Mirosła
w Tyrka

Elektronicznie podpisany przez Mirosław Tyrka
Data: 2024.02.08 10:20:01 +01'00'

Tabela S1.1. Wyniki izolacji DNA z linii pszenicy badanych w 2023 roku. Pochodzenie SMH - HR Smolice, MHR - Małopolska HR, PHR - Poznańska HR, STH - HR Strzelce

Wydruk pierwszych 5 stron

Nr DNA	Symbol lini	Populacja	Pochodzen	Stężenieng	Płytka	Pozycja
1	SMH_497	DW	SMH	1000	P1	1
2	SMH_524	DW	SMH	936	P1	2
3	SMH_553	DW	SMH	527	P1	3
4	SMH_576	DW	SMH	1030	P1	4
5	SMH_578	DW	SMH	775	P1	5
6	SMH_643	DW	SMH	1000	P1	6
7	SMH_710	DW	SMH	995	P1	7
8	SMH_761	DW	SMH	740	P1	8
9	SMH_796	DW	SMH	874	P1	9
10	SMH_804	DW	SMH	721	P1	10
11	SMH_825	DW	SMH	1150	P1	11
12	SMH_520	DW	SMH	876	P1	12
13	SMH_530	DW	SMH	858	P1	13
14	SMH_574	DW	SMH	931	P1	14
15	SMH_592	DW	SMH	1050	P1	15
16	SMH_644	DW	SMH	1230	P1	16
17	SMH_733	DW	SMH	810	P1	17
18	SMH_786	DW	SMH	719	P1	18
19	SMH_797	DW	SMH	1070	P1	19
20	SMH_816	DW	SMH	824	P1	20
21	SMH_829	DW	SMH	773	P1	21
22	SMH_840	DW	SMH	541	P1	22
23	SMH_521	DW	SMH	706	P1	23
24	SMH_533	DW	SMH	463	P1	24
25	SMH_575	DW	SMH	950	P1	25
26	SMH_577	DW	SMH	995	P1	26
27	SMH_633	DW	SMH	680	P1	27
28	SMH_652	DW	SMH	789	P1	28
29	SMH_754	DW	SMH	1120	P1	29
30	SMH_798	DW	SMH	1070	P1	30
31	SMH_820	DW	SMH	878	P1	31
32	SMH_839	DW	SMH	858	P1	32
33	SMH_1_22	DPW	SMH	475	P1	33
34	SMH_2_22	DPW	SMH	703	P1	34
35	SMH_10_2	DPW	SMH	760	P1	35
36	SMH_17_2	DPW	SMH	574	P1	36
37	SMH_23_2	DPW	SMH	835	P1	37
38	SMH_24_2	DPW	SMH	1000	P1	38
39	SMH_28_2	DPW	SMH	805	P1	39
40	SMH_30_2	DPW	SMH	995	P1	40
41	SMH_31_2	DPW	SMH	898	P1	41
42	SMH_33_2	DPW	SMH	711	P1	42

43	SMH_35_2	DPW	SMH	551	P1	43
44	SMH_39_2	DPW	SMH	661	P1	44
45	SMH_43_2	DPW	SMH	439	P1	45
46	SMH_45_2	DPW	SMH	653	P1	46
47	SMH_46_2	DPW	SMH	936	P1	47
48	SMH_47_2	DPW	SMH	867	P1	48
49	SMH_48_2	DPW	SMH	575	P1	49
50	SMH_50_2	DPW	SMH	798	P1	50
51	SMH_56_2	DPW	SMH	856	P1	51
52	SMH_61_2	DPW	SMH	1230	P1	52
53	SMH_64_2	DPW	SMH	877	P1	53
54	SMH_65_2	DPW	SMH	953	P1	54
55	SMH_66_2	DPW	SMH	676	P1	55
56	SMH_67_2	DPW	SMH	784	P1	56
57	SMH_68_2	DPW	SMH	596	P1	57
58	SMH_69_2	DPW	SMH	967	P1	58
59	SMH_70_2	DPW	SMH	686	P1	59
60	SMH_71_2	DPW	SMH	831	P1	60
61	SMH_72_2	DPW	SMH	684	P1	61
62	SMH_73_2	DPW	SMH	673	P1	62
63	SMH_74_2	DPW	SMH	549	P1	63
64	SMH_75_2	DPW	SMH	604	P1	64
65	SMH_83_2	DPW	SMH	600	P1	65
66	SMH_92_2	DPW	SMH	634	P1	66
67	SMH_93_2	DPW	SMH	581	P1	67
68	SMH_94_2	DPW	SMH	658	P1	68
69	SMH_95_2	DPW	SMH	769	P1	69
70	SMH_100_	DPW	SMH	751	P1	70
71	SMH_101_	DPW	SMH	861	P1	71
72	SMH_102_	DPW	SMH	800	P1	72
73	SMH_103_	DPW	SMH	684	P1	73
74	SMH_104_	DPW	SMH	753	P1	74
75	SMH_105_	DPW	SMH	853	P1	75
76	SMH_107_	DPW	SMH	852	P1	76
77	SMH_111_	DPW	SMH	847	P1	77
78	SMH_112_	DPW	SMH	733	P1	78
79	SMH_113_	DPW	SMH	805	P1	79
80	SMH_114_	DPW	SMH	688	P1	80
81	SMH_115_	DPW	SMH	734	P1	81
82	SMH_117_	DPW	SMH	771	P1	82
83	SMH_120_	DPW	SMH	642	P1	83
84	SMH_121_	DPW	SMH	699	P1	84
85	SMH_123_	DPW	SMH	1190	P1	85
86	SMH_124_	DPW	SMH	749	P1	86
87	SMH_126_	DPW	SMH	983	P1	87
88	SMH_128_	DPW	SMH	719	P1	88
89	SMH_129_	DPW	SMH	636	P1	89
90	SMH_130_	DPW	SMH	697	P1	90
91	SMH_132_	DPW	SMH	536	P1	91
92	SMH_133_	DPW	SMH	666	P1	92

93	SMH_134_	DPW	SMH	640	P1	93
94	SMH_136_	DPW	SMH	579	P1	94
95	SMH_137_	DPW	SMH	373	P2	1
96	SMH_138_	DPW	SMH	555	P2	2
97	SMH_139_	DPW	SMH	337	P2	3
98	SMH_141_	DPW	SMH	587	P2	4
99	SMH_144_	DPW	SMH	571	P2	5
100	SMH_145_	DPW	SMH	793	P2	6
101	C_19_104	DW	DANKO	417	P2	7
102	C_19_573	DW	DANKO	451	P2	8
103	DI_2_38	DW	DANKO	719	P2	9
104	C_2738_14	DW	DANKO	563	P2	10
105	DD_197_1	DW	DANKO	516	P2	11
106	DD_531_1	DW	DANKO	687	P2	12
107	DD_559_1	DW	DANKO	749	P2	13
108	DD_868_1	DW	DANKO	527	P2	14
109	DL_1027_1	DW	DANKO	676	P2	15
110	DL_1028_1	DW	DANKO	479	P2	16
111	DL_1091_1	DW	DANKO	702	P2	17
112	DL_1095_1	DW	DANKO	428	P2	18
113	MIB_0245	DW	MHR	854	P2	19
114	MIB_0534	DW	MHR	781	P2	20
115	POB_0122	DW	MHR	750	P2	21
116	POB_0222	DW	MHR	626	P2	22
117	POB_0322	DW	MHR	880	P2	23
118	KBP_21.25	DW	MHR	895	P2	24
119	KBP21.16	DW	MHR	913	P2	25
120	KBP_21.41	DW	MHR	674	P2	26
121	KBP_21.28	DW	MHR	791	P2	27
122	KBP_21.47	DW	MHR	977	P2	28
123	AND_1905	DW	PHR	1150	P2	29
124	AND_1906	DW	PHR	951	P2	30
125	AND_1924	DW	PHR	872	P2	31
126	AND_1956	DW	PHR	790	P2	32
127	AND_1979	DW	PHR	981	P2	33
128	AND_1979	DW	PHR	822	P2	34
129	NAD_Z_19	DW	PHR	579	P2	35
130	NAD_Z_19	DW	PHR	819	P2	36
131	NAD_Z_19	DW	PHR	1070	P2	37
132	NAD_Z_19	DW	PHR	885	P2	38
133	NAD_Z_19	DW	PHR	869	P2	39
134	NAD_Z_19	DW	PHR	875	P2	40
135	STHD_042	DW	STH	890	P2	41
136	STHD_043	DW	STH	1090	P2	42
137	STH_0244L	DW	STH	868	P2	43
138	STH_0244L	DW	STH	976	P2	44
139	STH_0307	DW	STH	1130	P2	45
140	STHD_041	DW	STH	947	P2	46
141	STHD_044	DW	STH	938	P2	47
142	STHD_054	DW	STH	1260	P2	48

143	STHD_112	DW	STH	837	P2	49
144	STHD_112	DW	STH	1000	P2	50
145	STHD_143	DW	STH	596	P2	51
146	STHD_144	DW	STH	1100	P2	52
147	ARTIST	DW	WZ1	704	P2	53
148	KILIMANJA	DW	WZ2	552	P2	54
149	SYMETRIA	DW	WZ3	812	P2	55
150	C_19_186	DW	DANKO	639	P2	56
151	C_3279_1	DW	DANKO	800	P2	57
152	C17_263	DW	DANKO	884	P2	58
153	C_16_397	DW	DANKO	770	P2	59
154	DD_198_1	DW	DANKO	767	P2	60
155	DD_530_1	DW	DANKO	767	P2	61
156	DD_561_1	DW	DANKO	701	P2	62
157	DD_909_1	DW	DANKO	614	P2	63
158	DL_1102_1	DW	DANKO	796	P2	64
159	DL_1121_1	DW	DANKO	624	P2	65
160	DL_1156_1	DW	DANKO	776	P2	66
161	DL_1175_1	DW	DANKO	627	P2	67
162	DL_1220_1	DW	DANKO	790	P2	68
163	MIB_0100	DW	MHR	685	P2	69
164	POB_0422	DW	MHR	605	P2	78
165	POB_0522	DW	MHR	687	P2	71
166	POB_0622	DW	MHR	848	P2	72
167	KBP_21.9	DW	MHR	719	P2	73
168	KBP_21.17	DW	MHR	1020	P2	74
169	KBP_21.43	DW	MHR	833	P2	75
170	KBP_21.32	DW	MHR	1030	P2	76
171	KBP_21.50	DW	MHR	724	P2	77
172	KBP_21.42	DW	MHR	698	P2	70
173	AND_1907	DW	PHR	934	P2	79
174	AND_1979	DW	PHR	808	P2	80
175	AND_1982	DW	PHR	990	P2	81
176	AND_1986	DW	PHR	1020	P2	82
177	AND_1910	DW	PHR	977	P2	83
178	AND_1910	DW	PHR	988	P2	84
179	AND_1910	DW	PHR	927	P2	85
180	NAD_Z_19	DW	PHR	925	P2	86
181	NAD_Z_19	DW	PHR	485	P2	87
182	NAD_Z_19	DW	PHR	1170	P2	88
183	NAD_Z_19	DW	PHR	901	P2	89
184	NAD_Z_19	DW	PHR	1470	P2	90
185	STHD_146	DW	STH	1160	P2	91
186	STHD_146	DW	STH	1130	P2	92
187	STHD_146	DW	STH	941	P2	93
188	STHD_200	DW	STH	842	P2	94
189	STHD_147	DW	STH	1090	P3	1
190	STHD_147	DW	STH	971	P3	2
191	STHD_147	DW	STH	844	P3	3
192	STHD_147	DW	STH	1310	P3	4

193	STHD_147	DW	STH	1340	P3	5
194	STHD_147	DW	STH	1400	P3	6
195	STHD_147	DW	STH	885	P3	7
196	POB_3392	PW1	MHR	143	P3	8
197	POB_3702	PW1	MHR	87.2	P3	9
198	KBP_22.11	PW1	MHR	233	P3	10
199	C_19318	DW	DANKO	1110	P3	11
200	C_1854_17	DW	DANKO	908	P3	12
201	C_18_238	DW	DANKO	1250	P3	13
202	C_2815_15	DW	DANKO	1570	P3	14
203	DD_470_1	DW	DANKO	751	P3	15
204	DD_522_1	DW	DANKO	1100	P3	16
205	DD_800_1	DW	DANKO	1050	P3	17
206	DD_910_1	DW	DANKO	1130	P3	18
207	DL_1278_1	DW	DANKO	1020	P3	19
208	DL_1348_1	DW	DANKO	1390	P3	20
209	DL_1359_1	DW	DANKO	1340	P3	21
210	DL_1410_1	DW	DANKO	1400	P3	22
211	DL_1552_1	DW	DANKO	885	P3	23
212	MIB_0115	DW	MHR	1350	P3	24
213	POB_0722	DW	MHR	1350	P3	25
214	POB_0822	DW	MHR	1080	P3	26
215	POB_0922	DW	MHR	1110	P3	27
216	POB_1022	DW	MHR	471	P3	28
217	KBP_21.10	DW	MHR	855	P3	29
218	KBP_21.19	DW	MHR	878	P3	30
219	KBP_21.20	DW	MHR	766	P3	31
220	KBP_21.33	DW	MHR	772	P3	32
221	KBP_21.56	DW	MHR	545	P3	33
222	AND_1933	DW	PHR	709	P3	34
223	AND_1980	DW	PHR	907	P3	35
224	AND_27_1	DW	PHR	772	P3	36
225	AND_33_1	DW	PHR	835	P3	37
226	AND_1902	DW	PHR	762	P3	38
227	AND_1901	DW	PHR	1020	P3	39
228	AND_267_	DW	PHR	818	P3	40
229	NAD_Z_19	DW	PHR	708	P3	41
230	NAD_Z_19	DW	PHR	793	P3	42
231	NAD_Z_19	DW	PHR	676	P3	43
232	NAD_Z_19	DW	PHR	864	P3	44
233	NAD_Z_19	DW	PHR	826	P3	45
234	STHD_200	DW	STH	729	P3	46
235	STHD_200	DW	STH	632	P3	47
236	STHD_200	DW	STH	635	P3	48
237	STHD_200	DW	STH	794	P3	49
238	STHD_200	DW	STH	563	P3	50
239	STHD_200	DW	STH	592	P3	51
240	STH_2008	DW	STH	517	P3	52
241	STH_2009	DW	STH	415	P3	53
242	STH_2010	DW	STH	541	P3	54

