

Supplementary Table S1:

SHEATP42	SHEAOV38	SHEARO210	SHEATS34	SHEASW27	SHEAST37	SHEAS17	SHEABS23	SHEATS110	SHEATP110	SHEATA28
SHEATP44	SHEAHP37	SHEABS27	SHEATS310	SHEAHP29	SHEARO35	SHEAEP210	SHEATP49	SHEASM14	SHEASP56	SHEARS24
SHEATP39	SHEAHA29	SHEABS17	SHEAHP39	SHEARO36	SHEAST36	SHEASP29	SHEATS51	SHEATS15	SHEAEL34	SHEARS15
SHEARO16	SHEAST34	SHEARO17	SHEADT27	SHEAHP22	SHEASW32	SHEAHP24	SHEAEL19	SHEARO34	SHEABO36	SHEARS28
SHEATP12	SHEAST110	SHEATA11	SHEAHP16	SHEABO18	SHEASM26	SHEAHP12	SHEASW39	SHEASM11	SHEAST39	SHEABS42
SHEABO14	SHEAST17	SHEASM39	SHEAOV18	SHEAEL55	SHEARS210	SHEASP21	SHEAOV21	SHEARO310	SHEARS29	SHEATP24
SHEASP11	SHEATS43	SHEAHA13	SHEASP18	SHEASW38	SHEAEL28	SHEARS16	SHEAHA18	SHEASP31	SHEATP210	SHEATP28
SHEASM17	SHEASW14	SHEASW33	SHEAEL24	SHEASM22	SHEATA13	SHEASP23	SHEASW19	SHEAHA11	SHEATP11	SHEARS17
SHEABO17	SHEAEL13	SHEAHP35	SHEAHA26	SHEABS38	SHEABO39	SHEASW310	SHEAHA310	SHEASP36	SHEATS510	SHEAOV11
SHEAOV24	SHEATS410	SHEARE35	SHEAPH210	SHEADT22	SHEAHA39	SHEARO27	SHEASP41	SHEASW28	SHEAEL18	SHEASM15
SHEASW11	SHEAOV210	SHEASP34	SHEAEL37	SHEARO18	SHEASW311	SHEAEL33	SHEABO23	SHEARS23	SHEAOV16	SHEATP21
SHEAHA32	SHEATS11	SHEAEL36	SHEAHP15	SHEATS12	SHEASW13	SHEAHA110	SHEASP25	SHEARS27	SHEABO11	SHEARS13
SHEAEP11	SHEATS21	SHEAOV26	SHEASM18	SHEARO13	SHEASW17	SHEAHP210	SHEATP18	SHEASM32	SHEAST28	SHEATS52
SHEARE23	SHEATS24	SHEASM33	SHEABO15	SHEABO16	SHEARO47	SHEAHP34	SHEASM21	SHEAHP27	SHEASP37	SHEASW35
SHEASW22	SHEATS27	SHEADT29	SHEAHP25	SHEARO42	SHEABO13	SHEAST22	SHEABO29	SHEAEL410	SHEAHP11	SHEATP32
SHEABS18	SHEATS29	SHEASW16	SHEAOV13	SHEAEL21	SHEAHA19	SHEASW110	SHEARS12	SHEAHP33	SHEATP36	SHEAHA15
SHEAST210	SHEASP17	SHEADT24	SHEABS39	SHEAEP12	SHEAHP36	SHEABS11	SHEAEL53	SHEATP15	SHEASM27	SHEAHP38
SHEASW24	SHEAEL38	SHEABO35	SHEAST31	SHEAHP23	SHEAST12	SHEABO21	SHEAST13	SHEATP27	SHEAHP19	SHEASP14
SHEAEL22	SHEARE21	SHEAEL46	SHEAST32	SHEAHA16	SHEARO28	SHEASP26	SHEATS58	SHEASP35	SHEASM24	SHEABO32
SHEAHP26	SHEATA18	SHEAEL17	SHEARO15	SHEABO28	SHEAST16	SHEASM25	SHEATS16	SHEASM19	SHEATP16	SHEATS210
SHEAST23	SHEASP39	SHEASP410	SHEAPH25	SHEABS12	SHEASM310	SHEAEL12	SHEAOV31	SHEAEL26	SHEAOV35	SHEAOV22
SHEAOV37	SHEARO11	SHEASP12	SHEASW44	SHEAOV32	SHEABO27	SHEASP22	SHEARO38	SHEASP510	SHEASP110	SHEABS14
SHEARO24	SHEABS13	SHEAEL210	SHEATS41	SHEABS15	SHEABO37	SHEARO32	SHEATP43	SHEABO25	SHEABO38	SHEARO29
SHEASP19	SHEASP27	SHEAHA21	SHEATS17	SHEAST33	SHEATP41	SHEABO110	SHEAOV28	SHEATP19	SHEAOV14	SHEAEL43
SHEABS46	SHEATA32	SHEAHA25	SHEASM110	SHEASM38	SHEARE33	SHEASP310	SHEASP33	SHEARO39	SHEATP47	SHEAEL45

