

Supplementary Tables

Table S1. Read summary statistics. Number of sequences before (column: ‘Number of raw reads’) and after (column: ‘Number of filtered 2bRAD tags’) quality filtering for each sample. Excluded samples included (1) low coverage individuals, (2) samples with over 30% of missing loci and (3) individuals which were not considered for SNP calling and R analysis due to a lack of additional replicates within their corresponding population. These excluded samples are indicated with ‘0’ in the column: ‘Retained Individuals’. Summarized information across all samples can be found at the bottom of the table. Table is divided with a bold line between Slender and Stocky individuals.

Sample ID	Number of raw reads	Number of filtered 2bRAD tags	Sample ID (concatenated)	Number of filtered 2bRAD tags (after concatenation)	Retained Individuals
T_Pax_ALA_10_CAGAGAC_L005.fasta	2,346,871	1,942,124	T_Pax_ALA_10_concatenated.fasta	1,942,124	1,942,124
T_Pax_ALA_11_TTGCGGA_L005.fasta	2,019,483	1,336,875	T_Pax_ALA_11_concatenated.fasta	1,336,875	1,336,875
T_Pax_ALA_12_CCGTGAA_L005.fasta	1,375,730	904,238	T_Pax_ALA_12_concatenated.fasta	904,238	904,238
T_Pax_ALA_13_AGCTCGT_L005.fasta	2,117,007	1,569,395	T_Pax_ALA_13_concatenated.fasta	1,569,395	1,569,395
T_Pax_ALA_14_GCTTGTG_L005.fasta	2,329,648	1,954,734	T_Pax_ALA_14_concatenated.fasta	1,954,734	1,954,734
T_Pax_ALA_15_TTCCTCG_L005.fasta	1,865,563	1,584,392	T_Pax_ALA_15_concatenated.fasta	1,584,392	1,584,392
T_Pax_ALA_16_GATGCAG_L005.fasta	2,997,892	2,259,411	T_Pax_ALA_16_concatenated.fasta	2,259,411	2,259,411
T_Pax_ALA_17_AATGGGC_L007.fasta	25,614	20	T_Pax_ALA_17_concatenated.fasta	20	0
T_Pax_ALA_19_CAACGGA_L005.fasta	2,473,445	2,034,841	T_Pax_ALA_19_concatenated.fasta	2,034,841	2,034,841
T_Pax_ALA_1_ACACTGC_L005.fasta	2,391,304	2,210,551	T_Pax_ALA_1_concatenated.fasta	3,269,804	3,269,804
T_Pax_ALA_1_CTAGCCA_L005.fasta	1,134,079	1,059,253			
T_Pax_ALA_20_CGTCGAA_L005.fasta	2,041,063	1,636,330	T_Pax_ALA_20_concatenated.fasta	1,636,330	1,636,330
T_Pax_ALA_21_ACGACGT_L005.fasta	2,373,630	2,070,740	T_Pax_ALA_21_concatenated.fasta	2,070,740	2,070,740
T_Pax_ALA_22_GTCACCA_L007.fasta	109,342	16,776	T_Pax_ALA_22_concatenated.fasta	16,776	0
T_Pax_ALA_2_GACTGAC_L005.fasta	1,483,311	1,343,551	T_Pax_ALA_2_concatenated.fasta	1,343,551	1,343,551
T_Pax_ALA_3_ACTCGGA_L005.fasta	1,131,774	1,020,503	T_Pax_ALA_3_concat	2,639,480	2,639,480

