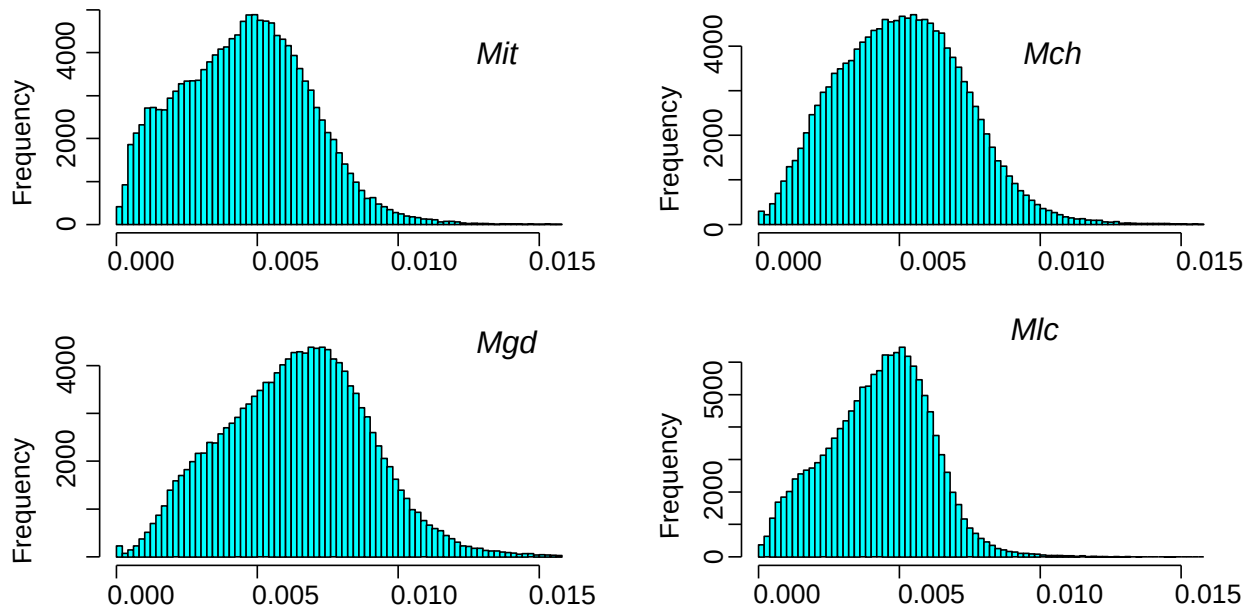


Table S1 The summary of sequencing depth and coverage for each sample accession of *Musa itinerans* used in this study

Varieties	Sample accession	Uniq mapping			Multiple-mapping		
		Depth (X)	Coverage (%)	Reads	Depth (X)	Coverage (%)	Reads
<i>M. itinerans</i> subsp. <i>chinensis</i>	CH1	8.73	85.12	41012748	10.92	90.68	51296411
	CH2	8.95	84.96	42059451	11.22	90.54	52742177
	CH3	8.54	84.97	40133752	10.68	90.5	50195517
	CH4	6.99	84.66	32848354	8.68	90.13	40802440
<i>M. itinerans</i> var. <i>itinerans</i>	HN1	20.34	89.82	95553637	24.96	95.18	117223525
	HN2	11.35	88.76	53313501	14.06	94.1	66053039
	HN3	11.08	88.36	52046835	13.74	93.74	64563856
	HN4	13.17	88.83	61861709	16.23	94.2	76240833
	HN5	10.67	87.44	50147590	13.31	92.89	62546088
	HN6	9.18	88.01	43147176	11.37	93.35	53398835
	HN7	8.39	87.56	39400227	10.38	92.85	48746947
	HN9	61.96	94.5	285824400	75.66	99.12	349013348
<i>M. itinerans</i> var. <i>guangdongensis</i>	LC1	10.39	85.49	48869340	13.23	91.08	62168683
	LC2	9.87	85.84	46423820	12.46	91.4	58564442
	LC3	8.62	84.83	40514166	10.8	90.42	50776531
	LC4	8.24	85.08	38740464	10.43	90.62	49002962
	LC8	7.29	83.74	34293584	9.14	89.28	42970700
	LC9	8.17	84.04	38409259	10.36	89.62	48723583
	YC1	10.78	86.39	50694500	13.49	91.95	63435851
	YC2	8.75	85.24	41144289	11.01	90.85	51766385
	YC3	54.82	89.61	252505816	68.87	94.82	317147704
<i>M. itinerans</i> var. <i>lechangensis</i>	BX1	8.53	86.29	40126714	10.64	91.75	50013421
	BX2	8.72	86.45	40984484	10.93	91.9	51361507
	BX3	48.38	90.35	223335542	59.96	95.48	276712458

(a).



