Table S3. The Primer list of sequencing of *Zoysia macrostachya*

Primer ID	Sequence(5'-3')	Strand[*]	Position
256	CTGGGGAGGTCCGTTTGATA	+	135042
		-	82236
W81925	GGTAGAATGCTAGATGCCCG	+	81588
		-	135690
W137891	TCTCACCATCCCCATAGTGT	-	83150
		+	134128
W-3	AATCCACTGCCTTGATCCAC	-	135501
		+	81855
H414	GGGGCGCTTCCGGTTCTGTT	+	82810
		-	134468
W-2	TTCTCGCTATTTGGAATGGA	-	84163
		+	133115
18	GTCTGTAAATACTGCATATTTGATTCCATC	+	83758
		-	133556
340	TTGGAACGAGCATGAAGAAA	-	84968
		+	132310
W84777	CGTTTTCATTTACCATCTCATG	+	84412
		-	132864
W133811	TGGGATCGTTTGATCGATTT	-	85736
		+	131542
W88291	GAAGCCCAAAGAGGTGCATA	-	86458
		+	130820
W135950	GGGTCGCTTCTTATGGACT	+	85074
		-	132205
H422	CTAAAGAGCGTGGAGGTTCG	-	131106
		+	86172
H423	GGTCTTCCTCCACTAGCAGG	+	130181
		-	87097
99	GTAGATGCTACATAGTTGGTTCTCAT	+	129316
		-	87956
106	TTGGGTTCATTGATATTCCTGGTATAG	+	86834
		-	130437
H424	TTTCGACCTTGGTTCCGTAG	+	87809
		-	129469
W90942	AATAAGGTTTGATCCTATTCATGG	+	128153
		-	89121
W92518	ATCCTTACTGTCCCTCTACAGAA	-	90697
		+	126578
W130055	ATGGCAAGTGCTCTTCCTTG	+	89512
		-	127078
W92021	CGAATTGTTTGTTGACACGG	+	90200
		-	127029
W93455	ATGAGAGAAGCACAGAGGTCA	-	91650
		+	125627

W94612	TCCCAAGGGCAGGTTCTTAC	+	124455
		-	92774
W128213	ATGATCCGATCGATTGC	+	91367
		-	125914
H427	ACCTTGACGTGGTGGAAGTC	+	92392
		-	124886
H428	AAGGGGCATGATGACTTGAC	+	123472
		-	93806
W95255	CCATCGTTTACGGCTAGGAC	-	123861
		+	93417
W125083	TACCACTGAGCTAATAGCCCG	+	122812
		-	94465
W124160	CCCGAAAAGGAGTCTATTGA	-	95144
		+	122134
W125409	GCTGGATCACCTCCTTTTCA	+	94141
		-	123137
H429	CGCATCTTCACAGACCAAGA	+	94864
		-	122414
W122891	TGCTTATTTTCAACTCCCCG	+	120861
		-	96417
10	CGAACTGCTGCTGAATCCATGGGCAGGCAAG	+	96470
		-	120796
W100297	GGTCTCCGCAAAGTCGTAAG	-	98222
		+	119056
W99809	GTCCATCGACTACGCCTTTC	-	119544
		+	97734
W119602	TGCGGTGACGATACTGTAGG	+	117568
		-	99710
96	GTAACTATAACGGTCCTAAGGTAGC	+	98344
		-	118929
W104124	GCAAGTCTCCGTATCTTATTGG	-	115218
		+	102115
W118951	CTGGTCGTAGGTTCGAATCC	-	116917
		+	100361
W105880	ACGTGAAGAGGGAATTGTGC	+	103814
W107400	GCAATAGATGTCTTTCACATACAA	+	105306
W108711	TCTCAGTGGTTAATGATGCATG	-	106613
W108608	AAGCACAATAACTACGCCAAG	+	106510
W109967	CCGATAAATCCATGGATA	-	107857
W110557	TAATTCTAACTCCCACATGATAAAA	-	108447
W-9	GAACAAAATCTGGATAGATACCGA	+	107435
W111122	GATAGAGCCATGCTGCG	-	109008
W112176	CGATTCATTTCAATCTGAGGA	+	110127
W114051	TTCGGTTTGATAACCTGCTA	-	112002
W112816	CCTAGTAGAAGAACAAATCCCC	+	110708
W116493	CGATGCGAAAGTAATTATGC	-	114460