Tabela S1.2. Segregacje markerów silicoDArT dla 428 genotypów pszenicy badanych w 2023 roku

Wydruk pierwszych 5 stron z 9360

CloneID	AlleleSequence	TrimmedSequence	Chrom_Wheat_ChineseSpring21	ChromPosTag_Wheat_ChineseSpring21	AlnCnt_Wheat_ChineseSpring21	AlnEvalue_Wheat_ChineseSpring21
5563173	TGCAGAGACGGCGGCTTGA	TGCAGAGACG	Chr5B	2.38E+08	2	1.21E-27
1138028	TGCAGATTAGCCTCTACGGT	TGCAGATTAGCCTCTACGG		0	0	999
1119271	TGCAGATTGCGAAATGGGTT	TGCAGATTGCGAAATGGGT		0	0	999
1058651	TGCAGCATTTCGTAAGAACA	TGCAGCATTTC	Chr6D	59424035	1	1.21E-27
978972	TGCAGCTAGGGAGGGGAAC	TGCAGCTAGG	Chr7A	38727462	1	7.80E-24
1059762	TGCAGTAACAGTGGACATGA	TGCAGTAACA	Chr4A	4.99E+08	1	1.21E-27
2289085	TGCAGTGCTCCGTGTGTCCC	TGCAGTGCTCC	Chr6B	5.25E+08	3	1.21E-27
12737595	TGCAGATGCGTGACGGCGG	TGCAGATGCG	Chr3D	6.01E+08	2	1.21E-27
41420416	TGCAGGAGCTCACCGAGGC	TGCAGGAGCTCACCGAGG		0	0	999
1048444	TGCAGTACCAAGAGAGGAA	TGCAGTACCA	Chr2A	6.44E+08	7	5.62E-26
1034916	TGCAGTGGGTCGGCCTGGTG	TGCAGTGGGT	Chr6D	3.5E+08	3	1.21E-27
1020557	TGCAGTTGTCAGTGGAGGTG	TGCAGTTGTCA	Chr3B	7.32E+08	3	5.62E-26
2241646	TGCAGTTGCGGTTCGATTCG	TGCAGTTGCG	Chr1D	3.73E+08	2	1.21E-27
1107907	TGCAGAAAAGTAAATGATAG	TGCAGAAAAG	Chr4B	1.83E+08	4	1.21E-27
1109646	TGCAGAAACTACATCACGTA	TGCAGAAACT	Chr2A	28519595	1	7.80E-24
1218137	TGCAGAAACTTTAGTTTTCCT	TGCAGAAACTT	Chr2D	74023469	7	1.22E-22
1129401	TGCAGAAAGACTCGTTTTTTT	TGCAGAAAGA	Chr3A	6.86E+08	1	2.02E-25
2288857	TGCAGAAATATGCCGATGGA	TGCAGAAATAT	Chr7B	3.88E+08	2	1.21E-27
1122897	TGCAGAAATATGCTATGAGT	TGCAGAAATATGCTATGAG		0	0	999
4009389	TGCAGAAATCAGGAACGCCC	TGCAGAAATC	Chr3B	4.92E+08	3	5.62E-26
1203668	TGCAGAAATTTGACTTAAAT	TGCAGAAATTT	Chr2D	72813210	1	5.62E-26
1233797	TGCAGAACACGTGCCTACTC	TGCAGAACACGTGCCTACT		0	0	999
1405153	TGCAGAACATATGTAATGGA	TGCAGAACAT	Chr5B	5.02E+08	1	1.21E-27
1109388	TGCAGAACATGTAAGCCAGG	TGCAGAACATGTAAGCCAG		0	0	999
1667629	TGCAGAACCGATTCGGCGTC	TGCAGAACCG	Chr2D	3.4E+08	3	1.21E-27
2264479	TGCAGAACCTCAGGTTGCGT	TGCAGAACCTC	Chr6D	4.83E+08	2	1.21E-27
5328706	TGCAGAACCTTGGAGTTGGA	TGCAGAACCTTGGAGTTGG		0	0	999
2320037	TGCAGAACGAGGCTGTGGG	TGCAGAACGA	Chr2A	16090941	7	1.21E-27
1089360	TGCAGAACGCCAACATGCTG	TGCAGAACGC	Chr5D	3.05E+08	3	1.21E-27
1269124	TGCAGAACGGACAAGGGAT	TGCAGAACGGACAAGGGA		0	0	999
1071333	TGCAGAACGTACTCTAGTCA	TGCAGAACGTACTCTAGTC		0	0	999
1109343	TGCAGAAGAAATCAGCACAA	TGCAGAAGAA	Chr1B	6.77E+08	1	1.21E-27
2289492	TGCAGAAGAAATTACCACTA	TGCAGAAGAA	Chr6A	6.18E+08	1	1.21E-27
1106701	TGCAGAAGAAGACAAAGGTT	TGCAGAAGAA	Chr2B	5374380	2	5.62E-26

1124449	TGCAGAAGAAGACGGGGTC	TGCAGAAGAA	Chr6B	7.11E+08	1	1.21E-27
1108207	TGCAGAAGACCATGCTAATC	TGCAGAAGAC	Chr5A	7.1E+08	1	1.21E-27
1232949	TGCAGAAGAGGCACACAGT	TGCAGAAGAGGCACACAG		0	0	999
1073478	TGCAGAAGAGGTAGCATAA	TGCAGAAGAG	Chr2D	5.8E+08	2	2.62E-24
1116306	TGCAGAAGCAATTGCCTGCA	TGCAGAAGCA	Chr3B	8.05E+08	1	1.21E-27
1070267	TGCAGAAGCAGAACAGACA	TGCAGAAGCAGAACAGAC		0	0	999
1686062	TGCAGAAGCATCGAAGGAA	TGCAGAAGCA	Chr5B	5.15E+08	7	2.02E-25
1231607	TGCAGAAGCATGTTGTGCAG	TGCAGAAGCATGTTGTGCA		0	0	999
1378950	TGCAGAAGCGAGGGCTTGC	TGCAGAAGCG	Chr6B	1.65E+08	2	1.21E-27
1214808	TGCAGAAGGAGAAATCGTCC	TGCAGAAGGA	Chr2D	3.4E+08	3	1.21E-27
990757	TGCAGAAGGCACAAGCTGCC	TGCAGAAGGCACAAGCTG		0	0	999
2324435	TGCAGAATAAGCAGCGGCG	TGCAGAATAA	Chr3D	6.07E+08	4	4.38E-22
2325332	TGCAGAATAGCTAGAATGTG	TGCAGAATAG	Chr4B	5076340	1	1.22E-22
1037525	TGCAGAATATACGTGTGTTC	TGCAGAATATA	Chr3D	1.48E+08	1	1.21E-27
3024272	TGCAGAATATTGTTTTTTTTT	TGCAGAATATT	Chr2B	7.98E+08	1	2.64E-19
11914663	TGCAGAATCATCTTCGCAGG	TGCAGAATCAT	Chr3B	4491041	6	5.62E-26
1118238	TGCAGAATCCTCTCCCCCATC	TGCAGAATCCTCTCCCCCAT		0	0	999
1398116	TGCAGAATCGACGCGAGGAA	TGCAGAATCG	Chr7A	2680560	1	1.21E-27
4994335	TGCAGAATCTCGTTCGAAGA	TGCAGAATCTC	Chr6A	39091903	1	1.21E-27
1121304	TGCAGAATGCGACGACAGG	TGCAGAATGCGACGACAG		0	0	999
1081172	TGCAGAATGGTATGACAAAA	TGCAGAATGGTATGACAAA		0	0	999
1090558	TGCAGAATGTATGCCGAGGT	TGCAGAATGTA	Chr4A	5.98E+08	2	7.27E-25
2241566	TGCAGACAAAATACTGTGCA	TGCAGACAAA	Chr7D	1.78E+08	2	1.21E-27
1016499	TGCAGACAAACAAAAAAGGT	TGCAGACAAA	Chr2D	90171119	1	4.35E-27
1127027	TGCAGACAAATACATGCACG	TGCAGACAAA	Chr4A	7.18E+08	1	4.35E-27
1107268	TGCAGACAAATTTTCTGTGCC	TGCAGACAAA	Chr5A	7.09E+08	1	1.21E-27
1065585	TGCAGACAATGTATAATGTA	TGCAGACAATGTATAATGT		0	0	999
1050592	TGCAGACAATTAAGCACAGC	TGCAGACAATT	Chr3A	6.09E+08	1	1.21E-27
3030784	TGCAGACACGCAGCCGCAGC	TGCAGACACG	Chr7A	1.27E+08	3	9.41E-24
1024092	TGCAGACAGACATACAGCAA	TGCAGACAGACATACAGCA		0	0	999
1721508	TGCAGACAGGACAGCGAGT	TGCAGACAGGACAGCGAG		0	0	999
1159192	TGCAGACAGTGTAAATAAAG	TGCAGACAGT	Chr3B	7.92E+08	1	1.21E-27
1213718	TGCAGACATGCCTGCCAGGC	TGCAGACATG	Chr7A	72467910	1	1.21E-27
1275494	TGCAGACCAATTGCATCCAA	TGCAGACCAA	Chr7B	7.46E+08	1	5.62E-26
2303939	TGCAGACCACATCGAGAGGC	TGCAGACCAC	Chr7B	7.29E+08	1	1.21E-27
1071277	TGCAGACCACGCGGAAAGTA	TGCAGACCACGCGGAAAG		0	0	999
2278029	TGCAGACCATCATCGACTAC	TGCAGACCATC	Chr7B	4.98E+08	1	1.21E-27
2244843	TGCAGACCCAGAGGATGAA	TGCAGACCCA	Chr7D	5.78E+08	3	1.21E-27
2334851	TGCAGACCCCTGACCCGTCC	TGCAGACCCCT	Chr5A	5.81E+08	2	2.97E-23
1719529	TGCAGACCGCCCTGAAGCGG	TGCAGACCGC	Chr3A	7.39E+08	1	1.21E-27
1279527	TGCAGACCTGGGGTGCTCGG	TGCAGACCTGGGGTGCTCG		0	0	999
1215753	TGCAGACGAAAGCGTCGGCA	TGCAGACGAA	Chr1A	5.77E+08	1	1.23E-17
5325756	TGCAGACGACGAGCCAGCG	TGCAGACGAC	Chr3A	6.87E+08	2	1.21E-27
1088746	TGCAGACGAGATGGGGTGC	TGCAGACGAG	Chr3D	6041939	1	1.21E-27
1192964	TGCAGACGAGGAAGCAGTTA	TGCAGACGAG	Chr6D	30035826	5	5.62E-26
1107041	TGCAGACGCACATAGCGAAT	TGCAGACGCA	Chr3D	7334939	1	1.21E-27
33847086	TGCAGACGCATGGAGAACCA	TGCAGACGCATGGAGAAC		0	0	999
23919161	TGCAGACGCGAAGCTCACCC	TGCAGACGCG	Chr7A	1999888	2	9.41E-24
1125691	TGCAGACGCGCGAACCACCA	TGCAGACGCG	Chr6A	31765468	1	1.21E-27
7929739	TGCAGACGGACATAAGTAGC	TGCAGACGGACATAAGTA		0	0	999