5.fasta					
T_Pax_ALA_3_bis_TTCGGAG_L007.fasta	822,013	736,414	enated.fasta		
T_Pax_ALA_3_TTCGGAG_L005.fasta	959,865	882,563			
T_Pax_ALA_4_CTGCATC_L005.fasta	1,130,160	902,155	T_Pax_ALA_4_concat	2,162,938	2,162,938
T_Pax_ALA_4_TCCCACA_L005.fasta	1,412,409	1,260,783	enated.fasta		
T_Pax_ALA_5_CAGTCGT_L005.fasta	1,338,263	1,135,166	T_Pax_ALA_5_concat	1,135,166	1,135,166
T_Pax_ALA_6_CCCATTG_L005.fasta	1,766,513	1,519,391	enated.fasta		
T_Pax_ALA_6_CTCCTGA_L005.fasta	737,957	648,490	T_Pax_ALA_6_concat	2,167,881	2,167,881
T_Pax_ALA_7_GGTTTCG_L005.fasta	5,648,509	4,811,674	enated.fasta		
T_Pax_ALA_8_CGTTTCAG_L005.fasta	1,214,715	805,448	T_Pax_ALA_8_concat	805,448	805,448
T_Pax_ALA_9_TAGTGGC_L005.fasta	1,947,492	1,589,539	enated.fasta		
T_Pax_CAMP_10_CGACAAC_L005.fasta	1,955,984	1,704,828	T_Pax_CAMP_10_co	1,704,828	1,704,828
T_Pax_CAMP_11_CCAATCC_L005.fasta	2,263,444	1,541,888	ncatenated.fasta		
T_Pax_CAMP_1_TACGGGT_L005.fasta	2,593,852	2,314,714	T_Pax_CAMP_11_co	1,541,888	1,541,888
T_Pax_CAMP_2_TGGCCAT_L005.fasta	1,416,126	1,252,648	ncatenated.fasta		
T_Pax_CAMP_3_ATGGAGG_L005.fasta	1,979,401	1,819,480	T_Pax_CAMP_1_con	2,314,714	2,314,714
T_Pax_CAMP_4_CTACGAG_L005.fasta	1,715,633	1,547,270	catenated.fasta		
T_Pax_CAMP_5_CCAGAGT_L005.fasta	2,157,367	1,725,683	T_Pax_CAMP_2_con	1,252,648	1,252,648
T_Pax_CAMP_6_GTGTCTG_L005.fasta	2,257,527	1,859,229	catenated.fasta		
T_Pax_CAMP_7_ATGTGCG_L005.fasta	1,780,577	1,295,542	T_Pax_CAMP_3_con	1,819,480	1,819,480
T_Pax_CAMP_8_GGGATTC_L005.fasta	1,953,188	1,662,418	catenated.fasta		
T_Pax_CAMP_9_ACCTAGC_L005.fasta	2,009,792	1,683,357	T_Pax_CAMP_4_con	1,547,270	1,547,270
T_Pax_CAMP_9_TGTCGTC_L005.fasta	1,807,453	1,227,065	catenated.fasta		
T_Pax_CUB_10a_S47.fasta	6,733,063	5,697,715	T_Pax_CAMP_5_con	1,725,683	1,725,683
T_Pax_CUB_10c_S56.fasta	1,596,920	1,423,067	catenated.fasta		
T_Pax_CUB_1a_S48.fasta	787,182	663,198	T_Pax_CAMP_6_con	1,859,229	1,859,229
T_Pax_CUB_1b_S46.fasta	4,500,060	55,778	catenated.fasta		
			T_Pax_CAMP_7_con	1,295,542	1,295,542
			catenated.fasta		
			T_Pax_CAMP_8_con	1,662,418	1,662,418
			catenated.fasta		
			T_Pax_CAMP_9_con	2,910,422	2,910,422
			catenated.fasta		
			T_Pax_CUB_10a_con	5,697,715	5,697,715
			catenated.fasta		
			T_Pax_CUB_10c_con	1,423,067	1,423,067
			catenated.fasta		
			T_Pax_CUB_1a_conc	663,198	663,198
			atenated.fasta		
			T_Pax_CUB_1b_conc	55,778	0
			atenated.fasta		

