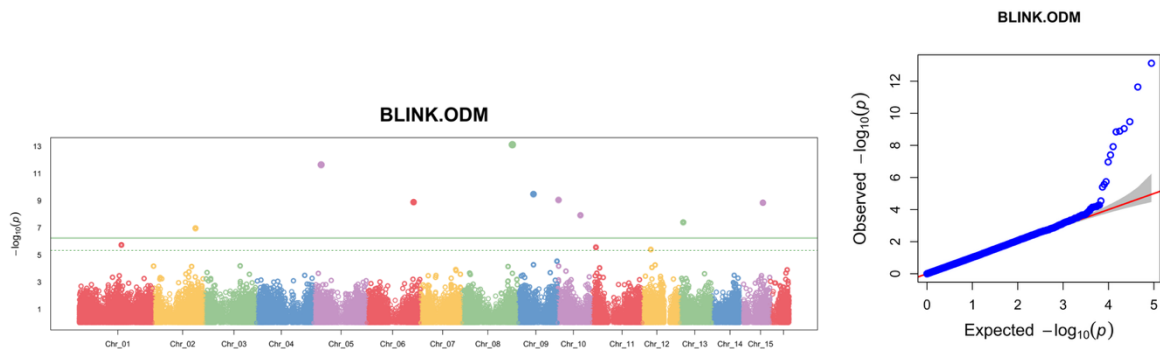
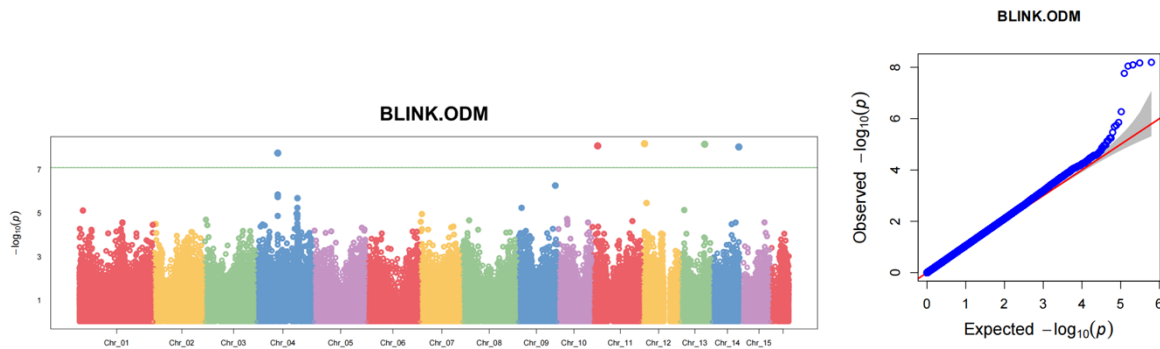


