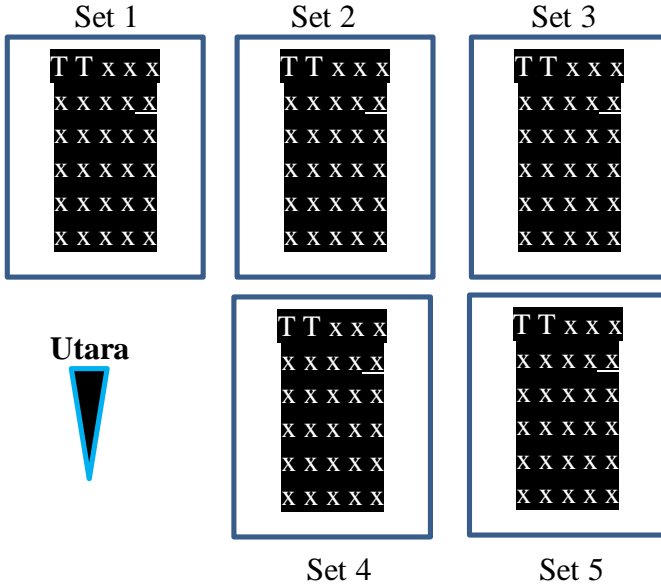


# LAMPIRAN

## Lampiran 1. Bagan di rumah kaca



Ket:  
T: Tetua  
X: Sampel

### Lampiran 2. Benih yang ditanam

Set	Varietas/ Galur	Persilangan	Kode	Jumlah	Ket
Set 1&2	Situ Bagendit	Tatua	1	3	Bak 1, 2, 3 dan 4
	Cabacu	Kontrol	2	3	
	77	BC1F <sub>1</sub> Situ Bagendit /Cabacu	SBC- 1	28	
	88	BC1F <sub>1</sub> Situ Bagendit /Cabacu	SBC- 2	28	Bak 3 dan Bak 4
	89	BC1F <sub>1</sub> Situ Bagendit /Cabacu	SBC- 3	28	
	91	BC1F <sub>1</sub> Situ Bagendit /Cabacu	SBC- 4	28	
	93	BC1F <sub>1</sub> Situ Bagendit /Cabacu	SBC- 5	28	

### Lampiran 3. Daftar primer *background*

No	Primer	Posisi	Kromosom	Sekuens	Ukuran
1	RM1282	4.2-4.2	1	F: AAGCATGACAGCTGCAAGAC	157
				R: GGGGATGAAGGGTAATTTTCG	
2	RM24	78.4- 78.4	1	F: GAAGTGTGATCACTGTAACC	192
				R: TACAGTGGACGGCGAAGTCG	
3	RM3475	107.6- 107.6	1	F: GTCGGTTTGCCTAGTTGAGC	150
				R: TTCCTCGGTGTATGGGTCTC	
4	RM3817	122.1- 122.1	1	F: AAGGAAGGGGAAGCTGAGAG	207
				R: CGGACTCGAGAAAAAAGCAG	
5	RM431	178.3- 178.3	1	F: TCCTGCGAACTGAAGAGTTG	251
				R: AGAGCAAAACCTGGTTTAC	
6	RM165	197.8- 197.8	1	F: CCGAACGCCTAGAAGCGCGTCC	185
				R: CGGCGAGGTTTGCTAATGGCGG	
7	OSR17	1.1-1.1	2	F: GCTGGTTGATTACAGTAGTC	0
				R: GCCTCGTTGTCGTTACCACAC	