23919162	TGCAGACGGCGGGCGTACT	TGCAGACGGCGGGCGTACT		0	0	999
1243958	TGCAGACGGTGGTGCGCGA	TGCAGACGGTGGTGCGCG		0	0	999
1220293	TGCAGACGTACTTGTTACGG	TGCAGACGTA	Chr1B	53720462	3	1.21E-27
3533301	TGCAGACGTCATAGACGGTG	TGCAGACGTCATAGACGGT		0	0	999
1261047	TGCAGACGTTGTAGTACAGG	TGCAGACGTT	Chr5A	30323849	2	9.48E-19
1082732	TGCAGACTACGGGGAGGAG	TGCAGACTAC	Chr6D	2.77E+08	2	2.23E-24
1124086	TGCAGACTAGAAAACGGGT	TGCAGACTAG	Chr2A	6.99E+08	3	1.21E-27
1860579	TGCAGACTAGCATGTCCCCC	TGCAGACTAG	Chr2A	66614468	1	5.66E-21
1266721	TGCAGACTAGCTGCATGCAT	TGCAGACTAG	Chr7B	7.3E+08	1	1.21E-27
1033696	TGCAGACTATGTGACAATGA	TGCAGACTATG	Chr5B	97900989	3	1.21E-27
23919163	TGCAGACTCCTCGTCACCAA	TGCAGACTCCTCGTCACCA		0	0	999
2303265	TGCAGACTCGCCATCGATGT	TGCAGACTCG	Chr7B	5.85E+08	1	1.21E-27
1374372	TGCAGACTCGGAGCCATCTA	TGCAGACTCG	Chr7B	4.53E+08	1	1.21E-27
23919164	TGCAGACTGAGGAGGCGCC	TGCAGACTGAGGAGGCGC		0	0	999
1106117	TGCAGACTGCGTAGTTGGGC	TGCAGACTGC	Chr7B	1.5E+08	2	1.04E-22
2324476	TGCAGACTGGAGTCTGATCC	TGCAGACTGG	Chr1A	8621710	7	1.35E-16
1209754	TGCAGAGAAACAACAAGATA	TGCAGAGAAA	Chr1B	6.48E+08	1	1.21E-27
1203934	TGCAGAGAAAGGCTCCCTCC	TGCAGAGAAA	Chr1A	4.94E+08	2	7.80E-24
68425876	TGCAGAGAACAGGCGAAAA	TGCAGAGAACAGGCGAAA		0	0	999
3384748	TGCAGAGAAGCTTTCCCTTC	TGCAGAGAAG	Chr3B	6.21E+08	6	2.62E-24
2363377	TGCAGAGAATGAACGAAGC	TGCAGAGAAT	Chr3B	6.21E+08	1	2.97E-23
1056533	TGCAGAGAATGAATCAACAG	TGCAGAGAAT	Chr2B	46405379	2	1.21E-27
1065555	TGCAGAGACCGAGGGACAC	TGCAGAGACC	ChrUnkno	2.14E+08	3	1.21E-27
999775	TGCAGAGAGCGAAGATATGA	TGCAGAGAGC	Chr5A	5.81E+08	2	1.21E-27
997868	TGCAGAGAGCGATAGAATCT	TGCAGAGAGC	Chr2A	18421993	2	1.21E-27
1131851	TGCAGAGAGTGGTGAATTTC	TGCAGAGAGTGGTGAATTT		0	0	999
1126666	TGCAGAGCACGTAGGTGGG	TGCAGAGCACGTAGGTGG		0	0	999
1106383	TGCAGAGCACTGTGGAGTTG	TGCAGAGCACTGTGGAGTT		0	0	999
12753276	TGCAGAGCATTGTACGTGCG	TGCAGAGCATTGTACGTGC		0	0	999
979471	TGCAGAGCCCGCATGCTACT	TGCAGAGCCC	Chr7D	14652031	3	1.21E-27
1100213	TGCAGAGCCTTATCTGTGGG	TGCAGAGCCTT	Chr3D	18704297	1	1.21E-27
1238843	TGCAGAGCTCATGGGACGCA	TGCAGAGCTC	Chr3A	7.34E+08	1	1.21E-27
1291909	TGCAGAGCTCGGACACAAGC	TGCAGAGCTC	Chr6A	39638170	12	1.21E-27
1106464	TGCAGAGGAAAAGGCAACA	TGCAGAGGAAAAGGCAAC		0	0	999
1020552	TGCAGAGGAAGAAGCGGCT	TGCAGAGGAA	Chr6D	2.09E+08	3	1.21E-27
1388893	TGCAGAGGAAGGCAAGAAT	TGCAGAGGAAGGCAAGAA		0	0	999
1122328	TGCAGAGGAGCCGAACCCAT	TGCAGAGGAGCCGAACCC		0	0	999
1130437	TGCAGAGGATGACGGCGGT	TGCAGAGGATGACGGCGG		0	0	999
1206682	TGCAGAGGCAAGTAGCGAG	TGCAGAGGCA	Chr6D	4.86E+08	1	1.21E-27
33847091	TGCAGAGGCAGGAGAAGTT	TGCAGAGGCA	Chr3B	1.63E+08	1	1.22E-22
1139755	TGCAGAGGGTCGTCAGGAA	TGCAGAGGGTCGTCAGGA		0	0	999
1131114	TGCAGAGTACGTGTTGGAGT	TGCAGAGTAC	Chr3A	5.26E+08	1	3.38E-23
1107187	TGCAGAGTCTGCGTTGGAGG	TGCAGAGTCT	Chr2A	7.82E+08	1	1.21E-27
2254661	TGCAGAGTTCACATGCATTT	TGCAGAGTTC	Chr1B	3249965	1	1.21E-27
1136258	TGCAGAGTTGCGGGTGACAC	TGCAGAGTTG	Chr2A	6.09E+08	3	1.21E-27
1379966	TGCAGATAAACCATGGCATA	TGCAGATAAACCATGGCAT		0	0	999
1232937	TGCAGATAACATTTTCGTTTC	TGCAGATAAC	Chr2A	18474998	2	1.21E-27
1065518	TGCAGATAAGATAGTTTCCTT	TGCAGATAAGATAGTTTCC		0	0	999
1099949	TGCAGATAAGCCAAACTCAA	TGCAGATAAG	Chr6D	4.89E+08	1	1.21E-27
1055759	TGCAGATAAGCTAGGGAATC	TGCAGATAAG	Chr6B	6.87E+08	1	1.21E-27

982599	TGCAGATAAGGCTCAAGTGT	TGCAGATAAGGCTCAAGTG		0	0	999
1206319	TGCAGATACAGATATCTACG	TGCAGATACA	Chr7A	78254899	4	2.64E-19
2243546	TGCAGATACCTCGTAGCTGC	TGCAGATACCTCGTAGCTG		0	0	999
1127970	TGCAGATACGAGGTTGGCA	TGCAGATACG	Chr5D	3598360	7	1.21E-27
1078249	TGCAGATAGGGCCGCACTTT	TGCAGATAGG	Chr6D	65848341	2	1.21E-27
1056902	TGCAGATATCGGCAACTTGG	TGCAGATATC	Chr3A	24290984	1	7.80E-24
33847222	TGCAGATATTCGCCATCTCCC	TGCAGATATTC	Chr6B	51153561	1	1.59E-16
12753277	TGCAGATCAACAAAGAGAG	TGCAGATCAACAAAGAGA		0	0	999
1722197	TGCAGATCAATGCAGAGCGA	TGCAGATCAAT	Chr1A	11975674	1	4.83E-21
1379114	TGCAGATCACGGGCGTGGT	TGCAGATCAC	Chr3A	2.49E+08	2	2.65E-14
1120767	TGCAGATCACTTTGGCACCT	TGCAGATCACT	Chr6B	6.21E+08	1	2.02E-25
1121763	TGCAGATCAGTTATTTGCTA	TGCAGATCAGTTATTTGCT		0	0	999
1255018	TGCAGATCATGGAAAAGAG	TGCAGATCATG	Chr7B	5.63E+08	1	1.21E-27
1217429	TGCAGATCATGGTGTACCCA	TGCAGATCATG	Chr7B	7.58E+08	1	1.21E-27
1061505	TGCAGATCCAACACTGCCAG	TGCAGATCCA	Chr3A	19705696	3	1.21E-27
1070118	TGCAGATCCAACACTTACAG	TGCAGATCCA	Chr7A	2242365	1	1.21E-27
986833	TGCAGATCCACCACCCCCAA	TGCAGATCCACCACCCCCA		0	0	999
33847097	TGCAGATCCCGCCATTGATG	TGCAGATCCCGCCATTGAT		0	0	999
23919292	TGCAGATCCTCGGGCAGATG	TGCAGATCCTC	Chr2A	7.8E+08	1	2.04E-20
33847098	TGCAGATCCTTCTCACCTGCT	TGCAGATCCTTCTCACCTGC		0	0	999
1118206	TGCAGATCGACGACTTTGTA	TGCAGATCGA	Chr5A	6.24E+08	1	5.62E-26
2279876	TGCAGATCGAGAGAGGATG	TGCAGATCGA	Chr7B	6.48E+08	2	2.19E-19
1118005	TGCAGATCGCCCCGACCGCA	TGCAGATCGC	Chr1A	4.79E+08	1	1.21E-27
1045223	TGCAGATCGGATGGGAGGG	TGCAGATCGG	Chr4A	5.7E+08	1	1.21E-27
1030421	TGCAGATCGGCGGGCTCTCC	TGCAGATCGG	Chr4B	3.85E+08	2	1.21E-27
29429512	TGCAGATCGGGAGGCTTTGC	TGCAGATCGG	ChrUnknov	1.4E+08	2	5.62E-26
1075695	TGCAGATCGTCCCCAGTAGT	TGCAGATCGTC	Chr5D	25767343	1	1.21E-27
2328160	TGCAGATCGTGAGCTCCTGC	TGCAGATCGT	Chr7A	4.67E+08	5	1.21E-27
1288584	TGCAGATCTCATACGCATTCT	TGCAGATCTCA	Chr2A	7.81E+08	1	1.21E-27
1673314	TGCAGATCTCGAGGCAGGCA	TGCAGATCTCG	Chr2A	6870644	1	1.21E-27
4990391	TGCAGATCTGGCGATCGCGA	TGCAGATCTG	Chr1D	53505098	1	1.21E-27
1079590	TGCAGATCTTTATCAATTGTC	TGCAGATCTTT	Chr7B	25395420	1	1.21E-27
1067211	TGCAGATCTTTCTGTTTTCCG	TGCAGATCTTT	Chr2A	7.62E+08	1	5.62E-26
1054158	TGCAGATGACTAAAGCGTCG	TGCAGATGACT	Chr2A	7.72E+08	1	1.21E-27
1235327	TGCAGATGACTACTCTCGTC	TGCAGATGACT	Chr7B	6.15E+08	1	1.21E-27
1211721	TGCAGATGACTCTGACGCAA	TGCAGATGACT	Chr5B	5.29E+08	2	1.21E-27
2325280	TGCAGATGAGAAGGTTTGA	TGCAGATGAGAAGGTTTG		0	0	999
2250418	TGCAGATGAGTACTAGAAGA	TGCAGATGAG	Chr2A	5707008	1	1.21E-27
4991389	TGCAGATGCATGGCAGGAA	TGCAGATGCAT	Chr2D	2.06E+08	1	1.21E-27
1266729	TGCAGATGCGACGTGACGCC	TGCAGATGCGACGTGACG		0	0	999
17972258	TGCAGATGCGGCTCGGGGC	TGCAGATGCG	Chr4D	3.37E+08	21	1.21E-27
1114887	TGCAGATGCGTGGAGGGAG	TGCAGATGCGTGGAGGGA		0	0	999
1127443	TGCAGATGCTCTTAGCACGT	TGCAGATGCT	Chr7B	7.52E+08	1	5.66E-21
1115201	TGCAGATGCTCTTGAGGTGG	TGCAGATGCT	Chr7B	7.19E+08	2	3.38E-23
1724581	TGCAGATGCTGTCCTTCGGC	TGCAGATGCT	Chr7B	6.49E+08	1	5.66E-21
1100616	TGCAGATGCTTATGACAAGA	TGCAGATGCTT	Chr5B	2235423	1	2.23E-24
4405283	TGCAGATGGCGGCGTTTGCG	TGCAGATGGC	Chr5B	4.87E+08	1	1.21E-27
1266732	TGCAGATGGCGTGTCTTCGG	TGCAGATGGCGTGTCTTCG		0	0	999
3949879	TGCAGATGGGGAGGATCTTC	TGCAGATGGGGAGGATCT		0	0	999
1195188	TGCAGATGGTGGAGGGACA	TGCAGATGGT	Chr1B	2963537	4	1.21E-27