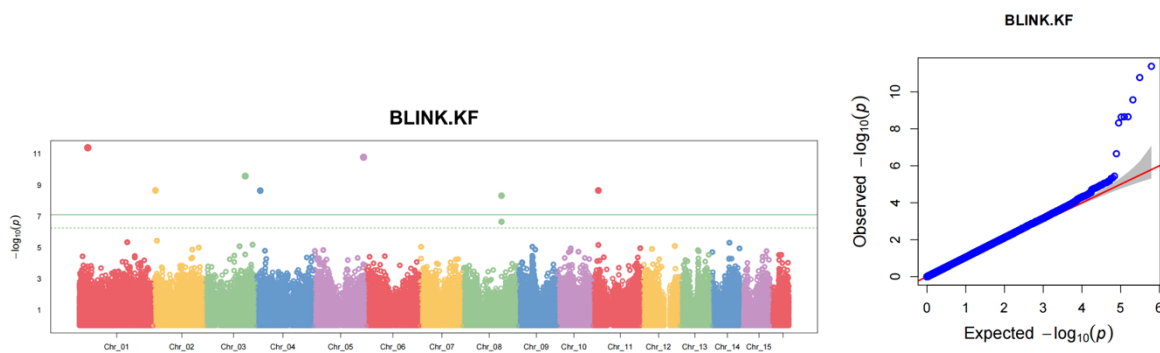
Supplementary data



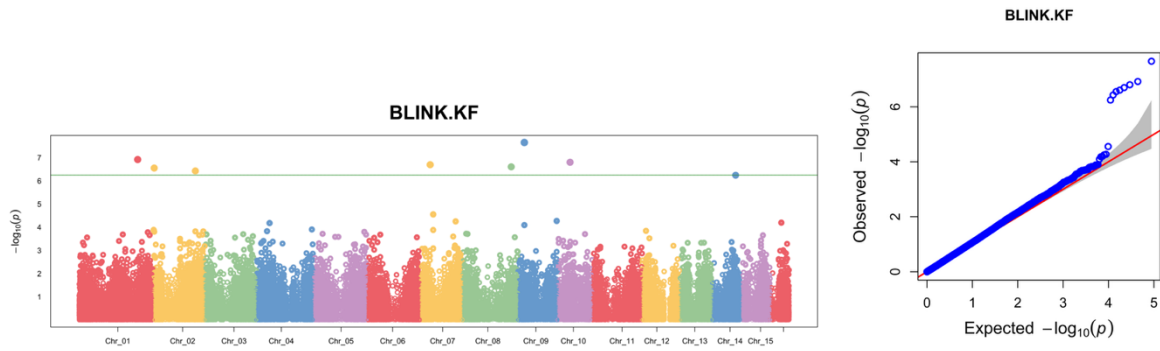
Supplementary Figure S1. Manhattan and quantile–quantile plots for oil-to-dry mesocarp ratio (ODM) using the MNP panel under the BLINK model.



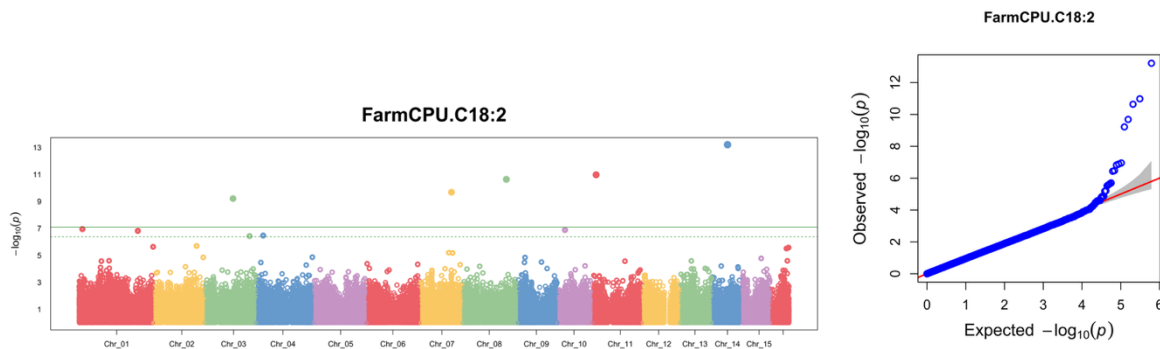
Supplementary Figure S2. Manhattan and quantile–quantile plots for oil-to-dry mesocarp ratio (ODM) using the SNP panel under the BLINK model.



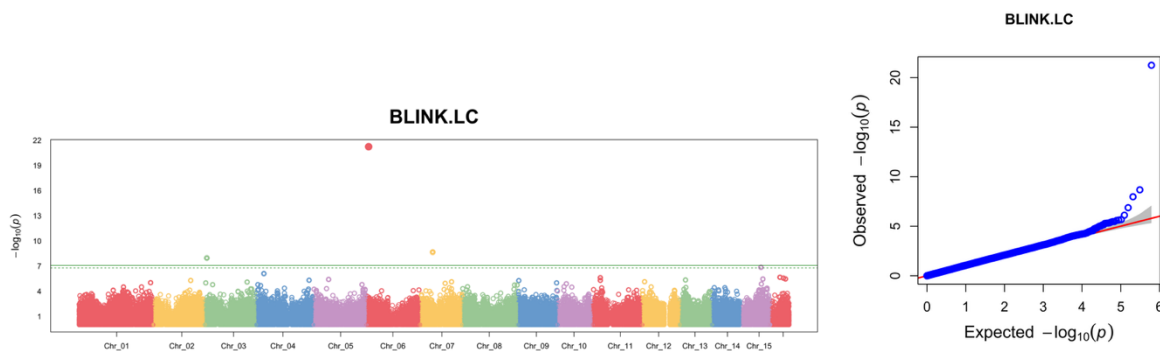
Supplementary Figure S3. Manhattan and quantile–quantile plots for kernel-to-fruit ratio (KF) using the SNP panel under the BLINK model.



