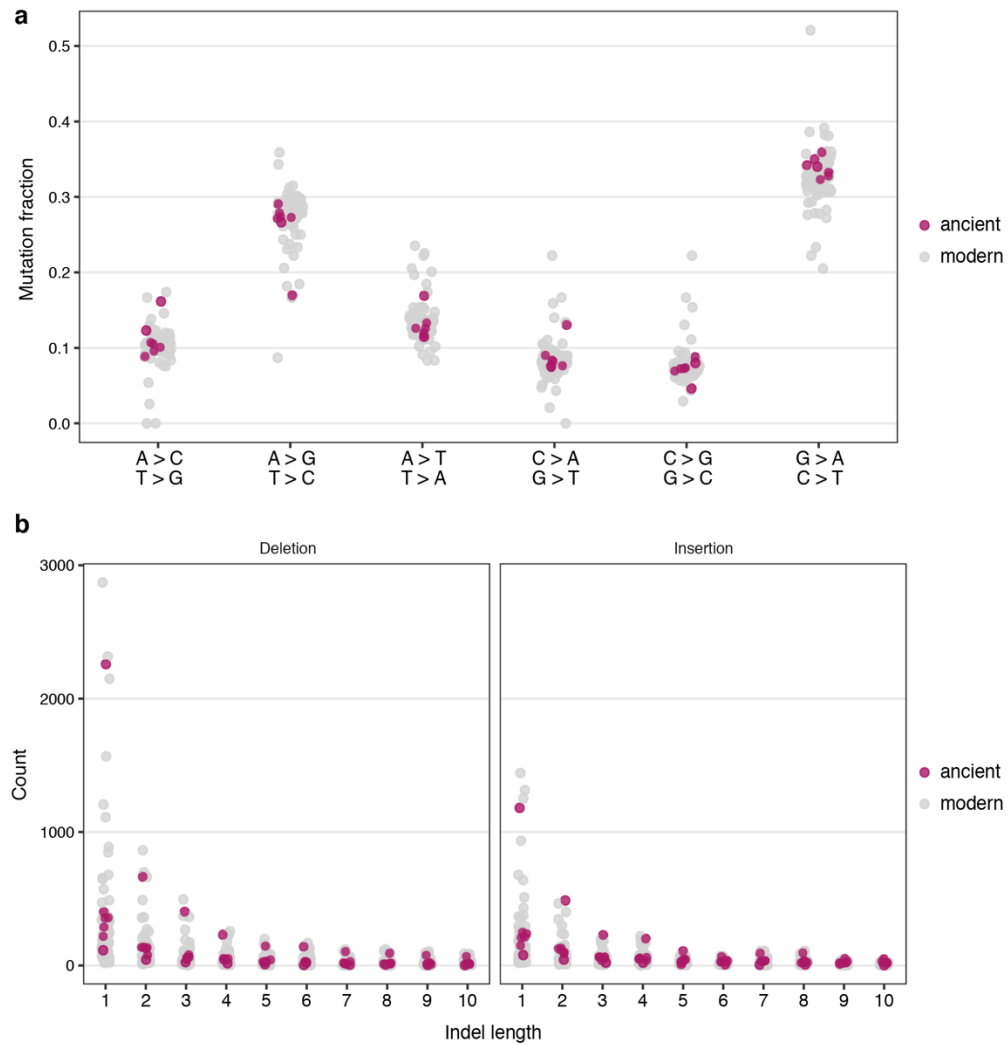
**Chromosome painting and introgression tract lengths.** We performed local ancestry estimation *aka* chromosome painting with the software RFMix (27) v2.03-r0, restricting our analysis to the non-admixed samples and to the 18 linkage groups (see above). We first phased the VCF with Beagle (28) v. 4.1 using the genotype field (*gt* option). We then ran RFMix using default parameters and with query samples being the Judean and North African date palms while the reference samples were West Asian date palms and *P. theophrasti*. In the absence of a genetic map, we assumed that 1cM=1Mb. We then identified all the *P. theophrasti* tracts in the query genomes along with their length. Statistical tests to compare Judean and North African date palms were performed using either Student's tests (*t.test* in R) if data were normally distributed (as evidenced by Anderson-Darling tests for normality, *ad.test*) or Wilcoxon rank sum tests (*wilcox.test* in R).

**Genotyping of the fruit color and sugar composition loci.** We genotyped the Judean date palms at key loci involved in fruit color and sugar content identified by Hazzouri *et al.* 2015 and 2019 (3, 8). Fruit color varies between yellow and red at khalal stage and has been mapped to the *VIRESCENS* locus identified on linkage group 4 (3, 8). Three alleles have been proposed (8): *VIR*<sup>+</sup> (wild type allele), *VIR*<sup>IM</sup>, *VIR*<sup>IM</sup> and *vir*<sup>saf</sup>. The *VIR*<sup>IM</sup> allele has a retrotransposon inserted in the third exon which introduces a premature stop codon at position 169 of the translated protein (3). Our reference genome assembly contains this retrotransposon and to genotype this allele we manually examined reads that map to the breakpoint between exon 3 and the retrotransposon. Samples that do not have the insertion show clipped reads at the flanking regions of the retrotransposon. Mapped

reads from alleles with the retrotransposon insertion span the junction while non-insertion alleles have soft-clipped reads at the breakpoint in either some (heterozygotes) or all junction-spanning reads (homozygotes). All genotypes were confirmed to have matching patterns at both 5' and 3' ends of the insertion. Finally, the *vir<sup>saf</sup>* allele is defined by a SNP at position 24,051,180 which modifies the predicted translation initiation codon of *VIR* from ATG to ATA, likely resulting in a loss-of-function allele (8).

Sugar composition is a major agronomic trait in date palm and varieties are classified as reducing-sugar type (defined by high concentrations of glucose and fructose) or sucrose (high concentration of sucrose) (29). This phenotype is associated with a deletion that spans ~40 kb at approximately 2.467 to 2.507 Mb of linkage group 14, a region with multiple invertase genes (8). To genotype this locus, we identified, in each Judean date palm, whether they have a homozygote deletion in the region as evidenced by an absence of mapped reads (our genome assembly does not have the deletion).

## Supplementary Information Figures

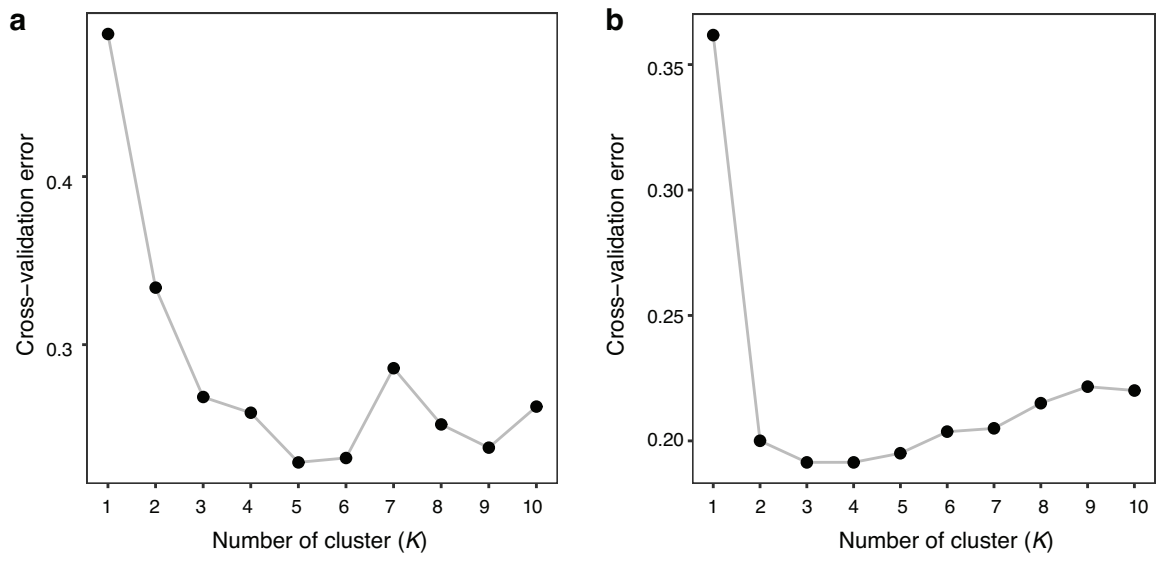


**Figure S1. Singleton mutational profile in modern and ancient Judean date palms.** a, Singleton substitution profile where the fraction of each mutation type is calculated as the mutation type count over the total number of mutations in each accession. No differences between ancient and modern samples were found using Wilcoxon rank sum tests: A>C/T>G:  $W = 243.5$ ,  $P = 0.80$ ; A>G/T>C:  $W = 345$ ,  $P = 0.15$ ; A>T/T>A:  $W = 325$ ,  $P = 0.27$ ; C>A/G>T:  $W = 276.5$ ,  $P = 0.78$ ; C>G/G>C:  $W = 255$ ,  $P = 0.95$ ; G>A/C>T:  $W = 155$ ,  $P = 0.082$ ; b, Singleton indel counts in each accession for length comprised between 1 and 10bp.