1404162	TGCAGATGTAATATAATGCCA	TGCAGATGTAA	Chr1B	5.84E+08	1	1.21E-27
1110440	TGCAGATGTATACAACCTGA	TGCAGATGTATACAACCTGA		0	0	999
1399115	TGCAGATGTCGTCGAGCTCC	TGCAGATGTCG	Chr3B	6.02E+08	4	5.62E-26
1696024	TGCAGATTAGGATCGCGGTA	TGCAGATTAGG	Chr3B	5.61E+08	2	1.21E-27
1006305	TGCAGATTCCTACGGCGGCG	TGCAGATTCCT	Chr3D	6.16E+08	1	1.21E-27
1697067	TGCAGATTCGAAAAGAGCCC	TGCAGATTCGAAAAGAGCC		0	0	999
2244041	TGCAGATTCTGCCACTAGTA	TGCAGATTCTG	Chr7D	4.02E+08	3	1.21E-27
1215959	TGCAGATTGCCTCTGCTTGC	TGCAGATTGCCTCTGCTTG		0	0	999
2330265	TGCAGATTGCTCCACTGATTG	TGCAGATTGCT	Chr7B	5.43E+08	12	1.56E-26
7345063	TGCAGATTGGAGCACTGCTT	TGCAGATTGGA	Chr1B	5.79E+08	2	2.62E-24
2249203	TGCAGATTTAAAAACGCACG	TGCAGATTTAA	Chr4A	6.78E+08	2	1.21E-27
1099962	TGCAGATTTGCACTCTGAAAA	TGCAGATTTGC	Chr6A	6.06E+08	3	5.62E-26
1071140	TGCAGATTTTCAGCCAGACG	TGCAGATTTTCA	Chr6D	1.32E+08	2	1.21E-27
1127141	TGCAGCAAAGCACTCACCAG	TGCAGCAAAG	Chr3D	46047220	3	1.21E-27
1124739	TGCAGCAAAGGGACAGATAG	TGCAGCAAAG	Chr7D	6.38E+08	5	1.21E-27
1385308	TGCAGCAAATCACCGACAAA	TGCAGCAAATCACCGACAA		0	0	999
1183644	TGCAGCAAATTTCAATAACTT	TGCAGCAAATT	Chr1A	5.36E+08	1	1.21E-27
994479	TGCAGCAACGCAGTGGCAGT	TGCAGCAACGCAGTGGCAG		0	0	999
4991407	TGCAGCAAGAAAGCGGTTGT	TGCAGCAAGAA	Chr5B	5.32E+08	1	1.21E-27
1125716	TGCAGCAAGAGGCACTGGG	TGCAGCAAGA	Chr6D	1.09E+08	1	7.80E-24
2276539	TGCAGCAAGCGCAGCGGTTG	TGCAGCAAGC	Chr4A	7.2E+08	1	1.21E-27
1233579	TGCAGCAAGCGCGAGTGTG	TGCAGCAAGC	ChrUnknow	3.36E+08	1	2.62E-24
1087241	TGCAGCAAGCGGGGCTGGA	TGCAGCAAGCGGGGCTGGA		0	0	999
1035371	TGCAGCAATAAGAGCTGTTG	TGCAGCAATAA	Chr7A	1.95E+08	1	1.21E-27
1092303	TGCAGCAATTAACAATAGCG	TGCAGCAATTA	Chr6B	2.12E+08	2	1.21E-27
1696981	TGCAGCAATTAGTCTCTCCTC	TGCAGCAATTA	Chr7B	7.57E+08	1	5.70E-16
1243126	TGCAGCAATTCTTAGGCTGC	TGCAGCAATTC	Chr1B	6.38E+08	2	2.64E-19
1270512	TGCAGCACAACAATAATTTCA	TGCAGCACAA	Chr2B	21932091	1	1.57E-21
1126759	TGCAGCACAACAGTTGCTAC	TGCAGCACAA	Chr1D	49591264	4	2.02E-25
1216002	TGCAGCACACACAGCACAAC	TGCAGCACACA	Chr1B	6.42E+08	2	1.21E-27
1695769	TGCAGCACATAAAACTGAAA	TGCAGCACATA	Chr5B	33142078	1	1.21E-27
1268373	TGCAGCACATCAATTGTCGG	TGCAGCACATC	Chr2D	6.43E+08	4	1.21E-27
1724576	TGCAGCACCAACGCTGTTGC	TGCAGCACCAACGCTGTTG		0	0	999
2303322	TGCAGCACCCTCGATTGAGC	TGCAGCACCCT	Chr2B	8.06E+08	2	1.21E-27
1397912	TGCAGCACGCACCCATCCAT	TGCAGCACGCA	Chr4B	4.13E+08	3	1.21E-27
1221591	TGCAGCACGCGAAACCCGCA	TGCAGCACGCGAAACCCGC		0	0	999
1062180	TGCAGCACTGGCATGCACGG	TGCAGCACTGG	Chr4A	38864274	1	1.21E-27
1099649	TGCAGCAGAAAGATTTGTCA	TGCAGCAGAAA	Chr1B	3116246	2	1.21E-27
1211136	TGCAGCAGAAGAGTTGCTGC	TGCAGCAGAA	ChrUnknow	48329118	17	1.01E-22
1050091	TGCAGCAGAAGTATACTGTTA	TGCAGCAGAA	Chr3A	22758667	2	1.21E-27
2323645	TGCAGCAGACAATTGGGTCC	TGCAGCAGACAATTGGGTC		0	0	999
1235056	TGCAGCAGAGGGCGATGCA	TGCAGCAGAG	Chr3A	4.24E+08	4	1.21E-27
1122024	TGCAGCAGATGGATGGACCC	TGCAGCAGATG	Chr2B	8.03E+08	1	1.21E-27
2322662	TGCAGCAGCAATAGTATTCGA	TGCAGCAGCAA	Chr3D	6987689	3	5.62E-26
1019056	TGCAGCAGCACCTGCGCAGG	TGCAGCAGCA	Chr4D	28214137	4	1.21E-27
1238421	TGCAGCAGCCGTTCCCAACTA	TGCAGCAGCCG	Chr6B	47090872	3	1.79E-20
5325867	TGCAGCAGCTAGTCTCGTCGA	TGCAGCAGCTAGTCTCGTC		0	0	999
23919169	TGCAGCAGTATTTCCACCTGA	TGCAGCAGTATTTCCACCTG		0	0	999
3950574	TGCAGCAGTGTGGATGAGG	TGCAGCAGTGT	Chr5A	5.87E+08	1	1.21E-27
1087680	TGCAGCAGTTCAGTGAGTAG	TGCAGCAGTTC	Chr4B	6.68E+08	2	2.02E-25

Tabela S1.3. Segregacje markerów silicoDArT dla 428 genotypów pszenicy badanych w 2023 roku w formacie Tassel 5.0. (1->AA, 0->CC)

Wydruk pierwszych 5 z 7266 stron

	rs#	alleles	chrom	pos	strand	assembly#	center	protLSID
76	1215753	A/C	Chr1A	577487742	+	IWGSC2	DArTSNP	NA
100	2324476	A/C	Chr1A	8621710	+	IWGSC2	DArTSNP	NA
102	1203934	A/C	Chr1A	494336665	-	IWGSC2	DArTSNP	NA
143	1722197	A/C	Chr1A	11975674	-	IWGSC2	DArTSNP	NA
157	1118005	A/C	Chr1A	478601867	-	IWGSC2	DArTSNP	NA
201	1183644	A/C	Chr1A	535598267	+	IWGSC2	DArTSNP	NA
292	2322425	A/C	Chr1A	497015826	+	IWGSC2	DArTSNP	NA
329	1062875	A/C	Chr1A	402883138	+	IWGSC2	DArTSNP	NA
448	1130184	A/C	Chr1A	253994919	-	IWGSC2	DArTSNP	NA
540	4990402	A/C	Chr1A	7216254	-	IWGSC2	DArTSNP	NA
567	1685855	A/C	Chr1A	260047132	+	IWGSC2	DArTSNP	NA
587	1080140	A/C	Chr1A	437524541	-	IWGSC2	DArTSNP	NA
593	1860815	A/C	Chr1A	3385473	+	IWGSC2	DArTSNP	NA
617	2277764	A/C	Chr1A	51858137	+	IWGSC2	DArTSNP	NA
619	1122959	A/C	Chr1A	584948277	-	IWGSC2	DArTSNP	NA
683	1105405	A/C	Chr1A	550841558	+	IWGSC2	DArTSNP	NA
694	4989894	A/C	Chr1A	585108728	+	IWGSC2	DArTSNP	NA
710	979810	A/C	Chr1A	559176866	+	IWGSC2	DArTSNP	NA
747	1058211	A/C	Chr1A	63471738	-	IWGSC2	DArTSNP	NA
750	3946324	A/C	Chr1A	533884844	+	IWGSC2	DArTSNP	NA
753	1088048	A/C	Chr1A	405301157	-	IWGSC2	DArTSNP	NA
872	1108857	A/C	Chr1A	587053970	+	IWGSC2	DArTSNP	NA
941	991333	A/C	Chr1A	259850024	-	IWGSC2	DArTSNP	NA
949	3934946	A/C	Chr1A	504861460	+	IWGSC2	DArTSNP	NA
1111	3935791	A/C	Chr1A	7206317	-	IWGSC2	DArTSNP	NA
1113	1057437	A/C	Chr1A	31388445	+	IWGSC2	DArTSNP	NA
1162	3023013	A/C	Chr1A	507766319	-	IWGSC2	DArTSNP	NA
1203	3938885	A/C	Chr1A	152962271	+	IWGSC2	DArTSNP	NA
1297	1405339	A/C	Chr1A	22910421	-	IWGSC2	DArTSNP	NA
1399	989382	A/C	Chr1A	52511327	+	IWGSC2	DArTSNP	NA
1575	3026226	A/C	Chr1A	478593561	+	IWGSC2	DArTSNP	NA
1580	4261370	A/C	Chr1A	55554227	-	IWGSC2	DArTSNP	NA
1589	1013527	A/C	Chr1A	10624438	+	IWGSC2	DArTSNP	NA
1593	3940711	A/C	Chr1A	62196637	+	IWGSC2	DArTSNP	NA
1614	3947631	A/C	Chr1A	596514054	+	IWGSC2	DArTSNP	NA
1623	1068748	A/C	Chr1A	5554758	-	IWGSC2	DArTSNP	NA
1700	1021518	A/C	Chr1A	486934235	-	IWGSC2	DArTSNP	NA
1925	3024016	A/C	Chr1A	15699296	+	IWGSC2	DArTSNP	NA
1999	4262489	A/C	Chr1A	1632059	-	IWGSC2	DArTSNP	NA
2318	4261359	A/C	Chr1A	7206248	+	IWGSC2	DArTSNP	NA
2326	1062507	A/C	Chr1A	573350332	-	IWGSC2	DArTSNP	NA

2340	3943550	A/C	Chr1A	473109528	-	IWGSC2	DArTSNP	NA
2348	3937333	A/C	Chr1A	152962274	-	IWGSC2	DArTSNP	NA
2376	4397724	A/C	Chr1A	362647445	-	IWGSC2	DArTSNP	NA
2486	1068263	A/C	Chr1A	454055461	-	IWGSC2	DArTSNP	NA
2508	1252727	A/C	Chr1A	1160397	+	IWGSC2	DArTSNP	NA
2533	1226319	A/C	Chr1A	478601867	-	IWGSC2	DArTSNP	NA
2567	1115883	A/C	Chr1A	24862708	+	IWGSC2	DArTSNP	NA
2593	1719190	A/C	Chr1A	20423536	+	IWGSC2	DArTSNP	NA
2595	2335340	A/C	Chr1A	22346531	+	IWGSC2	DArTSNP	NA
2605	5325782	A/C	Chr1A	452894520	-	IWGSC2	DArTSNP	NA
2612	1236098	A/C	Chr1A	510928214	-	IWGSC2	DArTSNP	NA
2623	1200935	A/C	Chr1A	23422540	-	IWGSC2	DArTSNP	NA
2624	983655	A/C	Chr1A	576443981	+	IWGSC2	DArTSNP	NA
2634	1105601	A/C	Chr1A	31383614	-	IWGSC2	DArTSNP	NA
2641	4394165	A/C	Chr1A	451397750	-	IWGSC2	DArTSNP	NA
2650	1161343	A/C	Chr1A	32253106	-	IWGSC2	DArTSNP	NA
2692	1254322	A/C	Chr1A	13795445	+	IWGSC2	DArTSNP	NA
2807	1101782	A/C	Chr1A	556531337	+	IWGSC2	DArTSNP	NA
2829	1099404	A/C	Chr1A	473352727	-	IWGSC2	DArTSNP	NA
2958	1132858	A/C	Chr1A	581578440	+	IWGSC2	DArTSNP	NA
3120	4538767	A/C	Chr1A	585109336	-	IWGSC2	DArTSNP	NA
3133	4989939	A/C	Chr1A	490957187	+	IWGSC2	DArTSNP	NA
3179	3021568	A/C	Chr1A	102147699	-	IWGSC2	DArTSNP	NA
3198	3953211	A/C	Chr1A	11975247	+	IWGSC2	DArTSNP	NA
3255	1101285	A/C	Chr1A	543210000	+	IWGSC2	DArTSNP	NA
3317	1092671	A/C	Chr1A	521536011	+	IWGSC2	DArTSNP	NA
3321	2294185	A/C	Chr1A	590739226	+	IWGSC2	DArTSNP	NA
3375	1266903	A/C	Chr1A	51904859	+	IWGSC2	DArTSNP	NA
3387	3956100	A/C	Chr1A	449092175	+	IWGSC2	DArTSNP	NA
3467	3940256	A/C	Chr1A	543197614	-	IWGSC2	DArTSNP	NA
3494	3384726	A/C	Chr1A	485452762	-	IWGSC2	DArTSNP	NA
3523	3934300	A/C	Chr1A	54756038	+	IWGSC2	DArTSNP	NA
3712	1116485	A/C	Chr1A	11848840	+	IWGSC2	DArTSNP	NA
3827	1211547	A/C	Chr1A	11541613	+	IWGSC2	DArTSNP	NA
3848	3937058	A/C	Chr1A	1910079	-	IWGSC2	DArTSNP	NA
3980	1406706	A/C	Chr1A	253117714	+	IWGSC2	DArTSNP	NA
4020	1125761	A/C	Chr1A	120322241	+	IWGSC2	DArTSNP	NA
4022	1256079	A/C	Chr1A	13705320	+	IWGSC2	DArTSNP	NA
4156	1246643	A/C	Chr1A	374147124	-	IWGSC2	DArTSNP	NA
4174	1765789	A/C	Chr1A	5849521	+	IWGSC2	DArTSNP	NA
4202	1102329	A/C	Chr1A	3341067	+	IWGSC2	DArTSNP	NA
4405	1102202	A/C	Chr1A	584106035	+	IWGSC2	DArTSNP	NA
4423	2300698	A/C	Chr1A	12617311	+	IWGSC2	DArTSNP	NA
4542	1142052	A/C	Chr1A	15205819	+	IWGSC2	DArTSNP	NA
4681	3937206	A/C	Chr1A	44938832	-	IWGSC2	DArTSNP	NA
4683	3955429	A/C	Chr1A	374147121	+	IWGSC2	DArTSNP	NA
4709	3951661	A/C	Chr1A	534459845	+	IWGSC2	DArTSNP	NA
4833	1105832	A/C	Chr1A	353118934	-	IWGSC2	DArTSNP	NA
4835	1675600	A/C	Chr1A	68038670	-	IWGSC2	DArTSNP	NA
4851	1124870	A/C	Chr1A	358338537	+	IWGSC2	DArTSNP	NA

