Table S2. The Primer list of sequencing of *Zoysia japonica*

Primer ID	Sequence(5'-3')	Strand[*]	Position
320	TAGCCTTTGTTTGGCAAGCT	-	7389
395	CTTCGGGATCGAACATCAAT	-	4643
petB	CGTCTTGAGATTCAGGCAATTGCG	-	72915
385	ACCTCCGGAGCTAATGAAAC	+	78020
381	TATTCAGGGGATCCTTTCCC	-	78630
rpoC1_1	GTGGATACACTTCTTGATAATGG	+	24530
rpoC1_4	CCAACTCAAGATATGCTTATGG	-	25127
rps16	GTTCTTGTAGGTTGAGCGCCTTT	-	4529
trnK5	TACTCTACCRTTGAGTTAGCAAC	+	3902
22	GTTCCTGTAGGTTGAGCCCCTTTTTCAAGG	-	4529
23	TTAAAAGCCGAGTACTCTACCGTTGAGTTA	+	3890
301	ATCCGTTACGGTCGTCATTC	+	44167
w54225f	TCCTGAAGTTCTTTGTAACGTTGT	+	53720
w55203	ACAGCTCTAACTCGATTATTTCCT	+	54698
w56135	AGACCCTGTCGTTGTGAGAA	+	55686
ccsAf	TTAGAACATATACTAACTCA	+	106187
ccsAr	TAATTTGGATCTGCTATTTT	-	107058
284	AAAAGAACCGGCACAATACG	-	129223
		+	87960
259	AAAAACCAAACTCTGCCTTACG	+	126586
		-	90596
40	CCTTGGCTAAACCTTGGAAATCGTAATGC	-	40118
370	GCAAGGCCTAATTGAAAAATGA	+	39140
247	TCTCCGTTCCAGAACCGTAC	-	44199
221	CAACCAATTATGCGCTTCAATATAATTACCAGGA	+	43084
99	GTAGATGCTACATAGTTGGTTCTCAT	+	129267
		-	87911
106	TTGGGTTCATTGATATTCCTGGTATAG	+	86789
		-	130388
182	GAAGGTCACGGCGAGACGAG	+	99278
		-	117906
9	GCCGACCGCTCTACCACTGAGCTACTGAGG	+	116828
		-	100346
339	AACTGCAAAATCCGATCCAA	+	127461
		-	89723
14	TAGCCCCAGAATGTTTCAGTTTATGCTCCT	-	128662
		+	88512
165	CATTACCAAGATTAGCACGG	+	165
168	TGCGTTTGTGGGTGGAATCCCCCGAG	-	39354
18	GTCTGTAAATACTGCATATTTGATTCCATC	+	83668
		-	133506
340	TTGGAACGAGCATGAAGAAA	-	84924
		+	132260
71	GTTGCTTTCTACCACATCGTTTCAAACGAA	+	5525

72	CCCGTTGCCTTACCACTTGGCCACGCCCCA	-	6862
27239F	CACTCATGGGGATCTGGT	+	26730
29456R	CAATACCAATTCCTTTTATTCCA	-	28968
29252F	TCAATTCGTTCGAACTTGCTT	+	28764
31653R	TATGACGAGGTTGCCTGACA	-	31180
13	GTAACGCGTAAGAACCTGCCCTTGGGAGGGG	-	92722
		+	124451
393	TCCGAATCCGCTTTGTCTAC	+	92569
		-	124615
43	GCCC-ACTATTGGCCAAACCACCTGGGCACTAG	+	42067
90	TCCAGGCTTATTTGTCAAAAAAAAATACACT	+	102112
		-	115061
8	GAACCACGGTGTCGGGGGTTCGAATCCCTC	+	100014
		-	117160
303	TAGGTTCGAATCCTACTTGGG	-	100308
		+	116875
39	ACCTTATATTCCCTGAGGAGGTTCTACCACGT	+	10042
38	TTGAAGAATCTTTTCCCTTCTTTGGTTATGTC	-	10454
25	CTGGGACGGAAGGATTCGAACCTCCGAATAGC	+	6820
37	ACTGTAAATTCGTTGGCAATATGTCTACGC	-	15660
161	GCCCTTTTAACTCAGTGGTAGAC	+	14882
148	GGCTTATATAGGTGAATCCTAGGA	+	32378
145	GATTGGCTGTAGGGCTTGCTTCT	-	33267
321	TGCTTAGTCTAGCTTTTATGGAAGC	-	33387
384	GAGGGGAAGGATGGATTGTT	+	10691
164	CTTAAAACTATACCGGTTTTCAAGA	-	11646
188	TCAACCACTCAGCCATCTCTCCG	-	11680
246	CCTTCCCTTAGAACCGTACTTG	-	43229
218	TTCCTTCCCTTAGAACCGTACTTGAGAG	-	43227
73	CGGAAAGAGAGGGATTCGAACCCTCGGTACG	+	8059
368	GTTGGTGTCAATTAGGCGGT	-	9337
76	AATCCACTGATTTCTGCCGCTTCCGTTATTGC	+	33230
356	TGCTGAATCGACGACCTATG	-	34490
24	CGCCGCTTTAGTCCACTCAGCCATCTCTCC	-	8117
15	GCTGTTAATACGAATAGAGAAACTCTGT	-	88595
		+	128580
19	GTTGGGCGCTTTAACCATTCAGCCATGGATGC	-	83917
		+	133255
H415	TATGGGGATGGTGAGAAGAG	-	134082
		+	83102
H428	AAGGGGCATGATGACTTGAC	+	123423
		-	93761
H427	ACCTTGACGTGGTGGAAGTC	+	92347
		-	124837
H429	CGCATCTTCACAGACCAAGA	+	94819
		-	122365

