

Table S1 The characteristic summary of three plant types within *Salix psammophila*.

ID	Clone number	Clone code	Plant types	Crown-height ratio	Height (m)	Crown width (east-west, m)	Crown (south-north, m)	Mean crown (m)
1	Clone1	5–25	Upright	0.58	3	1.8	1.7	1.75
2	Clone2	11 – 30	Upright	0.61	3.3	2.2	1.8	2.0
3	Clone3	12 – 27	Upright	0.61	3.2	2.1	1.8	1.95
4	Clone1	17 – 13	Intermediate	0.70	3.7	2.6	2.6	2.60
5	Clone2	17 – 12	Intermediate	0.95	2.8	2.8	2.5	2.65
6	Clone3	7 – 35	Intermediate	0.96	2.5	2.3	2.5	2.40
7	Clone1	19 – 49	Scattered	1.15	3	3.6	3.3	3.45
8	Clone2	16 – 36	Scattered	1.36	2.5	3	3.8	3.40
9	Clone3	13 – 15	Scattered	1.43	3	4.6	4	4.30

Table S2 Organs used for transcriptome sequencing for different plant types within *Salix psammophila*. Bud indicates the terminal bud.

Plant Type	Group	Clone1	Clone2	Clone3
Upright	A1	5 – 25-Bud	11 – 30-Bud	12 – 27-Bud
	A2	5 – 25-Stem	11 – 30-Stem	12 – 27-Stem
	A3	5 – 25-Root	11 – 30-Root	12 – 27-Root
Intermediate	B1	17 – 13-Bud	17 – 12-Bud	7 – 35-Bud
	B2	17 – 13-Stem	17 – 12-Stem	7 – 35-Stem
	B3	17 – 13-Root	17 – 12-Root	7 – 35-Root
Scattered	C1	19 – 49-Bud	16 – 36-Bud	13 – 15-Bud
	C2	19 – 49-Stem	16 – 36-Stem	13 – 15-Stem
	C3	19 – 49-Root	16 – 36-Root	13 – 15-Root

Table S3 Accession number of the *tubulin* genes used for phylogenetic analysis.