W-19	GTAAAGAGTTTACACTGCTTATG	+	112999
W98266	CTTATCTCCAGCCCGTGAAC	+	96182
		-	121096
W111245	ATTTGCTTGGCTTTACATCC	+	109131
W113787	TTGATCCATTCTCATCCTGG	+	111738
W114453	CGCTTCCGAATTGATCTCAT	+	112400
103	GATATCATATTCATGGAATATGATTC	+	131024
		-	86248
14	TAGCCCCAGAATGTTTCAGTTTATGCTCCT	-	128711
		+	88557
339	AACTGCAAAATCCGATCCAA	+	127510
		-	89768
W-1	CGAGATCCACCCTACAATA	+	127379
		-	89900
97	ATATAGCTCAGTTGGTAGAGCTCCG	-	95313
		+	121960
11	CATTTCGCTCGCCGCTACTACGGGAATCGC	+	120713
		-	96555
100	GGGCGAGGTCTCTGGTTCAAGTCCAGGA	+	95209
		-	122061
W98861	CTATCGGTCACCCAGGAGTATT	+	120495
		-	96781
98	ATGAAGCTTATCCCCCATCGTCTC	-	119953
		+	97321
95	TCGTGCGGGTCGGAACTTACCCGAC	+	118894
		-	98379
9	GCCGACCGCTCTACCACTGAGCTACTGAGG	+	116877
		-	100391
W-24	CTGTAGAGAATTGAGAATTTTCATG	+	101324
		-	115949
W-25	CGTGAGACATATAATCGTCGC	-	104205
H409	GGTGAAATTGGTAGACACGC	-	106069
W-26	GAATTTGACCTTCGCTTTATCTCC	+	105004
W110391	TCAATCTTTCCAAATCTAATCC	+	108236
W-27	GAATTAGCCAATAAATTGGCTAT	-	109475
H401	GCCAGTCCAATAGCTGCTTC	+	109808
W112922	CTGACTAAAACTAAAAGATTCAAGG	-	110814
W115117	AAATTAATAAGCTGTTTTGTTTCAC	-	113076
W115989	TTACATAAAGCTCTTGCTTTGATA	+	113956
W-4	TTGTTTACGAAGAAATAATAACAA	+	2520
W-5	CAGATCGGTTAAATTTCACTG	-	4067
24	CGCCGCTTTAGTCCACTCAGCCATCTCTCC	-	8119
25	CTGGGACGGAAGGATTCGAACCTCCGAATAGC	+	6821
W13690	AGAACGAATCACACTTTTACCAC	-	13842
W-12	TCCTACGAAAGCATAACAGAAAA	-	15346
W17778	AGAATGCAAGTCCTCCCCTT	+	17040

W-13	TTCTGACACCTTAACGCATAGTTT	-	18779
309	TCTTGCATTTATTGCTACTGCAC	+	17151
W18889	TTCTGCCCTAAGACTATGGATT	+	18212
W20819	GGAATGGAAATGAGGGAATG	-	20282
W27367	CCGACCTTGTACGATCCC	+	25861
W29456	CAATACCAATTCCTTTTATTCCA	-	28992
W27717	CGTCGATTACCAAAAACAAGC	+	27211
175	CTTGGGGATTCTTGATTGGTGCTG	-	29810
W30641	TTGGTTGAAAGGCCTGAAAG	+	30183
W31373	CAGCAAGTCAGGGAAAAAGC	-	30924
W34488	ACCGATATTTTAGCAACAAATCTAA	+	34022
W36012	TGCTCGTATTATAGGTCTTGGTGA	-	35551
40	CCTTGGCTAAACCTTGGAAATCGTAATGC	-	40139
165	CATTACCAAGATTAGCACGG	+	165
43	GCCCACTATTGGCCAAACCACCTGGGCACTAG	+	42088
246	CCTTCCCTTAGAACCGTACTTG	-	43249
H458	TGAGCCTTGGTATGGAAACC	-	47831
W47393	GCATTACAAATGCGATGCTC	-	46944
224	CCATGCATAAACTAAACCAACAA	+	50729
W53119	CCCTTGTCAGAGATATCTTAACAT	-	52677
w55203	ACAGCTCTAACTCGATTATTTCCT	+	54722
W-7	CTATCACATCGAACCCGTTC	-	56007
W-16	GTGGACTAGCACTTGATTTCG	+	55099
w56135	AGACCCTGTCGTTGTGAGAA	+	55705
W56293	CTTGGCAGCATTCCGAGTA	-	55893
W74410	GCATTCATTTTCTTTGCATCG	+	74027
W76331	TGGATTCTTCAATACCTACTATTGT	-	75946
W-17	GCCGTCAATGATTGGTGAGC	+	74660
W79014	GGTTTAACAACGGCTACCCA	-	78629
W-23	TAACGTGAATTGTATCGATTTC	-	80586
69	CAACCCCTTGGGGTTATCCTGCACTTGGAA	+	135249
		-	82019
W80090	TCCACATCCCTTTAGTTTTGC	+	79704
W105376	GACCAGAAGCAAGCAAGAGG	-	13310
W117523	AATAAAGAATGTACCCTTCTATCC	+	101794
		-	115479
W-35	GTGATAAATTCATATGAATTTATGGA	+	102749
W-36	GAATAGACAGGTGAACTGAGAATA	-	104376
W1683	ATTCACCAGGTCATCAATACG	+	1695
W-28	GATTGCAAACCCCTCAGATA	-	2904
W3004	TGCTGATACATTAGAAAAATTAAA	+	3016
395	CTTCGGGATCGAACATCAAT	-	4644
36	CCCATCGTCTAGTGGTTTAGGACATCTCTC	+	15503
W18757	ACCATTAAAGCAGCCCAAGC	-	18090
W16206	CATCTCTCTTTCAAGGAGGCA	+	15525
W-20	TTCAATTGGTTAGAGCACCG	+	16081