4868	1114966	A/C	Chr1A	357363681	-	IWGSC2	DArTSNP	NA
4869	3960706	A/C	Chr1A	459858650	+	IWGSC2	DArTSNP	NA
4877	2354508	A/C	Chr1A	68038667	+	IWGSC2	DArTSNP	NA
4960	1088792	A/C	Chr1A	575763511	+	IWGSC2	DArTSNP	NA
4962	4395843	A/C	Chr1A	22910554	+	IWGSC2	DArTSNP	NA
4984	1140807	A/C	Chr1A	538360324	+	IWGSC2	DArTSNP	NA
4999	1121364	A/C	Chr1A	11989801	-	IWGSC2	DArTSNP	NA
5141	1137407	A/C	Chr1A	435419307	+	IWGSC2	DArTSNP	NA
5142	996865	A/C	Chr1A	8616644	+	IWGSC2	DArTSNP	NA
5156	1267529	A/C	Chr1A	464504196	-	IWGSC2	DArTSNP	NA
5163	2303757	A/C	Chr1A	478675826	-	IWGSC2	DArTSNP	NA
5164	1123867	A/C	Chr1A	126615978	-	IWGSC2	DArTSNP	NA
5176	3949999	A/C	Chr1A	343480558	+	IWGSC2	DArTSNP	NA
7476	1131917	A/C	Chr1A	549095877	-	IWGSC2	DArTSNP	NA
8097	1236950	A/C	Chr1A	478604668	-	IWGSC2	DArTSNP	NA
8177	5346147	A/C	Chr1A	578989227	-	IWGSC2	DArTSNP	NA
8349	1083146	A/C	Chr1A	62532255	+	IWGSC2	DArTSNP	NA
8398	1119170	A/C	Chr1A	22779857	-	IWGSC2	DArTSNP	NA
8406	1069296	A/C	Chr1A	473517988	-	IWGSC2	DArTSNP	NA
8452	1101719	A/C	Chr1A	15378506	+	IWGSC2	DArTSNP	NA
8554	2275134	A/C	Chr1A	529472207	+	IWGSC2	DArTSNP	NA
8565	1667191	A/C	Chr1A	529472350	-	IWGSC2	DArTSNP	NA
8740	5342778	A/C	Chr1A	580545314	-	IWGSC2	DArTSNP	NA
8760	1721385	A/C	Chr1A	11792609	+	IWGSC2	DArTSNP	NA
8821	2.7E+07	A/C	Chr1A	307849745	+	IWGSC2	DArTSNP	NA
8889	1159766	A/C	Chr1A	39784410	+	IWGSC2	DArTSNP	NA
8906	1263969	A/C	Chr1A	222126199	+	IWGSC2	DArTSNP	NA
8927	1152254	A/C	Chr1A	386976876	+	IWGSC2	DArTSNP	NA
8958	2311770	A/C	Chr1A	9326346	-	IWGSC2	DArTSNP	NA
8973	1160569	A/C	Chr1A	468905532	-	IWGSC2	DArTSNP	NA
9018	1075139	A/C	Chr1A	586229395	+	IWGSC2	DArTSNP	NA
9031	1060474	A/C	Chr1A	553811010	-	IWGSC2	DArTSNP	NA
9038	5410374	A/C	Chr1A	480107207	-	IWGSC2	DArTSNP	NA
9056	1.9E+07	A/C	Chr1A	562717947	-	IWGSC2	DArTSNP	NA
9059	1252775	A/C	Chr1A	521536011	+	IWGSC2	DArTSNP	NA
9060	1057186	A/C	Chr1A	588937277	-	IWGSC2	DArTSNP	NA
9081	1102942	A/C	Chr1A	153404634	-	IWGSC2	DArTSNP	NA
9089	1126005	A/C	Chr1A	7520585	+	IWGSC2	DArTSNP	NA
9206	2310479	A/C	Chr1A	534446986	-	IWGSC2	DArTSNP	NA
9219	1062584	A/C	Chr1A	140403006	+	IWGSC2	DArTSNP	NA
9269	1051556	A/C	Chr1A	251530600	-	IWGSC2	DArTSNP	NA
9280	2289064	A/C	Chr1A	549620251	-	IWGSC2	DArTSNP	NA
9306	1023595	A/C	Chr1A	7338933	-	IWGSC2	DArTSNP	NA
9328	1078628	A/C	Chr1A	559837259	+	IWGSC2	DArTSNP	NA
9337	1077302	A/C	Chr1A	5595391	-	IWGSC2	DArTSNP	NA
9412	1045015	A/C	Chr1A	8411496	-	IWGSC2	DArTSNP	NA
9459	1087705	A/C	Chr1A	482843284	+	IWGSC2	DArTSNP	NA
9511	1107257	A/C	Chr1A	9470140	+	IWGSC2	DArTSNP	NA
9646	1118559	A/C	Chr1A	15772579	-	IWGSC2	DArTSNP	NA
9647	1128039	A/C	Chr1A	8656323	-	IWGSC2	DArTSNP	NA

9700	5325747	A/C	Chr1A	407860941	-	IWGSC2	DArTSNP	NA
9714	1088699	A/C	Chr1A	566965771	-	IWGSC2	DArTSNP	NA
9741	3946318	A/C	Chr1A	570907982	-	IWGSC2	DArTSNP	NA
9742	2302257	A/C	Chr1A	571003298	-	IWGSC2	DArTSNP	NA
9878	1041189	A/C	Chr1A	505611670	+	IWGSC2	DArTSNP	NA
9883	1079519	A/C	Chr1A	517928347	-	IWGSC2	DArTSNP	NA
9946	1012142	A/C	Chr1A	517725513	+	IWGSC2	DArTSNP	NA
9959	1039050	A/C	Chr1A	412082544	+	IWGSC2	DArTSNP	NA
10192	1205976	A/C	Chr1A	538307115	-	IWGSC2	DArTSNP	NA
10218	1164220	A/C	Chr1A	13099532	+	IWGSC2	DArTSNP	NA
10367	1221062	A/C	Chr1A	48771409	-	IWGSC2	DArTSNP	NA
10485	1231766	A/C	Chr1A	341085873	+	IWGSC2	DArTSNP	NA
10487	1102229	A/C	Chr1A	53463260	-	IWGSC2	DArTSNP	NA
10567	1120323	A/C	Chr1A	539820169	+	IWGSC2	DArTSNP	NA
11071	1102623	A/C	Chr1A	11974864	+	IWGSC2	DArTSNP	NA
11082	3033625	A/C	Chr1A	83002949	-	IWGSC2	DArTSNP	NA
11107	3020474	A/C	Chr1A	24547228	+	IWGSC2	DArTSNP	NA
11159	3025386	A/C	Chr1A	550067551	-	IWGSC2	DArTSNP	NA
11215	4439800	A/C	Chr1A	14561662	-	IWGSC2	DArTSNP	NA
11216	3935402	A/C	Chr1A	509470025	+	IWGSC2	DArTSNP	NA
11270	3952681	A/C	Chr1A	564337742	+	IWGSC2	DArTSNP	NA
11495	3532646	A/C	Chr1A	552007373	-	IWGSC2	DArTSNP	NA
11560	1403995	A/C	Chr1A	559843130	-	IWGSC2	DArTSNP	NA
11651	3937719	A/C	Chr1A	491868717	-	IWGSC2	DArTSNP	NA
11678	994857	A/C	Chr1A	40642046	-	IWGSC2	DArTSNP	NA
11813	4439965	A/C	Chr1A	4912787	+	IWGSC2	DArTSNP	NA
11986	1065035	A/C	Chr1A	543926728	+	IWGSC2	DArTSNP	NA
12033	1075681	A/C	Chr1A	511769676	-	IWGSC2	DArTSNP	NA
12107	4262527	A/C	Chr1A	249154099	-	IWGSC2	DArTSNP	NA
12241	1210851	A/C	Chr1A	39783993	+	IWGSC2	DArTSNP	NA
12366	4395958	A/C	Chr1A	4968391	-	IWGSC2	DArTSNP	NA
12492	2275476	A/C	Chr1A	242152044	+	IWGSC2	DArTSNP	NA
12534	3022649	A/C	Chr1A	569292652	+	IWGSC2	DArTSNP	NA
12581	3028941	A/C	Chr1A	12628226	+	IWGSC2	DArTSNP	NA
12601	4542043	A/C	Chr1A	504998371	+	IWGSC2	DArTSNP	NA
12610	1126979	A/C	Chr1A	516028106	+	IWGSC2	DArTSNP	NA
12671	1149784	A/C	Chr1A	345078440	+	IWGSC2	DArTSNP	NA
12674	3024292	A/C	Chr1A	12628229	-	IWGSC2	DArTSNP	NA
12754	3960417	A/C	Chr1A	506584487	+	IWGSC2	DArTSNP	NA
12831	3022792	A/C	Chr1A	521745696	+	IWGSC2	DArTSNP	NA
13046	1087917	A/C	Chr1A	39783993	+	IWGSC2	DArTSNP	NA
13072	1124599	A/C	Chr1A	590163356	+	IWGSC2	DArTSNP	NA
13106	1103189	A/C	Chr1A	523650758	+	IWGSC2	DArTSNP	NA
13112	3534261	A/C	Chr1A	8626960	+	IWGSC2	DArTSNP	NA
13116	3532686	A/C	Chr1A	415378202	-	IWGSC2	DArTSNP	NA
13230	1273059	A/C	Chr1A	592395772	-	IWGSC2	DArTSNP	NA
13441	1380604	A/C	Chr1A	359966503	-	IWGSC2	DArTSNP	NA
13472	1233332	A/C	Chr1A	504849803	-	IWGSC2	DArTSNP	NA
13478	1127111	A/C	Chr1A	359649615	-	IWGSC2	DArTSNP	NA
13634	1076929	A/C	Chr1A	376341545	-	IWGSC2	DArTSNP	NA

13726	4404770	A/C	Chr1A	12796056	-	IWGSC2	DArTSNP	NA
13728	4004912	A/C	Chr1A	24848358	-	IWGSC2	DArTSNP	NA
13729	1077077	A/C	Chr1A	9151458	-	IWGSC2	DArTSNP	NA
13731	1100401	A/C	Chr1A	31071086	+	IWGSC2	DArTSNP	NA
13765	1695042	A/C	Chr1A	538349857	-	IWGSC2	DArTSNP	NA
13918	1019609	A/C	Chr1A	345841290	-	IWGSC2	DArTSNP	NA
13947	980414	A/C	Chr1A	13268918	-	IWGSC2	DArTSNP	NA
13962	1063576	A/C	Chr1A	560344630	-	IWGSC2	DArTSNP	NA
13964	5340674	A/C	Chr1A	155425702	+	IWGSC2	DArTSNP	NA
13971	1136542	A/C	Chr1A	46586638	-	IWGSC2	DArTSNP	NA
13998	992176	A/C	Chr1A	51843724	-	IWGSC2	DArTSNP	NA
14101	2250404	A/C	Chr1A	590739226	+	IWGSC2	DArTSNP	NA
14102	992113	A/C	Chr1A	5686515	+	IWGSC2	DArTSNP	NA
14116	5370345	A/C	Chr1A	1868201	+	IWGSC2	DArTSNP	NA
14128	2351729	A/C	Chr1A	7688525	-	IWGSC2	DArTSNP	NA
14148	983365	A/C	Chr1A	548508344	-	IWGSC2	DArTSNP	NA
14160	1110184	A/C	Chr1A	542417335	+	IWGSC2	DArTSNP	NA
14186	978510	A/C	Chr1A	406574665	-	IWGSC2	DArTSNP	NA
14208	1234131	A/C	Chr1A	24688007	-	IWGSC2	DArTSNP	NA
14249	1026677	A/C	Chr1A	30909944	-	IWGSC2	DArTSNP	NA
14290	1210333	A/C	Chr1A	585109336	-	IWGSC2	DArTSNP	NA
14295	2275375	A/C	Chr1A	8236316	+	IWGSC2	DArTSNP	NA
14313	1054997	A/C	Chr1A	23537509	+	IWGSC2	DArTSNP	NA
14319	1070550	A/C	Chr1A	157171200	+	IWGSC2	DArTSNP	NA
14345	1088935	A/C	Chr1A	577404229	-	IWGSC2	DArTSNP	NA
14384	1256583	A/C	Chr1A	11583187	-	IWGSC2	DArTSNP	NA
14440	1041649	A/C	Chr1A	494753515	-	IWGSC2	DArTSNP	NA
14466	1045584	A/C	Chr1A	32765129	-	IWGSC2	DArTSNP	NA
14650	1221906	A/C	Chr1A	3919892	-	IWGSC2	DArTSNP	NA
14679	3951616	A/C	Chr1A	207675913	+	IWGSC2	DArTSNP	NA
14724	976975	A/C	Chr1A	560398043	+	IWGSC2	DArTSNP	NA
14730	1162440	A/C	Chr1A	15479229	-	IWGSC2	DArTSNP	NA
14752	3944829	A/C	Chr1A	56026318	+	IWGSC2	DArTSNP	NA
14813	1118912	A/C	Chr1A	15125867	+	IWGSC2	DArTSNP	NA
14851	2258970	A/C	Chr1A	592350777	-	IWGSC2	DArTSNP	NA
14910	1195763	A/C	Chr1A	505938944	-	IWGSC2	DArTSNP	NA
14940	1126728	A/C	Chr1A	594005313	+	IWGSC2	DArTSNP	NA
14961	1118051	A/C	Chr1A	594005316	-	IWGSC2	DArTSNP	NA
15017	1103933	A/C	Chr1A	56460948	+	IWGSC2	DArTSNP	NA
15018	2261520	A/C	Chr1A	1902482	+	IWGSC2	DArTSNP	NA
15071	4991245	A/C	Chr1A	1311189	-	IWGSC2	DArTSNP	NA
15129	1132024	A/C	Chr1A	583558533	+	IWGSC2	DArTSNP	NA
15189	1234731	A/C	Chr1A	26649332	-	IWGSC2	DArTSNP	NA
15293	1166905	A/C	Chr1A	484270839	-	IWGSC2	DArTSNP	NA
15578	5569907	A/C	Chr1A	367685700	+	IWGSC2	DArTSNP	NA
15604	1160536	A/C	Chr1A	572192993	-	IWGSC2	DArTSNP	NA
15634	3020618	A/C	Chr1A	52063275	-	IWGSC2	DArTSNP	NA
15701	3027260	A/C	Chr1A	562641178	-	IWGSC2	DArTSNP	NA
15703	3020657	A/C	Chr1A	580322979	-	IWGSC2	DArTSNP	NA
15753	3028141	A/C	Chr1A	15510260	-	IWGSC2	DArTSNP	NA