<i>Populus trichocarpa</i> (NCBI)			<i>Salix arbutifolia</i> NCBI)		<i>Salix purpurea</i> (Phytozome 13)		<i>Manihot esculenta</i> (Phytozome 13)		<i>Arabidopsis thaliana</i> (NCBI)	
ID	Gene Name	Gene ID	Gene Name	Gene ID	Gene Name	Gene ID	Gene Name	Gene ID	Gene Name	Gene ID
1	PtTUA1	LOC7467233	CaTUA1	KC238439	SpTUA1	Sapur.002G090500.1	MeTubulin1	Manes.08G061700	AtTUA1	AT1G64740.1
2	PtTUA2	LOC7463572	CaTUA2	KC238440	SpTUA2	Sapur.003G166900.1	MeTubulin2	Manes.08G024800	AtTUA2	AT1G50010.1
3	PtTUA3	LOC7478676	CaTUA3	KC238441	SpTUA3	Sapur.016G172500.1	MeTubulin3	Manes.02G136200	AtTUA3	AT5G19770.1
4	PtTUA4	LOC7457696	CaTUA4	KC238442	SpTUA4	Sapur.001G003500.1	MeTubulin4	Manes.02G123600	AtTUA4	AT1G04820.1
5	PtTUA5	LOC7478755	CaTUA5	KC238443	SpTUA5	Sapur.009G066800.1	MeTubulin5	Manes.05G200200	AtTUA5	AT5G19780.1
6	PtTUA6	LOC7489664	CaTUA6	KC238444	SpTUA6	Sapur.013G052700.1	MeTubulin6	Manes.05G025900	AtTUA6	AT4G14960.2
7	PtTUA7	LOC7482463	CaTUA7	KC238445	SpTUA7	Sapur.017G067300.1	MeTubulin7	Manes.05G147000	AtTUB1	AT1G75780.1
8	PtTUA8	LOC7491044	CaTUA8	KC238446	SpTUA8	Sapur.019G035200.1	MeTubulin8	Manes.13G106300	AtTUB2	AT5G62690.1
9	PtTUB1	LOC7468015	CaTUB1	KC243688	SpTUB1	Sapur.016G138000.1	MeTubulin9	Manes.09G100400	AtTUB3	AT5G62700.1
10	PtTUB2	LOC7481503	CaTUB2	KC243693	SpTUB2	Sapur.009G029500.1	MeTubulin10	Manes.09G055800	AtTUB4	AT5G44340.1
11	PtTUB3	LOC7478050	CaTUB3	KC243687	SpTUB3	Sapur.001G086500.1	MeTubulin11	Manes.09G140200	AtTUB5	AT1G20010.1
12	PtTUB4	LOC7465852	CaTUB4	KC243682	SpTUB4	Sapur.003G090100.1	MeTubulin12	Manes.06G058600	AtTUB6	AT5G12250.1
13	PtTUB5	LOC7487287	CaTUB5	KC243698	SpTUB5	Sapur.006G078000.1	MeTubulin13	Manes.06G007200	AtTUB7	AT2G29550.1
14	PtTUB6	LOC7487442	CaTUB6	KC243679	SpTUB6	Sapur.016G094800.1	MeTubulin14	Manes.06G147900	AtTUB8	AT5G23860.1
15	PtTUB7	LOC7471684	CaTUB7	KC243685	SpTUB7	Sapur.016G301900.1	MeTubulin15	Manes.15G108500	AtTUB9	AT4G20890.1
16	PtTUB8	LOC18103507	CaTUB8	KC243697	SpTUB8	Sapur.011G119600.1	MeTubulin16	Manes.01G249000		
17	PtTUB9	LOC7472769	CaTUB9	KC243686	SpTUB9	Sapur.001G085400.1	MeTubulin17	Manes.01G061400		
18	PtTUB10	LOC7465861	CaTUB10	KC243683	SpTUB10	Sapur.003G091100.1	MeTubulin18	Manes.01G166100		
19	PtTUB11	LOC7486729	CaTUB11	KC243690	SpTUB13	Sapur.016G158100.1	MeTubulin19	Manes.14G124600		
20	PtTUB12	LOC7462497	CaTUB12	KC243696	SpTUB14	Sapur.009G052100.1	MeTubulin20	Manes.03G135500		
21	PtTUB13	LOC105126006	CaTUB13	KC243694	SpTUB15	Sapur.016G158200.1	MeTubulin21	Manes.03G098100		

22	PtTUB14	LOC7454884	CaTUB14	KC243691	SpTUB16	Sapur.009G052200.1	MeTubulin22	Manes.10G087300
23	PtTUB15	LOC7480106	CaTUB15	KC243695	SpTUB17	Sapur.006G025400.1	MeTubulin23	Manes.10G087200
24	PtTUB16	LOC18108966	CaTUB16	KC243692	SpTUB18	Sapur.016G030100.1		
25	PtTUB17	LOC7479658	CaTUB17	KC243684	SpTUB19	Sapur.002G015900.1		
26	PtTUB18	LOC7464075	CaTUB18	KC243680	SpTUB20	Sapur.005G192400.1		
27	PtTUB19	LOC7479116	CaTUB19	KC243681				
28	PtTUB20	LOC7477677	CaTUB20	KC243689				

Table S4 Detail information of the sequenced transcriptomes for different organs from the clones of the three plant types.