T_Pax_CUB_2A_S49.fasta	182,297	26,641	T_Pax_CUB_2A_conc atenated.fasta	26,641	0
T_Pax_CUB_2B_S42.fasta	3,330,976	1,171,857	T_Pax_CUB_2B_conc atenated.fasta	1,171,857	0
T_Pax_CUB_3A_S50.fasta	5,501,169	4,896,475	T_Pax_CUB_3A_conc atenated.fasta	4,896,475	4,896,475
T_Pax_CUB_3b_S38.fasta	37,272	18,111	T_Pax_CUB_3b_conc atenated.fasta	18,111	0
T_Pax_CUB_4a_S51.fasta	1,072,978	992,506	T_Pax_CUB_4a_conc atenated.fasta	992,506	992,506
T_Pax_CUB_4b_S31.fasta	103,763	63,049	T_Pax_CUB_4b_conc atenated.fasta	63,049	0
T_Pax_CUB_7a_S55.fasta	1,587,343	1,260,420	T_Pax_CUB_7a_conc atenated.fasta	1,260,420	1,260,420
T_Pax_GIA_15_CGAAGTG_L0 05.fasta	2,022,399	1,758,814	T_Pax_GIA_15_conc atenated.fasta	3,415,184	3,415,184
T_Pax_GIA_15_GAGCGTA_L0 05.fasta	1,951,376	1,656,370			
T_Pax_GIA_16_GTCTGGT_L0 05.fasta	695,071	7,363	T_Pax_GIA_16_conc atenated.fasta	7,621	0
T_Pax_GIA_16_L1bis_GTCTG GT_L001.fasta	35,064	258			
T_Pax_GIA_18_CAGATCG_L0 05.fasta	2,207,390	1,522,595	T_Pax_GIA_18_conc atenated.fasta	1,522,595	1,522,595
T_Pax_GIA_19_CTCGTTT_L00 5.fasta	1,565,711	1,244,260	T_Pax_GIA_19_conc atenated.fasta	1,244,260	1,244,260
T_Pax_GIA_21_ACCGTAG_L0 05.fasta	2,060,423	1,788,331	T_Pax_GIA_21_conc atenated.fasta	1,788,331	1,788,331
T_Pax_GIA_24_ACCAGTC_L0 05.fasta	2,395,661	1,896,931	T_Pax_GIA_24_conc atenated.fasta	1,896,931	1,896,931
T_Pax_GIA_25_AAAGCCC_L0 05.fasta	2,268,640	2,052,284	T_Pax_GIA_25_conc atenated.fasta	2,052,284	2,052,284
T_Pax_GIA_30_ACTCGGA_L0 07.fasta	1,949,847	1,071,742	T_Pax_GIA_30_conc atenated.fasta	4,010,046	4,010,046
T_Pax_GIA_30_bis_TTGCGGA _L007.fasta	5,604,772	2,938,304			
T_Pax_GIA_31_bis_CCGTGAA _L007.fasta	3,130,424	2,514,943	T_Pax_GIA_31_conc atenated.fasta	10,125,557	10,125,557
T_Pax_GIA_31_TCCACA_L0 07.fasta	9,345,347	7,610,614			
T_Pax_GIA_33_CGTACCA_L0 05.fasta	2,651,068	1,873,516	T_Pax_GIA_33_conc atenated.fasta	1,873,516	1,873,516
T_Pax_GIA_34_bis_TCGCGTT _L007.fasta	7,301,432	149,319	T_Pax_GIA_34_conc atenated.fasta	226,371	226,371
T_Pax_GIA_34_TCTGTGG_L0 07.fasta	1,372,049	77,052			
T_Pax_GIA_36_bis_ACGGGAT _L007.fasta	2,472,713	53,103	T_Pax_GIA_36_conc atenated.fasta	53,103	0
T_Pax_GIA_37_bis_GTACTGG _L007.fasta	1,729,348	26,822	T_Pax_GIA_37_conc atenated.fasta	48,884	0
T_Pax_GIA_37_TCCTGGA_L0 07.fasta	1,050,706	22,062			
T_Pax_GIA_5_TAGTGGC_L00	189,757	2,364	T_Pax_GIA_5_concat	2,364	0

