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Supplementary data

QTL for grain yield under water stress and non-stress conditions over years in rice (*Oryza sativa* L.)

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Supplementary Table 1. Primers used for developing genotypic data

S.No.	Markers	Forward Sequence (5’ --------->3’)	Reverse Sequence (5’ --------->3’)
1	**RM - 499**	TACCAAACACCAACACTGCG	ACCTGCAGTATCCAAGTGTACG
2	**HvSSR 1-24**	ACGCAGTTACACCCACTACT	ATAAGTGCCTATGCATGGTT
3	**HvSSR 1-33**	AACTTGGGCTCTTTAATTCC	CAGAGTTCGAGAGAGACCAG
4	**HvSSR 1-34**	AAACTGGAGATGAACTCGAA	GTAACGAACTAGAGCATGGG
5	**HvSSR 1-49**	TCCTAAAGTTCACACCAACC	TGTCGATTCTCCTTCACTTT
6	**RM - 428**	AACAGATGGCATCGTCTTCC	CGCTGCATCCACTACTGTTG
7	**HvSSR 1-55**	ACACCATACCAATACGAAGG	ACACCGTACTGTTTATTGGG
8	**RM - 84**	TAAGGGTCCATCCACAAGATG	TTGCAAATGCAGCTAGAGTAC
9	**RM - 1**	GCGAAAACACAATGCAAAAA	GCGTTGGTTGGACCTGAC
10	**HvSSR 1-80**	TTTGAGCAAATAAACTTGAGG	GCTTCTACTTCCACAAGGC
11	**HvSSR 1-87**	TTGGTACACGACCATGATTA	ATGGATCTGTGTGTGCGT
12	**HvSSR 1-89**	TGCGACGGATAGAGTACATA	GGATGCAAAGAAAGAACAAG
13	**RM - 259**	TGGAGTTTGAGAGGAGGG	CTTGTTGCATGGTGCCATGT
14	**RM - 243**	GATCTGCAGACTGCAGTTGC	AGCTGCAACGATGTTGTCC
15	**RM - 572**	CGGTTAATGTCATCTGATTGG	TTCGAGATCCAAGACTGACC
16	**RM - 24**	GAAGTGTGATCACTGTAACC	TACAGTGGACGGCGAAGTCG
17	**RM - 449**	TTGGGAGGTGTTGATAAGGC	ACCACCAGCGTCTCTCTCTC
18	**RM - 5**	TGCAACTTCTAGCTGCTCGA	GCATCCGATCTTGATGGG
19	**RM - 212**	CCACTTTCAGCTACTACCAG	CACCCATTTGTCTCTCATTATG
20	**RM - 3825**	AAAGCCCCCAAAAGCAGTAC	GTGAAACTCTGGGGTGTTCG
21	**RM - 302***	TCATGTCATCTACCATCACAC	ATGGAGAAGATGGAATACTTGC
22	**RM - 486**	CCCCCCTCTCTCTCTCTCTC	TAGCCACATCAACAGCTTGC
23	**RM - 14**	CCGAGGAGAGGAGTTCGAC	GTGCCAATTTCCTCGAAAAA
24	**RM - 109**	GCCGCCGGAGAGGGAGAGAGAG	CCCCGACGGGATCTCCATCGTC
25	**RM - 485***	CACACTTTCCAGTCCTCTCC	CATCTTCCTCTCTTCGGCAC
26	**HvSSR 2-1**	AAGAGATGAGAAGAGCAATGA	CAACTTAGAGGAAGAAGGAGG
27	**HvSSR 2-12**	TCTCCAATTCTCCATCAAAC	CTTGCTTGAGCGAGTCTAAT
28	**HvSSR 2-23**	AGCTAGCTACACACTTTCCG	ATAGATGCATGGCGATATTT
