

Supporting Information

Article title: **Population genomics in wild tomatoes - the interplay of divergence and admixture**

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The following **Supporting Information** is available for this article:

Supplemental Methods Materials and methods for flow cytometry and notes on $\partial a\partial i$.

Fig. S1 Read mapping data by individual

Fig. S2 Polymorphism count by category

Fig. S3 Count and read coverage of polymorphisms

Fig. S4 Principle component analysis

Fig. S5 STRUCTURE Likelihoods

Fig. S6 Heterozygosity for all accessions

Fig. S7 F_{ST} between species and subpopulations of *S. peruvianum*

Fig. S8 Relationship between heterozygosity and latitude in *S. chilense*

Fig. S9 $\partial a\partial i$ data and residuals

Fig. S10 Comparison of parental and hybrid phenotypes

Fig. S11 Flow cytometry data

Fig. S12 Haplotypes of hybrid individuals identified with HAPMIX

Fig. S13 Number of seed and seed-like structures for all crosses

Fig. S14 ML phylogeny with all data

Fig. S15 Phenotype of *S. chilense* LA0752

Fig. S16 Location of wild tomato collections

Fig. S17 Phenotypes of herbarium specimens

Table S1 Information on the individual accessions used in this study

Table S2 Data of accessions used only for $\partial a\partial i$ analysis

Table S3 Heterozygosity for all accessions

Table S4 Maximum likelihood parameters returned by $\partial a\partial i$

Table S5 Number of seeds and seed-like structures for all individual crosses

Ploidy (C-value) determination by flow cytometry

To determine if two cryptic hybrid individuals (LA1930, LA1932) were allopolyploids, they, two *S.per* (LA2732, LA1954), *S.chi*-LA2930, and two diploid *S. lycopersicum* controls were analyzed on the FACS Aria II Flow Cytometer. Leaf tissue from one individual from these accessions was chopped in 500 μ L of 15 mM PBS buffer containing 2 mM EDTA, 15 mM 2-Mercaptoethanol, 0.1% Triton X-100, 0.5 mM Spermine, 100 μ g/mL RNase, and 5 μ g/mL propidium iodide. The nuclei suspension was then run through a 50 μ m filter and the filtered nuclei were then immediately analyzed. A minimum of 10,000 nuclei from each accession were analyzed. Samples were normalized to the diploid *S. lycopersicum* controls. The flow cytometry data for all samples is shown in Fig. S12.

$\partial a \partial i$ Notes

Our analysis using $\partial a \partial i$ highlighted two informative problems. First, the number of singleton SNPs appeared to be underestimated, perhaps due to low sequencing coverage of these rare variants (Nielsen et al. 2011). We addressed this by masking singletons in the JSFS before running $\partial a \partial i$. Second, according to $\partial a \partial i$, too many high-frequency shared derived alleles were detected. This could result from ancestral state misidentification, and a misidentification rate of 1.1 – 1.5% in the outgroup could account for these high-frequency shared derived alleles. To address this potential problem, an additional outgroup misidentification rate parameter was added to the model.

According to the branching order in the coalescent analysis and the ML analysis using all data, the divergence of *S. chilense* predates the divergence between *S. peruvianum* and the Arc+Esc lineage. This is surprising and goes against what is known from morphology and the literature. However, a large degree of uncertainty on the branching order of these lineages is evident (for example, if taxa with >10% admixture are removed), and it is also difficult distinguish these patterns from a concurrent divergence of all three lineages (a true polytomy).

Therefore, we wanted to directly test four alternative evolutionary scenarios to help determine the branching order of *S. chilense*, *S. peruvianum*, and Arc+Esc. For this we used $\partial a \partial i$ because it is able to estimate demographic parameters from a three-dimensional site frequency spectrum (Gutenkunst et al. 2009). The four alternative hypotheses are: (Arc+Esc, (*S. chilense*, *S. peruvianum*)), (*S. chilense*, (Arc+Esc, *S. peruvianum*)), (*S. peruvianum*, (*S. chilense*, Arc+Esc)), or simultaneous divergence (polytomy). The model written for this purpose had two ancestral splits (T1 and T2) which were both followed by growth in all populations. The time interval of T1 was restricted to 0 to estimate a simultaneous speciation event.

Unfortunately, the multispecies Arc+Esc lineage did not have an appropriate site frequency spectrum for demographic analysis in $\partial a\partial i$. As an alternative we downloaded 17 *S. pimpinellifolium* ('Esculentum group) accessions reported by Lin et al. 2014 (NCBI SRA SRP045767). These are described in Supplemental Table S2. All of these *S. pimpinellifolium* accessions were then used to represent the Arc+Esc group. After excluding the admixed individuals identified in STRUCTURE, the three-dimensional JSFS was derived from 92,939 synonymous variants with a nonzero MAF. Ten independent runs of 10,000 iterations and 10 bootstraps were computed for each scenario and the scenario with the highest composite log-likelihood was selected. The model with the highest composite likelihood was (Arc+Esc), (*S. chilense*, *S. peruvianum*)), supporting *S. chilense* and *S. peruvianum* as sister species:

The four alternative demographic scenarios tested in $\partial a\partial i$ and the maximum log-likelihood returned from 10 independent runs from randomized starting parameters.				
Hypothesis	<i>S. chilense</i> diverges first	<i>S. peruvianum</i> diverges first	Arc+Esc diverges first	Simultaneous divergence
Demographic scenario				
Maximum log-likelihood	-20,538	-23,119	-20,059	-22,026

Fig. S1. (a) Number of reads mapping to the reference genome sequence for the 80 wild tomato accessions. The colored segment represents the proportion of reads uniquely aligning to the genome and the gray segment the proportion of reads non-uniquely aligned or not aligned. Mapping data for these and the additional accessions is in Supplemental Table S1. **(b)** Distribution of read coverage in the 80 libraries following mapping.

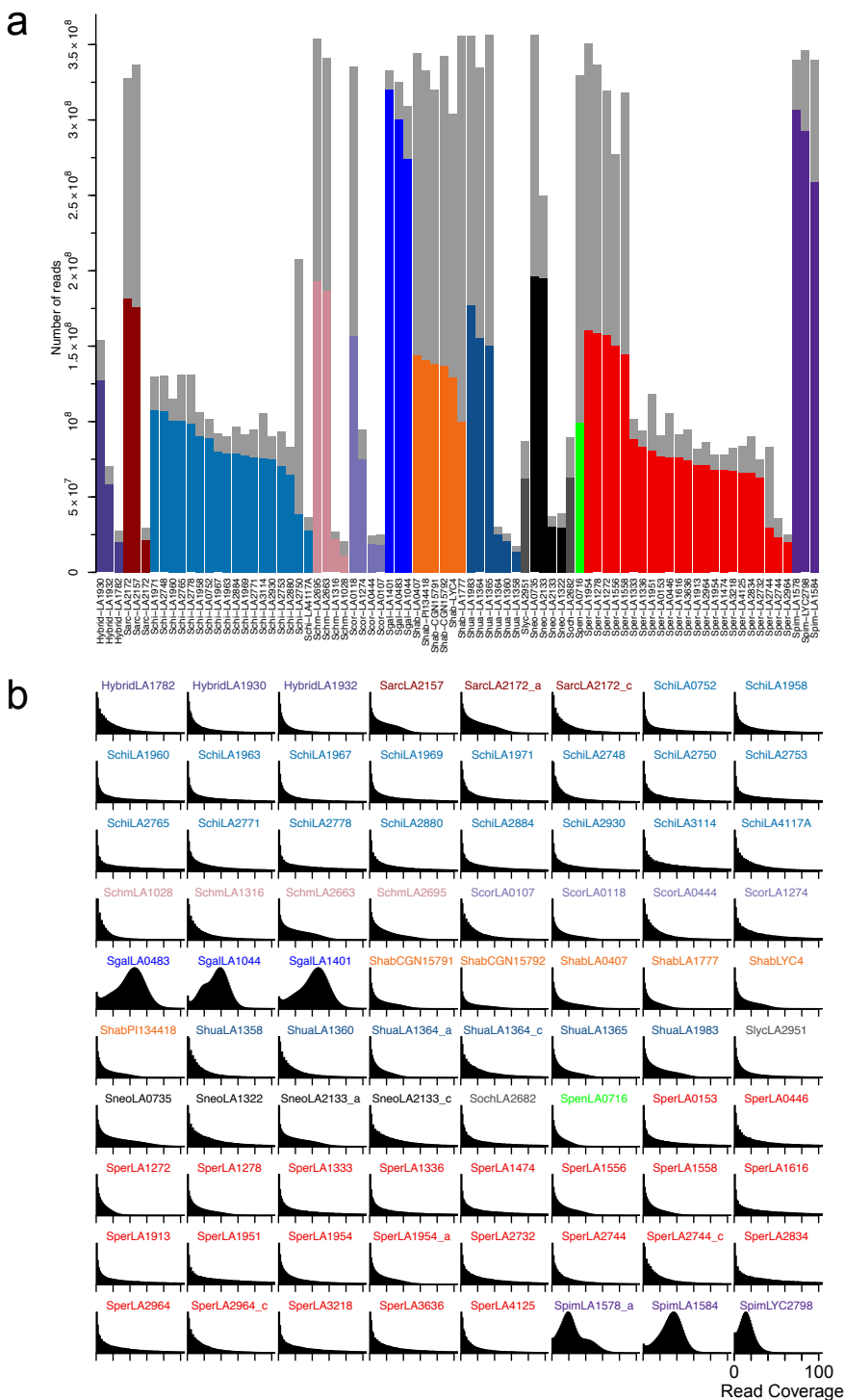


Fig. S2. Number of positions (y-axis) sequenced to a minimum coverage (x-axis) in all 80 individuals. The number of positions is divided into categories following the reference GFF file. Note that the number of positions sequenced to a minimum depth also includes all positions sequenced to a greater depth of coverage. For example, 527,655 positions were sequenced to ≥ 10 coverage but only 56,433 had a depth of 10. The remaining positions had a depth >10 .

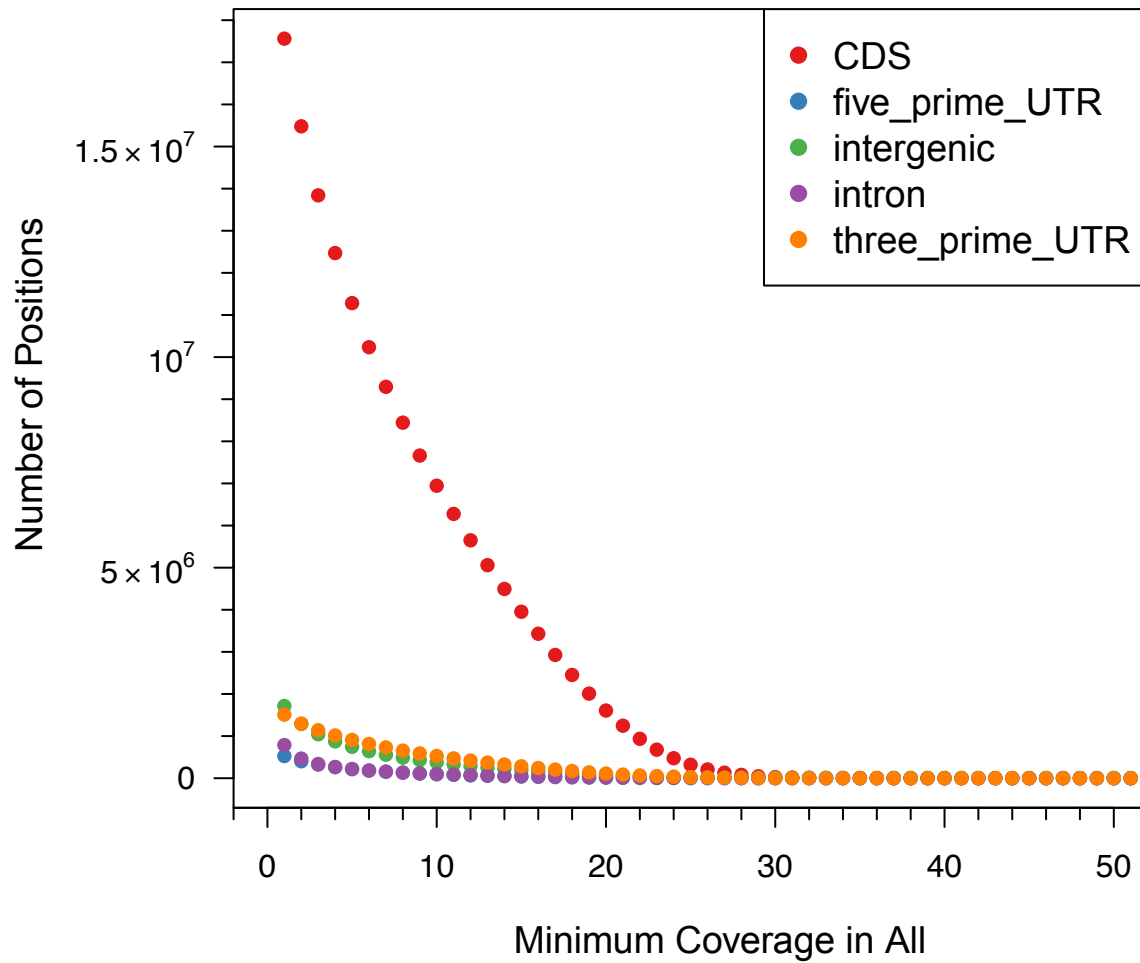


Fig. S3. Annotation and coverage in the high-quality variant dataset. (a) Number of variants assigned as 5'UTR, CDS (synonymous + nonsynonymous), intron, 3'UTR, and intergenic. The number of positions which change a start or stop codon and nonsense mutations are also given (b) Median depth of coverage at variable sites for the classes in (a). (c) The distribution of read depth at variable positions. Depth (from 0-250) is on the x-axis.