8	RM211	14.4-14.4	2	F: CCGATCTCATCAACCAACTG	161
				R: CTTACAGAGGATCTCAAAGG	
9	RM233A	16.3-16.3	2	F: CCAAATGAACCTACATGTTG	162
				R: GCATTGCAGACAGCTATTGA	
10	RM1075	17.6-17.6	2	F: CCAGTTCAGTAGTTCACACACC	200
				R: GTTGGGTTGCTGTGTGTTC	
11	RM438	58.4-66	2	F: CTTATCCCCCGTCTCTCTC	137
				R: CTCTCTGCCACCGATCTAC	
12	OSR4		2	F: TGGGATGCAGAGTGCAGTTGGC	346
				R: CGCAGGCACGGTGCCTTGTAAG	
13	RM1942	102.6-102.6	2	F: CTGCTCAATGATACAGGA	132
				R: GGCATCCACTAAATTTAGATA	
14	RM1920	103.4-103.4	2	F: CAAACACAGTGTGACAGAA	127
				R: GCTATTGACTTATCCGTTCA	
15	RM497	150.8-150.8	2	F: TCCTCTTACCTATGGGTGG	213
				R: GCCAGTGCTAGGAGAGTTGG	
16	RM530	158-158	2	F: GCACTGACCACGACTGTTTG	161
				R: ACCGTAACCCGATCTATCC	
17	RM250	170.1-170.1	2	F: GGTTCAAACCAAGCTGATCA	153
				R: GATGAAGGCCTTCCACGCAG	
18	RM208	172.7-172.7	2	F: TCTGCAAGCCTTGTCTGATG	178
				R: TAAGTCGATCATTGTGTGGACC	
19	RM138	196.8-196.8	2		233
20	RM263	127.5-127.5	2	F: CCCAGGCTAGCTCATGAACC	199
				R: GCTACGTTTGAGCTACCACG	
21	RM266	192.2-192.2	2	F: TAGTTTAACCAAGACTCTC	127
				R: GGTGAACCCAAATCTGCA	
22	RM523	11.0-13	3	F: AAGGCATTGCAGCTAGAAGC	148
				R: GCACTTGGGAGGTTTGCTAG	
23	RM22	7.2-7.2	3	F: GGTTTGGGAGCCATAATCT	194

				R: CTGGGCTTCTTTCACCTCGTC	
24	RM569	11.0- 11.0	3	F: GACATTCTCGCTTGCTCCTC	175
				R: TGTCCCCTCTAAAACCCTCC	
25	RM545	35.3- 35.3	3	F: CAATGGCAGAGACCCAAAAG	226
				R: CTGCATGTAACGACAGTGG	
26	RM232	76.7- 76.7	3	F: CCGGTATCCTTCGATATTGC	158
				R: CCGACTTCTCTCCTGACG	
27	RM554	100.6- 100.6	3	F: GTTCGTCCGTCTCTCGTCTC	259
				R: CCCAAAATCTGTGCCTCTC	
28	RM165	131.5- 131.5	3	F: CGCTAGGGCAGCATCTAAA	181
				R: AACACAGCAGGTACGCGC	
29	RM426	157.3- 157.3	3	F: ATGAGATGAGTTCAAGCCC	150
				R: AACTCTGTACCTCCATCGCC	
30	RM532		3		180
31	RM504	138.8- 138.8	3	F: TCTATAATGTAGCCCCCCC	180
				R: TTTCAGGGGCTTCTACCAAC	
32	RM448	189.6- 191.6	3	F: TCTGATCTTGATGCAGGCAC	228
				R: TCTCCCATTGGACAGATC	
33	RM520	191.6- 191.6	3	F: AGGAGCAAGAAAAGTTCCCC	247
				R: GCCAATGTGTGACGCAATAG	
34	RM143	207.3- 207.3	3	F: GTCCCGAACCTAGCCCGAGGG	207
				R: AGAGGCCCTCCACATGGCGACC	
35	RM514	216.4- 216.4	3	F: AGATTGATCTCCCATTCCCC	259
				R: CACGAGCATATTACTAGTGG	
36	RM570	221.1- 221.1	3	F: GTTCTTCAACTCCCAGTGCG	208
				R: TGACGATGTGGAAGAGCAAG	
37	RM442	224.2- 224.2	3	F: CTTAAGCCGATGCATGAAGG	257
				R: ATCCTATCGACGAATGCACC	
38	RM401	63.4- 63.4	4	F: TGGAACAGATAGGGTGTAAAGGG	283
				R: CCGTTCACAACACTATACAAGC	