29	**HvSSR 2-27**	GGTGCAATTCTTATTCCTTG	AATTTGGATTCAGATGTTGC
30	**HvSSR 2-78**	GTTTCCTTGCAAACAGACAT	AGTCATTCTAGCATTTCCCA
31	**RM - 174**	AGCGACGCCAAGACAAGTCGGG	TCCACGTCGATCGACACGACGG
32	**RM - 492**	CCAAAAATAGCGCGAGAGAG	AAGACGTACATGGGTCAGGC
33	**RM - 475**	CCTCACGATTTTCCTCCAAC	ACGGTGGGATTAGACTGTGC
34	**RM - 341**	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC
35	**RM - 221**	ACATGTCAGCATGCCACATC	TGCAAGAATCTGACCCGG
36	**HvSSR 3-6**	AGATGAGCTTCAGTGCTAGG	TTCACCACAAAGTTCACAAA
37	**HvSSR 3-9**	TGTATTCAAGGAGGGCTAGA	CAACTGTTTCCTGGAATGAT
38	**HvSSR 3-35**	TTGATTACGTGAATAGCTCG	CATAGCTAACTTGTGCGTTG
39	**HvSSR 3-40**	CGAGAGGTTCAGAGAGAATG	GCATTCACCCTAAGGATACA
40	**HvSSR 3-41**	ATGCAATTACTTGTTGCCTT	AAGTTCTGAACAACCACCAC
41	**RM - 231**	CCAGATTATTTCCTGAGGTC	CACTTGCATAGTTCTGCATTG
42	**HvSSR 3-56**	GCCTATCAGGCTATCATCAC	GTGATCGACATTGAGGAGTT
43	**HvSSR 3-71**	CACACCAACTCACTCTTGAA	CCGTTTCGTCTATGTTCATT

44	**HvSSR 3-85**	GCAAACGACACAAGTCATTA	ATAGTGCCCTTTCTTTCACA
45	**RM - 517**	GGCTTACTGGCTTCGATTTG	CGTCTCCTTTGGTTAGTGCC
46	**RM - 7**	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTCGTTGTT
47	**RM - 232**	CCGGTATCCTTCGATATTGC	CCGACTTTTCCTCCTGACG
48	**RM - 411**	ACACCAACTCTTGCCTGCAT	TGAAGCAAAAACATGGCTAGG
49	**RM - 135**	CTCTGTCTCCTCCCCCGCGTCG	TCAGCTTCTGGCCGGCCTCCTC
50	**RM - 55**	CCGTCGCCGTAGTAGAGAAG	TCCCGGTTATTTTAAGGCG
51	**RM - 85**	CCAAAGATGAAACCTGGATTG	GCACAAGGTGAGCAGTCC
52	**RM - 307**	GTACTACCGACCTACCGTTCAC	CTGCTATGCATGAACTGCTC
53	**HvSSR 4-26**	GAGGAATTCATTCATCATGC	ATTTCGTTATTTGCATTGGT
54	**HvSSR 4-35**	ACCAACCTAATACCGATGTG	CGCGAGTGTTGTAACTTTAAC
55	**HvSSR 4-38**	CCAAGCACCTCTTAACTTGA	CCGTTCTTATTAGGTTGTGG
56	**HvSSR 4-39**	CAAATAAGATCGCTGAAACC	TTCGGAGTAAATTGGACATC
57	**HvSSR 4-42**	GATGGTGAATCTCGGTCTAA	TGTCCCATCATCACAAACTA
58	**RM - 564**	CATGGCCTTGTGTATGCATC	ATGCAGAGGATTGGCTTGAG
59	**RM - 273**	GAAGCCGTCGTGAAGTTACC	GTTTCCTACCTGATCGCGAC
60	**RM - 348**	CCGCTACTAATAGCAGAGAG	GGAGCTTTGTTCTTGCGAAC
61	**RM - 317**	CATACTTACCAGTTCACCGCC	CTGGAGAGTGTCAGCTAGTTGA
62	**RM - 559**	ACGTACACTTGGCCCTATGC	ATGGGTGTCAGTTTGCTTCC