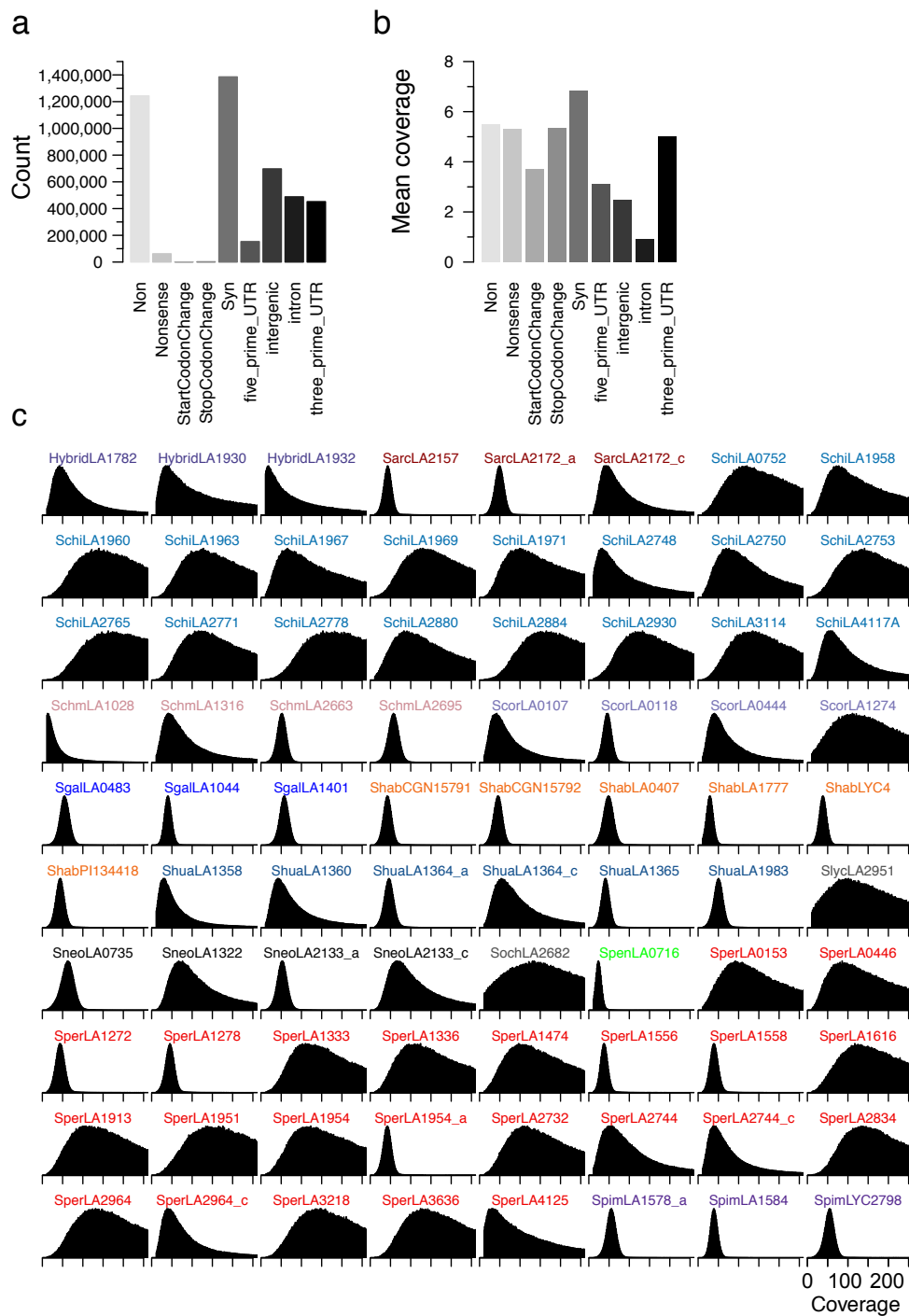


Fig S4. Principle component analysis of all accessions excluding the 'Hirsutum' and 'Lycopersicon' groups. The first principle component explained 29.98% of the variance and delineated *S. chilense* (*S.chi*) from the 'Arcanum' and 'Peruvianum' group species. Species abbreviations are given in Fig. 2.

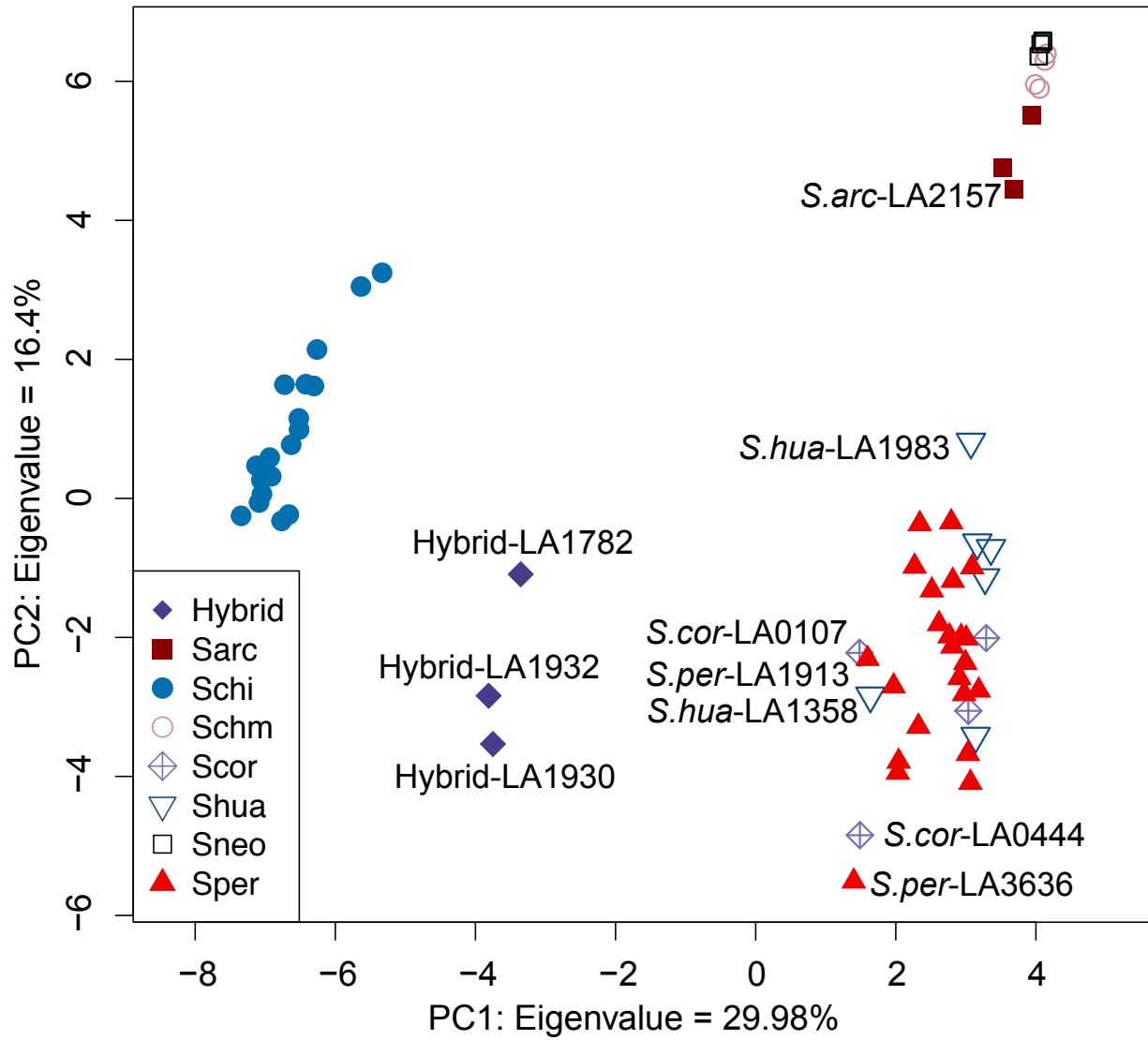


Fig. S5. Log-likelihood of the data from STRUCTURE. **(a)** The average log likelihood \pm s.d. over 10 runs (y-axis) modelled for $K=1 - K=7$ (x-axis). **(b)** The average difference between successive likelihood values of K , $L'(K) = L(K) - L(K-1)$. **(c)** The second order rate change of $L'(K)$, $|L''(K)| = |L'(K+1) - L'(K)|$. **(d)** The ad hoc ΔK statistic which is the average second order rate change ($|L''(K)|$) divided by the standard deviation of $L(K)$ [see Evanno *et al.* (2005) for full details]. The log likelihood and ΔK both indicate that $K=3$ is most likely.

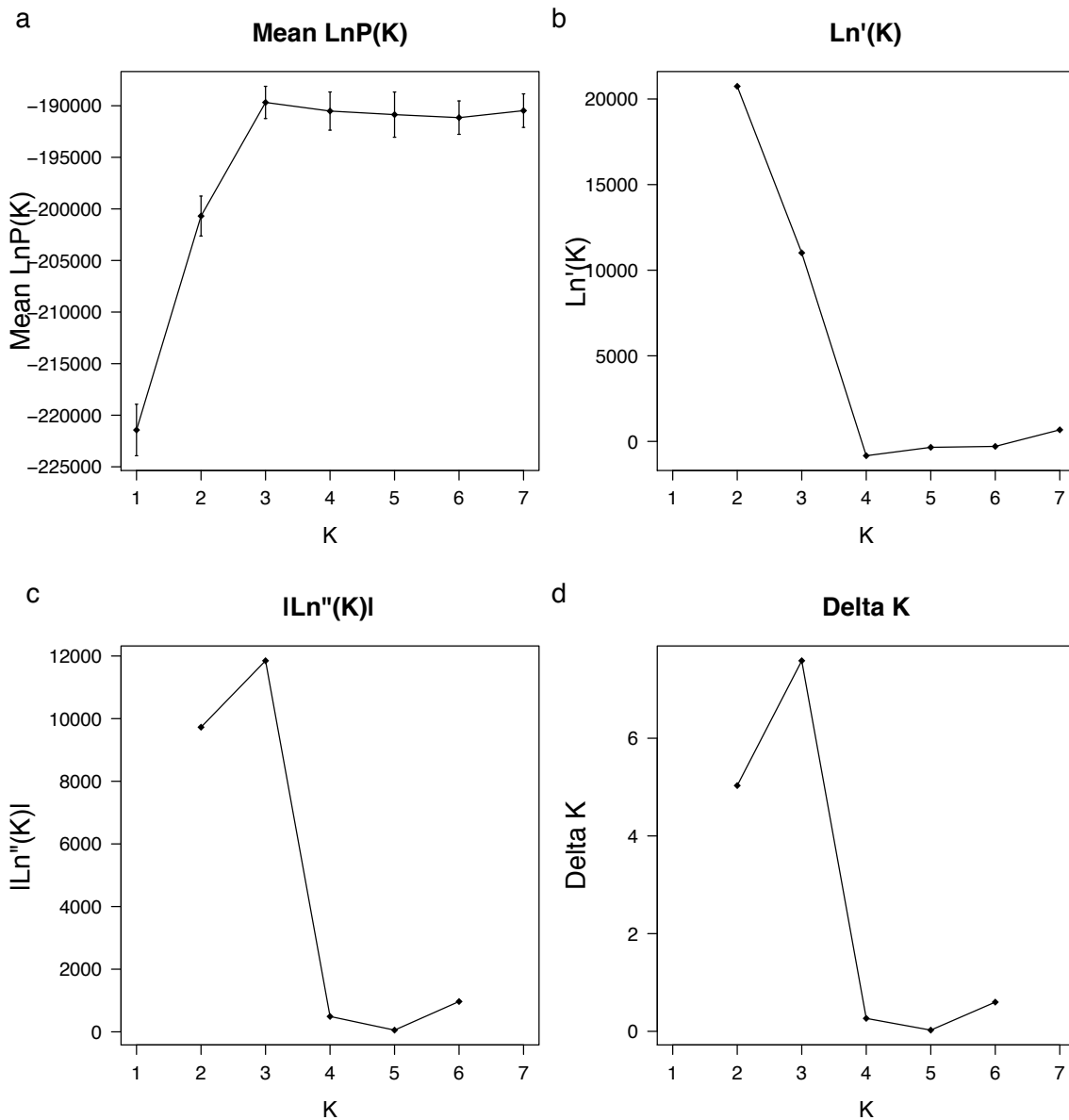


Fig S6. Heterozygosity per accession. Individual heterozygosity was calculated for each accession by dividing the number of heterozygous sites by the number of positions. For example, from the 4,866,729 bi-allelic polymorphisms 154,538 had ≥ 10 coverage and were heterozygous in *S.chi*-LA1958. These bi-allelic polymorphisms were drawn from the 34,617,016 positions with ≥ 10 coverage with $\leq 50\%$ missing data. However, only 28,448,837 of the 34,617,016 positions had ≥ 10 coverage in *S.chi*-LA1958. Thus, the heterozygosity for this accession is 154,538 divided by 28,448,837.