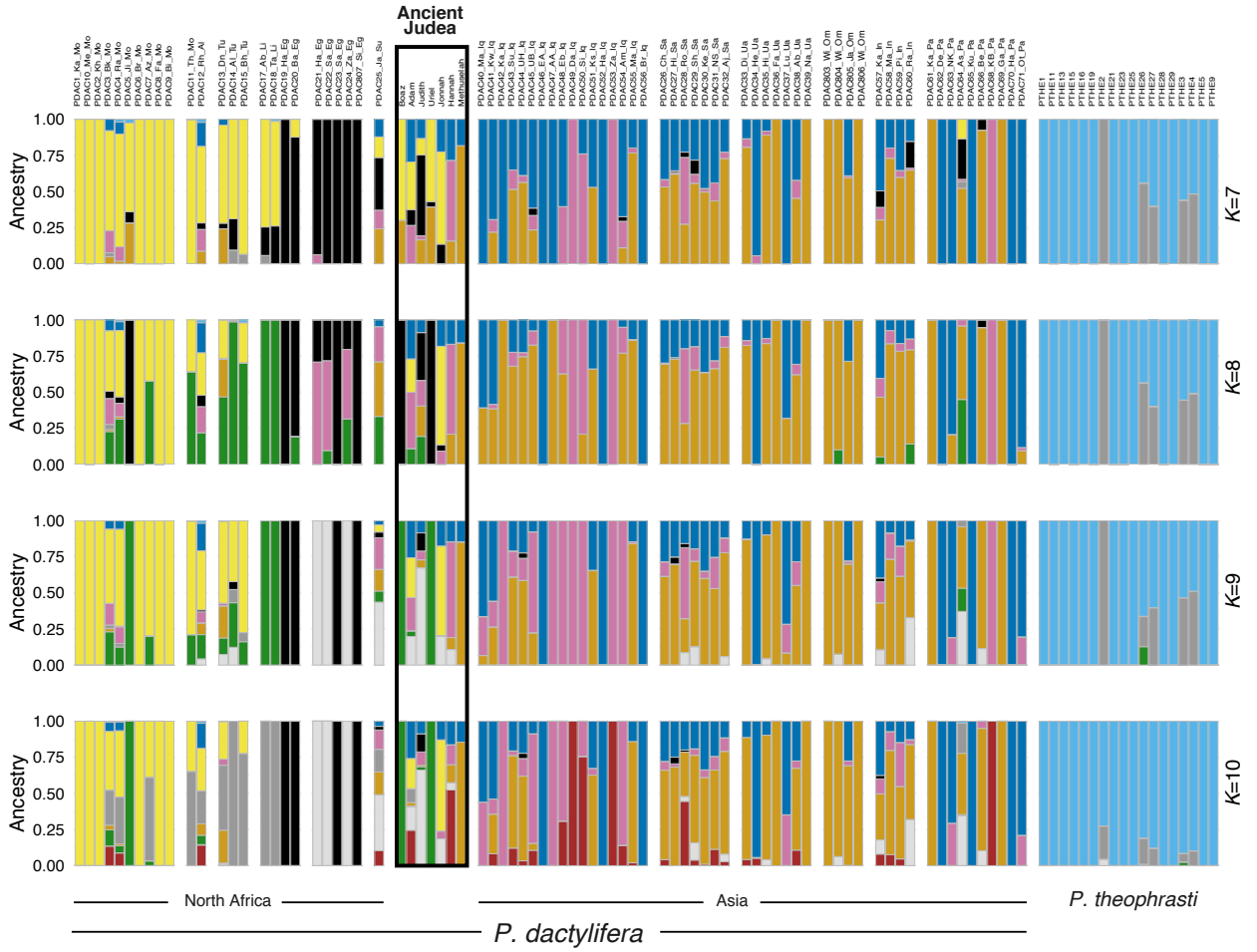




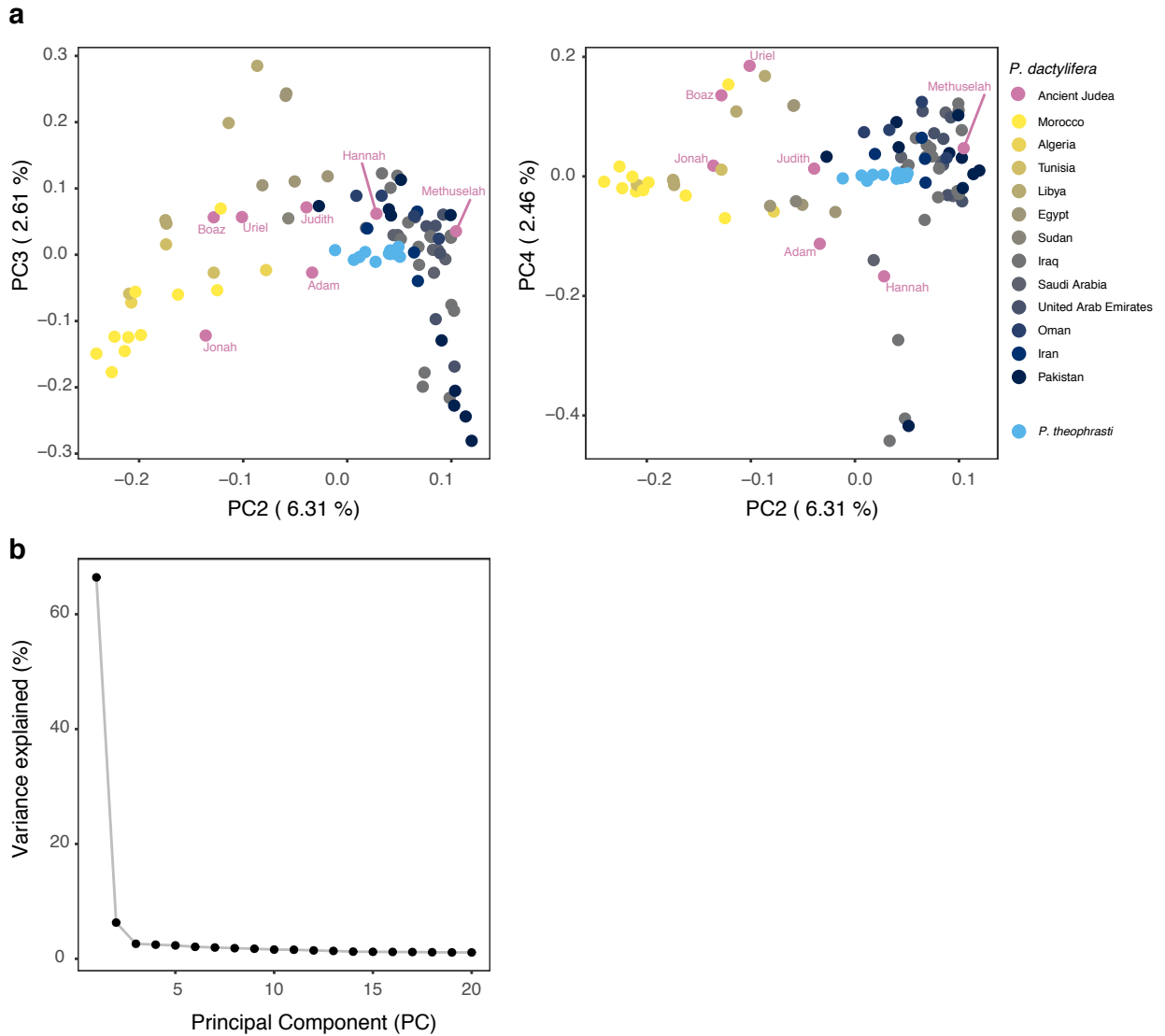
**Figure S2.** Ancestry coefficients inferred in 117 date palms and *Phoenix* spp. accessions using a randomly downsampled set of 53,845 SNPs. Cross-validation error plot may be found in Fig. S3a.



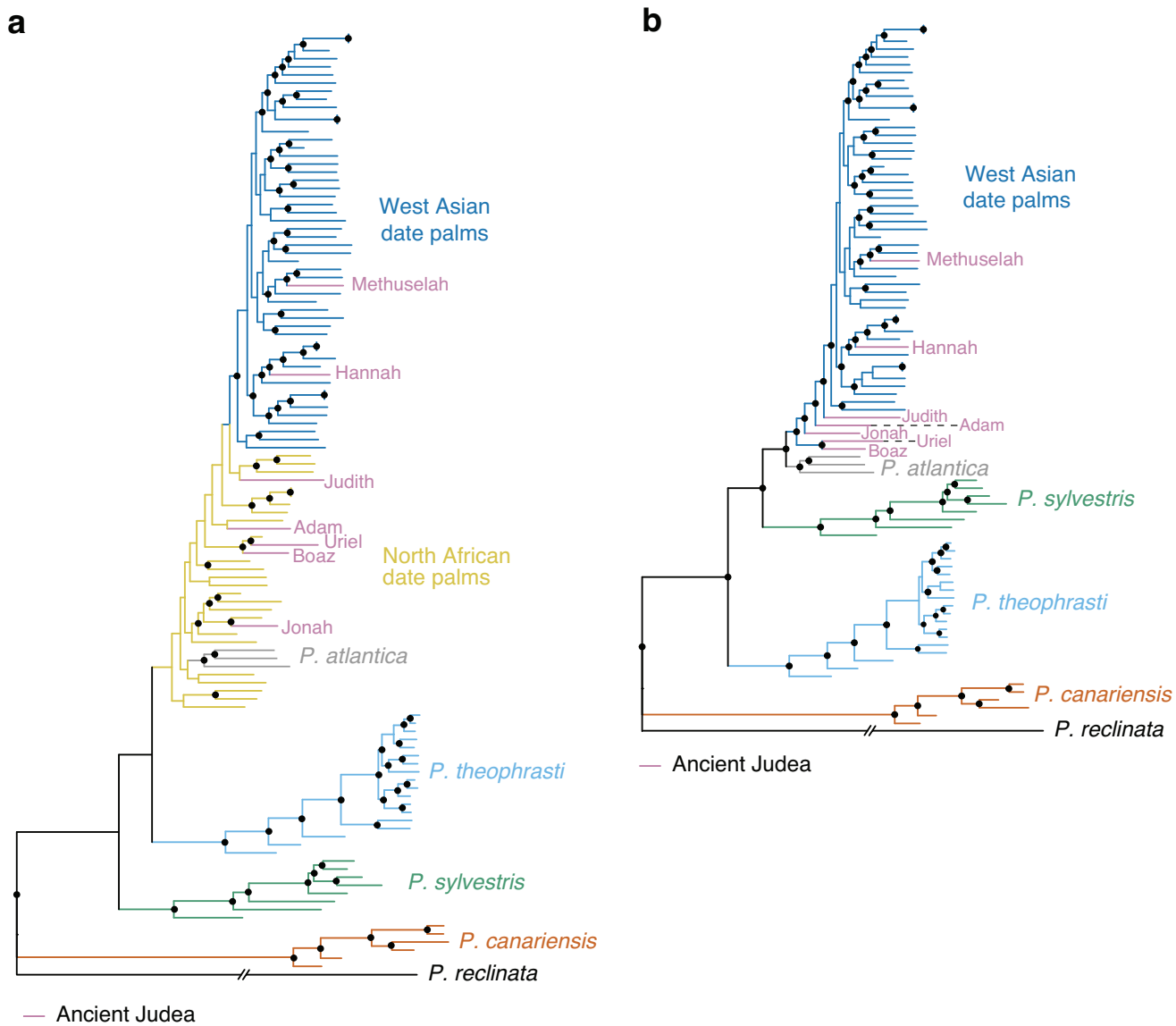
**Figure S3. Cross-validation error of the admixture models.** a, Model including all *Phoenix* species included in this manuscript; b, Model with *P. dactylifera* and *P. theophrasti*. Corresponding ancestry plots may be found in Figs. S2 and Fig. S3, respectively.



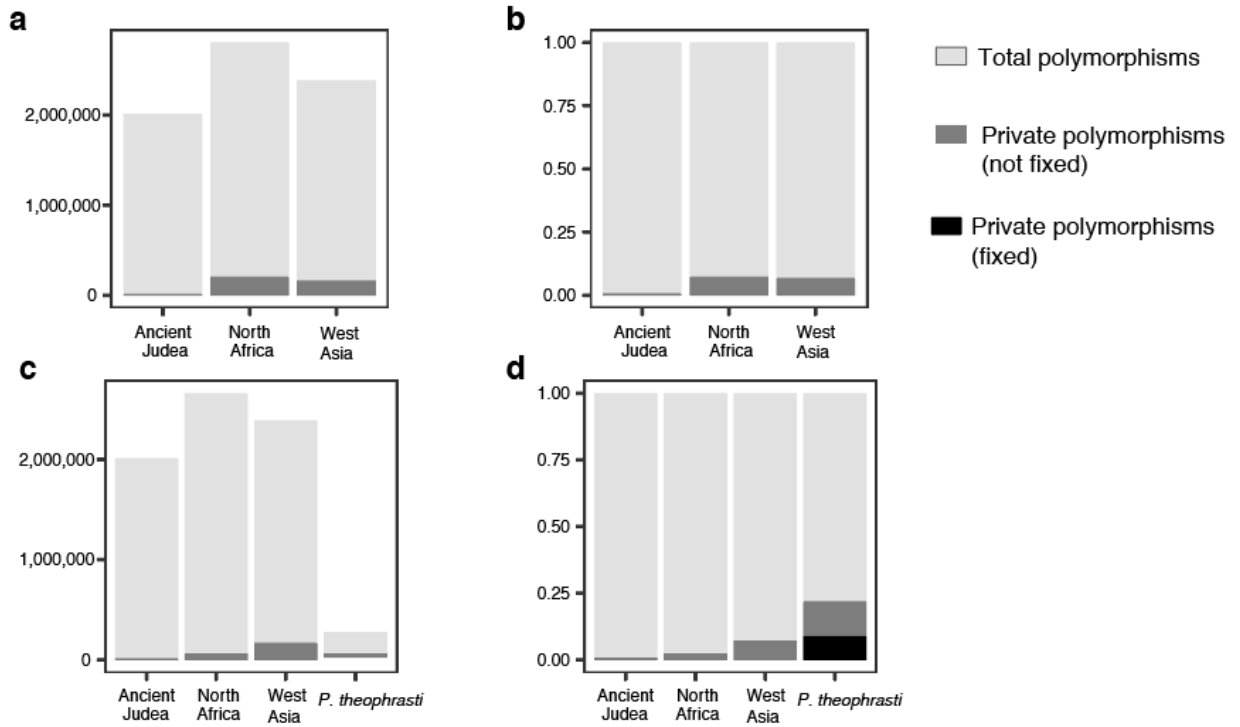
**Figure S4.** Ancestry coefficients inferred in 99 date palms and *P. theophrasti* accessions using a randomly downsampled set of 53,845 SNPs. The number of cluster ( $K$ ) ranges from seven to ten ( $K = 2$  to 6 can be found in Fig. 2). The Judean date palms are ordered as follow from left to right: Boaz, Adam, Judith, Uriel, Jonah, Hannah, Methuselah. Cross-validation error plot may be found in Fig. S3b.