7.fasta			enated.fasta		
T_Pax_GIA_6_CAGAGAC_L007.fasta	174,712	4,768	T_Pax_GIA_6_concatenated_L007.fasta	4,768	0
T_Pax_PTF_11_TACGGGT_L007.fasta	1,846,154	1,605,303	T_Pax_PTF_11_concatenated.fasta	1,605,303	1,605,303
T_Pax_PTF_12_bis_TGGCCAT_L007.fasta	2,165,766	1,728,125	T_Pax_PTF_12_concatenated.fasta	7,184,415	7,184,415
T_Pax_PTF_12_TCGAACCC_L007.fasta	6,425,419	5,456,290			
T_Pax_PTF_13_bis_ATGGAGG_L007.fasta	2,216,147	1,913,023	T_Pax_PTF_13_concatenated.fasta	1,924,249	1,924,249
T_Pax_PTF_13_GGAGTGA_L007.fasta	28,655	11,226			
T_Pax_PTF_14_bis_CTACGAG_L007.fasta	1,684,345	1,134,462	T_Pax_PTF_14_concatenated.fasta	3,564,976	3,564,976
T_Pax_PTF_14_CGTACCA_L007.fasta	2,858,961	2,430,514			
T_Pax_PTF_15_ACACTGC_L007.fasta	1,950,381	1,346,524	T_Pax_PTF_15_concatenated.fasta	3,128,115	3,128,115
T_Pax_PTF_15_bis_CCTGCAA_L007.fasta	2,194,952	1,781,591			
T_Pax_PTF_16_bis_AGTCCTG_L007.fasta	2,128,878	1,005,638	T_Pax_PTF_16_concatenated.fasta	2,338,987	2,338,987
T_Pax_PTF_16_GACTGAC_L007.fasta	3,638,944	1,333,349			
T_Pax_PTF_17_CAGATCG_L007.fasta	2,590,598	1,484,401	T_Pax_PTF_17_concatenated.fasta	1,484,401	1,484,401
T_Pax_PTF_18_GGGAGAA_L007.fasta	2,191,073	1,973,065	T_Pax_PTF_18_concatenated.fasta	1,973,065	1,973,065
T_Pax_PTF_1_TGGGCTA_L007.fasta	34,729	23,564	T_Pax_PTF_1_concatenated.fasta	23,564	0
T_Pax_PUG_A1_GGAGGTT_L007.fasta	1,549,287	472,414	T_Pax_PUG_A1_concatenated.fasta	472,414	472,414
T_Pax_PUG_A2_GAGACCT_L007.fasta	1,215,300	567,402	T_Pax_PUG_A2_concatenated.fasta	567,402	567,402
T_Pax_PUG_A4_GCAACTC_L007.fasta	4,574,694	3,386,260	T_Pax_PUG_A4_concatenated.fasta	3,386,260	3,386,260
T_Pax_PUG_C14_CGATTGC_L007.fasta	320,575	2,242	T_Pax_PUG_C14_concatenated.fasta	2,242	0
T_Pax_PUG_C1_CGTGCTT_L005.fasta	1,207,460	6,240	T_Pax_PUG_C1_concatenated.fasta	6,240	0
T_Pax_PUG_C4_AGCAACC_L005.fasta	1,185,719	9,318	T_Pax_PUG_C4_concatenated.fasta	9,318	0
T_Pax_PUG_C5_GCTCCAT_L005.fasta	1,891,766	12,893	T_Pax_PUG_C5_concatenated.fasta	12,893	0
T_Pax_PUG_C8_GCGTAGA_L005.fasta	1,349,020	14,742	T_Pax_PUG_C8_concatenated.fasta	14,742	0
T_Pax_PVEN_11_TGGTTCC_L005.fasta	695,743	25,273	T_Pax_PVEN_11_concatenated.fasta	25,273	0
T_Pax_PVEN_12_CTTTGGG_L007.fasta	603,892	3,378	T_Pax_PVEN_12_concatenated.fasta	3,378	0
T_Pax_PVEN_13_TACACGG_L005.fasta	1,327,872	190,171	T_Pax_PVEN_13_concatenated.fasta	190,171	190,171