Samples	Raw reads	Clean reads	Clean data (bp)	GC Content(%)	≥Q30 (%)	Total mapped (%)	Uniquely mapped (%)	Multiple mapped (%)
G12 – 27-Bud	46639672	46406080	6926713892	44.80	91.77	37566753 (83.57%)	33403115 (74.31%)	4163638 (9.26%)
H11 – 30-Bud	49874082	49618266	7402843050	44.50	91.59	40066626 (82.69%)	35744125 (73.77%)	4322501 (8.92%)
J5 – 25-Bud	40902996	40708318	6063120948	44.95	92.37	32620836 (83.25%)	28972565 (73.94%)	3648271 (9.31%)
G12 – 27-shoot	41508676	41261368	6162859751	44.18	91.42	34034494 (82.67%)	30210074 (73.38%)	3824420 (9.29%)
H11 – 30-shoot	48672594	48337300	7217628104	44.23	91.21	39549533 (81.94%)	35155014 (72.83%)	4394519 (9.10%)
J5 – 25-shoot	43368666	43135998	6427665968	44.39	91.72	35225790 (81.79%)	31286616 (72.64%)	3939174 (9.15%)
G12 – 27-Root	40742408	40526754	6046240497	44.19	91.86	33462833 (83.17%)	29859986 (74.21%)	3602847 (8.95%)
H11 – 30-Root	42270446	42062374	6279087121	44.33	91.69	35863074 (85.44%)	31930093 (76.07%)	3932981 (9.37%)
J5 – 25-Root	44508702	44306080	6616871584	44.38	92.06	37703210 (85.29%)	33454894 (75.68%)	4248316 (9.61%)
D7 – 35-Bud	55700008	55424934	8256278468	44.66	91.98	45541954 (83.64%)	40517540 (74.41%)	5024414 (9.23%)
E17 – 12-Bud	46413642	46176498	6863291065	44.52	91.74	36960078 (81.55%)	32813839 (72.40%)	4146239 (9.15%)
F17 – 13-Bud	52306386	52000898	7758687647	44.61	91.56	42262625 (83.32%)	37646886 (74.22%)	4615739 (9.10%)
D7 – 35- shoot	42820444	42602240	6354732426	44.34	91.79	35378133 (83.22%)	31405374 (73.87%)	3972759 (9.34%)
E17 – 12-shoot	52100372	51818444	7723231977	44.23	91.68	41672233 (80.64%)	36661044 (70.94%)	5011189 (9.70%)
F17 – 13-shoot	53122022	52838666	7884172331	44.40	91.81	44079804 (83.58%)	39057193 (74.06%)	5022611 (9.52%)
D7 – 35-Root	40352560	40144920	5992465970	44.43	92.17	34306704 (85.74%)	30490271 (76.20%)	3816433 (9.54%)
E17 – 12-Root	44626744	44369948	6613113455	44.63	91.65	37560732 (85.44%)	33320050 (75.79%)	4240682 (9.65%)
F17 – 13-Root	50549028	50310526	7504818672	44.57	91.86	43051449 (86.06%)	38160895 (76.28%)	4890554 (9.78%)
A13 – 15-Bud	42364722	42094584	6272978155	44.04	91.54	34286375 (81.95%)	30727154 (73.44%)	3559221 (8.51%)
B16 – 36-Bud	47180942	46805734	6980639794	44.64	91.01	38191438 (82.96%)	33986287 (73.83%)	4205151 (9.13%)
C19 – 49-Bud	43306150	43062706	6426896922	44.64	91.64	34952764 (82.96%)	31106976 (73.83%)	3845788 (9.13%)

A13 – 15-shoot	43628016	43395440	6470910433	44.31	91.79	35807774 (82.76%)	31800568 (73.50%)	4007206 (9.26%)
B16 – 36-shoot	43461428	43246212	6456675235	44.39	91.76	36035579 (83.51%)	32038947 (74.25%)	3996632 (9.26%)
C19 – 49-shoot	43970108	43739114	6527316152	44.39	91.91	36140643 (82.77%)	32076268 (73.47%)	4064375 (9.31%)
A13 – 15-Root	47243528	47022196	7017842949	44.57	91.73	40267743 (85.87%)	35711570 (76.16%)	4556173 (9.72%)
B16 – 36-Root	50518430	50256956	7503674946	45.04	91.77	41215730 (85.70%)	36560978 (76.02%)	4654752 (9.68%)
C19 – 49-Root	50023056	49725374	7418216858	44.54	91.41	42423670 (85.62%)	37673546 (76.04%)	4750124 (9.59%)
Total		1241397928		44.477778	91.721852			

Table S5 Information on primers used in this study.