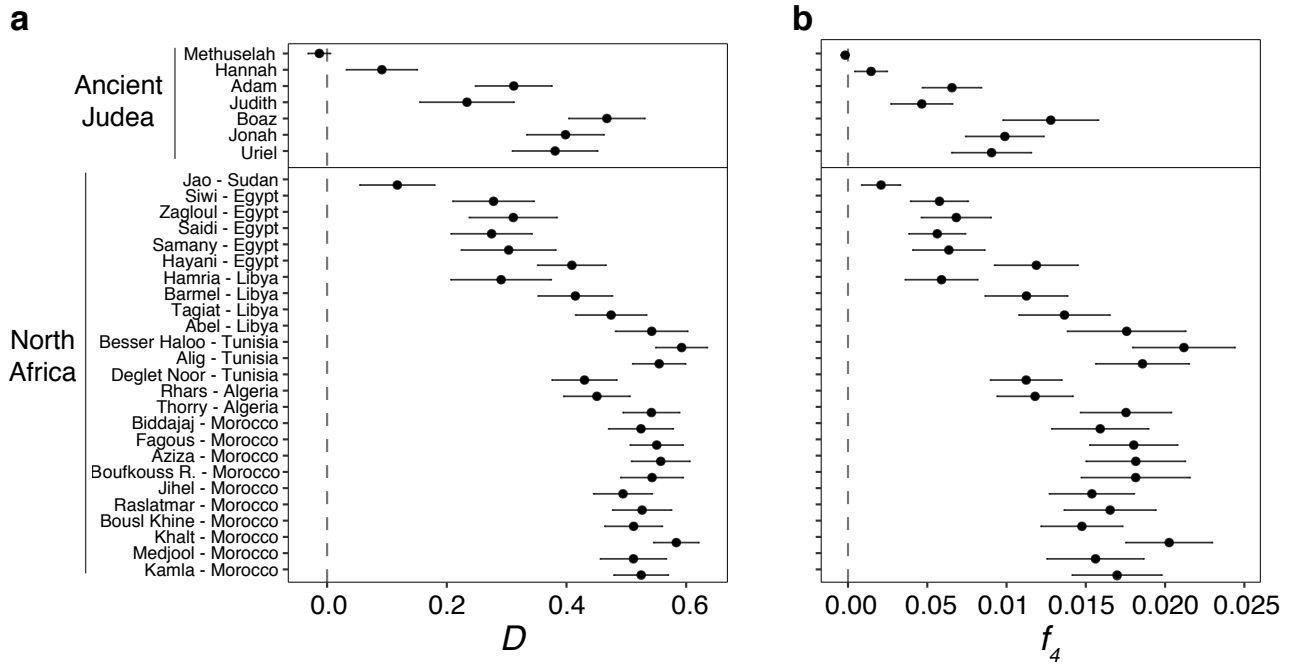
**Figure S5. Principal component analysis of 99 *Phoenix* spp. accessions including the seven Judean date palms genotyped on 24,689 SNPs. a, PCA plots of PC2/PC3 (left) and PC2/PC4 (right). The variance explained by each principal component is given in parentheses. The plot showing PC1/PC2 is in Fig. 3a; b, Variance explained by each principal component.**



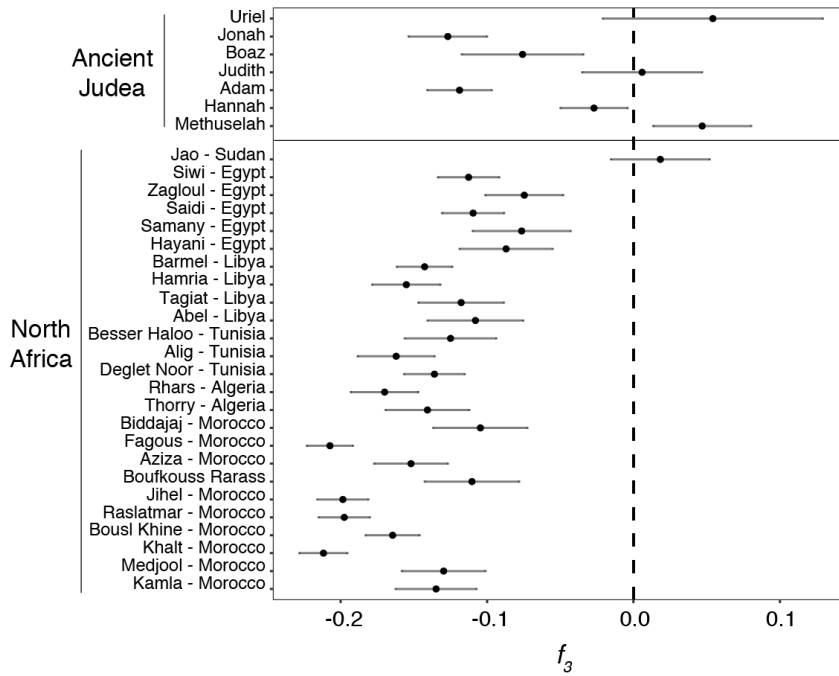
**Figure S6. Phylogenetic relationships among *Phoenix* inferred from 53,845 SNPs.** a, Inference including all 117 *Phoenix* spp. accessions; b, Inference after exclusion of the North African date palms and an admixed Asian sample. The trees were rooted with *Phoenix reclinata*. Black circles indicate nodes with >80% bootstrap support.



**Figure S7. Summary of polymorphisms and private alleles in date palm and *Phoenix theophrasti*.** On the left panels (a and c), we show the actual number of polymorphisms while in the right panels (b and d), we show the fraction of private and private fixed SNPs over the total number of polymorphisms. a and b show the level of polymorphism in three date palm populations, while in c and d the wild relative *Phoenix theophrasti* have been included in the analysis.

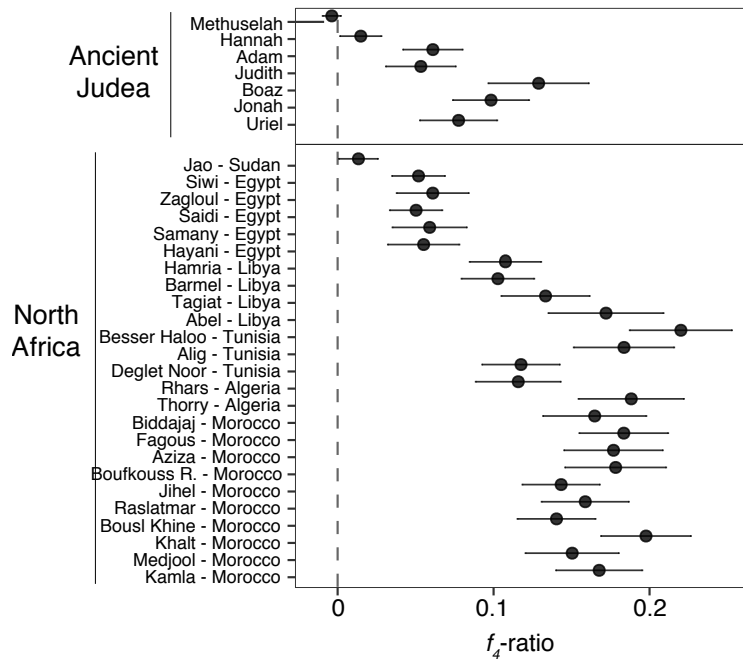


**Figure S8. Admixture between ancient Judean / modern North African date palms and *Phoenix theophrasti*.** a, Admixture  $D$ -statistic and b, Admixture  $f_4$ -statistic, both testing whether ancient Judean and modern North African date palms show an excess of shared derived alleles with *Phoenix theophrasti*, in which case they are significantly positive. We estimated both the  $D$ -statistics and  $f_4$ -statistics using the following tree: (((test sample, West Asian date palms), *P. theophrasti*), *P. canariensis*). The same analyses with *Phoenix reclinata* as the outgroup are in Fig. 4.



**Figure S9. Admixture  $f_3$ -statistic, testing whether ancient Judean and modern North African date palms are mixed from West Asian date palms and *Phoenix theophrasti*.** We estimated the  $f_3$ -statistics as  $f_3(\text{test sample}; \text{West Asian date palms}; P. \textit{theophrasti})$ . A negative  $f_3$ -statistic indicate that the test sample is likely mixed from these two populations/species.





**Figure S10. Admixture proportion in ancient Judean and modern North African date palms.** The  $f_4$ -ratio statistic is indicating the fraction of *P. theophrasti* genomes found in the test sample. We calculated the  $f_4$ -ratio statistics as  $f_4(A,O;X,C)/f_4(A,O;B,C)$ , where X is the test sample, A is a sister species, namely *P. sylvestris*, B and C are the mixing populations, namely West Asian date palms and *P. theophrasti*, respectively, and O is the outgroup, that is *P. canariensis*. The same analysis with *Phoenix reclinata* as the outgroup is in Fig. 5a.

## Supplementary Information Tables

**Table S1. List of Phoenix spp. accessions, their geographic origin and source**

<b>ID</b>	<b>Species</b>	<b>Cultivar</b>	<b>Country of collect</b>	<b>Country of origin</b>	<b>Source</b>	<b>GenBank accession</b>
PATL1	<i>P. atlantica</i>	NA	Cape Verde	Cape Verde	1	SAMN10272237
PATL2	<i>P. atlantica</i>	NA	Cape Verde	Cape Verde	1	SAMN10272238
PATL9	<i>P. atlantica</i>	NA	Cape Verde	Cape Verde	2	SAMN04413862
PCAN1	<i>P. canariensis</i>	NA	France	Canary Islands, Spain	1	SAMN10272206
PCAN2	<i>P. canariensis</i>	NA	France	Canary Islands, Spain	1	SAMN10272207
PCAN3	<i>P. canariensis</i>	NA	Italy	Canary Islands, Spain	1	SAMN10272208
PCAN4	<i>P. canariensis</i>	NA	Italy	Canary Islands, Spain	1	SAMN10272209
PCAN5	<i>P. canariensis</i>	NA	Italy	Canary Islands, Spain	1	SAMN10272210
PCAN6	<i>P. canariensis</i>	NA	USA	Canary Islands, Spain	1	SAMN10272211
PDAC11_Th_Al	<i>P. dactylifera</i>	Thory	USA	Algeria	3	SAMN04108817
PDAC12_Rh_Al	<i>P. dactylifera</i>	Rhars	USA	Algeria	3	SAMN04108818
PDAC21_Ha_Eg	<i>P. dactylifera</i>	Hayany	USA	Egypt	3	SAMN04108822
PDAC22_Sa_Eg	<i>P. dactylifera</i>	Samany	USA	Egypt	3	SAMN04108823
PDAC23_Sa_Eg	<i>P. dactylifera</i>	Saidi	USA	Egypt	3	SAMN04108820
PDAC24_Za_Eg	<i>P. dactylifera</i>	Zagloul	Syria	Egypt	3	SAMN04108821
PDAC807_Si_Eg	<i>P. dactylifera</i>	Siwi	Egypt	Egypt	2	SAMN04413858
PDAC57_Ka_In	<i>P. dactylifera</i>	Kabkab Red	Syria	Iran	3	SAMN04108827
PDAC58_Ma_In	<i>P. dactylifera</i>	Mazafati	Qatar	Iran	3	SAMN04108826
PDAC59_Pi_In	<i>P. dactylifera</i>	Piavom	Qatar	Iran	3	SAMN04108824
PDAC60_Ra_In	<i>P. dactylifera</i>	Rabee	Qatar	Iran	3	SAMN04108825

PDAC40_Ma_Iq	<i>P. dactylifera</i>	Maktoumi	UAE	Iraq	3	SAMN04108860
PDAC41_Kw_Iq	<i>P. dactylifera</i>	Khadrawy	USA	Iraq	3	SAMN04108831
PDAC42_Ka_Iq	<i>P. dactylifera</i>	Khastawi	USA	Iraq	3	SAMN04108832
PDAC43_Su_Iq	<i>P. dactylifera</i>	Sultana	UAE	Iraq	3	SAMN04108836
PDAC44_UH_Iq	<i>P. dactylifera</i>	Um al hamam	Iraq	Iraq	3	SAMN04108835
PDAC45_UB_Iq	<i>P. dactylifera</i>	Um al blaliz	Iraq	Iraq	3	SAMN04108834
PDAC46_EA_Iq	<i>P. dactylifera</i>	Ewent Ayob	Iraq	Iraq	3	SAMN04108839
PDAC47_AA_Iq	<i>P. dactylifera</i>	Azraq Azraq	Iraq	Iraq	3	SAMN04108837
PDAC48_Eb_Iq	<i>P. dactylifera</i>	Ebrahimi	Iraq	Iraq	3	SAMN04108838
PDAC49_Da_Iq	<i>P. dactylifera</i>	Dajwani	Iraq	Iraq	3	SAMN04108876
PDAC50_Si_Iq	<i>P. dactylifera</i>	Silani	Iraq	Iraq	3	SAMN04108840
PDAC51_Ks_Iq	<i>P. dactylifera</i>	Khisab	USA	Iraq	3	SAMN04108864
PDAC52_Ha_Iq	<i>P. dactylifera</i>	Halawy	USA	Iraq	3	SAMN04108863
PDAC53_Za_Iq	<i>P. dactylifera</i>	Zahidi	USA	Iraq	3	SAMN04108833
PDAC54_Am_Iq	<i>P. dactylifera</i>	Amir Haj	USA	Iraq	3	SAMN04108819
PDAC55_Ma_Iq	<i>P. dactylifera</i>	Manjouma	Iraq	Iraq	1	SAMN10272193
PDAC56_Br_Iq	<i>P. dactylifera</i>	Braim	USA	Iraq	3	SAMN04108845
PDAC17_Ab_Li	<i>P. dactylifera</i>	Abel	Libya	Libya	3	SAMN04108830
PDAC18-Ta_Li	<i>P. dactylifera</i>	Tagiat	Libya	Libya	3	SAMN04108828
PDAC19_Ha_Li	<i>P. dactylifera</i>	Hamria	Libya	Libya	1	SAMN10272197
PDAC20_Ba_Li	<i>P. dactylifera</i>	Barmel	Libya	Libya	1	SAMN10272198
PDAC1_Ka_Mo	<i>P. dactylifera</i>	Kamla	Morocco	Morocco	1	SAMN10272199
PDAC10_Me_Mo	<i>P. dactylifera</i>	Medjool	UAE	Morocco	3	SAMN04108841
PDAC2_Kh_Mo	<i>P. dactylifera</i>	Khalt	Morocco	Morocco	1	SAMN10272204