63	**HvSSR 5-13**	TCCTCTACAGTTGTCTGCCT	CATTCCTCTCCACTTTCTTG
64	**HvSSR 5-23**	GCAGCCATCTATCATCTAGC	CTAGCTGCACCAGTTTGATT
65	**HvSSR 5-31**	TGGAGCTGTGTTGTTGATTA	ATTGTGACATGCTGATGTTG
66	**HvSSR 5-39**	TGAGAGGATACTTGGGACTG	CCAGCATGCAACTGTAACTA
67	**HvSSR 5-48**	GAATTGAAGGTGGGACATAA	GAAGATGGCATGTAAACGAT
68	**HvSSR 5-51**	CCATGAAATAGTTCTAGGGAA	TAATTAATGCCTTCGTGGAT
69	**HvSSR 5-52**	GCTTAGTACTTGCGGCTAAA	CCATCTTACATGTCCTCACC
70	**HvSSR 5-56**	AAACTATCCGCTTGTGAAAT	CCGGTTAAGGACTCCTATCT
71	**HvSSR 5-65**	ATTAAACGCACACTGGAAGT	AAACGGAGGGAGTAGTTAGC
72	**HvSSR 5-66**	GTTATGCGCTTCTGCTTATT	AGTTGGCTTCTGGATTACAA
73	**RM - 163**	ATCCATGTGCGCCTTTATGAGGA	CGCTACCTCCTTCACTTACTAGT
74	**RM - 440**	CATGCAACAACGTCACCTTC	ATGGTTGGTAGGCACCAAAG
75	**RM - 459**	CTGCAATGCTGCATGACC	CACTTTCTCTGCAGCACCAG
76	**RM - 188**	TCCGCCTCTCCTCTCGCTTCCC	GCAACGCACAACCGAACCGAGC
77	**RM - 421**	AGCTCAGGTGAAACATCCAC	ATCCAGAATCCATTGACCCC
78	**RM - 178**	TCGCGTGAAAGATAAGCGGCGC	GATCACCGTTCCCTCCGCCTGC
79	**RM - 26**	GAGTCGACGAGCGGCAGA	CTGCGAGCGACGGTAACA
80	**RM - 274**	CCTCGCTTATGAGAGCTTCG	CTTCTCCATCACTCCCATGG
81	**RM - 87**	CCTCTCCGATACACCGTATG	GCGAAGGTACGAAAGGAAAG
82	**HvSSR 6-35**	GAAAGGAAATCAGGTTGTGA	CCCATTAGACATTTCGGATA
83	**HvSSR 6-44**	GGAGCATCCATCACAATATC	GTAATTTCAGTCAGCCAAGC
84	**HvSSR 6-56**	AGCATTTGTGTGTGCAATAG	ATGCTTGCCTCATCAGTAGT
85	**RM - 225**	TGCCCATATGGTCTGGATG	GAAAGTGGATCAGGAAGGC
86	**HvSSR 6-65**	GTGTGGCAATTTAACATCCT	TTGTTGCTTGTTCTTCACTG
87	**RM - 217**	ATCGCAGCAATGCCTCGT	GGGTGTGAACAAAGACAC
88	**RM - 136**	GAGAGCTCAGCTGCTGCCTCTAGC	GAGGAGCGCCACGGTGTACGCC
89	**RM - 340**	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC
90	**RM - 400**	ACACCAGGCTACCCAAACTC	CGGAGAGATCTGACATGTGG
91	**RM - 481**	TAGCTAGCCGATTGAATGGC	CTCCACCTCCTATGTTGTTG
92	**HvSSR 7-40**	GATTTACTCGCAAGTTACCG	TGTTTCAGGTTCGTCTATCC
93	**HvSSR 7-43**	CAACTCAGTTCCAATCCCTA	TTGTGTGTTTCATATACGGC
94	**HvSSR 7-46**	ACAGCTGTAGAGGATGAGGA	TCCCTAATTCGAATCACAAC
95	**RM - 125**	ATCAGCAGCCATGGCAGCGACC	AGGGGATCATGTGCCGAAGGCC
96	**HvSSR 7-53**	CGAGCATGTCTGTCAAGTAA	GTTCGAATGTAATGTTGGCT