W-29	GCACCCAGATTTGAACTGGGGAT	+	19048
W21210	CTCGGAATTAGACCATAAGGG	-	20673
W31653	TATGACGAGGTTGCCTGACA	-	31204
145	GATTGGCTGTAGGGCTTGCTTCT	-	33290
W-14	GGGGTTGTATGATATATCAGGC	+	31729
321	TGCTTAGTCTAGCTTTTATGGAAGC	-	33410
W39284	GTCTTACCATGAGCAGATTGTAT	-	38762
W44580	CCTTTGTATGCTCTCCATTGC	+	44044
W-30	GAGTGGTTTTATTCAAATTCAAAGC	+	43066
W48442-1	GGATAGGTGCAGAGACTCAATG	-	47966
W48442	GGATAGGTGCAGAGACTCAATG	+	47966
W49145	TGAAAATCCTCGTGTCACCA	-	48802
235	TAGGGCTATACGGACTCG	-	52009
W51430	TACCAAAATAGGAATAAGGCTTG	+	50993
212	CAGGAGCAGGGTCGGTCAAAT	-	53934
W52686	CCAAAGTGTTTCAAAGGAGGA	+	52244
H437	CATGAGTTGTAGGGAGGGAT	-	55734
W55204	CAGCTCTAACTCGATTATTTCCTAA	+	54752
W56293-1	CTTGGCAGCATTCCGAGTA	-	55863
W56344	AGGGGCTGCAGTAGCTG	-	55914
W80234	GGATCTCGACAATACGAAGCA	-	79844
W-33	GCTCCTATGACTCGAATACACATC	+	78325
W80924	TGACGTGGATTGTATCGATTTC	+	80586
W81925-1	GGTAGAATGCTAGATGCCCG	-	81588
		+	135690
W947	GAAACAGGCTCACGAATACCA	+	947
72	CCCGTTGCCTTACCACTTGGCCACGCCCCA	-	6863
W4463	TCAAAGTTCTTTCTTTATCTTTAAA	+	4474
W-21	TTCTGCCCTAAGACTCTGGATG	-	18212
276	ACCATTAAAGCAGCCCAAGC	-	18086
W23499	TGAGCAAGAGGCTTCAAGAAA	+	22962
W25894-1	GCTCCGATGGAAACTAGATCA	-	25348
W32396	GCAAAACTCAGATTGGAGAAGAA	-	31918
W41129	CGACTGCATTTTCCAACTGA	-	40607
W41797	TGTGGTGTGTGAACAAGGAAA	-	41254
W45138	TGTGGTGTGTGAACAAGGAAA	-	41275
W47393-1	GCATTACAAATGCGATGCTC	-	46944
W-31	TCTAGGCATAATTCCCAATCC	+	45047
W-32	GGTATGAGTACTGCGCCGAACATAAACT	-	50076
W48828	CCTCTATCCCCAAACCCTCT	+	48415
320	TAGCCTTTGTTTGGCAAGCT	-	7390
W7487	TGGATCTGTGCGGTAAGGAAAA	+	7764
W-11	TAAGGAGGTATTTTGTCTTTGG	-	7108
W114453-1	CGCTTCCGAATTGATCTCAT	-	112400
W48828-1	CCTCTATCCCCAAACCCTCT	-	48415

374	CATCTCGGAAATATTCAGCCA	-	54165
W54841	CGGATACGCCTCCATGA	+	54360
W55204-1	CAGCTCTAACTCGATTATTTCCTAA	-	54723
W-34	CTCAACGGATAAAAGTTACT	-	98858
W5430	CTATGTCGAGCCAAGAGCATT	-	5441
W25382	ATTGTATGGGAAATACTTCAAGAA	-	24845
W80234-1	GGATCTCGACAATACGAAGCA	+	79844
W33791	CTGCTGCAGGACAAGCTGTA	-	33338
W34156	GCCCTCTTCCTTCCCG	-	33692
W-10	AGTGGTATCGAGAATTGATCC	+	5596
71	GTTGCTTTCTACCACATCGTTTCAAACGAA	+	5526

*Primer sequences mentioned with both a "+" and "-" strand position are located in the Inverted Repeat region.