Tabela S1.4. Segregacje markerów SNP dla genotypów pszenicy badanych w 2023 roku

Wydruk pierwszych 5 z 12848 stron

CloneID	AlleleID	TrimmedSe	AlnCnt_Wh	AlnEvalue_	rs#	Chrom_Wh
1206275	1206275|F|0-62:T>C-62:T>C	TGCAGCAG	3	1.21E-27	1206275	Chr2B
1045184	1045184|F|0-14:G>A-14:G>A	TGCAGCAG	3	1.21E-27	1045184	Chr5D
977659	977659|F|0-45:G>A-45:G>A	TGCAGCCA	1	1.21E-27	977659	Chr3B
2278762	2278762|F|0-60:G>C-60:G>C	TGCAGCGC	4	1.21E-27	2278762	Chr2B
1204116	1204116|F|0-9:G>A-9:G>A	TGCAGCTC	1	1.21E-27	1204116	Chr6B
1001344	1001344|F|0-35:G>C-35:G>C	TGCAGCTT	12	1.21E-27	1001344	Chr3D
9723682	9723682|F|0-16:T>C-16:T>C	TGCAGGAC	1	1.21E-27	9723682	Chr3B
2253134	2253134|F|0-30:G>C-30:G>C	TGCAGGCC	1	1.21E-27	2253134	Chr3B
1219494	1219494|F|0-34:C>T-34:C>T	TGCAGTCT	1	1.56E-26	1219494	Chr2D
2322423	2322423|F|0-14:A>G-14:A>G	TGCAGACT	2	1.21E-27	2322423	Chr7A
5580983	5580983|F|0-27:G>A-27:G>A	TGCAGATT	4	2.62E-24	5580983	ChrUnknov
14582313	14582313|F|0-32:A>G-32:A>G	TGCAGCCA	6	1.22E-22	14582313	Chr2A
2252238	2252238|F|0-35:G>A-35:G>A	TGCAGCCC	3	2.23E-24	2252238	Chr4D
1054608	1054608|F|0-26:A>G-26:A>G	TGCAGCCC	1	1.21E-27	1054608	Chr5D
1E+08	100009501|F|0-58:T>C-58:T>C	TGCAGCGG	10	5.62E-26	1E+08	Chr2D
991053	991053|F|0-31:C>G-31:C>G	TGCAGGAA	1	5.62E-26	991053	Chr4B
1097044	1097044|F|0-20:T>C-20:T>C	TGCAGGCG	1	1.21E-27	1097044	Chr6A
1043238	1043238|F|0-66:G>A-66:G>A	TGCAGGTG	3	1.21E-27	1043238	Chr5D
1135903	1135903|F|0-19:G>A-19:G>A	TGCAGGTG	1	1.21E-27	1135903	Chr1A
2295526	2295526|F|0-35:C>T-35:C>T	TGCAGAGC	0	999	2295526	
1092368	1092368|F|0-18:T>C-18:T>C	TGCAGCGT	2	7.80E-24	1092368	Chr3B
2275392	2275392|F|0-57:C>A-57:C>A	TGCAGCTA	1	1.21E-27	2275392	Chr2A
3021994	3021994|F|0-19:G>A-19:G>A	TGCAGCTT	2	2.02E-25	3021994	Chr5B
1108996	1108996|F|0-9:T>C-9:T>C	TGCAGGAA	17	1.21E-27	1108996	Chr6D
1053920	1053920|F|0-22:A>C-22:A>C	TGCAGGTA	2	1.21E-27	1053920	Chr3B
1112179	1112179|F|0-53:C>T-53:C>T	TGCAGAAA	1	2.04E-20	1112179	Chr2D
1E+08	100009527|F|0-46:C>T-46:C>T	TGCAGAAA	31	2.62E-24	1E+08	ChrUnknov
1075947	1075947|F|0-17:G>C-17:G>C	TGCAGAAA	1	1.21E-27	1075947	Chr6A
982867	982867|F|0-50:T>A-50:T>A	TGCAGAAA	1	1.21E-27	982867	Chr5B
1286103	1286103|F|0-29:A>T-29:A>T	TGCAGAAA	1	1.21E-27	1286103	Chr1D
993943	993943|F|0-23:A>G-23:A>G	TGCAGAAA	4	1.21E-27	993943	Chr2A
979691	979691|F|0-18:A>T-18:A>T	TGCAGAAA	3	1.21E-27	979691	Chr1A
1001962	1001962|F|0-62:G>T-62:G>T	TGCAGAAA	1	1.21E-27	1001962	Chr7B
1221252	1221252|F|0-19:C>A-19:C>A	TGCAGAAA	1	1.21E-27	1221252	Chr2B
978141	978141|F|0-12:T>C-12:T>C	TGCAGAAA	1	1.21E-27	978141	Chr2D
1101784	1101784|F|0-47:A>G-47:A>G	TGCAGAAA	1	1.21E-27	1101784	Chr6B
1121560	1121560|F|0-60:T>C-60:T>C	TGCAGAAA	1	1.21E-27	1121560	Chr5D
2275336	2275336|F|0-28:T>C-28:T>C	TGCAGAAA	1	1.21E-27	2275336	Chr2A
1185856	1185856|F|0-33:T>A-33:T>A	TGCAGAAA	9	1.21E-27	1185856	Chr6A
1037900	1037900|F|0-32:A>G-32:A>G	TGCAGAAA	3	1.21E-27	1037900	Chr7B
1052289	1052289|F|0-33:C>T-33:C>T	TGCAGAAA	1	1.21E-27	1052289	Chr7B
1394848	1394848|F|0-11:A>G-11:A>G	TGCAGAAA	1	1.21E-27	1394848	Chr3A
1202549	1202549|F|0-19:T>C-19:T>C	TGCAGAAA	4	5.62E-26	1202549	Chr7B
992564	992564|F|0-56:T>C-56:T>C	TGCAGAAA	1	5.62E-26	992564	Chr4B

1090542	1090542|F|0-55:G>A-55:G>A	TGCAGAAA	2	1.21E-27	1090542	Chr7B
1117799	1117799|F|0-20:G>A-20:G>A	TGCAGAAA	1	1.21E-27	1117799	Chr1D
1135829	1135829|F|0-43:C>G-43:C>G	TGCAGAAA	3	5.62E-26	1135829	Chr3B
1220475	1220475|F|0-12:T>C-12:T>C	TGCAGAAA	3	1.21E-27	1220475	Chr5B
1031060	1031060|F|0-31:A>G-31:A>G	TGCAGAAA	3	1.21E-27	1031060	Chr1D
70233546	70233546|F|0-32:G>A-32:G>A	TGCAGAAA	1	5.62E-26	70233546	Chr1A
1088472	1088472|F|0-42:G>A-42:G>A	TGCAGAAA	2	1.21E-27	1088472	Chr1B
1131881	1131881|F|0-33:A>G-33:A>G	TGCAGAAA	0	999	1131881	
1213910	1213910|F|0-50:G>A-50:G>A	TGCAGAAA	4	5.62E-26	1213910	Chr7A
1094515	1094515|F|0-8:C>G-8:C>G	TGCAGAAA	1	1.21E-27	1094515	Chr7A
5324560	5324560|F|0-28:A>G-28:A>G	TGCAGAAA	2	1.21E-27	5324560	Chr3A
1127148	1127148|F|0-39:T>C-39:T>C	TGCAGAAA	8	1.21E-27	1127148	Chr6B
3222192	3222192|F|0-37:T>C-37:T>C	TGCAGAAA	1	1.21E-27	3222192	Chr6A
1090818	1090818|F|0-27:T>C-27:T>C	TGCAGAAA	1	1.21E-27	1090818	Chr1B
3944426	3944426|F|0-6:A>G-6:A>G	TGCAGAGA	2	1.22E-22	3944426	Chr3A
4989902	4989902|F|0-55:A>G-55:A>G	TGCAGAAA	3	1.21E-27	4989902	Chr4A
2277300	2277300|F|0-35:T>C-35:T>C	TGCAGAAA	1	1.21E-27	2277300	Chr2B
1005316	1005316|F|0-65:A>G-65:A>G	TGCAGAAA	3	5.62E-26	1005316	Chr1D
1115539	1115539|F|0-8:C>T-8:C>T	TGCAGAAA	1	1.21E-27	1115539	Chr5A
1113277	1113277|F|0-36:C>T-36:C>T	TGCAGAAA	0	999	1113277	
1103701	1103701|F|0-44:A>G-44:A>G	TGCAGAAA	1	5.62E-26	1103701	Chr2B
1103248	1103248|F|0-24:G>A-24:G>A	TGCAGAAA	1	1.21E-27	1103248	Chr5A
1088482	1088482|F|0-6:A>G-6:A>G	TGCAGAGA	9	2.62E-24	1088482	Chr3B
1138199	1138199|F|0-57:A>G-57:A>G	TGCAGAAA	6	1.21E-27	1138199	ChrUnknov
2275935	2275935|F|0-10:G>A-10:G>A	TGCAGAAA	3	1.21E-27	2275935	Chr5B
1103891	1103891|F|0-24:G>A-24:G>A	TGCAGAAA	1	1.21E-27	1103891	Chr5B
1205318	1205318|F|0-21:A>G-21:A>G	TGCAGAAA	2	1.21E-27	1205318	Chr5A
981297	981297|F|0-13:T>C-13:T>C	TGCAGAAA	1	1.21E-27	981297	Chr2B
1088359	1088359|F|0-43:C>T-43:C>T	TGCAGAAA	1	1.21E-27	1088359	Chr5A
6027430	6027430|F|0-34:C>T-34:C>T	TGCAGAAA	1	1.21E-27	6027430	Chr3D
1128177	1128177|F|0-36:T>C-36:T>C	TGCAGAAA	1	1.21E-27	1128177	Chr3A
2290787	2290787|F|0-5:A>G-5:A>G	TGCAGGAA	4	1.21E-27	2290787	Chr5B
1032558	1032558|F|0-66:G>T-66:G>T	TGCAGAAA	2	1.21E-27	1032558	Chr1A
1079818	1079818|F|0-28:A>G-28:A>G	TGCAGAAA	2	1.21E-27	1079818	Chr1B
1066488	1066488|F|0-59:T>C-59:T>C	TGCAGAAA	1	1.21E-27	1066488	Chr5B
1256734	1256734|F|0-23:T>A-23:T>A	TGCAGAAA	2	1.21E-27	1256734	Chr5B
1062944	1062944|F|0-19:C>G-19:C>G	TGCAGAAA	0	999	1062944	
1029555	1029555|F|0-26:C>G-26:C>G	TGCAGAAA	1	5.62E-26	1029555	Chr5B
2285557	2285557|F|0-23:T>C-23:T>C	TGCAGAAA	2	5.62E-26	2285557	Chr1B
2340381	2340381|F|0-56:G>T-56:G>T	TGCAGAAA	8	5.62E-26	2340381	Chr7D
1163777	1163777|F|0-50:A>T-50:A>T	TGCAGAAA	3	1.21E-27	1163777	Chr5A
1245435	1245435|F|0-9:T>G-9:T>G	TGCAGAAA	1	1.22E-22	1245435	Chr7B
1010420	1010420|F|0-11:T>G-11:T>G	TGCAGAAA	3	1.21E-27	1010420	Chr7B
1094312	1094312|F|0-65:G>A-65:G>A	TGCAGAAA	1	1.21E-27	1094312	Chr3D
982838	982838|F|0-44:C>T-44:C>T	TGCAGAAA	1	2.23E-24	982838	Chr1A
1031049	1031049|F|0-39:A>G-39:A>G	TGCAGAAA	1	1.21E-27	1031049	Chr7D
1345323	1345323|F|0-8:G>T-8:G>T	TGCAGAAA	0	999	1345323	
1691561	1691561|F|0-60:G>C-60:G>C	TGCAGAAA	2	1.21E-27	1691561	Chr5D
2254084	2254084|F|0-44:C>G-44:C>G	TGCAGAAA	3	1.21E-27	2254084	Chr2A
1053625	1053625|F|0-5:C>A-5:C>A	TGCAGAAA	5	1.22E-22	1053625	Chr6B
1033949	1033949|F|0-45:T>C-45:T>C	TGCAGAAA	3	1.21E-27	1033949	Chr4B
1139142	1139142|F|0-21:A>G-21:A>G	TGCAGAAA	1	1.21E-27	1139142	Chr7D
1107195	1107195|F|0-38:C>A-38:C>A	TGCAGAAA	0	999	1107195	