PDAC3_Bk_Mo	<i>P. dactylifera</i>	Bouisl Khine	Morocco	Morocco	1	SAMN10272200
PDAC4_Ra_Mo	<i>P. dactylifera</i>	Raslatmar	Morocco	Morocco	1	SAMN10272201
PDAC5_Ji_Mo	<i>P. dactylifera</i>	Jihl	Morocco	Morocco	1	SAMN10272202
PDAC6_Br_Mo	<i>P. dactylifera</i>	Boufkouss Rarass	Morocco	Morocco	1	SAMN10272203
PDAC7_Az_Mo	<i>P. dactylifera</i>	Aziza	Morocco	Morocco	3	SAMN04108844
PDAC8_Fa_Mo	<i>P. dactylifera</i>	Fagous	Morocco	Morocco	3	SAMN04108842
PDAC9_Bi_Mo	<i>P. dactylifera</i>	Biddajaj	Morocco	Morocco	3	SAMN04108843
PDAC803_Wi_Om	<i>P. dactylifera</i>	NA	Oman	Oman	2	SAMN04413859
PDAC804_Wi_Om	<i>P. dactylifera</i>	NA	Oman	Oman	2	SAMN04413860
PDAC805_Ja_Om	<i>P. dactylifera</i>	Jabri	Oman	Oman	2	SAMN04413857
PDAC806_Wi_Om	<i>P. dactylifera</i>	NA	Oman	Oman	2	SAMN04413861
PDAC61_Ka_Pa	<i>P. dactylifera</i>	Kashoowari	Pakistan	Pakistan	3	SAMN04108846
PDAC62_De_Pa	<i>P. dactylifera</i>	Dedhi	Pakistan	Pakistan	3	SAMN04108849
PDAC63_NK_Pa	<i>P. dactylifera</i>	Naquel Khuh	Pakistan	Pakistan	3	SAMN04108847
PDAC64_As_Pa	<i>P. dactylifera</i>	Aseel	Pakistan	Pakistan	3	SAMN04108850
PDAC65_Ku_Pa	<i>P. dactylifera</i>	Kuproo	Pakistan	Pakistan	3	SAMN04108851
PDAC66_Be_Pa	<i>P. dactylifera</i>	Began	Pakistan	Pakistan	3	SAMN04108829
PDAC68_KB_Pa	<i>P. dactylifera</i>	Karbali	Pakistan	Pakistan	3	SAMN04108848
PDAC69_Ga_Pa	<i>P. dactylifera</i>	Gajar	Pakistan	Pakistan	1	SAMN10272194
PDAC70_Ha_Pa	<i>P. dactylifera</i>	Hawawiri	Pakistan	Pakistan	1	SAMN10272195
PDAC71_Ot_Pa	<i>P. dactylifera</i>	Otaquin	Pakistan	Pakistan	1	SAMN10272196
PDAC26_Ch_Sa	<i>P. dactylifera</i>	Chichi	UAE	Saudi Arabia	3	SAMN04103916
PDAC27_Hi_Sa	<i>P. dactylifera</i>	Hilali	USA	Saudi Arabia	3	SAMN04108853
PDAC28_Ro_Sa	<i>P. dactylifera</i>	Rothan	UAE	Saudi Arabia	3	SAMN04108857

PDAC29_Sh_Sa	<i>P. dactylifera</i>	Shagri	UAE	Saudi Arabia	3	SAMN04108859
PDAC30_Ke_Sa	<i>P. dactylifera</i>	Khenezi	UAE	Saudi Arabia	3	SAMN04108854
PDAC31_NS_Sa	<i>P. dactylifera</i>	Nebeit Seif	UAE	Saudi Arabia	3	SAMN04108855
PDAC32_Aj_Sa	<i>P. dactylifera</i>	Ajwa	UAE	Saudi Arabia	3	SAMN04108856
PDAC25_Ja_Su	<i>P. dactylifera</i>	Jao	UAE	Sudan	3	SAMN04108865
PDAC13_Dn_Tu	<i>P. dactylifera</i>	Deglet Noor	Tunisia	Tunisia	3	SAMN04108868
PDAC14_Al_Tu	<i>P. dactylifera</i>	Alig	Tunisia	Tunisia	3	SAMN04108866
PDAC15_Bh_Tu	<i>P. dactylifera</i>	Besser Haloo	Tunisia	Tunisia	3	SAMN04108867
PDAC33_Di_Ua	<i>P. dactylifera</i>	Dibbas	UAE	UAE	3	SAMN04108545
PDAC34_He_Ua	<i>P. dactylifera</i>	Helwa	UAE	UAE	3	SAMN04108870
PDAC35_Hi_Ua	<i>P. dactylifera</i>	Hiri	UAE	UAE	3	SAMN04108874
PDAC36_Fa_Ua	<i>P. dactylifera</i>	Fard4	USA	UAE	3	SAMN04108875
PDAC37_Lu_Ua	<i>P. dactylifera</i>	Lulu	UAE	UAE	3	SAMN04108871
PDAC38_Ab_Ua	<i>P. dactylifera</i>	Abouman	UAE	UAE	3	SAMN04108873
PDAC39_Na_Ua	<i>P. dactylifera</i>	Nagal	UAE	UAE	3	SAMN04108872
PREC2	<i>P. reclinata</i>	NA	USA	Rwanda	1	SAMN10272205
PSYL1	<i>P. sylvestris</i>	NA	USA	NA	1	SAMN10272212
PSYL2	<i>P. sylvestris</i>	NA	USA	NA	1	SAMN10272213
PSYL3	<i>P. sylvestris</i>	NA	USA	NA	1	SAMN10272214
PSYL4	<i>P. sylvestris</i>	NA	USA	NA	1	SAMN10272215
PSYL44	<i>P. sylvestris</i>	NA	India	India	2	SAMN04413863
PSYL5	<i>P. sylvestris</i>	NA	USA	NA	1	SAMN10272216
PSYL6	<i>P. sylvestris</i>	NA	Spain	NA	1	SAMN10272217
PSYL7	<i>P. sylvestris</i>	NA	Pakistan	Pakistan	1	SAMN10272218

PTHE1	<i>P. theophrasti</i>	NA	Italy	Greece	3	SAMN10272219
PTHE11	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272225
PTHE13	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272226
PTHE15	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272227
PTHE16	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272228
PTHE19	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272229
PTHE2	<i>P. theophrasti</i>	NA	Italy	NA	1	SAMN10272220
PTHE21	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272230
PTHE23	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272231
PTHE25	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272232
PTHE26	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272233
PTHE27	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272234
PTHE28	<i>P. theophrasti</i>	NA	Greece	Libya	1	SAMN10272235
PTHE29	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272236
PTHE3	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272221
PTHE4	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272222
PTHE5	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272223
PTHE9	<i>P. theophrasti</i>	NA	Greece	Crete, Greece	1	SAMN10272224

Source: 1 – Flowers et al. 2019. Cross-species hybridization and the origin of North African date palms. Proc. Natl. Acad. Sci. U. S. A. 116, 1651–1658; 2 - Gros-Balthazard et al. 2017. The discovery of wild date palms in Oman reveals a complex domestication history involving centers in the Middle East and Africa. Curr. Biol. 27, 2211–2218; 3 – Hazzouri et al. 2015. Whole genome re-sequencing of date palms yields insights into diversification of a fruit tree crop. Nat. Commun. 6, 8824

**Table S2. Sequencing and read alignments metrics.**

<b>ID</b>	<b># reads</b>	<b># mapped reads</b>	<b>Proportion mapped</b>	<b>Depth</b>
PATL1	197,158,412	195,548,314	99.2	23.3
PATL2	177,816,454	176,063,722	99.0	21.0
PATL9	77,525,586	76,827,615	99.1	10.4
PCAN1	192,687,974	190,031,402	98.6	23.6
PCAN2	174,401,608	172,211,870	98.7	21.4
PCAN3	184,205,404	181,720,551	98.7	22.5
PCAN4	200,974,554	198,210,043	98.6	25.1
PCAN5	182,193,640	179,664,201	98.6	22.3
PCAN6	101,872,484	100,362,011	98.5	13.9
PDAC1_Ka_Mo	64,295,532	63,623,840	99.0	8.1
PDAC10_Me_Mo	119,940,728	119,068,553	99.3	14.5
Boaz	340,936,352	333,724,692	97.9	41.1
Adam	295,123,720	287,493,700	97.4	35.8
Judith	307,846,880	301,073,499	97.8	35.9
Uriel	357,116,030	349,387,223	97.8	42.3
Jonnah	344,095,200	336,110,891	97.7	40.6
Hannah	331,863,442	324,193,419	97.7	40.2
PDAC11_Th_Mo	149,799,322	148,613,125	99.2	18.0
PDAC12_Rh_Al	163,712,090	162,438,077	99.2	19.5
PDAC13_Dn_Tu	138,303,880	137,123,535	99.1	16.6
PDAC14_Al_Tu	142,887,896	141,736,208	99.2	16.8
PDAC15_Bh_Tu	161,563,172	160,219,397	99.2	18.5
PDAC17_Ab_Li	151,405,024	150,325,950	99.3	18.1
PDAC18-Ta_Li	228,882,532	227,284,180	99.3	27.3
PDAC19_Ha_Li	61,282,522	50,490,461	82.4	6.5
PDAC2_Kh_Mo	105,332,060	104,048,946	98.8	12.7
PDAC20_Ba_Li	63,021,546	62,458,390	99.1	8.0
PDAC21_Ha_Eg	413,069,026	406,452,682	98.4	46.4
PDAC22_Sa_Eg	304,948,916	297,389,629	97.5	34.9
PDAC23_Sa_Eg	144,017,910	143,000,478	99.3	17.1
PDAC24_Za_Eg	172,140,454	171,005,631	99.3	20.4
PDAC25_Ja_Su	149,538,326	148,274,447	99.2	18.2
PDAC26_Ch_Sa	103,075,942	102,513,577	99.5	12.5
PDAC27_Hi_Sa	40,812,836	40,587,230	99.4	5.3
PDAC28_Ro_Sa	151,663,576	150,219,998	99.0	18.1
PDAC29_Sh_Sa	124,625,060	123,664,433	99.2	15.0
PDAC3_Bk_Mo	77,950,280	76,600,812	98.3	9.6