T_Pax_PVEN_14_GTTCACG_L005.fasta	3,615,590	1,862,411	T_Pax_PVEN_14_concatenated.fasta	1,862,411	1,862,411
T_Pax_PVEN_15_S96.fasta	1,296,910	1,177,448	T_Pax_PVEN_15_concatenated.fasta	1,177,448	0
T_Pax_PVEN_16_GGCATAG_L007.fasta	159,750	8,186	T_Pax_PVEN_16_concatenated.fasta	8,186	0
T_Pax_PVEN_1_TCTCGAG_L005.fasta	5,586	3,889	T_Pax_PVEN_1_concatenated.fasta	3,889	0
T_Pax_PVEN_3_ACGGTCA_L005.fasta	3,056,352	908,298	T_Pax_PVEN_3_concatenated.fasta	916,830	916,830
T_Pax_PVEN_3_CAGCACA_L005.fasta	30,331	8,532			
T_Pax_PVEN_4_TCAGCCT_L005.fasta	711,171	6,582	T_Pax_PVEN_4_concatenated.fasta	6,582	0
T_Pax_PVEN_5_GTCCGAT_L007.fasta	517,352	11,159	T_Pax_PVEN_5_concatenated.fasta	11,159	0
T_Pax_PVEN_6_AGCCCAA_L005.fasta	3,604,827	2,354,020	T_Pax_PVEN_6_concatenated.fasta	2,426,460	2,426,460
T_Pax_PVEN_6_TGCACAC_L005.fasta	214,122	72,440			
T_Pax_PVEN_7_AGTCCCTG_L005.fasta	441,110	18,681	T_Pax_PVEN_7_concatenated.fasta	18,681	0
T_Pax_PVEN_8_GAGGATG_L005.fasta	667,840	5,246	T_Pax_PVEN_8_concatenated.fasta	23,978	0
T_Pax_PVEN_8_L1bis_GAGGATG_L001.fasta	4,415,813	18,732			
T_Pax_SAR_20_AGAAGGC_L005.fasta	414,214	254,046	T_Pax_SAR_20_concatenated.fasta	990,614	990,614
T_Pax_SAR_20_CGATGCA_L005.fasta	1,103,018	736,568			
T_Pax_SAR_21_CGCGAAA_L005.fasta	1,208,545	914,370	T_Pax_SAR_21_concatenated.fasta	1,414,804	1,414,804
T_Pax_SAR_21_GTGGAAC_L005.fasta	895,829	500,434			
T_Pax_SAR_23_TCTGTGG_L005.fasta	1,185,073	950,074	T_Pax_SAR_23_concatenated.fasta	950,074	950,074
T_Pax_SAR_24_ACGGGAT_L005.fasta	2,385,855	2,038,763	T_Pax_SAR_24_concatenated.fasta	2,038,763	2,038,763
T_Pax_SAR_25_GTACTGG_L005.fasta	3,294,983	3,078,794	T_Pax_SAR_25_concatenated.fasta	3,078,794	3,078,794
T_Pax_SAR_26_TGGTGAG_L005.fasta	2,217,707	1,788,832	T_Pax_SAR_26_concatenated.fasta	1,788,832	1,788,832
T_Pax_ALAOR_10_ACGGGAT_L001.fasta	176,127	150,515	T_Pax_ALAOR_10_concatenated.fasta	150,515	150,515
T_Pax_ALAOR_11_GTACTGG_L001.fasta	4,562	61	T_Pax_ALAOR_11_concatenated.fasta	61	0
T_Pax_ALAOR_12_TGGTGAG_L001.fasta	219,529	186,685	T_Pax_ALAOR_12_concatenated.fasta	186,685	186,685
T_Pax_ALAOR_14_GTGGAAC_L001.fasta	4,646	92	T_Pax_ALAOR_14_concatenated.fasta	92	0
T_Pax_ALAOR_15_GCGTAGA_L001.fasta	101,899	61,318	T_Pax_ALAOR_15_concatenated.fasta	61,318	0
T_Pax_ALAOR_16_GGGAGAA	83,253	54,340	T_Pax_ALAOR_16_c	54,340	0