2301896	2301896|F|0-17:G>A-17:G>A	TGCAGAAA	1	1.21E-27	2301896	Chr6B
1164347	1164347|F|0-23:G>A-23:G>A	TGCAGAAA	2	5.62E-26	1164347	Chr6A
1084839	1084839|F|0-50:C>T-50:C>T	TGCAGAAA	3	1.21E-27	1084839	ChrUnknov
5325707	5325707|F|0-30:G>A-30:G>A	TGCAGAAA	1	1.21E-27	5325707	Chr6B
2260177	2260177|F|0-68:C>T-68:C>T	TGCAGAAA	2	1.21E-27	2260177	Chr1B
1126203	1126203|F|0-20:T>G-20:T>G	TGCAGAAC	0	999	1126203	
1021108	1021108|F|0-6:A>G-6:A>G	TGCAGAGC	3	1.21E-27	1021108	Chr3D
1079802	1079802|F|0-18:G>T-18:G>T	TGCAGAAC	1	5.62E-26	1079802	Chr3A
1217270	1217270|F|0-35:T>A-35:T>A	TGCAGAAC	1	9.48E-19	1217270	Chr2B
1089114	1089114|F|0-34:A>G-34:A>G	TGCAGAAC	1	2.02E-25	1089114	ChrUnknov
1039288	1039288|F|0-30:C>A-30:C>A	TGCAGAAC	3	1.21E-27	1039288	Chr4B
1233872	1233872|F|0-62:A>C-62:A>C	TGCAGAAC	6	1.21E-27	1233872	ChrUnknov
1233399	1233399|F|0-39:T>G-39:T>G	TGCAGAAC	1	1.21E-27	1233399	Chr2B
1E+08	100009636|F|0-51:G>A-51:G>A	TGCAGAAC	2	5.62E-26	1E+08	Chr2A
1109519	1109519|F|0-20:G>A-20:G>A	TGCAGAAC	0	999	1109519	
1102515	1102515|F|0-44:C>T-44:C>T	TGCAGAAC	2	1.21E-27	1102515	Chr5D
2275333	2275333|F|0-21:C>T-21:C>T	TGCAGAAC	1	1.21E-27	2275333	Chr5B
1155386	1155386|F|0-17:T>C-17:T>C	TGCAGAAC	1	1.21E-27	1155386	Chr3B
978099	978099|F|0-12:G>A-12:G>A	TGCAGAAC	2	1.21E-27	978099	Chr5D
1100082	1100082|F|0-19:A>G-19:A>G	TGCAGAAC	1	1.21E-27	1100082	Chr1A
985735	985735|F|0-17:A>G-17:A>G	TGCAGAAC	1	4.35E-27	985735	Chr6A
1106627	1106627|F|0-33:T>C-33:T>C	TGCAGAAC	1	1.21E-27	1106627	Chr7B
2245154	2245154|F|0-6:A>T-6:A>T	TGCAGATC	2	1.21E-27	2245154	Chr3D
1089656	1089656|F|0-20:T>C-20:T>C	TGCAGAAC	2	1.21E-27	1089656	Chr1B
1110156	1110156|F|0-46:T>C-46:T>C	TGCAGAAC	1	1.21E-27	1110156	Chr3A
979649	979649|F|0-12:G>C-12:G>C	TGCAGAAC	1	1.21E-27	979649	Chr7D
1137912	1137912|F|0-12:C>T-12:C>T	TGCAGAAC	3	1.21E-27	1137912	Chr3A
1069296	1069296|F|0-21:A>G-21:A>G	TGCAGAAC	3	7.80E-24	1069296	Chr1A
2256116	2256116|F|0-26:G>A-26:G>A	TGCAGAAC	1	1.21E-27	2256116	Chr2B
1091514	1091514|F|0-56:A>T-56:A>T	TGCAGAAC	4	1.21E-27	1091514	Chr3A
1090229	1090229|F|0-21:G>A-21:G>A	TGCAGAAC	2	1.21E-27	1090229	Chr4D
1125188	1125188|F|0-48:A>C-48:A>C	TGCAGAAC	3	1.21E-27	1125188	Chr6D
1018097	1018097|F|0-9:T>A-9:T>A	TGCAGAAC	5	1.21E-27	1018097	Chr5D
1111800	1111800|F|0-8:C>G-8:C>G	TGCAGAAC	3	1.21E-27	1111800	Chr7B
1216111	1216111|F|0-21:A>G-21:A>G	TGCAGAAC	7	6.39E-25	1216111	Chr1D
2252616	2252616|F|0-37:C>G-37:C>G	TGCAGAAC	2	1.21E-27	2252616	Chr5D
2247236	2247236|F|0-26:A>C-26:A>C	TGCAGAAC	2	1.21E-27	2247236	Chr1D
2298173	2298173|F|0-40:A>G-40:A>G	TGCAGAAC	5	1.21E-27	2298173	Chr4D
2335624	2335624|F|0-67:G>A-67:G>A	TGCAGAAC	1	1.21E-27	2335624	Chr3B
3570089	3570089|F|0-18:C>T-18:C>T	TGCAGAAC	1	1.21E-27	3570089	Chr7D
1123196	1123196|F|0-7:C>T-7:C>T	TGCAGAAT	2	1.21E-27	1123196	Chr5B
982239	982239|F|0-15:T>C-15:T>C	TGCAGAAC	1	1.21E-27	982239	Chr6B
1090849	1090849|F|0-47:A>G-47:A>G	TGCAGAAC	4	1.21E-27	1090849	Chr3B
1219989	1219989|F|0-56:G>A-56:G>A	TGCAGAAC	1	7.80E-24	1219989	Chr3A
2333056	2333056|F|0-27:A>C-27:A>C	TGCAGAAC	1	1.21E-27	2333056	Chr4B
978093	978093|F|0-42:G>A-42:G>A	TGCAGAAC	1	1.21E-27	978093	Chr2D
1241932	1241932|F|0-32:T>C-32:T>C	TGCAGAAC	1	1.22E-22	1241932	Chr3B
16661436	16661436|F|0-28:A>T-28:A>T	TGCAGAAC	3	1.21E-27	16661436	Chr3B
1102292	1102292|F|0-8:G>A-8:G>A	TGCAGAAC	2	1.21E-27	1102292	Chr4D
1120800	1120800|F|0-21:G>A-21:G>A	TGCAGAAC	1	1.21E-27	1120800	Chr3A
1220863	1220863|F|0-42:T>A-42:T>A	TGCAGAAC	1	1.59E-16	1220863	Chr1A
1204275	1204275|F|0-23:C>T-23:C>T	TGCAGAAC	1	2.62E-24	1204275	Chr3A
1083182	1083182|F|0-11:T>A-11:T>A	TGCAGAAC	1	1.21E-27	1083182	Chr3B

1118247	1118247|F|0-23:T>C-23:T>C	TGCAGAAC	1	1.21E-27	1118247	Chr1A
1087758	1087758|F|0-27:T>A-27:T>A	TGCAGAAC	1	1.21E-27	1087758	Chr2A
5323829	5323829|F|0-68:T>A-68:T>A	TGCAGAAC	2	4.35E-27	5323829	Chr3A
1208004	1208004|F|0-18:A>G-18:A>G	TGCAGAAG	3	1.21E-27	1208004	Chr2B
1092678	1092678|F|0-48:C>T-48:C>T	TGCAGAAG	2	1.56E-26	1092678	Chr3B
1214807	1214807|F|0-42:A>G-42:A>G	TGCAGAAG	1	4.35E-27	1214807	Chr5D
1116122	1116122|F|0-55:T>C-55:T>C	TGCAGAAG	1	1.21E-27	1116122	Chr1D
1113408	1113408|F|0-41:G>A-41:G>A	TGCAGAAG	3	1.21E-27	1113408	Chr2B
1108862	1108862|F|0-67:A>G-67:A>G	TGCAGAAG	2	1.21E-27	1108862	Chr7D
1159680	1159680|F|0-59:G>A-59:G>A	TGCAGAAG	1	5.62E-26	1159680	Chr1B
2334853	2334853|F|0-18:A>G-18:A>G	TGCAGAAG	1	2.62E-24	2334853	Chr3A
1126182	1126182|F|0-29:A>C-29:A>C	TGCAGAAG	3	1.21E-27	1126182	Chr1D
2273055	2273055|F|0-41:T>C-41:T>C	TGCAGAAG	1	1.21E-27	2273055	Chr5D
1240590	1240590|F|0-46:T>C-46:T>C	TGCAGAAG	2	1.21E-27	1240590	Chr3B
1243384	1243384|F|0-41:G>A-41:G>A	TGCAGAAG	3	1.21E-27	1243384	Chr5A
1219469	1219469|F|0-34:A>G-34:A>G	TGCAGAAG	1	1.21E-27	1219469	Chr5D
1402444	1402444|F|0-18:T>G-18:T>G	TGCAGAAG	1	1.21E-27	1402444	Chr4B
1031087	1031087|F|0-25:G>C-25:G>C	TGCAGAAG	1	1.21E-27	1031087	Chr3B
2327407	2327407|F|0-11:A>T-11:A>T	TGCAGAAG	1	1.21E-27	2327407	Chr3A
1095244	1095244|F|0-43:T>A-43:T>A	TGCAGAAG	1	1.21E-27	1095244	Chr5B
1090144	1090144|F|0-68:G>C-68:G>C	TGCAGAAG	1	1.21E-27	1090144	Chr1B
2251028	2251028|F|0-29:C>T-29:C>T	TGCAGAAG	6	1.21E-27	2251028	Chr5D
49091207	49091207|F|0-31:A>G-31:A>G	TGCAGAAG	1	2.62E-24	49091207	Chr1D
2278684	2278684|F|0-68:G>A-68:G>A	TGCAGAAG	1	1.21E-27	2278684	Chr6B
1268113	1268113|F|0-15:T>C-15:T>C	TGCAGAAG	2	1.21E-27	1268113	Chr5B
1211266	1211266|F|0-23:T>C-23:T>C	TGCAGAAG	3	1.21E-27	1211266	Chr7D
995501	995501|F|0-19:T>G-19:T>G	TGCAGAAG	4	1.21E-27	995501	Chr6B
1089000	1089000|F|0-42:T>A-42:T>A	TGCAGAAG	1	1.56E-26	1089000	Chr3D
1102843	1102843|F|0-40:G>A-40:G>A	TGCAGAAG	1	7.80E-24	1102843	Chr6D
1113946	1113946|F|0-39:T>C-39:T>C	TGCAGAAG	2	1.21E-27	1113946	Chr5D
1185264	1185264|F|0-54:G>A-54:G>A	TGCAGAAG	1	1.21E-27	1185264	Chr4D
1028238	1028238|F|0-22:G>A-22:G>A	TGCAGAAG	1	1.57E-21	1028238	Chr6B
1068275	1068275|F|0-5:A>C-5:A>C	TGCAGCAG	1	1.21E-27	1068275	Chr1D
1104000	1104000|F|0-58:C>A-58:C>A	TGCAGAAG	1	1.21E-27	1104000	Chr4B
1053729	1053729|F|0-38:A>G-38:A>G	TGCAGAAG	2	1.21E-27	1053729	Chr6A
2294721	2294721|F|0-53:A>G-53:A>G	TGCAGAAG	2	5.62E-26	2294721	Chr7B
1084637	1084637|F|0-43:T>C-43:T>C	TGCAGAAG	2	1.21E-27	1084637	Chr5B
1256445	1256445|F|0-41:C>T-41:C>T	TGCAGAAG	1	1.21E-27	1256445	Chr2A
1052749	1052749|F|0-48:C>T-48:C>T	TGCAGAAG	1	1.21E-27	1052749	Chr2B
2290120	2290120|F|0-13:C>T-13:C>T	TGCAGAAG	8	1.21E-27	2290120	Chr7B
1114532	1114532|F|0-12:C>T-12:C>T	TGCAGAAG	1	1.21E-27	1114532	Chr2B
1052267	1052267|F|0-31:C>A-31:C>A	TGCAGAAG	1	1.21E-27	1052267	Chr5D
1338378	1338378|F|0-48:C>T-48:C>T	TGCAGAAG	2	1.21E-27	1338378	Chr6B
1092666	1092666|F|0-68:G>A-68:G>A	TGCAGAAG	1	1.21E-27	1092666	Chr6A
1130446	1130446|F|0-9:G>C-9:G>C	TGCAGAAG	1	1.21E-27	1130446	Chr4A
1001902	1001902|F|0-33:C>T-33:C>T	TGCAGAAG	1	5.62E-26	1001902	Chr5B
1093202	1093202|F|0-10:A>G-10:A>G	TGCAGAAG	5	1.21E-27	1093202	Chr4B
39692798	39692798|F|0-39:C>G-39:C>G	TGCAGAAG	1	1.21E-27	39692798	Chr5B
1090426	1090426|F|0-8:T>C-8:T>C	TGCAGAAG	1	1.21E-27	1090426	Chr3D
1043394	1043394|F|0-58:A>G-58:A>G	TGCAGAAG	1	1.21E-27	1043394	Chr2A
993205	993205|F|0-37:T>G-37:T>G	TGCAGAAG	1	5.62E-26	993205	Chr1B
1210760	1210760|F|0-28:A>T-28:A>T	TGCAGAAT	1	1.21E-27	1210760	Chr5A
1125460	1125460|F|0-31:C>G-31:C>G	TGCAGAAT	1	1.21E-27	1125460	Chr1B