97	**RM - 2**	ACGTGTCACCGCTTCCT	ATGTCCGGGATCTCATCG
98	**RM - 11**	TCTCCTCTTCCCCCGATC	ATAGCGGGCGAGGCTTAG
99	**RM - 234**	ACAGTATCCAAGGCCCTGG	CACGTGAGACAAAGACGGAG
100	**RM - 248**	TCCTTGTGAAATCTGGTCCC	GTAGCCTAGCATGGTGCATG
101	**RM - 337**	GTAGGAAAGGAAGGGCAGAG	CGATAGATAGCTAGATGTGGCC

102	**RM - 152**	GAAACCACCACACCTCACCG	CCGTAGACCTTCTTGAAGTAG
103	**HvSSR 8-29**	AACTGAGAGGCTGCTTGTAT	TAAAGGGTTCACTCATGGAC
104	**RM - 310**	CCAAAACATTTAAAATATCATG	GCTTGTTGGTCATTACCATTC
105	**RM - 44**	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCTACC
106	**RM - 483**	CTTCCACCATAAAACCGGAG	ACACCGGTGATCTTGTAGCC
107	**RM - 72**	CCGGCGATAAAACAATGAG	GCATCGGTCCTAACTAAGGG
108	**RM - 515**	TAGGACGACCAAAGGGTGAG	TGGCCTGCTCTCTCTCTCTC
109	**RM - 256**	GACAGGGAGTGATTGAAGGC	GTTGATTTCGCCAAGGGC
110	**RM - 230**	GCCAGACCGTGGATGTTC	CACCGCAGTCACTTTTCAAG
111	**RM - 433**	TGCGCTGAACTAAACACAGC	AGACAAACCTGGCCATTCAC
112	**RM - 281**	ACCAAGCATCCAGTGACCAG	GTTCTTCATACAGTCCACATG
113	**HvSSR 9-5**	GAACGGAGGGAGGTTGTT	AAAGTGTCCTAAAGCCAAGTC
114	**RM - 444**	GCTCCACCTGCTTAAGCATC	TGAAGACCATGTTCTGCAGG
115	**HvSSR 9-7**	CATCTCAGCAAACAAGAACA	GTAAAGACTCCAGCTTTCTCC
116	**HvSSR 9-19**	TCGAATTTAGTCCAGGGTAA	GGTGAGAGATCTTGAGTTCG
117	**HvSSR 9-25**	GATCGATCTCATCATCACCT	TAGCTTCCTACTGGGAGTGA
118	**HvSSR 9-27**	TGGGCATCTGGTACTATCTT	AGCTCATTCCACAGGTTAGA
119	**HvSSR 9-37**	AATCTCAACTGCTCGGATTA	TTGATTGATTGATTGAACGA
120	**HvSSR 9-57**	GGAGGTTGTTGTTACGTTGT	GGGAGGGTAATTCAGGTAAG
121	**RM - 296**	CACATGGCACCAACCTCC	GCCAAGTCATTCACTACTCTGG
122	**RM - 434**	GCCTCATCCCTCTAACCCTC	CAAGAAAGATCAGTGCGTGG
123	**RM - 410**	GCTCAACGTTTCGTTCCTG	GAAGATGCGTAAAGTGAACGG
124	**RM - 108**	TCTCTTGCGCGCACACTGGCAC	CGTGCACCACCACCACCACCAC
125	**RM - 242**	GGCCAACGTGTGTATGTCTC	TATATGCCAAGACGGATGGG
126	**RM - 288**	CCGGTCAGTTCAAGCTCTG	ACGTACGGACGTGACGAC
127	**RM - 553**	AACTCCACATGATTCCACCC	GAGAAGGTGGTTGCAGAAGC
128	**RM - 278**	GTAGTGAGCCTAACAATAATC	TCAACTCAGCATCTCTGTCC
129	**RM - 201**	CTCGTTTATTACCTACAGTACC	CTACCTCCTTTCTAGACCGATA
130	**RM - 245**	ATGCCGCCAGTGAATAGC	CTGAGAATCCAATTATCTGGGG
