

Supplementary material:

**Insights for the Captive Management of South China Tigers Basing
on Large-Scale Genetic Survey**

Supplementary figure legend:

Figure S1: The K value of Bayesian Clustering Analyses through software STRUCTURE (Usepopinfo = 1), admixture model, and burn-in and replication values set at 50000 and 100000, respectively. The figure was based on all 320 captive South China tigers and the 108 voucher tigers (Luo et al. 2004 and 2008) as the reference tiger population data set. The figure showed K = 15 is the highest probability among choices of K.

Figure S2: The Pearson correlation between f_M and f_P .

Figure S3: The Pearson correlation between heterozygous loci ratio and f_P .

Figure S4: The Pearson correlation between heterozygous loci ratio and f_M .

Figure S5: The Pearson correlation between f_P and generation.

Figure S6: The Pearson correlation between f_M and generation.

Figure S7: The Pearson correlation between heterozygous loci ratio and generation.

Figure S8: The distribution of f_M among the institutes with more than 3 living pureblood SCTs. The differences among locations were not significant with $P > 0.05$ (ANOVA test).

Figure S9: The Pearson correlation between heterozygosity and nucleotide diversity (π) at genome level.

Figure S10: The Pearson correlation between heterozygosity and F_{ROH} at genome level.

Figure S11: The comparison of F_{ROH} for total ROH between hybridization in Meihua mountain and pureblood SCTs ($P = 0.0026$, ANOVA).

Figure S12: The comparison of F_{ROH} for different ROH length between hybridization in Meihua mountain and pureblood SCTs. (A) the ROH length $< 0.1M$ ($P = 0.0001205$, ANOVA); (B) $0.1M \leq$ the ROH length $< 1M$ ($P = 0.001006$, ANOVA); (C) $1M \leq$ the ROH length $< 3M$ ($P = 0.0001264$, ANOVA); (D) $3M \leq$ the ROH length $< 5M$ ($P = 0.09333$, ANOVA); (E) $5M \leq$ the ROH length $< 10M$ ($P = 0.6082$, ANOVA); (F) $10M \leq$ the ROH length ($P = 0.0002751$, ANOVA).

Figure S13 The principal component analysis of PC1 and PC2 following autosomal variants. South China tigers included SCT and Mei. SCT denoted the 23 pureblood SCTs and Mei denoted the hybridization SCTs in Meihua mountain. ptal: *P. t. altaica*, ptco: *P. t. corbetti*, ptja: *P. t. jacksoni*, ptsu: *P. t. sumatrae*, ptti: *P. t. tigris*.

Supplementary table legend

Table S1. The samples information in this study. (a separated file)

Table S2. Structure results basing on microsatellite. (a separated file)

Table S3. Re-sequencing data statistics in this study.

Table S4 the genomic heterozygosity and F_{ROH} in this study

Table S5 the F_{ROH} under different ROH length (a separated file)

Table S6. the detail about ADMIXTURE under genome level for the living six tiger subspecies. K is set from 4 to 10. (a separated file)

Table S7 Individual homozygote SNP counts per impact category.

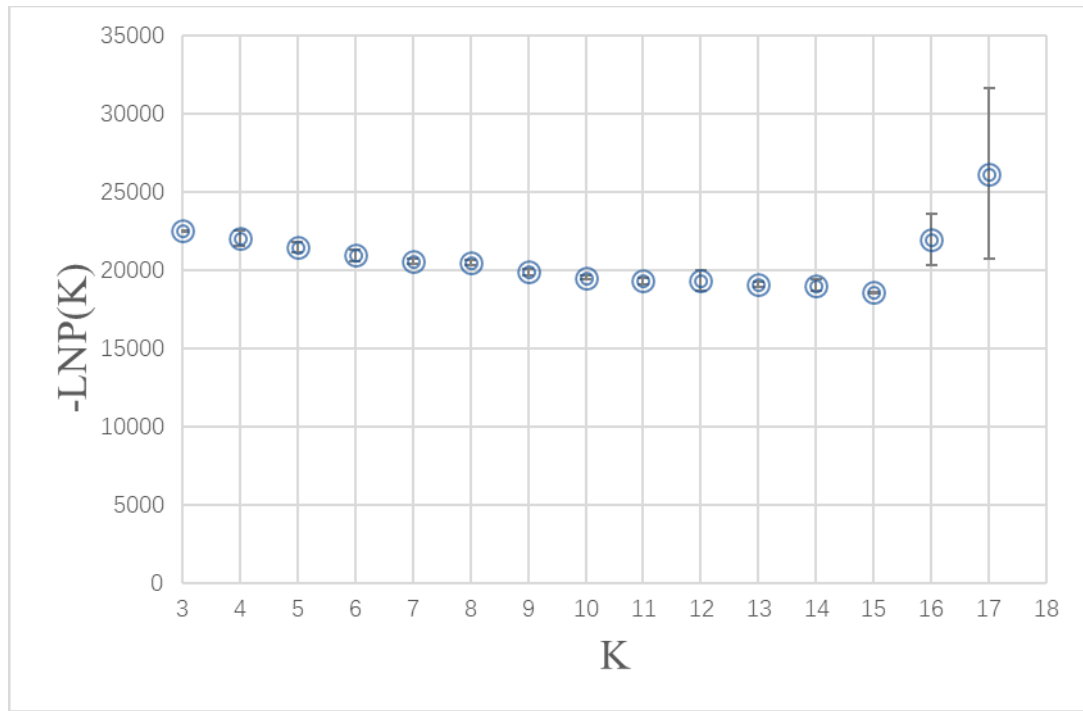


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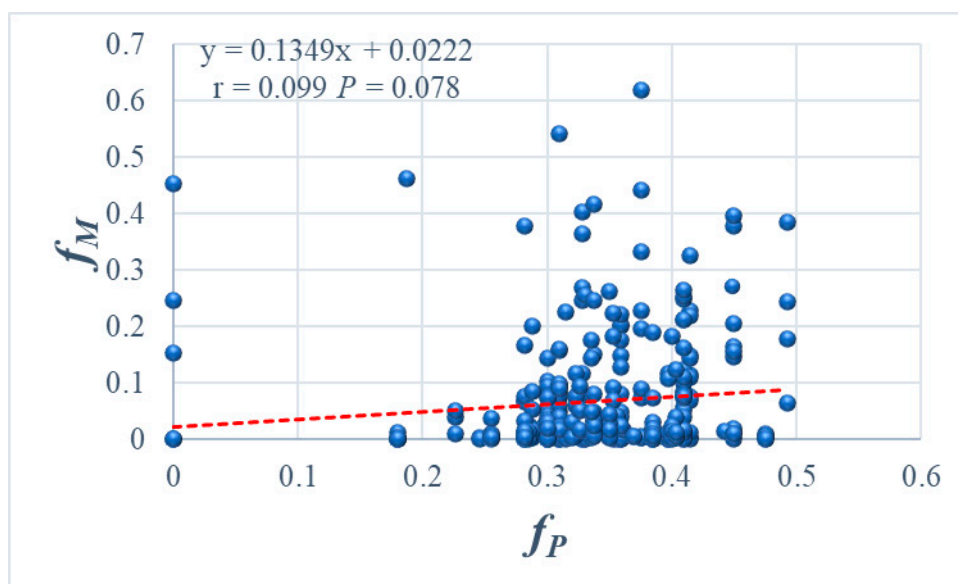


Figure S2: The Pearson correlation between f_M and f_P .

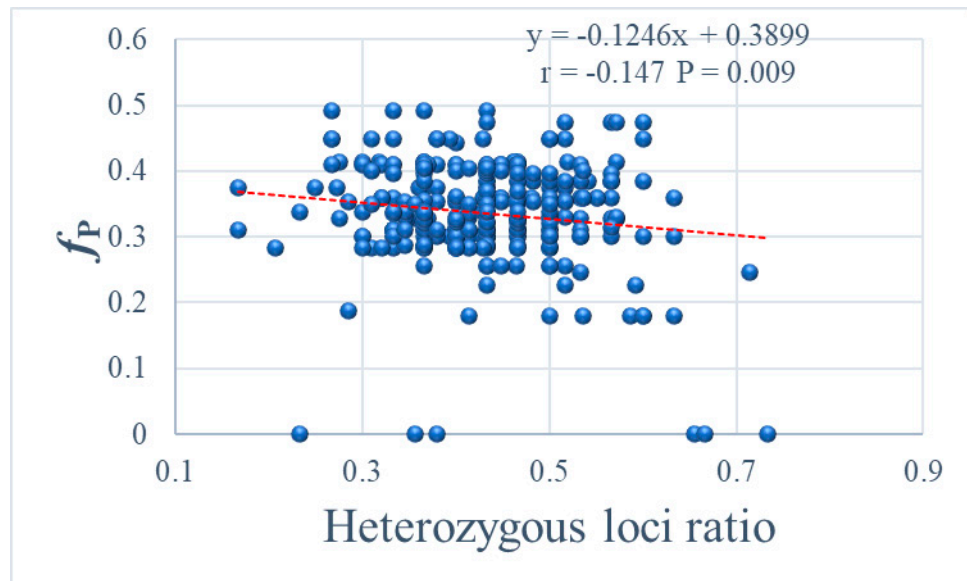


Figure S3: The Pearson correlation between heterozygous loci ratio and f_P .

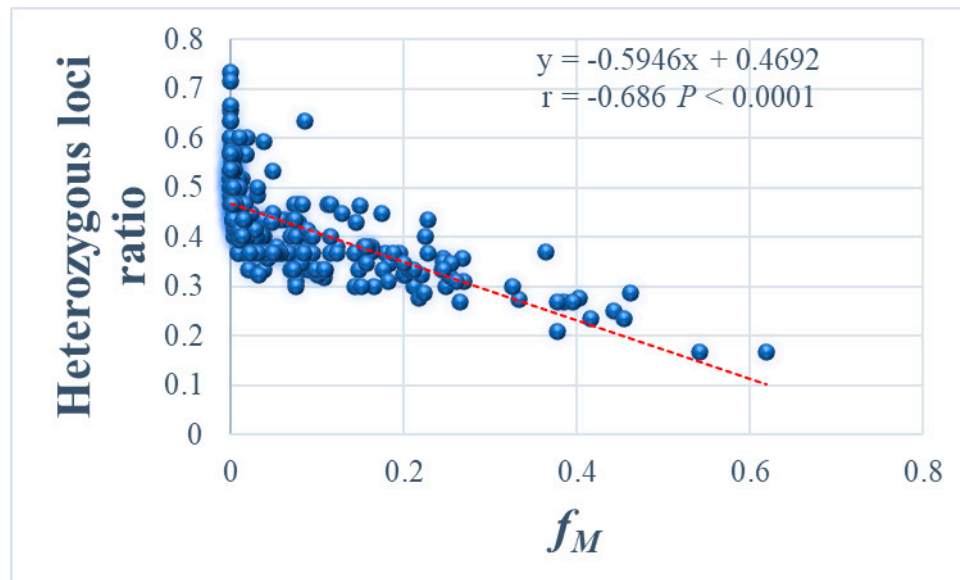


Figure S4: The Pearson correlation between heterozygous loci ratio and f_M .

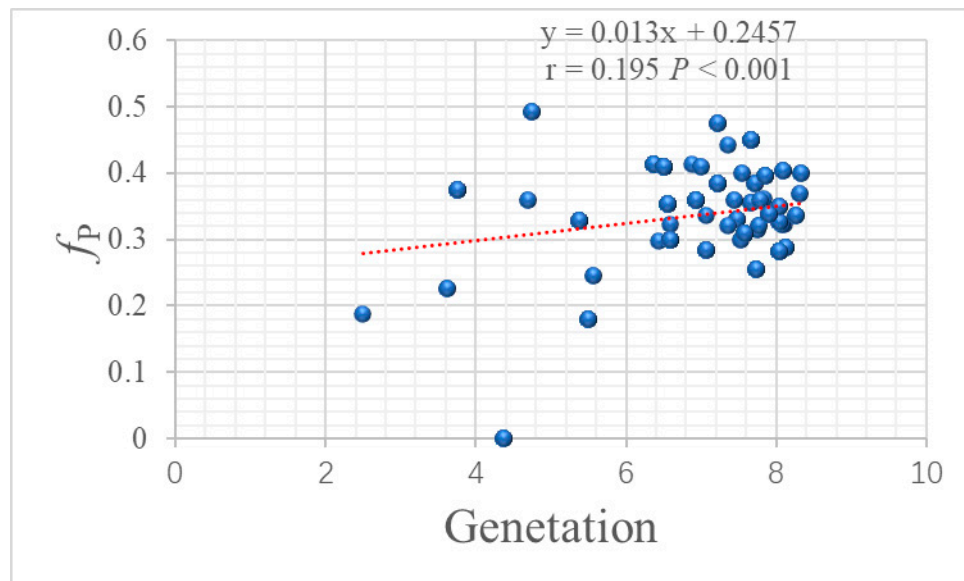


Figure S5: The Pearson correlation between f_P and generation.

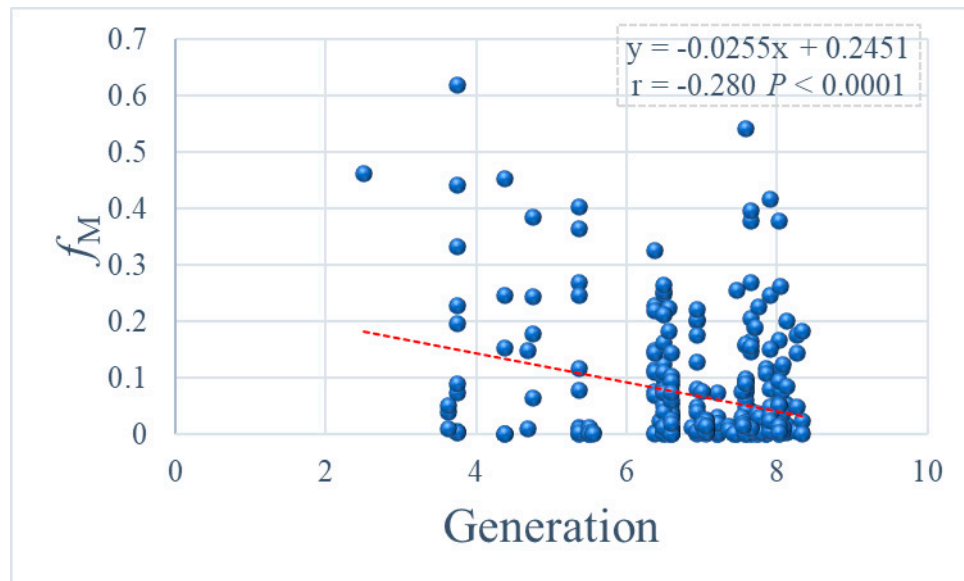


Figure S6: The Pearson correlation between f_M and generation.

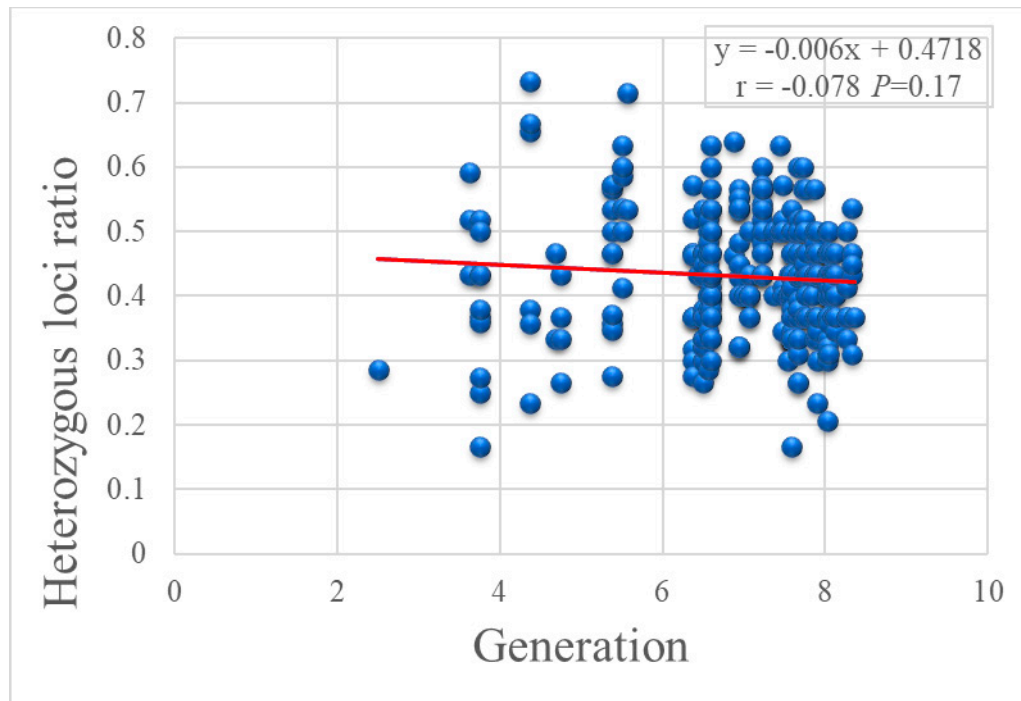


Figure S7: The Pearson correlation between heterozygous loci ratio and generation.

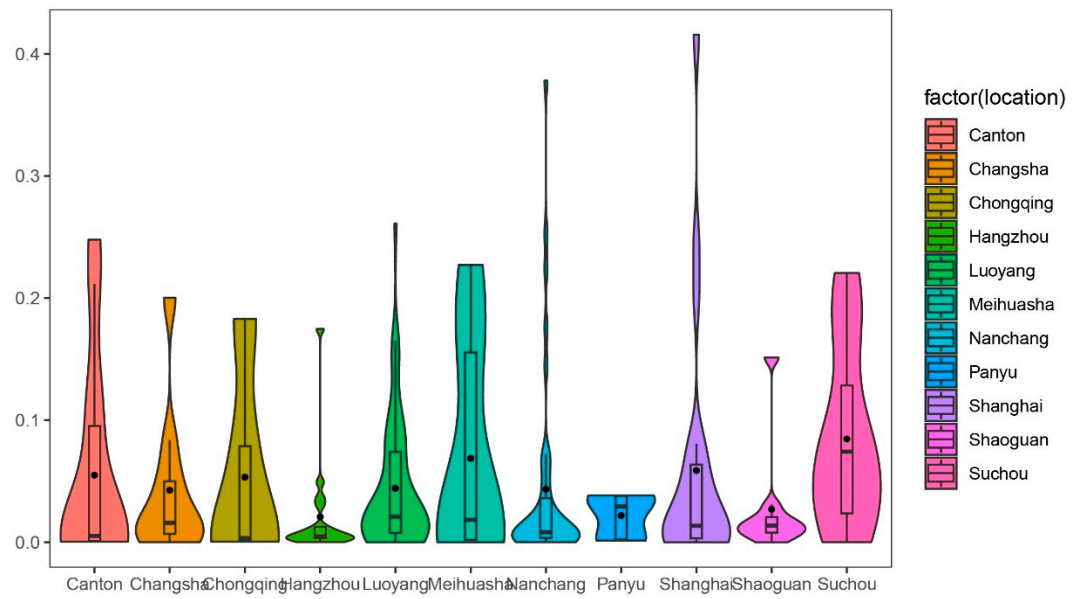


Figure S8: The distribution of f_M among the institutes with more than 3 living pureblood SCTs. The differences among locations were not significant with $P > 0.05$ (ANOVA test).

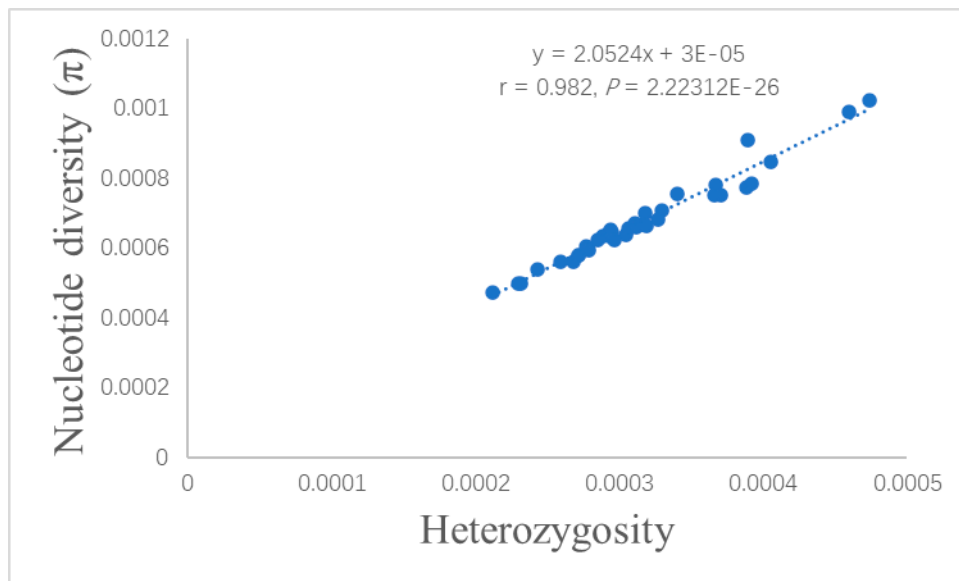


Figure S9: The Pearson correlation between heterozygosity and nucleotide diversity (π) at genome level.

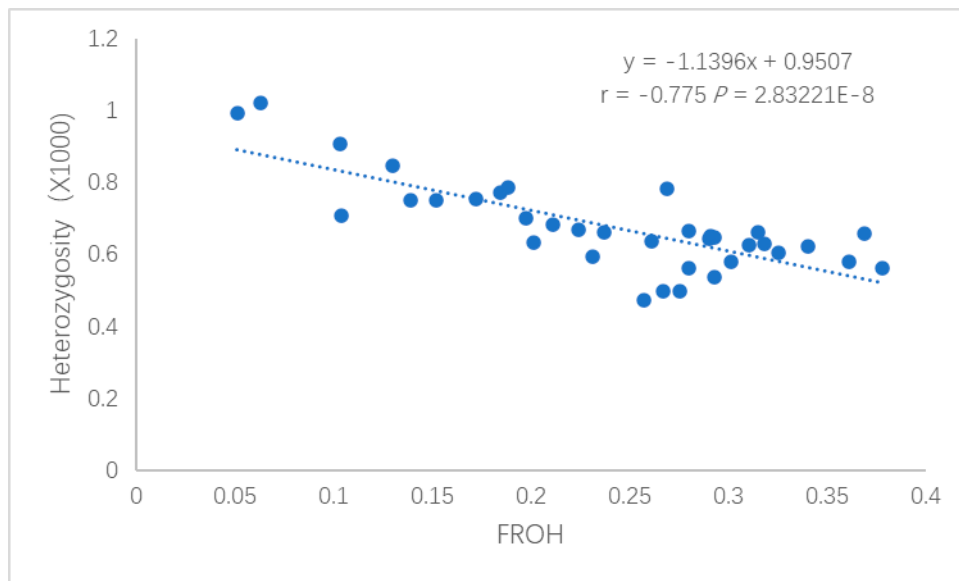


Figure S10: The Pearson correlation between heterozygosity and F_{ROH} at genome level.

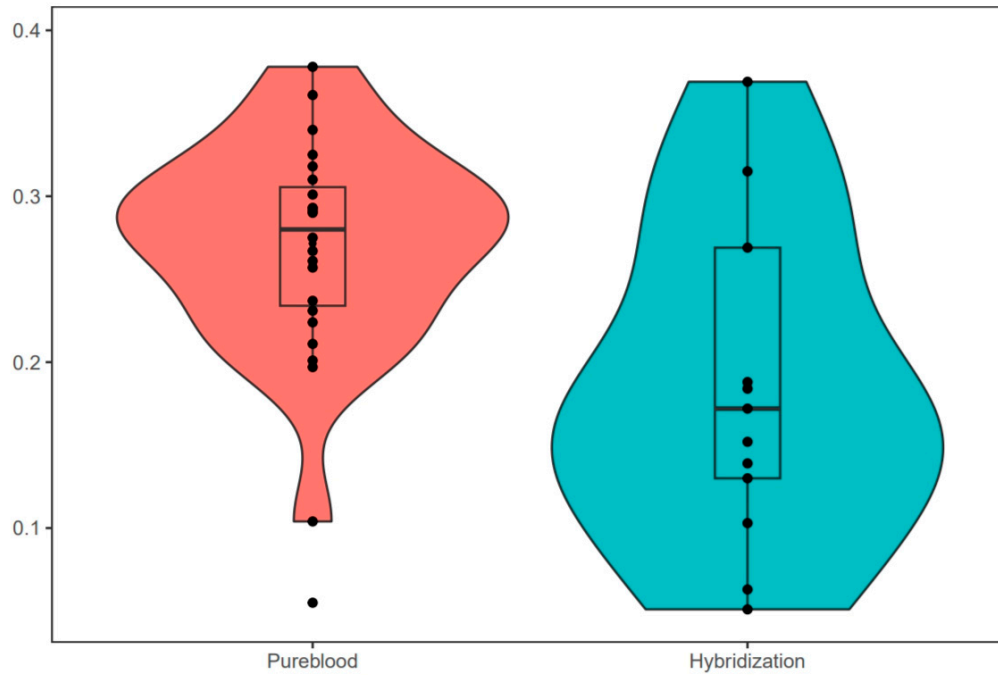


Figure S11: The comparison of F_{ROH} for total ROH between hybridization in Meihua mountain and pureblood SCTs ($P = 0.0026$, ANOVA).

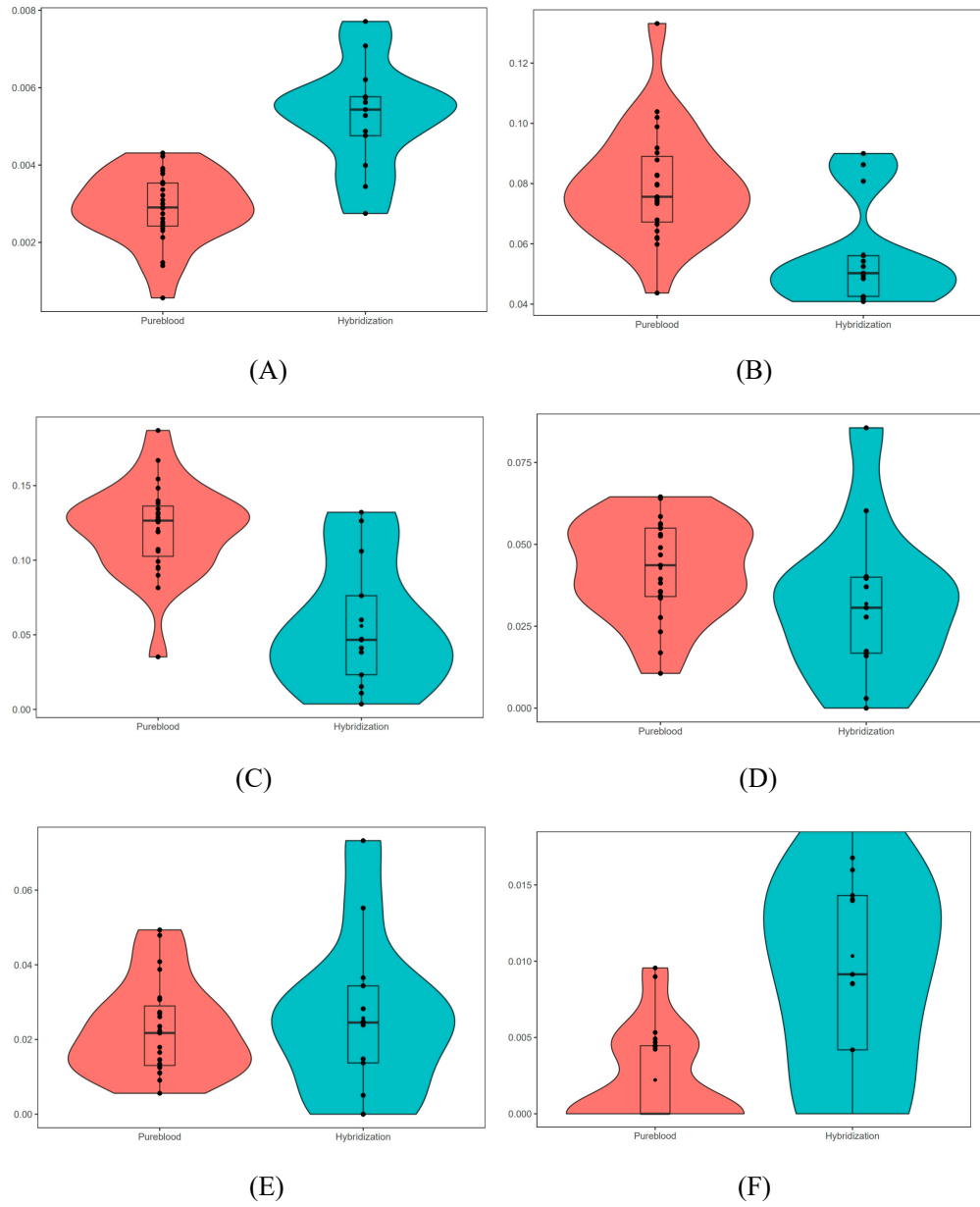


Figure S12: The comparison of F_{ROH} for different ROH length between hybridization in Meihua mountain and pureblood SCTs. (A) the ROH length $< 0.1M$ ($P = 0.0001205$, ANOVA); (B) $0.1M \leq$ the ROH length $< 1M$ ($P = 0.001006$, ANOVA); (C) $1M \leq$ the ROH length $< 3M$ ($P = 0.0001264$, ANOVA); (D) $3M \leq$ the ROH length $< 5M$ ($P = 0.09333$, ANOVA); (E) $5M \leq$ the ROH length $< 10M$ ($P = 0.6082$, ANOVA); (F) $10M \leq$ the ROH length ($P = 0.0002751$, ANOVA).

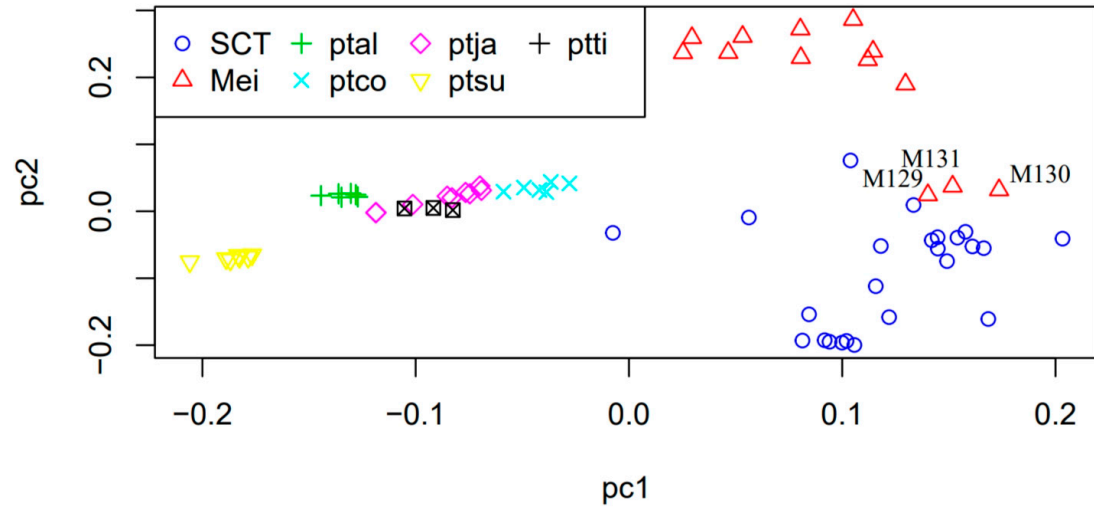


Figure S13 The principal component analysis of PC1 and PC2 following autosomal variants. South China tigers included SCT and Mei. SCT denoted the 23 pureblood SCTs and Mei denoted the hybridization SCTs in Meihua mountain. ptal: *P. t. altaica*, ptco: *P. t. corbetti*, ptja: *P. t. jacksoni*, ptsu: *P. t. sumatrae*, ptti: *P. t. tigris*.

Table S1. The samples information in this study. (a separated file)

Table S2. Structure results basing on microsatellite. (a separated file)

Table S3. Re-sequencing data statistics in this study.

Sample	Read_length(bp)	RawBases(Gb)	RawCoverage(X)	CleanBases(Gb)	CleanCoverage(X)
#267	150_150	49.90826	20.8	47.94401278	19.98
#296	150_150	44.61216	18.59	43.0103104	17.92
#299	150_150	39.07528	16.27	37.50236	15.62
#348	150_150	37.65111	15.67	36.254522	15.1
#393	150_150	38.72085	16.12	36.747563	15.29
#441	150_150	46.13822	19.21	43.827861	18.25
#457	150_150	34.10595	14.2	32.957172	13.73
#467	150_150	37.90963	15.78	36.580036	15.23
#468	150_150	44.13163	18.38	41.101204	17.11
#489	150_150	44.93985	18.71	42.607143	17.73
#522	150_150	40.3453	16.8	38.747885	16.13
#530	150_150	41.69762	17.36	39.582499	16.47
#531	150_150	41.50857	17.27	39.477911	16.43
#544	150_150	34.67444	14.43	33.165348	13.81
#551	150_150	47.24652	19.67	44.92909	18.71
#553	150_150	46.49082	19.36	44.311691	18.45
#558	150_150	48.53714	20.2	46.351285	19.3
#616	150_150	41.2668	17.18	39.281961	16.35
#625	150_150	44.37436	18.47	42.410637	17.66
#635	150_150	35.00888	14.57	33.61567	14
#701	150_150	42.69144	17.77	40.710288	16.95
#702	150_150	43.09487	17.94	41.207888	17.15
#712	150_150	32.83035	13.67	31.538613	13.13
M118	150_150	44.48234	18.53	43.886367	18.27
M129	150_150	47.38267	19.74	39.466503	16.43
M130	150_150	43.25693	18.02	40.379301	16.81
M131	150_150	51.26582	21.36	42.877485	17.85
M29	150_150	45.30731	18.88	43.819113	18.24
M31	150_150	48.864211	20.36	46.599321	19.4
M36	150_150	43.080932	17.95	41.194761	17.15
M44	150_150	45.5760134	18.99	43.428646	18.08
M64	150_150	45.192257	18.83	43.236483	18
M67	150_150	40.968016	17.07	39.393241	16.4
M70	150_150	46.93199	19.56	44.768306	18.65

M74	150_150	52.45002	21.85	50.145154	20.89
M77	150_150	43.17973	17.99	41.141724	17.14

Table S4 the genomic heterozygosity and F_{ROH} in this study

Individual	Total ROH length (Kb)	the number of ROH	Average ROH length (Kb)	Number of heterozygotes	F_{ROH}	non-ROH	Heterozygosity	N_SITES	Coverged(bp)	CoveredRatio(%)	Origin
#267	693753	739	938.772	1539512	0.29	0.71	0.000643078	2376436	2393974405	99.1	pureblood
#296	905833	895	1012.1	1342943	0.378	0.62	0.00056107	2367254	2393537867	99.08	pureblood
#299	478368	613	780.372	1504520	0.201	0.79	0.000633491	2009701	2374965919	98.31	pureblood
#441	856086	961	890.828	1373068	0.361	0.63	0.000578736	2257874	2372530894	98.21	pureblood
#530	694938	816	851.639	1533596	0.293	0.70	0.000646195	2415206	2373270732	98.24	pureblood
#551	807383	999	808.191	1480910	0.34	0.66	0.000623663	2444966	2374537488	98.3	pureblood
#616	619749	726	853.648	1516877	0.261	0.73	0.000638408	2189493	2376028907	98.36	pureblood
#701	530718	717	740.193	1589963	0.224	0.77	0.000669779	2259842	2373861531	98.27	pureblood
#702	563601	739	762.654	1575202	0.237	0.76	0.000663101	2249524	2375507455	98.34	pureblood
#348	246572	448	550.383	1684277	0.104	0.89	0.000708491	2069506	2377275259	98.41	pureblood
#393	664980	768	865.85	1584009	0.28	0.72	0.000666514	237556	2376556699	98.38	pureblood

			9					3			
#45 7	610577	52 0	117 4.1 9	11189 68	0. 25 7	0.74 3	0.0004 71408	151 881 2	23736 72443	98.26	pureb lood
#46 7	652237	68 6	950 .78 3	11845 68	0. 27 5	0.72 5	0.0004 98584	170 198 2	23758 62752	98.35	pureb lood
#46 8	632885	62 1	101 9.1 4	11833 72	0. 26 7	0.73 3	0.0004 98352	167 294 0	23745 70114	98.3	pureb lood
#48 9	772474	84 5	914 .17	14350 47	0. 32 5	0.67 5	0.0006 04443	232 842 9	23741 62803	98.28	pureb lood
#52 2	467853	82 4	567 .78 3	16615 72	0. 19 7	0.80 3	0.0006 99608	227 725 8	23750 03370	98.32	pureb lood
#53 1	755879	92 9	813 .64 8	14963 92	0. 31 8	0.68 2	0.0006 30478	241 395 9	23734 24450	98.25	pureb lood
#54 4	695086	82 3	844 .57 6	12786 00	0. 29 3	0.70 7	0.0005 3857	192 981 0	23740 64437	98.28	pureb lood
#55 3	691404	94 8	729 .33	15493 46	0. 29 1	0.70 9	0.0006 52548	242 402 4	23743 00162	98.29	pureb lood
#55 8	715804	83 8	854 .18 1	13773 23	0. 30 1	0.69 9	0.0005 79561	210 154 9	23764 93772	98.38	pureb lood
#62 5	500523	66 7	750 .40 9	16231 29	0. 21 1	0.78 9	0.0006 82882	225 205 8	23768 81704	98.39	pureb lood
#63 5	735365	11 85	620 .56 1	14845 02	0. 31	0.69	0.0006 24977	235 242 0	23752 89131	98.33	pureb lood
#71 2	548027	62 0	883 .91 5	14100 43	0. 23 1	0.76 9	0.0005 93776	193 997 3	23747 03827	98.3	pureb lood
M2 9	151309	72 9	207 .55 7	24505 24	0. 06 3	0.93 7	0.0010 23128	328 850 7	23951 29796	99.15	hybri dizati on
M3 1	120311	66 1	182 .01 3	23557 04	0. 05 1	0.94 9	0.0009 91829	309 188 2	23751 11375	98.32	hybri dizati on
M3	223962	72	309	19832	0.	0.89	0.0009	283	21835	90.39	hybri

6		3	.76 8	93	10 3	7	0829	522 4	46758		dizati on
M4 4	310632	64 8	479 .37	20298 31	0. 13	0.87	0.0008 46703	281 273 0	23973 35770	99.24	hybri dizati on
M6 4	440750	66 5	662 .78 2	18551 34	0. 18 4	0.81 6	0.0007 73832	264 670 3	23973 35770	99.24	hybri dizati on
M6 7	451466	76 0	594 .03 4	18838 45	0. 18 8	0.81 2	0.0007 85333	276 613 7	23987 85187	99.3	hybri dizati on
M7 0	644717	96 0	671 .58	18728 65	0. 26 9	0.73 1	0.0007 81398	291 968 3	23968 12652	99.22	hybri dizati on
M7 4	754580	94 7	796 .81 1	15825 20	0. 31 5	0.68 5	0.0006 60159	263 490 8	23971 80527	99.23	hybri dizati on
M7 7	883849	10 13	872 .50 7	15738 54	0. 36 9	0.63 1	0.0006 56754	276 227 1	23964 13501	99.2	hybri dizati on
M11 8	634363	73 6	861 .90 6	12725 69	0. 28	0.72	0.0005 61193	219 572 8	22676 12945	93.87	hybri dizati on
M1 29	362488	57 0	635 .94 4	17864 77	0. 15 2	0.84 8	0.0007 50562	243 086 1	23801 84335	98.53	hybri dizati on
M1 30	332556	49 7	669 .12 7	18033 46	0. 13 9	0.86 1	0.0007 52305	238 258 5	23970 94200	99.23	hybri dizati on
M1 31	412917	63 0	655 .42 4	18134 23	0. 17 2	0.82 8	0.0007 56204	253 428 5	23980 60478	99.27	hybri dizati on

Table S5 the F_{ROH} under different ROH length (a separated file)

Table S6. the detail about ADMIXTURE under genome level for the living six tiger subspecies. K is set from 4 to 10. (a separated file)

Table S7
homozygote
impact category.

Individual	High	Moderate	Low	Total
M129	10	625	989	1624
M130	6	520	951	1477
M131	11	752	1032	1795

Individual
SNP counts per