Primer	Primer sequence (5'-3')
SpsTUB10-F	GGGGACAACCTGTACAAAAAAGTTGGAATGAGAGAAATCCTCCATATT
SpsTUB10-R	GGCGGCCCGCACAACTTTGTACAAGAAAGTTGGGTATTAGTTGTCCAGTGCCTC
q-SpsTUB10-F	ATGAGTGGAGTGACGTGCTG
q-SpsTUB10-R	CATCCCACATTGCTGTGTC

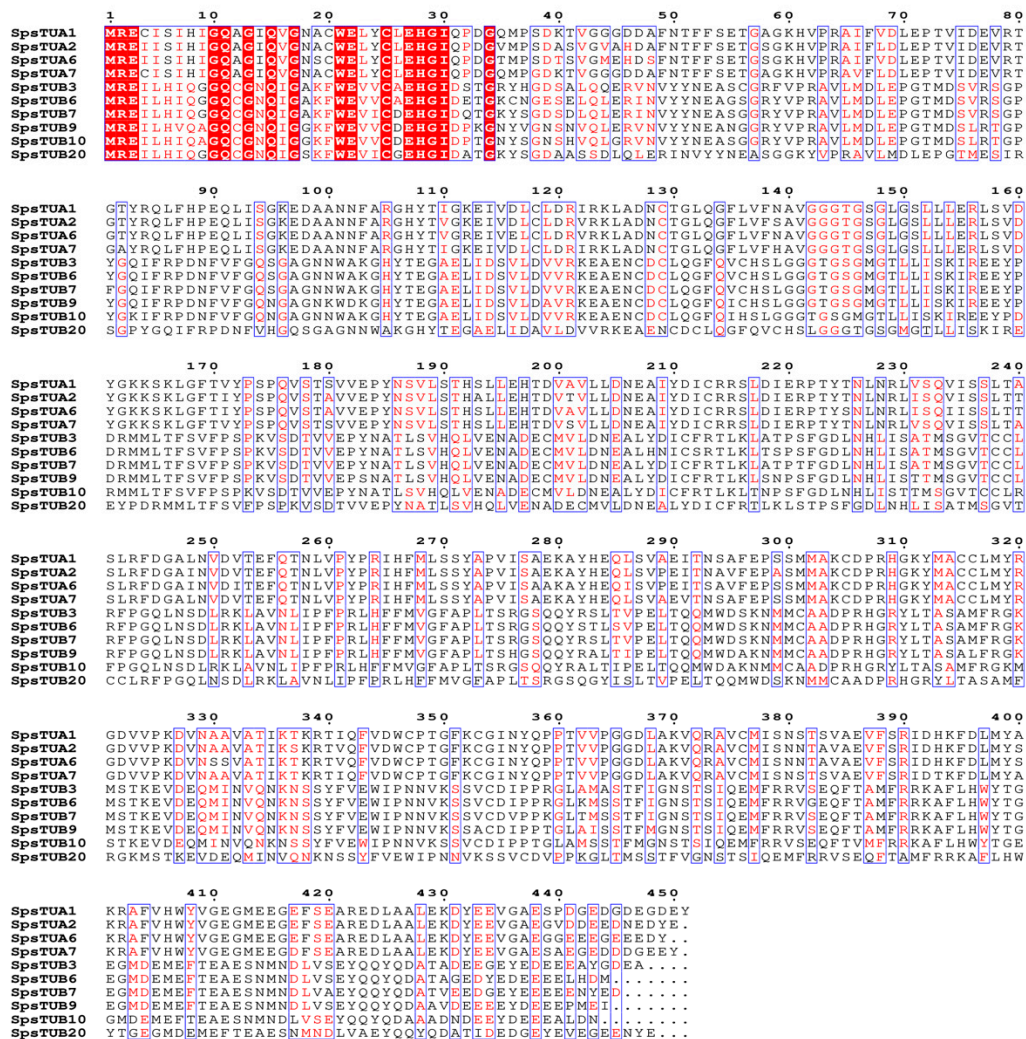


Figure S1 Alignment of the amino acid sequences of the tubulin genes within *Salix psammophila*.