(b)

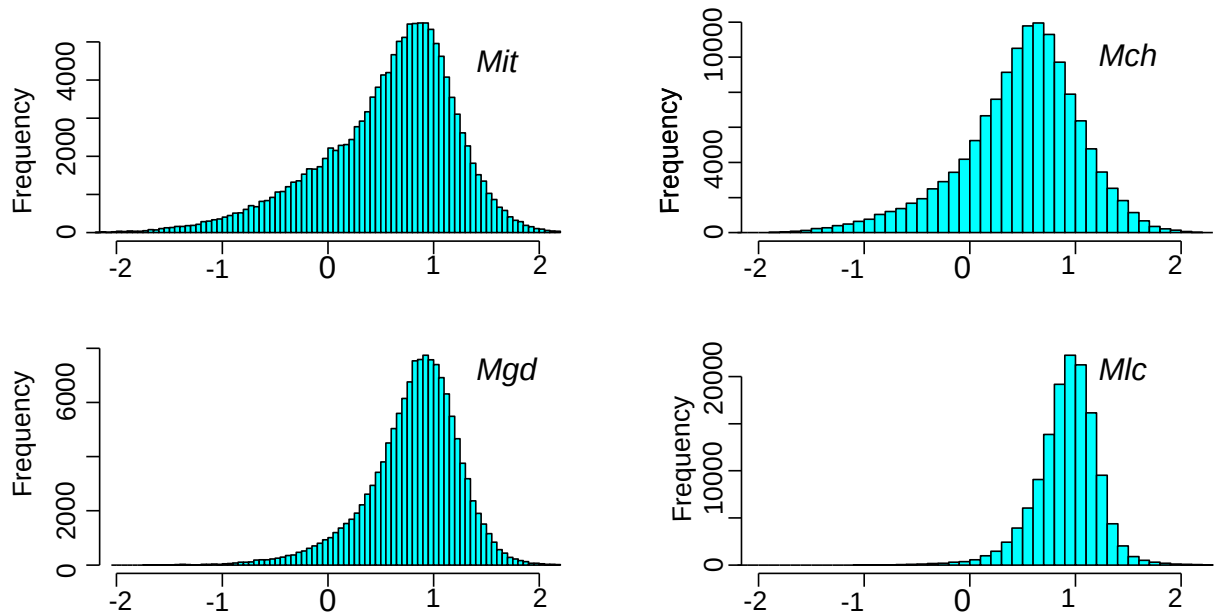
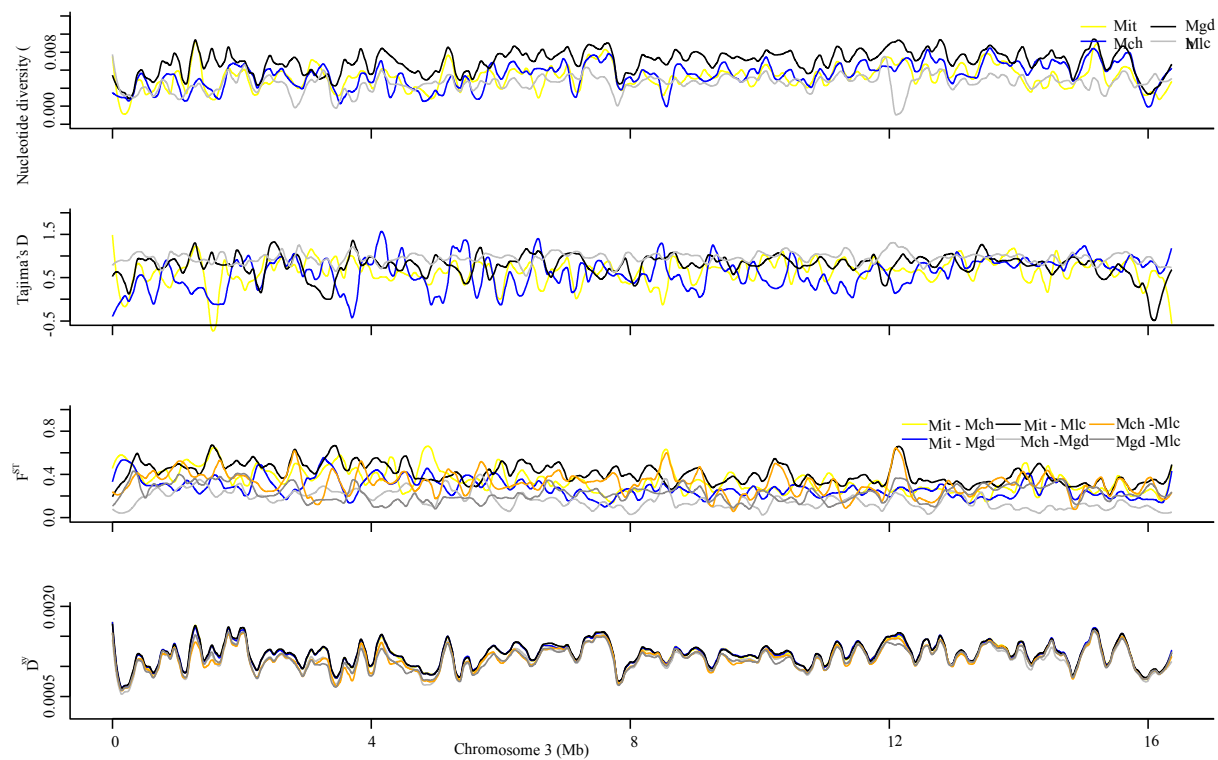
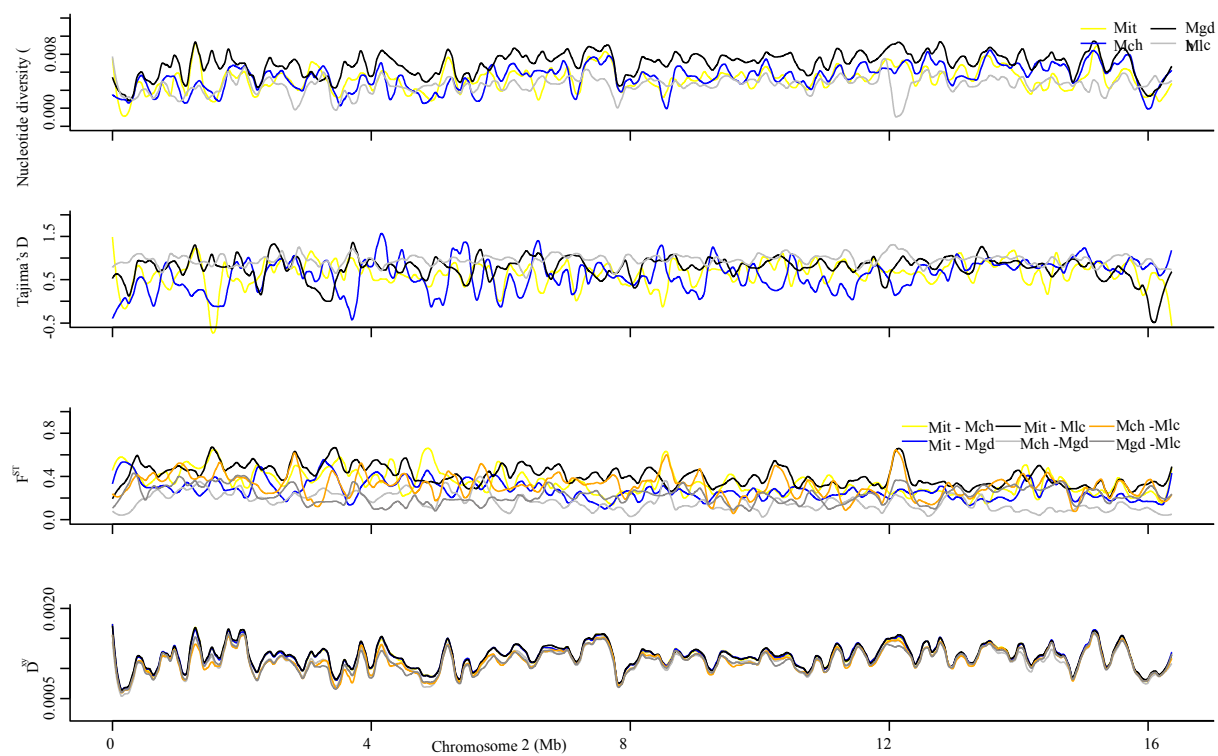
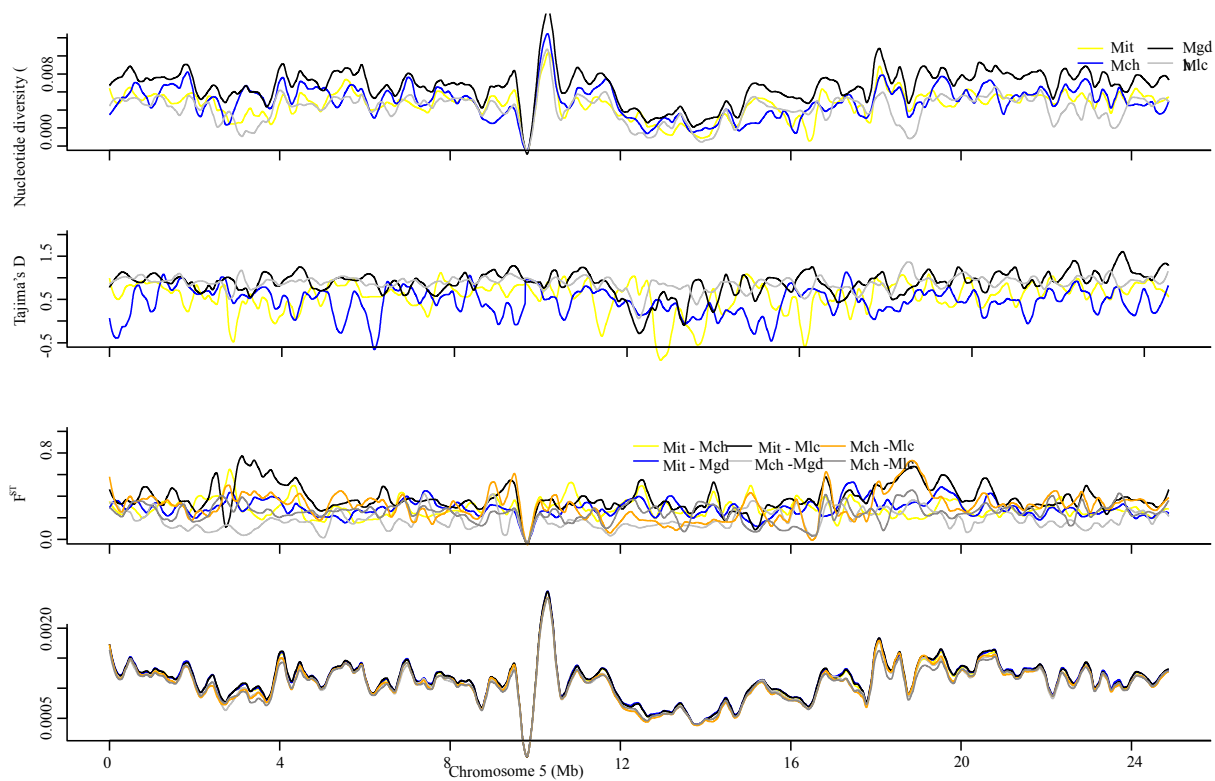
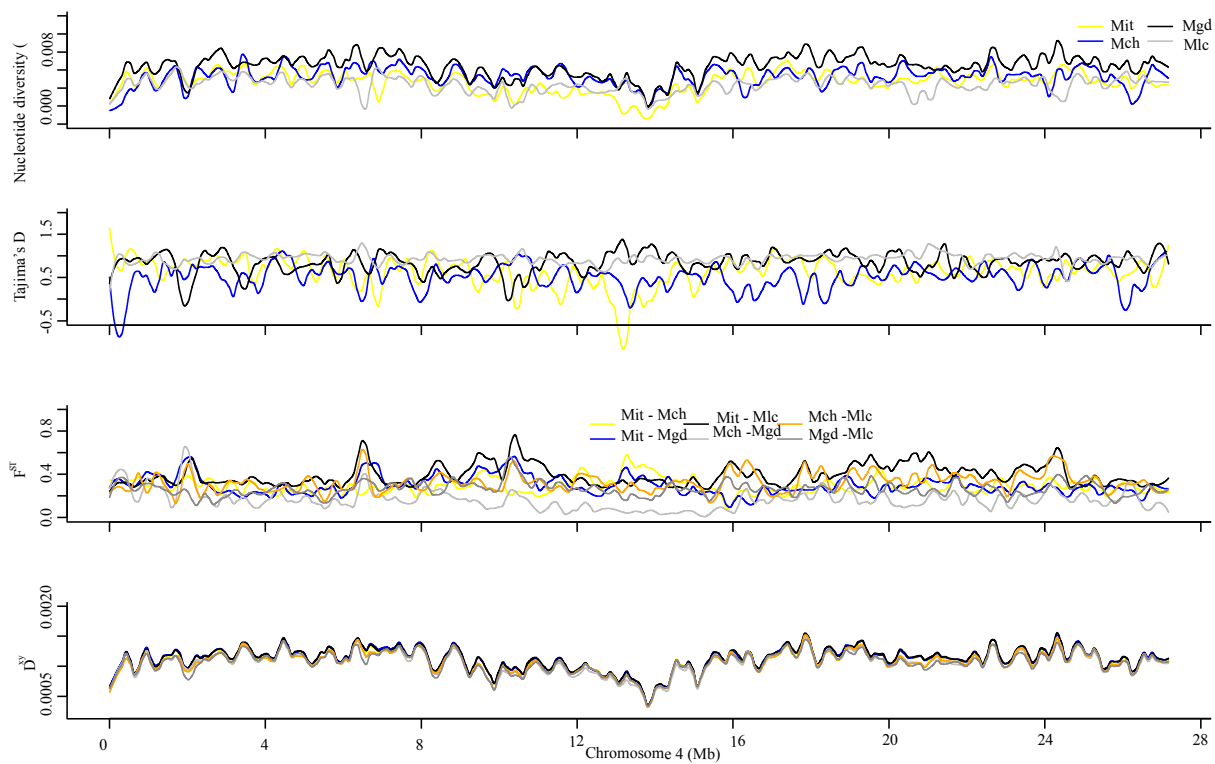