_L001.fasta			onconcatenated.fasta		
T_Pax_ALAOR_5_ACGACGT_L001.fasta	492,467	414,849	T_Pax_ALAOR_5_concatenated.fasta	414,849	414,849
T_Pax_ALAOR_6_CGAAGTG_L001.fasta	297,547	248,930	T_Pax_ALAOR_6_concatenated.fasta	248,930	248,930
T_Pax_ALAOR_7_CAGATCG_L001.fasta	166,990	1,598	T_Pax_ALAOR_7_concatenated.fasta	1,598	0
T_Pax_ALAOR_8_CTCGTTC_L001.fasta	269,328	213,038	T_Pax_ALAOR_8_concatenated.fasta	213,038	213,038
T_Pax_ALAOR_9_TCGCGTT_L001.fasta	232,699	207,509	T_Pax_ALAOR_9_concatenated.fasta	207,509	207,509
T_Pax_GIAOR_32_concatenated.fasta	1,986,366	1,769,616	T_Pax_GIAOR_32_concatenated.fasta	1,769,616	1,769,616
T_Pax_GIAOR_35_concatenated.fasta	2,710,527	2,263,867	T_Pax_GIAOR_35_concatenated.fasta	2,263,867	2,263,867
T_Pax_GIAOR_36_concatenated.fasta	8,103,103	5,085,369	T_Pax_GIAOR_36_concatenated.fasta	5,085,369	5,085,369
T_Pax_GIAOR_38_concatenated.fasta	3,103,136	2,771,368	T_Pax_GIAOR_38_concatenated.fasta	2,771,368	2,771,368
T_Pax_GIAOR_39_concatenated.fasta	1,746,265	1,288,523	T_Pax_GIAOR_39_concatenated.fasta	1,288,523	1,288,523
T_Pax_GIAOR_40_concatenated.fasta	2,462,102	2,178,109	T_Pax_GIAOR_40_concatenated.fasta	2,178,109	2,178,109
T_Pax_PVENOR_10_TCGAAC_L001.fasta	308,024	274,760	T_Pax_PVENOR_10_concatenated.fasta	274,760	274,760
T_Pax_PVENOR_11_GGAGTGA_L001.fasta	149,708	1,351	T_Pax_PVENOR_11_concatenated.fasta	1,351	0
T_Pax_PVENOR_12_CGTACCA_L001.fasta	157,859	509	T_Pax_PVENOR_12_concatenated.fasta	509	0
T_Pax_PVENOR_13_TACGGGT_L001.fasta	243,318	211,388	T_Pax_PVENOR_13_concatenated.fasta	211,388	211,388
T_Pax_PVENOR_14_TGGCCAT_L001.fasta	337,722	283,858	T_Pax_PVENOR_14_concatenated.fasta	283,858	283,858
T_Pax_PVENOR_15_ATGGAGG_L001.fasta	299,345	250,069	T_Pax_PVENOR_15_concatenated.fasta	250,069	250,069
T_Pax_PVENOR_16_CTACGAG_L001.fasta	328,380	270,374	T_Pax_PVENOR_16_concatenated.fasta	270,374	270,374
T_Pax_PVENOR_17_ACACTGC_L001.fasta	323,368	255,090	T_Pax_PVENOR_17_concatenated.fasta	255,090	255,090
T_Pax_PVENOR_18_GACTGAC_L001.fasta	169,710	143,274	T_Pax_PVENOR_18_concatenated.fasta	143,274	143,274
T_Pax_PVENOR_19_ACTCGGA_L001.fasta	331,476	282,607	T_Pax_PVENOR_19_concatenated.fasta	282,607	282,607
T_Pax_PVENOR_1_GCTCCAT_L001.fasta	1,337,857	1,180,019	T_Pax_PVENOR_1_concatenated.fasta	1,180,019	1,180,019
T_Pax_PVENOR_20_TCCCACA_L001.fasta	180,009	107,291	T_Pax_PVENOR_20_concatenated.fasta	107,291	107,291
T_Pax_PVENOR_2_TCCTGGA_L001.fasta	1,771,297	1,602,053	T_Pax_PVENOR_2_concatenated.fasta	1,602,053	1,602,053
T_Pax_PVENOR_3_CAGCACAL001.fasta	2,014,360	1,791,374	T_Pax_PVENOR_3_concatenated.fasta	1,791,374	1,791,374
T_Pax_PVENOR_5_AGCTCGT_L001.fasta	1,214,286	1,068,485	T_Pax_PVENOR_5_concatenated.fasta	1,068,485	1,068,485

T_Pax_PVENOR_6_GCTTGTG_L001.fasta	1,384,866	1,203,862	T_Pax_PVENOR_6_concatenated.fasta	1,203,862	1,203,862
T_Pax_PVENOR_7_GTTACG_L001.fasta	867,589	2,967	T_Pax_PVENOR_7_concatenated.fasta	2,967	0
T_Pax_PVENOR_8_CGATGCA_L001.fasta	576,192	9,985	T_Pax_PVENOR_8_concatenated.fasta	9,985	0
T_Pax_PVENOR_9_GGCTATC_L001.fasta	335,329	1,607	T_Pax_PVENOR_9_concatenated.fasta	1,607	0
T_Pax_SAROR_16_concatenated.fasta	665,132	230,140	T_Pax_SAROR_16_concatenated.fasta	230,140	230,140
T_Pax_SAROR_17_concatenated.fasta	2,513,006	2,398,323	T_Pax_SAROR_17_concatenated.fasta	2,398,323	2,398,323
T_Pax_SAROR_18_concatenated.fasta	993,991	890,035	T_Pax_SAROR_18_concatenated.fasta	890,035	890,035
T_Pax_SAROR_19_concatenated.fasta	1,792,278	1,353,237	T_Pax_SAROR_19_concatenated.fasta	1,353,237	1,353,237
T_Pax_SAROR_1_concatenated.fasta	1,896,100	1,797,027	T_Pax_SAROR_1_concatenated.fasta	1,797,027	1,797,027
T_Pax_SAROR_2_concatenated.fasta	1,568,708	1,480,054	T_Pax_SAROR_2_concatenated.fasta	1,480,054	1,480,054
T_Pax_SAROR_3_concatenated.fasta	4,294,098	4,060,932	T_Pax_SAROR_3_concatenated.fasta	4,060,932	4,060,932
TOTAL	274,223,791			184,091,482	183,758,244
AVERAGE	1,724,678			1,157,808	1,155,712
SD	1,596,305			1,251,355	1,253,289
Retained [%]				67.13	67.01
MIN	4,562			20	77,052
MAX	9,345,347			7,610,614	7,610,614