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1   ATGAGAGAAATCCTCCATATTCAAGCCGGTCAATGTGGTAACCAGATTGGTGGCAAGTTCTGGGAGGTGGTGTGCGATGAACACGGGATT
1   M R E I L H I Q A G Q C G N Q I G G K F W E V V C D E H G I
91  GATCCAACAGGGAATTACTCTGGCAACTCTCAGTTTCAGTTGGGAGGGTCAATGTTTACTACAATGAGGCTAGTGGTGGCCGCTATGTG
31  D P T G N Y S G N S H V Q L G R V N V Y Y N E A S G G R Y V
181 CCCAGGGCTGTCCTGATGGACCTCGAGCCAGGACCATGGACAGCTTGAGGACTGGTCCTTATGGGAAAATCTTCAGGCCTGACAACTTT
61  P R A V L M D L E P G T M D S L R T G P Y G K I F R P D N F
271 GTTTTCGGCCAGAATGGAGCTGGAAATAACTGGGCTAAGGGACATTACACTGAGGGAGCGGAAGTATCGACTCTGTTCTTGATGTTGTT
91  V F G Q N G A G N N W A K G H Y T E G A E L I D S V L D V V
361 CGAAAGAAGCTGAGAATTGTGATTGCTTGCAAGGCTTCCAATCTGACATTCTCTGGGAGGTGGAAGTGGATCAGGAATGGGGACTCG
121 R K E A E N C D C L Q G F Q I * H S L G G G T G S G M G T L
451 CTTATATCAAAGATCAGGGAAGAATACCTGACAGGATGATGCTGACTTTCTCAGTATTTCCTCCCTAAGGTTTCTGATACTGTGGTC
151 L I S K I R E E Y P D R M M L T F S V F P S P K V S D T V V
541 GAGCCTTACAATGCCACCTCTCTGTACACCAACTGGTTGAAAATGTGATGAATGTATGGTCCTTGACAACGAAGCTCTCTACGATATC
181 E P Y N A T L S V H Q L V E N A D E C M V L D N E A L Y D I
631 TGCTTTCGAAGCTCTCAAGCTCACCACCCAAGCTTTGGTGATCTCAACCATCTTATCTCAACGACCATGAGTGGAGTGACGTGCTGCCTT
211 C F R T L K L T N P S F G D L N H L I S T T M S G V T C C L
721 CGATTCCGGGTCAACTCAACTCCGATCTTCGAAAACAGCGTGAACCTAATCCCTTCCACGCTCCATTCTTCATGGTTGGTTT
241 R F P G Q L N S D L R K L A V N L I P F P R L H F F M V G F
811 GCACCATTAACATCCCGGGGCTCGCAGCAGTACCGGCCCTAACCATCCCGGAGCTGACACAGCAAATGTGGGATGCTAAAAACATGATG
271 A P L T S R G S Q Q Y R A L T I P E L T Q Q M W D A K N M M
901 TGTGCAGTGACCTCGGCATGGAAGGTACTTAAGTGCCTCAGCCATGTTCCGAGGCAAAATGAGCACCAAGGAAGTCGATGAACAGATG
301 C A A D P R H G R Y L T A S A M F R G K M S T K E V D E Q M
991 ATAAATGTGCAGAACAAAGAACTCATCTACTTTGTGGAGTGGATTCTAATAATGTAATAAAGTGGTTGTGACATCCACCAACCGGG
331 I N V Q N K N S S Y F V E W I P N N V K S S V C D I P P T G

1081 CTGGCAATGTCATCGACATTGATGGGAATTCTACCTCCATTCAAGAGATGTTTAGAGTGTTCGGAACAATTACAGTCATGTTTAGG
361 L A M S S T F M G N S T S I Q E M F R R V S E Q F T V M F R
1171 AGAAAGGCGTTTTTGCAATTGGTACACCGGGAAGGAATGGATGAAATGGAGTTTACTGAGGCTGAAAGCAACATGAACGATTGGTTTCT
391 R K A F L H W Y T G E G M D E M E F T E A E S N M N D L V S
1261 GAATATCAACAATCAAGATGCCGCTGCGGATAATGACGAGGAGTATGATGAAGAAGAGGCACTGGACAACATAA
421 E Y Q Q Y Q D A A A D N D E E Y D E E E A L D N *

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Figure S2 Full-length of the cDNA of the *SpsTUB10* and its amino acid sequence.