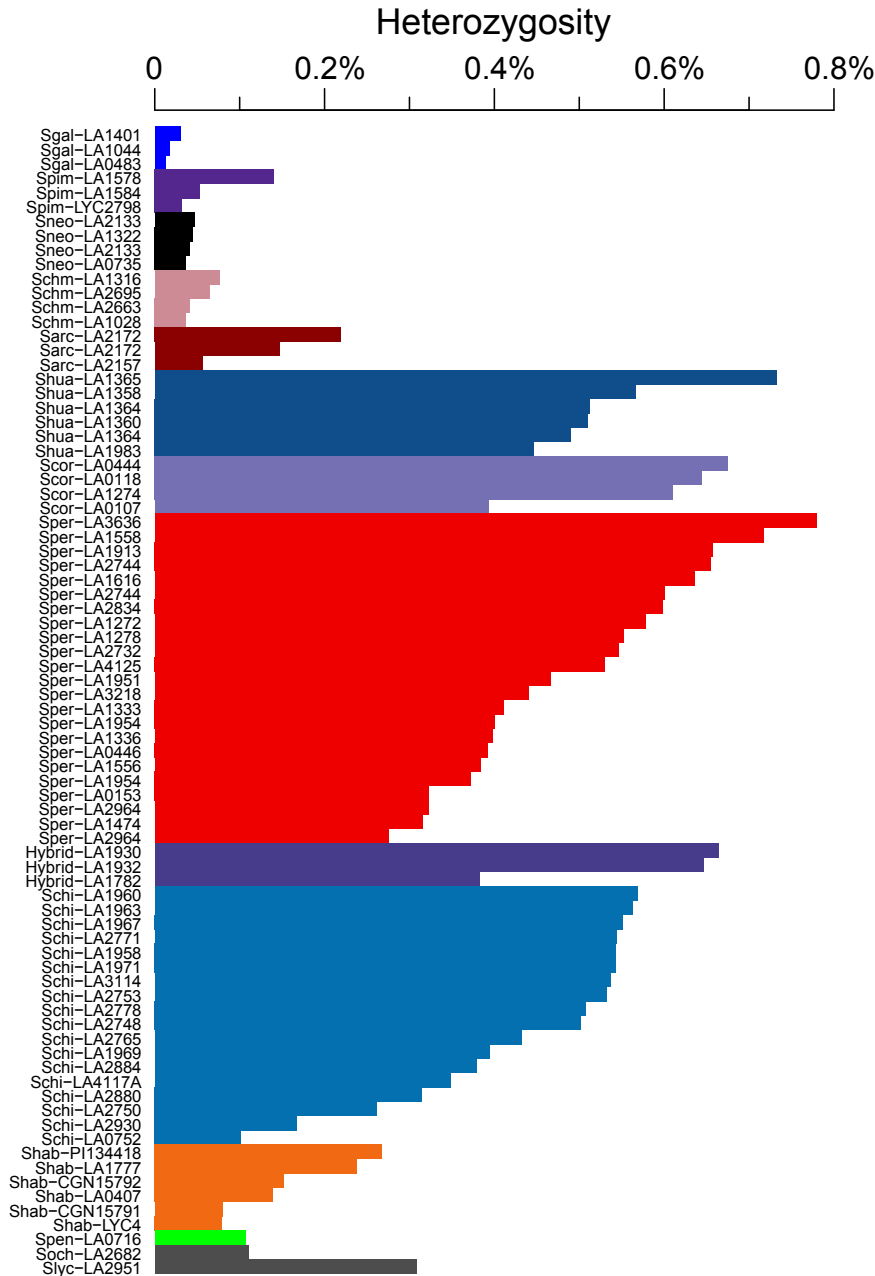


Fig S7. F_{ST} between species and subpopulations of *S. peruvianum*. The mean F_{ST} was calculated using VCFTools for all genes in pairwise comparisons between all populations shown. The species/accessions included in the Arcanum and Esculentum species groups is indicated in Fig. 2. For the *S.per* subpopulations were assigned based on the STRUCTURE result (Fig. 3) with a majority rule.

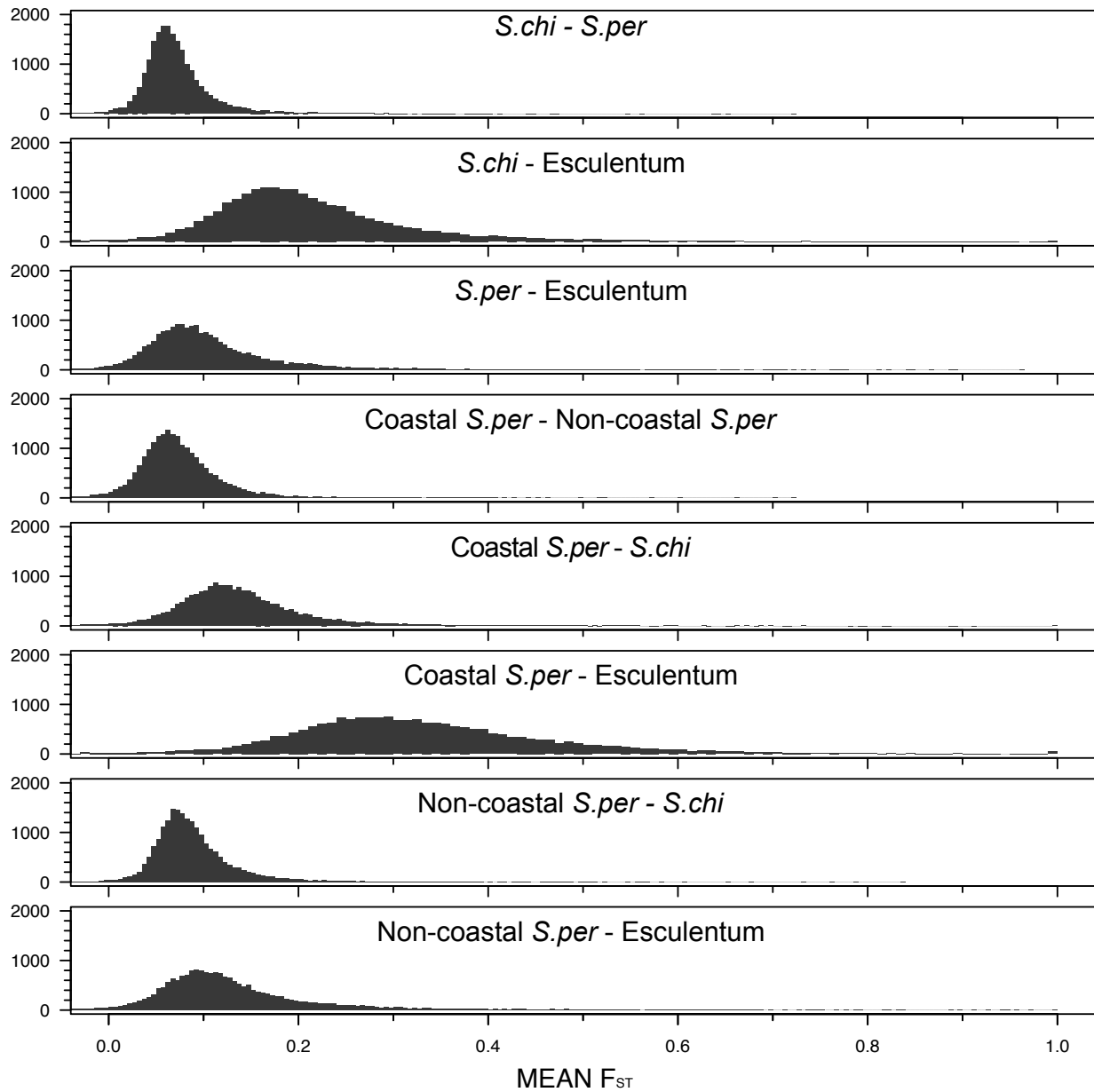


Fig. S8. The relationships of heterozygosity (x-axis) and latitude (y-axis) of *S. chilense* accessions. The anomolous *S. chilense* accession LA0752 is labelled.

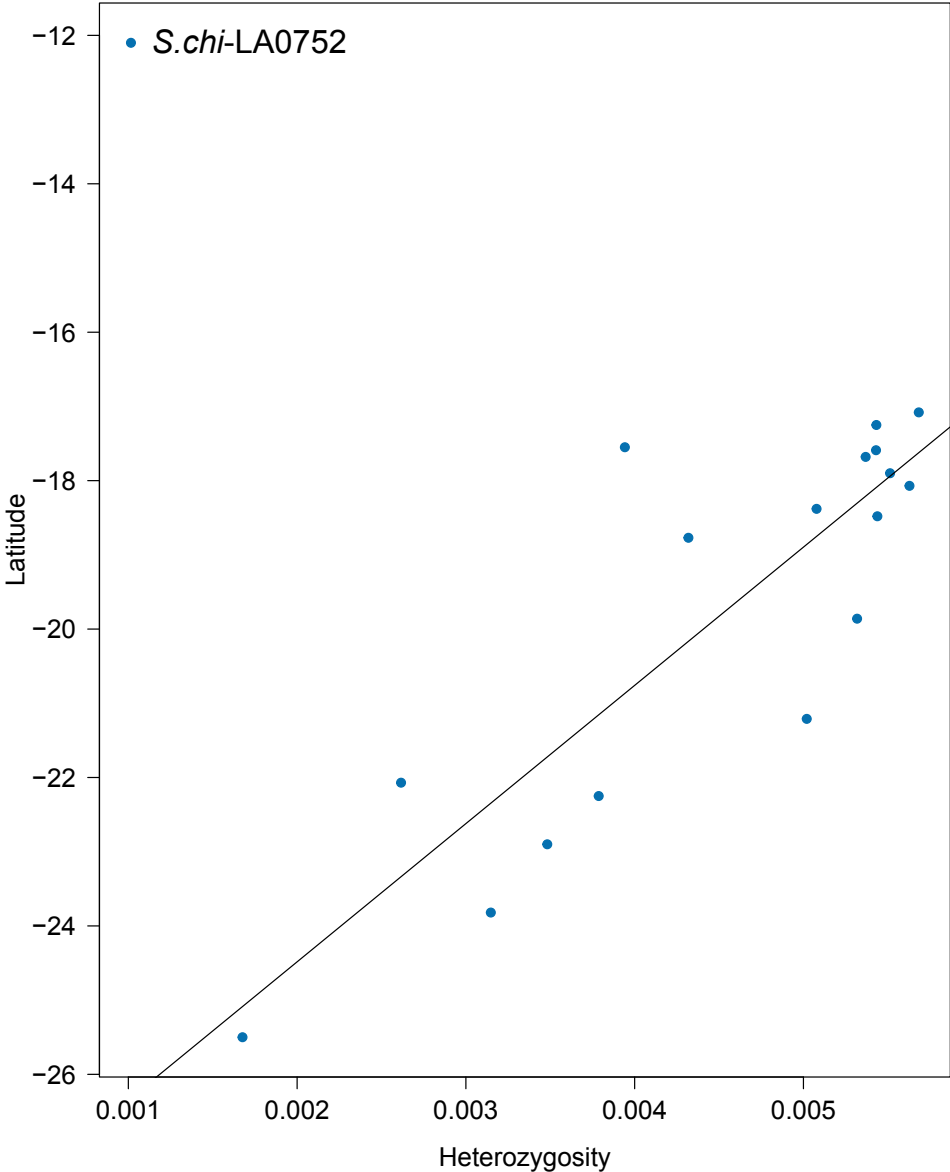


Fig. S9. Fit of the *S. chilense* and *S. peruvianum* speciation event to the model in $\partial a \partial i$. (a) The synonymous joint site frequency spectrum (JSFS) of *S. chilense* and *S. peruvianum*. (b) the modeled JSFS. (c) The residuals (data - model). (d) Histogram of the residual values showing a good model fit.

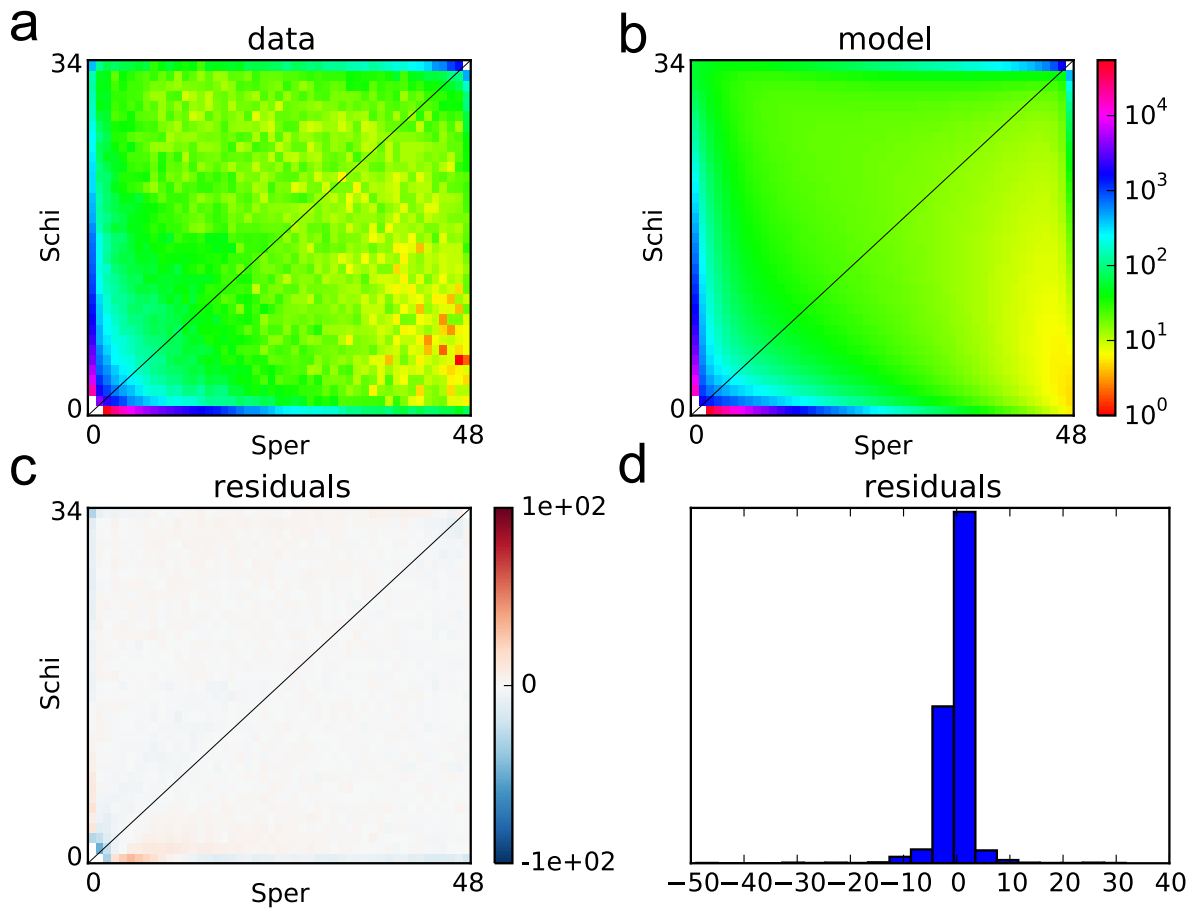


Fig. S10. Distinct phenotypes of hybrid populations LA1930 and LA1932. Approximately four seeds from LA1930, LA1932, *S.chi*-LA2930, *S.chi*-LA0572, three *S.per*, and one *S.cor* accession were germinated and grown together in a greenhouse in Düsseldorf, Germany (29 plants total). Measurements were taken after three months for all individuals and grouped by accession. Bars with no shared letters indicates significant difference between groups (pairwise t-test, $P < 0.01$) and error bars show the s.e.m. Measurements for **(a)** Leaf length and **(b)** stem diameter were taken at nodes 1 through 10 for 3-5 individuals per accession. **(c)** The number of lateral branches >5 cm.

