Table S5.

Dsuite analyses of excess allele sharing among regional lineages. (A) Dsuite Dtrios results based on ABBA–BABA site-pattern tests. D statistic, *Z*-score, *p*-value, f4-ratio, and ABBA/BABA counts are shown for each regional trio. The *p*-values are nominal and were interpreted cautiously. (B) Fbranch *Z*-score matrix summarizing branch-level signals of excess allele sharing. NA values indicate non-applicable comparisons. No branch-level signal exceeded $Z = 3$. KansaiChugoku corresponds to Kansai–Chugoku.

(A)

P1	P2	P3	D statistic	*Z* -score	*p* -value	f4-ratio	ABBA	BABA	Statistical inference
Hokuriku	Kyushu	KansaiChugoku	0.4134	2.314	0.0207	0.1	36.15	15	Nominal $p < 0.05$; $Z < 3$; not retained in Fbranch at default threshold.
Shiga	KansaiChugoku	Hokuriku	0.05232	0.2813	0.778	0.00464	10.48	9.435	Not significant.
Tokai	KansaiChugoku	Hokuriku	0.09902	0.6496	0.516	0.0119	15.21	12.47	Not significant.
Hokuriku	Kyushu	Shiga	0.4766	2.501	0.0124	0.102	35.2	12.48	Nominal $p < 0.05$; $Z < 3$; not retained in Fbranch at default threshold.
Hokuriku	Kyushu	Tokai	0.3031	1.666	0.0957	0.073	32.45	17.35	$p \geq 0.05$.
Tokai	Shiga	Hokuriku	0.02542	0.1397	0.889	0.00311	14.11	13.41	Not significant.
Shiga	KansaiChugoku	Kyushu	0.01324	0.0685	0.945	0.00147	10.32	10.05	Not significant.
Tokai	KansaiChugoku	Kyushu	0.335	1.84	0.0658	0.0487	18.91	9.422	$p \geq 0.05$.
KansaiChugoku	Shiga	Tokai	0.1669	1.343	0.179	0.182	24.9	17.78	Not significant.
Tokai	Shiga	Kyushu	0.2961	1.756	0.0791	0.0429	17.99	9.771	$p \geq 0.05$.

(B)

branch	branch descendants	Outgroup	Shiga	Hokuriku	Kyushu	Tokai	KansaiChugoku
b2	Shiga, Tokai, KansaiChugoku	NA	NA	NA	NA	NA	NA
b3	Hokuriku, Kyushu	NA	NA	NA	NA	NA	NA
b4	Shiga	NA	NA	0.0698705	0.877915	NA	NA
b5	Tokai, KansaiChugoku	NA	NA	0	0	NA	NA
b6	Hokuriku	NA	0	NA	NA	0	0
b7	Kyushu	NA	2.50141	NA	NA	1.666	2.31376
b8	Tokai	NA	0	0	0	NA	NA
b9	KansaiChugoku	NA	1.75757	0.649585	1.83983	NA	NA