SHEAHA36	SHEAEL15	SHEATA27	SHEAST24	SHEARO37	SHEARO31	SHEAST26	SHEAHA14	SHEAHA31	SHEAEL29	SHEASW12
SHEAHA23	SHEADT26	SHEAHA27	SHEASP38	SHEARS111	SHEATP13	SHEAEP25	SHEASW26	SHEATP34	SHEASM210	SHEATS49
SHEATS55	SHEABO26	SHEAOV34	SHEATP310	SHEATA22	SHEABO24	SHEAST21	SHEAHP110	SHEARO12	SHEAEL39	SHEAOV29
SHEATS14	SHEATA21	SHEASW23	SHEAST18	SHEASM35	SHEAOV23	SHEAEL14	SHEAHP13	SHEARO26	SHEAEL310	SHEASW18
SHEAHA17	SHEATS18	SHEABO34	SHEASP13	SHEAHP14	SHEASM12	SHEARO19	SHEARO14	SHEASN12	SHEABS210	SHEASM31
SHEAOV25	SHEAHA38	SHEAST310	SHEABS28	SHEATS19	SHEABO12	SHEARO110	SHEATP25	SHEASW21	SHEASP58	SHEARS26
SHEAOV39	SHEASW25	SHEAST29	SHEASP16	SHEABS21	SHEATP23	SHEABS45	SHEASW210	SHEAHP31	SHEASW29	SHEAHP18
SHEABO19	SHEAST19	SHEARO21	SHEASP45	SHEABO22	SHEABS16	SHEAOV19	SHEASM13	SHEATP17	SHEASW34	SHEAHA24
SHEARO22	SHEABS22	SHEASM36	SHEAHA28	SHEATA29	SHEAHA12	SHEAHP28	SHEAEL35	SHEARE22	SHEASW312	SHEASP15

Supplementary Table S2: Candidate genes at QTL region searched within approximately ± 20 Kb region of significant SNP markers. The identified genes is believed to be playing an important part in oil yield variation in shea tree.

SNP	Chr	SNP Position	Start	End	Genes	Annotation
						Gene Ontology (GO.OBO)
Trait: Kernel length						
S1_76647305	1	76647305	76642517	76649841	Acyl-ACP Thioesterase Fat B (FATB)	GO:0005634;GO:0006334 PTHR11875:SF126: NAP1-RELATED PROTEIN 2; IPR037231: NAP-like superfamily; G3DSA:3.30.1120.90: -; Coil: Coil; IPR002164: Nucleosome assembly protein (NAP)
S6_46530240	6	46530240	46538324	46541412	Fatty acid desaturases (FADs)	PTHR23155: DISEASE RESISTANCE PROTEIN RP; SSF52047: RNI-like; PTHR23155:SF962: OS08G0539900 PROTEIN
Trait: Kernel width						
S7_45737117	7	45737117	45731235	45739404	Long Chain Acyl-CoA Synthetas (LACS)	GO:0003824;GO:0004619;GO:0005737;GO:0006007;GO:0030145;GO:0046872 IPR011258: BPG-independent PGAM, N-terminal; IPR036646: BPG-independent phosphoglycerate mutase, domain B superfamily; Coil: Coil; IPR005995: Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent; IPR006124: Metalloenzyme; PTHR31637:SF7: 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE 2-RELATED; IPR017850: Alkaline-phosphatase-like, core domain superfamily
S12_32853547	12	32853547	32850936	32857952	3-ketoacyl-ACP synthase II (KASII)	GO:0003824 IPR000192: Aminotransferase class V domain; cd06451: AGAT_like; IPR015424: Pyridoxal phosphate-dependent transferase; IPR020578: Aminotransferase class-V, pyridoxal-phosphate binding site; PTHR21152:SF24: SERINE--PYRUVATE

						AMINOTRANSFERASE; IPR015421: Pyridoxal phosphate-dependent transferase, major domain; PTHR21152: AMINOTRANSFERASE CLASS V; IPR015422: Pyridoxal phosphate-dependent transferase domain 1; IPR024169: Serine-pyruvate aminotransferase/2-aminoethylphosphonate-pyruvate transaminase
Trait: Oil content						
S8_41696703	8	41696703	41709109	41713918	Acyl-CoA-binding protein (ACBP)	GO:0046872 PTHR12506: PROTEIN PHOSPHATASE RELATED; PTHR12506:SF51: ZINC FINGER CCCH DOMAIN-CONTAINING PROTEIN 67-LIKE ISOFORM X1; G3DSA:2.30.30.1190: -; mobidb-lite: consensus disorder prediction; IPR000571: Zinc finger, CCCH-type; IPR036855: Zinc finger, CCCH-type superfamily; G3DSA:4.10.1000.10: CCCH zinc finger
S9_8298654	9	8298654	8284421	8294168	Fatty acid exporter (FAX2)	GO:0003993;GO:0005515;GO:0016787;GO:0046872 IPR004843: Calcineurin-like phosphoesterase domain, ApaH type; IPR029052: Metallo-dependent phosphatase-like; SignalP-noTM: SignalP-noTM; PTHR22953:SF130: PURPLE ACID PHOSPHATASE; SIGNAL_PEPTIDE_C_REGION: C-terminal region of a signal peptide.; SSF56300: Metallo-dependent phosphatases; IPR039331: Purple acid phosphatase-like; IPR003961: Fibronectin type III; SIGNAL_PEPTIDE_N_REGION: N-terminal region of a signal peptide.; IPR015914: Purple acid phosphatase, N-terminal; IPR008963: Purple acid phosphatase-like, N-terminal; SIGNAL_PEPTIDE_H_REGION: Hydrophobic region of a signal peptide.; SIGNAL_PEPTIDE: Signal peptide region; IPR025733: Iron/zinc purple acid phosphatase-like C-terminal domain; IPR041792: Purple acid phosphatase, metallophosphatase domain; PS51257: Prokaryotic membrane lipoprotein lipid attachment site

						profile.; NON_CYTOPLASMIC_DOMAIN: Region of a membrane-bound protein predicted to be outside the membrane, in the extracellular region
S9_32689981	9	32689981	32688415	32689337	Acyl-CoA-binding protein (ACBP)	IPR005050: Early nodulin 93 ENOD93 protein; TMhelix: Region of a membrane-bound protein predicted to be embedded in the membrane.