131	**HvSSR 10-1**	ATGTATCGCTCGACAGATTT	CCGATTCATTGATGATTTCT
132	**HvSSR 10-5**	TCTCGCTCACTACCAGACTT	AATTTCGCTTCACATCACTT
133	**HvSSR 10-17**	CGTCTTGAATCAATTTCCAT	GATTGCCCGTAGAACTATTG
134	**RM - 222**	CTTAAATGGGCCACATGCG	CAAAGCTTCCGGCCAAAAG
135	**HvSSR 10-34**	TAGACCGAGGAATTGAAAGA	TTTGGGCTTATTGTCAGTTT
136	**RM - 171**	AACGCGAGGACACGTACTTAC	ACGAGATACGTACGCCTTTG
137	**RM - 228**	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC
138	**RM - 484**	TCTCCCTCCTCACCATTGTC	TGCTGCCCTCTCTCTCTCTC
139	**HvSSR 11-1**	TGTGTGTCCGCATACTTAAA	ATGTCAAAGTCCGAAAGTGT
140	**HvSSR 11-2**	TAGATTGGGTGATGGATAGC	CTACTTGATCCAGGGAAATG
141	**HvSSR 11-3**	GGTTGACACCGTTAACATTT	TGGAACTACCTACCTAGCCA
142	**HvSSR 11-13**	TGAAACCACAATGAGTCAAA	GCCCTAAACCCAAATAGAAG
143	**RM - 202**	CAGATTGGAGATGAAGTCCTCC	CCAGCAAGCATGTCAATGTA
144	**RM - 229**	CACTCACACGAACGACTGAC	CGCAGGTTCTTGTGAAATGT
145	**RM - 21**	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG
146	**RM - 26334**	GACTCCCTACTAGTGGTTCTGATTCG	CCTTTGACGATTGTGATGCTACG
147	**RM - 206**	CCCATGCGTTTAACTATTCT	CGTTCCATCGATCCGTATGG
148	**RM - 254**	AGCCCCGAATAAATCCACCT	CTGGAGGAGCATTTGGTAGC
149	**RM - 224**	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCGGG
150	**RM - 20**	ATCTTGTCCCTGCAGGTCAT	GAAACAGAGGCACATTTCATTG
151	**HvSSR 12-35**	ATGACCATAATCCCAACAAA	GTCGTGGTGTTATTCTTGGT
152	**HvSSR 12-36**	ATCAGCGACTAAGGATCTCA	CTAATGTTGCCACATACGAA
153	**HvSSR 12-40**	ATCTAACAACAACAATCCCG	CATCTTCATCCCTCGTGTAT
154	**HvSSR 12-48**	AAACTCGATCAGACTTAGAGAAG	TCTCTGATGGCAATACAACA
155	**HvSSR 12-51**	AATCATCATATTGCCGAAAG	ATCACCATCTATCATTGCAC
156	**RM - 277**	CGGTCAAATCATCACCTGAC	CAAGGCTTGCAAGGGAAG
157	**RM - 511**	CTTCGATCCGGTGACGAC	AACGAAAGCGAAGCTGTCTC
158	**RM - 260**	ACTCCACTATGACCCAGAG	GAACAATCCCTTCTACGATCG
159	**RM - 519**	AGAGAGCCCCTAAATTTCCG	AGGTACGCTCACCTGTGGAC

160	**RM - 28305**	GTCATCTTCGCAAATGGTGATGG	GGTCGTCGTGGTGTTATTCTTGG
161	**RM - 270**	GGCCGTTGGTTCTAAAATC	TGCGCAGTATCATCGGCGAG
162	**RM - 17**	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA