

Table S1. Summary statistics and coefficient of variation for fat content and fatty acids in superior shea trees.

	Minimum	Maximum	Mean $\pm$ sd	Coefficient of variation(%)
Fat content	36.24	58.09	49.73 $\pm$ 3.7	7.44
Palmitic acid	2.01	6.12	3.53 $\pm$ 0.52	14.73
Stearic acid	22.33	50.54	38.76 $\pm$ 4.67	12.05
Oleic acid	40.27	65.66	51.26 $\pm$ 4.21	8.21
Linoleic acid	4.78	9.03	6.45 $\pm$ 0.76	11.78

Table S2. Statistical summary of fat content and fatty acid composition of superior shea trees across different districts.

	District	Min.	Max.	Mean $\pm$ sd	CV(%)	Skewness	Kurtosis	F-value	p-value
Fat c.	Hamb.	41.28	54.49	49.02 $\pm$ 3.22	6.57	-0.5	-0.56	0.57	0.57
	Poro	36.24	55.86	49.9 $\pm$ 3.9	7.82	-0.95	1.33		
	Tchol.	41.01	58.09	49.91 $\pm$ 3.77	7.55	-0.49	-0.28		
C16:0	Hamb.	2.91	4.69	3.65 $\pm$ 0.43	11.78	0.66	-0.27	1.06	0.35
	Poro	2.01	4.11	3.47 $\pm$ 0.6	17.29	1.35	6.39		
	Tchol.	2.43	4.86	3.55 $\pm$ 0.48	13.52	0.49	0.31		
C18:0	Hamb.	22.33	43.24	36.87a $\pm$ 5.77	15.65	-0.99	-0.02	3.51	0.03*
	Poro	32.25	48.16	39.84b $\pm$ 3.8	9.54	-0.18	-0.4		
	Tchol.	26.59	50.54	38.64ab $\pm$ 4.88	12.63	-0.09	-0.16		
C18:1	Hamb.	46.4	65.66	52.91a $\pm$ 5.31	10.04	0.93	-0.11	3.04	0.05
	Poro	42.13	57.51	50.4b $\pm$ 3.04	6.03	0.08	0.09		
	Tchol.	40.27	63.51	51.28ab $\pm$ 4.41	8.6	0.15	0.17		
C18:2	Hamb.	4.93	8.59	6.57 $\pm$ 0.79	12.02	0.48	0.2	1.77	0.18
	Poro	4.78	7.64	6.29 $\pm$ 0.69	10.97	0.19	-0.72		
	Tchol.	5.12	9.03	6.55 $\pm$ 0.81	12.37	0.95	1.16		

Min: minimum, Max: maximum, CV: coefficient of variation, Fat c: Fat content, Hamb.: Hambol, Tchol.: Tchologo

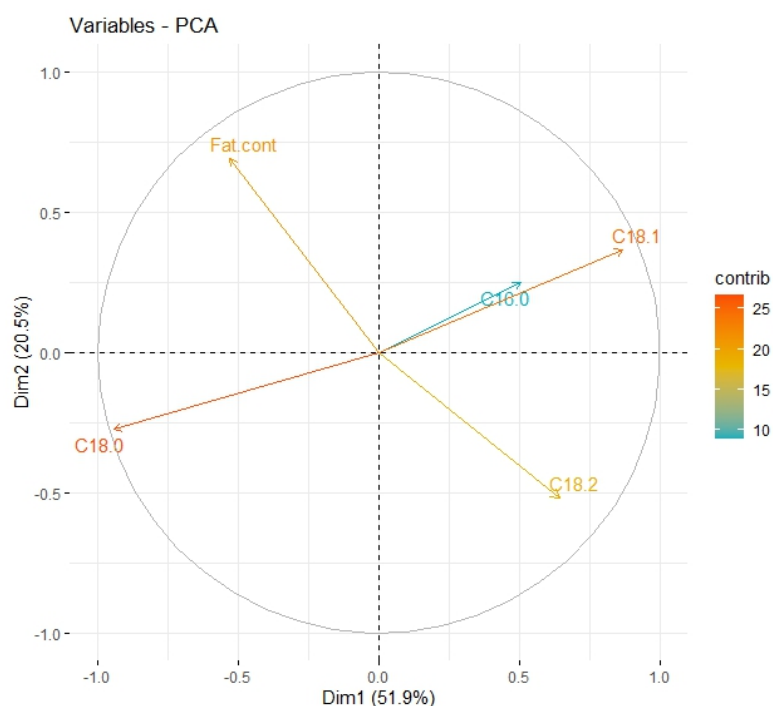


Figure S1. Loading and score plots of PC1-PC2, "Variables-PCA".

Table S3. Results of bayesian model-based clustering implemented in structure of 122 SSTs

Cluster No	GG1	GG2	GG3	HE	F _{ST}	Number of genotypes	Admixed genotypes
GG1	0			0.2599	0.012	52	19
GG2	0.0016	0		0.2604	0.018	30	10
GG3	0.0018	0.0022	0	0.2597	0.021	40	19
Total	-	-	-	0.26	-	122	48

HE: Expected heterozygosity; F_{ST}: Fixation index; GG1, GG2, GG3: genetic groups 1, 2 and 3 respectively.

Table S4. Quantitative trait nucleotides (QTNs) associated with fat content and fatty acid content in *V. paradoxa* accessions.

Traits	Marker	Gwas Method	Chr	Pos	QTN effect	LOD Score	-log10	r ²	MAF
C16:0	q3_57006090 ^b	1, 5	3	57006090	0.2264, 0.1699	36.933, 36.351	44.291, 43.678	97.826, 66.324	0.238
	q7_45956782	1, 2, 4, 5	7	45956782	-0.537, -0.397, -0.376, -0.454	62.718, 42.023, 69.118, 76.237	71.139, 49.637, 77.737, 85.058	336.766, 24.47, 197.545, 289.897	0.092
	q9_42857113 ^b	1, 2	9	42857113	-0.193, -0.135	30.231, 34.732	37.198, 41.969	73.341, 47.868	0.27
	q12_1933151 ^b	1, 2, 4, 5	12	1933151	0.3395, 0.2786, 0.2322, 0.2222	41.414, 46.872, 42.555, 31.404	48.999, 54.704, 50.194, 38.445	162.921, 14.562, 91.167, 83.967	0.12
	q2_4344942	4	2	4344942	0.1786	34.622	41.853	68.075	0.17
	q2_14738783	4	2	14738783	-0.1623	37.044	44.408	57.715	0.2
	q5_55626422	4	5	55626422	-0.1625	52.575	60.638	56.337	0.2
	q10_35612747	4	10	35612747	0.1377	39.578	47.073	44.096	0.23
	q10_8515795	5	10	8515795	-0.2066	45.518	53.291	86.167	0.17
C18:0	q2_70518009 ^{a, b}	1, 2, 4	2	70518009	25.630, 2.206, 19.779	41.425, 41.509, 42.318	49.01, 49.098, 49.945	88.886, 112.583, 86.867	0.11
	q2_5991246 ^{a, b}	1, 2, 4	2	5991246	-27.37, -17.753, -17.607	59.194, 36.946, 41.381	67.497, 44.305, 48.964	145.993, 10.503, 99.159	0.19
	q2_19257675	1	2	19257675	-21.959	33.436	40.599	82.528	0.15
	q3_43202766 ^a	1	3	43202766	-27.761	62.683	71.102	163.817	0.21
	q6_3096993 ^a	1, 2, 4	6	3096993	25.763, 17.085, 19.205	73.867, 37.316, 51.863	82.623, 44.694, 59.898	130.982, 98.484, 119.445	0.2
	q8_9172814	1	8	9172814	-22.456	37.054	44.419	84.533	0.15
	q9_1135448 ^b	1	9	1135448	25.697	38.323	45.754	97.945	0.12
	q3_45009201 ^a	2, 4	3	45009201	14.201, 14.498	37.756, 49.525	45.158, 57.467	71.634, 71.662	0.43
	q6_48934498 ^a	2, 5	6	48934498	-11.776, -17.598	30.555, 52.002	37.543, 60.042	51.283, 116.913	0.28
	q1_78304163 ^a	4	1	78304163	11.464	36.487	43.821	46.408	0.39
	q2_15731361 ^a	4, 5	2	15731361	-0.739, -11.788	34.676, 38.989	4.191, 46.454	17.213, 46.655	0.5

	<i>q5_36247653</i>	4	5	36247653	15.118	30.657	37.651	58.664	0.14
	<i>q7_34884350</i>	4	7	34884350	10.663	35.243	42.509	39.662	0.39
	q9_1241251^{a, b}	4	9	1241251	-24.055	56.843	65.063	11.968	0.1
	<i>q2_51742656</i>	5	2	51742656	15.183	45.893	53.682	88.938	0.33
	<i>q5_19261711</i>	5	5	19261711	14.429	43.614	51.302	79.295	0.38
	<i>q5_55907613</i>	5	5	55907613	14.107	35.712	43.004	75.486	0.25
	<i>q6_28898438^b</i>	5	6	28898438	-12.941	39.253	46.731	64.615	0.33
C18:1	<i>q1_78304163^a</i>	1	1	78304163	-15.724	40.431	47.968	76.142	0.39
	q2_5991246^{a, b}	1, 2, 4, 5	2	5991246	20.125, 17.516, 16.691, 2.054	38.52, 40.963, 42.476, 66.346	45.961, 48.526, 50.111, 74.881	112.983, 11.87, 105.835, 15.845	0.19
	<i>q3_43202766^a</i>	1	3	43202766	19.558	36.107	43.421	116.374	0.21
	q6_3096993^a	1, 2, 3, 4, 5	6	3096993	-31.50, - 2.172, - 36.43, - 19.473, -19.201	95.051, 57.854, 34.979, 49.996, 45.514	104.33, 6.611, 4.223, 57.957, 53.287	280.241, 184.793, 66.249, 145.848, 140.201	0.2
	q9_1241251^{a, b}	1	9	1241251	26.178	40.873	48.431	123.613	0.1
	q2_70518009^{a, b}	2, 4, 5	2	70518009	-20.44, - 20.77, - 16.874	43.335, 48.946, 36.178	5.101, 56.864, 43.495	112.221, 113.747, 74.243	0.11
	q3_45009201^a	2, 4, 5	3	45009201	-12.423, -14.148, -13.787	35.626, 50.611, 56.447	42.913, 58.597, 64.653	63.643, 84.045, 76.098	0.43
	<i>q4_49530029</i>	4	4	49530029	-0.9213	36.584	43.923	36.494	0.32
	q6_48934498^a	4, 5	6	48934498	10.153, 10.259	31.444, 36.152	38.488, 43.468	43.455, 43.871	0.28
	<i>q2_15731361^a</i>	5	2	15731361	0.6843	34.004	4.12	17.355	0.5
	<i>q4_7790254</i>	5	4	7790254	-12.237	5.027	58.242	62.963	0.27
	<i>q8_41435892</i>	5	8	41435892	-0.9015	32.746	39.868	25.686	0.14
C18:2	<i>q1_20786407</i>	1, 2, 4, 5	1	20786407	0.3172, 0.2385, 0.275, 0.2518	42.493, 35.764, 53.124, 53.254	50.129, 43.059, 61.207, 61.342	98.526, 67.616, 96.032, 72.536	0.47
	<i>q2_51742656</i>	1, 2, 3, 5	2	51742656	-0.354, - 0.307, - 0.457, - 0.337	53.915, 58.718, 31.075, 88.003	62.028, 67.004, 38.095, 9.712	142.896, 130.252, 48.076, 151.484	0.33
	<i>q5_9317929</i>	1, 2, 5	5	9317929	0.2994, 0.2262, 0.246	39.459, 34.047, 45.983	46.948, 41.246, 53.776	102.34, 70.849, 80.684	0.33
	<i>q6_43871960</i>	1, 2, 5	6	43871960	-0.316, - 0.255, - 0.218	37.103, 42.238, 31.335	44.47, 49.862, 38.372	109.756, 86.752, 60.655	0.36
	<i>q6_10189604</i>	1, 2, 4, 5	6	10189604	0.429, 0.3224, 0.4396, 0.3415	51.462, 47.971, 85.302, 66.999	59.481, 55.849, 94.355, 75.554	45.464, 31.151, 61.879, 33.654	0.22
	<i>q7_48678186</i>	1, 2, 4, 5	7	48678186	0.4206, 0.3462, 0.3936, 0.3498	40.838, 41.728, 59.801, 45.359	48.395, 49.328, 68.125, 53.125	175.724, 144.471, 199.426, 142.037	0.18
	<i>q7_5074043</i>	4	7	5074043	0.2227	44.244	5.196	72.687	0.31
	<i>q8_2105500</i>	4	8	2105500	-0.2147	37.457	44.843	58.519	0.19

	<i>q10_3420702^b</i>	5	10	3420702	0.1426	38.003	45.417	25.685	0.42
FC	<i>q4_46157457</i>	1, 2, 3, 4, 5	4	46157457	26.41, 22.561, 42.502, 19.889, 21.292	47.868, 52.273, 49.296, 48.381, 47.381	55.742, 60.324, 57.229, 56.276, 55.234	289.169, 239.309, 93.099, 174.944, 215.294	0.16
	<i>q11_13733557</i>	1, 2, 3, 4	11	13733557	-20.44, - 16.825, -34.31, - 14.766	40.872, 36.559, 38.836, 46.511	48.43, 43.897, 46.293, 54.327	204.689, 15.735, 85.125, 114.002	0.24
	<i>q8_11065258</i>	3	8	11065258	-20.333	31.227	38.257	41.936	0.49
	<i>q2_13023583</i>	4, 5	2	13023583	-1.22, -0.9671	42.896, 35.059	5.055, 42.315	34.697, 23.412	0.29
	<i>q2_49928619</i>	4, 5	2	49928619	-18.571, -15.523	45.411, 34.502	53.179, 41.726	135.098, 101.353	0.13
	<i>q4_56145911</i>	4	4	56145911	-0.879	36.305	43.629	41.206	0.36
	<i>q9_23061170</i>	4	9	23061170	-12.269	38.858	46.316	58.967	0.14
	<i>q11_14542132</i>	4	11	14542132	10.248	52.239	60.289	56.696	0.32

GWAS method: (1) mrMLM, (2) FASTmrMLM, (3) FASTmrEMMA, (4) pLARM and (5) ISIS EM-BLASSO; Chr: chromosome; Pos: QTN position; MAF: Minor allele frequency; Markers with letter **a** were associated with both stearic acid (C18:0) and oleic acid (C18:1); Markers with letter **b** were detected near a putative coding region that are involved in shea tree lipid biosynthesis; markers in **bold** were tightly associated with both C18:0 and C18:1.