97	ATATAGCTCAGTTGGTAGAGCTCCG	-	95268
		+	121911
102	CGCTCTACCACTGAGCTAATAGCCC	-	122758
		+	94421
H426	CCCTATTGTTCCGATGGAGA	+	128422
		-	88762
H424	TTTCGACCTTGGTTCCGTAG	+	87764
		-	129420
H422	CTAAAGAGCGTGGAGGTTCG	-	131057
		+	86127
11	CATTTCGCTCGCCGCTACTACGGGAATCGC	+	120664
		-	96510
21	AACAGCAATCCAAGGTCGCATACCCAGACGGA	+	715
W4052	CAAAATAAACAGATCGGT	+	4059
48	CCCCAGAACCAGAAGTAGTAGGATTGATTCT	-	54894
W-2	TTCTCGCTATTTGGAATGGA	-	84119
		+	133065
W90942	AATAAGGTTTGATCCTATTCATGG	+	128104
		-	89076
256	CTGGGGAGGTCCGTTTGATA	+	134992
		-	82192
W-3	AATCCACTGCCTTGATCCAC	-	135373
		+	81811
W3004	TGCTGATACATTAGAAAAATTAAA	+	3015
W7487	TGGATCTGTGCGGTAAGGAAAA	+	7762
W27367	CCGACCTTGTACGATCCC	+	26858
W108608	AAGCACAATAACTACGCCAAG	+	106485
W110557	TAATTCTAACTCCCACATGATAAAA	-	108402
W112176	CGATTCATTTCAATCTGAGGA	+	110020
W114051	TTCGGTTTGATAACCTGCTA	-	111953
W-1	CGAGATCCACCCTACAATA	+	127330
		-	89855
W6509	TTTTGTGTCGTGCAGAGC	+	6770
H465	AGTGGTTCAAGGCGTAGCAT	-	45638
210	GTGTGTATTTTTCGTTGGGGATTT	-	58812
288	ATCAATATATCTGTTATGTAGCTTACCCCTTAGAC	+	56020
129	GCTCTGTAGGATTTGAACCTACGACATC	+	64771
237	AAGTATTTTACGATTAAGAAG	-	67258
264	CCTTTTTCATTGCTTTTCGA	-	80331
W113787	TTGATCCATTCTCATCCTGG	+	111689
W115436	CAAAACGATATCCCAAAGGG	-	113345
212	CAGGAGCAGGGTCGGTCAAAT	-	53910
C011	GGGCTATACGGACTCGAACC	+	51987
374	CATCTCGGAAATATTCAGCCA	-	54141
82	CTATGGAGAAATTGGTAGACACGCTGCTCT	-	106020
C002	GACCCCATACCTAGAGCTAACA	+	103499