39	RM537	8.5-21.5	4	F: CCGTCCCTCTCTCTCCTTC	236
				R: ACGGGAAACCATCCATCCTCCTC	
40	RM564	73.1-73.1	4	F: CATGGCTTGTGTATGCATC	228
				R: ATGCAGAGGATTGGCTTGAG	
41	RM564A	73.1-73.1	4	F: CATGGCTTGTGTATGCATC	228
				R: ATGCAGAGGATTGGCTTGAG	
42	RM303	116.9-116.9	4	F: GCATGGCCAAATATTAAGG	200
				R: GGTTGGAAATAGAAGTTCGGT	
43	RM255	120.8-120.8	4	F: TGTTGCGTGTGGAGATGTG	144
				R: CGAAACGGCTCAGTTCAAC	
44	RM217	38.5-38.5	4	F: ATCGCAGCAATGCCTCGT	133
				R: GGGTGTGAAXAAGACAC	
45	RM131	148.5-148.5	4	F: TCCTCCCTCCCCTTCGCCACTG	215
				R: CGATGTTCCGCATGGCTGCTCC	
46	RM307	0-0	4	F: GTECTACCGACCTACCGTTCAC	174
				R: CTGCTATGCATGAACGTCTC	
47	RM437	18.2-18.2	5	F: ACACCAACCAGATCAGGGAG	275
				R: TGCTCGCAATGGTGAGTTC	
48	RM245	86.5-86.5	5	F: GTTGCACTACGTATTCTGAG	245
				R: GATCCAGATAAATGAGGCAC	
49	RM163	91.4-91.4	5	F: ATCCATGTGCGCCTTATGAGGA	124
				R: CGCTACCTCCTTCACTTACTAGT	
50	RM233B	16.3-16.3	5	F: CCAAATGAACCTACATGTTG	55
				R: GCATTGCAGACAGCTATTGA	
51	RM274	126.6-126.6	5	F: CCTCGCTTATGAGAGCTTCG	160
				R: CTTCTCCATCACTCCCATGG	
52	RM406	156.3-156.3	5	F: GAGGGAGAAAGTGGACATG	146
				R: TGTGCTCCTTGGGAAGAAAG	
53	RM540	0-0	6	F: GCCTTCTGGCTCATTTATGC	172
				R: CTAGGCCTGCCAGATTGAAC	
54	RM435	2.2-2.2	6	F: ATTACGTGCATGTCTGGCTG	166

				R: CGTACCTGACCATGCATCTG	
55	RM588		6		126
56	RM586	7.4-7.4	6	F: ACCTCGCGTTATTAGGTACCC R: GAGATACGCCAACGAGATACC	271
57	RM111	35.3-35.3	6	F: CACAACCTTTGAGCACCGGGTC R: ACGCCTGCAGTTGATCACCGG	124
58	RM276	30.8-30.8	6	F: CTCAACGTTGACACCTCGTG R: TCCTCCATCGAGCAGTATCA	149
59	RM549	42.7-42.7	6	F: ACGAACTGATCATATCCGCC R: CTGTGGTTGATCCCTGAACC	148
60	RM3431	43.4-43.4	6	F: ATCCAAATCCAATGGTGC R: GCGAAAGGGAACATTCTG	161
61	RM539	45.1-45.1	6	F: GAGCGTGGTTGTTAAAACCG R: AGTAGGGTATCACGCATCCG	272
62	RM3330	61.6-61.6	6	F: ATTATCCCCTCTTCCGCTC R: AAGAAACCCTCGGATTCCTG	145
63	RM465B	79.2-79.2	6	F: GTGCCCTCCATCATCATCATC R: TAGGACAAGCGAAGAAACCG	212
64	RM1340	82.9-82.9	6	F: TCCAACTAGTGGGAACGC R: CTCAACGCATGAACCTC	163
65	RM162	114.9-114.9	6		229
66	RM1370	137.2-137.2	6	F: AAACGAGAACCAACCGACAC R: GGAGGGAGGAATGGGTACAC	173
67	RM400	134.5-134.5	6	F: ACACCAGGCTACCCAAACTC R: CGGAGAGATCTGACATGTGG	321
68	OSR21	143.7-143.7	6	F: TTTCTTTGGCCACAGGCGA R: CCCAGATTCGGAACAAGAAGAAC	0
69	RM481	3.2-3.2	7	F: TAGCTAGCCGATTGAATGGC R: CTCCACCTCCTATGTTGTTG	169