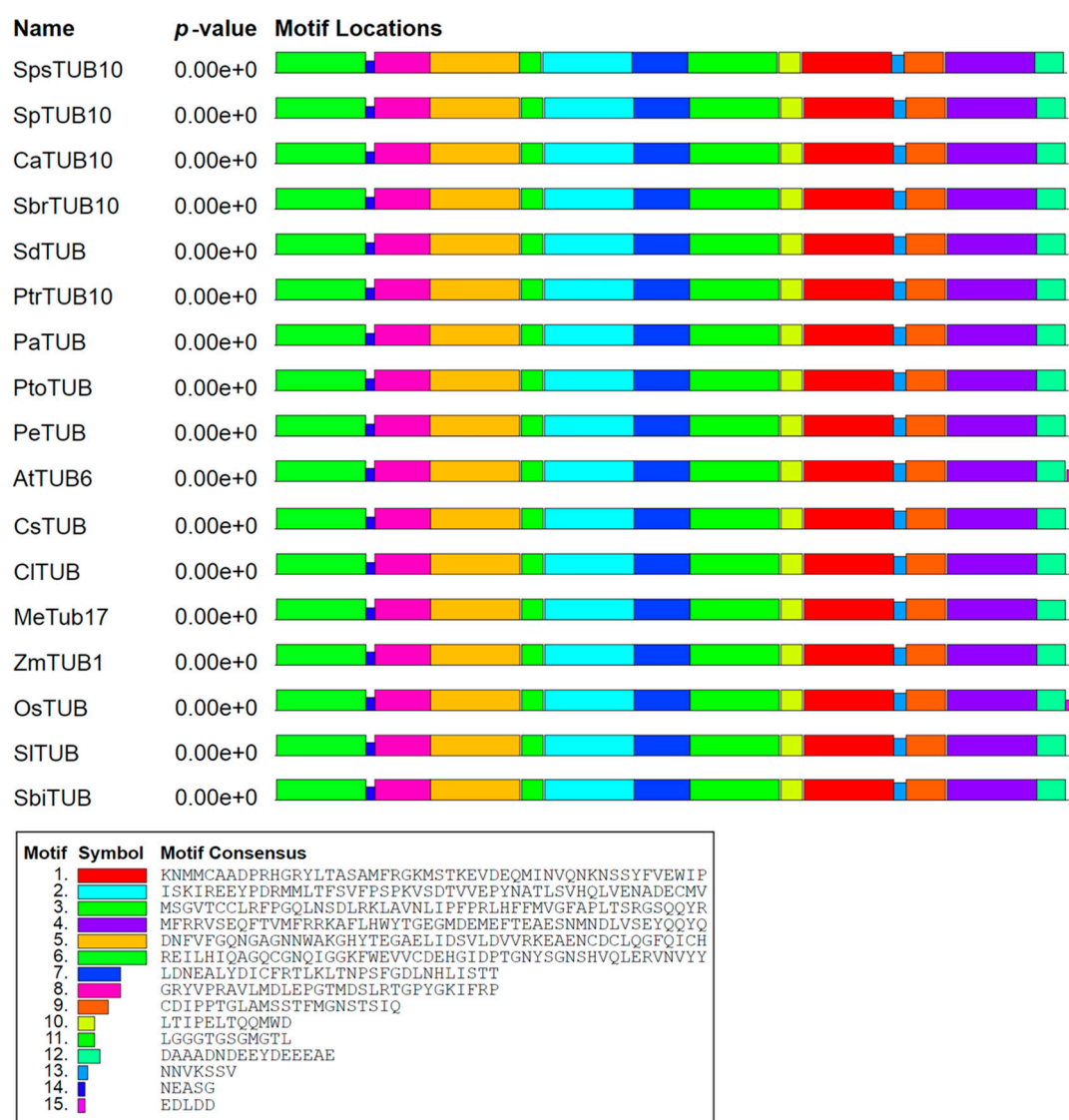


Figure S3 Homologous structure alignment of the amino acid sequences of *TUB* genes. Bar=0.1 substitutions per site. *TUB* gene accessions retrieved from NCBI and Phytozome 13: *Salix psammophila* SpsTUB10, *Salix purpurea* SpTUB, *Salix arbutifolia* CaTUB, *Salix brachista* SbrTUB, *Salix dunnii* SdTUB, *Populus trichocarpa* PtrTUB, *Populus alba* PaTUB, *Populus tomentosa* PtoTUB, *Populus euphratica* PeTUB, *Arabidopsis thaliana* AtTUB6, *Camellia sinensis* CsTUB, *Camellia lanceoleosa* CITUB, *Manihot esculenta* MeTub17, *Zea mays* ZmTUB1, *Oryza sativa* OsTUB, *Solanum lycopersicum* SITUB, and *Sorghum bicolor* SbiTUB. Motif symbol and motif consensus shown in the end.