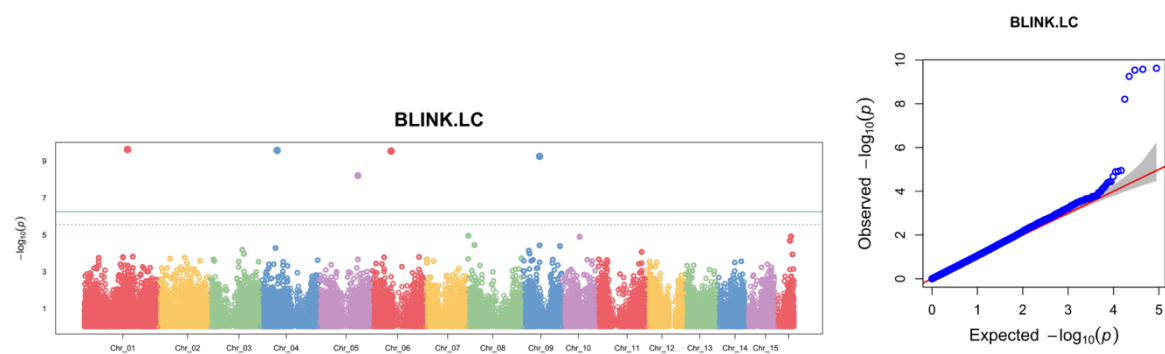
Supplementary Figure S4. Manhattan and quantile–quantile plots for kernel-to-fruit ratio (KF) using the MNP panel under the BLINK model.



Supplementary Figure S5. Manhattan and quantile–quantile plots for linoleic acid (C18:2) using the SNP panel under the FarmCPU model.



Supplementary Figure S6. Manhattan and quantile–quantile plots for leaflet count (LC) using the SNP panel under the BLINK model.



Supplementary Figure S7. Manhattan and quantile–quantile plots for leaflet count (LC) using the MNP panel under the BLINK model.

Supplementary Table S1. Full list of significant loci associated with focal and additional traits in oil palm pan-GWAS.

Trait	Variant ID	Variant panel	Chr	Position (Mb)	P-value	MAF	Effect	Region	Gene ID/ gene name/ Nearest Gene	Nearest Gene distance (bp)	Relative position
SF	MNP1	MNP	1	89.4	2.16E-08	0.41	-1.35	intergenic	LOC105045285	2,933	upstream
SF	MNP2	MNP	1	109.4	2.73E-09	0.24	1.95	intergenic			
SF	MNP3	MNP	2	104.2	6.39E-13	0.26	2.08	intergenic			
SF	MNP4	MNP	7	62.8	1.49E-07	0.49	-9.51	intergenic			
SF	MNP5	MNP	7	75.6	2.89E-07	0.37	-1.74	intergenic			
SF	MNP6	MNP	8	137.1	1.26E-12	0.01	-3.13	mRNA	LOC114914420	0	within
SF	MNP7	MNP	9	22.7	2.32E-07	0.39	2.59	intergenic	LOC105051336	3,974	downstream
SF	MNP8	MNP	9	48.7	6.00E-09	0.38	-1.39	intergenic			
SF	MNP9	MNP	9	72	4.32E-11	0.42	4.11	intergenic			
SF	MNP10	MNP	11	14.7	4.18E-07	0.47	1.25	intergenic	LOC140852689	4,532	upstream
SF	MNP11	MNP	16	37.4	3.25E-10	0.25	2.86	intergenic			
SF	MNP12	MNP	16	43	2.84E-08	0.23	2.13	CDS	LOC105059033	0	within
SF	SNP1*	SNP	1	3.8	1.87E-10	0.06	17.63	CDS	LOC105034563	0	within
SF	SNP2	SNP	9	27	2.27E-08	0.05	2.65	CDS	LOC105033745	0	within
SF	SNP3	SNP	16	1.3	1.76E-13	0.27	-3.59	exon	LOC140854322	0	within
SF	SNP4	SNP	16	46.3	4.34E-10	0.49	7.82	intergenic			
SF	MI1	micro-indel	9	8.5	1.06E-08	0.05	3.96	intergenic	LOC105051902	7,397	upstream
SF	MI2	micro-indel	11	13.4	3.57E-08	0.32	-1.28	intergenic	LOC105032486	2,604	downstream
SF	MI3	micro-indel	11	13.5	6.76E-10	0.31	0.04	intergenic			
SF	MI4	micro-indel	11	90.2	2.02E-08	0.18	1.83	intergenic			
SF	LI1	larger indel	1	25.4	2.00E-07	0.04	-6.97	intergenic			
SF	LI2	larger indel	9	0.8	5.04E-09	0.38	2.9	intergenic	LOC105059160	7,876	upstream
SF	LI3	larger indel	11	14.7	2.07E-09	0.43	1.96	intergenic			
SF	LI4	larger indel	13	21.3	1.09E-08	0.49	-17.77	intergenic	LOC105056267	9,301	downstream
SF	LI5	larger indel	15	61	1.84E-10	0.49	-14.73	intergenic			