70	RM501	30.1-34.7	7	F: GCCCAATTAATGTACAGGCG	179
				R: ATATCGTTAGCCGTGCTGC	
71	RM325B	33.3-33.3	7	F: GACGATGAATCAGGAGAACG	201
				R: GGCATGCATCTGAGTAATGG	
72	RM500	77.3-77.3	7	F: GAGCTTGCCAGAGTGGAAAG	259
				R: GTTACACCGAGAGCCAGCTC	
73	RM418	42.1-42.1	7	F: TCGCGTATCGTCATGCATAG	283
				R: GAGCACATATGCCACGTACG	
74	RM1186	42.8-42.8	7	F: AATAATCTGAGCCAGCTGCG	108
				R: CTGCGGGTAGGCAGCTATAC	
75	RM336	61-61	7	F: CTTACAGAGAAACGGCATCG	154
				R: GCTGGTTGTTCAGGTTTCG	
76	RM505	78.6-78.6	7	F: GAGTTATGAGCCGGGTGTG	199
				R: GATTTGGCGATCTTAGCAGC	
77	RM478	93.8-93.8	7	F: CAGCTGGGGAAGAGAGAGAG	205
				R: CAGAACTAAACGCACCCC	
78	RM429	131.4-131.4	7	F: TCCCTCCAGCAATGTCTTTC	159
				R: CCTTCATCTTGCTTTCACC	
79	RM337	0.1-0.1	8	F: GTAGGAAAGGAAGGGCAGAG	192
				R: CGATAGATAGCTAGATGTGGCC	
80	RM1295	13.35-13.35	8	F: GAGAAGAGGTGGAAGTTGAA	134
				R: GACGGAAGAATTCTTAATGG	
81	RM2819	26.3-26.3	8	F: AATGTTGCTAGATTTAAAC	182
				R: CAGTAGGATATCTTACAACC	
82	RM310	57-57	8	F: CCAAAAACATTTAAAATATCATG	105
				R: GCTTGTGGTCATTACCATTTC	
83	RM547	27.3-27.3	8	F: TAGGTTGGCAGACCTTTTCG	235
				R: GTCAAGATCATCCTCGTAGCG	
84	RM72	60.9-60.9	8	F: CCGGCGATAAAACAATGAG	166
				R: GCATCGGTCTAACTAAGGG	
85	RM339		8	F: GTAATCGATGCTGTGGGAAG	148

		72.2-72.2		R: GAGTCATGTGATAGCCGATATG	
86	RM42	78.4-78.4	8	F: ATCCTACCGCTGACCATGAG	166
				R: TTTGGTCTACGTGGCGTACA	
87	RM223	80.5-80.5	8	F: GAGTGAGCTTGGGCGYAAAAC	165
				R: GAAGGCAAGTCTTGGCACTG	
88	RM531	90.3-90.3	8	F: GAAACATCCCATGTTCCAC	128
				R: TCGGTTTTTCAGACTCGGTC	
89	RM340	133.5-133.5	8	F: GGTAATGGACAATCCTATGGC	163
				R: GACAAATATAAGGGCAGTGTGC	
90	RM408	0.1-1	8	F: CAACGAGCTAACTTCCGTCC	128
				R: CTGCTACTTGGGTAGCTGACC	
91	RM404	60.9-60.9	8	F: CCAATCATTAAACCCCTGAGC	236
				R: GCTTCATGCTTCAGAAGAC	
92	RM149	122.1-122.1	8		253
93	RM316	1.8-1.8	9	F: CTAGTTGGGCATACGATGGC	192
				R: ACGCTTATATGTTACGTCAAC	
94	RM321	32.1-32.1	9	F: CTAGTTGGGCATACGATGGC	200
				R: ACGCTTATATGTTACGTCAAC	
95	RM1553	68.2-68.2	9	F: AATTAGAGGGTCCACATGTC	161
				R: ATTACCTCATTTTCTACGC	
96	RM242	73.3-73.3	9	F: GGCCAACGTGTGTCTGTCTC	225
				R: TATATGCCAAGACGGATGGG	
97	RM1026	102.3-102.3	9	F: GCCTCTGGCAGAATAGCATC	164
				R: TATCACTTTGCTGCCTAGGC	
98	RM105	32.1-32.1	9	F: GTCGTGACCCATCGGAGCCAC	134
				R: TGGTCGAGGTGGGGATCGGGTC	
99	RM474	0-0	10	F: AAGATGTACGGGTGGCATTTC	252
				R: TATGAGCTGGTGAGCAATGG	
100	RM330A	60.9-60.9	10	F: CAATGAAGTGATCTCGGAG	177
				R: CATCAATCAGCGAAGGTCC	



