

Supplementary Tables

Table S1. Statistics of Sequencing Data Quality for All Samples.

Sampies_ID	Clean_Reads	Clean_Base	Q20(%)	Q30(%)	GC(%)
A1	36466434	10907725307	99.5	98.27	37.72
A10	38220521	11430832146	99.52	98.19	38.05
A11	38601026	11544219409	99.52	98.22	38.19
A12	37397278	11180309070	99.47	98.07	37.84
A13	39372768	11774339424	99.51	98.17	38.04
A14	34715379	10382583667	99.46	98.02	37.99
A15	35145257	10508715813	99.48	98.09	38.2
A16	34698721	10374952279	99.48	98.11	38.05
A17	37374751	11174624809	99.55	98.31	37.96
A18	37906145	11324816911	99.5	98.14	37.8
A19	38252728	11442601893	99.53	98.24	37.89
A2	34920710	10445248885	99.52	98.27	37.68
A20	37089702	11093840864	99.47	98.04	38.15
A3	37645176	11260179937	99.51	98.21	37.78
A4	35649630	10662194879	99.54	98.31	37.78
A5	36306726	10855414041	99.47	97.99	37.9
A6	33688852	10077969076	99.5	98.21	37.74
A7	37235119	11136494733	99.49	98.13	37.99
A8	37980122	11355696408	99.49	98.13	38.07
A9	34209483	10228813752	99.44	97.97	37.96
B1	36131563	10806676793	99.54	98.32	38.03
B10	39367634	11768342880	99.47	98.03	38.12
B11	35642412	10658397888	99.47	98.04	38.08
B12	34901743	10437662238	99.49	98.12	37.8
B13	34923142	10444735144	99.52	98.26	38.04
B14	34860536	10424501731	99.49	98.12	37.99
B15	37212433	11129901628	99.53	98.26	38.1
B16	35944358	10748981986	99.53	98.23	37.97
B17	35909419	10739873238	99.49	98.11	37.95
B18	35121756	10503075179	99.5	98.13	37.93
B19	35144423	10511052198	99.34	97.4	37.74
B2	35826459	10715965508	99.53	98.28	37.96
B20	34510894	10318654750	99.48	98.1	37.89
B3	36081183	10791681860	99.53	98.23	38.13
B4	36303575	10858508459	99.56	98.37	37.92
B5	35516697	10620472697	99.48	98.08	37.81
B6	36553848	10931850641	99.52	98.2	37.83
B7	36540869	10924580581	99.48	98.08	38.05
B8	38172904	11418236115	99.55	98.3	38.03
B9	39478753	11808728049	99.54	98.26	38.02
C1	33658107	10063247196	99.47	98.13	38.03
C10	36047017	10779548730	99.52	98.22	37.9
C11	34008559	10175624829	99.53	98.29	37.69
C12	34462871	10310773379	99.48	98.1	37.7
C13	37380446	11182683912	99.52	98.2	37.73
C14	35624423	10656922031	99.53	98.28	37.79