RL	MNP1	MNP	1	16.8	1.55E-10	0.41	27.34	intergenic	LOC105037980	5,256	downstream
RL	MNP2	MNP	2	100.7	1.27E-09	0.36	-44.46	exon	LOC105049717	7,518	downstream
RL	MNP3	MNP	7	4.1	1.07E-07	0.41	-20.82	intergenic	LOC105049192	2,293	upstream
RL	MNP4	MNP	9	94.1	8.95E-09	0.28	23.13	intergenic	LOC105051035	1,674	upstream
RL	MNP5	MNP	12	5.6	4.45E-07	0.48	18.77	CDS	LOC105054852	0	within
ODM	ODMMNP1	MNP	6	117.4	1.30E-09	0.5	1.34	intergenic	LOC105046718	7,339	downstream
ODM	ODMMNP2	MNP	9	39	3.34E-10	0.4	1.19	intergenic	-	-	-
ODM	ODMMNP3	MNP	10	57.7	1.20E-08	0.4	-1.02	intergenic	-	-	-
ODM	ODMSNP1	MNP	13	62	6.76E-09	0.48	3.98	intergenic	LOC114913045	8,986	downstream
KF	KFSNP1	SNP	1	21.9	4.14E-12	0.46	3.13	intergenic	LOC105033790	23,862	upstream
KF	KFSNP2	SNP	8	98.6	4.82E-09	0.49	4.75	intergenic	-	-	-
KF	KFSNP3	SNP	11	14.8	2.24E-09	0.4	1.17	intergenic	LOC105061553	25,217	downstream
KF	KFMNP1	SNP	2	1.9	2.80E-07	0.32	-1.16	intergenic	LOC140855532	24,693	upstream
KF	KFMNP2	SNP	2	105	3.73E-07	0.49	1.3	intergenic	LOC105045845	11,547	upstream
C18_2	C18_2SNP1	SNP	3	71	6.10E-10	0.43	-0.87	mRNA	LOC105042227	0	within
LC	LCSNP1	SNP	3	5.4	1.08E-08	0.11	6.27	intergenic	LOC140856037	25,747	downstream
LC	LCSNP2	SNP	7	31.5	2.13E-09	0.34	5.93	mRNA	LOC105061390	0	within
LC	LCMNP1	MNP	4	39.7	2.66E-10	0.19	5.19	intergenic	TRNAV-CAC	5,518	upstream
LC	LCMNP2	MNP	5	99	6.16E-09	0.17	-5.27	intergenic	-	-	-
LC	LCMNP3	MNP	6	48.9	2.90E-10	0.49	5.64	intergenic	-	-	-
LC	LCMNP4	MNP	9	41.7	5.60E-10	0.33	5.04	intergenic	-	-	-

Note: SNP1* corresponds to the known SHELL/AGL11 locus and was used as a positive control. The variant panel indicates the marker class used for association mapping. MI and LI denote micro-indel (1–5 bp) and larger indel (>5 bp), respectively. Positions are shown in megabases (Mb). Distance indicates the distance to the overlapping or nearest annotated gene; distance = 0 indicates that the variant overlaps an annotated gene feature. REF/ALT alleles were omitted for readability because allele representation differs among variant classes; full allele information is available in the variant call files.