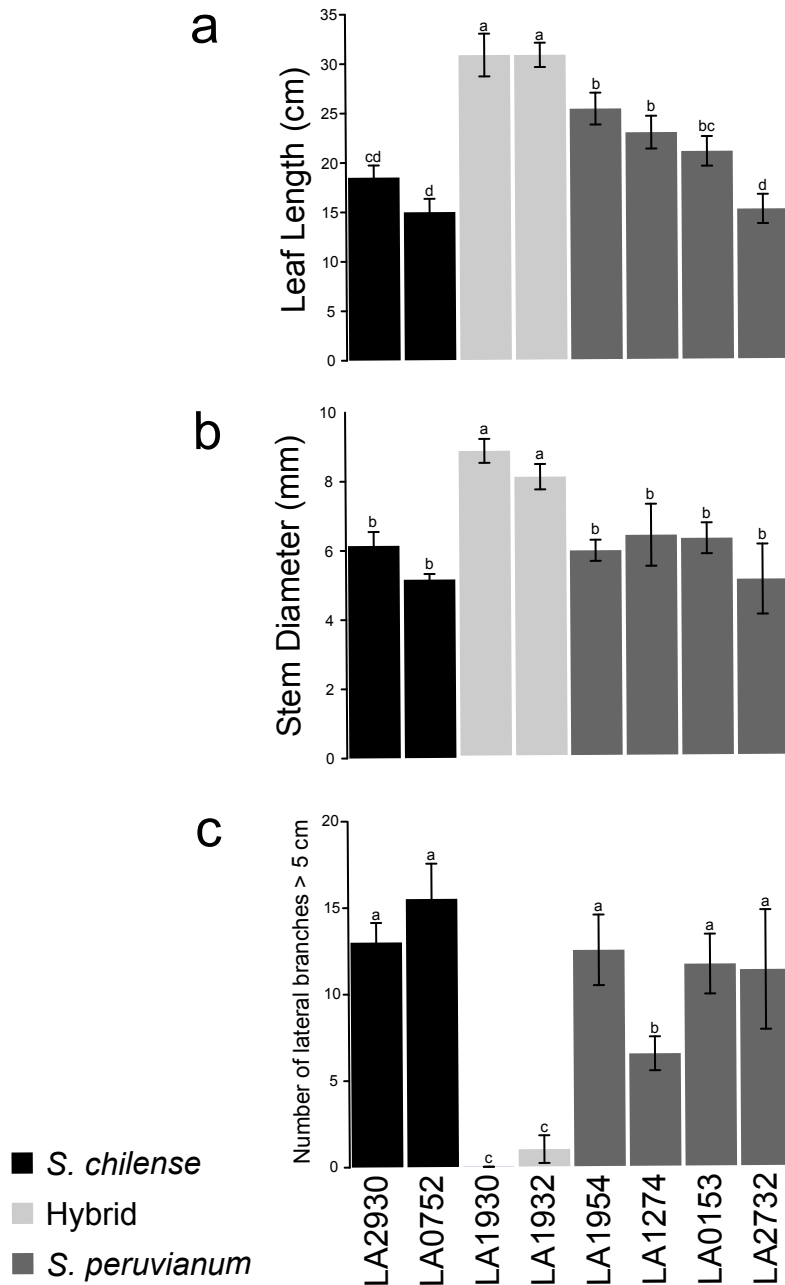


Fig. S11. Flow cytometry results. The two-dimensional plots show side scattered light (y-axis) and propidium iodide intensity (x-axis). The ploidy level gates were determined from the first wt tomato control and confirmed again with the same and a second diploid cultivated control.

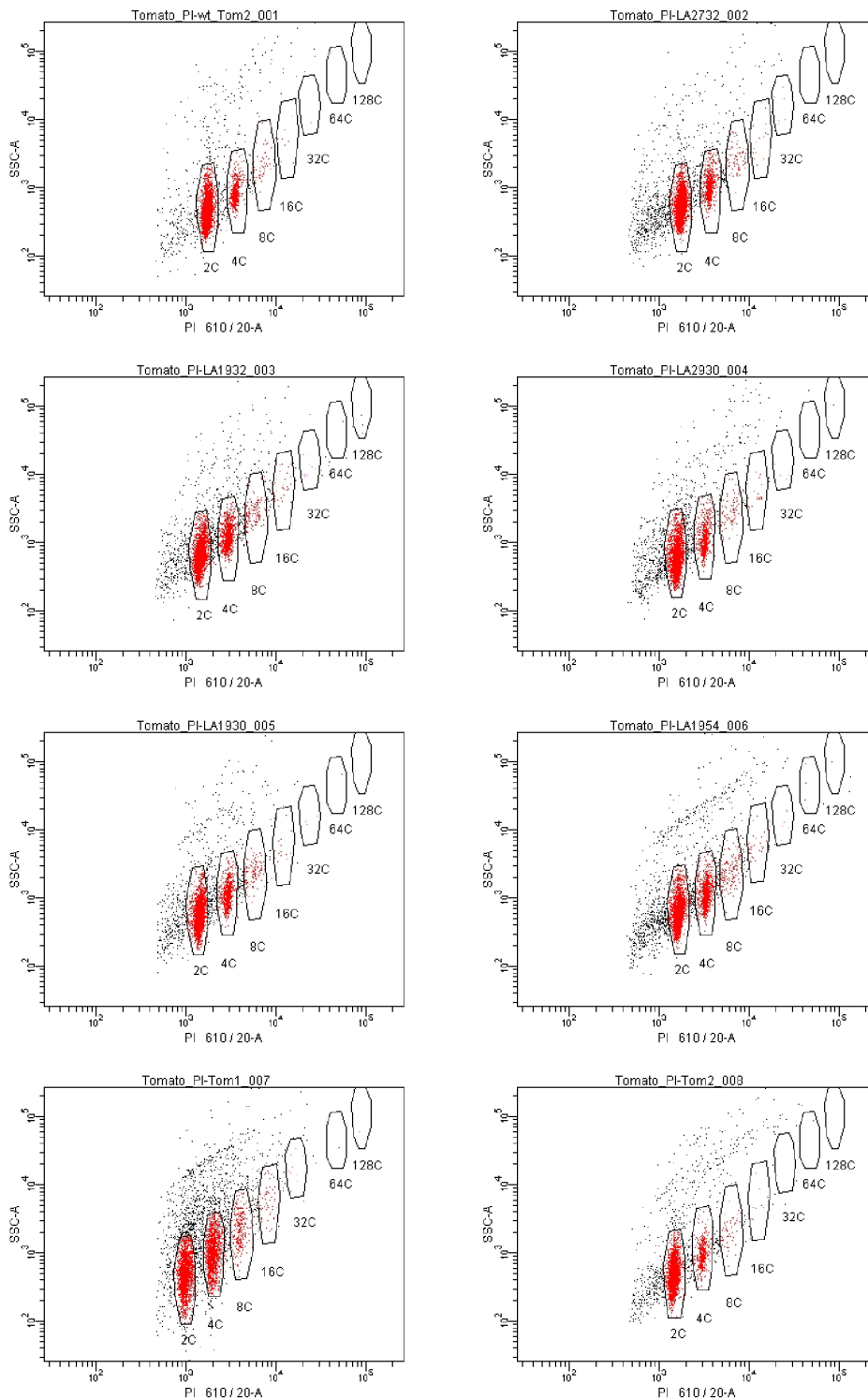
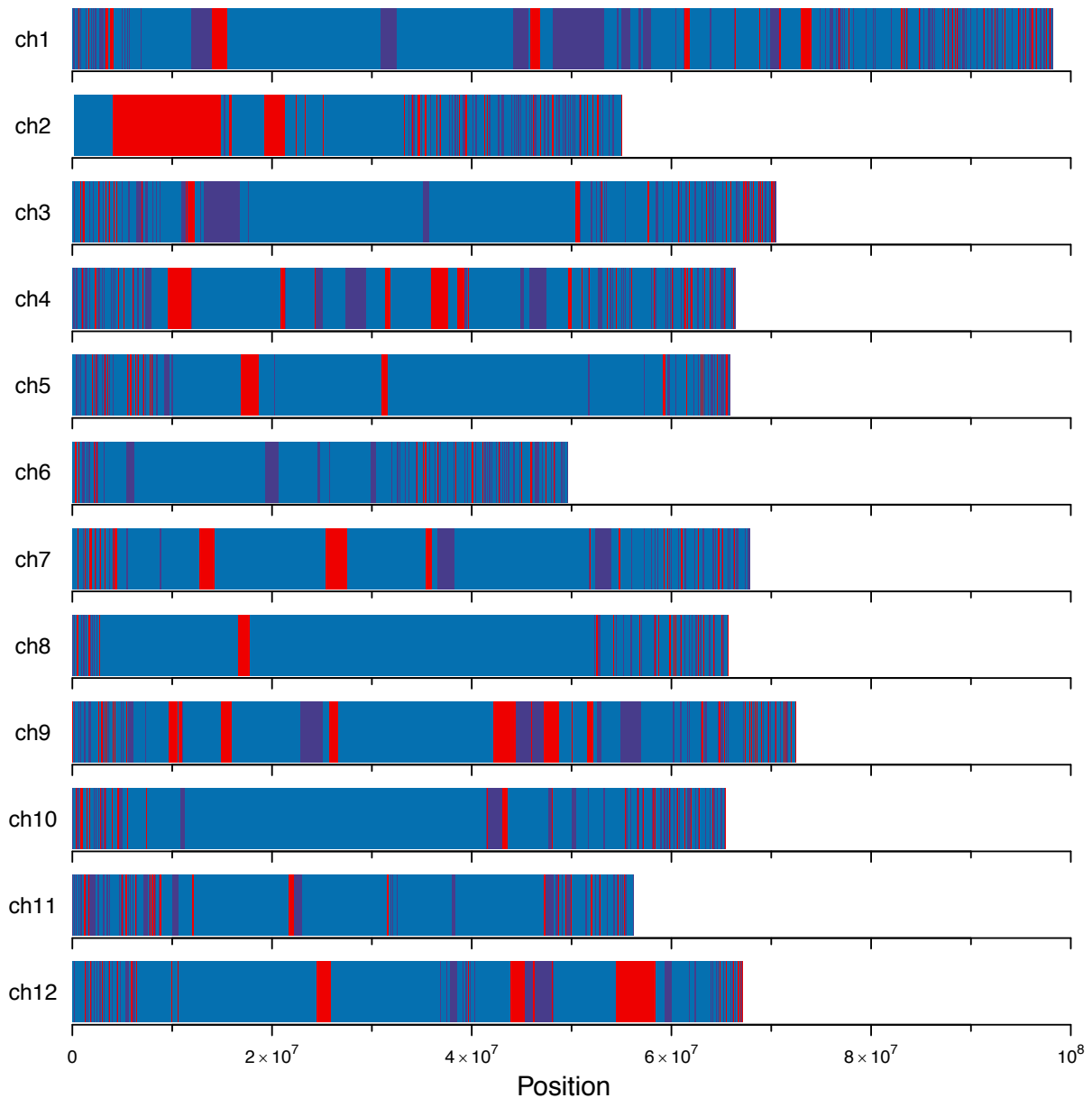
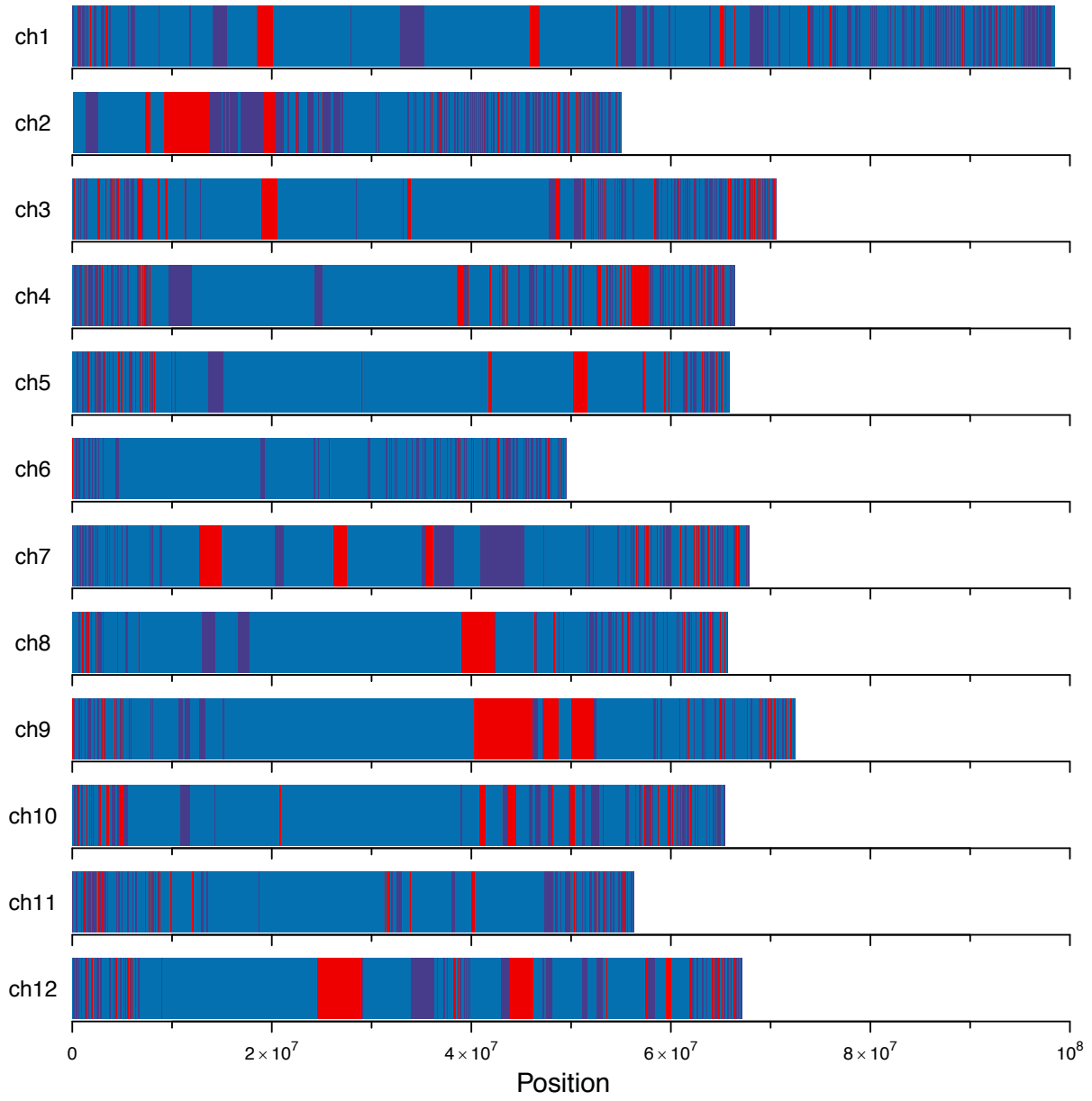


Fig. S12. Haplotype blocks identified in three hybrid individuals from HAPMIX. Parental haplotype blocks were identified in the three individual accessions identified as hybrids in this study. Blocks were assigned using all accessions from the parental species *S.chi* and *S.per*. Blocks were then plotted to the genomic position and colored depending on the parental species (red = *S.per* and blue = *S.chi*). Note that there is little coverage in non-genic regions for these accessions because it is RNAseq data, so the assignment of large blocks to *S.chi* in non-genic regions might be misleading. Data is shown for (a) LA1782, (b) LA1930, and (c) LA1932.

(a)



(b)



(c)

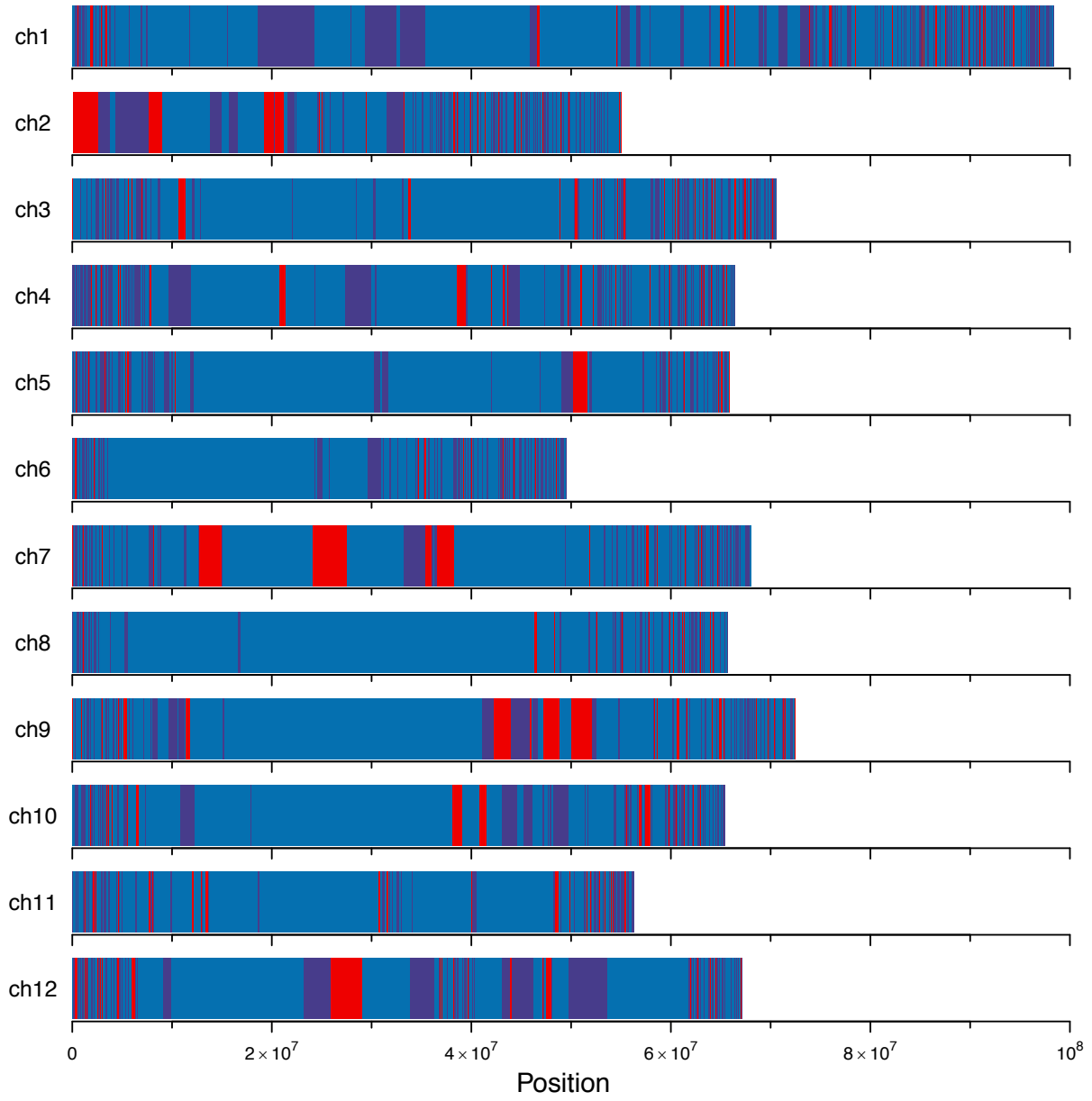


Fig. S13. Results of the crossing study. The number of seeds (top) and seed-like structures (bottom) for all crosses are shown as box and whisker plots. Crosses involving the hybrids are in blue (left), interspecific crosses are in green (middle) and intraspecific crosses are in black (right).

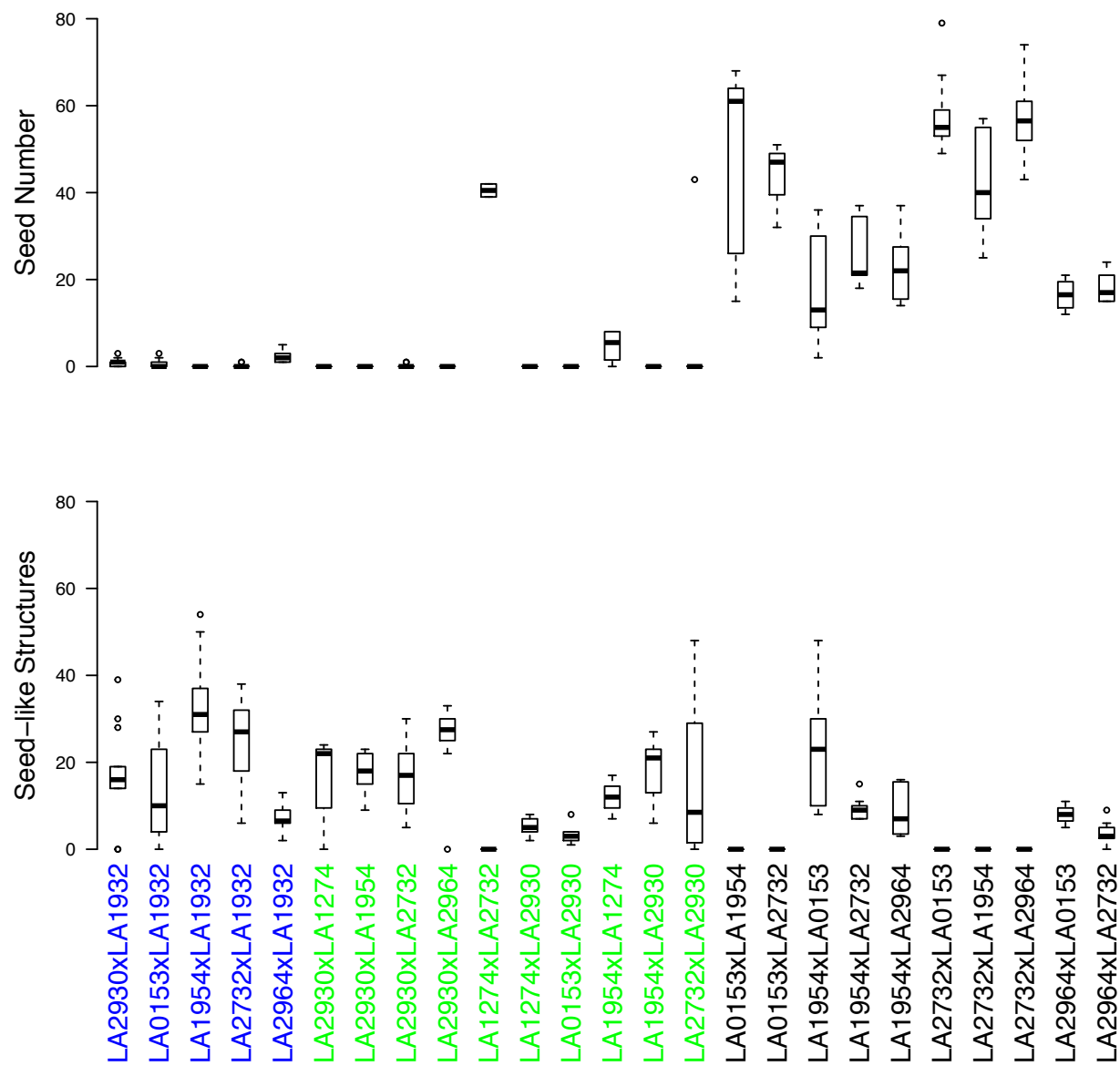


Fig. S14. Maximum-likelihood phylogeny with all accessions using 712,432 synonymous polymorphisms with less than 50% missing data.

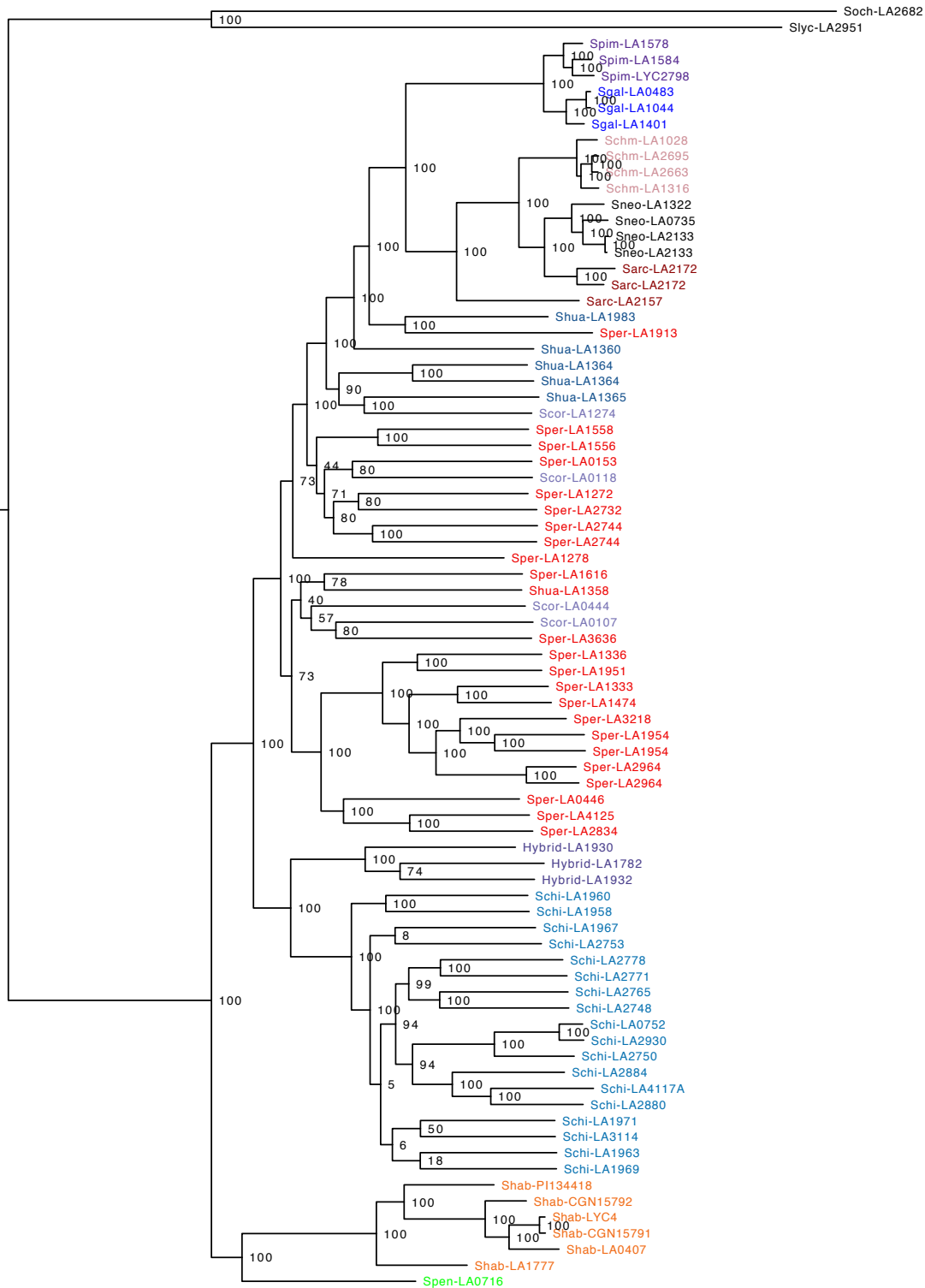


Fig. S15. Phenotype of the cryptic *S. chilense* populations LA0752. (a) Typical flower of *S.chi*-LA0752. (b) Typical leaflet of *S.chi*-LA0752 from several individuals. (c) Three-week-old individuals from *S.chi*-LA0752, *S. chilense* (LA2930), *S. peruvianum* (LA0153, LA1954 and LA2732), *S. corneliomulleri* (LA1272), and the two *S.chi* x *S.per* hybrid accessions (LA1930 and LA1932).

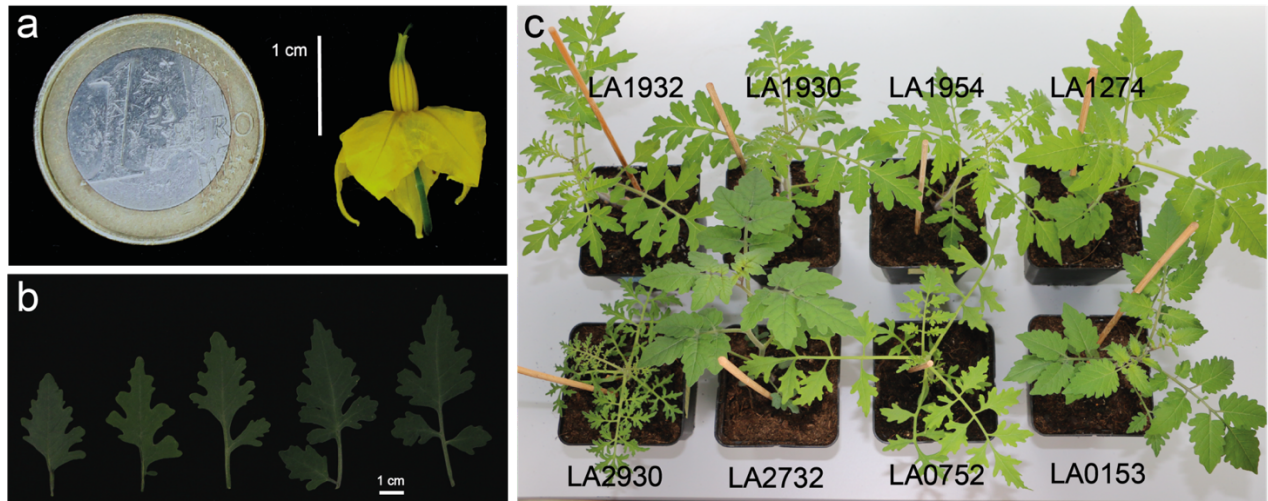


Fig. S16. Known distribution of *S. chilense*. (a) All known collections of *S. chilense* (dataset kindly provided by Sandra Knapp, Natural History Museum, London) show the discrete northern populations identified as hybrids in this study. *S.chi*-LA0752 is shown as the most northern *S. chilense* population. The 2004 collection sites of *S. chilense* (Roselius *et al.* 2005) are also shown (Nazca [NAZ], Tacna [TAC], Moquegua [MOQ], and Quicacha [QUI]). (b) Close up of the collection gap between *S. chilense* and hybrid individuals previously described as *S. chilense*. There are collections from other species within the gap which begins around 72° (indicated by a line).

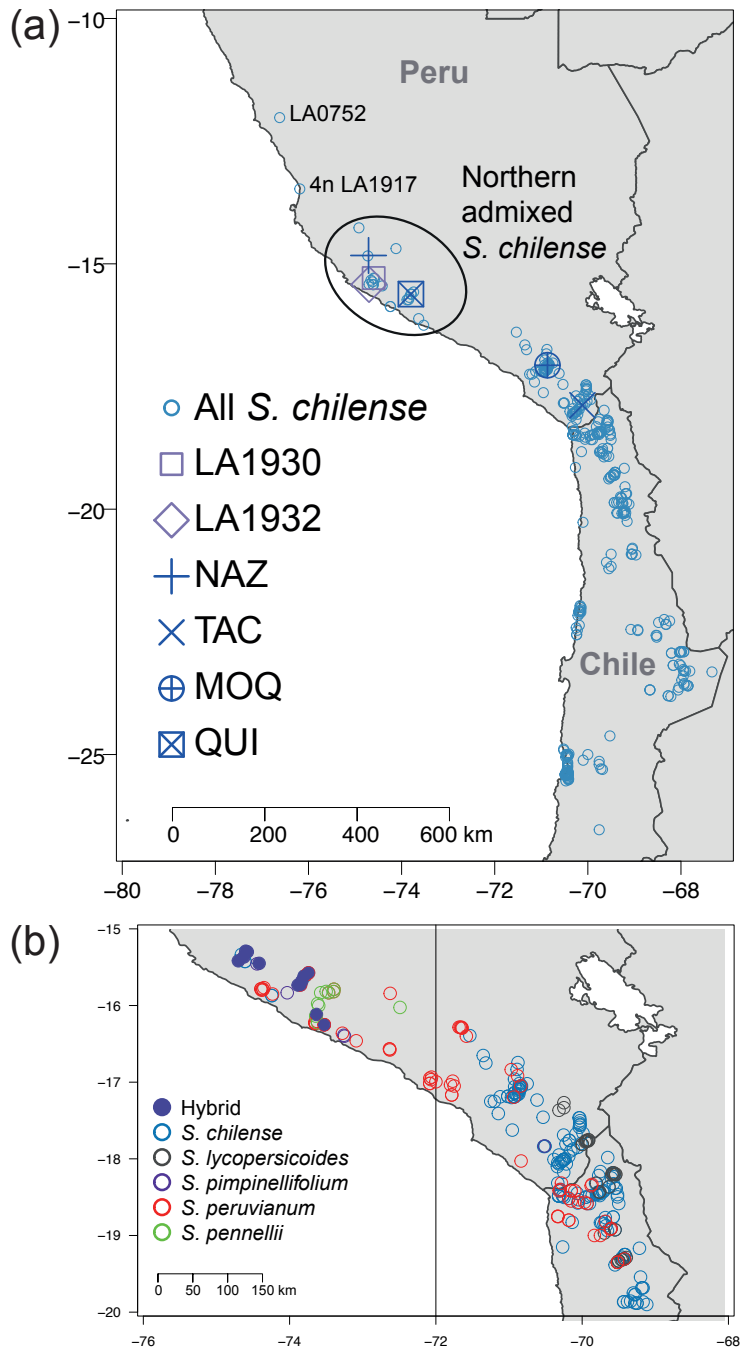
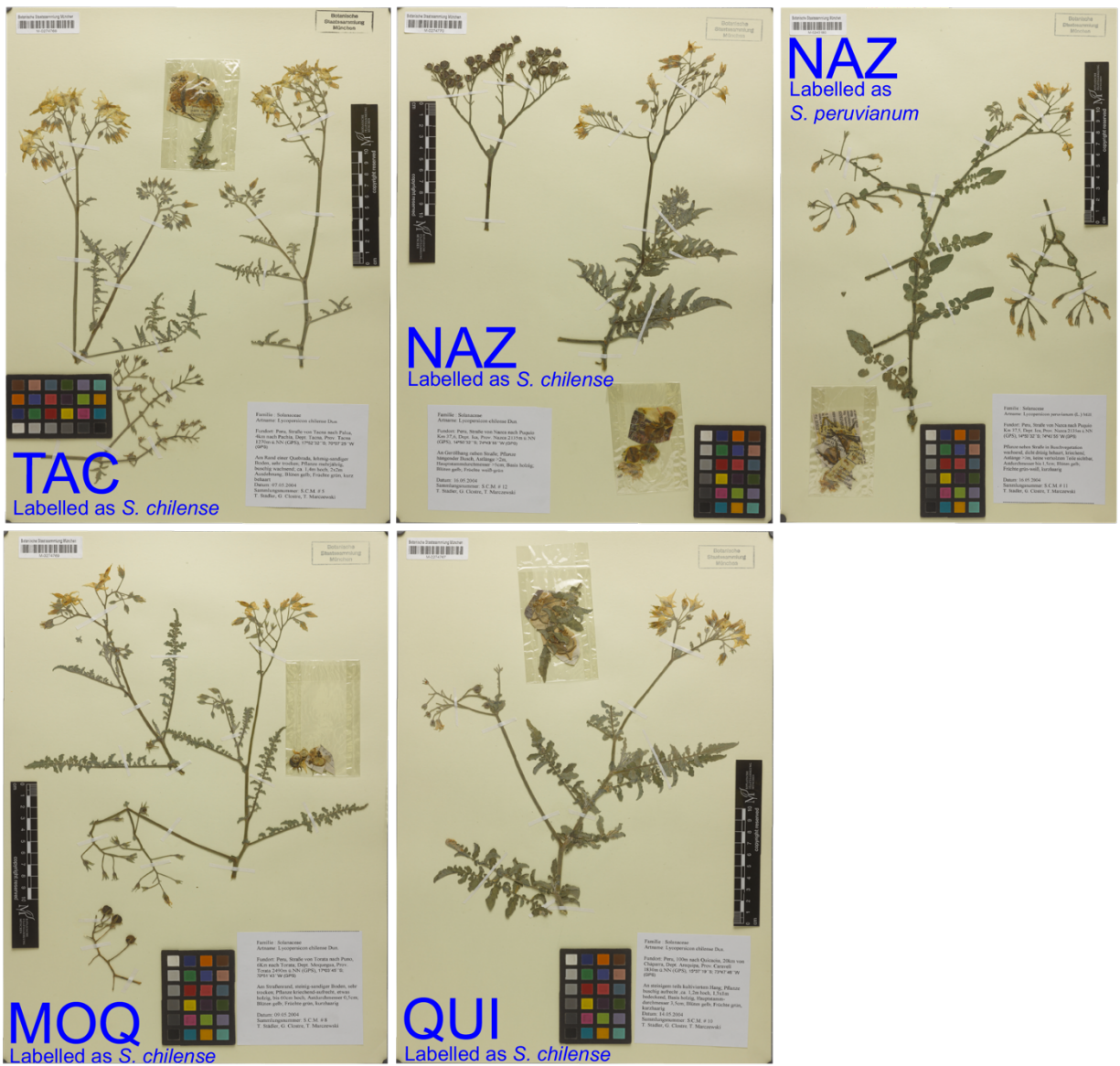


Fig. S17. Herbarium voucher specimens from Roselius *et al.* 2005. The location of these collections is indicated in Fig. S16. Note the similar phenotype of QUI and *S. chilense* NAZ, and the similarity of these collections to LA1930 and LA1932 in Fig. 6.



Supplemental Table 1. Details of the populations and data analyzed in this study.