PDAC30_Ke_Sa	180,780,780	179,533,343	99.3	21.0
PDAC31_NS_Sa	189,418,200	188,243,772	99.4	22.3
PDAC32_Aj_Sa	133,517,770	132,552,481	99.3	16.1
PDAC33_Di_Ua	68,469,304	68,073,960	99.4	8.3
PDAC34_He_Ua	94,791,162	94,297,142	99.5	11.5
PDAC35_Hi_Ua	34,479,912	34,293,353	99.5	4.7
PDAC36_Fa_Ua	173,990,458	172,677,258	99.2	20.8
PDAC37_Lu_Ua	156,410,544	155,327,741	99.3	18.4
PDAC38_Ab_Ua	265,572,440	263,586,381	99.3	30.7
PDAC39_Na_Ua	93,130,718	92,349,463	99.2	11.9
PDAC4_Ra_Mo	74,658,968	72,429,219	97.0	9.1
PDAC40_Ma_Iq	99,763,240	99,140,014	99.4	12.0
PDAC41_Kw_Iq	185,509,412	184,331,712	99.4	21.9
PDAC42_Ka_Iq	165,266,340	164,037,488	99.3	19.5
PDAC43_Su_Iq	164,736,418	163,688,120	99.4	19.7
PDAC44_UH_Iq	110,973,284	110,053,615	99.2	13.5
PDAC45_UB_Iq	79,016,884	78,290,182	99.1	9.8
PDAC46_EA_Iq	73,217,444	72,595,841	99.2	9.0
PDAC47_AA_Iq	76,291,000	75,717,851	99.2	9.6
PDAC48_Eb_Iq	80,351,780	79,543,999	99.0	9.9
PDAC49_Da_Iq	70,103,050	69,590,999	99.3	8.8
PDAC5_Ji_Mo	64,726,936	63,990,945	98.9	8.1
PDAC50_Si_Iq	112,156,326	111,025,337	99.0	13.6
PDAC51_Ks_Iq	173,421,696	172,358,512	99.4	23.3
PDAC52_Ha_Iq	169,972,110	168,996,581	99.4	22.8
PDAC53_Za_Iq	299,718,590	293,159,247	97.8	34.2
PDAC54_Am_Iq	359,465,904	352,576,817	98.1	40.9
PDAC55_Ma_Iq	79,554,634	78,925,401	99.2	9.9
PDAC56_Br_Iq	155,582,104	154,418,662	99.3	18.4
PDAC57_Ka_In	58,262,680	57,995,381	99.5	7.4
PDAC58_Ma_In	252,034,528	250,194,806	99.3	29.6
PDAC59_Pi_In	106,153,662	105,390,839	99.3	12.9
PDAC6_Br_Mo	67,285,164	66,654,559	99.1	8.5
PDAC60_Ra_In	83,820,956	83,085,276	99.1	10.4
PDAC61_Ka_Pa	142,039,272	138,828,675	97.7	16.7
PDAC62_De_Pa	81,853,532	80,831,262	98.8	10.0
PDAC63_NK_Pa	135,997,284	131,027,284	96.3	15.7
PDAC64_As_Pa	163,090,956	160,655,952	98.5	19.3
PDAC65_Ku_Pa	158,207,914	156,464,858	98.9	18.9
PDAC66_Be_Pa	211,230,860	208,830,598	98.9	24.6



PDAC68_KB_Pa	182,253,212	179,346,384	98.4	21.6
PDAC69_Ga_Pa	76,628,818	75,886,964	99.0	9.6
PDAC7_Az_Mo	142,790,544	141,545,499	99.1	17.1
PDAC70_Ha_Pa	70,521,848	69,844,614	99.0	8.9
PDAC71_Ot_Pa	64,498,294	63,752,197	98.8	8.0
PDAC8_Fa_Mo	124,292,474	122,326,434	98.4	14.7
PDAC803_Wi_Om	83,398,814	82,833,524	99.3	11.1
PDAC804_Wi_Om	70,626,734	69,924,397	99.0	9.4
PDAC805_Ja_Om	74,799,190	74,344,114	99.4	9.9
PDAC806_Wi_Om	63,212,222	62,833,027	99.4	8.5
PDAC807_Si_Eg	91,056,090	90,424,595	99.3	12.0
Methuselah	152,308,928	151,418,706	99.4	18.1
PDAC9_Bi_Mo	190,405,508	187,377,696	98.4	22.0
PREC2	82,238,884	81,055,410	98.6	11.2
PSYL1	185,277,266	183,487,724	99.0	22.3
PSYL2	178,945,780	177,312,053	99.1	21.5
PSYL3	169,782,932	168,354,829	99.2	20.3
PSYL4	188,981,576	187,206,228	99.1	22.7
PSYL44	71,938,838	71,220,814	99.0	10.0
PSYL5	192,403,206	190,714,457	99.1	22.6
PSYL6	180,363,028	178,713,178	99.1	21.7
PSYL7	179,608,912	178,058,712	99.1	21.2
PTHE1	168,776,628	166,654,034	98.7	21.7
PTHE11	187,574,316	185,210,867	98.7	26.2
PTHE13	188,852,064	186,314,936	98.7	26.3
PTHE15	188,829,858	185,926,905	98.5	26.2
PTHE16	200,513,310	198,171,160	98.8	27.7
PTHE19	180,548,836	178,201,122	98.7	25.1
PTHE2	186,618,412	184,358,907	98.8	22.2
PTHE21	190,144,102	187,890,377	98.8	26.4
PTHE23	174,751,714	172,541,163	98.7	24.5
PTHE25	198,198,222	195,811,479	98.8	27.5
PTHE26	168,707,556	166,742,774	98.8	21.9
PTHE27	211,708,886	209,190,604	98.8	27.8
PTHE28	59,691,270	59,045,277	98.9	9.1
PTHE29	56,456,840	55,824,818	98.9	8.8
PTHE3	220,226,168	217,868,745	98.9	29.6
PTHE4	198,200,168	196,013,962	98.9	26.2
PTHE5	134,889,884	133,183,708	98.7	19.2
PTHE9	163,077,408	161,232,727	98.9	22.7

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**Table S3. Heterozygosity in date palms**

<b>ID</b>	<b>Mean H<sup>a</sup></b>	<b>SD H<sup>b</sup></b>
PDAC1_Ka_Mo	0.200297	0.19055157
PDAC10_Me_Mo	0.27332094	0.2398702
PDAC100_Bo_Is	0.25750061	0.23654027
PDAC101_Ad_Is	0.24104859	0.225161
PDAC102_Ju_Is	0.23141093	0.21964016
PDAC103_Ur_Is	0.25604435	0.23239818
PDAC104_Jo_Is	0.2550906	0.23313845
PDAC105_Ha_Is	0.21780881	0.21114075
PDAC11_Th_Mo	0.27646702	0.24162057
PDAC12_Rh_Al	0.26092075	0.23468549
PDAC13_Dn_Tu	0.25627849	0.2321452
PDAC14_Al_Tu	0.27899395	0.24349829
PDAC15_Bh_Tu	0.28754525	0.24481589
PDAC17_Ab_Li	0.27211126	0.23971707
PDAC18_Ta_Li	0.26948538	0.23976827
PDAC19_Ha_Eg	0.16208026	0.15605693
PDAC2_Kh_Mo	0.28065715	0.23468901
PDAC20_Ba_Eg	0.19437373	0.17939066
PDAC21_Ha_Eg	0.23667846	0.22284738
PDAC22_Sa_Eg	0.24052955	0.22352226
PDAC23_Sa_Eg	0.23203156	0.21839205
PDAC24_Za_Eg	0.234884	0.2207314
PDAC25_Ja_Su	0.222365	0.21222625
PDAC26_Ch_Sa	0.19638698	0.19199911
PDAC27_Hi_Sa	0.13114107	0.1258111
PDAC28_Ro_Sa	0.21360565	0.20518711
PDAC29_Sh_Sa	0.20796644	0.20377121
PDAC3_Bk_Mo	0.21472788	0.19921558
PDAC30_Ke_Sa	0.20776517	0.20415663
PDAC31_NS_Sa	0.20809791	0.20630561
PDAC32_Aj_Sa	0.20381131	0.20250877
PDAC33_Di_Ua	0.1675022	0.16586321
PDAC34_He_Ua	0.19352745	0.19098859
PDAC35_Hi_Ua	0.10070154	0.09511435
PDAC36_Fa_Ua	0.19950071	0.20205376
PDAC37_Lu_Ua	0.20792227	0.20488339
PDAC38_Ab_Ua	0.20902782	0.20416256

PDAC39_Na_Ua	0.17139712	0.17016561
PDAC4_Ra_Mo	0.23821837	0.20637217
PDAC40_Ma_Iq	0.19359936	0.18808793
PDAC41_Kw_Iq	0.20537616	0.2030457
PDAC42_Ka_Iq	0.205141	0.2022006
PDAC43_Su_Iq	0.20604089	0.20292724
PDAC44_UH_Iq	0.20054049	0.19562735
PDAC45_UB_Iq	0.19689207	0.19059286
PDAC46_EA_Iq	0.19993956	0.19328168
PDAC47_AA_Iq	0.19184613	0.18773883
PDAC48_Eb_Iq	0.19979742	0.19158806
PDAC49_Da_Iq	0.19423464	0.18768937
PDAC5_Ji_Mo	0.2329454	0.20903128
PDAC50_Si_Iq	0.20487146	0.19778536
PDAC51_Ks_Iq	0.2101651	0.2047746
PDAC52_Ha_Iq	0.21505961	0.21030486
PDAC53_Za_Iq	0.21537373	0.2080215
PDAC54_Am_Iq	0.21175801	0.207616
PDAC55_Ma_Iq	0.19331466	0.1896056
PDAC56_Br_Iq	0.21708809	0.21199427
PDAC57_Ka_In	0.12306364	0.12011909
PDAC58_Ma_In	0.20761323	0.20492149
PDAC59_Pi_In	0.20444773	0.19735923
PDAC6_Br_Mo	0.21759102	0.19845778
PDAC60_Ra_In	0.20172884	0.19325068
PDAC61_Ka_Pa	0.20653305	0.20244752
PDAC62_De_Pa	0.19435102	0.19125316
PDAC63_NK_Pa	0.20725251	0.20324726
PDAC64_As_Pa	0.24155817	0.22307625
PDAC65_Ku_Pa	0.21194653	0.20808883
PDAC66_Be_Pa	0.21378957	0.206338
PDAC68_KB_Pa	0.21439602	0.20679358
PDAC69_Ga_Pa	0.1871054	0.18819124
PDAC7_Az_Mo	0.2685847	0.23701228
PDAC70_Ha_Pa	0.19282504	0.18675087
PDAC71_Ot_Pa	0.18389018	0.17741367
PDAC8_Fa_Mo	0.27994664	0.2335126
PDAC803_Wi_Om	0.18961433	0.19102521
PDAC804_Wi_Om	0.18055233	0.17798511
PDAC805_Ja_Om	0.19325963	0.18979133

PDAC806_Wi_Om	0.18182892	0.17946364
PDAC807_Si_Eg	0.22769753	0.21474822
PDAC810_Me_Is	0.20477883	0.20262644
PDAC9_Bi_Mo	0.25958485	0.23961948

<sup>a</sup>The proportion of heterozygote sites was calculated in non-overlapping sliding windows and the mean H reports the average across windows; <sup>b</sup>standard deviation of H

**Table S4. Summary of *D*-tests of admixture in date palm and wild *Phoenix* species<sup>a</sup>**

<b>W</b>	<b>Y</b>	<b>Z</b>	<b>D<sup>b</sup></b>	<b>SE<sup>c</sup></b>	<b>Zsc<sup>d</sup></b>	<b>BABA<sup>e</sup></b>	<b>ABBA<sup>e</sup></b>	<b>nsnps<sup>f</sup></b>
Adam	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.3119	0.031971	9.756	70386	37019	5087997
Adam	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.3028	0.031649	9.566	58520	31402	4184633
Boaz	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4675	0.031782	14.71	102376	37297	5088261
Boaz	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.4665	0.033548	13.906	86053	31437	4184860
Hannah	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0915	0.029572	3.095	44511	37109	5090309
Hannah	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0922	0.029568	3.119	37905	31556	4186577
Jonah	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.3983	0.032278	12.341	88564	38231	5088273
Jonah	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.3952	0.032116	12.304	74849	32550	4184999
Judith	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.2337	0.039366	5.938	62766	39118	5082287
Judith	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.2322	0.04088	5.68	53276	33320	4180009
Methuselah	<i>P. theophrasti</i>	<i>P. canariensis</i>	-0.013	0.009277	-1.407	34080	34979	5045765
Methuselah	<i>P. theophrasti</i>	<i>P. reclinata</i>	-0.0094	0.009204	-1.026	29060	29614	4150821
Uriel	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.381	0.03564	10.691	83752	37677	5088367
Uriel	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.3722	0.036379	10.233	70126	32198	4184942
PDAC1_Ka_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5248	0.022705	23.114	86307	26964	3496335
PDAC1_Ka_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5206	0.02268	22.954	72570	22932	2896189
PDAC10_Me_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5119	0.027551	18.58	113916	36895	4933406
PDAC10_Me_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5032	0.027785	18.111	95153	31540	4062069
PDAC11_Th_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5419	0.023633	22.93	125268	37310	5016174
PDAC11_Th_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5331	0.024727	21.56	105100	32090	4125410
PDAC12_Rh_Al	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4508	0.027686	16.282	95686	36321	5031448
PDAC12_Rh_Al	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.4458	0.02863	15.572	80073	30776	4137459
PDAC13_Dn_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4301	0.027069	15.89	93585	37381	5000681
PDAC13_Dn_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.4222	0.026083	16.186	78703	32049	4112542
PDAC14_Al_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5549	0.022104	25.102	130612	37484	5013359
PDAC14_Al_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5506	0.022858	24.087	109623	31854	4125405

