

***In silico* mining and characterization of simple sequence repeats (SSRs) from *Euphorbia esula* expressed sequence tags (ESTs): A potential crop for biofuel**

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Supplementary Table S1 Primer Details of EST-SSR Contigs.

Sl.No.	ID	SSR Motif	FORWARD PRIMER (5'-3')	Tm (°C)	REVERSE PRIMER (5'-3')	Tm (°C)	Expected product size (bp)
1	Contig1000	(T)10	CAGTTTGGGAAAATCGGAAA	59.91	CAGGTCAAATTCAGGATCAA	59.918	237
2	Contig1016	(GAA)5(A)10*	CAGCTGTTCTCTCTTTTCCC	59.638	ACGGTGATATTCTCCGATGC	59.923	272
3	Contig1028	(A)10	TTTCCGTTATATCACCCCA	60.009	AACTTGTCGCCATTCAGG	60.255	237
4	Contig1055	(GAA)5	TCGAAATGTCACGGTTGAA	60.088	ACATTGCAGAAAGCAAAGGC	60.395	222
5	Contig1058	(T)10	GATCGAAAGGATGGCTGTTT	59.635	GCATACATTTCCTTATCATCTGTCA	59.432	256
6	Contig1069	(AGC)5	ACTTCACTGCAGCCGATTTT	59.882	CTTAGATCGGCCAGCTCTTG	60.11	276
7	Contig107	(AGA)6	GTCCCTTGCTTCTTCCCTC	60.19	TCTTAATCACATGGCTCCCC	59.894	245
8	Contig1099	(TGG)5	AAACATCAACCTCATCGGG	59.79	GAGGGAGGCAGGGTATGAAT	60.293	220
9	Contig1111	(CAT)6	CCCACCTCCTTTTCCTC	60.186	GAAAAAGCTGCTGGAGTTGC	60.14	245
10	Contig1126	(T)13	ACAAGGTATGCCAAATTGC	59.829	TGCTAACGAACAAAGCTCAGA	58.859	203
11	Contig1149	(T)15	TGTCCACTGAAACCGAGTTG	59.72	AAACAAAATCTTCCATAAATCTAGC	57.691	222
12	Contig116	(CT)7	ACCTCTTTTCATTCCACG	59.028	TACAAATCAGCTCCAGCTCCA	59.547	260
13	Contig116	(T)10	AAAAGATGGTGGGGGAATTG	60.91	GAAATCCACTAGGGCAGGGT	60.328	201
14	Contig1206	(TCC)5	CAAGGCTGAAAAGAACGAGC	60.132	AAATTGCCACATGGGACTC	59.797	229
15	Contig1211	(GGA)5	CGAGTGAAAGAAAGTGGAGAAA	59.914	AATTGACTTCCCATTGCTCG	60.074	221
16	Contig1227	(A)10	TGTCGTAACGCTTAAAACCC	57.837	GAACTCGTAATCTCTCGGCG	59.978	234
17	Contig1229	(CAG)5	GGTCCCAGCAAGCACAATT	59.962	GAAAAACCAGGAGGAGGAGG	60.045	279
18	Contig1242	(CAC)5	GCAGGGGATTTCCCTTAG	60.032	GTAAGTACCCTGCAATTGGG	60.375	208
19	Contig126	(TCT)6	TCTTTTCACTGACGCAATTTTT	58.922	GCGATCAAGATCTGGCTTTG	60.884	238
20	Contig1265	(AC)6atgttactagcccgttg gttcacagaattggcagggaata gaatagaatagatctctgtcta ttctattctagcttgggtgg(T) 10	ATATGAATTGGCCCATGACG	60.553	GCGCTACTGCTCACACCATA	60.042	257
21	Contig1270	(T)12	ACGAGCTTGGCTCTCAAAGA	60.277	CAGGTACAAAATTACCCATTGA	59.01	217
22	Contig1282	(A)12	CACTATTTTCGTCGGAGGGA	60.066	AAAAAGCCTCATTTGGATGCTA	58.844	245
23	Contig1358	(T)16	TCTGTCTTGTACCCGAAAATGA	60.035	TTTCCCATTTTTGGCTGTTT	59.916	280
24	Contig136	(T)11	CGAAGATGAGGAAGCAAAGG	59.948	TTACCCCACTCAAATCCAA	60.162	242
25	Contig1373	(TCT)6	GTGAGACTCTGGCTTGGGAC	59.841	CTCCGAGGATCCCTTCTTCT	59.772	226
26	Contig1389	(GGT)6	GCAATTC AATACCCAATGCC	60.161	CTTGTTTCGTTCCCTCTCA	60.224	267
27	Contig1395	(A)14	TCTTCTCCCTCATCTGTGAA	59.935	AAGGCTATGGCGAAAGTGAA	59.845	215
28	Contig1406	(CT)7	CGTTGTTACAGAACACGATT	58.689	AAATGGAGCAGATAAGGGCA	59.668	251
29	Contig142	(GA)7	GGCACGAGGTTTTCATTCAT	59.939	CCAGGAAGAGAGCTACCCAG	60.127	250

30	Contig1460	(A)10	AATGAAAGCCAATCGCTGTC	60.221	GAAGGAGAGGCTTGCAAATG	59.955	262
31	Contig1461	(A)11	TTAGATCCCACCAATCAACA	57.93	TCTTCGGAAGCAAATCATCC	60.155	225
32	Contig1468	(AG)7	TGCGTTAGGGTTGAAAATCG	60.989	GCTTCCTCCAATGAAAACA	60.051	266
33	Contig1532	(AT)8	TCATTTGTGAAAGCTTCTGTC	59.519	ACATTTGATTTTGGAAACGCC	59.807	247
34	Contig154	(T)11	GGAGGAGAAAAAGGAGGAGC	59.397	TTCAACACAATGCATTCTCAA	59.206	209
35	Contig1545	(CAA)6	GAGCTGCTTTTCAGGACGAC	60.142	CTGCTCCCATTTTGTCCATT	59.933	262
36	Contig1611	(T)10	ATTGCAAGCATCAGATTCCA	59.23	TCATGGCAAGAATTTGAAACC	59.93	261
37	Contig1625	(AAG)5	TTGAGCAAAATGGAAAAGGA	59.685	AAGGTGGAATGAGGTTTGGGA	59.381	269
38	Contig1641	(T)11	GCTCCTACGAGAGTTGGTGG	59.867	GGTCTGCAAAAAGTGAAGGC	59.859	277
39	Contig1645	(AGC)6	AGGAGGATCGCCGATTAATA	60.893	TTGGAGTTGAAAAGGCCAC	60.088	248
40	Contig1650	(A)11	ACAGCATGCTCCACAATCAA	59.967	GCAAAACCTTCAAGAGTGGC	59.859	263
41	Contig1657	(T)12	ACGCTACCTATTTTCGCTG	59.384	TAACCCACCATGCATTTCAA	59.786	203
42	Contig1662	(T)13	TGAAAAGCTTCCCTCCA	59.926	TAACCACAACTCCCAAGC	59.971	223
43	Contig1735	(TGA)6	CGCGGAATCCATATAATGT	59.643	AATCTGAAGGCGGTCTCTT	60.212	247
44	Contig1773	(T)15	AAGGGAGAGCGATCTGAACA	59.95	CCCATTTCACAAGGCTAGGA	60.066	268
45	Contig1792	(T)11	GGGAAATCTAGCAGGCTCC	60.173	AGCCAACCTGCTCTGAGTGT	60.057	211
46	Contig1804	(T)11 gttatcattcctggtttaa atccatgaggagaaggagagga (GCC)5	TTTGTCCATGAGGAGCTGA	59.369	GCGAATCTACCCCAAGGTCT	60.464	248
47	Contig1815	(TA)8	TGGTCTAACCTTGTTTGTGTTG	59.929	GGTCCATGAATGTATGGGGA	60.404	275
48	Contig1821	(T)10	GAAGCCATTAATGCAGAGCC	59.813	CCCATTTCACAATCTCCAGT	59.779	275
49	Contig1847	(TCT)5	GATTACGGGTGACTTCGTGG	60.375	GTCGTAAGCGAGAGCAGCTT	59.927	255
50	Contig1851	(A)11	CCACATAACCGAAAGCTGGT	59.993	ATGACAAGGAAGCCATGGAG	60.073	264
51	Contig1856	(T)10	TTCGCCTCTCAAAAGCCTTA	60.089	CGTGTGACCTTTTCATAGC	59.623	240
52	Contig1862	(CTC)5	ACCAAGAACAACCCCT	59.707	CAAATGAGCGTTCGTCTTA	60.014	265
53	Contig1863	(A)10	CAACTGAACCAAAATCCAAA	59.876	GCACATTTACGAGATTGCGA	59.839	216
54	Contig1864	(A)13	CTCTCTCAACTGGGCTGGTC	59.986	CTTTGACATGCGCATGAAA	59.664	278
55	Contig1882	(T)15	GAAGAAGGGAAGGTGGCTCT	59.817	ATGGCAATTAAGCACACTG	58.651	279
56	Contig1886	(AG)7	TCTTCTCGACATTTTCCGC	60.331	TGATCTTCTCTGAGTCGCA	59.656	279
57	Contig1886	(T)11	AGCCGATATCTCGTTTGAAGA	58.941	CCCTATAAAAAGCACAGGCA	57.927	236
58	Contig1912	(TCC)5	CAACTCCGTTTCTCTTCCA	60.224	AGCGTTGAAAAAGGCGTCTA	60.018	278
59	Contig1912	(CCT)5	TCACTGTTCCGATTGCTGTC	59.837	AGCGTTGAAAAAGGCGTCTA	60.018	246
60	Contig1927	(A)10	GCCATCTTCCCTTTGTGCTA	60.214	ACACGACAACCACCTTCCCT	59.474	255
61	Contig1945	(A)11	TGTGCCTCCAAATCAAACA	60.088	TCTTGGATACGAAACCGGAG	60.066	244
62	Contig1955	(T)12	CAGAAGAAACGAATGGGGAG	59.665	TTTTGCTTTTCCAAAGACGG	60.215	273
63	Contig1958	(A)11	TTGGTATTCTTGTTAGGCGG	59.13	AGAAATCTTGCGACTCCGAA	59.955	236
64	Contig1964	(TCC)5	ACCCTTTTCTCCAGGAAGGA	60.045	ATCCTTGGCTTAATTTGCC	60.28	263
65	Contig1995	(TCT)5	CCAACCTCTCTTTCTTTCCA	60.586	TATTCGTACCACATGCCGAG	59.566	280
66	Contig1998	(TCT)5	CCCAAACCTCTATCTTGA	60.042	AACCTCTCTATCGCTACCA	59.694	235
67	Contig1999	(A)10	GTTGCTGTCGCTTCAAGTCA	60.183	GACCTTCTTTTACCGACCA	60.088	209
68	Contig2066	(CAC)5	GTTATGAGGAAGCCAGCGAG	59.978	CTCCAGCATGTCTTGAACA	59.988	251
69	Contig2071	(T)10	ATGAAGGTGACACAGTGA	60.005	ACAAAACGGGAACCTGAATG	59.83	270
70	Contig2099	(A)10	TTTGCTGTGTTATAGGGTGAA	59.514	AGAAGGAGGAGATTTGCC	59.651	209
71	Contig2116	(T)10	ATGGTGTCAATGTGAAGGCA	59.967	GCCAACTGCCACTTCAATTT	60.118	220