Id	Species	Species Abbreviation	Study	Duplicate	# Seed-Expansion Generations	# Total Reads	# Positions with MinDepth ≥ 10	# Aligned Reads	% Aligned	Province	Country	Elevation	Latitude	Longitude	Mating System
LA1782	Hybrid	Hybrid	c			27407970	56256043	20,234,125	74%	Arequipa	Peru		-15.36	-74.62	Allogamous-SI
LA1930	Hybrid	Hybrid			2	154021324	55483585	127,682,186	83%	Arequipa	Peru	500	-15.29	-74.6	Allogamous-SI
LA1932	Hybrid	Hybrid			3	70286604	41652129	58,739,548	84%	Arequipa	Peru	1100	-15.42	-74.7	Allogamous-SI
LA2157	S. arcanum	S.arc	a			336528946	269008348	175,818,877	52%	Cajamarca	Peru	1600	-6.51	-78.81	Facultative-SC
LA2172	S. arcanum	S.arc	a	YES		327920754	286177531	181,859,614	55%	Cajamarca	Peru		-6	-78.91	Allogamous-SI
LA2172	S. arcanum	S.arc	c	YES		29277492	55365171	21,413,972	73%	Cajamarca	Peru		-6	-78.91	Allogamous-SI
LA0752	S. chilense	S.chi			5	101970490	70492417	89,227,601	88%	Lima	Peru	1200	-12.1	-76.6	Allogamous-SI
LA1958	S. chilense	S.chi			2	106082222	63533072	90,323,189	85%	Moquegua	Peru	1250	-17.25	-71.25	Allogamous-SI
LA1960	S. chilense	S.chi			2	114906258	71767018	100,616,993	88%	Moquegua	Peru	1850	-17.08	-70.87	Allogamous-SI
LA1963	S. chilense	S.chi			1	90304024	69548517	78,906,333	87%	Tacna	Peru	200	-18.07	-70.32	Allogamous-SI
LA1967	S. chilense	S.chi			2	92496720	57229647	80,442,070	87%	Tacna	Peru	1000	-17.9	-70.16	Allogamous-SI
LA1969	S. chilense	S.chi			3	91197178	68639340	77,708,686	85%	Tacna	Peru	3250	-17.55	-70.03	Allogamous-SI
LA1971	S. chilense	S.chi			3	129813792	64394111	107,887,801	83%	Tacna	Peru	3150	-17.59	-70.04	Allogamous-SI
LA2748	S. chilense	S.chi			3	130209336	43278704	106,619,009	82%	Tarapaca	Chile	800	-21.21	-69.55	Allogamous-SI
LA2750	S. chilense	S.chi			2	207655754	63160144	38,750,231	19%	Antofagasta	Chile	300	-22.07	-70.16	Allogamous-SI
LA2753	S. chilense	S.chi			2	93241972	77690255	70,635,380	76%	Tarapaca	Chile	1650	-19.86	-69.34	Allogamous-SI
LA2765	S. chilense	S.chi			2	130974634	81499570	100,558,213	77%	Arica and	Chile	2400	-18.77	-69.68	Allogamous-SI
LA2771	S. chilense	S.chi			4	94589440	68362578	76,334,713	81%	Arica and	Chile	1800	-18.48	-69.87	Allogamous-SI
LA2778	S. chilense	S.chi			3	131261078	80666920	98,948,038	75%	Arica and	Chile	2900	-18.38	-69.55	Allogamous-SI
LA2880	S. chilense	S.chi			3	82840240	65348571	64,874,285	78%	Antofagasta	Chile	2500	-23.82	-68.22	Allogamous-SI
LA2884	S. chilense	S.chi			3	96468832	74182929	78,708,109	82%	Antofagasta	Chile	2900	-22.25	-68.36	Allogamous-SI
LA2930	S. chilense	S.chi			2	90023102	68485886	74,777,787	83%	Antofagasta	Chile	550	-25.5	-70.42	Allogamous-SI
LA3114	S. chilense	S.chi			2	105516090	76953459	75,527,578	72%	Tacna	Peru	2960	-17.68	-70.08	Allogamous-SI
LA4117A	S. chilense	S.chi	c			36321890	62670271	27,729,862	76%	Antofagasta	Chile	3540	-22.9	-67.94	Allogamous-SI
LA1028	S. chmielewskii	S.chm	c			20718540	32504920	11,328,013	55%	Apurimac	Peru	3000	-13.88	-73.01	Facultative-SC
LA1316	S. chmielewskii	S.chm	c			27282862	55100912	22,331,541	82%	Ayacucho	Peru	2920	-13.39	-73.92	Facultative-SC
LA2663	S. chmielewskii	S.chm	a			341164730	292981762	187,068,096	55%	Cusco	Peru	2500	-13.7	-71.99	Facultative-SC
LA2695	S. chmielewskii	S.chm	a			354078446	257609756	193,294,895	55%	Cusco	Peru	2300	-13.96	-71.76	Facultative-SC
LA0107	S. corneliomulleri	S.cor	c			25207286	52928891	18,464,348	73%	Lima	Peru	60	-13.01	-76.38	Allogamous-SI
LA0118	S. corneliomulleri	S.cor	a			335487318	196520686	156,957,493	47%						Allogamous-SI
LA0444	S. corneliomulleri	S.cor	c			24552910	52196803	18,856,869	77%	Ica	Peru	100	-13.43	-76.13	Allogamous-SI
LA1274	S. corneliomulleri	S.cor			2	94550118	66437945	75,389,974	80%	Lima	Peru	1440	-11.46	-76.9	Allogamous-SI
LA0483	S. galapagense	S.gal	a			325259616	653076473	300,903,738	93%	Galapagos Islands	Ecuador		-0.37	-91.6	Autogamous-SC
LA1044	S. galapagense	S.gal	a			309118016	662395936	274,029,941	89%	Galapagos Islands	Ecuador		-0.28	-90.55	Autogamous-SC
LA1401	S. galapagense	S.gal	a			332617086	663119779	319,895,925	96%	Galapagos Islands	Ecuador	5	-0.24	-91.39	Autogamous-SC
CGN15791	S. habrochaites	S.hab	a			320002236	155245404	138,286,664	43%						
CGN15792	S. habrochaites	S.hab	a			342613468	155762000	137,105,706	40%						
LA0407	S. habrochaites	S.hab	a			344461004	154612310	144,036,116	42%	Guayas	Ecuador	70	-2.18	-79.91	Facultative-SC
LA1777	S. habrochaites	S.hab	a			355583114	107272689	99,785,409	28%	Ancash	Peru	3216	-9.55	-77.67	Allogamous-SI
LYC4	S. habrochaites	S.hab	a			304186072	153083781	129,451,667	43%						
PI134418	S. habrochaites	S.hab	a			333175862	149837952	141,004,224	42%						
LA1358	S. huaylasense	S.hua	c			17653244	46515260	13,994,568	79%	Ancash	Peru	750	-9.53	-77.96	Allogamous-SI
LA1360	S. huaylasense	S.hua	c			25716052	54684140	20,772,720	81%	Ancash	Peru	1490	-9.54	-77.93	Allogamous-SI
LA1364	S. huaylasense	S.hua	a	YES		334812164	158063838	155,785,273	47%	Ancash	Peru	2920	-10.13	-77.39	Allogamous-SI
LA1364	S. huaylasense	S.hua	c	YES		30423044	61774387	25,354,397	83%	Ancash	Peru	2920	-10.13	-77.39	Allogamous-SI
LA1365	S. huaylasense	S.hua	a			356531462	193579086	150,431,862	42%	Ancash	Peru	2450	-10.16	-77.43	Allogamous-SI
LA1983	S. huaylasense	S.hua	a			355914006	253148108	177,188,003	50%	Ancash	Peru	940	-8.69	-77.97	Allogamous-SI
LA2951	S. lycopersicoides	S.lyc			4	87246466	46040360	62,720,955	72%	Tarapaca	Chile	2200	-19.32	-69.45	Allogamous-SI

LA0735	<i>S. neorickii</i>	S.neo	a			356305676	287714940	196,633,336	55%	Huanuco	Peru		-10.4	-76.2	Autogamous-SC
LA1322	<i>S. neorickii</i>	S.neo	c			38679884	69960549	29,641,067	77%	Cusco	Peru	2380	-13.45	-72.43	Autogamous-SC
LA2133	<i>S. neorickii</i>	S.neo	a	YES		249439256	288126468	195,162,489	78%	Azuay	Ecuador	1980	-3.4	-79.18	Autogamous-SC
LA2133	<i>S. neorickii</i>	S.neo	c	YES		37045366	71293598	30,268,114	82%	Azuay	Ecuador	1980	-3.4	-79.18	Autogamous-SC
LA2682	<i>S. ochranthum</i>	S.och			1	89755404	56376314	63,004,248	70%	Cusco	Peru	2500	-13.63	-72.24	Allogamous-SI
LA0716	<i>S. pennellii</i>	S.pen	a			329844716	114438071	99,403,464	30%	Arequipa	Peru	50	-16.2	-73.6	Facultative-SC
LA0153	<i>S. peruvianum</i>	S.per			6	90866996	68418645	77,375,883	85%	Ancash	Peru	90	-9.95	-78.22	Allogamous-SI
LA0446	<i>S. peruvianum</i>	S.per			4	105322468	66081629	76,578,198	73%	Arequipa	Peru	150	-15.78	-74.39	Allogamous-SI
LA1272	<i>S. peruvianum</i>	S.per	a			319497888	105046666	157,499,587	49%	Lima	Peru	1000	-11.52	-77	Allogamous-SI
LA1278	<i>S. peruvianum</i>	S.per	a			336836546	192320612	158,965,815	47%	Lima	Peru	800	-11.64	-76.96	Allogamous-SI
LA1333	<i>S. peruvianum</i>	S.per			3	101707500	67620815	88,724,222	87%	Arequipa	Peru	700	-16.57	-72.63	Allogamous-SI
LA1336	<i>S. peruvianum</i>	S.per			3	94154260	64819205	83,692,673	89%	Arequipa	Peru	10	-16.21	-73.62	Allogamous-SI
LA1474	<i>S. peruvianum</i>	S.per			2	77910156	70047648	68,197,814	88%	Arequipa	Peru	1300	-16.36	-73.02	Allogamous-SI
LA1556	<i>S. peruvianum</i>	S.per	a			277362664	188391821	150,555,118	54%	Lima	Peru	250	-12.13	-77.03	Allogamous-SI
LA1558	<i>S. peruvianum</i>	S.per	a			317996198	161196562	144,782,268	46%	Lima	Peru		-11.44	-76.48	Allogamous-SI
LA1616	<i>S. peruvianum</i>	S.per			2	91459430	76729666	76,457,864	84%	Lima	Peru	350	-12.08	-76.92	Allogamous-SI
LA1913	<i>S. peruvianum</i>	S.per			2	82115154	71664926	71,652,758	87%	Ica	Peru	900	-14.4	-75.2	Allogamous-SI
LA1951	<i>S. peruvianum</i>	S.per			2	118039694	79101191	80,529,978	68%	Arequipa	Peru	65	-16.46	-73.09	Allogamous-SI
LA1954	<i>S. peruvianum</i>	S.per		YES	1	78228862	60737907	68,249,537	87%	Arequipa	Peru	50	-17.02	-72.08	Allogamous-SI
LA1954	<i>S. peruvianum</i>	S.per	a	YES		350310992	190291649	160,499,579	46%	Arequipa	Peru	50	-17.02	-72.08	Allogamous-SI
LA2732	<i>S. peruvianum</i>	S.per			1	74996958	68517416	63,277,237	84%	Tarapaca	Chile	1750	-19.42	-69.58	Allogamous-SI
LA2744	<i>S. peruvianum</i>	S.per		YES	2	82672378	48268384	29,669,894	36%	Arica and	Chile	400	-18.55	-70.15	Allogamous-SI
LA2744	<i>S. peruvianum</i>	S.per	c	YES		35864470	52467877	23,167,401	65%	Arica and	Chile	400	-18.55	-70.15	Allogamous-SI
LA2834	<i>S. peruvianum</i>	S.per			3	90252506	76002730	66,065,914	73%	Ica	Peru	1200	-14.77	-74.82	Allogamous-SI
LA2964	<i>S. peruvianum</i>	S.per		YES	3	86482844	69973707	71,257,540	82%	Tacna	Peru	100	-18.03	-70.84	Allogamous-SI
LA2964	<i>S. peruvianum</i>	S.per	c	YES		24875770	54127010	20,010,110	80%	Tacna	Peru	100	-18.03	-70.84	Allogamous-SI
LA3218	<i>S. peruvianum</i>	S.per			2	82629604	74323523	67,628,976	82%	Arequipa	Peru	600	-16.95	-72.08	Allogamous-SI
LA3636	<i>S. peruvianum</i>	S.per			1	94711590	70088210	74,591,151	79%	Lima	Peru		-12.68	-76.4	Allogamous-SI
LA4125	<i>S. peruvianum</i>	S.per			1	83898054	44871634	66,134,403	79%	Tarapaca	Chile	2510	-19.31	-69.42	Facultative-SC
LA1578	<i>S. pimpinellifolium</i>	S.pim	a	YES		339542086	588512441	306,955,744	90%	La Libertad	Peru		-7.33	-79.58	Autogamous-SC
LA1584	<i>S. pimpinellifolium</i>	S.pim	a			339788834	657286470	258,871,034	76%	Lambayeque	Peru		-6.37	-79.79	Autogamous-SC
LYC2798	<i>S. pimpinellifolium</i>	S.pim	a			346344194	444970160	293,051,229	85%						

a Afflitto S, Schiilen E, de Jong H, et al. (2014) Exploring genetic variation in the tomato (*Solanum section Lycopersicon*) clade by whole-genome sequencing. *Plant Journal* 80, 136-148.
c Pease IR, Haak DC, Hahn MW, Mowle LC (2016) Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. *PLoS Biology* 14

Supplemental Table 2. Additional data from Lin T, Zhu G, Zhang J, et al. (2014) Genomic analyses provide insights into the history of tomato breeding. Nature Genetics 46, 1220-1226 used for a *daði* analysis.

Id	Species	Species Abbreviation	Duplicate	Total Reads	Province	Country	Elevation	Longitude	Latitude	Mating System
LA1237	<i>S. pimpinellifolium</i>	<i>S.pim</i>		61858842	Esmeraldes	Ecuador	5	0.87	79.85	Autogamous-SC
LA1242	<i>S. pimpinellifolium</i>	<i>S.pim</i>		67157190	Morona-Santiago	Ecuador	900			Autogamous-SC
LA1246	<i>S. pimpinellifolium</i>	<i>S.pim</i>		57831786	Loja	Ecuador	1200	-3.99	-79.36	Autogamous-SC
LA1341	<i>S. pimpinellifolium</i>	<i>S.pim</i>		49877478	Lima	Peru	500	-11.97	-76.79	Autogamous-SC
LA1547	<i>S. pimpinellifolium</i>	<i>S.pim</i>		58611708	Carchi	Ecuador	3000	0.58	-77.93	Autogamous-SC
LA1578	<i>S. pimpinellifolium</i>	<i>S.pim</i>	YES	55566326	La Libertad	Peru		-7.33	-79.58	Autogamous-SC
LA1591	<i>S. pimpinellifolium</i>	<i>S.pim</i>		59333440	La Libertad	Peru		-7.72	-79.12	Autogamous-SC
LA1595	<i>S. pimpinellifolium</i>	<i>S.pim</i>		56572400	Ancash	Peru	10	-9.27	-78.47	Autogamous-SC
LA1596	<i>S. pimpinellifolium</i>	<i>S.pim</i>		76571072	Ancash	Peru	15	-8.93	-78.57	Autogamous-SC
LA1933	<i>S. pimpinellifolium</i>	<i>S.pim</i>		59626428	Arequipa	Peru	140	-15.46	-74.45	Autogamous-SC
LA2147	<i>S. pimpinellifolium</i>	<i>S.pim</i>		55487778	Cajamarca	Peru	550	-7.2	-78.98	Autogamous-SC
LA2173	<i>S. pimpinellifolium</i>	<i>S.pim</i>		59361256	Cajamarca	Peru	1200			Autogamous-SC
LA2181	<i>S. pimpinellifolium</i>	<i>S.pim</i>		62378096	Cajamarca	Peru	850	-5.78	-78.78	Autogamous-SC
LA2184	<i>S. pimpinellifolium</i>	<i>S.pim</i>		55498628	Amazonas	Peru	450	-5.59	-78.55	Autogamous-SC
LA2187	<i>S. pimpinellifolium</i>	<i>S.pim</i>		56411540	Amazonas	Peru	650	-5.93	-78.05	Autogamous-SC
LA2656	<i>S. pimpinellifolium</i>	<i>S.pim</i>		65242236	Tumbez	Peru	70	-3.8	-80.7	Autogamous-SC
LA2857	<i>S. pimpinellifolium</i>	<i>S.pim</i>		55283766	Galapagos Islands	Peru	5	-0.95	-90.97	Autogamous-SC