101	RM5348	15.7- 15.7	10	F: AATCCGATAGGAGTACCGCC	183
				R: AAGTGTATGGGCTGGAATGG	
102	RM1375	80.8- 80.8	10	F: CTACACGCGCAAACCTCTGTC	180
				R: ATGAAGGTCTAGGCTGCACC	
103	RM596	54.7- 54.7	10	F: ATCTACAGGACGAATTGCC	188
				R: AGAAGCTTCAGCCTCTGCAG	
104	RM1374	72.8- 72.8	10	F: TAGATATGTTGGGCCGGAAG	168
				R: AGATCGATGCCGTTTCAGAC	
105	RM328	82.4- 82.4	10	F: CATAGTGGAGTATGCAGCTGC	172
				R: CCTTCTCCCAGTCGTATCTG	
106	RM222	11.3- 11.3	10	F: CTTAAATGGGCCACATGCG	213
				R: CAAAGCTTCCGGCCAAAAG	
106	RM244	15-15	10	F: CCGACTGTTTCGTCTTATCA	163
				R: CTGCTCTCGGGTGAACGT	
107	RM311	25.2- 25.2	10	F: TGGTAGTATAGGTAACAAAT	179
				R: TCCTATACACATACAAACATAC	
108	RM3717	4.8-4.8	11	F: AGCTCTACCTTTGCTGTCGG	123
				R: AACTCCCTAGACCCACCTGC	
109	RM1240	6.5-6.5	11	F: CCATGAGCTAGTAACTGCAGC	215
				R: GGATCGCAAAATCTGGCATC	
110	RM1812	10.3- 10.3	11	F: CAGCTAGTGAGCTCCTAGTG	136
				R: GCTAACCCACCAACTTATTC	
111	RM552	40.6- 40.6	11	F: CGCAGTTGTGGATTCAGTG	195
				R: TGCTCAACGTTTGACTGTCC	
112	RM441	43.9- 43.9	11	F: ACACCAGAGAGAGAGAGAGAGAG	189
				R: TCTGCAACGGCTGATAGATG	
113	RM1341	80.2- 80.2	11	F: AACCTGGAGGTGCTGGTCTC	183
				R: TTTCTCCCCCAACCAC	
114	RM21	85.7- 85.7	11	F: ACAGTATTCCGTAGGCACGG	157
				R: GCTCCATGAGGGTGGTAGAG	
115	RM4B	0-0	11	F: TTGACGAGGTCAGCACTGAC	159

				R: AGGGTGTATCCGACTCATCG	
116	RM286	0-0	11	F: GGCTTCATCTTTGGCGAC	110
				R: CCGGATTCACGAGATAACTC	
117	RM20A	3.2-3.2	12	F: ATCTTGTCCTGCAGGTCAT	140
				R: GAAACAGAGGCACATTTTCATTG	
118	RM4A	5.2-5.2	12	F: TTGACGAGGTCAGCACTGAC	159
				R: AGGGTGTATCCGACTCATCG	
119	RM6998		12	F: AGATGATAAGCTTGCGGACC	211
				R: ATGCAGATGAGTCCCTCCAC	
120	RM453	28.2- 28.2	12	F: CGCATCTCTCTCCCTTATCG	178
				R: CTCTCCTCCTCGTTGTGTCGTC	
121	RM453	38.1- 38.1	12	F: CTTGGTATGTATTGGCAGCG	196
				R: GAGGCAATAGGAGGGGAGAG	
122	RM3103	47-47	12	F: CAGACAACTTGTAAATGTACG	218
				R: ATGTCATGGGAGATAAATTA	
123	RM1036	48.2- 48.2	12	F: CTCATTTGTGCGATTGCCGTC	146
				R: ATGGGAGGAGTGATCAAACG	
124	RM511	59.8- 59.8	12	F: CTTCGATCCGGTGACGAC	130
				R: AACGAAAGCGAAGCTGTCTC	
125	RM519	62.6- 62.6	12	F: AGAGAGCCCTAAATTTCCG	122
				R: AGGTACGCTCACCTGTGGAC	
126	RM1246	65.3- 65.3	12	F: CTCGATCCCCTAGCTCTC	162
				R: TCACCTCGTTCTCGATCC	
127	RM309	74.5- 74.5	12	F: GTAGATCACGCACCTTCTGG	169
				R: AGAAGGCCTCCGGTGAAG	
128	RM1130	91.4- 91.4	12	F: CAGCTGCTGCTACTACACCG	216
				R: CTACTCCACGTCCATGCATG	
129	RM1296	108.2- 108.2	12	F: CAGCTAGCACTGATCAAATAAG	192
				R: GAAATTAACCAAGTTGGATTG	
130	RM1226	109.2- 109.2	12	F: TCCCTCACCTCACTCTCAC	103
				R: TCTTGTGCTTGTGCTGTCC	