H409	GGTGAAATTGGTAGACACGC	-	106024
W108711	TCTCAGTGGTTAATGATGCATG	-	106568
W947	GAAACAGGCTCACGAATACCA	+	947
W2279	GCGAGAAATTGACAAGGTAAGA	-	2290
W4463	TCAAAGTTCTTTCTTTATCTTTAAA	+	4473
W5430	CTATGTCGAGCCAAGAGCATT	-	5441
H481	AATGATGTCGAGCCAAGAGC	+	5439
W7136	GCGTTTGTTTGGCAAGC	+	7391
163	AGGAGAGAGAGGGATTCGAACCCT	+	11614
W13690	AGAACGAATCACACTTTTACCAC	-	13839
162	CATCGGTTCAAATCCGATAAGGGGCT	-	14928
W13308	CGGTTCTAGTAAACCAAAACCA	+	13458
W25288	GCTTTTTCAGCTATTTGTAATTCG	+	24748
W27428	CACACGTACCCGTCATGG	-	26919
W29987	TCAAATTTTCATTGTTAATATGGAC	+	29505
W31365	TTTTGATGCAGCAAGTCAGG	+	30892
146	GCAGCATGGTACTCTTTCTACCACTA	+	34319
W37015	AAAGCCATGAAACAAGTAGCTG	-	36531
W39972	TACTCGAATCAGGATTTTGG	+	39429
W41797	TGTGGTGTGTGAACAAGGAAA	-	41254
42	CTATCTACCAAAATTTTAACTTCTGGTTCCGGC	-	42381
W41549	TATGGCGGTATCCGAAAACA	+	41006
W54841	CGGATACGCCTCCATGA	+	54336
W54225	TCCTGAAGTTCTTTGTAACGTTGT	+	53720
69	CAACCCCTTGGGGTTATCCTGCACTTGGAA	+	135199
		-	81975
W80924	TGACGTGGATTGTATCGATTTC	+	80544
H432	GGGTTATCCTGCACTTGGAA	+	135209
		-	81975
W107400	GCAATAGATGTCTTTCACATACAA	+	105261
260	AAGGATTTACCCGGTGTGAG	-	126720
		+	90464
W94612	TCCCAAGGGCAGGTTCTTAC	+	124455
		-	92729
W95255	CCATCGTTTACGGCTAGGAC	-	123812
		+	93372
W98266	CTTATCTCCAGCCCGTGAAC	+	96137
		-	121047
W100297	GGTCTCCGCAAAGTCGTAAG	-	98177
		+	119007
W105011	CCGTTTCATGAGGATAGACAAA	-	102900
H401	GCCAGTCCAATAGCTGCTTC	+	109763
W18889	TTCTGCCCTAAGACTATGGATT	+	18208
W20819	GGAATGGAAATGAGGGAATG	-	20279
W19456	TTCTGACATCTTAGTCTCGTAGTTT	+	18775
W21210	CTCGGAATTAGACCATAAGGG	-	20670

W20900	GCTTGGCAGAAGAACTTGAGA	+	20360
W22691	GTATGCACCAAAAACCTCGG	-	22151
34	CTCGGGGATGGAAATGAGGGAATATCTACAAT	+	20275
156	AAGATGTGAATTAGGAAGGATTGG	+	21027
W22358	TTGCATGGGAACAGATTCAT	+	21818
W23878	GAAATACTTAATGCTACGATCTGGG	-	23338
W58483	GATTTTAACTTACCCTCTATTTTCG	+	58046
W60385	CTACTAATTCGTTGGGTCTACAA	-	59948
W61165	CCGACCGTATTTCTCCTGA	+	60708
W62668	AGAGATGAACCCAATCCAGAA	-	62212
W62250	GCTAGTTGAGTAGTTTTGATTAAGG	+	61777
W63625	CCCGAAACAGAATTCCTT	-	63169
W72808	TCATCAAGCGGTTCTTATTCG	+	72421
W74664	TTCAATGAGTAGTTATAGGCGCA	-	74261
58	CTGCCGTATTTATGTTAATGCACTTTCCAATG	+	73468
W74410	GCATTCATTTTCTTTGCATCG	+	74007
313	CAATTTTTGTTTTTCTTCTAGACGA	-	46416
W79014	GGTTTAACAACGGCTACCCA	-	78609
W5578	AATGGTATCGAGAATTGATCC	+	5595
W6851	CAAGGAGGTATTTGTGTTTGG	-	7107
W10898	CTAATGCGTTCCCCAACG	+	11056
W12264	ATAGAAAATGAAACGGTCGACC	-	12426
W14720	AATAGTCAAGTACCCATTTCC	-	14317
W32396	GCAAAACTCAGATTGGAGAAGAA	-	31918
W38034	ATCTTGTTGCACCCGGTAAC	+	37504
W39284	GTCTTACCATGAGCAGATTGTAT	-	38741
W57280	TCAGGACTGGGTATCCATGC	+	56831
W58952	TGAATTGGCGATCAGAACAC	-	58510
219	GGCCTAGTATTTCCGGCAAT	-	58082
W65036	CGAACAAATCGAAATGATTGAA	+	64518
W66044	CGTTTATTCCCAGATGCTTT	-	65523
W105880	ACGTGAAGAGGGAATTGTGC	+	103769
W11893	TTTCCAATTAGCTGTTTTTGCAT	+	12056
W12997	CATCGTTAGCTTGGAAGGCT	+	13146
W27717	CGTCGATTACCAAAAACAAGC	+	27208
W30641	TTGGTTGAAAGGCCTGAAAG	+	30159
W36871	GACGTTTCCGCCTATATTCC	+	36387
W38591	GAAAGAGCCACGGGCTTAT	-	38048
W51430	TACCAAAATAGGAATAAGGCTTG	+	50972
W53119	CCCTTGTCAGAGATATCTTAACAT	-	52653
W99809	GTCCATCGACTACGCCTTTC	-	119495
		+	97689
W119602	TGCGGTGACGATACTGTAGG	+	117519
		-	99665
W9275	CTGTTCAATTGCGGCCTTAT	-	9433
W80090	TCCACATCCCTTTAGTTTTGC	+	79683