72	Contig2130	(ACC)6	CGACAGGAACCAACCAAAAA	60.893	ACGTCAGGAACCGTGAAAAG	60.149	210
73	Contig2135	(AAT)6	TGCTGCATATGGTGAACACA	59.701	AACAGCGTAAGGAGGGGAAT	59.962	250
74	Contig2140	(A)10	TTTACCCTTCAAAAACACGA	59.145	AAGAACGAGCTCACAGCAT	60.02	247
75	Contig2141	(A)10	AAATAATTGTCCGCCACTGC	59.967	ATTTACTCTCGGATGGCTCG	60.096	264
76	Contig2145	(A)15	TAAGGGCAAGTGAAATTGGG	59.931	TTCATTCACCAAAAGAACCA	58.947	269
77	Contig2165	(A)14	CTTCTCTCCAAATGACCGTGG	60.646	ATTAAACCACTTGCCTCC	60.187	246
78	Contig2175	(GAT)6	TTCAGCAAAGCACTTGGAGA	59.716	AAGTGGACAATCAAGCCAGG	60.111	279
79	Contig2180	(TC)6	TGATGATTGGATTGGGGAT	59.952	TCTTCGCTCTTTTGCTCAGA	59.024	251
80	Contig2185	(T)11	CATGAGAACTCTACCCGGA	60.065	TAGCCTCGTCATTTGTGCC	60.074	253
81	Contig2189	(T)10	AACTGGGTTGGTTCAGGATG	59.82	CAGGAACCAACATCAATTCAAA	59.839	262
82	Contig2189	(ATC)5	AATCAAATCTTCCAACCCCC	59.996	TTTGAGCCGATGATGATGAA	60.159	212
83	Contig2190	(T)14	TAATTCGTGAGTGCAGTGGC	59.871	TGACCCTTTATCGAACACGA	59.123	220
84	Contig22	(A)11	TCTGGCTCAAAAACAAGCA	59.585	ACAGGGAATATGCAACAGCC	59.962	220
85	Contig222	(TC)9	GCTGCTCAAAAATCCAAGC	59.967	AAGGTCCAAACTTTTGATTGAGTT	59.481	210
86	Contig2226	(A)12	AAAGCAATGTCCATCCATCC	59.756	TTTCACAGGTGTGTGCTC	60.032	246
87	Contig2253	(A)10	ATGTCAAATCCAATCCCAA	59.991	TTGGAGATGTTC AAGCATGG	59.648	240
88	Contig2260	(A)11	TAGGGTGTGTGGTTTGTCTG	59.609	GAAACAATCCCGCATGAAAT	59.768	235
89	Contig2277	(T)10	TTTTATTGGCTCACAATGCG	59.702	GCCAAATCCAACCGTAAGAA	59.938	253
90	Contig2283	(AAC)6	GCTTCCAGGCGTTACAGAAG	60.015	TGAATCAACTGGCACAGAGC	59.992	269
91	Contig230	(T)11	ATGCTCTGCTCGAACTCCAC	60.564	GAACACATCCAAAACCCTTGA	59.822	206
92	Contig2303	(GGA)5	AATCTGACCCGTGCTTACG	59.989	CAGCATTTCCACTCGGACTT	60.255	252
93	Contig2303	(TA)6	TCAGCAAGATAGGGGTCAGG	60.21	GAAAAGCCAAGAGTCGTCACA	60.425	246
94	Contig234	(A)16	TGTCAGGCTTTTGTATTGTTCA	59.677	CATAGGCAGGGTGGAACTGT	59.989	272
95	Contig2360	(CTA)5	TGAGTGTCCACAGGAGCTTG	60.022	CTACAACTAAACCCATTGCCG	59.522	245
96	Contig2415	(T)12	CCAACCTGGTCTAGGGTTCA	59.959	GGGGGTGGTCTGTATATT	60.039	216
97	Contig2438	(T)15	TCTTGTCTCGATCCAAG	60.474	ATGTTTGTGCTCCAAAAGG	59.971	204
98	Contig2453	(TC)5	AAGGCACTCAACCCCTCTT	60.11	AAATACGCACAATCAGCCAG	58.799	238
99	Contig2462	(T)13	CGTTGATGCCGATGAGTTTA	59.688	CACAGAAACGCAGCAATTTT	58.967	236
100	Contig2469	(TC)6	CCTCACCTTACCTCACCAT	59.962	CGTCAATAACAAGCCAGCAA	59.872	237
101	Contig2472	(T)10gttatttgctagaaaaga tctacatatta(T)10	TTTGCCAAATGGGTGAAAGAT	60.309	GACTACACGAGGATGCACGA	59.862	256
102	Contig2503	(T)15	CGGAGGCTTAATGATGAGGA	60.17	TGACAATCAATAAATAAGCCATGAA	59.771	226
103	Contig2508	(CTD)6	AAAGAGGCGAAACAACCTGC	59.499	CCACGCCATTACCTCTGTTT	59.993	215
104	Contig2515	(T)10	TGAGAATGGAAGGCCAGAAG	60.331	GGCGAGGGATAACAACATTC	59.391	225
105	Contig2518	(T)11	CAGTGAAGGGACATAGCAA	59.864	TTCCTCGATTCAATGCTTC	60.155	247
106	Contig2544	(T)11	AAGCGAAATCAAAACCCCTCT	60.074	ACCTCGTTTTCTCTCATGC	59.288	201
107	Contig2558	(T)11	GTGTTGAAAGTTGCCCGTTT	60.015	CACATTCCAAACAGCTTCCC	60.495	258
108	Contig2570	(T)11	GCCCTTACGTCCGGTTAGTT	60.496	ATTTCTGCACTCCGTGCT	59.882	278
109	Contig2578	(A)10	GATGAGAAGCCACCATGAC	60.484	GAATTTAGCACGGCTGGAAA	60.209	278
110	Contig2588	(CAG)5	TCTCCTCCACCCAGAAACC	60.032	GTTGAGGATGAAATGGGATG	60.135	229
111	Contig2589	(TCA)6	TCGGTGGAGAAGAAGAAGGA	59.92	TTTGCCACTGTGAAAATCCA	60.088	275
112	Contig2599	(T)10	CTCTGTTACGTGGACGTTTCG	59.36	GCGGTGTGATTGATTGATTG	59.931	224
113	Contig2708	(A)10	ACGATGACAGTGGGACACAA	60.005	ATCACCCGCCATCATAAAAC	59.651	248
114	Contig2715	(T)13	AGGGAGTTTCGATGGACTA	59.694	CGCTCAATTTCCATGAAGAAG	59.831	267

115	Contig2731	(TAA)5	ATGATTTTGGAAATGGGGGT	60.245	TGGTCTTTGCTGCAAATGTC	59.847	232
116	Contig2739	(A)15	CCAATTTTCCCTTCGGGT	60.159	TTTACCAACTGGGCTTCC	59.943	235
117	Contig278	(T)14aaaagctctcattaatc cacaaagtgcattaagataga agtgactgatcc(A)10	AGCAGCCATGTTGGTACAAT	60.406	TCCTCTGAGTTTGGGCAGAT	59.803	270
118	Contig2781	(T)10	GCCCTTAGGCTTTCAATTC	60.041	TTGAAAGCCTGTTTGTAGTCA	59.633	275
119	Contig2799	(T)10	TTTCTTTCGGTTTTCGATT	59.699	ATAGAATGTGGGCGACAAGG	59.955	278
120	Contig2808	(T)11	AAAAGGTGAGCTCCTTGCCCT	60.382	GGAAGCAAGCTGATCTGTCC	59.957	226
121	Contig2859	(CT)5	CACCCATTTCTCTCTGTGTTG	58.741	CTTCTCTGGTTCATCCG	59.797	231
122	Contig2886	(TIC)5	TCGGTTTTCAGCGCTCAATTT	59.853	AGCGAAGCAGAAACAGCATT	60.162	250
123	Contig2932	(A)11	AAGATGGGAATTCGTGTTGA	59.629	ACAAATGGGAAACAAAACCG	59.702	269
124	Contig299	(T)16ctttataactgttttcatatg tttagttcaattctaaacctagg aattgaagaaacgtcccttttta tctcaaa(T)11	TAGGTGGAGTTGGCATAGCA	59.297	CCACATCCAGCCAAAATAA	60.692	266
125	Contig3007	(A)14	AACTCCATTACAGCCGTTGG	59.966	TGGTAAGGAGCATAATCCG	59.916	263
126	Contig3007	(CTC)6	TGGGATTATGCTCCTTACC	60.06	CATTTCCGAGCACATCCTT	60.074	231
127	Contig3019	(CCA)5	CCCAATTCACCTTCTCTCCA	60.042	GAGAGATCCACGAAAGGCTG	59.95	264
128	Contig303	(TG)7	AATCCAAGTGGGGCTTTTT	59.814	TTGCCGAGAATATTGCCTGT	60.606	235
129	Contig3051	(AT)8	GCTACCAACATGAAAGGGGA	59.933	TGGACCCCTGATCAAAAAGA	60.43	222
130	Contig3095	(AGA)5	GCTTATGTGGCGAGGATTC	59.674	GGGAACGTACTCCACCTCAA	59.966	260
131	Contig3103	(GAG)5	GGGAAATCTGAATGTAGGCA	60.014	GCCGGAGTTGCACTGACTAC	60.865	203
132	Contig3111	(GAG)5	GTTCTCCAACGCCTCAAATC	59.676	CGGCGAGTTTCCACTATCTC	59.836	273
133	Contig3113	(T)13	TGGAGCACAAAGGAAGGGAT	59.803	GCTCTGCCTGTCTTAGCAAC	60.164	270
134	Contig3121	(GCT)5	AACTGGACGGTTTTGATTGC	59.978	ACAGGGATAAAAATAAGAGCAGGT	57.485	276
135	Contig3122	(CT)9	CCTTCTGTGTCAGAGAGCC	60.134	GCGAGGATCTTCATCTTGG	59.91	270
136	Contig3132	(GGC)5	GCCTCTTCTCCACAACGAAG	59.989	CCAAACGCCCTGTTATTAT	59.985	217
137	Contig3160	(T)10	AGACAACAACAATCCCGAGG	59.966	TGGATACAAAATAGCCAACGC	59.978	272
138	Contig3207	(CAG)6	AGCGTTTCAGCAGTTGACCT	60.058	CGGGATCGGCTAAAAGTGTA	60.089	260
139	Contig3236	(AGC)5	TGAAGAGAAGGATGGGCTTG	60.331	GGAGCTGTTTTGCTTGAAC	59.859	235
140	Contig3242	(ATC)6	TGAAGAACAACCTAGGCGCT	60.015	TAACAAGTCCCACGGGAAAC	59.83	217
141	Contig3251	(AAG)5	TCGGATCTTACATCACATCA	60.006	CTTCTCGGGCTTCCCTTCT	59.955	225
142	Contig3252	(T)11	AACTAAGAAATGCACACGGGG	59.993	GCGAAACTTTGAAGCAGACC	60	270
143	Contig3252	(GTG)5	GGTCTGCTTCAAAGTTTCGC	60	CCATGAACAGAACTACCGCA	59.716	262
144	Contig3263	(AGG)5	CTATTCTCCGATTCCACA	59.887	ATTACAAGTGCCCATACCGC	59.851	247
145	Contig3284	(T)10	TCCCTAAGAAAAACCATTCAACA	59.83	GAAGGTCGGAGTCCATTTT	60.306	237
146	Contig3307	(A)16	GGTACTGGCTTGAACCTCG	60.015	GCTGAGTGCCAAATAGGACC	59.7	245
147	Contig332	(AG)6	GCTACAGAGAGAGAAAGAAAGATT	58.667	TCAAAAATGTGGCACTGGA	60.088	232
148	Contig3332	(TA)9	AAGCATGGAGGAGAATCCAA	59.629	TGAATGAGGCAAAATGACCA	60.049	251
149	Contig3346	(T)10	GGCAAATTCAGCCAAAAGA	60.188	CATTGATGTGTCACAGTTG	59.864	226
150	Contig336	(T)10	GAGATTGGGATTGCCGTTTA	59.901	CATGGCAACGAATTTGAGAA	59.664	256
151	Contig3369	(ATC)6	TCCTCTGATTGGAGCCAGAC	60.349	CCGTCCGATCGTTGTAAAAA	60.856	244
152	Contig3372	(T)13	TTTTCGGAGTGGAAAGTGGAC	60.088	CCAACACCAATCCATCAAT	60.439	213
153	Contig3373	(TCT)6(TC)6*	CGTTGAAAGTCTGCCAAAGT	60.291	ACAGGACACTCTGGCTTTGA	58.435	212
154	Contig3377	(GAA)5	GGCTAACAGCAACAGCAACA	60.058	CCATTACATTTGGGGCAATC	60.016	265
155	Contig3391	(A)10	CCAAGTGGACATCAAAAACCC	60.21	TTTGGGGTGTAGAGACGGG	60.103	224
156	Contig3406	(T)10	AAATGGGTTGCAAGAGTTCG	60.11	TTTGGAGGAGGCTTGAACAC	60.232	277

157	Contig3436	(AAG)5	AACAAGGGGAAGGGAAAGAA	59.912	TTTGAGCACTCCGGTCTCTT	59.989	259
158	Contig3445	(AAG)6	TGAGTCCAGCATGTGCGAAG	59.984	ATGGTGATTTGAACGGTGTT	57.766	211
159	Contig345	(AG)8	CACCATATCCGTTTTCTACG	59.348	TCCGACCTCTTTTCCATGTC	60.05	240
160	Contig3487	(T)15	TTGATGAAAATCCTTTTCCGC	60.016	GTGACGATGATTTTGGGGAC	60.181	262
161	Contig3501	(T)10	GGGAATCAAAAAGCACTGGA	60.051	AGGGAAGTTTCTTATTGTCAAAAAG	59.552	265
162	Contig3508	(GAT)5	TTGATGCTGCAGAAAAGACG	60.134	CCTGCATAGCAATCAAGCAA	59.976	239
163	Contig3517	(T)14	TGCTGCACTTTTAAAGCTCA	59.752	CCTGCTCGGAGGATAGAAGA	59.526	279
164	Contig3534	(A)10	CCTCCATCTCCAAAACAAA	59.903	TGTGCGGTTTCAGATGAGAG	59.984	274
165	Contig3545	(TCA)5	CTGCTCTATTTTCGAAGGG	59.975	AATGTGGATCTGCGGCTAC	60.103	258
166	Contig3545	(A)10	TTGCTCTCGGAGATTTTCAT	59.773	CCCTTGGCAAAAATAGAGCAG	59.975	248
167	Contig3556	(CAG)5	AGCAAGATGTGCCCTCGAGT	60.02	GGACCCGATACAGGTGCTAA	59.955	232
168	Contig3574	(T)10	ATGTCATCCGATCATCGACA	59.882	TTTTTCATTAGCATCAITTAATTGC	57.545	207
169	Contig3584	(AAG)5	TTTTCTGTAGCAATCATGGCG	59.833	AAATCTCCCCCAGTTTCGAC	60.306	255
170	Contig3597	(TC)7ttcagcttgcacaatc atccgatccaataaattttgct caac(T)13	GAAGATCGTTTCCAGGCAAG	59.813	CATTCTCAGAGCAAAAAGAAACAA	59.933	210
171	Contig3604	(T)14	TACATCATGAATGGGCGCTA	60.058	AAGTTATAAACAGGTCTCGGTCG	59.958	229
172	Contig361	(TCA)5	GGAACAGGTTTTTGAGCAG	59.711	TGCATCTGATTTTGACTCCG	59.799	262
173	Contig3634	(AAT)6	GGCTCAACAAAGGCAGTTTC	59.859	CTCTAATGGCTGCTCAGGG	59.971	254
174	Contig3637	(T)12	CCCCTCAATGCCACTCAAT	60.924	CCCCCGATTTTATTGTCTCT	60.013	274
175	Contig3649	(T)11	TCATGTGAGCCCAATTGCTA	60.22	TTAACTACACCAGGCATCG	59.609	255
176	Contig3655	(T)14aaaacaactttgtctctatt tattctttgtaagtgcataatga cattttcatattgatccagttttta ac(T)10	TATCCAGACACTTGGTGGA	60.112	CACCACATTACAAGTGCCAAA	59.497	228
177	Contig3664	(T)12	AAGTTCTTGGTTTTCCGGC	60.463	ACGGCAAGTAAAAGACCCAA	59.609	268
178	Contig3667	(T)16	TGCCCCTTTCTCAAGTTTTG	60.22	GGGGGTGTGACGTGTCTAAT	59.703	232
179	Contig3690	(GGA)5	TACCTCCCATIGATCGACCT	59.361	TGATCTTCGTGGCAGCAATA	60.366	264
180	Contig370	(TGC)5	ATATGGTCCCTCCGGCTGTG	59.95	CCGGTATTGTGGTGACCTCT	59.989	228
181	Contig3718	(ATC)5	GGTAATCCGACAACCAACG	60.227	TGGGTTATGATTCCAAGGG	59.617	277
182	Contig372	(AGA)5	GCTATGGCAGAGCAACATCA	59.979	GGAGCATCTGGATTTGAGC	59.78	209
183	Contig3744	(TCT)5	GCGGTACCAATGTTCAGGAT	59.82	TCGAAATTGCATTTGTGAG	59.953	227
184	Contig3792	(T)10	AATTCCTGATCAATCGGTGC	59.9	AATGGCTTTGTCCAACCTTA	59.429	259
185	Contig3809	(T)10	GGTGTGGAAGAGGGATTGAA	59.903	AGGAAGTTTCTGTTTCAGACCA	57.964	236
186	Contig3812	(AAG)5	GCAGTTGTGCCCCTTCTCTC	59.997	AAACAGGACCGAAACCTCCT	59.972	277
187	Contig3822	(A)12	GTGTGCTTTTGTGTGTCAT	59.918	CTAATGGTCCGAATGCAGTG	59.148	213
188	Contig3825	(T)10	CTTTGTATCTCATCGTCCCC	60.011	TTGGGATGAGGATTTGAAGC	60.014	256
189	Contig386	(AGA)6	GGCAAATTGGCAGAAAGAAA	60.188	TCTCCAGTCCAAAGCATTCC	60.195	254
190	Contig3881	(A)15	TGGAGAAGTTTGAGATCCCG	60.187	TGGTAAAAGGGTGGACAAAA	59.343	276
191	Contig389	(TTC)6	GCGGTCAACGGAAACAGTAT	60	ATCCATCGGTTATCATGGGA	59.975	247
192	Contig3905	(ATA)5	CTTCTGACCAAACTTCCCA	60.081	CAAAGGTTGATGATGATGCG	60.073	240
193	Contig391	(T)10	CAGGATTCAGATGCACCAAG	59.241	AACTGGACTTGAATGCGG	60.074	246
194	Contig3948	(GAA)5	GGCGATTAACCAATCTGGA	59.901	TTTATTC'TCCCTTTTTCGCA	59.655	230
195	Contig3958	(T)10	CTTTGATTCGCATGTTCG	59.809	CCAACCCACACCTCAAAGAT	59.82	247
196	Contig4	(CT)8	CCTCGCACTCGTCTATCTCC	59.973	CCCTCTCAC'TCCGTAACCTC	59.835	241
197	Contig402	(A)11	GGGTTTTGTGTTGTCGATTA	59.938	AGGTGAAGCCATTTTCAACG	60.11	239
198	Contig4070	(TCT)6	ATCCAGATTCCAGAAACC	60.133	ATCTGCTGGGACAAAGAGA	59.803	263

199	Contig4071	(A)13	TTCCCTCTCAAGTGCCAG	60.229	TCGATTGCGTCACTTATTGG	59.688	200
200	Contig4084	(TA)6	TTGCTTGCTTGCTGCTTCTA	60.037	TCATGTGGAAAACCTTATTAACAACA	58.978	242
201	Contig4141	(GCT)6	TTGAAATTTTCGGTCTGTTCC	59.916	AATCCATCCGGGATAAAACC	59.852	205
202	Contig4163	(T)11	TTCATCAGCTCATCCACTG	59.787	AAAAC TCCGAGGAAAAGGGA	60.046	209
203	Contig4194	(A)12	ATCACCTTCAGGAACAAGCG	60.255	CGAGATCAACCATTTCTCA	58.643	271
204	Contig4225	(CA)9	GTC TCTACGGCCTCATCGTC	59.834	TGAGGAAGTGAGTGTGTGGG	59.705	269
205	Contig423	(CAG)5	TGCAATTGATCCTGCAAAAG	59.809	AGAGCAAAGCATCCCGATAA	59.807	279
206	Contig4235	(ATG)5	TCCCGTTGAAAGAAAATTGC	60.053	TTC TTTCGCTTCTTCCCTG	59.564	201
207	Contig4252	(TGG)5	TGCTCTGCGTTAGGGTTTT	59.883	TCTCCAGTCAAACCTGCT	59.844	231
208	Contig4270	(A)12	TCTCTTCAACTAACACTGCAA	60.081	ATTGAAACTTGCGCTCCTA	59.845	279
209	Contig4350	(GAT)6	GCGAGAGGCAGAAGGATATG	59.939	GCTGTCGGAAGATGGCTTAG	59.978	250
210	Contig4371	(T)14	AGCAATCTTGAGGTGGGTC	59.141	TGGTGGTGTGTGTGTGTGTG	59.923	278
211	Contig4391	(G)16	TGATTTGAATTCGTTGGGGT	60.17	TTCATCAAAAACCCGATCC	59.739	270
212	Contig4402	(T)12	TTTTCAACCGGAATCTTGC	60.053	ATCCAATTTGCAACTCCAAG	57.67	223
213	Contig4413	(A)10	ATCCGGTGTCCAATATCCA	60.195	ACAGAAATTATCGGGGACC	60.017	236
214	Contig442	(TTC)5	GCCATCTCCAAAAACAAAGC	59.691	GATGACCCCTGT TTTGCTGT	59.973	259
215	Contig4422	(A)13gtaaacgcctcaacc atcaatttaagccccctctctt tcttgattttgcagacacc(T)11	TCTTCCAGTTTTGCCTCC	59.405	TGCTCAGTGTACTTGGTTGGA	59.35	278
216	Contig4431	(A)10	TAAGAACGGCAAAACATCCG	60.989	AGCATTTTGAAGCCGAAGAA	59.96	213
217	Contig4468	(T)16	GTTGAGCACATGGCTCTCA	59.992	TGCAACAATGAATGCGTAGC	60.817	279
218	Contig4469	(T)10	CTCAAGGTTTCGGCCACTTA	60.241	TGGCACATTTGGATGACATT	59.781	256
219	Contig4478	(CT)8	TTGTTCTTAACTTTGAGATCG	57.644	TATTTCCCAATCAAAATCCG	59.593	235
220	Contig448	(AAG)6	TTAGAGCTTAAGCGTCCCA	59.975	CGTAAGTCCGGTGAATGCT	60.132	274
221	Contig4488	(T)19	GACCTTCCAATCGCACTGTT	60.119	ATGGTTGGAATTCGAGAGA	60.603	253
222	Contig4488	(CTGCAA)5	AATGACTTTTACCTTGGCGC	59.229	GTGGGAGGATCAAGTGCTTC	59.661	250
223	Contig4507	(AT)7	CGTTCTGAAAACACGAGCAA	60.027	TCAAACAAGGCATGAAA	60.088	266
224	Contig4512	(A)10	TTGAGAAGCAAAGCAATCAA	57.227	AAGACGAGCACGACGAGAAT	60.02	214
225	Contig4514	(A)11	GGATATGGTGGTGGAAATGG	59.871	AAGCCCTATTTCCACTTGCT	60.096	247
226	Contig4558	(CTD)5	CACCAGTAATGGCAGCTCAA	59.864	AGTGAGAATCCAATTGGGCA	60.461	240
227	Contig4564	(A)10	GAAAGATATTGCGAGCCAGC	59.951	GCAAAACGAGTCCGGAAGTA	60.249	250
228	Contig4573	(GGT)5	TGGAAC TCCGGGACATATT	61.46	TTGCTGGTGTCTGTACTTGG	59.904	206
229	Contig4587	(AGG)5	CCGGCTTCATTGACTTGTTT	60.11	GCAAAATGATGACGACGAAGA	59.805	212
230	Contig4588	(T)11	AGTGGCATCAAATCAAAGCC	60.081	ATAGTATTTGGAGGCCCG	60.164	239
231	Contig4589	(A)10	TCCTAAACAGCATATTTCCCC	60.157	GTTCTCTTGACAAAGGGGTG	60.69	261
232	Contig4597	(GGC)5	TTGCTTCAATTTGAGCTGGA	59.542	GACTTCCCGTCTATCACGGA	60.073	249
233	Contig4599	(A)10	CACGAGATCCAGTTTGGGAT	59.927	TGCAAAACAAGAAATGGCAGT	59.322	243
234	Contig460	(T)12	GCGAGACAAGGAAGAGGAGA	59.679	CTGAAGAAATGAAATGGCCG	60.576	241
235	Contig4600	(A)11	CGGAAAAACTGAAAAGCCAG	59.855	GCAAAATGCATTCATAAAAATAATACG	58.96	271
236	Contig4610	(A)12	GGTTAAGTTTATTTGGCGCTG	60.637	TCGGTATCAGGACGGGTATC	59.773	229
237	Contig4617	(AAG)5	GAGAGGTTGTTTATGAGGGA	59.903	TAGCTGGTTCCACAACATGC	59.722	238
238	Contig4635	(T)11	GGAGCCAAAAATTTCTGTTGA	60.053	TGTAAGCACATTGCTGCTATTTT	59.016	207
239	Contig4686	(T)19	TGTGCCAATTTTCACTCCC	59.767	CCCCTGGGTGTGTGTTTTT	60.246	235
240	Contig4692	(CTD)5	GAACCAATTGACCACCGATTT	59.653	TACAAGCCCTCCAATGATCC	59.894	229

241	Contig4698	(A)10	TGGGAACCTAACGTCTCGG	60.103	TTTGAATCAGGTAGATGGGAA	58.556	236
242	Contig4704	(CTA)5	TTCGTGCCCAAGATGGAGC	60.195	CTTTGCAGGTGTGCAATG	60.293	280
243	Contig4706	(C)10	TC'TCCCCATTTCTCTCT	57.839	GTTTGGTCTTGACGGAGA	60.088	250
244	Contig4718	(T)12	GTCGTTTTTGGCAATGGAAT	59.807	TCGTGATGCATGTAGGCAAT	60.104	276
245	Contig4718	(A)11	GAGCCATGTAGCTTCCAAG	59.836	GCAGGCTTGAGCTTTGAGAT	59.723	262
246	Contig4768	(ATC)5	ATTCCAGCACAAACCCCTT	60.723	TCTGAGGCACCCAGTAGCTT	60.156	213
247	Contig4785	(A)10	TTTGTGGAGAAAATGAAAATCTGA	59.984	GTAAGCCATATGCCAGGA	59.923	204
248	Contig4829	(AGA)6	GCAAGTCATCAGAGTTTGGC	58.444	TGGAGCAAGAATGAGGGTTC	60.195	252
249	Contig4869	(CTD)5	ACCAAAGAGACCAATGGCTT	58.646	CAAATACACATTCCCGCTT	59.823	218
250	Contig4909	(A)13	AGTTTGGAGGACTGTGGGTG	60.002	AAGTGTCAAATTATGGGTCTAATTG	58.889	239
251	Contig4957	(GCT)6gatgtgatgattctc atctgctgcacaaaggctcacc tcaaatgctggaatgaagagtc cctgaagcaaaaaggaggta gcat(GAA)5	TCCTCCTCCTCGACAATTA	60.734	CAACAAGTGGATGAGCATGG	60.112	272
252	Contig4957	(ATC)6	CCAATGCTCAICCACTTGTG	60.112	ACAAGGGAGGGAATGATGTG	59.779	246
253	Contig4960	(T)10	GGAATCGGAAAAGAAAAACG	58.762	CAAGAAGCAAAATGGGCATT	60.074	239
254	Contig4964	(AAG)5	TTTACTCCACTTTTTCGCCG	60.236	GCCCTGTCAGCTTTC AACTC	59.997	231
255	Contig4986	(T)11	TTCGTGCCCTTGATCAACTT	60.636	CTGGTTGTGTTTCCAAGCGT	60.147	228
256	Contig5021	(GGT)6	GCTGGAAATGTCGAGATGGT	60.081	TCAACACCCCATGAAAGGTT	60.21	278
257	Contig5035	(AAD)5	CTTTGGAGGAGTTTCTTGCC	58.909	GGGCTGAGATAGTGGCTGAG	59.973	278
258	Contig504	(ATC)5	TCCATGTTACGGAGTGAAG	59.864	GCATCTCAACAAGCTGCTCA	60.296	223
259	Contig5057	(ATC)5aagggttctctctcc atgaattcaccacctagacactat ta(TCC)5	AATAGCGCCAGATCAGCAAT	59.835	TTTCCCAAAGAAATCCCAGTG	59.903	203
260	Contig5062	(T)11	GGAAGCATAAGCACACCGAT	60.103	TGCATCTAGAACTTGAAAGCAC	57.332	261
261	Contig507	(CAG)5	CCATFACCTTCCCCCATT	60.011	TTCGGTTATGGACCTTGGAG	59.926	216
262	Contig5078	(T)11	CCGAAGATCCGTTTTTACA	57.755	TGTTTCC'TGTTCTTGGCAAT	59.601	238
263	Contig5111	(A)15	TCTCAAAACCTTCACTTCTTTT	58.941	TTTGTCTCAAGAAGGGGT	58.909	276
264	Contig5116	(TTC)6	GGGAGCAAATGTTCTGAC	60.646	TCTGGAAGCTCGAACAAATCA	59.522	254
265	Contig5122	(ATC)5	GAGTGCCGGTGAATCACTT	60.119	GGCTACACAAAACCAATCCGT	59.859	272
266	Contig5123	(C)12	TTAAGGGCTTGTATCGTTGG	60.067	TCACCTCTTTGAGATCGCCT	59.95	251
267	Contig513	(A)12	TCTAGGGTTTTACCTGCCA	59.702	GAACTCCGGTATGAGGACCA	59.927	261
268	Contig5153	(A)10	CCAATCCAATCCTTCTCA	59.864	TGCTGGTGAGGTGCTAAATG	59.864	222
269	Contig5159	(TGA)5	ACATACACATGGACCAGCCA	59.837	GCTTCCACAGGCCATACATT	59.962	248
270	Contig5166	(CTG)5	TAACGGGAAAAGATCATGGC	59.901	CGTCAAAC'TCTCTCATCAA	57.938	268
271	Contig5189	(CAG)5	ATCAAAATATCCGTGGCGTC	59.791	TACTCTTACCCGAGGCACC	60.218	212
272	Contig5190	(A)15	CGGAAACTCAAGAATCCAGC	59.813	GATAGTGGCGGTATGGTTT	59.988	228
273	Contig5191	(ACA)5	ATCATGTCCGGTATCCTCA	60.448	GTCACCGTAAGGAGCTGAT	60.285	235
274	Contig5194	(A)14	TCTTCTTCTTTACCCCTCACG	58.448	ACTCGCCATTTCTGCTCTCA	61.087	274
275	Contig5198	(CCA)6	CCCAAGAAGGACAAGACAA	60.366	GCTCTCCCAATCTTGATGA	60.158	226
276	Contig522	(A)12	GTTTTCGCCGTGCTGTC	60.399	ATGGAAAGGGGAAAGGAGT	61.029	227
277	Contig5223	(TTC)5	GGTAACAAGTGGGCAGCAAT	60	TGGTGGAGGAGGATATGG	59.92	253

278	Contig5244	(CAT)5	ATGCTCCCTCTCTCATGGTGG	60.223	CCCAAATCACCAGCATTTTT	59.801	275
279	Contig525	(A)11	TTGAAACATGCGAGACATTCA	60.25	CACAGTGATTGAGATGGTGAAAA	60.023	258
280	Contig5273	(TTC)5gcagaagctagaagacaaatgaagctagctatcaggatgcagatactgtggtgaatt(A)11	CAAGCAGTTGCTCTCAGTCG	59.922	TTATCGGGATTCTTCAGCC	59.115	204
281	Contig5289	(T)10	TTTCGCTGTCTGGTCTTCA	59.566	GTCACATATTAGCAGCCGGT	57.725	213
282	Contig5304	(CTC)5	TGATTTGAGGCTGATTTCC	60.155	CTCTTTGCGGATTTTTCAGC	59.96	204
283	Contig5315	(T)13	CGAGGAATATAGCGGCTGAG	59.96	TGGGTGCTATTCTATCCCAA	58.718	266
284	Contig5321	(TA)6	CGCTTTGGGTTTAAGCAATC	59.72	ACCAATCTGTGGAGCAACC	59.973	255
285	Contig5322	(GAG)5	GCCAAAATAAAGGGCACTGA	60.074	TCTCTTGCTGTGTGCTG	60.175	228
286	Contig5330	(A)14	GTAATCTTCGTTTCGTTCCGGG	59.569	TTCCATGATGCACACAAACC	60.376	207
287	Contig5333	(CCG)6	CTCACTCACCACCTGATCCA	59.659	AGGTGAAGGAGCAAAGGAT	60.212	219
288	Contig5335	(CCA)6	GGCAAGATAACAAGCAGGG	59.708	CTCCACATCCATCCAGGACT	59.92	270
289	Contig5335	(A)12	CTGGATATTAGGTGGCGAA	59.916	GAGGAATCTCCGTTGGGAT	60.272	204
290	Contig5336	(A)10	CGCCAGCTTCTCTAGTCTCA	59.906	CCAAATTAGTCGCCGTTGTT	59.996	212
291	Contig5337	(T)10	CTATCAGCCGTGCCATTTCT	60.235	ACCCTTCCCTCATTTTGACC	60.169	270
292	Contig5371	(TTC)5	ACTCTGCATTTCCACTGGCT	59.874	TC AACCAGAGAACCAAAGGC	60.232	203
293	Contig54	(CT)9	GCAACTATGGTGCTGGAGGT	60.142	TTCCTTCACAAAACCAATCG	59.244	271
294	Contig5482	(GGT)5	AGAACGCCCTTGACCTTTAT	59.962	TTCGCTGTTCGTCATC	59.847	240
295	Contig5487	(TTG)5	AGTCGTGGCGATCTCTGT	59.874	GGGTTTTCTCCGAAGGTA	60.291	258
296	Contig5499	(AAG)5	CTTCGCCAAAAGATTCCAAG	59.817	AACTTCCACTCGCTTTCCAA	59.853	278
297	Contig5516	(AAT)5	CGGAGCCAGTTGCTGATAGT	60.419	ACATTCACACCCATCCATCTC	59.652	210
298	Contig5524	(A)11	CCCACCATTTCCAAACCTTA	59.657	GTAAGTGGCCGTGGAAGAAA	60.11	269
299	Contig5537	(T)12ggtaacagacatgctttttagatatatcaggactaattaagctaatTTGactatagacaaataatgc(T)10caaaattgaggatcatttaacatattggaacttatgaagaagtattcatt(A)10	CATAGTGCCCATCAGCTTCA	59.823	AATCAGCATGTATCTAAAAACAATCA	58.3	261
300	Contig5552	(CT)7tgtgctttgc(T)10	CATCAATCTCAAAAACCTGG	59.415	GGCGGATTATTTCGACTCTTG	59.668	247
301	Contig5596	(GGGTCC)5	TATTCTTTGGGGTCTGGTIG	59.784	GCTCTCTGCCACCCTCTTTA	59.574	225
302	Contig5607	(T)10	CACAGCCTTTGTCTTCCTT	59.328	AGGGTTCCTTTGAGTGATG	60.111	217
303	Contig5615	(A)11	GCCCGAAAGAAAACACATA	59.938	GGAGCAGTAACGGGAATGAC	59.556	253
304	Contig5633	(A)13	TTCCTCTTTGTAGTCTTTGGA	59.548	ATGGTACCTCATCTGGTGGG	59.655	278
305	Contig5643	(T)10	TTTGGGATGAGAACTAACGA	59.555	GATTCCAAGAAGCCAAGCTG	59.955	206
306	Contig5682	(A)15	TGGATTGCATTTTCTAATGTTGA	59.485	TTCCCTTTTTGTCTTCA	59.518	259
307	Contig5713	(AGA)5	TGAGCTTCGTGTTGTGTCT	59.528	GTGGGATGGTCAAGAAGGA	59.903	223
308	Contig5744	(T)13	ATCCAAAACAATCTACCG	59.79	AAAAGCCAGGCACTGAAGAA	59.993	220
309	Contig5754	(GCT)5	CACGAAGACCCAACAACAAA	59.585	GTGGAATTACGGTGGCAGT	59.859	232
310	Contig5764	(T)10	GGTGATATGCTTGATCGCCT	60.066	ATGCACCTTCAATTCCCAGG	59.933	278
311	Contig5765	(GCT)5	TTTCGTTACAGCGTTTGCAG	60.052	GAAAAGCCCTCTTAGCACC	60.208	207
312	Contig5765	(CCT)5	GCCAAACAACATTCAACAA	59.42	GCCTCCACTGCTCTCAATC	59.957	263
313	Contig5778	(T)16	TGCAGCTTCACTGGAAGAG	59.314	GAGCAGAAACCATAACCCCA	59.933	278
314	Contig5778	(AGA)6	TGCAGACAGAAGAGGAAAGTGA	60.171	TGGGTGGTTTTTCAGATTGAG	58.541	251
315	Contig5780	(A)10	AATGTGGCACTTCTCACC	59.973	ATTGCAGAGATAACGCCACC	60.103	279
316	Contig5850	(TCC)5	GATGAGACGGAAGGAGTCCA	60.199	AGCATGAGCTGCAGGATTTT	59.985	264
317	Contig5884	(A)10	TACAACCTTAGCCTGCCTG	60.262	GCTCTCAATGGGGTGAAAAA	60.051	246

318	Contig5898	(A)10	ACGGATCATTTTCCTTGTGC	59.939	CGGATGAGTCAAACCTGGAA	61.034	279
319	Contig5916	(T)15	TTCATTGTCTACAAGCCCC	59.933	CGAATTGGAAGTCGAGGAA	60.184	206
320	Contig5917	(A)10	ATAAAACCCGGGAGACCACT	59.691	ATTGTCTGAACCACCTTCCA	60.495	202
321	Contig5932	(CT)6	TCTTCCTACTCCCAACCCCT	59.928	GCTGGTCCTTGAGCTTATCG	59.978	259
322	Contig5948	(T)11	GCTCTCAATCTCAATCTCACTTC	59.92	GGAGGGAACCTTGAGGGAAC	59.912	207
323	Contig5967	(T)10	TCTCTGAGCTGCTTCATTTC	59.708	ACGAACAGATCTGCCTGTA	58.315	278
324	Contig5974	(AT)7	CTGCTGCTGCCAATTAGACC	60.934	CAGTTGGGGAGGCTAACAAA	60.103	276
325	Contig5983	(AG)6	TCTCGCCCAATTTCCACTATT	59.528	CCGATGAGCACAACTTTGAA	59.84	231
326	Contig5986	(T)10	CCCTTTCAAAATCGGTGAAG	59.541	GAGTCCCAATTTCTCGACA	60.05	221
327	Contig5994	(T)11	GAGTTTGGGATTACAGCCGA	60.074	TGGATTCTGTGCTCATTICA	59.262	263
328	Contig5997	(T)10	AGATTAGGGTAGGGGGCTTG	59.438	GCGAATGACAAGAGCTTATTTTG	60.264	252
329	Contig6021	(T)11	TTTTTCCCCCTTTGCTTTTC	60.393	CCCAAACATCACCTTCTTCAA	59.956	204
330	Contig6028	(T)17	ATTGGCAAAGTTGTGAGGG	59.971	ATGAAAACAATTAAGCCAGA	57.351	223
331	Contig6045	(T)10	TAGGGTGTCCAGTGGCAAAT	60.375	AAAAACCTTAAACCCACAGAA	58.948	232
332	Contig6059	(AGA)5	CATCCCTGCAAACAACCAC	59.951	GAAGCAGCCATATCCAGAGC	59.946	238
333	Contig6064	(T)10	CCCCCTTCAACTGCAATAGT	59.052	ACATATCGATCCGACCTTGG	59.773	268
334	Contig6073	(A)12	AAATCCGACCTGAAAAACCTT	59.805	AGGGAAAGGAGATACGGGTG	60.319	279
335	Contig6100	(AGT)5	TGTGTCTTCCAATAGTGAATGAGC	59.256	GCAATCTTGGTTTGGTTTTTIG	59.483	204
336	Contig6104	(ACT)5	TTACCAGCATGTGGTTTGGA	59.964	GGACAAGCTGAAGCGAGAAG	60.277	228
337	Contig6165	(TTC)5	GCCACCCTCAAACCTCTCTTG	59.844	CAACCACCGTTTCGATTCTT	59.971	269
338	Contig6166	(CT)8	CATCGAAAAGAGGAAACACGA	60.234	GCTCTTCTTGGATGACTCG	59.95	226
339	Contig6236	(T)10	CAAGGAGGCTTCTCAACTGG	59.982	TCAAAATTCAGGTACAAGCAACA	59.677	210
340	Contig6268	(AGA)5	GTAACCTTTGGTTGCGGGAA	59.975	AGCAGGTTGGAGCTCTTGAA	60.134	256
341	Contig6274	(GCA)5	ATCTTGCCGCTGAGGTATTG	60.235	TAGTAGCCTTGGCTGTGTCT	60.037	252
342	Contig6298	(CCT)5	CATGACCATCGCCCTTTC	60.006	GCAACCACATTTCTCACAA	59.697	263
343	Contig6302	(GA)7	CTCGTTTGTAGCCGTCCATT	60.132	AATGTCTGCCATTTAGGTCTG	60.096	222
344	Contig631	(T)10	TTTCATCACTGCTCATCTTCC	60.211	ACGCCGTTGGTGAAGATAC	60	255
345	Contig6328	(AGA)5	ATTCTACCCACCACCACGAG	59.844	CTTCTCCATCTCCCTGTTCCA	60.34	269
346	Contig6328	(T)14	TGTACGGGGAAAGTGAATC	59.79	TGGTTGGTTTGGTTTGGTTT	60.103	254
347	Contig6332	(T)11	GAAGAAATGCGGGAACAAA	60.053	CCTGTGGTTTTATACCTCTTGA	59.42	274
348	Contig6336	(TCT)5	TGTTAGGTGGTAGAGGGCG	60.125	ACTGTCTGAACCCCATCTG	60.111	278
349	Contig6347	(T)13	GTCGGCTAAATTTACAGAGC	59.851	TGAGAGCGTTGGTTTCACAC	59.88	251
350	Contig6364	(GCG)5	ATTCGGTGTGCTGCGAGAAG	60.397	ATTGATACGGCGAGAGCAAG	60.374	215
351	Contig6369	(TCC)5	ATCGGATTCAGCAATGACC	59.9	GCCCGTTGTGAGTACGAAAT	60	271
352	Contig6398	(T)12	TACACCAGTCTTGGTCCCAT	60.238	AACCGTGAACCAACCCTTC	59.867	255
353	Contig6403	(T)12	GCTGAGCTCTGGTCCGAAAG	60.284	ACTCTGTTTGATATGCCGC	60.103	237
354	Contig6438	(T)16	CTGGCAACAGGCCCTTCTTA	60.529	TTGATCCCCATATGAAGCC	59.722	250
355	Contig6462	(CAC)5	CTCCCGCTCGACCTCTTT	60.191	CCGTCACCGTCAAGAGTACA	59.745	223
356	Contig6507	(AGG)5	CCAACCCACACAAAAAGC	59.992	GAAAGAACAGAGCAGCAGCC	60.285	265
357	Contig6515	(CCT)5	AGACCCCATCTCTTCTGT	59.929	CTTCTTAACCTCCACGCAGC	60.015	260
358	Contig6537	(T)11	CATTGGAGGACCTGCTCTG	60.791	AAATGCACTCTGCCATTTC	60.081	265
359	Contig6559	(TAC)5	CCAATGGGACCAAAAACACT	59.688	AAAATGAGAAGACTAAAACTAAACCA	57.47	274
360	Contig6573	(T)10	TTCATCATTTTGGGGCTACA	58.965	AAACCCAGATGAGCAACTGAA	59.726	254

361	Contig6595	(GCC)5	CGACTACGGCACCGTTTAAT	60.018	GGAGGTGGTGGTTGTTATGG	60.088	237
362	Contig6603	(T)15	ATATGGTAGGAACACCGGCA	60.214	GGCCAGACTATGAGGATTGC	59.658	258
363	Contig6619	(T)10	TGGCCTTTTGTTCAGTG	60.131	TTCCAAGTCTCGGTAGCCTC	59.43	267
364	Contig6624	(A)11	TCCTCTCATATCTTCTCATCTTCTC	59.797	GATAGCGACGCACCCATAGT	60.125	233
365	Contig6627	(TC)5	AGAAGATGAGATGGGAGGGG	60.412	ATTGATCAGGAATGAACCCG	59.75	254
366	Contig6643	(T)15gctttgggttctgcaatt ttgctcttctttaagcctgagaat ttgatgaatc(T)13	CATGGCGATTTTCAGGTCT	60.074	TGCTCTTCAAAAACTCCTCC	60.548	245
367	Contig6648	(T)11	TCTCTGTTCACCCACCTCT	59.682	AATTTTGACCAGAAGTGCCG	60.11	245
368	Contig6662	(AAG)5	CGGAGGATGGAATAGCAAAA	60.031	TACAACCCAGCCATAGAGCC	60.096	219
369	Contig6732	(T)11	AGGGGCTGGTCTCGTTTTAT	59.962	TGTAATCTCTCCACAACCTCAATC	59.526	209
370	Contig6741	(AGG)5	ACACCACCACCTTCAACC	59.859	TCTCCTCCTCTGTAGCCA	59.943	251
371	Contig6748	(T)10	CCTTGGCATCTCTCCTTTG	59.948	TTGAACCATGTGCTACTACCAA	59.036	230
372	Contig6749	(TC)5	TGTGCTGTGTAACCAACGTCCT	60.102	GTTCAATCCAGCAGCAAT	60.081	269
373	Contig6782	(A)11	CCCGGTCTCCTTCGAGTAGT	60.64	TGCTGTGCTATCAACCAGT	59.621	261
374	Contig6785	(TTC)5	TCGTTTCGATTCAAGCTGC	61.42	ATCTTGCCCTCCGAAGTTTT	60.074	256
375	Contig6790	(TGA)5	TACACTCGGGAATCCGAG	60.066	GATGCTCCCTATAGCCCC	60.024	265
376	Contig6801	(A)12	CTTTCTGGAGTGCTTTGGG	59.846	TCACCAACCAACATCTCTGC	59.547	280
377	Contig6815	(AGA)5	AGAGAATTGCTCAAGCCGAA	60.096	TGTTGCTTGCAATGGTTTCA	60.142	223
378	Contig6865	(T)10	GAAGACGGTTATGAACCCGA	59.933	ATGATGTTAAACGAAGCCCG	59.96	278
379	Contig6883	(C)10	GATTCCTCTGCTCCTTTTC	60.154	TGGCTGAAAATCTGAAAACC	60.051	254
380	Contig6897	(ATC)5	TTTTGGAAAGTGAGCCCATC	60.051	ATGGCATGGTGCAATTAGGT	60.221	230
381	Contig6916	(TCC)5	ACAACCAAAAACCCATTTGA	60.066	AACCAACGAAGTCACTGCC	60.156	238
382	Contig6951	(T)11	TGATGAGAAGGATGATGGCA	60.161	AATCCTCAGCCGTGTGTTTC	60.119	257
383	Contig6992	(CTA)5	GGTTTTCTTGGACCCAAAGG	60.694	TCCACTGAAGACATTTTCGCA	60.39	247
384	Contig6996	(A)11	GCAACTCACTCGCAACAGAA	60.183	GGCAAAAGGTTGAACCAAGA	60.088	256
385	Contig7003	(ACC)5	GTGAATGTCCCATCTGCCTT	59.934	TTATCGTCACTGGCTGCTG	59.972	278
386	Contig7025	(GGA)6	GATAGGCGAGAGCACAAAGC	60.125	TTCACATGGCTAAACTACCA	59.184	219
387	Contig7060	(T)13	GCTGTGAAGGGAGCAACTTT	59.478	TTCCCAGCCATTAACCTCAG	60.066	241
388	Contig7068	(T)11	ATGGCAAGATGGTTACACGA	59.002	GCTCTGCACTGTGATCTTC	59.957	278
389	Contig7068	(T)11ggt(A)10	GAAGGATCAAGTGCAGGAGC	59.957	ATTTTCGGTTTGTATTGTAAAAGCA	59.06	218
390	Contig7070	(GGAACC)5	CGGAGTTTTCAGGATAACGGA	60.066	TTCAGGCTCTCCGTTCAAAAT	59.813	272
391	Contig7079	(TCT)6	TCTACACTTTCTCCAGGCC	59.284	AAGAATGGTGCCTTGACCAG	60.111	275
392	Contig708	(T)12	CCCACCGAGTTCTACAAAA	59.964	CAGAGGGTTGTAAGAAAAGCAGA	59.935	258
393	Contig7093	(TCT)6	CCTGCTGGACGCTCTGGTTAT	60.134	CCCACGCTCTTCCAATGAT	59.927	274
394	Contig7108	(ATA)5	AAGCCAAATCAGAGCCAGAA	59.955	GAAAAAGCAAGGAAAAGCC	60.184	228
395	Contig7150	(ACT)7	GACAACCAAACTTCGCAA	59.74	GGCATAGCCGTTTGGTTAAA	59.964	229
396	Contig719	(T)16	CATTTGGGAGTTTCGGGTA	59.795	CTCTGCGAGCAATCTGATGA	60.249	218
397	Contig7194	(T)13	TGGTGAATGTCTTGCTTGA	60.24	TACCTCACCGGCCATTACAT	60.214	221
398	Contig7197	(TC)8	CTGCCTTTCTCCCTTCTC	60.319	GTGTCCGGGTTCTCTGTG	60.545	268
399	Contig7198	(A)10	TTCACCCTTCGGTATCTGAAA	59.555	TTGATACATTTGACAGCGAAAA	58.355	279
400	Contig7204	(T)10	GCGGTTATGATTCAGGCACT	60.103	CAAAAACCGCTCAAGTTTCA	58.939	278
401	Contig726	(A)16	TTACAGCAACAGCCGATGAG	60.011	GGGAGGGGGACAAGAGATA	60.264	259

402	Contig7275	(T)12	TATGGAAGGGAAGACGGTGG	59.926	CACATAAAGGGAAGATGCCA	59.946	216
403	Contig73	(TGA)6	TTGGAGCTATGAAGTTGCC	60.214	ACATGCAAAATGCACAACCAT	59.854	259
404	Contig7312	(A)13ggagatatttttttct ag(T)12	GGCGAGTGGATCTAAGCAAA	60.352	ATTAGTTCCACCCACCTA	58.24	280
405	Contig732	(T)13	GATGATGAGCAGCAAAAGCA	60.104	AGGGGTCAACTCATACCCA	59.259	265
406	Contig7341	(T)10	AAGAAATTTGCTGCATGGC	60.217	TGAAGAGGAGGGAGAGGAGA	59.049	205
407	Contig7349	(T)10attaggccctgtcttttt acttatttcagtaaatcagttca	GCCCTGCTTTTCTCTCTCT	60.096	CCCGGTATGAATCTTGCCATC	60.296	244
408	Contig7400	g(A)15 (T)13	GGAGGAAGAAAGTGGTGAGC	58.868	CCACCAATCCTCAAAACAACC	60.21	237
409	Contig7407	(A)10	CCCACATTTTGGATTTCAG	60.301	GCAGTCAAGTGTGCAAAAGC	59.646	255
410	Contig7415	(T)12	GATGATGACGGCCTTGAGAT	60.042	ACAGACACCTCTCACCATAAAAA	57.792	271
411	Contig743	(CCG)5	TCGCTCTCTCTCTCTCTG	59.973	CTTGAATCCTTTCCCGCATA	60.031	239
412	Contig7438	(T)13	AAGGCTTGGCCGAAAAGT	60.11	GCCCAATGATGGGATAAAAA	59.599	249
413	Contig7461	(AGT)11	AAAATGCGAGGCATCAACTC	60.081	TAGCAGCAAGGCAGAGCATA	59.879	210
414	Contig7463	(T)10	AAGCCATTGTGGTGGAAAAG	59.971	GACGCAACAACACGTCAGTT	59.801	280
415	Contig7469	(A)10	GAACCCAAAAGGAAGAGCC	60.053	TGATAATCTCAACCACCATCTATA	60.04	274
416	Contig7494	(GAA)5	ACCGAACCAGCAAGTTTCAC	60.156	GGATGTGCCCTCTCCACTAA	60.073	274
417	Contig7510	(A)18	CTCTGGTCCCCTCCCTCCTC	60.336	CATGACCTGCTTCAGAGCAA	60.136	260
418	Contig7510	(CT)7	TGCCATGTTGACTTGGGTTA	59.964	TAAAGGTGGCAAGAAGTCGC	60.386	217
419	Contig7510	(A)10	TCCTTCGACCAGATGTTCT	59.655	ATGCTCTCAGGCTGGTTGG	60.261	203
420	Contig7535	(T)15	TCGGGTTGAGCTACTATGGG	60.088	AAAACCTCTCATACAATTAGCA	57.071	244
421	Contig7540	(T)12	GTGATGGGACTTGAGGAGGA	60.048	AACATTC AAGACGTTTTCTAGG	58.106	254
422	Contig7559	(AT)6	TGATTCGGCCCTTGTCAC	59.831	AACCCACAGATCAAAATCACA	60.225	231
423	Contig7617	(T)10	GGAAACGGGATTTGCTCATA	59.901	CAGAAGGCACAAAATGTCAC	59.78	223
424	Contig7626	(TA)7	GTGAAGCTAAGGTGGTGGGT	59.065	TCCAAAAGGCTTGAAATTGG	60.046	242
425	Contig7642	(GAA)5	TGTTCATTTCGTGGTTCA	59.941	TTAGGGTAAACAACCGTGGC	59.861	249
426	Contig767	(T)10	CAAATGCACCAAGGATGATG	59.924	CAATCCGTCTCAATTGCTT	60.074	270
427	Contig7689	(A)10catacaacttaaatgc taagattaaaattaaacacaat gattaactagtacaagagg(T)1 5	ATTGATGCATGGGAGCTACA	59.105	TGACTGAATCTGTTGGCCTT	58.287	251
428	Contig7693	(T)14	AGGTTTCTGCTGATGTGGCT	59.874	TGCTATTTGAAAAGGCGAGC	60.476	272
429	Contig7695	(TCC)5	CCTTCTCTCTGCTTCCCG	60.126	CACGGAGCAATTC A AACA	59.84	266
430	Contig7696	(T)12	AAAGTGCAACCTTTTCGAG	60.42	GTCAGCAACTTGGGCTTTT	60.118	275
431	Contig77	(AG)7	AACAAAGCAAGGAAGGACCA	59.711	CCAACTCCGGAGAAGATCA	60.187	238
432	Contig7708	(T)13	AATCGCTGCTGTTTTGTTT	60.257	AGCAACCAAGAAACATCAATA	59.939	232
433	Contig7708	(A)14	CCTCTCAGCTTTCCAATTCA	58.02	TGAGCTTCACTTTGTGTGCC	60.032	213
434	Contig7718	(TGT)5	AACCTTCTTCAAGCCCCAA	59.711	TTGGTCTCAAAAGGCAGTCA	59.415	271
435	Contig7723	(GAA)5	TACAGGGCTAAGCAGGATGG	60.227	AACCACGCTCAAAACGAAAT	59.615	262
436	Contig7737	(A)11	GCTTCACTTTGGCCCTCTAA	59.41	TTTCCCATAGAACAACCG	59.795	235
437	Contig7757	(TGT)5	TAATCAAAAGGCTGGGCAGT	59.708	TCATGCAGATTCCTGATTGTC	60.081	271
438	Contig7760	(T)10	AGTGCTCTGGATTCTGTTGG	60.261	TGCGAGATAGATGCTCATGC	60.088	237
439	Contig7792	(AC)8	GCTCAAGAAGTTTCGTTTTCTCTC	60.063	AAGGAGCCTCTCACCTCCTC	59.952	206
440	Contig7796	(TAA)5	AACGTCGTGTAAGGCTGAT	60.02	GGTCATGTTTCGCTTGAT	60.935	231
441	Contig7799	(T)12	GCTTTTGTAGCTGGGCAGAC	60.022	TCAAATAGCAACATCAGAAAATA	59.827	216
442	Contig7812	(T)11	GCCACTATACCGTACCCAT	59.7	GTAATAGACCAGTCCGCCCA	59.955	236
443	Contig7836	(TAA)5	CGGCAGTGCATTC AAGTA	60.011	GCCTGGGAATTAGCAACAGA	60.214	238

444	Contig7861	(T)12	CGAGAGTTCCATCAGAGCG	59.666	GAAACAGAACTAATACTTTCCAATGC	58.795	221
445	Contig787	(A)10tggaaatataatgttctctctcttcttctta(T)12	ATGCTGTGGCAGTACAAGA	59.47	TGCAAAGTTTACATTTGTGTAAGA	58.894	236
446	Contig787	(A)17	CGCATTTTATATTTCTCCCAA	58.212	TTTTAGGCAAGCTGTTACAG	59.108	220
447	Contig7893	(ATD)5	CTATTGGAAAAATGGCGGAGA	60.031	TCATTTTAAATCACTTGAGAAGCAA	59.363	276
448	Contig7899	(A)11	CACATCACAAACCAACTAATTGA	59.107	TCAAGCCATTCAGGAGGAGT	59.803	280
449	Contig791	(T)12	TTGGGAAAGTGAATCAGGG	59.903	CAAGCGAAGAAAACAGTGTC	59.906	254
450	Contig7937	(TCC)5	TCTCCAAGCTCAAGTCGGTT	59.989	ACAATCGGACTCACCAGACC	59.969	233
451	Contig7941	(A)17	TTC TTCACA TCCCTTCGTC	60.05	TGTGGATTGATCGGTTC	60.526	273
452	Contig795	(CCA)5gctgtcaacagcttgagttggcaataata(T)10	ACAACGTGTTTTCGGAGACC	60.012	AACACAACACCTTTCCTCCG	60.005	251
453	Contig796	(GAA)5	GTTCTCACTCGCCACCTCTC	59.993	GTTACCGGGTGAACGCTTTA	59.996	238
454	Contig7970	(T)10	TCCGATGTAAGAGAGGTCGG	60.21	GCACCTACCCAAGCCAGTAA	60.132	231
455	Contig7976	(A)16	CACGGCTTC TTTCTTGGAG	59.986	GGGCTTTCGATCCACTGTAA	60.074	230
456	Contig7983	(A)11	ACCCATTCCAACAAGACCAA	60.21	CATGAAAGCAAATAAGATTGGG	58.629	215
457	Contig8015	(T)12	CTCCCTTGC AATTTCTTT	60.423	TTGGGTCTACGAGGGTCTG	60.103	203
458	Contig8016	(T)11caagtgaagggtgacatctgagagaccacaaaagggtgaaataatgatg(T)10	GAATTGATGTTTTGAAGCCAA	59.101	TTTAAGACTGCCAACCGAC	60.11	271
459	Contig8018	(T)12	TTGGGCTGTTC AAGGTGT	60.529	TCCACAATTTCAAGCAAAA	59.133	267
460	Contig8019	(AT)6g(A)11tgggtcttggatag(T)12	TGTGTTATGGAAGGCATTGG	59.395	TTTTCTTGGCACACTCTCA	59.415	235
461	Contig8044	(A)10	AAATTACACGTGCGGTTTT	59.652	GICCAAAAATTCATCATCAAACTAA	57.278	256
462	Contig8067	(T)10	CAGAGAAGACAATGGGGGAG	59.649	CCAAGAACGCCACACTAAT	59.993	235
463	Contig807	(GAT)5	AGTTCAATCCAGCATTGGCT	59.7	ATTTCCAATGCGTGCTCC	60.119	279
464	Contig8084	(TGA)6	GTTACCCATTAGCAAGGAGGG	59.843	ACATGCAAAATGCACAACCAT	59.854	246
465	Contig809	(TTC)5	TGCATCCCACTATCAACCAA	59.924	ACATAGGTTTATGCCCTGGA	60.34	223
466	Contig8150	(A)12	GCTTTGTGGCAAGCTGAGTA	59.224	TGATGGAGACATTAGCACGC	59.83	280
467	Contig8198	(A)10	GGCCAAAGCCAATACAAGAA	60.074	TGCAAAATTTCTCCCATCTC	60.014	218
468	Contig8206	(T)10	TGCAGCACATGATGTATGGTT	60.011	CAAGTGCCACAGTTCTGGA	59.873	275
469	Contig8272	(ATC)5	TTGTCCTCGGTTTTCAAGG	60.081	AAACAAAGAACTAATCCAGCC	58.694	280
470	Contig8290	(ACA)6	TATTTGGGGCATTGCTTTTC	59.907	AGCCAGATGGAAACCTGATG	60.073	269
471	Contig8304	(CTD)5	GTTCAACAAGCAGAGCATGG	59.445	TGATAGGGAGAAGCCTTGG	59.767	244
472	Contig8310	(GAT)5	TTTCAATGATGCTGAGAGCG	60.096	CATTTCAACACCAACGATGC	59.972	270
473	Contig8330	(TA)6	TCTGTTATCCCTCCCTCGTG	60.065	TTGCACAAAATTTAAGGTCCA	59.511	202
474	Contig834	(A)10	TTGCACACAAAACCCAGAAA	60.127	AGGATGATTTTCCAGCTCCA	59.629	247
475	Contig834	(AGA)5	GGTTTTGCACCATGGAACCT	59.836	ATTGCTGGAAAAGCTGTTGG	60.249	200
476	Contig837	(TC)7	TGCTTATGTTCAGTTTGGG	59.982	TCTTATCAGTTCGATCCCC	58.934	254
477	Contig8389	(GT)9	GGGAGAGACTCGTTCGTCTG	59.986	AGCATAACACTCCAGGGGA	60.678	261
478	Contig8393	(TC)7	CAGGAAGGAGAAGAAGACCA	59.988	CGAGGTTAACACGGGGTAGA	59.986	222
479	Contig8395	(T)17	TTGGGATTCACAGTGTGTG	59.831	GAGGCCCAAGAAGGAAAATC	60.017	254
480	Contig842	(T)14	ATGATTTCCGTTTAAACGACG	57.925	AACAACCTTCTCAAATAGGACAAGA	57.692	273
481	Contig842	(TAC)5	GAGATAAGCGAATTCGTGGC	59.813	GTACCGAGTTACCGAGCCAG	59.757	249
482	Contig8435	(T)10	TCCGGTAAGAACATGCTTTG	58.771	CCGGTTCACAACAATCAGC	60.104	277
483	Contig8437	(T)11	TGAGCATCCAACGAATACCA	60.073	CAGACACATGAAATTTGAACTAAA	58.759	280
484	Contig8455	(T)11	ATCTACTGCCTTTTCAGGCG	59.476	CTCACAAAAATCAATTAGCTTCA	59.68	214
485	Contig8464	(T)14	ATACCAAGACGCCGATGAAG	60.096	AAACCTGATGAGTTCCTCAATTT	58.87	267

486	Contig8481	(A)11ttcagtcacctaaag agatgcagaatttgaatagtcgc tgcagttgtgaccaaaaagataa caattttgtggagag(A)10	AGATTATCGTTTTTGGGGCG	61.155	TGAAAAGTGTATTAAACCACCG	58.176	253
487	Contig8483	(A)10	GAGCCCTATCGTGGTCACTC	59.685	CCAGCTTCGTGGGTGTTGA	59.873	264
488	Contig8505	(T)14	CAGGGAAGAAAGTTTGCCA	60.22	TCAGACTGCTCCATCTAGCA	60.154	250
489	Contig8507	(T)10ccttcataaatgaatcet gggattgcaattgttcacattatc cttatgggtttgttcatttaggatt taccatgtttgaattcttccc(T	ATTGGATTTCGACAGTTTCCG	59.933	TTTTTCCATTTTCATCCATCG	59.759	271
490	Contig8541	(T)12	TAATGAGCTGGATGCGAATG	59.792	TTCAAAAATGACACAAACCCA	58.903	234
491	Contig8547	(ATG)5	CCACTCTTGGAAAGCCTCAG	59.982	CACAATCTCCCTAACCCCA	59.784	279
492	Contig8558	(T)17	AGGGAGCAACTTGGAAACAGA	59.844	AGCCCCATCATTACCTACCC	60.039	226
493	Contig8565	(T)14	AGTGTGCCCTCAAAATGAACC	59.973	AACACAGCGAGATGAGGTCC	60.269	223
494	Contig8574	(TA)6	TTTCCAAGCCGTCTGATICT	59.813	TCTCATAAATGCGAGTATTGTTTT	58.41	253
495	Contig8612	(T)11	GTAGGAGGAGGAAAAAGGC	59.171	TTTCCACCATCAAGCACAAA	60.088	241
496	Contig8613	(T)11	CCATGAAAATCACCTGCTT	59.933	GGGCTCACCTAACCTATCCC	59.789	279
497	Contig8617	(TAA)6	GGAACACAAAGTAGGCCCAA	59.971	TAAACCAGCTCCACCTCGTC	60.255	241
498	Contig8649	(GAT)5	AAGCGTCATGCAAATATCCC	59.929	CAGAGAAAATCCCCACAATG	59.415	219
499	Contig8656	(ACC)5	AACCCCTAATCGGAAAATGG	60.013	CGAGTTAGCTGGAAGATCCG	59.971	255
500	Contig8660	(A)10	TCGGTAGATGCTCAACCCCT	59.694	GCAACTCCAAATCAAGCTC	58.965	264
501	Contig8663	(T)11	CTGGTTCGAGGATGTGGAGT	60.112	ATTATCCAAAATATGAAAAGCACAT	57.314	202
502	Contig8667	(AGA)5	ATTCGTAATGGCACCAAAGG	59.823	TGTTCAATAATCCCCATGGCT	60.155	239
503	Contig87	(T)10	TGAGGGACATACTTCCCAGG	59.92	GGCAAAAATCGCTAGAACC	58.976	241
504	Contig8761	(CAT)5	GGGACTAGAACTGCCACCA	60.111	ACTCACAACTGCTGACACCG	59.94	208
505	Contig8840	(T)11	GCGAGGAATGTGACAAGGTT	60.119	CCCAATTCACAATACAAAGAAAGA	59.432	251
506	Contig8892	(TC)6	TTCCGTTATCCATTGTCTTCTC	59.493	CGAGCATCTAGCTTGCCTG	59.911	262
507	Contig8904	(T)10	GCAGCAGCAAATCTCCTCTT	59.723	TCTCCTCAAATCCCTGAAAAA	58.749	280
508	Contig8928	(T)10	CAGGGTACCAAAACTCTGGC	59.592	TGCTGAACTAAGGGATTAATAATG	58.797	245
509	Contig8967	(TG)6	GGAGAAAGTGAAGAGCGTGG	59.989	ATCAGTGCAACACCAAAGCA	60.31	228
510	Contig90	(T)10	ATGCTTGACCAACCCAGTTC	59.973	TTCCCAATCCAATCACAAACC	60.56	244
511	Contig9006	(A)14	GCCGCTTAGGTGTGGTGT	60.035	TGGTATTGCCTCAAAACTCAA	59.625	257
512	Contig9015	(T)10	TAGTGAAGGAAATGAGGCGG	60.206	CAGTAGTTGCCCAAAATGCC	60.502	247
513	Contig9083	(T)10	TGGAAAGATGAAACTTGGGG	59.903	TTGGATTGAACCACCACAAA	59.792	229
514	Contig91	(A)10	TCACCCCTTCAGTCTCCAC	60.088	CAGTATCGCCCTTCTCTCA	60.353	270
515	Contig9102	(T)11	CAGGAAAGTGGTTGGTTGCT	60.149	AAACCGCTTCTACCACATCA	59.623	255
516	Contig9118	(A)16	GAAAGCTGATGTGGCAATGA	59.805	AGCCTGGATTCCACAAAACA	60.495	271
517	Contig9133	(T)14	GCACCTTCCACTACTCTCA	57.87	TCATGTTTATTAATTATGGGCTCG	59.321	280
518	Contig9166	(CTC)5	CCTCTCTATCCACCACCAA	59.92	TTTTAGTTGCGGATTTGGCT	59.72	252
519	Contig9173	(AAG)6	GGATAATGAAGCACCGAAA	59.901	CCATAGCCACTGGGTCTTAA	59.948	234
520	Contig919	(T)10	AGGTGTGCAAAAGCAGGAGT	59.914	GGACAAATCTAGCTAATTGCCCTA	60.016	254
521	Contig9210	(A)10	CAAGAGACGCATGCAGGATA	59.972	TCAACAAAGCATCATTAACAAA	57.473	202
522	Contig9221	(T)10	TGTGACAGCTGAAAACCTCGG	60.025	GCAATGTCCAAAATCTCTCAA	59.93	259
523	Contig9222	(T)12	TAGCAGTGTGAAACAAGCGG	60.05	CACAGTTGCTCCACAACCTCA	58.401	265
524	Contig924	(T)12	CAAAGACGCCCTCTGTATC	59.694	TGAACAAGTAGCCACTGATG	58.787	232

525	Contig928	(GAC)6	AACGGTGGTAAGAAAAGGCA	59.609	AAGAGGAGGAGGAGGAGGTG	59.801	241
526	Contig967	(AGA)5	AACGAATCTGGGCTTTTCCT	60.074	CAGGCAGATCCCCACTTACT	59.162	247
527	Contig969	(CCT)5	TCAGCAGAAAATCCACCTC	60.195	GCGGTTATCCGATGATGAG	60.435	234

Table S2. BLASTx results of EST-SSR Contigs.

Sl. No.	ID	Function
1	Contig1000	tubby-like f-box protein 5-like
2	Contig1016	aspartic proteinase-like protein 2-like
3	Contig1028	spx domain-containing protein 2-like
4	Contig1055	vacuolar iron transporter homolog 4-like
5	Contig1058	protein kinase g11a-like
6	Contig1069	protein mon2 homolog isoform x2
7	Contig107	stem-specific protein tsj1-like
8	Contig1099	dnaj heat shock n-terminal domain-containing protein
9	Contig1111	ring-h2 finger protein at146-like
10	Contig1126	e3 ubiquitin ligase big brother
11	Contig1149	31 kda chloroplastic-like
12	Contig116	glucan endo- β -glucosidase-like protein
13	Contig1206	transcription factor ilr3-like
14	Contig1211	phd finger family protein
15	Contig1227	glucuronosyltransferase pgsip8-like
16	Contig1229	kinase-related family protein
17	Contig1242	transcription factor lux-like
18	Contig126	at hook motif-containing
19	Contig1265	arid bright dna-binding domain-containing protein
20	Contig1270	50s ribosomal protein 112-a
21	Contig1282	della protein
22	Contig1358	lysine-ketoglutarate reductase saccharopine dehydrogenase bifunctional enzyme
23	Contig136	calreticulin family protein
24	Contig1373	ethylene-responsive transcription factor 9-like
25	Contig1389	ribosomal rna methyltransferase nop2-like
26	Contig1395	expp1 protein precursor
27	Contig1406	el14-like 4 isoform 1
28	Contig142	aquaporin pip1 2
29	Contig1460	l-aspartate oxidase
30	Contig1461	pseudouridine synthase and archaeosine transglycosylase domain-containing family protein

31	Contig1468	glutaredoxin
32	Contig1532	snf1-related protein kinase regulatory subunit beta-1
33	Contig154	60s acidic ribosomal protein
34	Contig1545	two-component response regulator-like aprr7-like
35	Contig1611	glycosyl hydrolase family protein
36	Contig1625	cation calcium exchanger 2-like
37	Contig1641	swi snf-related matrix-associated actin-dependent regulator of chromatin subfamily a member 3-like 2-like
38	Contig1645	transcription factor tcp8-like
39	Contig1650	hydrolase family protein
40	Contig1657	dctp pyrophosphatase 1-like
41	Contig1662	kda class iii heat shock
42	Contig1735	dentin sialophospho isoform x2
43	Contig1773	cbl-interacting serine threonine-protein kinase 1-like
44	Contig1792	protein transparent testa 12-like
45	Contig1804	ethylene-responsive transcription factor 3-like
46	Contig1815	beta-galactosidase 9 isoform 2
47	Contig1821	tetratricopeptide repeat-containing protein
48	Contig1847	ethylene-responsive transcription factor 12-like
49	Contig1851	ubiquitin-conjugating enzyme e2 variant 1d-like
50	Contig1856	upf0136 membrane protein at2g26240-like
51	Contig1862	utp--glucose-1-phosphate uridylyltransferase-like
52	Contig1863	54s ribosomal protein mitochondrial-like
53	Contig1864	cytochrome p450 734a1-like
54	Contig1882	ribosome-recycling chloroplastic-like
55	Contig1886	ca-responsive protein
56	Contig1912	mediator-associated protein 1-like
57	Contig1927	f-box lrr-repeat protein at5g02930-like
58	Contig1945	brassinosteroid-regulated protein bru1
59	Contig1955	pre-mrna cleavage complex-related family protein
60	Contig1958	omega-6 fatty acid chloroplastic-like
61	Contig1964	nucleic acid binding
62	Contig1995	rubisco accumulation factor chloroplastic-like
63	Contig1998	wat1-related protein chloroplastic-like
64	Contig1999	proteasome subunit alpha type-4-like
65	Contig2066	btb poz domain-containing protein at4g08455-like
66	Contig2071	26s proteasome regulatory subunit 4 homolog a
67	Contig2099	benzyl alcohol o-benzoyltransferase-like
68	Contig2116	enhancer of polycomb-like transcription factor isoform 1
69	Contig2130	transcription factor hy5-like protein
70	Contig2135	dna binding
71	Contig2140	protein lurp-one-related 12-like

72	Contig2141	udp-glucuronate:xylan alpha-glucuronosyltransferase 4-like
73	Contig2145	ein3-like family protein
74	Contig2165	signal recognition particle receptor subunit beta-like
75	Contig2175	periodic tryptophan protein
76	Contig2180	pra1 family protein b1
77	Contig2185	glutathione reductase
78	Contig2189	harpin-induced protein 1 containing expressed
79	Contig2190	nadh dehydrogenase
80	Contig22	sugar isoform partial
81	Contig222	aminocyclopropane carboxylate oxidase family protein
82	Contig2226	tetraspanin-6-like
83	Contig2253	seven in absentia of 2 isoform 1
84	Contig2260	flavonol 3-
85	Contig2277	calmodulin binding
86	Contig2283	cell division cycle 5-like
87	Contig230	trm1 12-like protein at 1g78190-like
88	Contig2303	microtubule-associated family protein
89	Contig234	triosephosphate cytosolic
90	Contig2360	uba and ubx domain-containing protein at 4g15410-like
91	Contig2415	zinc finger ccch domain-containing protein 32
92	Contig2438	dof zinc finger
93	Contig2453	protein kinase pt11
94	Contig2462	calcium-binding ef hand family protein
95	Contig2469	cytochrome b5-like
96	Contig2472	vacuolar fusion protein mon1 homolog a-like
97	Contig2503	nad-dependent malic enzyme 62 kda mitochondrial-like
98	Contig2508	haloacid dehalogenase-like hydrolase superfamily protein
99	Contig2515	splicing factor u2af large subunit b-like
100	Contig2518	gc-rich sequence dna-binding factor 1-like
101	Contig2544	t-complex protein 1 subunit alpha-like
102	Contig2558	histone deacetylase
103	Contig2570	mitogen-activated protein kinase kinase 6-like
104	Contig2578	cinnamoyl-reductase family protein
105	Contig2588	rubredoxin family protein
106	Contig2589	endonuclease v-like
107	Contig2599	reverse transcriptase
108	Contig2708	methyltransferase-like protein 13-like
109	Contig2715	serine threonine-protein kinase pbs 1-like
110	Contig2731	wrky transcription factor 48 family protein
111	Contig2739	zinc finger family protein
112	Contig278	homeobox-leucine zipper protein athb-6-like

113	Contig2781	transcription factor tcp13-like
114	Contig2799	wd repeat-containing protein 18-like
115	Contig2808	serine threonine-protein kinase atm
116	Contig2859	dehydration-responsive element-binding protein 3-like
117	Contig2886	isoamylase chloroplastic-like
118	Contig2932	no apical meristem-like family protein
119	Contig299	sulfite exporter family protein
120	Contig3007	gem-like protein 1-like
121	Contig3019	mediator of rna polymerase ii transcription subunit 4-like
122	Contig303	thioredoxin-like 1- chloroplastic-like
123	Contig3051	downward leaf curling protein
124	Contig3095	abscisic insensitive 1b
125	Contig3103	late embryogenesis abundant domain-containing protein
126	Contig3111	adenylate terminal-differentiation specific-like
127	Contig3113	n-alpha-acetyltransferase auxiliary subunit-like
128	Contig3121	transferring glycosyl groups
129	Contig3122	adenine phosphoribosyltransferase chloroplastic-like
130	Contig3132	system protein c
131	Contig3160	legumin a
132	Contig3207	alpha beta
133	Contig3236	p-loop containing nucleoside triphosphate hydrolases superfamily protein isoform 1
134	Contig3242	bag family molecular chaperone regulator 1-like
135	Contig3251	homeobox-leucine zipper protein hat22-like
136	Contig3252	calcium-dependent protein kinase
137	Contig3263	cche-type zinc knuckle protein
138	Contig3284	myb family transcription factor family protein
139	Contig3307	membrane protein
140	Contig332	bidirectional sugar transporter n3-like
141	Contig3332	metal ion binding
142	Contig3346	hnh endonuclease domain-containing family protein
143	Contig336	fe(2+) transport protein chloroplastic-like
144	Contig3369	transcription factor bhlh1 12-like isoform xl
145	Contig3372	nudix hydrolase 25-like
146	Contig3373	ubiquitin family protein
147	Contig3377	humj1 family protein
148	Contig3391	abscisic acid receptor pyl4-like
149	Contig3406	protease 2-like
150	Contig3436	rna binding
151	Contig3445	e3 ubiquitin-protein ligase atl23-like
152	Contig345	lanc-like protein 2-like
153	Contig3487	nuclear movement protein

154	Contig3501	trab domain-containing
155	Contig3505	shaggy-related protein kinase theta-like
156	Contig3508	zinc finger with ufm1-specific peptidase domain
157	Contig3517	kinase family protein
158	Contig3534	2-oxoglutarate and fe -dependent oxygenase superfamily protein
159	Contig3545	serine threonine-protein phosphatase pp-z
160	Contig3574	30s ribosomal protein s6 chloroplastic-like
161	Contig3584	eukaryotic translation initiation factor 2 beta subunit family protein
162	Contig3597	translation initiation
163	Contig3604	serine threonine-protein phosphatase 6 regulatory subunit 3-like isoform x1
164	Contig361	n-alpha-acetyltransferase 10-like
165	Contig3634	rna-binding region-containing
166	Contig3637	short-chain dehydrogenase reductase family protein
167	Contig3649	histone-lysine n-methyltransferase atx2
168	Contig3655	tropomyosin-like isoform x1
169	Contig3664	protein clavata3 esr-related 9
170	Contig3667	nodal modulator 1-like
171	Contig3690	core-2 i-branching beta- -n-acetylglucosaminyltransferase family protein
172	Contig370	peroxisome biogenesis protein 1-like
173	Contig3718	nodulin family protein
174	Contig372	caffeic acid methyltransferase
175	Contig3744	lateral root primordium family protein
176	Contig3792	f-box domain-containing protein
177	Contig3809	dna polymerase zeta catalytic
178	Contig3812	g-type lectin s-receptor-like serine threonine-protein kinase at4g03230-like
179	Contig3822	sugar transporter erd6-like 6-like
180	Contig3825	biotin carboxyl carrier protein
181	Contig386	cyclin-d1-binding protein 1 homolog
182	Contig3881	long chain acyl- synthetase chloroplastic-like
183	Contig389	wrky transcription factor 6-like
184	Contig3905	calcium-binding ef-hand-containing protein
185	Contig391	integrin-linked protein kinase-like protein
186	Contig3948	zinc finger protein chloroplastic-like
187	Contig3958	auxin-binding protein abp19a-like
188	Contig4	dnaj protein homolog atj3
189	Contig402	vesicle-associated membrane protein 726-like
190	Contig4070	pyridoxamine 5 -phosphate oxidase-like protein
191	Contig4071	protein transport protein sec23-like
192	Contig4084	amino acid permease 2-like
193	Contig4141	mitochondrial glycoprotein family protein
194	Contig4163	ein3-binding f-box protein 1-like

195	Contig4194	golgin candidate 1-like
196	Contig4225	vacuolar h
197	Contig423	frigida-like protein 3-like isoform x1
198	Contig4235	rna binding
199	Contig4252	dof zinc finger
200	Contig4270	aquaporin sip1-1-like
201	Contig4350	cd2 antigen cytoplasmic tail-binding protein 2
202	Contig4371	zf-hd homeobox protein at5g65410-like
203	Contig4391	zinc finger family protein
204	Contig4402	senescence-associated family protein
205	Contig4413	zinc finger ccch domain-containing protein 58-like
206	Contig442	ferredoxin-like protein
207	Contig4422	ethylene-responsive transcription factor crf4-like
208	Contig4431	histidine protein methyltransferase 1 homolog
209	Contig4468	protein tplate-like
210	Contig4469	aspartate aminotransferase
211	Contig4478	kinase interacting family isoform 1
212	Contig448	glucan endo- β -glucosidase 14-like
213	Contig4488	pyridoxine 5-phosphate oxidase-related family protein
214	Contig4507	dnaj heat shock n-terminal domain-containing family protein
215	Contig4512	at1g71970 fl7m19_12
216	Contig4514	short-chain alcohol dehydrogenase family protein
217	Contig4558	duf246 domain-containing protein at1g04910-like
218	Contig4564	retrotransposon unclassified
219	Contig4573	lateral root primordium protein
220	Contig4587	ethylene-responsive transcription factor shine 2-like
221	Contig4588	heparanase-like protein 3-like
222	Contig4589	abc transporter c family member 3-like
223	Contig4597	amino acid dehydrogenase family protein isoform 1
224	Contig4599	mitochondrial carnitine acylcarnitine carrier-like
225	Contig460	histidine kinase- dna gyrase b- and hsp90-like atpase family protein
226	Contig4600	abhydrolase domain-containing protein fam108b1-like
227	Contig4610	e3 ubiquitin-protein ligase at4g11680-like
228	Contig4617	transcription initiation factor
229	Contig4635	udp-glucuronate decarboxylase protein 1
230	Contig4686	homeobox protein knotted-1-like 2-like
231	Contig4692	membrane-anchored ubiquitin-fold protein 2-like
232	Contig4698	f-box protein skip5
233	Contig4704	phytoalexin deficient 4 family protein
234	Contig4706	proline-rich family protein
235	Contig4718	protein phloem protein 2-like a1-like

236	Contig4768	myelin-associated oligodendrocyte basic protein isoform 2
237	Contig4785	cytochrome p450 90b1-like
238	Contig4829	protein yls7-like
239	Contig4858	sterol-4alpha-methyl oxidase 1-1 family protein
240	Contig4869	siroheme synthase-like
241	Contig4909	phytochrome-interacting factor
242	Contig4957	phd finger family protein
243	Contig4960	ring u-box domain-containing protein
244	Contig4964	disease resistance protein
245	Contig4986	replication factor a protein 1-like
246	Contig5021	29 kda ribonucleoprotein
247	Contig5035	dna binding
248	Contig504	dna binding
249	Contig5057	frigida-like protein
250	Contig5062	rpp4 candidate
251	Contig507	transcription initiation factor tfiid subunit 12-like
252	Contig5078	ubx domain-containing protein 6-like
253	Contig5111	gibberellin 2-oxidase
254	Contig5116	dolichyl-phosphate beta-d-mannosyltransferase family protein
255	Contig5122	f-box kelch-repeat protein at3g23880-like
256	Contig5123	ankyrin repeat family protein
257	Contig513	squint family protein
258	Contig5153	dna-binding protein gt-1
259	Contig5159	ribonucleoside-diphosphate reductase large subunit-like
260	Contig5166	glutamate--trna chloroplastic mitochondrial-like
261	Contig5189	photosystem ii repair protein psb27- chloroplastic-like
262	Contig5190	methyltransferase domain-containing protein
263	Contig5191	calcium-binding ef hand family protein
264	Contig5194	chaperone protein dnaj
265	Contig5198	tcp4
266	Contig522	transcriptional factor nac 11
267	Contig5223	myb-related protein 306-like
268	Contig5244	non-symbiotic hemoglobin class 1
269	Contig525	proline-rich extensin-like protein epr1-like
270	Contig5273	regulator of nonsense transcripts upf3-like isoform x2
271	Contig5289	proteasome subunit alpha
272	Contig5304	transcription factor isoform 1
273	Contig5315	prolyl 4-hydroxylase subunit alpha-1-like
274	Contig5321	methionine sulfoxide
275	Contig5322	late embryogenesis
276	Contig5330	granule-bound starch synthase i

277	Contig5333	hmg-y-related protein a-like
278	Contig5335	zf-hd homeobox protein at4g24660-like
279	Contig5336	scarecrow-like protein 8-like
280	Contig5337	importin subunit beta-1-like
281	Contig5371	serine carboxypeptidase-like 45-like
282	Contig54	glycine-rich rna-binding protein 3
283	Contig5482	translation machinery-associated protein 22-like
284	Contig5487	glucose-6-phosphate phosphate-translocator precursor family protein
285	Contig5499	phd finger family protein
286	Contig5516	ocs element-binding
287	Contig5524	bri1 kinase inhibitor 1-like
288	Contig5537	l-ascorbate oxidase-like
289	Contig5552	transcription factor myb1r1-like
290	Contig5596	vacuolar proton atpase a1-like
291	Contig5607	lim transcription factor
292	Contig5615	outer envelope pore protein 16- chloroplastic-like
293	Contig5633	cationic amino acid transporter 3 family protein
294	Contig5643	sorbitol dehydrogenase
295	Contig5682	ubiquitin carboxyl-terminal hydrolase 3-like
296	Contig5713	zinc finger
297	Contig5744	phosphate transporter pho1 homolog 3-like
298	Contig5754	zf-hd homeobox protein at4g24660-like
299	Contig5764	atp synthase subunit mitochondrial-like
300	Contig5765	kinase interacting family protein
301	Contig5778	casp-like protein at3g53850-like
302	Contig5780	dentin sialophosphoprotein
303	Contig5850	transcription factor lhy
304	Contig5884	ethanolamine-phosphate cytidyltransferase-like
305	Contig5898	acetamidase formamidase family protein
306	Contig5916	ribulose biphosphate carboxylase small chloroplastic-like
307	Contig5917	homeobox protein knotted-
308	Contig5932	very-long-chain 3-oxoacyl-reductase 1-like
309	Contig5948	superoxide dismutase
310	Contig5967	auxin signaling f-box 2
311	Contig5974	yggf family protein
312	Contig5983	gtp-binding protein
313	Contig5986	e3 ubiquitin-protein ligase ring1-like
314	Contig5994	transketolase
315	Contig5997	aaa-type atpase family protein
316	Contig6021	homeobox protein 12-like
317	Contig6028	peptidyl-prolyl cis-trans isomerase cyp19-3-like

318	Contig6045	cellulose synthase family protein
319	Contig6059	polyneuridine-aldehyde esterase
320	Contig6064	protein phosphatase
321	Contig6066	succinate dehydrogenase
322	Contig6073	xylosyltransferase 1-like
323	Contig6100	mediator of rna polymerase ii transcription subunit
324	Contig6104	atp binding
325	Contig6165	udp-glucose:flavonoid 3-o-glucosyltransferase
326	Contig6166	peroxisome biogenesis protein 22-like
327	Contig6236	set domain-containing protein
328	Contig6268	calcium-binding ef hand family protein
329	Contig6274	histone h2a-like
330	Contig6298	guanine nucleotide-binding protein subunit beta-2-like
331	Contig6302	adenosine 3 -phospho 5 -phosphosulfate transporter
332	Contig631	transcription factor hb29-like
333	Contig6328	dna glycosylase superfamily protein
334	Contig6332	serine threonine protein phosphatase 2a 59 kda regulatory subunit b eta isoform-like
335	Contig6336	zinc ion binding
336	Contig6347	galactosyltransferase family protein
337	Contig6364	ribosome biogenesis protein brx1 homolog
338	Contig6369	peroxisome biogenesis factor 10-like
339	Contig6398	pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta-like
340	Contig6403	thylakoid lumenal kda chloroplastic-like
341	Contig6438	cytosolic phosphoglucose isomerase
342	Contig6462	trihelix transcription factor gt-2-like
343	Contig6507	protein iq-domain 14-like
344	Contig6515	asymmetric leaves 1 and rough
345	Contig6537	tbc domain-containing family protein
346	Contig6559	gata transcription factor 9-like
347	Contig6573	pentatricopeptide repeat-containing
348	Contig6595	nadph-dependent pterin aldehyde reductase
349	Contig6603	prolyl 4-hydroxylase subunit alpha-1-like
350	Contig6624	f-box protein pp2-a15-like
351	Contig6627	e3 ubiquitin-protein ligase rglg2-like
352	Contig6643	senescence-associated family protein
353	Contig6648	ctc-interacting domain 11 isoform 1
354	Contig6662	diacylglycerol acyltransferase type 2
355	Contig6732	adp atp translocase 1
356	Contig6741	water-stress inducible protein 1
357	Contig6748	fmn binding protein
358	Contig6749	gds1 esterase lipase

359	Contig6782	small related domain-containing family protein
360	Contig6785	sec-independent protein translocase protein chloroplastic-like
361	Contig6790	vacuolar cation proton exchanger 5-like
362	Contig6801	glycine-rich family protein
363	Contig6815	30s ribosomal protein chloroplastic-like
364	Contig6865	pentatricopeptide repeat-containing protein at2g35130-like
365	Contig6883	myb-like protein a
366	Contig6897	ring fyve phd zinc finger-containing protein
367	Contig6916	aspartic proteinase nepenthesin-2-like
368	Contig6951	cc-nbs-lrr resistance protein
369	Contig6992	40s ribosomal protein
370	Contig6996	ormdl family protein
371	Contig7003	e3 ubiquitin-protein ligase sis3-like
372	Contig7025	latex abundant family protein
373	Contig7060	s-adenosylmethionine decarboxylase
374	Contig7068	beta-glucosidase d4
375	Contig7070	at5g56980 mhm17_10
376	Contig7079	magnesium transporter -like family protein
377	Contig708	growth-regulating factor 6-like
378	Contig7093	transcription isoform 1
379	Contig7108	drought-responsive family protein
380	Contig7150	nucleoporin family protein
381	Contig719	gtp-binding protein sar1a-like
382	Contig7194	elongator complex protein 3-like
383	Contig7197	tryptophan synthase alpha chain family protein
384	Contig7198	protein abil1-like
385	Contig7204	cbs domain-containing protein cbsx5-like
386	Contig726	ecotropic viral integration site 5 protein
387	Contig7275	lachrymatory-factor synthase-like
388	Contig73	late embryogenesis abundant group 2 isoform 1
389	Contig7312	beta-xylosidase
390	Contig732	dna-directed rna polymerase e subunit 1-like
391	Contig7341	transmembrane protein 147-like
392	Contig7349	s-adenosyl-l-methionine-dependent methyltransferases superfamily protein isoform 1
393	Contig7400	50s ribosomal protein l10
394	Contig7407	auxin-responsive protein
395	Contig7415	mfp1 attachment factor 1-like
396	Contig743	protein sensitive to proton rhizotoxicity 1-like
397	Contig7438	e3 ubiquitin-protein ligase ring1-like
398	Contig7461	photosystem i reaction center subunit chloroplastic-like
399	Contig7463	rubisco subunit binding-protein alpha subunit

400	Contig7469	metal ion binding
401	Contig7494	dna-binding family protein
402	Contig7510	alpha- -glucan-protein synthase
403	Contig7535	scarecrow-like protein 3-like
404	Contig7540	acyl carrier protein
405	Contig7559	major latex
406	Contig7617	replication factor c subunit 2-like
407	Contig7626	transcription factor
408	Contig7642	cold-regulated protein
409	Contig767	helix-loop-helix dna-binding domain containing expressed
410	Contig7689	cytochrome p450 71a26-like
411	Contig7693	haca ribonucleoprotein complex subunit 2-like
412	Contig7695	polyketide cyclase dehydrase and lipid transport superfamily protein
413	Contig7696	upf0690 protein c1orf52 homolog
414	Contig77	protein tify 6b-like
415	Contig7708	ferredoxin- chloroplastic-like
416	Contig7718	senescence-associated family protein
417	Contig7723	nadh dehydrogenase
418	Contig7737	60s acidic ribosomal protein p0
419	Contig7757	peptidyl-prolyl cis-trans isomerase-like 1-like
420	Contig7760	ubiquitin-conjugating enzyme e2 27-like
421	Contig7792	acyl carrier protein
422	Contig7796	pre-mrna-processing protein 40c-like
423	Contig7799	gata transcription factor 11-like
424	Contig7812	atp-citrate lyase b-1
425	Contig7836	bah helical bundle-like domain isoform 1
426	Contig7861	transport family protein
427	Contig787	cbl-interacting serine threonine-protein kinase 1-like
428	Contig7893	dna repair protein rad23
429	Contig7899	chlorophyll a b-binding protein type ii precursor
430	Contig791	ferredoxin- chloroplastic-like
431	Contig7937	saur family protein
432	Contig7941	ERF4
433	Contig795	udp-xylose synthase 4 family protein
434	Contig796	methylesterase chloroplastic-like
435	Contig7970	pleckstrin homology domain-containing family protein
436	Contig7976	lob domain-containing protein 38-like
437	Contig7983	gibberellin-regulated protein 3
438	Contig8015	protein transport protein sec61 subunit alpha-like
439	Contig8016	intracellular protein transport protein
440	Contig8018	major allergen pru

441	Contig8019	speckle-type poz family protein
442	Contig8044	cyclin-dependent protein kinase inhibitor sim-like
443	Contig8067	swi snf-related matrix-associated actin-dependent regulator of chromatin subfamily a containing dead h box 1b-like
444	Contig807	gpi inositol-deacylase
445	Contig8084	desiccation protectant protein lea14-like protein
446	Contig809	3-oxoacyl-
447	Contig8150	rna methyltransferase at5g10620-like
448	Contig8198	inositol-tetrakisphosphate 1-kinase 2
449	Contig8206	transcription initiation factor tfiid subunit 13-like
450	Contig8272	syntaxin-24-like
451	Contig8290	lesion inducing family protein
452	Contig8304	wound-responsive family protein
453	Contig8310	crs2-associated factor mitochondrial-like
454	Contig8330	pre-mrna-splicing factor slu7-like
455	Contig834	abc transporter g family member 5-like
456	Contig837	exostosin family protein
457	Contig8389	stress-responsive family protein
458	Contig8393	lipid binding
459	Contig8395	hexose transporter
460	Contig842	gibberellin receptor gid1c-like
461	Contig8435	heat shock factor-binding protein 1-like
462	Contig8437	stem-specific protein tsjt1-like
463	Contig8455	peptidyl-prolyl cis-trans isomerase fkbp42-like
464	Contig8464	protein sgt1 homolog
465	Contig8481	ethylene responsive element binding factor 5 family protein
466	Contig8483	subtilisin-like protease-like
467	Contig8505	60s ribosomal protein
468	Contig8507	ribulose -bisphosphate carboxylase small chain precursor
469	Contig8541	phosphoenolpyruvate carboxylase
470	Contig8547	rpm1-interacting protein 4-like
471	Contig8558	late embryogenesis abundant protein
472	Contig8565	gdp-mannose transporter
473	Contig8574	seed maturation protein
474	Contig8612	udp-glucuronate 4-epimerase 3-like
475	Contig8613	at5g66780 mud21_2
476	Contig8617	transcriptional corepressor
477	Contig8649	40s ribosomal protein
478	Contig8656	transcription factor tcp11-like
479	Contig8660	btb poz domain-containing protein at5g41330-like
480	Contig8663	bifunctional inhibitor lipid-transfer protein seed storage 2s albumin superfamily protein
481	Contig8667	histone -like

482	Contig87	ribosomal protein l19 family protein
483	Contig8761	hyponastic leaves 1 family protein
484	Contig8840	phenylalanine ammonia- partial
485	Contig8892	anti-virus transcriptional factor
486	Contig8904	transcription factor bhlh13-like
487	Contig8928	upf0098 protein mth_273-like
488	Contig8967	late embryogenesis abundant protein 2-like
489	Contig90	nuclear transport factor 2-like
490	Contig9006	2s albumin
491	Contig9015	deacetylvindoline o-acetyltransferase-like
492	Contig9083	cellulose synthase-like protein e6-like
493	Contig91	gtpase -like
494	Contig9102	40s ribosomal protein
495	Contig9118	solanesyl diphosphate synthase
496	Contig9133	blue copper
497	Contig9166	u-box domain-containing protein 26-like
498	Contig9173	palmitoyl protein thioesterase family protein
499	Contig919	snakin-1
500	Contig9210	oleosin 2
501	Contig9221	spx domain-containing protein 4-like
502	Contig9222	syntaxin-52-like isoform x1
503	Contig924	protoheme ix mitochondrial-like
504	Contig967	conserved oligomeric golgi complex subunit 8-like
505	Contig969	protein yls9-like