Supplemental Table 3. Heterozygosity for each individual.		
Species	Id	Heterozygosity
Hybrid	LA1782	0.38%
Hybrid	LA1930	0.66%
Hybrid	LA1932	0.65%
<i>S.arc</i>	LA2157	0.06%
<i>S.arc</i>	LA2172	0.15%
<i>S.arc</i>	LA2172	0.22%
<i>S.chi</i>	LA0752	0.10%
<i>S.chi</i>	LA1958	0.54%
<i>S.chi</i>	LA1960	0.57%
<i>S.chi</i>	LA1963	0.56%
<i>S.chi</i>	LA1967	0.55%
<i>S.chi</i>	LA1969	0.39%
<i>S.chi</i>	LA1971	0.54%
<i>S.chi</i>	LA2748	0.50%
<i>S.chi</i>	LA2750	0.26%
<i>S.chi</i>	LA2753	0.53%
<i>S.chi</i>	LA2765	0.43%
<i>S.chi</i>	LA2771	0.54%
<i>S.chi</i>	LA2778	0.51%
<i>S.chi</i>	LA2880	0.31%
<i>S.chi</i>	LA2884	0.38%
<i>S.chi</i>	LA2930	0.17%
<i>S.chi</i>	LA3114	0.54%
<i>S.chi</i>	LA4117A	0.35%
<i>S.chm</i>	LA1028	0.04%
<i>S.chm</i>	LA1316	0.08%
<i>S.chm</i>	LA2663	0.04%
<i>S.chm</i>	LA2695	0.06%
<i>S.cor</i>	LA0107	0.39%
<i>S.cor</i>	LA0118	0.64%
<i>S.cor</i>	LA0444	0.68%
<i>S.cor</i>	LA1274	0.61%
<i>S.gal</i>	LA0483	0.01%
<i>S.gal</i>	LA1044	0.02%
<i>S.gal</i>	LA1401	0.03%
<i>S.hab</i>	CGN15791	0.08%
<i>S.hab</i>	CGN15792	0.15%
<i>S.hab</i>	LA0407	0.14%
<i>S.hab</i>	LA1777	0.24%
<i>S.hab</i>	LYC4	0.08%
<i>S.hab</i>	PI134418	0.27%
<i>S.hua</i>	LA1358	0.57%
<i>S.hua</i>	LA1360	0.51%
<i>S.hua</i>	LA1364	0.49%
<i>S.hua</i>	LA1364	0.51%

<i>S.hua</i>	LA1365	0.73%
<i>S.hua</i>	LA1983	0.45%
<i>S.lyc</i>	LA2951	0.31%
<i>S.neo</i>	LA0735	0.04%
<i>S.neo</i>	LA1322	0.04%
<i>S.neo</i>	LA2133	0.05%
<i>S.neo</i>	LA2133	0.04%
<i>S.och</i>	LA2682	0.11%
<i>S.pen</i>	LA0716	0.11%
<i>S.per</i>	LA0153	0.32%
<i>S.per</i>	LA0446	0.39%
<i>S.per</i>	LA1272	0.58%
<i>S.per</i>	LA1278	0.55%
<i>S.per</i>	LA1333	0.41%
<i>S.per</i>	LA1336	0.40%
<i>S.per</i>	LA1474	0.32%
<i>S.per</i>	LA1556	0.38%
<i>S.per</i>	LA1558	0.72%
<i>S.per</i>	LA1616	0.64%
<i>S.per</i>	LA1913	0.66%
<i>S.per</i>	LA1951	0.47%
<i>S.per</i>	LA1954	0.40%
<i>S.per</i>	LA1954	0.37%
<i>S.per</i>	LA2732	0.55%
<i>S.per</i>	LA2744	0.66%
<i>S.per</i>	LA2744	0.60%
<i>S.per</i>	LA2834	0.60%
<i>S.per</i>	LA2964	0.28%
<i>S.per</i>	LA2964	0.32%
<i>S.per</i>	LA3218	0.44%
<i>S.per</i>	LA3636	0.78%
<i>S.per</i>	LA4125	0.53%
<i>S.pim</i>	LA1578	0.14%
<i>S.pim</i>	LA1584	0.05%
<i>S.pim</i>	LYC2798	0.03%

Supplemental Table 4. Highest log-likelihood parameters inferred from $\partial a \partial i$ with confidence intervals from 100 conventional bootstraps.		
Parameter	Value	Description
Maximum Log-Likelihood	-11,786	
Theta	(24,409, 25,758)	Ancestral population size ($4 \cdot N_{\text{ref}} \cdot L \cdot \mu$)
N_{ref}	(417,486, 440,556)	Individuals in the ancestral population ($\text{Theta} / L \cdot \mu \cdot 4$)
L	2,866,063.30	Effective length. The number of synonymous nucleotides sequenced to a depth of 3 reads in all individuals
Tau	(1.46, 1.56)	Speciation event in $2 \cdot N_{\text{ref}}$
Split Time	(1,216,455, 1,374,108)	Speciation event in years ($2 \cdot N_{\text{ref}} \cdot \text{Tau} \cdot g$), if $g = 1$
Nu1F	(1.26, 1.32)	<i>S. chilense</i> population size relative to the ancestral population (N_{ref})
Nu2F	(3.69, 3.87)	<i>S. peruvianum</i> population size
m12	(0.26, 0.28)	<i>S. chilense</i> individuals introduced into <i>S. peruvianum</i> population in 1 generation
m21	(0.13, 0.14)	<i>S. peruvianum</i> individuals introduced into <i>S. chilense</i> population in 1 generation
M12	(3.11×10^{-7} , 3.23×10^{-7})	Fraction of <i>S. chilense</i> individuals derived from <i>S. peruvianum</i> in 1 generation
M21	(1.54×10^{-7} , 1.61×10^{-7})	Fraction of <i>S. peruvianum</i> individuals derived from <i>S. chilense</i> in 1 generation
outgr_misid	(0.11, 0.15)	Outgroup misidentification rate
μ	$5.1 \cdot 10^{-9}$	Mutation rate (Roselius et al. 2005)

Supplemental Table 5. Number of seeds and seed-like structures (SLS) for individual crosses.						
Cross	Parent1	Parent2	SpeciesParent1	SpeciesParent2	Seed	SLS
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	2	9
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	1	10
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	1	11
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	3	4
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	0
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	2	4
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	29
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	31
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	34
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	23
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	21
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	6
LA0153xLA1932	LA0153	LA1932	Sper	Hybrid	0	2
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	54
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	42
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	46
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	50
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	35
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	39
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	48
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	29
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	32
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	36
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	32
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	38
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	36
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	31
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	28
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	26
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	27
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	33
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	27
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	29
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	23

LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	25
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	29
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	27
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	23
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	15
LA1954xLA1932	LA1954	LA1932	Sper	Hybrid	0	26
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	1	6
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	6
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	21
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	16
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	19
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	14
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	16
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	18
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	1	32
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	34
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	38
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	36
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	26
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	34
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	31
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	28
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	27
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	22
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	31
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	38
LA2732xLA1932	LA2732	LA1932	Sper	Hybrid	0	32
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	1	30
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	1	15
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	2	15
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	1	16
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	0	14
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	1	18
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	0	19
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	0	16
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	1	39
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	2	28
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	0	0
LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	0	0

LA2930xLA1932	LA2930	LA1932	Schi	Hybrid	3	14
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	5	9
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	1	13
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	5	6
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	1	12
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	3	3
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	3	2
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	2	9
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	1	6
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	2	7
LA2964xLA1932	LA2964	LA1932	Sper	Hybrid	1	6
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	8
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	3
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	2
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	3
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	4
LA0153xLA2930	LA0153	LA2930	Sper	Schi	0	1
LA1274xLA2732	LA1274	LA2732	Scor	Sper	42	0
LA1274xLA2732	LA1274	LA2732	Scor	Sper	39	0
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	6
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	8
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	7
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	4
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	4
LA1274xLA2930	LA1274	LA2930	Scor	Schi	0	2
LA1954xLA1274	LA1954	LA1274	Sper	Scor	8	12
LA1954xLA1274	LA1954	LA1274	Sper	Scor	8	17
LA1954xLA1274	LA1954	LA1274	Sper	Scor	3	12
LA1954xLA1274	LA1954	LA1274	Sper	Scor	0	7
LA1954xLA2930	LA1954	LA2930	Sper	Schi	0	21
LA1954xLA2930	LA1954	LA2930	Sper	Schi	0	27
LA1954xLA2930	LA1954	LA2930	Sper	Schi	0	13
LA1954xLA2930	LA1954	LA2930	Sper	Schi	0	6
LA1954xLA2930	LA1954	LA2930	Sper	Schi	0	23
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	24
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	10
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	7
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	48
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	34

LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	2
LA2732xLA2930	LA2732	LA2930	Sper	Schi	0	1
LA2732xLA2930	LA2732	LA2930	Sper	Schi	43	0
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	23
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	19
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	0
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	0
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	24
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	22
LA2930xLA1274	LA2930	LA1274	Schi	Scor	0	23
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	9
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	22
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	16
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	23
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	20
LA2930xLA1954	LA2930	LA1954	Schi	Sper	0	15
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	26
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	21
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	30
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	21
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	18
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	23
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	17
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	25
LA2930xLA2732	LA2930	LA2732	Schi	Sper	1	16
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	13
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	15
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	17
LA2930xLA2732	LA2930	LA2732	Schi	Sper	1	8
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	6
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	5
LA2930xLA2732	LA2930	LA2732	Schi	Sper	0	5
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	25
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	28
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	26
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	22
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	33
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	26
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	28

LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	33
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	30
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	27
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	25
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	29
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	31
LA2930xLA2964	LA2930	LA2964	Schi	Sper	0	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	68	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	61	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	67	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	29	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	61	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	15	0
LA0153xLA1954	LA0153	LA1954	Sper	Sper	23	0
LA0153xLA2732	LA0153	LA2732	Sper	Sper	51	0
LA0153xLA2732	LA0153	LA2732	Sper	Sper	47	0
LA0153xLA2732	LA0153	LA2732	Sper	Sper	32	0
LA1954xLA0153	LA1954	LA0153	Sper	Sper	9	48
LA1954xLA0153	LA1954	LA0153	Sper	Sper	10	45
LA1954xLA0153	LA1954	LA0153	Sper	Sper	30	29
LA1954xLA0153	LA1954	LA0153	Sper	Sper	2	8
LA1954xLA0153	LA1954	LA0153	Sper	Sper	33	14
LA1954xLA0153	LA1954	LA0153	Sper	Sper	36	10
LA1954xLA0153	LA1954	LA0153	Sper	Sper	25	19
LA1954xLA0153	LA1954	LA0153	Sper	Sper	11	8
LA1954xLA0153	LA1954	LA0153	Sper	Sper	8	9
LA1954xLA0153	LA1954	LA0153	Sper	Sper	25	23
LA1954xLA0153	LA1954	LA0153	Sper	Sper	33	23
LA1954xLA0153	LA1954	LA0153	Sper	Sper	15	25
LA1954xLA0153	LA1954	LA0153	Sper	Sper	8	32
LA1954xLA0153	LA1954	LA0153	Sper	Sper	10	30
LA1954xLA2732	LA1954	LA2732	Sper	Sper	35	7
LA1954xLA2732	LA1954	LA2732	Sper	Sper	37	15
LA1954xLA2732	LA1954	LA2732	Sper	Sper	34	9
LA1954xLA2732	LA1954	LA2732	Sper	Sper	21	9
LA1954xLA2732	LA1954	LA2732	Sper	Sper	21	7
LA1954xLA2732	LA1954	LA2732	Sper	Sper	21	11
LA1954xLA2732	LA1954	LA2732	Sper	Sper	18	9
LA1954xLA2732	LA1954	LA2732	Sper	Sper	22	7

LA1954xLA2964	LA1954	LA2964	Sper	Sper	37	7
LA1954xLA2964	LA1954	LA2964	Sper	Sper	22	16
LA1954xLA2964	LA1954	LA2964	Sper	Sper	14	16
LA1954xLA2964	LA1954	LA2964	Sper	Sper	9	15
LA1954xLA2964	LA1954	LA2964	Sper	Sper	14	3
LA1954xLA2964	LA1954	LA2964	Sper	Sper	6	3
LA1954xLA2964	LA1954	LA2964	Sper	Sper	3	4
LA2732xLA0153	LA2732	LA0153	Sper	Sper	79	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	54	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	56	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	53	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	54	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	52	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	57	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	61	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	56	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	53	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	67	0
LA2732xLA0153	LA2732	LA0153	Sper	Sper	49	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	25	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	35	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	33	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	40	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	36	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	29	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	55	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	57	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	55	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	56	0
LA2732xLA1954	LA2732	LA1954	Sper	Sper	51	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	74	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	54	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	53	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	43	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	60	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	66	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	52	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	59	0
LA2732xLA2964	LA2732	LA2964	Sper	Sper	48	0

LA2732xLA2964	LA2732	LA2964	Sper	Sper	61	0
LA2964xLA0153	LA2964	LA0153	Sper	Sper	21	5
LA2964xLA0153	LA2964	LA0153	Sper	Sper	15	11
LA2964xLA0153	LA2964	LA0153	Sper	Sper	12	8
LA2964xLA0153	LA2964	LA0153	Sper	Sper	18	8
LA2964xLA2732	LA2964	LA2732	Sper	Sper	20	0
LA2964xLA2732	LA2964	LA2732	Sper	Sper	24	3
LA2964xLA2732	LA2964	LA2732	Sper	Sper	15	9
LA2964xLA2732	LA2964	LA2732	Sper	Sper	22	2
LA2964xLA2732	LA2964	LA2732	Sper	Sper	15	3
LA2964xLA2732	LA2964	LA2732	Sper	Sper	15	6
LA2964xLA2732	LA2964	LA2732	Sper	Sper	17	4