PDAC15_Bh_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5924	0.021551	27.489	143329	36781	5028671
PDAC15_Bh_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5915	0.021768	27.174	119655	30790	4137668
PDAC17_Ab_Li	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5424	0.030183	17.971	125462	37378	5011772
PDAC17_Ab_Li	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5398	0.029894	18.058	105325	31603	4125286
PDAC18-Ta_Li	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4746	0.029663	15.999	107939	38585	5079573
PDAC18-Ta_Li	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.4726	0.030092	15.706	91252	32784	4178192
PDAC19_Ha_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.409	0.028576	14.314	48971	20597	2388140
PDAC19_Ha_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.3983	0.02833	14.06	41508	17905	1988090
PDAC2_Kh_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5835	0.018827	30.994	130365	34351	4739752
PDAC2_Kh_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5786	0.019075	30.331	108930	29135	3906173
PDAC20_Ba_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4148	0.030993	13.383	64790	26882	3367971
PDAC20_Ba_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.4056	0.030458	13.316	54274	23014	2789897
PDAC21_Ha_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.2908	0.041848	6.948	67028	36998	5090322
PDAC21_Ha_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.2877	0.042793	6.722	56646	31481	4186568
PDAC22_Sa_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.3034	0.039478	7.684	69884	37510	5089655
PDAC22_Sa_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.3012	0.039316	7.66	59087	31863	4186039
PDAC23_Sa_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.2749	0.033842	8.124	64863	36983	4952832
PDAC23_Sa_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.2704	0.032417	8.342	54376	31299	4071369
PDAC24_Za_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.3111	0.036676	8.483	71425	37661	4943903
PDAC24_Za_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.303	0.036256	8.359	60009	32203	4068560
PDAC25_Ja_Su	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.1173	0.031267	3.752	50329	39825	5036738
PDAC25_Ja_Su	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.1289	0.0289	4.461	43113	33314	4145012
PDAC3_Bk_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5122	0.024014	21.331	90027	29112	4128984
PDAC3_Bk_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5015	0.024212	20.714	75335	25068	3414094
PDAC4_Ra_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5264	0.024591	21.407	95281	29643	3970236
PDAC4_Ra_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5191	0.024876	20.867	80555	25567	3284569
PDAC5_Ji_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.4945	0.024454	20.222	83864	28432	3603358
PDAC5_Ji_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.488	0.025149	19.405	70616	24355	2988238
PDAC6_Br_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.543	0.026091	20.813	95523	28385	3699658

PDAC6_Br_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5314	0.025883	20.531	80062	24574	3065333
PDAC7_Az_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5575	0.024376	22.87	124884	35587	4919509
PDAC7_Az_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5515	0.024828	22.215	104657	30334	4050963
PDAC8_Fa_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5508	0.022071	24.957	120881	35091	4759397
PDAC8_Fa_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5458	0.021648	25.212	101908	30006	3922119
PDAC807_Si_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.2781	0.033951	8.192	62908	35623	4729474
PDAC807_Si_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.2746	0.032371	8.483	52973	30217	3901541
PDAC9_Bi_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.5245	0.026957	19.455	116119	36340	5014741
PDAC9_Bi_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.5099	0.027817	18.332	96697	31480	4126416
Adam	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0987	0.014465	-6.822	58779	71621	5079594
Adam	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0986	0.014306	-6.893	47174	57472	4177947
Boaz	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1802	0.018392	-9.797	61877	89007	5079853
Boaz	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1679	0.015833	-10.605	49928	70034	4178168
Hannah	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.027	0.011923	-2.266	56458	59584	5081900
Hannah	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0223	0.011177	-1.995	45493	47562	4179885
Jonah	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1444	0.015505	-9.316	61444	82147	5079865
Jonah	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.136	0.014802	-9.191	49584	65164	4178308
Judith	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0856	0.016684	-5.133	60089	71308	5073895
Judith	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0806	0.01432	-5.626	48438	56905	4173331
Methuseah	<i>P. sylvestris</i>	<i>P. canariensis</i>	0.0074	0.005857	1.26	52785	52011	5037383
Methuseah	<i>P. sylvestris</i>	<i>P. reclinata</i>	0.0108	0.00705	1.536	42365	41457	4144148
Uriel	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1175	0.016803	-6.991	61493	77825	5079959
Uriel	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1152	0.016053	-7.173	49392	62216	4178250
PDAC1_Ka_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2145	0.014882	-14.412	44547	68840	3489628
PDAC1_Ka_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2019	0.01446	-13.961	36435	54839	2890864
PDAC10_Me_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1995	0.016013	-12.458	61780	92516	4925133
PDAC10_Me_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1946	0.015906	-12.232	50065	74203	4055494
PDAC11_Th_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2359	0.018085	-13.043	63350	102393	5007831
PDAC11_Th_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.228	0.015932	-14.31	50887	80897	4118770



PDAC12_Rh_Al	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1676	0.017957	-9.334	59912	83991	5023085
PDAC12_Rh_Al	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1581	0.016242	-9.735	48142	66195	4130804
PDAC13_Dn_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1667	0.015813	-10.544	60882	85203	4992361
PDAC13_Dn_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1596	0.015603	-10.228	49380	68102	4105920
PDAC14_Al_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2284	0.015566	-14.673	64436	102520	5005015
PDAC14_Al_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2137	0.014295	-14.948	52269	80637	4118769
PDAC15_Bh_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2642	0.015112	-17.481	63839	109612	5020338
PDAC15_Bh_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2525	0.014839	-17.015	52005	87088	4131041
PDAC17_Ab_Li	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2186	0.018689	-11.697	63861	99514	5003433
PDAC17_Ab_Li	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2052	0.018782	-10.925	52091	78921	4118648
PDAC18-Ta_Li	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1795	0.01613	-11.126	64129	92132	5071185
PDAC18-Ta_Li	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1662	0.015489	-10.728	52262	73053	4171518
PDAC19_Ha_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1408	0.013896	-10.134	33114	43953	2383115
PDAC19_Ha_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1346	0.013655	-9.854	27062	35464	1984139
PDAC2_Kh_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2401	0.013402	-17.916	59509	97072	4731717
PDAC2_Kh_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2306	0.013339	-17.288	48135	76955	3899769
PDAC20_Ba_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1422	0.014672	-9.691	43312	57652	3361384
PDAC20_Ba_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1406	0.015129	-9.292	35056	46507	2784686
PDAC21_Ha_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0902	0.017113	-5.273	58772	70390	5081915
PDAC21_Ha_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0827	0.015561	-5.313	47278	55775	4179877
PDAC22_Sa_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0942	0.017274	-5.456	59944	72373	5081261
PDAC22_Sa_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0861	0.01665	-5.173	48320	57396	4179351
PDAC23_Sa_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0812	0.012874	-6.311	58323	68623	4944566
PDAC23_Sa_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0771	0.013424	-5.745	46868	54688	4064787
PDAC24_Za_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0937	0.016376	-5.719	60528	73005	4935673
PDAC24_Za_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0891	0.015205	-5.86	48630	58122	4062022
PDAC25_Ja_Su	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0224	0.01035	-2.166	60882	63667	5028384
PDAC25_Ja_Su	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.014	0.011707	-1.2	49048	50437	4138354
PDAC3_Bk_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1952	0.014715	-13.264	48891	72571	4121534

PDAC3_Bk_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1877	0.01501	-12.506	39871	58272	3408171
PDAC4_Ra_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.207	0.015297	-13.531	49594	75443	3962892
PDAC4_Ra_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1969	0.01497	-13.152	40228	59921	3278689
PDAC5_Ji_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.1865	0.014281	-13.057	47272	68915	3596629
PDAC5_Ji_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.1764	0.013081	-13.483	38429	54867	2982897
PDAC6_Br_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2259	0.016589	-13.615	47251	74770	3692735
PDAC6_Br_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2237	0.017002	-13.156	38413	60503	3059850
PDAC7_Az_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.224	0.015445	-14.502	61335	96683	4911307
PDAC7_Az_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.215	0.01544	-13.924	49655	76806	4044434
PDAC8_Fa_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2297	0.014838	-15.479	59039	94200	4751429
PDAC8_Fa_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2173	0.014935	-14.55	47874	74419	3915788
PDAC807_Si_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.083	0.012842	-6.461	56186	66338	4721397
PDAC807_Si_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0778	0.013501	-5.76	45418	53066	3895120
PDAC9_Bi_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.2171	0.018262	-11.885	61428	95413	5006443
PDAC9_Bi_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.2149	0.017829	-12.051	49435	76432	4119804

<sup>a</sup>The test was performed using *admixr* with the following tree, as stated in the Methods: (((W, X), Y), Z), where X is West Asian date palms; <sup>b</sup>D-statistic value; <sup>c</sup>standard error of the *D*-statistic calculated using the block jackknife; <sup>d</sup>Z-score is the number of standard errors *D* is from 0; <sup>e</sup>BABA and ABBA are the counts of observed site patterns; <sup>f</sup>number of SNPs used for a given calculation

**Table S5. Summary of f4-statistics for testing of admixture in date palm and wild *Phoenix* species<sup>a</sup>**

<b>W</b>	<b>Y</b>	<b>Z</b>	<b><math>f_4^b</math></b>	<b>SE<sup>c</sup></b>	<b>Zsc<sup>d</sup></b>	<b>BABA<sup>e</sup></b>	<b>ABBA<sup>e</sup></b>	<b>Nsnps<sup>f</sup></b>
Boaz	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0128	0.0015	8.505	102376	37297	5088261
Boaz	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0131	0.00159	8.209	86053	31437	4184860
Adam	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0066	0.00093	7.045	70386	37019	5087997
Adam	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0065	0.00092	7.022	58520	31402	4184633
Judith	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0047	0.00097	4.79	62766	39118	5082287
Judith	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0048	0.00104	4.602	53276	33320	4180009
Uriel	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0091	0.00126	7.21	83752	37677	5088367
Uriel	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0091	0.00128	7.074	70126	32198	4184942
Jonah	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0099	0.00123	8.017	88564	38231	5088273
Jonah	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0101	0.00125	8.104	74849	32550	4184999
Hannah	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0015	0.00051	2.847	44511	37109	5090309
Hannah	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0015	0.00053	2.87	37905	31556	4186577
Methuselah	<i>P. theophrasti</i>	<i>P. canariensis</i>	-0.0002	0.00013	-1.4	34080	34979	5045765
Methuselah	<i>P. theophrasti</i>	<i>P. reclinata</i>	-0.0001	0.00013	-1.026	29060	29614	4150821
PDAC1_Ka_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.017	0.00141	12.015	86307	26964	3496335
PDAC1_Ka_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0171	0.00142	12.059	72570	22932	2896189
PDAC10_Me_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0156	0.00153	10.233	113916	36895	4933406
PDAC10_Me_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0157	0.00151	10.353	95153	31540	4062069
PDAC11_Th_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0175	0.00143	12.247	125268	37310	5016174
PDAC11_Th_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0177	0.00151	11.749	105100	32090	4125410
PDAC12_Rh_Al	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0118	0.0012	9.875	95686	36321	5031448
PDAC12_Rh_Al	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0119	0.00123	9.683	80073	30776	4137459
PDAC13_Dn_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0112	0.00112	9.996	93585	37381	5000681
PDAC13_Dn_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0113	0.00113	10.088	78703	32049	4112542
PDAC14_Al_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0186	0.00148	12.594	130612	37484	5013359
PDAC14_Al_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0189	0.00154	12.281	109623	31854	4125405

PDAC15_Bh_Tu	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0212	0.00161	13.146	143329	36781	5028671
PDAC15_Bh_Tu	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0215	0.00164	13.135	119655	30790	4137668
PDAC17_Ab_Li	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0176	0.00187	9.423	125462	37378	5011772
PDAC17_Ab_Li	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0179	0.00186	9.616	105325	31603	4125286
PDAC18-Ta_Li	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0137	0.00144	9.513	107939	38585	5079573
PDAC18-Ta_Li	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.014	0.00147	9.501	91252	32784	4178192
PDAC19_Ha_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0119	0.00132	9.027	48971	20597	2388140
PDAC19_Ha_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0119	0.0013	9.158	41508	17905	1988090
PDAC2_Kh_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0203	0.00137	14.841	130365	34351	4739752
PDAC2_Kh_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0204	0.00138	14.856	108930	29135	3906173
PDAC20_Ba_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0113	0.0013	8.651	64790	26882	3367971
PDAC20_Ba_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0112	0.00126	8.884	54274	23014	2789897
PDAC21_Ha_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0059	0.00114	5.164	67028	36998	5090322
PDAC21_Ha_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.006	0.00119	5.048	56646	31481	4186568
PDAC22_Sa_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0064	0.00114	5.602	69884	37510	5089655
PDAC22_Sa_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0065	0.00116	5.623	59087	31863	4186039
PDAC23_Sa_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0056	0.00089	6.319	64863	36983	4952832
PDAC23_Sa_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0057	0.00087	6.544	54376	31299	4071369
PDAC24_Za_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0068	0.0011	6.211	71425	37661	4943903
PDAC24_Za_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0068	0.0011	6.189	60009	32203	4068560
PDAC25_Ja_Su	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0021	0.00061	3.421	50329	39825	5036738
PDAC25_Ja_Su	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0024	0.00059	4.021	43113	33314	4145012
PDAC3_Bk_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0148	0.00129	11.464	90027	29112	4128984
PDAC3_Bk_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0147	0.00127	11.59	75335	25068	3414094
PDAC4_Ra_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0165	0.00145	11.435	95281	29643	3970236
PDAC4_Ra_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0167	0.00145	11.572	80555	25567	3284569
PDAC5_Ji_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0154	0.00134	11.518	83864	28432	3603358
PDAC5_Ji_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0155	0.00137	11.303	70616	24355	2988238
PDAC6_Br_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0181	0.00171	10.587	95523	28385	3699658

PDAC6_Br_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0181	0.00168	10.769	80062	24574	3065333
PDAC7_Az_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0182	0.00157	11.601	124884	35587	4919509
PDAC7_Az_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0183	0.00157	11.668	104657	30334	4050963
PDAC8_Fa_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.018	0.00139	13.01	120881	35091	4759397
PDAC8_Fa_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0183	0.00136	13.464	101908	30006	3922119
PDAC807_Si_Eg	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0058	0.00091	6.344	62908	35623	4729474
PDAC807_Si_Eg	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0058	0.00088	6.62	52973	30217	3901541
PDAC9_Bi_Mo	<i>P. theophrasti</i>	<i>P. canariensis</i>	0.0159	0.00153	10.422	116119	36340	5014741
PDAC9_Bi_Mo	<i>P. theophrasti</i>	<i>P. reclinata</i>	0.0158	0.00153	10.342	96697	31480	4126416
Boaz	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0053	0.00066	-8.072	61877	89007	5079853
Boaz	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0048	0.00055	-8.732	49928	70034	4178168
Adam	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0025	0.00041	-6.209	58779	71621	5079594
Adam	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0025	0.0004	-6.236	47174	57472	4177947
Judith	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0022	0.00046	-4.762	60089	71308	5073895
Judith	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.002	0.00039	-5.225	48438	56905	4173331
Uriel	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0032	0.00051	-6.325	61493	77825	5079959
Uriel	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0031	0.00048	-6.419	49392	62216	4178250
Jonah	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0041	0.00051	-7.973	61444	82147	5079865
Jonah	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0037	0.00048	-7.831	49584	65164	4178308
Hannah	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0006	0.00028	-2.23	56458	59584	5081900
Hannah	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0005	0.00025	-1.97	45493	47562	4179885
Methuselah	<i>P. sylvestris</i>	<i>P. canariensis</i>	0.0002	0.00012	1.26	52785	52011	5037383
Methuselah	<i>P. sylvestris</i>	<i>P. reclinata</i>	0.0002	0.00014	1.536	42365	41457	4144148
PDAC1_Ka_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.007	0.0006	-11.66	44547	68840	3489628
PDAC1_Ka_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0064	0.00056	-11.32	36435	54839	2890864
PDAC10_Me_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0062	0.00062	-10.1	61780	92516	4925133
PDAC10_Me_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.006	0.00061	-9.786	50065	74203	4055494
PDAC11_Th_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0078	0.00074	-10.54	63350	1E+05	5007831
PDAC11_Th_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0073	0.00064	-11.44	50887	80897	4118770

PDAC12_Rh_Al	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0048	0.00059	-8.077	59912	83991	5023085
PDAC12_Rh_Al	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0044	0.00052	-8.472	48142	66195	4130804
PDAC13_Dn_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0049	0.00054	-9.046	60882	85203	4992361
PDAC13_Dn_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0046	0.00052	-8.819	49380	68102	4105920
PDAC14_Al_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0076	0.00067	-11.36	64436	1E+05	5005015
PDAC14_Al_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0069	0.00058	-11.8	52269	80637	4118769
PDAC15_Bh_Tu	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0091	0.00069	-13.16	63839	1E+05	5020338
PDAC15_Bh_Tu	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0085	0.00066	-12.94	52005	87088	4131041
PDAC17_Ab_Li	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0071	0.00076	-9.327	63861	99514	5003433
PDAC17_Ab_Li	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0065	0.00074	-8.809	52091	78921	4118648
PDAC18-Ta_Li	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0055	0.00059	-9.369	64129	92132	5071185
PDAC18-Ta_Li	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.005	0.00055	-9.077	52262	73053	4171518
PDAC19_Ha_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0045	0.00051	-8.898	33114	43953	2383115
PDAC19_Ha_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0042	0.00049	-8.701	27062	35464	1984139
PDAC2_Kh_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0079	0.00058	-13.72	59509	97072	4731717
PDAC2_Kh_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0074	0.00055	-13.45	48135	76955	3899769
PDAC20_Ba_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0043	0.00049	-8.663	43312	57652	3361384
PDAC20_Ba_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0041	0.0005	-8.315	35056	46507	2784686
PDAC21_Ha_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0023	0.00047	-4.833	58772	70390	5081915
PDAC21_Ha_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.002	0.00041	-4.908	47278	55775	4179877
PDAC22_Sa_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0024	0.00049	-4.952	59944	72373	5081261
PDAC22_Sa_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0022	0.00046	-4.754	48320	57396	4179351
PDAC23_Sa_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0021	0.00035	-5.946	58323	68623	4944566
PDAC23_Sa_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0019	0.00035	-5.458	46868	54688	4064787
PDAC24_Za_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0025	0.00048	-5.307	60528	73005	4935673
PDAC24_Za_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0023	0.00043	-5.448	48630	58122	4062022
PDAC25_Ja_Su	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0006	0.00026	-2.138	60882	63667	5028384
PDAC25_Ja_Su	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0003	0.00028	-1.185	49048	50437	4138354
PDAC3_Bk_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0057	0.00052	-10.96	48891	72571	4121534

PDAC3_Bk_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0054	0.00052	-10.39	39871	58272	3408171
PDAC4_Ra_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0065	0.0006	-10.96	49594	75443	3962892
PDAC4_Ra_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.006	0.00056	-10.68	40228	59921	3278689
PDAC5_Ji_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.006	0.00054	-11.06	47272	68915	3596629
PDAC5_Ji_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0055	0.00049	-11.35	38429	54867	2982897
PDAC6_Br_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0075	0.0007	-10.58	47251	74770	3692735
PDAC6_Br_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0072	0.00071	-10.2	38413	60503	3059850
PDAC7_Az_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0072	0.00064	-11.28	61335	96683	4911307
PDAC7_Az_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0067	0.00061	-10.93	49655	76806	4044434
PDAC8_Fa_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0074	0.0006	-12.28	59039	94200	4751429
PDAC8_Fa_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0068	0.00059	-11.57	47874	74419	3915788
PDAC807_Si_Eg	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0022	0.00035	-6.077	56186	66338	4721397
PDAC807_Si_Eg	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.002	0.00036	-5.472	45418	53066	3895120
PDAC9_Bi_Mo	<i>P. sylvestris</i>	<i>P. canariensis</i>	-0.0068	0.00072	-9.483	61428	95413	5006443
PDAC9_Bi_Mo	<i>P. sylvestris</i>	<i>P. reclinata</i>	-0.0066	0.00069	-9.512	49435	76432	4119804

<sup>a</sup>The test was performed using *admixr* with the following tree, as stated in the Methods: (((W, X), Y), Z), where X is West Asian date palms; <sup>b</sup> $f_4$ -statistic value; <sup>c</sup>standard error of the  $f_4$ -statistic calculated using the block jackknife; <sup>d</sup>Z-score is the number of standard errors  $f_4$  is from 0; <sup>e</sup>BABA and ABBA are the counts of observed site patterns; <sup>f</sup>number of SNPs used for a given calculation

**Table S6. Summary of f3-statistics for testing of admixture in date palm and wild *Phoenix* species<sup>a</sup>**

<b>C</b>	<b>A</b>	<b>B</b>	<b><math>f_3^b</math></b>	<b>SE<sup>c</sup></b>	<b>Zs<sup>d</sup></b>	<b>Nsnps<sup>e</sup></b>
Adam	<i>P. theophrasti</i>	West Asian date palms	-0.118809	0.011043	-10.759	2948922
Boaz	<i>P. theophrasti</i>	West Asian date palms	-0.075744	0.020792	-3.643	2957757
Hannah	<i>P. theophrasti</i>	West Asian date palms	-0.026978	0.011471	-2.352	2944442
Jonah	<i>P. theophrasti</i>	West Asian date palms	-0.12681	0.013453	-9.426	2956696
Judith	<i>P. theophrasti</i>	West Asian date palms	0.005873	0.020502	0.286	2955779
Methuselah	<i>P. theophrasti</i>	West Asian date palms	0.046912	0.016765	2.798	2911108
Uriel	<i>P. theophrasti</i>	West Asian date palms	0.054206	0.037589	1.442	2952214
PDAC1_Ka_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.134801	0.013852	-9.732	2033698
PDAC10_Me_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.129639	0.014303	-9.064	2873384
PDAC11_Th_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.140723	0.014361	-9.799	2920402
PDAC12_Rh_Al	<i>P. theophrasti</i>	West Asian date palms	-0.169976	0.011542	-14.726	2921322
PDAC13_Dn_Tu	<i>P. theophrasti</i>	West Asian date palms	-0.135955	0.010362	-13.12	2909137
PDAC14_Al_Tu	<i>P. theophrasti</i>	West Asian date palms	-0.162077	0.013148	-12.327	2921781
PDAC15_Bh_Tu	<i>P. theophrasti</i>	West Asian date palms	-0.124935	0.015689	-7.963	2929982
PDAC17_Ab_Li	<i>P. theophrasti</i>	West Asian date palms	-0.107931	0.016389	-6.585	2917329
PDAC18-Ta_Li	<i>P. theophrasti</i>	West Asian date palms	-0.117694	0.014638	-8.04	2955438
PDAC19_Ha_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.155136	0.01167	-13.294	1430252
PDAC2_Kh_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.211745	0.008194	-25.842	2717214
PDAC20_Ba_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.142667	0.009484	-15.042	1968998
PDAC21_Ha_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.087003	0.015923	-5.464	2953964
PDAC22_Sa_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.076366	0.016754	-4.558	2953428
PDAC23_Sa_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.109542	0.01066	-10.276	2872522
PDAC24_Za_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.074581	0.013319	-5.599	2867517
PDAC25_Ja_Su	<i>P. theophrasti</i>	West Asian date palms	0.018337	0.016889	1.086	2919978
PDAC3_Bk_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.164486	0.009228	-17.825	2367784
PDAC4_Ra_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.197528	0.008763	-22.541	2292843



