Table S4. The Primer list of sequencing of *Zoysia sinica*

Primer ID	Sequence(5'-3')	Strand*	Position
256	CTGGGGAGGTCCGTTTGATA	+	135010
		-	82210
W81925	GGTAGAATGCTAGATGCCCG	+	81562
		-	135658
W137891	TCTCACCATCCCCATAGTGT	-	83124
		+	134096
W-3	AATCCACTGCCTTGATCCAC	-	135391
		+	81829
H414	GGGGCGCTTCCGGTTCTGTT	+	82784
		-	134436
W-2	TTCTCGCTATTTGGAATGGA	-	84137
		+	133083
18	GTCTGTAAATACTGCATATTTGATTCCATC	+	83686
		-	133524
340	TTGGAACGAGCATGAAGAAA	-	84942
		+	132278
W84777	CGTTTTCATTTACCATCTCATG	+	84386
		-	132832
W133811	TGGGATCGTTTGATCGATTT	-	85710
		+	131510
W88291	GAAGCCCAAAGAGGTGCATA	-	86431
		+	130771
W135950	GGGTCGCTTCTTATGGACT	+	85048
		-	132173
H422	CTAAAGAGCGTGGAGGTTCG	-	131075
		+	86145
H423	GGTCTTCCTCCACTAGCAGG	+	130150
		-	87070
99	GTAGATGCTACATAGTTGGTTCTCAT	+	129285
		-	87929
106	TTGGGTTCATTGATATTCCTGGTATAG	+	86807
		-	130406
H424	TTTCGACCTTGGTTCCGTAG	+	87782
		-	129438
W90942	AATAAGGTTTGATCCTATTCATGG	+	128122
		-	89094
W92518	ATCCTTACTGTCCCTCTACAGAA	-	90670
		+	126547
W130055	ATGGCAAGTGCTCTTCCTTG	+	89485
		-	127735
W92021	CGAATTGTTTGTTGACACGG	+	90173
		-	127047
W93455	ATGAGAGAAGCACAGAGGTCA	-	91623
		+	125596

W94612	TCCCAAGGGCAGGTTCTTAC	+	124473
		-	92747
W128213	ATGATCCGATCGATTGC	+	91340
		-	125883
H427	ACCTTGACGTGGTGGAAGTC	+	92365
		-	124855
H428	AAGGGGCATGATGACTTGAC	+	123441
		-	93779
W95255	CCATCGTTACGGCTAGGAC	-	123830
		+	93390
W125083	TACCACTGAGCTAATAGCCCG	+	122781
		-	94438
W124160-1	TCAATAGACTCCTTTTCGGG	+	122103
		-	95117
W125409	GCTGGATCACCTCCTTTTCA	+	94114
		-	123106
H429	CGCATCTTCACAGACCAAGA	+	94837
		-	122383
W122891	TGCTTATTTTCAACTCCCCG	+	120830
		-	96390
10	CGAACTGCTGCTGAATCCATGGGCAGGCAAG	+	96443
		-	120765
W100297	GGTCTCCGCAAAGTCGTAAG	-	98195
		+	119025
97	ATATAGCTCAGTTGGTAGAGCTCCG	-	95286
		+	121929
98	ATGAAGCTTATCCCCCATCGTCTC	-	119922
		+	97294
W99809	GTCCATCGACTACGCCTTTC	-	119513
		+	97707
W119602-1	CCTACAGTATCGTCACCGCA	+	117537
		-	99683
96	GTAACTATAACGGTCCTAAGGTAGC	+	98317
		-	118898
9	GCCGACCGCTCTACCACTGAGCTACTGAGG	+	116846
		-	100364
94	GAAGGTCTCGGCGAGACGAGCCG	+	99296
		-	117921
W118236	TCGTGAAAAGTGATACCTGTGAA	+	116159
		-	101058
W119602	TGCGGTGACGATACTGTAGG	+	117537
		-	99683
W104124-1	GCAAGTCTCCGTATCTTATTGG	+	115187
		-	102031