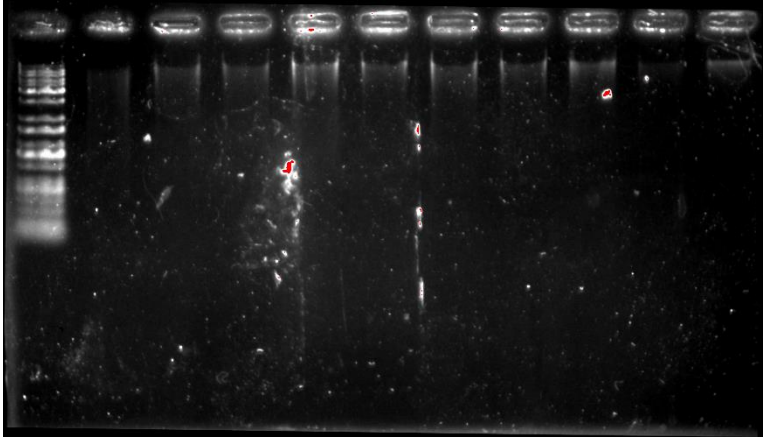
131	RM1226	130.8- 130.8	12	F: CATGGTAGCACACACCCTTG	176
				R: CATCGACATGTGGACCACTC	

average -: 17.5 cM; 1.0 %  
average A: 15.6 cM; 0.9 %  
average B: 749.3 cM; 44.3 %  
average H: 910.1 cM; 53.8 %  
Average # of recombinations(1): 48.5

#### Lampiran 4. Daftar Primer Foreground

1	RM13596	98.25- 98.25	2	F: TATTGCCACTTCATGGCAAAGC	98
				R: TTGCCGTTACATCTCCAACAAGC	
2	RM13599	100.4- 100.4	2	F: GTTCATGGCACTCCTCTCCTAGC	98
				R: GAGGAATGAACAGTGCCTACACG	
3	RM12865	45.4- 45.4	2	F: TTGAAATCAGGGCAGAGCATTCC	156
				R: CGAGCTCTGATAATTCGGTGAGC	
4	RM3680	45.4- 45.4	2	F: AAGCTGCTGCTACGAGGAAG	107
				R: ATTGAACTCCGCCTCTCCTC	
5	RM5473	107.35 - 107.35	4	F: ACACGGAGATAAGACACGAG	105
				R: CGAGATTAACGTCGTCCTC	
6	RM17509	130.1- 130.1	4	F: ATTCAGGTGATCCCTCTCCCTACC	177
				R: CAATCCAAGCCTCAGAAATCG	
7	RM23679	5.6-5.6	9	F: TCACAGCTTAGTGCATGTTGAGC	189
				R: GATTCACCTGGCAATGAGAACG	
8	RM6920	32.4- 36.9	9	F: AGAGCGTACCACAAATGAGG	209
				R: AATCGTATTGCCAGCGAGAC	

Lampiran 5. Uji Kualitatif DNA



Lampiran 6. Gambar hasil *Genome Genotyping*