C15	35297245	10558703522	99.5	98.15	37.74
C16	34649502	10367096629	99.51	98.16	37.85
C17	34690967	10380704111	99.57	98.45	37.7
C18	35952168	10757625213	99.55	98.37	37.83
C19	36569533	10937690949	99.56	98.38	37.99
C2	33659927	10054393919	99.43	97.92	37.26
C20	34739788	10393630779	99.48	98.11	37.85
C3	38971406	11656164820	99.58	98.44	37.84
C4	35106049	10502173115	99.53	98.24	38.14
C5	34278917	10253957861	99.55	98.29	38.07
C6	37677492	11268218076	99.57	98.39	38.1
C7	34964496	10455840450	99.5	98.15	38.19
C8	39173088	11714913154	99.51	98.13	38.08
C9	36716443	10981311237	99.51	98.21	37.96
D1	33718794	10089303905	99.46	97.99	37.96
D10	35131555	10509421163	99.36	97.39	37.69
D11	36513656	10924916346	99.52	98.26	37.69
D12	36736714	10990091204	99.56	98.3	37.76
D13	37991068	11365058911	99.57	98.4	37.6
D14	36899510	11041948983	99.51	98.21	38.34
D15	35572863	10642891478	99.63	98.59	37.72
D16	36364854	10878288387	99.44	98.05	37.63
D17	35954044	10755846359	99.54	98.29	37.55
D18	37419665	11196079894	99.6	98.48	37.77
D19	34450117	10305953551	99.56	98.37	37.82
D2	37425329	11198269684	99.56	98.34	37.62
D20	34615083	10354857596	99.53	98.28	37.8
D3	36577137	10942099302	99.52	98.2	37.89
D4	33858315	10129117322	99.53	98.29	37.71
D5	36877296	11032571045	99.56	98.37	37.72
D6	35966350	10759092296	99.51	98.17	37.81
D7	36376035	10881725749	99.55	98.31	37.78
D8	33959192	10157016042	99.57	98.37	37.8
D9	35589139	10645853753	99.5	98.17	37.75
E1	34223630	10238825878	99.54	98.34	37.44
E10	34770791	10398778760	99.54	98.31	37.69
E11	34599203	10349524008	99.55	98.36	37.76
E12	34507143	10321076261	99.53	98.3	37.75
E13	34141171	10212377349	99.49	98.15	37.84
E14	34611809	10351835779	99.52	98.24	37.71
E15	34083732	10196759390	99.53	98.29	37.75
E16	34137591	10211556778	99.51	98.23	37.76
E17	38417527	11492381318	99.48	98.05	37.7
E18	34714931	10380046378	99.5	98.21	37.35
E19	36529507	10928543293	99.52	98.21	37.7
E2	35745099	10691074640	99.48	98.1	37.62
E20	35491778	10618013560	99.54	98.32	37.63
E3	37271876	11151381366	99.52	98.23	37.75
E4	36173742	10820948279	99.49	98.11	37.81
E5	37034721	11077292595	99.52	98.22	37.65
E6	35144280	10516430524	99.5	98.13	37.84

E7	35580998	10643261242	99.51	98.21	37.9
E8	36243573	10842465950	99.53	98.25	37.75
E9	35308183	10564378818	99.55	98.37	37.72
H1	35399288	10590439165	99.54	98.28	37.73
H10	33875473	10132063425	99.49	98.13	37.65
H11	36982829	11063664211	99.56	98.34	37.74
H12	36923535	11046228320	99.52	98.23	37.81
H13	35926069	10746821120	99.49	98.11	37.75
H14	39059227	11683797707	99.46	98.08	37.61
H15	36245139	10846026726	99.57	98.41	37.67
H16	34524357	10327836226	99.51	98.23	37.41
H17	34949159	10454241914	99.52	98.22	37.65
H18	34011828	10174623868	99.44	97.95	37.71
H19	33397886	9987294759	99.46	98.05	37.55
H2	37180819	11122791593	99.56	98.37	37.76
H20	34643055	10362532986	99.52	98.22	37.67
H3	32178783	9624847988	99.53	98.27	37.74
H4	36685082	10974495815	99.52	98.23	37.72
H5	35125211	10508331061	99.54	98.29	37.7
H6	35178771	10523555624	99.52	98.25	37.67
H7	34493578	10318724336	99.53	98.26	37.75
H8	34414793	10296148302	99.53	98.29	37.71
H9	35366571	10577808778	99.5	98.17	37.67
K1	35463895	10607523198	99.5	98.14	37.69
K10	37416597	11194457702	99.52	98.2	37.68
K11	34453300	10306429327	99.47	98.03	37.77
K12	37142744	11113649434	99.54	98.28	37.66
K13	36097855	10799491799	99.52	98.22	37.67
K14	34789733	10406882231	99.51	98.18	37.71
K15	35782446	10705415172	99.58	98.48	37.69
K16	37757597	11294737411	99.52	98.2	37.8
K17	35413561	10592552807	99.52	98.25	37.71
K18	39366453	11776623951	99.55	98.31	37.75
K19	37330480	11166727673	99.53	98.23	37.86
K2	36308680	10861195127	99.53	98.22	37.72
K20	36201325	10827844186	99.52	98.21	37.3
K3	36807107	11011204106	99.51	98.16	37.71
K4	33857120	10127349394	99.47	98.08	37.78
K5	37651664	11263871190	99.49	98.07	37.44
K6	35327180	10567574256	99.54	98.31	37.68
K7	34553936	10334513648	99.5	98.18	37.36
K8	34027355	10178313781	99.52	98.24	37.59
K9	35272639	10552466562	99.52	98.25	37.72

Notes: Sample_ID refers to the unique identifier for each sample; Clean_Reads represents the number of reads after quality filtering; Clean_Base means the total number of filtered bases, calculated by multiplying the number of clean reads by the read length; Q20(%) indicates the percentage of bases with a Phred quality score of no less than 20 among all clean bases; Q30(%) is the percentage of bases with a Phred quality score of no less than 30; GC(%) stands for the GC content of the sample, which is the proportion of G and C bases in all total bases.

Table S2. Mapping Statistics of Sequencing Reads.

Sample ID	Total_reads	Mapped (%)	Properly_mapped (%)	Ave_depth	Cov_ratio_1X (%)	Cov_ratio_5X (%)	Cov_ratio_10X (%)
A1	72932868	99.75	95.1	10	95.86	86.69	56.88
A10	76441042	99.69	95.3	11	96.01	87.44	59.42
A11	77202052	99.75	95.41	11	95.59	86.75	59.06
A12	74794556	99.63	94.24	10	95.87	87.1	57.43
A13	78745536	99.74	95.31	11	96.27	87.98	61.22
A14	69430758	99.7	95.05	10	95.67	85.12	51.81
A15	70290514	99.77	94.84	10	95.25	84.05	50.77
A16	69397442	99.76	94.41	10	95.83	84.78	50.89
A17	74749502	99.75	94.8	10	95.74	86.31	55.81
A18	75812290	99.73	94.8	11	95.74	87.36	58.22
A19	76505456	99.74	95.7	11	95.77	87.47	60.61
A2	69841420	99.7	95.04	10	95.77	85.93	53.18
A20	74179404	99.73	95.09	10	95.51	84.9	54.83
A3	75290352	99.72	94.77	10	95.64	87.24	59.81
A4	71299260	99.73	94.91	10	95.69	86.33	55.4
A5	72613452	99.73	94.39	10	95.58	86.57	56.11
A6	67377704	99.69	95.67	9	95.56	84.76	50.53
A7	74470238	99.75	95.5	10	96.31	87.08	57.76
A8	75960244	99.74	94.97	11	95.8	86.33	56.58
A9	68418966	99.69	94.06	9	95.78	84.49	49.59
B1	72263126	99.45	95.24	10	95.88	85.09	53.09
B10	78735268	99.72	94.19	11	96.68	87.99	59.3
B11	71284824	99.76	95.24	10	96.62	86.01	53.23
B12	69803486	99.76	95.31	10	96.82	86.53	53.16
B13	69846284	99.72	95.01	10	96.04	84.71	51.02
B14	69721072	99.67	94.78	10	97.16	85.46	51.01
B15	74424866	99.73	95.13	10	96.81	86.52	55.07
B16	71888716	99.76	95.78	10	97.29	87.29	54.89
B17	71818838	99.75	95.13	10	96.39	86.31	54.63
B18	70243512	99.75	95.53	10	96.63	86.43	53.4
B19	70288846	99.77	95.64	10	97.37	86.57	53.61
B2	71652918	99.64	95.55	10	97.26	86.63	54.52
B20	69021788	99.77	95.32	10	97.05	86.01	51.82
B3	72162366	99.76	95.08	10	96.75	85.84	53.62
B4	72607150	99.74	95.37	10	96.15	86.34	55.02
B5	71033394	99.71	95.09	10	97.01	86.66	53.96
B6	73107696	99.75	95.06	10	96.29	86.75	56.32
B7	73081738	99.75	94.32	10	96.5	86.54	54.15
B8	76345808	99.74	95.53	11	96.46	87.58	59.38
B9	78957506	99.78	95.37	11	96.83	87.99	61.13
C1	67316214	99.75	94.78	9	96.08	84.36	48.25
C10	72094034	99.72	94.16	10	96.23	85.47	52.87
C11	68017118	99.69	96.36	9	96.36	84.53	50.4
C12	68925742	99.67	96.35	10	95.61	82.7	50.15
C13	74760892	99.74	96.1	10	95.88	87.13	59.44
C14	71248846	99.71	96.02	10	96.06	86.36	54.98
C15	70594490	99.72	95.82	10	96.22	86.32	54.53
C16	69299004	99.7	95.93	10	95.85	84.41	51.57
C17	69381934	99.68	96.55	10	95.41	83.81	51.57
C18	71904336	99.7	96.06	10	95.91	84.74	53.73
C19	73139066	99.77	95.91	10	96.47	87.13	56.56
C2	67319854	99.71	93.35	9	96.22	83.91	45.91
C20	69479576	99.67	95.68	10	95.73	83.34	50.7
C3	77942812	99.75	94.86	11	96.75	88.6	61.43
C4	70212098	99.76	95.85	10	96	84.95	52.35
C5	68557834	99.73	94.93	10	96.19	84.07	49.35
C6	75354984	99.76	95.22	11	96.31	86.87	56.95
C7	69928992	99.73	94.97	10	96.26	84.73	50.23
C8	78346176	99.71	94.85	11	96.55	87.89	59.82
C9	73432886	99.73	94.98	10	96.18	86.62	55.88
D1	67437588	99.69	95.42	9	96.12	83.5	48.97
D10	70263110	99.61	95.97	10	96.24	86.01	53.85

D11	73027312	99.57	95.91	10	96.25	85.57	55.22
D12	73473428	99.74	96.04	10	96.28	87.3	58.13
D13	75982136	99.77	96.33	11	96.42	87.74	60.23
D14	73799020	99.62	95.24	10	96.04	84.24	53.63
D15	71145726	99.76	96.24	10	97.01	86.33	54.65
D16	72729708	99.73	95.92	10	96.28	86.92	56.89
D17	71908088	99.61	95.88	10	96.74	86.93	56.19
D18	74839330	99.71	96.07	10	96.49	87.53	59.25
D19	68900234	99.72	96	10	96.23	85.71	52.37
D2	74850658	99.73	96.11	10	96.35	87	59.08
D20	69230166	99.71	95.88	10	96.16	85.91	52.66
D3	73154274	99.75	95.83	10	96.04	86.63	56.9
D4	67716630	99.74	95.92	9	96.97	85.18	50.66
D5	73754592	99.72	96.02	10	96.43	87.04	58.24
D6	71932700	99.77	96.18	10	96	86.13	55.6
D7	72752070	99.77	96.09	10	96.22	86.95	57.24
D8	67918384	99.7	95.74	9	96.57	85.53	51.12
D9	71178278	99.76	95.84	10	96.31	86.49	54.67
E1	68447260	99.71	95.88	9	95.92	85.23	51.64
E10	69541582	99.65	95.79	10	96.2	86.1	52.73
E11	69198406	99.7	95.87	10	96.17	85.84	52.27
E12	69014286	99.72	95.77	10	96.57	85.89	52.2
E13	68282342	99.73	96.05	9	96.1	85.53	51.26
E14	69223618	99.74	96.19	10	96.32	86.15	52.8
E15	68167464	99.74	96.09	9	96.08	85.39	51.22
E16	68275182	99.76	96.29	9	96.49	85.93	51.57
E17	76835054	99.72	95.9	11	96.14	87.85	61.55
E18	69429862	99.74	94.29	10	96.34	86.29	52.73
E19	73059014	99.73	95.87	10	96.36	87.22	57.46
E2	71490198	99.73	95.28	10	96.11	86.77	55.68
E20	70983556	99.71	95.96	10	96.21	86.43	55.1
E3	74543752	99.69	95.99	10	96.17	87.34	59.38
E4	72347484	99.72	95.97	10	96.45	86.99	56.48
E5	74069442	99.7	95.45	10	96.49	87.69	58.42
E6	70288560	99.69	95.95	10	95.75	85.04	53.41
E7	71161996	99.76	95.9	10	96.45	86.74	54.69
E8	72487146	99.69	96.01	10	96.18	86.93	56.72
E9	70616366	99.7	96.35	10	96.17	86.04	54.03
H1	70798576	99.66	95.8	10	95.79	85.86	54.51
H10	67750946	99.7	95.78	9	95.51	84.92	51.05
H11	73965658	99.73	95.98	10	96.42	87.07	58.35
H12	73847070	99.72	95.73	10	96.13	86.97	58.05
H13	71852138	99.73	95.79	10	96.74	86.66	56.26
H14	78118454	99.72	95.44	11	96.73	88.33	62.78
H15	72490278	99.7	96.26	10	96.43	86.17	55.85
H16	69048714	99.7	95.76	10	96.32	85.4	52.4
H17	69898318	99.7	95.73	10	96.14	85.91	53.72
H18	68023656	99.72	95.77	9	95.98	85.19	51.11
H19	66795772	99.72	94.57	9	96.02	85.02	49.67
H2	74361638	99.74	96.1	10	96.02	87.15	58.84
H20	69286110	99.7	95.67	10	96.31	85.87	52.77
H3	64357566	99.71	95.62	9	95.76	83.51	46.38
H4	73370164	99.72	95.28	10	96.25	87.08	57.69
H5	70250422	99.72	95.87	10	96.15	86.16	53.96
H6	70357542	99.71	95.69	10	95.84	85.79	54.33
H7	68987156	99.73	95.89	10	96.2	85.88	52.44
H8	68829586	99.67	95.77	10	95.92	85.5	52.26
H9	70733142	99.71	95.65	10	95.89	86.14	54.73
K1	70927790	99.64	95.53	10	96.56	86.65	54.86
K10	74833194	99.69	95.93	10	96.37	87.46	59.42
K11	68906600	99.74	95.9	10	96.08	85.6	52.66
K12	74285488	99.69	96.1	10	96.16	86.18	57.1
K13	72195710	99.71	95.88	10	95.99	86.44	56.35
K14	69579466	99.74	95.77	10	96.24	86.23	53.42
K15	71564892	99.61	95.69	10	95.86	84.91	53.69
K16	75515194	99.72	95.94	11	96.35	87.69	60.07

K17	70827122	99.59	95.61	10	96.04	86.37	54.98
K18	78732906	99.49	95.5	11	96.48	88.16	62.8
K19	74660960	99.44	95.2	10	96.4	87.42	58.32
K2	72617360	99.7	95.72	10	96.23	86.83	56.9
K20	72402650	99.73	95.61	10	96.61	87	56.26
K3	73614214	99.72	95.41	10	96.55	87.41	57.76
K4	67714240	99.74	95.79	9	96.5	85.64	50.62
K5	75303328	99.74	95.89	11	96.32	87.53	59.62
K6	70654360	99.71	95.86	10	96.37	86.48	54.35
K7	69107872	99.75	94.99	10	96.27	86.05	52.26
K8	68054710	99.74	95.71	9	96.28	85.46	51.04
K9	70545278	99.45	95.57	10	96.3	86.24	54.01

Notes: Sample ID: Unique identifier for each sample, Total_reads: Total number of clean reads used for alignment Mapped (%):Percentage of clean reads successfully mapped to the reference genome , Properly_mapped (%): Percentage of paired-end reads where both ends align to the reference genome with insert sizes consistent with the sequenced fragment library, Ave_depth: Average sequencing depth of the sample, Cov_ratio_X (%): Proportion of bases in the reference genome covered by at least the specified sequencing depth (1×, 5×, and 10×, respectively). For example, Cov_ratio_1X (%) indicates the percentage of bases across the reference genome covered by at least one read.

Supplementary Figure

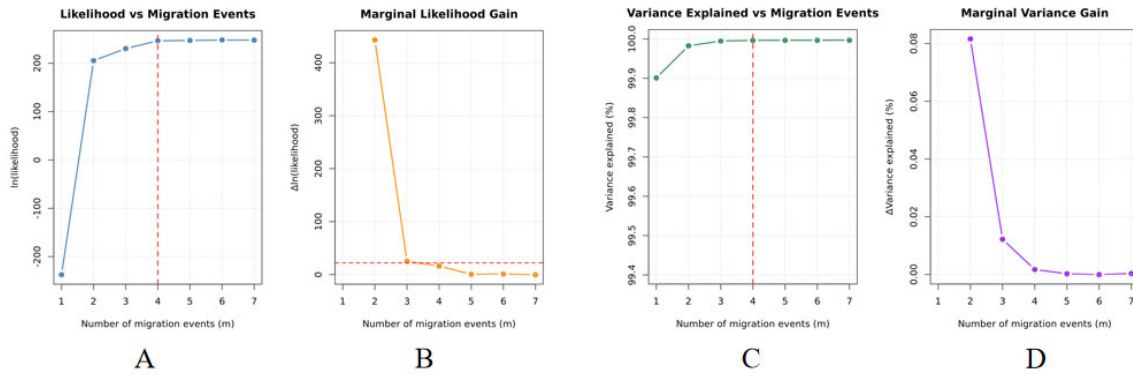


Figure S1. Determination of optimal migration edges (m) for TreeMix. (A) Log-likelihood across different migration event counts; saturation at $m = 4$. (B) Marginal log-likelihood gain for each added migration edge. (C) Percentage of variance explained by TreeMix models with varying m values. (D) Marginal gain in explained variance for each migration edge increment.