W82197	TCAAGGCAGTGGATTGTGAA	+	81816
		-	135368
98	ATGAAGCTTATCCCCCATCGTCTC	-	119904
		+	97276
W80234	GGATCTCGACAATACGAAGCA	-	79823
W104124	GCAAGTCTCCGTATCTTATTGG	-	115169
		+	102013
W115355	ATCCCGCCATGAGAAG	+	113264
W16232	GATTCGACTTCCCCTAGGG	-	15546
276	ACCATTAAAGCAGCCCAAGC	-	18086
W17778	AGAATGCAAGTCCTCCCCTT	+	17035
W23499	TGAGCAAGAGGCTTCAAGAAA	+	22959
W25382	ATTGTATGGGAAATACTTCAAGAA	-	24842
W31373	CAGCAAGTCAGGGAAAAAGC	-	30900
W46254	TAGCAAATTACTGTGGTATGTAAAA	-	45806
W48442	GGATAGGTGCAGAGACTCAATG	+	47943
W50280	AGATAACCAACCCTGCTGCA	-	49821
W59953	AACAAATGTCTGGAACTTTGGA	+	59516
W61817	TCCTTATTTCTATCTCATGCAAA	-	61361
242	GGAGATGCAGAAATAGTACTTCAAGA	-	61166
130	GTATTTCTAATAAGTTGTTTAATAGTTGG	-	68318
W67189	GGCTCGTATTTTATCTTTCTTACCA	+	66749
W73004	AAATAGGGAAGAGAAAAGTCAAG	+	72603
W76846	GGGTGATGCTTTTCTTGAGC	+	76439
W78260	GCAATAGTGTCCTTGCCCAT	-	77854
253	GCATTGTCATCATATCGTATTATCA	-	78134
66	AGGGCATTTCCCATTGATATAGGAACTTTT	-	83018
		+	134156
W81925	GGTAGAATGCTAGATGCCCG	+	81544
		-	135640
W77590	ATTTTGACCCTATCCCCCAT	-	77187
W3692	GGCTCTATCCATTTATTCACTAGAC	-	3695
W-4	TTGTTTACGAAGAAATAATAACAA	+	2519
W-5	CAGATCGGTTAAATTTCACTG	-	4068
W34488	ACCGATATTTTAGCAACAAATCTAA	+	33999
W36012	TGCTCGTATTATAGGTCTTGGTGA	-	35528
W-6	TGAATACCGATTTACATTTCCG	+	35250
174	GAGATGGCCGAGTGGTTGAAGGCG	-	45628
W44580	CCTTTGTATGCTCTCCATTGC	+	44024
W45797	GCGTAACGTACCTTATGCAA	+	45331
W47393	GCATTACAAATGCGATGCTC	-	46918
W46864	CAGACCATAATGAAAACGCAAT	+	46398
W49145	TGAAAATCCTCGTGTCACCA	-	48779
W48828	CCTCTATCCCCAAACCCTCT	+	48392
W50130	AGCACATTGGGAACGTAAAT	+	49671
W51362	CCCGATTCATAACTAGAAAGC	-	50904