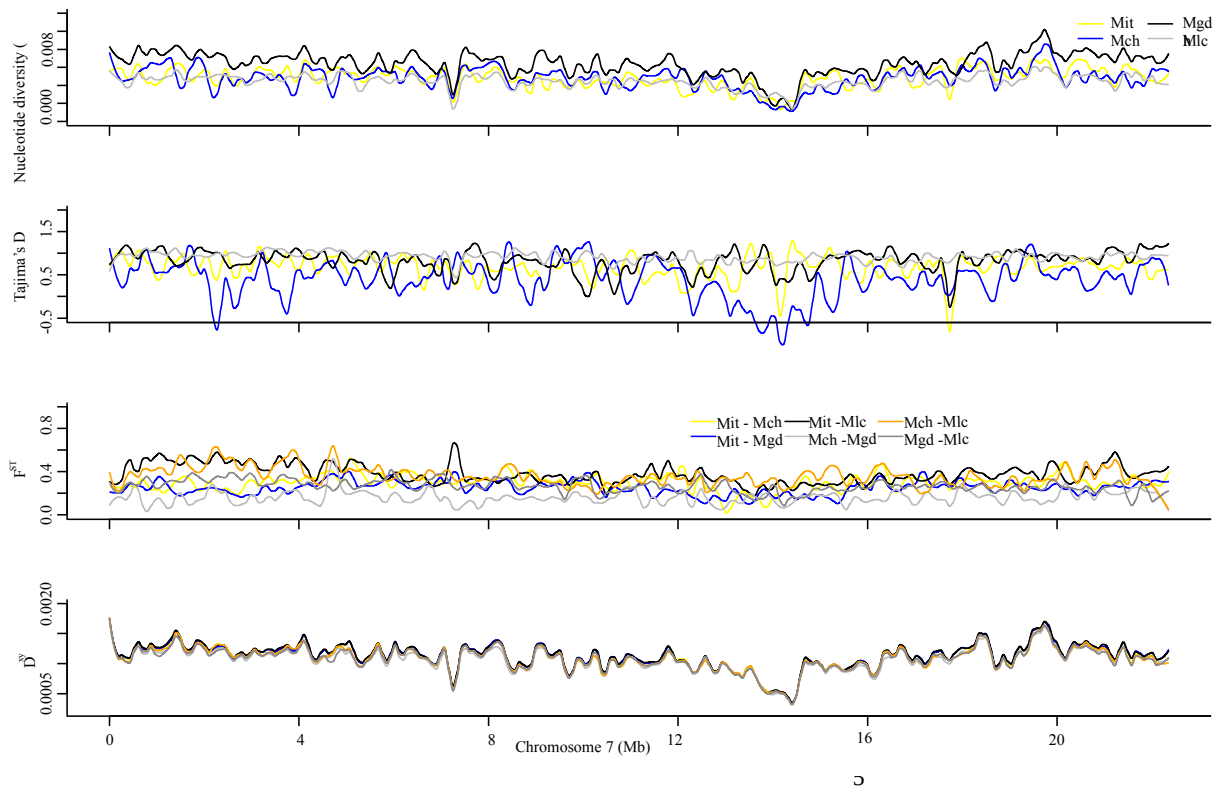
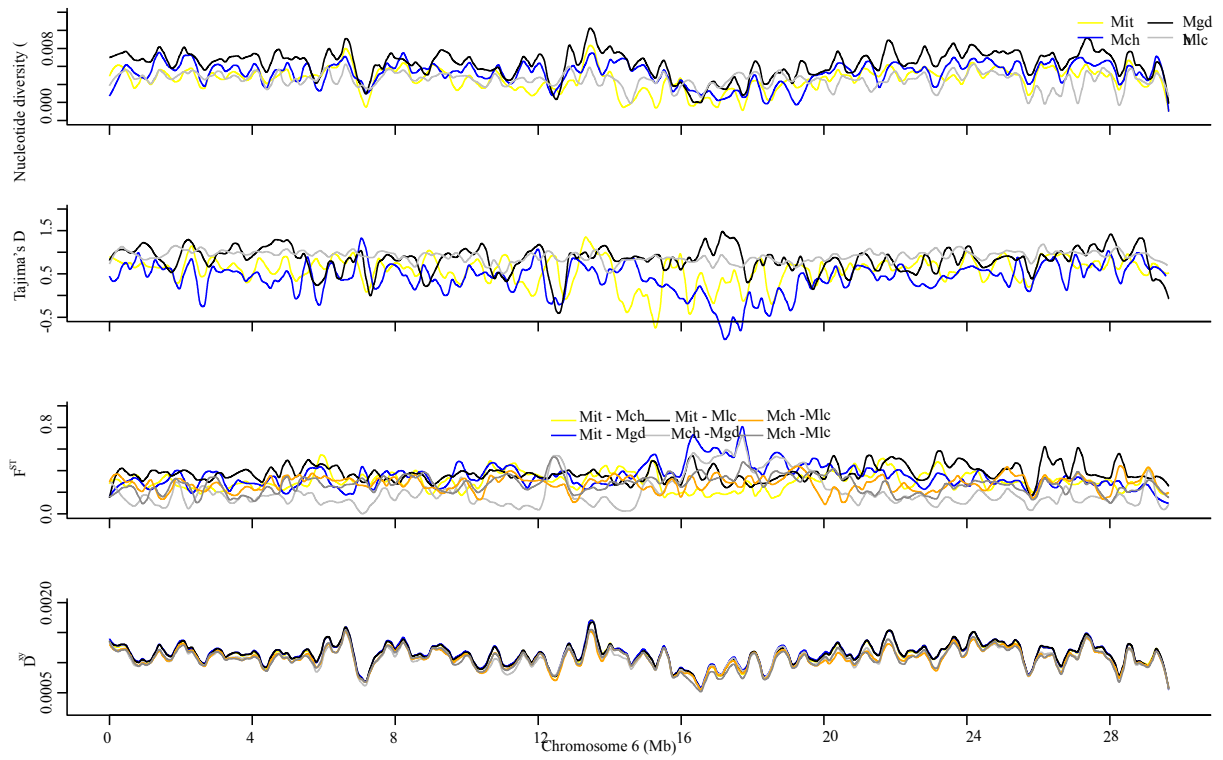
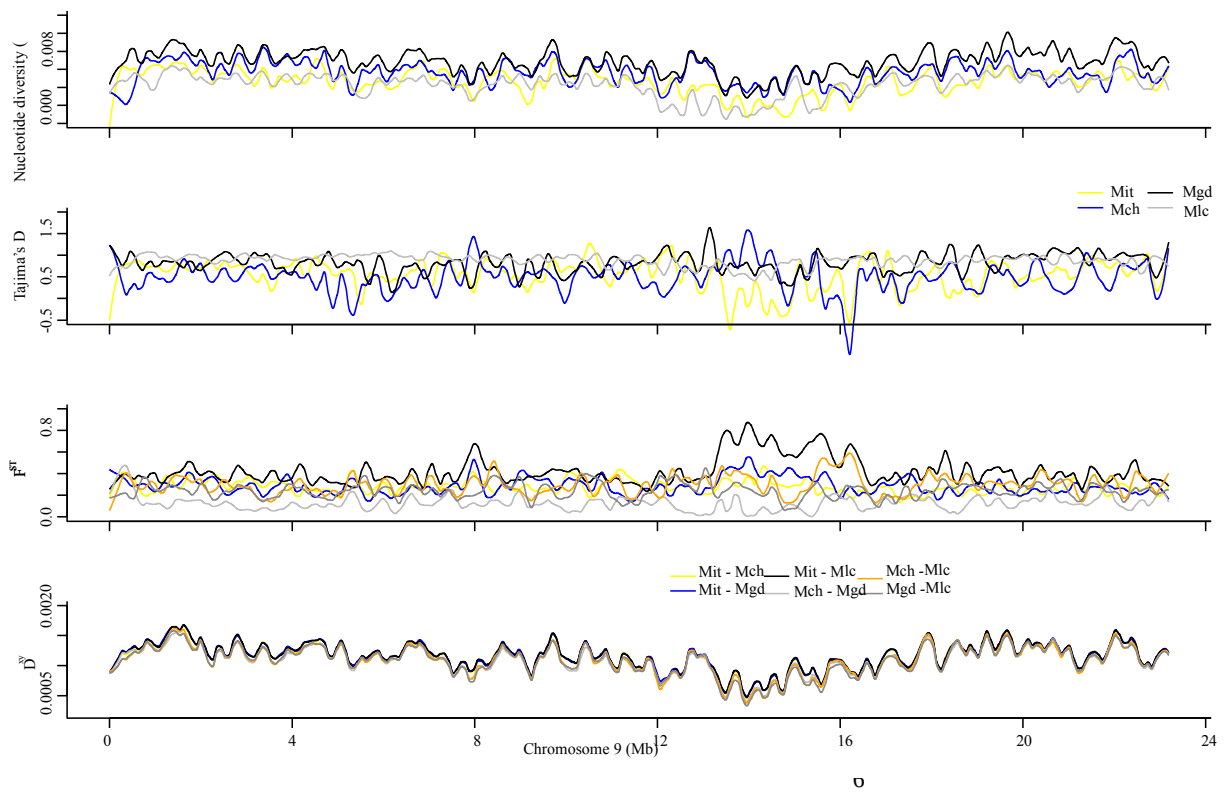
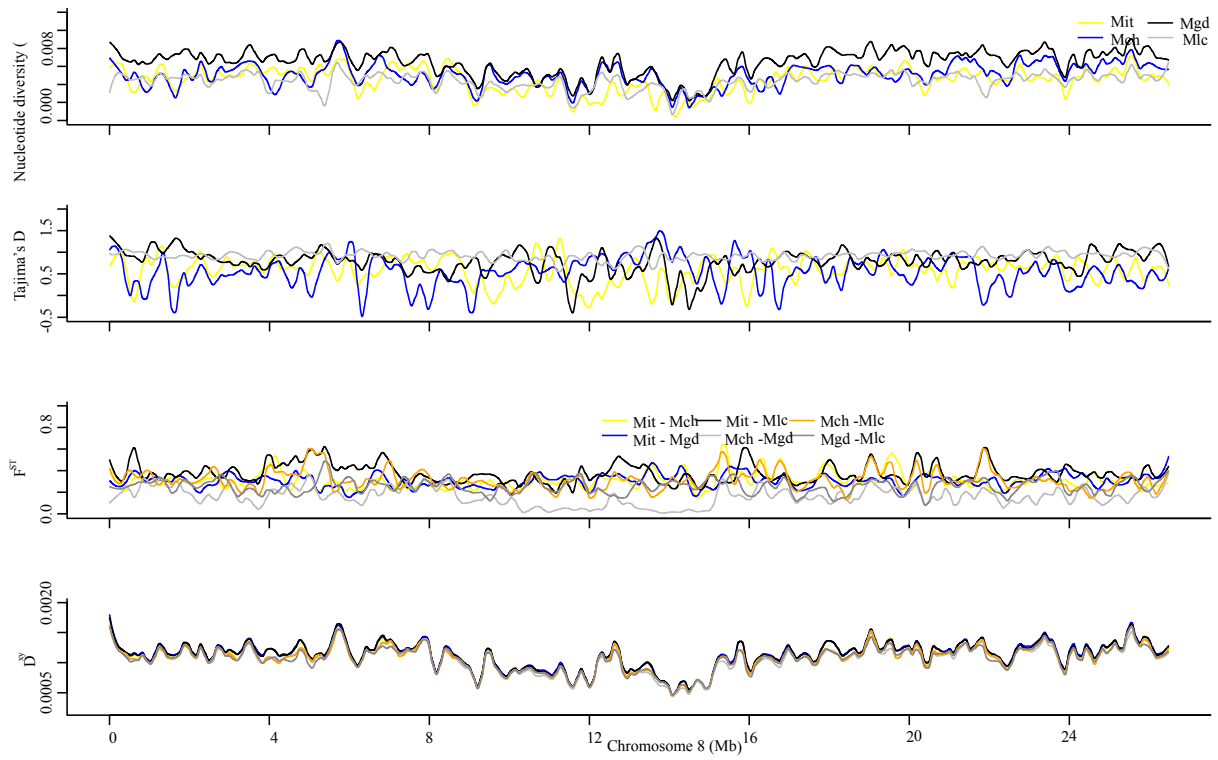


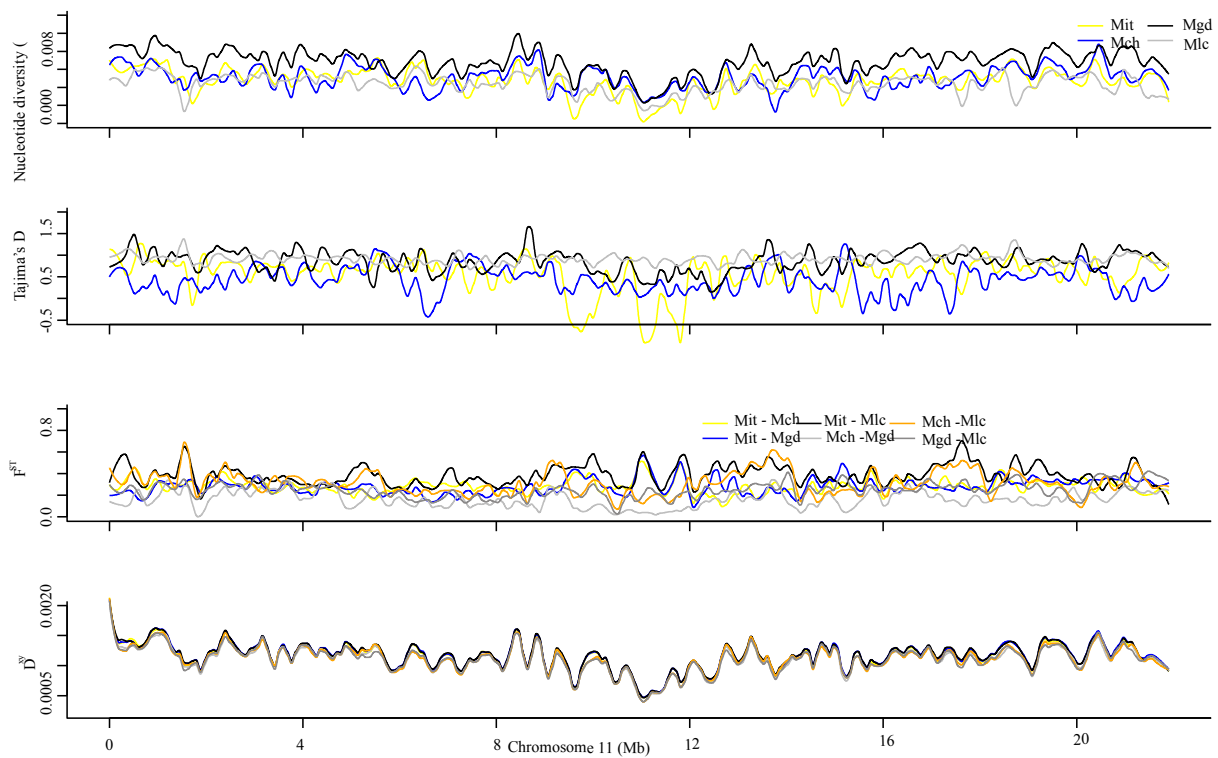