PDAC5_Ji_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.19849	0.008755	-22.673	2124227
PDAC6_Br_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.110322	0.016178	-6.819	2159712
PDAC7_Az_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.151952	0.012602	-12.058	2836570
PDAC8_Fa_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.207316	0.007907	-26.221	2734011
PDAC807_Si_Eg	<i>P. theophrasti</i>	West Asian date palms	-0.112598	0.010501	-10.723	2746996
PDAC9_Bi_Mo	<i>P. theophrasti</i>	West Asian date palms	-0.104555	0.016092	-6.497	2906443
Adam	<i>P. sylvestris</i>	West Asian date palms	-0.05265	0.005135	-10.253	3124186
Boaz	<i>P. sylvestris</i>	West Asian date palms	0.071698	0.026447	2.711	3179383
Hannah	<i>P. sylvestris</i>	West Asian date palms	-0.008484	0.008381	-1.012	3069804
Jonah	<i>P. sylvestris</i>	West Asian date palms	-0.028615	0.00697	-4.105	3170817
Judith	<i>P. sylvestris</i>	West Asian date palms	0.068791	0.021151	3.252	3107096
Methuselah	<i>P. sylvestris</i>	West Asian date palms	0.043275	0.016461	2.629	3026272
Uriel	<i>P. sylvestris</i>	West Asian date palms	0.183267	0.039201	4.675	3148575
PDAC1_Ka_Mo	<i>P. sylvestris</i>	West Asian date palms	0.021545	0.012647	1.704	2212811
PDAC10_Me_Mo	<i>P. sylvestris</i>	West Asian date palms	0.022578	0.013815	1.634	3118448
PDAC11_Th_Mo	<i>P. sylvestris</i>	West Asian date palms	0.03244	0.011406	2.844	3197119
PDAC12_Rh_Al	<i>P. sylvestris</i>	West Asian date palms	-0.06313	0.004377	-14.422	3146971
PDAC13_Dn_Tu	<i>P. sylvestris</i>	West Asian date palms	-0.026739	0.00685	-3.904	3124169
PDAC14_Al_Tu	<i>P. sylvestris</i>	West Asian date palms	0.006835	0.011431	0.598	3195739
PDAC15_Bh_Tu	<i>P. sylvestris</i>	West Asian date palms	0.095536	0.019503	4.899	3209014
PDAC17_Ab_Li	<i>P. sylvestris</i>	West Asian date palms	0.075564	0.017165	4.402	3175060
PDAC18-Ta_Li	<i>P. sylvestris</i>	West Asian date palms	0.017681	0.011446	1.545	3191817
PDAC19_Ha_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.069187	0.007428	-9.314	1523771
PDAC2_Kh_Mo	<i>P. sylvestris</i>	West Asian date palms	-0.057152	0.005885	-9.712	3025595
PDAC20_Ba_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.049062	0.006741	-7.278	2108790
PDAC21_Ha_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.022291	0.00864	-2.58	3119444
PDAC22_Sa_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.005994	0.009384	-0.639	3123539
PDAC23_Sa_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.053893	0.005172	-10.42	3029592
PDAC24_Za_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.002398	0.009172	-0.261	3035641

PDAC25_Ja_Su	<i>P. sylvestris</i>	West Asian date palms	0.042675	0.014878	2.868	3055285
PDAC3_Bk_Mo	<i>P. sylvestris</i>	West Asian date palms	-0.031818	0.009382	-3.391	2578108
PDAC4_Ra_Mo	<i>P. sylvestris</i>	West Asian date palms	-0.073333	0.007768	-9.44	2512705
PDAC5_Ji_Mo	<i>P. sylvestris</i>	West Asian date palms	-0.088485	0.003506	-25.236	2304246
PDAC6_Br_Mo	<i>P. sylvestris</i>	West Asian date palms	0.069742	0.017713	3.937	2344223
PDAC7_Az_Mo	<i>P. sylvestris</i>	West Asian date palms	0.017106	0.014269	1.199	3106611
PDAC8_Fa_Mo	<i>P. sylvestris</i>	West Asian date palms	-0.068818	0.005554	-12.392	3025843
PDAC807_Si_Eg	<i>P. sylvestris</i>	West Asian date palms	-0.05672	0.005041	-11.251	2897667
PDAC9_Bi_Mo	<i>P. sylvestris</i>	West Asian date palms	0.069417	0.015541	4.467	3160929

<sup>a</sup>The test was performed using *admixr* to see if population C is an admixture of populations A and B; <sup>b</sup> $f_3$  statistic value; <sup>c</sup>standard error of the  $f_3$ -statistic calculated using the block jackknife; <sup>d</sup>Z-score is the number of standard errors  $f_3$  is from 0; <sup>e</sup>number of SNPs used for a given calculation

**Table S7. Summary of  $f_4$ -ratio statistics for inferring the proportion of *P. theophrasti* ancestry in the North African and Judean date palm genomes<sup>a</sup>**

<b>X<sup>b</sup></b>	<b>O<sup>c</sup></b>	<b><math>\alpha^d</math></b>	<b><math>1 - \alpha^e</math></b>	<b>SE<sup>f</sup></b>	<b>Zsc<sup>g</sup></b>
Boaz	<i>P. canariensis</i>	0.871112	0.128888	0.016107	54.084
Boaz	<i>P. reclinata</i>	0.872225	0.127775	0.01481	58.894
Adam	<i>P. canariensis</i>	0.938934	0.061066	0.009558	98.24
Adam	<i>P. reclinata</i>	0.93449	0.06551	0.010168	91.906
Judith	<i>P. canariensis</i>	0.946642	0.053358	0.011221	84.364
Judith	<i>P. reclinata</i>	0.946157	0.053843	0.010484	90.248
Uriel	<i>P. canariensis</i>	0.922431	0.077569	0.012408	74.34
Uriel	<i>P. reclinata</i>	0.91851	0.08149	0.012768	71.937
Jonah	<i>P. canariensis</i>	0.90164	0.09836	0.012234	73.698
Jonah	<i>P. reclinata</i>	0.900977	0.099023	0.012573	71.661
Hannah	<i>P. canariensis</i>	0.985159	0.014841	0.006643	148.301
Hannah	<i>P. reclinata</i>	0.986859	0.013141	0.00666	148.172
Methuselah	<i>P. canariensis</i>	1.003711	-0.003711	0.002945	340.851
Methuselah	<i>P. reclinata</i>	1.005817	-0.005817	0.003791	265.336
PDAC1_Ka_Mo	<i>P. canariensis</i>	0.832294	0.167706	0.013849	60.1
PDAC1_Ka_Mo	<i>P. reclinata</i>	0.831107	0.168893	0.014261	58.277
PDAC10_Me_Mo	<i>P. canariensis</i>	0.8496	0.1504	0.014971	56.751
PDAC10_Me_Mo	<i>P. reclinata</i>	0.842171	0.157829	0.015967	52.745
PDAC11_Th_Mo	<i>P. canariensis</i>	0.81172	0.18828	0.016909	48.006
PDAC11_Th_Mo	<i>P. reclinata</i>	0.806423	0.193577	0.016201	49.778
PDAC12_Rh_Al	<i>P. canariensis</i>	0.884192	0.115808	0.013643	64.811
PDAC12_Rh_Al	<i>P. reclinata</i>	0.883844	0.116156	0.013077	67.59
PDAC13_Dn_Tu	<i>P. canariensis</i>	0.882408	0.117592	0.012457	70.837
PDAC13_Dn_Tu	<i>P. reclinata</i>	0.878829	0.121171	0.013275	66.204
PDAC14_Al_Tu	<i>P. canariensis</i>	0.816388	0.183612	0.016121	50.642

PDAC14_Al_Tu	<i>P. reclinata</i>	0.81725	0.18275	0.015592	52.415
PDAC15_Bh_Tu	<i>P. canariensis</i>	0.779914	0.220086	0.016406	47.539
PDAC15_Bh_Tu	<i>P. reclinata</i>	0.774489	0.225511	0.016841	45.989
PDAC17_Ab_Li	<i>P. canariensis</i>	0.827914	0.172086	0.018451	44.872
PDAC17_Ab_Li	<i>P. reclinata</i>	0.826914	0.173086	0.019382	42.664
PDAC18-Ta_Li	<i>P. canariensis</i>	0.866673	0.133327	0.014163	61.191
PDAC18-Ta_Li	<i>P. reclinata</i>	0.867587	0.132413	0.014354	60.444
PDAC19_Ha_Eg	<i>P. canariensis</i>	0.892389	0.107611	0.011477	77.753
PDAC19_Ha_Eg	<i>P. reclinata</i>	0.889411	0.110589	0.012032	73.92
PDAC2_Kh_Mo	<i>P. canariensis</i>	0.802281	0.197719	0.01443	55.598
PDAC2_Kh_Mo	<i>P. reclinata</i>	0.797359	0.202641	0.014839	53.733
PDAC20_Ba_Eg	<i>P. canariensis</i>	0.897229	0.102771	0.011674	76.859
PDAC20_Ba_Eg	<i>P. reclinata</i>	0.890611	0.109389	0.012575	70.822
PDAC21_Ha_Eg	<i>P. canariensis</i>	0.944846	0.055154	0.01148	82.307
PDAC21_Ha_Eg	<i>P. reclinata</i>	0.946027	0.053973	0.011035	85.729
PDAC22_Sa_Eg	<i>P. canariensis</i>	0.940975	0.059025	0.01193	78.876
PDAC22_Sa_Eg	<i>P. reclinata</i>	0.942321	0.057679	0.012054	78.172
PDAC23_Sa_Eg	<i>P. canariensis</i>	0.949691	0.050309	0.008425	112.726
PDAC23_Sa_Eg	<i>P. reclinata</i>	0.948842	0.051158	0.009243	102.652
PDAC24_Za_Eg	<i>P. canariensis</i>	0.939006	0.060994	0.011567	81.177
PDAC24_Za_Eg	<i>P. reclinata</i>	0.938029	0.061971	0.011415	82.177
PDAC25_Ja_Su	<i>P. canariensis</i>	0.98664	0.01336	0.006269	157.391
PDAC25_Ja_Su	<i>P. reclinata</i>	0.991066	0.008934	0.007534	131.544
PDAC3_Bk_Mo	<i>P. canariensis</i>	0.859644	0.140356	0.012516	68.684
PDAC3_Bk_Mo	<i>P. reclinata</i>	0.854289	0.145711	0.013542	63.084
PDAC4_Ra_Mo	<i>P. canariensis</i>	0.841218	0.158782	0.014	60.089
PDAC4_Ra_Mo	<i>P. reclinata</i>	0.838607	0.161393	0.014568	57.565
PDAC5_Ji_Mo	<i>P. canariensis</i>	0.856681	0.143319	0.012422	68.967
PDAC5_Ji_Mo	<i>P. reclinata</i>	0.855472	0.144528	0.012141	70.461

PDAC6_Br_Mo	<i>P. canariensis</i>	0.821729	0.178271	0.016209	50.696
PDAC6_Br_Mo	<i>P. reclinata</i>	0.81079	0.18921	0.017619	46.018
PDAC7_Az_Mo	<i>P. canariensis</i>	0.823104	0.176896	0.015826	52.01
PDAC7_Az_Mo	<i>P. reclinata</i>	0.818516	0.181484	0.016576	49.381
PDAC8_Fa_Mo	<i>P. canariensis</i>	0.816507	0.183493	0.014251	57.293
PDAC8_Fa_Mo	<i>P. reclinata</i>	0.814917	0.185083	0.015288	53.304
PDAC807_Si_Eg	<i>P. canariensis</i>	0.948102	0.051898	0.008496	111.593
PDAC807_Si_Eg	<i>P. reclinata</i>	0.947875	0.052125	0.009383	101.017
PDAC9_Bi_Mo	<i>P. canariensis</i>	0.835152	0.164848	0.016573	50.393
PDAC9_Bi_Mo	<i>P. reclinata</i>	0.824877	0.175123	0.01753	47.055

<sup>a</sup>The ancestry proportion was estimated using *admixr*; <sup>b</sup>X is the focal individual whose ancestry we are testing (Judean date palm or North African variety); <sup>c</sup>outgroup species used; <sup>d</sup>proportion of West Asian date palm ancestry in the North African and Judean date palm genomes; <sup>e</sup>proportion of *P. theophrasti* ancestry; <sup>f</sup>standard error of the *f4*-ratio statistic calculated using the block jackknife; <sup>g</sup>Z-score is the number of standard errors the *f4*-ratio statistics is from 0

**Table S8. Genotypes of the Judean date palms at loci controlling fruit color (*VIR* locus) and sugar content (invertase genes region).**

<i>Accession</i>	<i>Genotype at the VIR locus</i>	<i>Genotype at the invertase genes region</i>
<i>Methuselah</i>	<i>VIR</i> <sup>+</sup> / <i>VIR</i> <sup>+</sup>	No homozygote deletion
<i>Hannah</i>	<i>vir</i> <sup>saf</sup> / <i>VIR</i> <sup>IM</sup>	No homozygote deletion
<i>Adam</i>	<i>VIR</i> <sup>+</sup> / <i>VIR</i> <sup>+</sup>	No homozygote deletion
<i>Judith</i>	<i>vir</i> <sup>saf</sup> / <i>vir</i> <sup>saf</sup>	No homozygote deletion
<i>Boaz</i>	<i>VIR</i> <sup>+</sup> / <i>VIR</i> <sup>IM</sup>	No homozygote deletion
<i>Jonah</i>	<i>VIR</i> <sup>IM</sup> / <i>VIR</i> <sup>IM</sup>	No homozygote deletion
<i>Uriel</i>	<i>VIR</i> <sup>+</sup> / <i>VIR</i> <sup>+</sup>	No homozygote deletion

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