BAD AVG GOOD

SpS1TUB10	:	99
SpTUB10	:	99
CaTUB10	:	99
SbrTUB10	:	99
SdTUB	:	99
PtrTUB10	:	99
PaTUB	:	99
PtoTUB	:	99
PeTUB	:	99
AtTUB6	:	99
CsTUB	:	99
CTUB	:	99
MeTub17	:	99
ZmTUB1	:	99
OsTUB	:	99
SLTUB	:	99
SbiTUB	:	99
cons	:	99

SpsTUB10	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
CaTUB10	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
CaTUB10	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
SrTUB10	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
SdTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
PtTUB10	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
PaTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
PoTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
PeTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
AtTUB6	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
CsTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
MREI LHTIQA GCGN IGTGGK FWEV	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
MeTub17	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
ZmTUB1	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
OsTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
SlTUB	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
SbTUB1	1	MREI LHTIQA GCGN IGTGGK FWEV	CDEHGD IPTGTG NYS GNSH VQL ERNV NYNE ASGGR VY PRAV L HMLEP GTMDS LRTG PYGKI FRPDM VFVGNG	96
cons	1	*****	*****	96

[illegible]

SpsTUB10	192	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2877
SptTUB10	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2878
CaTUB10	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2880
SbrTUB10	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2881
SdTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2882
PrTUB10	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2883
PaTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2884
ToTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2885
PeTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2886
AlaTUB6	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2887
CaTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2888
CLTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2889
MeTub17	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2890
ZmTub17	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2891
OsTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2892
SLTUB	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2893
SbTUB10	193	VENADECMVLNDNEALDYICFRTLKLTNP	SGDGLNHLISITMS	GVTCCLRFFPGQLNSDRKL	LAVNL1PPRLHF	FMVGFAPL	TSRGSQOYRAL	TIPE	2894

SpsTUB10	288	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	383
SptUB10	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
CapTUB10	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
CatTUB10	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
SdTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
PrtTUB10	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
PaTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
PtoTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
PeTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
AtTUB6	289	LTQOMDSKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIAPGLSMASTFGNSTIQEMFRVSEQ	384
CsTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
ClTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
MeTUB17	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMINVNQKNSYF	VEWIPNNVKSSVCDIPTGLAMSTFMGNSTIQEMFRVSEQ	384
ZmTUB1	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMLNVNQNKSIF	VEWIPNNKVTCTCDIPTGLKMASTFGNSTIQEMFRVSEQ	384
AtTUB	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMLNVNQNKSIF	VEWIPNNKVTCTCDIPTGLKMASTFGNSTIQEMFRVSEQ	384
SbTUB1	289	LTQOMDAKNMCMCAADPRHGRYL TASAMFRGKMSKTE	DEQMLNVNQNKSIF	VEWIPNNKVTCTCDIPTGLKMASTFGNSTIQEMFRVSEQ	384
cons	289	*****	*****	*****	384

SpSUTB10	384	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	LD--N	443
SptB10	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	LD--N	444
CaTb10	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	LD--N	444
SpTb10	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	LD--N	444
dTbTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	LD--N	444
PtUTb10	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEI----	VE--N	444
PaTbTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	ME--N	444
PtOTbTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	VE--N	444
PeTbTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAAADNDEEYD	-EEA----	ME--N	444
AttB6	385	FTAMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
CSUTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
CLTbTb	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
MeTbTb17	385	FTVMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
ZmTb17	385	FTAMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
MeTb17	385	FTAMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
SLTbTb	385	FTAMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
SbTbTbTb	385	FTAMFRKFAFLHWYTGEGDMEFTAEASNNDLVSEYQQYQDAADNDEGEYEE	-DEEETLH-	E--	449
cons	385	*****	*****	*****	452

Figure S4 Amino acid sequence alignment of the SpsTUB10 with other 16 TUB homologous genes from different plant species.