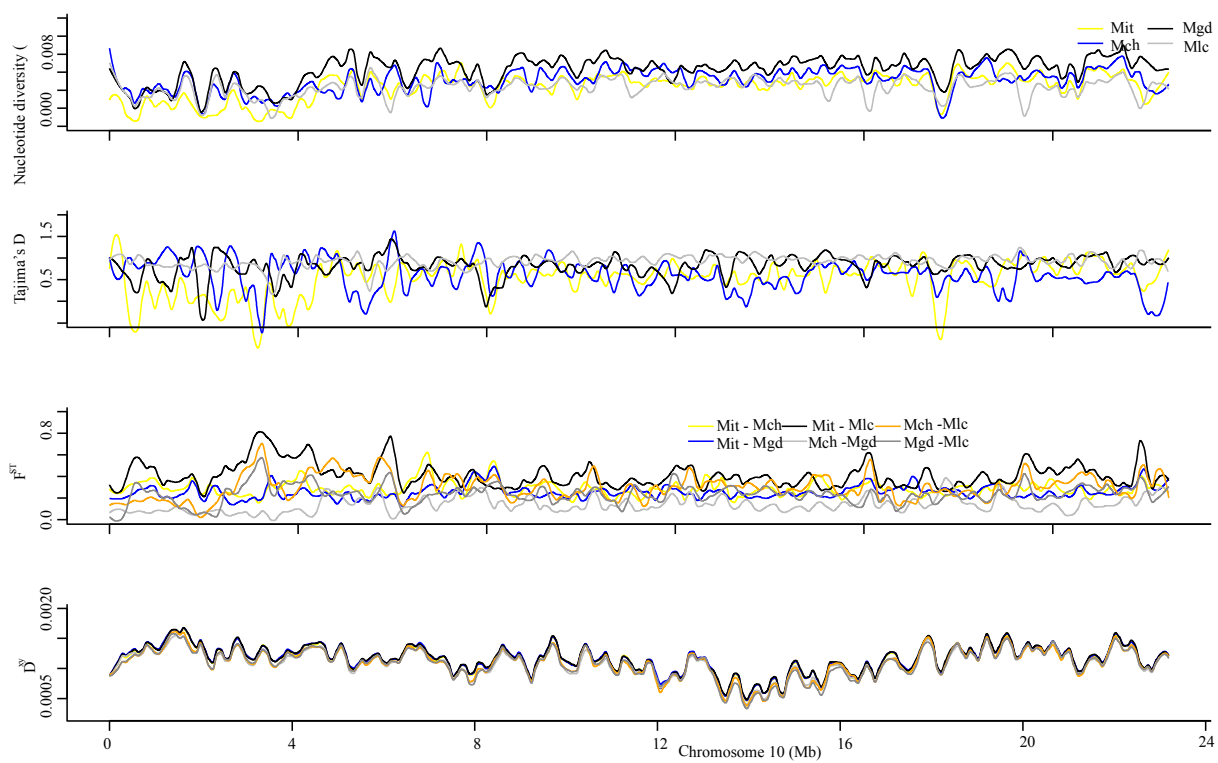
Fig S1. The overall genome-wide polymorphisms distributions with 20kb overlapped window size and 2kb step size among four *Musa itinerans* varieties. (a) pairwise