W118951	CTGGTCGTAGGTTCGAATCC	-	116886
		+	100334
W105880	ACGTGAAGAGGGAATTGTGC	+	103787
W107400-1	GCAATAGATGTCTTTCACATACAA	-	105279
W107400	GCAATAGATGTCTTTCACATACAA	+	105279
W108711	TCTCAGTGGTTAATGATGCATG	-	106586
W108608	AAGCACAATAACTACGCCAAG	+	106483
W109967	CCGATAAATCCATGGGATA	-	107830
W110557	TAATTCTAACTCCCACATGATAAAA	-	108420
W-9	GAACAAAATCTGGATAGATACCGA	+	107408
W111122	GATAGAGCCATGCTGCG	-	108981
W112176	CGATTCATTTCAATCTGAGGA	+	110038
W114051	TTCGGTTTGATAACCTGCTA	-	111971
W112816	CCTAGTAGAAGAACAAATCCCC	+	110677
W116493	CGATGCGAAAGTAATTATGC	-	114429
W-19	GTAAAGAGTTTACACTGCTTATG	+	112968
W98266	CTTATCTCCAGCCCGTGAAC	+	96155
		-	121065
W104124	GCAAGTCTCCGTATCTTATTGG	-	115187
		+	102031
82	CTATGGAGAAATTGGTAGACACGCTGCTCT	-	106038
W111245	ATTTGCTTGGCTTTACATCC	+	109104
W113787	TTGATCCATTCTCATCCTGG	+	111707
W114453	CGCTTCCGAATTGATCTCAT	+	112369
15	GCTGTTAATACGAATAGAGAAACTCTGT	-	88613
		+	128598
H426	CCCTATTGTTCCGATGGAGA	+	128440
		-	88780
259	AAAAACCAAACTCTGCCTTACG	+	126604
		-	90614
W130741	GAACAATAGGGCCGTTATGC	+	88789
		-	128431
11	CATTTCGCTCGCCGCTACTACGGGAATCGC	+	120682
		-	96528
100	GGGCGAGGTCTCTGGTTCAAGTCCAGGA	+	65182
		-	122030
W98861	AATACTCCTGGGTGACCGATAG	-	96754
		+	120464
W-24	CTGTAGAGAATTGAGAATTTTCATG	+	101297
		-	115918
W-25	CGTGAGACATATAATCGTCGC	-	104178
W110391	TCAATCTTTCCAAATCTAATCC	+	108254
W-27	GAATTAGCCAATAAATTGGCTAT	-	109448
W115989	TTACATAAAGCTCTTGCTTTGATA	+	113925
395	CTTCGGGATCGAACATCAAT	-	4642

W4052	CAAAATAAACAGATCGGT	+	4058
23	TTAAAAGCCGAGTACTCTACCGTTGAGTTA	+	3889
276	ACCATTAAAGCAGCCCAAGC	-	18088
W-22	AAGATCTTCTTTTCTCCATCTC	+	16695
W31365	TTTTGATGCAGCAAGTCAGG	+	30894
W32396	GCAAAACTCAGATTGGAGAAGAA	-	31920
W34488	ACCGATATTTTAGCAACAAATCTAA	+	34001
W36012	TGCTCGTATTATAGGTCTTGGTGA	-	35530
251	GTAGCCCAAACAAGATGTCCA	-	38175
W36871	GACGTTTCCGCCTATATTCC	+	36389
43	GCCCACTATTGGCCAAACCACCTGGGCACTAG	+	42068
246	CCTTCCCTTAGAACCGTACTTG	-	43230
H458	TGAGCCTTGGTATGGAAACC	-	47809
W47393	GCATTACAAATGCGATGCTC	-	46919
W49145	TGAAAATCCTCGTGTCACCA	-	48780
224	CCATGCATAAACTAAACCAACAA	+	50709
235	CCATGCATAAACTAAACCAACAA	-	51986
W56293	CTTGGCAGCATTCCGAGTA	-	55840
W56135	AGACCCTGTCGTTGTGAGAA	+	55682
244	AAAACAAACGCGCTACCAAG	+	65003
W67341	GAAACTCCAACCAGAATTTAAGA	-	66897
W76331	TGGATTCTTCAATACCTACTATTGT	-	75923
W-17	GCCGTCAATGATTGGTGAGC	+	74637
253	GCATTGTCATCATATCGTATTATCA	-	78131
W76846	GGGTGATGCTTTTCTTGAGC	+	76436
W18889	TTCTGCCCTAAGACTATGGATT	+	18210
W-20	TTCAATTGGTTAGAGCACCG	+	16078
W20819	GGAATGGAAATGAGGGAATG	-	20281
76	AATCCACTGATTCTGCCGCTTCCGTTATTGC	+	33232
40	CCTTGGCTAAACCTTGGAAATCGTAATGC	-	40119
165	CATTACCAAGATTAGCACGG	+	165
127	GAATGACCCAGTATCGAATACTGGTAA	+	62906
231	TATAATAGGTAGGGATGACAGGA	-	64959
W65536	AAAACAAACGCGCTACCAAG	-	65003
237	AAGTATTTTACGATTAAGAAG	-	67254
238	CGCTCTGTAGGATTTGAACCTAC	+	64766
129	GCTCTGTAGGATTTGAACCTACGACATC	+	64767
58	CTGCCGTATTTATGTTAATGCACTTTCCAATG	+	103787
W71818	TCTTCTTCCGAGAACCACCT	+	71416
69	CAACCCCTTGGGGTTATCCTGCACTTGGAA	+	135217
		-	81993
W80090	TCCACATCCCTTTAGTTTTGC	+	79680
W105376	GACCAGAAGCAAGCAAGAGG	-	103283
W117523	GGATAGAAGGGTACATTCTTTTATT	-	115448
		+	101767
W-35	GTGATAAATTCATATGAATTTATGGA	+	102722

W-36	GAATAGACAGGTGAACTGAGAATA	-	104349
W1683	ATTCACCAGGTCATCAATACG	+	1694
W-28	GATTGCAAACCCCTCAGATA	-	2903
24	CGCCGCTTTAGTCCACTCAGCCATCTCTCC	-	8118
25	CTGGGACGGAAGGATTCGAACCTCCGAATAGC	+	6821
320	TAGCCTTTGTTTGGCAAGCT	-	7390
W6509	TTTTGTGTCGTGCAGAGC	+	6771
W7136	GCGTTTGTTTGGCAAGC	+	7391
W-29	GCACCCAGATTTGAACTGGGGAT	+	19046
W21210	CTCGGAATTAGACCATAAGGG	-	20672
145	GATTGGCTGTAGGGCTTGCTTCT	-	33269
W-14	GGGGTTGTATGATATATCAGGC	+	31708
321	TGCTTAGTCTAGCTTTTATGGAAGC	-	33389
W48442-1	GGATAGGTGCAGAGACTCAATG	-	47944
218	TTCCTTCCCTTAGAACCGTACTTGAGAG	-	43228
W46864	CAGACCATAATGAAAACGCAAT	+	46390
W73004-1	AAATAGGGAAGAGAAAAGTCAAG	-	72600
W77590	ATTTTGACCCTATCCCCCAT	-	77184
W80234	GGATCTCGACAATACGAAGCA	-	79820
W-33	GCTCCTATGACTCGAATACACATC	+	78302
W947	GAAACAGGCTCACGAATACCA	+	947
W4463	TCAAAGTTCTTTCTTTATCTTTAAA	+	4472
W5430	CTATGTCGAGCCAAGAGCATT	-	5440
W-10	AGTGGTATCGAGAATTGATCC	+	5594
W-11	TAAGGAGGTATTTTGTCTTTGG	-	7108
W33791	CTGCTGCAGGACAAGCTGTA	-	33317
W-15	CAATATATAGAATTCCGGAATTG	-	32780
H465	AGTGGTTCAAGGCGTAGCAT	-	45639
W47393-1	GCATTACAAATGCGATGCTC	-	46919
W-31	TCTAGGCATAATTCCCAATCC	+	45028
W48828	CCTCTATCCCCAAACCCTCT	+	48393
W50130	AGCACATTGGGAACGTAAAT	+	49672
W-32	GGTATGAGTACTGCGCCGAACATAAACT	-	50056
W51430	TACCAAAATAGGAATAAGGCTTG	+	50973
212	CAGGAGCAGGGTCGGTCAAAT	-	53911
374	CATCTCGGAAATATTCAGCCA	-	54142
W52686	CCAAAGTGTTTCAAAGGAGGA	+	52221
W71184-1	GAATTGTGAGAGCGGACGTT	+	70775
W72808	TCATCAAGCGGTTCTTATTCG	+	72418
W78260	GCAATAGTGTCCTTGCCCAT	-	77851
W81925-1	GGTAGAATGCTAGATGCCCG	-	81562
W-23	TAACGTGAATTGTATCGATTTC	-	80562

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