W-7	CTATCACATCGAACCCGTTC	-	55988
W64314	TTTCTTCTCCTCTTATTCCATATGG	+	63823
W65536	AAAACAAACGCGCTACCAAG	-	65007
128	CCACGTTCTACCGAACTGAACTAAGAGC	-	64812
231	TATAATAGGTAGGGATGACAGGA	-	64959
W67341	GAAACTCCAACCAGAATTTAAGA	-	66901
W-8	TGATCATATATGTATTCCAATAAGG	+	65394
W69005	CCATAAGCTTTGGCTTCGTC	-	68579
W69829	AAGCTACCCATTGCATATTG	+	69428
W71184	GAATTGTGAGAGCGGACGTT	-	70779
W70884	GGGATCAGGGATACTTTCAGC	+	70479
W71750	CGAATCTATGGAAGCATTGG	-	71352
W72170	GGCTACACAAACCGTTGAAGA	-	71750
W122891	TGCTTATTTTCAACTCCCCG	+	120812
		-	96372
W118236	TCGTGAAAAGTGATACCTGTGAA	+	116141
		-	101040
W137891	TCTCACCATCCCCATAGTGT	-	83106
		+	134078
W92021	CGAATTGTTTGTTGACACGG	+	90155
		-	127029
W93455	ATGAGAGAAGCACAGAGGTCA	-	91605
		+	125578
W128213	ATGATCCGATCGATTGC	+	91322
		-	125865
W92518	ATCCTTACTGTCCCTCTACAGAA	-	90652
		+	126529
W130055	ATGGCAAGTGCTCTTCCTTG	+	89467
		-	127717
W125083	TACCACTGAGCTAATAGCCCG	+	122763
		-	94420
W126193	GCCGACACTGACACTGAGAG	+	93312
		-	123872
W124160	CCCGAAAAGGAGTCTATTGA	-	95099
		+	122085
W125409	GCTGGATCACCTCCTTTTCA	+	94096
		-	123088
W118951	CTGGTCGTAGGTTCGAATCC	-	116868
		+	100316
W109967	CCGATAAATCCATGGGATA	-	107812
W111122	GATAGAGCCATGCTGCG	-	108963
W-9	GAACAAAATCTGGATAGATACCGA	+	107390
W110391	TCAATCTTTCCAAATCTAATCC	+	108236
W112816	CCTAGTAGAAGAACAAATCCCC	+	110659
W-10	AGTGGTATCGAGAATTGATCC	+	5595
W-11	TAAGGAGGTATTTTGTCTTTGG	-	7107

W-14	GGGGTTGTATGATATATCAGGC	+	31706
W-15	CAATATATAGAATTCCGGAATTG	-	32778
W31723	GCCATTTTGGGGATTCCTAC	+	31250
W33791	CTGCTGCAGGACAAGCTGTA	-	33315
W-16	GTGGACTAGCACTTGATTTCG	+	55074
W56293	CTTGGCAGCATTCCGAGTA	-	55844
W56344	AGGGGCTGCAGTAGCTG	-	55895
W55204	CAGCTCTAACTCGATTATTTCCTAA	+	54699
W76331	TGGATTCTTCAATACCTACTATTGT	-	75926
W-17	GCCGTCAATGATTGGTGAGC	+	74640
W-18	GCATCTATAGGATAACTTCCATC	+	75655
W116493	CGATGCGAAAGTAATTATGC	-	114411
W-19	GTAAAGAGTTTACACTGCTTATG	+	112950
W115989	TTACATAAAGCTCTTGCTTTGATA	+	113907
W-12	TCCTACGAAAGCATAACAGAAAA	-	15341
W-13	TTCTGACACCTTAACGCATAGTTT	-	18775
W16206	CATCTCTCTTTCAAGGAGGCA	+	15520
W8579	TTAAAAGATAGGCTTTGAAATAGG	+	8742
W10070-1	GGAGCAATGAACCTATTTGAAG	-	10228
W10070	GGAGCAATGAACCTATTTGAAG	+	10228
W11523	ACTCAGCCATCTCTCCACAG	-	11686
W26767	CGGATCCTCAAGGACAAATG	-	26258
W25894	GCTCCGATGGAAACTAGATCA	+	25345
W84777	CGTTTTCATTTACCATCTCATG	+	84368
		-	132814
W88291	GAAGCCCAAAGAGGTGCATA	-	86413
		+	130771
W18055	CCGGTTGGAATCATAAAGTG	-	17314
W71818	TCTTCTTCCGAGAACCACCT	+	71420
W111245	ATTTGCTTGGCTTTACATCC	+	109086
W112337	TTCTAAGTATTTCTTATTGTCGAGC	-	110180
W111787	TTTCTATTCATCTTAATGTTCCG	-	109627
W-20	TTCAATTGGTTAGAGCACCG	+	16076
W-21	TTCTGCCCTAAGACTCTGGATG	-	18208
W133811	TGGGATCGTTTGATCGATTT	-	85692
		+	131492
W135950	GGGTCGCTTCTTATGGACT	+	85030
		-	132155
W-23	TAACGTGAATTGTATCGATTTC	-	80544
W-22	AAGATCTTCTTTTCTCCATCTC	+	16693

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