nucleotide diversity θ_{π} , (b) Tajima's D . The varieties were designated as: *Mit*: *Musa itinerans* var *itinerans*; *Mch*: *Musa itinerans* var *guangdongensis*; *Mgd*: *Musa itinerans* var *chinensis*; *Mlc*: *Musa itinerans* var *lechangensis*











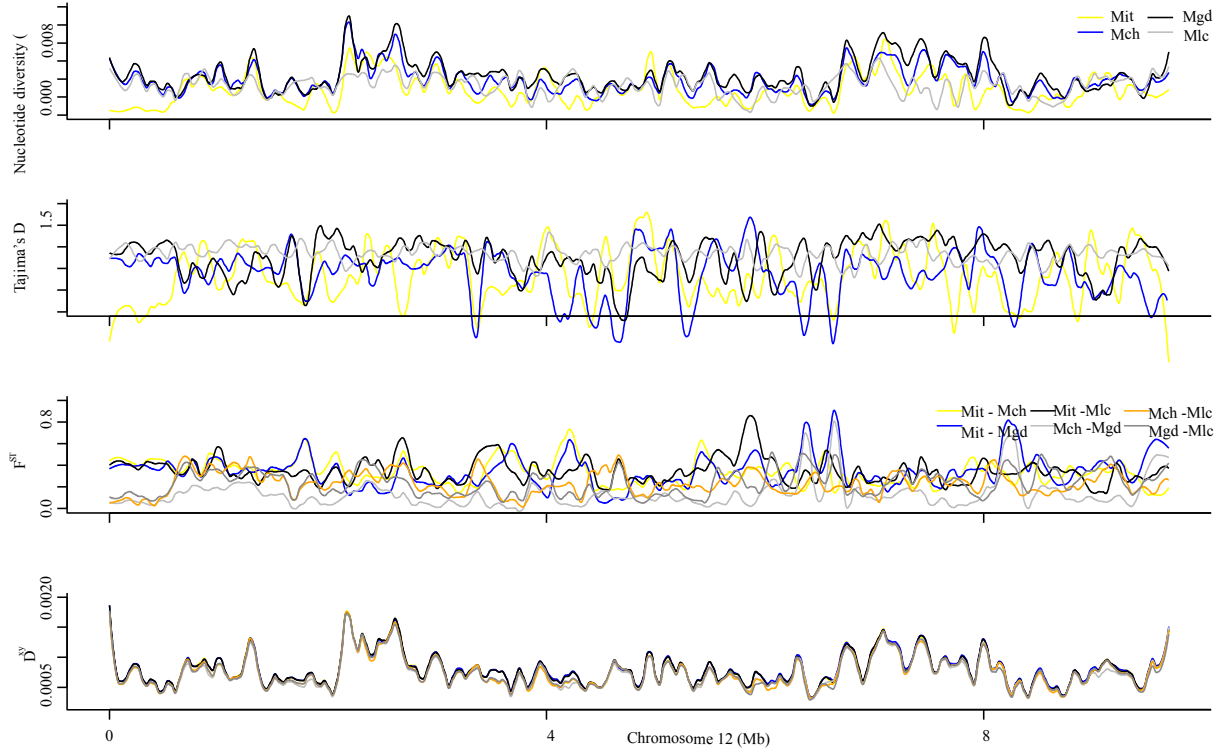


Figure S2 The distribution of average pairwise nucleotide diversity θ_{π} , and Tajima's D, Wright's fixation index F_{ST} and absolute genetic divergence D_{xy} across the chromosome 2 ~12 with 20k b overlapped window size and 2kb step size among four *Musa itinerans* varieties; The the varieties were designated as: *Mit*: *Musa itinerans* var *itinerans*; *Mch*: *Musa itinerans* var *guangdongensis*; *Mgd*: *Musa itinerans* var *chinensis*; *Mlc*: *Musa itinerans* var *lechangensi*.