Table S2. Outlier loci selection. The number of outlier loci detected in BayeScan is shown for each of the hierarchical levels: 1) between Slender and Stocky morphotypes ('Y&O' level), and within 2) Slender and 3) Stocky morphotypes.

Hierarchical levels	Number of outliers (BayeScan)
Between the morphotypes	469
Slender	4
Stocky	23

Table S3. AMOVA summary statistics. The 'AMOVA: Overall results' table shows degrees of freedom (Df), sum of squares (Sum Sq) and mean of squares (Mean Sq). The 'AMOVA: Components of covariance' table shows how much variance is detected at each hierarchical level, with sigma (σ) representing the variance [Sigma (σ) column]. Most variance is expected to derive from the 'Within Populations' level for groups that are not genetically structured. The 'AMOVA: Phi statistics' table provides the ϕ population differentiation statistics, and a higher ϕ statistic is expected to represent a higher amount of differentiation. The 'AMOVA: Testing significance with 999 Monte-Carlo tests' table shows p values inferred based on 999 permutations at each hierarchical level. AMOVA results are shown as separate tables for each of the hierarchical levels: (1) 'Slender & Stocky', (2) Stocky and (3) Slender.

Slender & Stocky				
AMOVA: Overall results				
Test	Df	Sum Sq	Mean Sq	
Between Morphotypes	1.00	41,405.77	41,405.76	
Between Populations (nested within Morphotypes)	10.00	1,668.03	166.80	
Within Populations	89.00	4,636.66	52.09	
Total	100.00	47,710.45	477.10	
AMOVA: Components of covariance				
Test	Sigma (σ)		%	
Variations Between Morphotypes	927.39		93.32	
Variations Between Populations (nested within Morphotype)	14.29		1.44	
Variations Within Populations	52.10		5.24	
Total variations	993.78		100.00	
AMOVA: Phi statistics				
Test	Phi			
Phi-Populations-total	0.95			
Phi-Populations-Morphotypes	0.21			
Phi-Morphotypes-total	0.93			
AMOVA: Testing significance with 999 Monte-Carlo tests				
Test	Obs	Std.Obs	Alter	P value
Variations within Populations	52.097	-21.650	less	0.001
Variations between Populations, nested within Morphotype	14.289	21.095	greater	0.001
Variations between Morphotypes	927.394	6.632	greater	0.002

Stocky						
AMOVA: Overall results						
Test			Df	Sum Sq	Mean Sq	
Between Populations			3	5,763.05	1,921.02	
Within Populations			29	3,074.03	106.01	
Total			32	8,837.08	276.16	
AMOVA: Components of covariance						
Test				Sigma (σ)	%	
Variations Between Populations				232.75	68.71	
Variations Within Populations				106.01	31.29	
Total variations				338.76	100.00	
AMOVA: Phi statistics						
Test						Phi
Phi-Populations-total						0.69
AMOVA: Testing significance with 999 Monte-Carlo tests						
Test	Observation	Std.Obs	Expectation	Variance	Alter	P value
Variations between Populations	232.75	17.76	0.97	170.27	greater	0.001

Slender						
AMOVA: Overall results						
Test		Df	Sum Sq	Mean Sq		
Between Populations		7	6327.08	903.87		
Within Populations		60	16714.13	278.57		
Total		67	23041.21	343.90		
AMOVA: Components of covariance						
Test			Sigma (σ)	%		
Variations Between Populations			76.95	21.64		
Variations Within Populations			278.57	78.36		
Total variations			355.52	100.00		
AMOVA: Phi statistics						
Test						Phi
Phi-Populations-total						0.22
AMOVA: Testing significance with 999 Monte-Carlo tests						
Test	Observation	Std.Obs	Expectation	Variance	Alter	P value
Variations between Populations	76.95	18.96	0.17	16.40	greater	0.001