2260164	2260164|F|0-25:G>A-25:G>A	TGCAGAAT	0	999	2260164	
2289240	2289240|F|0-10:T>G-10:T>G	TGCAGAAT	1	1.21E-27	2289240	Chr3A
12419524	12419524|F|0-15:C>G-15:C>G	TGCAGAAT	0	999	12419524	
1711309	1711309|F|0-51:G>A-51:G>A	TGCAGAAT	3	1.21E-27	1711309	Chr5D
39692018	39692018|F|0-47:T>A-47:T>A	TGCAGAAT	2	2.62E-24	39692018	Chr5A
2247535	2247535|F|0-30:C>T-30:C>T	TGCAGAAT	1	1.21E-27	2247535	Chr1D
2289400	2289400|F|0-28:T>C-28:T>C	TGCAGAAT	1	1.21E-27	2289400	Chr2A
1120052	1120052|F|0-16:T>C-16:T>C	TGCAGAAT	1	1.21E-27	1120052	Chr6D
2277242	2277242|F|0-56:C>G-56:C>G	TGCAGAAT	0	999	2277242	
1063189	1063189|F|0-63:T>C-63:T>C	TGCAGAAT	1	1.21E-27	1063189	Chr4A
992529	992529|F|0-13:G>C-13:G>C	TGCAGAAT	2	5.62E-26	992529	Chr5A
1094732	1094732|F|0-22:G>A-22:G>A	TGCAGAAT	1	6.39E-25	1094732	Chr7A
1131720	1131720|F|0-5:C>A-5:C>A	TGCAGAAT	1	5.62E-26	1131720	Chr5A
2290381	2290381|F|0-12:G>A-12:G>A	TGCAGAAT	1	1.21E-27	2290381	Chr7A
1034758	1034758|F|0-49:T>G-49:T>G	TGCAGAAT	1	1.21E-27	1034758	Chr3B
997914	997914|F|0-64:C>T-64:C>T	TGCAGAAT	0	999	997914	
1696389	1696389|F|0-20:G>T-20:G>T	TGCAGAAT	1	1.56E-26	1696389	Chr1D
988637	988637|F|0-51:C>G-51:C>G	TGCAGAAT	1	1.21E-27	988637	Chr5D
1212339	1212339|F|0-27:A>G-27:A>G	TGCAGAAT	1	5.62E-26	1212339	Chr3B
1049837	1049837|F|0-35:T>C-35:T>C	TGCAGAAT	1	5.62E-26	1049837	Chr5A
982759	982759|F|0-7:T>G-7:T>G	TGCAGAAG	1	1.21E-27	982759	Chr2B
1106892	1106892|F|0-13:G>A-13:G>A	TGCAGAAT	2	1.21E-27	1106892	Chr3A
989603	989603|F|0-31:C>T-31:C>T	TGCAGAAT	4	1.21E-27	989603	Chr3B
1211780	1211780|F|0-28:C>T-28:C>T	TGCAGAAT	2	5.62E-26	1211780	Chr4A
1030466	1030466|F|0-27:T>G-27:T>G	TGCAGAAT	1	1.21E-27	1030466	Chr5D
1119104	1119104|F|0-37:T>C-37:T>C	TGCAGAAT	4	1.21E-27	1119104	Chr3A
1072346	1072346|F|0-20:G>T-20:G>T	TGCAGAAT	1	9.48E-19	1072346	Chr6D
1106388	1106388|F|0-55:T>A-55:T>A	TGCAGAAT	1	1.21E-27	1106388	Chr7B
1061588	1061588|F|0-5:A>G-5:A>G	TGCAGGAT	2	1.21E-27	1061588	Chr3B
1203947	1203947|F|0-45:C>G-45:C>G	TGCAGAAT	2	1.21E-27	1203947	Chr7B
2287690	2287690|F|0-58:T>C-58:T>C	TGCAGAAT	1	1.21E-27	2287690	Chr7A
1279273	1279273|F|0-11:G>A-11:G>A	TGCAGAAT	0	999	1279273	
1010359	1010359|F|0-39:T>A-39:T>A	TGCAGAAT	1	1.21E-27	1010359	Chr5B
1696167	1696167|F|0-8:T>C-8:T>C	TGCAGAAT	1	1.21E-27	1696167	Chr1D
1053718	1053718|F|0-7:A>G-7:A>G	TGCAGACG	5	1.21E-27	1053718	ChrUnknov
1102550	1102550|F|0-8:A>G-8:A>G	TGCAGACA	3	7.80E-24	1102550	Chr5D
1074666	1074666|F|0-12:G>T-12:G>T	TGCAGACA	1	9.41E-24	1074666	Chr1A
988631	988631|F|0-41:C>G-41:C>G	TGCAGACA	4	1.21E-27	988631	Chr6D
978032	978032|F|0-33:C>A-33:C>A	TGCAGACA	3	1.21E-27	978032	Chr6D
989098	989098|F|0-40:C>T-40:C>T	TGCAGACA	13	1.21E-27	989098	Chr3D
2279559	2279559|F|0-29:C>T-29:C>T	TGCAGACA	2	1.21E-27	2279559	Chr4A
1172052	1172052|F|0-12:C>T-12:C>T	TGCAGACA	1	1.21E-27	1172052	Chr2D
2291097	2291097|F|0-9:A>G-9:A>G	TGCAGACA	3	1.21E-27	2291097	Chr5B
1051025	1051025|F|0-66:G>A-66:G>A	TGCAGACA	1	1.21E-27	1051025	Chr6B
1240475	1240475|F|0-17:A>C-17:A>C	TGCAGACA	1	2.23E-24	1240475	Chr5B
1319073	1319073|F|0-9:G>A-9:G>A	TGCAGACA	2	1.21E-27	1319073	Chr4B
2279701	2279701|F|0-67:G>A-67:G>A	TGCAGACA	3	1.21E-27	2279701	Chr7A
2325016	2325016|F|0-52:C>T-52:C>T	TGCAGACA	3	1.21E-27	2325016	Chr2D
1123770	1123770|F|0-14:A>C-14:A>C	TGCAGACA	4	1.21E-27	1123770	Chr7B
1114411	1114411|F|0-25:C>G-25:C>G	TGCAGACA	1	1.56E-26	1114411	Chr5A
2244959	2244959|F|0-38:G>A-38:G>A	TGCAGACA	2	1.21E-27	2244959	Chr1D
1313363	1313363|F|0-15:G>A-15:G>A	TGCAGACA	2	5.62E-26	1313363	Chr3B
3024869	3024869|F|0-13:T>C-13:T>C	TGCAGACA	1	1.21E-27	3024869	Chr2B

Tabela S1.5. Segregacje markerów SNP genotypów pszenicy badanych w 2023 roku do analiz asocjacyjnych

Wydruk pierwszych 5 z 12765 stron

	rs#	alleles		Chrom	ChromPosSnp_	strand	assembly#	center
895	2294102	C/A	A	1A	63202868	-	IWGSC2	DArTSNP
1414	1132236	C/A	A	1A	79654005	+	IWGSC2	DArTSNP
2502	1221148	C/A	A	1A	23548617	-	IWGSC2	DArTSNP
2578	1364191	C/A	A	1A	236671119	-	IWGSC2	DArTSNP
3290	1004489	C/A	A	1A	165699437	+	IWGSC2	DArTSNP
4312	2262808	C/A	A	1A	2609211	-	IWGSC2	DArTSNP
4796	1097106	C/A	A	1A	2981550	+	IWGSC2	DArTSNP
5050	1126766	C/A	A	1A	526306057	-	IWGSC2	DArTSNP
5073	3020862	C/A	A	1A	484386429	-	IWGSC2	DArTSNP
5437	5345633	C/A	A	1A	550861629	+	IWGSC2	DArTSNP
5892	5968414	C/A	A	1A	347391874	+	IWGSC2	DArTSNP
8142	2252203	C/A	A	1A	350392400	-	IWGSC2	DArTSNP
9090	1060723	C/A	A	1A	376857933	+	IWGSC2	DArTSNP
9304	1067105	C/A	A	1A	574062075	-	IWGSC2	DArTSNP
10284	2330803	C/A	A	1A	558132725	-	IWGSC2	DArTSNP
10306	1335844	C/A	A	1A	533266984	-	IWGSC2	DArTSNP
10471	2281776	C/A	A	1A	17724052	+	IWGSC2	DArTSNP
10996	1126484	C/A	A	1A	32439454	+	IWGSC2	DArTSNP
11031	1084276	C/A	A	1A	467152573	+	IWGSC2	DArTSNP
11465	1141154	C/A	A	1A	375161242	+	IWGSC2	DArTSNP
11466	1141154	C/A	A	1A	375161243	+	IWGSC2	DArTSNP
11504	978646	C/A	A	1A	0	+	IWGSC2	DArTSNP
11752	1039774	C/A	A	1A	524810047	-	IWGSC2	DArTSNP
12653	999895	C/A	A	1A	567382281	-	IWGSC2	DArTSNP
12718	2271780	C/A	A	1A	496325317	-	IWGSC2	DArTSNP
12812	1314631	C/A	A	1A	98716898	-	IWGSC2	DArTSNP
13696	39661826	C/A	A	1A	100173445	-	IWGSC2	DArTSNP
13878	11313351	C/A	A	1A	257910507	+	IWGSC2	DArTSNP
14614	3935974	C/A	A	1A	120686202	+	IWGSC2	DArTSNP
15449	3021967	C/A	A	1A	8542998	+	IWGSC2	DArTSNP
16455	990732	C/A	A	1A	321962024	+	IWGSC2	DArTSNP
17387	1106679	C/A	A	1A	355709044	+	IWGSC2	DArTSNP
18540	1201355	C/A	A	1A	507239870	+	IWGSC2	DArTSNP
18998	49097139	C/A	A	1A	542425956	+	IWGSC2	DArTSNP
19225	1093668	C/A	A	1A	4968173	+	IWGSC2	DArTSNP
19615	1078943	C/A	A	1A	518269791	-	IWGSC2	DArTSNP
20125	979990	C/A	A	1A	547747938	-	IWGSC2	DArTSNP
20867	1130340	C/A	A	1A	594705776	-	IWGSC2	DArTSNP
21015	1112515	C/A	A	1A	448113315	+	IWGSC2	DArTSNP
21185	1081508	C/A	A	1A	587523427	+	IWGSC2	DArTSNP
21511	1093295	C/A	A	1A	11994534	+	IWGSC2	DArTSNP

23500	1106808	C/A	A	1A	18759329	+	IWGSC2	DArTSNP
23575	1011620	C/A	A	1A	51795022	+	IWGSC2	DArTSNP
24606	1077939	C/A	A	1A	557806494	+	IWGSC2	DArTSNP
24903	2334587	C/A	A	1A	8656388	+	IWGSC2	DArTSNP
25657	1293074	C/A	A	1A	10970374	+	IWGSC2	DArTSNP
26951	979743	C/A	A	1A	594437814	-	IWGSC2	DArTSNP
27452	1299519	C/A	A	1A	383314091	-	IWGSC2	DArTSNP
28035	3027649	C/A	A	1A	63137275	-	IWGSC2	DArTSNP
28366	7487803	C/A	A	1A	5857442	+	IWGSC2	DArTSNP
29917	1303334	C/A	A	1A	497216581	+	IWGSC2	DArTSNP
32218	5578231	C/A	A	1A	55004011	+	IWGSC2	DArTSNP
32639	2258784	C/A	A	1A	9970776	+	IWGSC2	DArTSNP
34034	1042991	C/A	A	1A	510981611	+	IWGSC2	DArTSNP
34422	1104397	C/A	A	1A	96744751	+	IWGSC2	DArTSNP
34459	996215	C/A	A	1A	592492395	-	IWGSC2	DArTSNP
34555	1251432	C/A	A	1A	3141565	-	IWGSC2	DArTSNP
34845	1219440	C/A	A	1A	307224970	-	IWGSC2	DArTSNP
35544	1167826	C/A	A	1A	44184737	+	IWGSC2	DArTSNP
36399	1001137	C/A	A	1A	15367397	-	IWGSC2	DArTSNP
36451	1088821	C/A	A	1A	47218959	-	IWGSC2	DArTSNP
37132	12419618	C/A	A	1A	591022403	-	IWGSC2	DArTSNP
37134	2260436	C/A	A	1A	591022388	-	IWGSC2	DArTSNP
37638	1E+08	C/A	A	1A	313833095	+	IWGSC2	DArTSNP
38140	1098334	C/A	A	1A	580835231	-	IWGSC2	DArTSNP
38618	1036957	C/A	A	1A	258801764	+	IWGSC2	DArTSNP
38659	1103517	C/A	A	1A	48877895	+	IWGSC2	DArTSNP
38705	989937	C/A	A	1A	534468481	+	IWGSC2	DArTSNP
38805	1E+08	C/A	A	1A	11338585	+	IWGSC2	DArTSNP
40185	12692132	C/A	A	1A	510527389	+	IWGSC2	DArTSNP
41707	1020196	C/A	A	1A	450968930	+	IWGSC2	DArTSNP
41930	3958664	C/A	A	1A	470074778	-	IWGSC2	DArTSNP
19	1135903	G/A	A	1A	501079058	-	IWGSC2	DArTSNP
50	70233546	G/A	A	1A	146578012	+	IWGSC2	DArTSNP
357	1203080	G/A	A	1A	533666804	+	IWGSC2	DArTSNP
436	1205643	G/A	A	1A	74872761	+	IWGSC2	DArTSNP
455	1094555	G/A	A	1A	521858494	+	IWGSC2	DArTSNP
825	2277135	G/A	A	1A	356854040	+	IWGSC2	DArTSNP
857	2327657	G/A	A	1A	440541426	+	IWGSC2	DArTSNP
990	4989129	G/A	A	1A	534984815	-	IWGSC2	DArTSNP
1028	1043544	G/A	A	1A	29654130	+	IWGSC2	DArTSNP
1391	1238410	G/A	A	1A	451451664	-	IWGSC2	DArTSNP
1588	1118630	G/A	A	1A	24601373	+	IWGSC2	DArTSNP
1665	1396845	G/A	A	1A	71574989	+	IWGSC2	DArTSNP
1674	2259602	G/A	A	1A	34014674	-	IWGSC2	DArTSNP
1813	3025653	G/A	A	1A	394214474	-	IWGSC2	DArTSNP
1981	1012492	G/A	A	1A	165673614	+	IWGSC2	DArTSNP
2255	1140682	G/A	A	1A	110867652	+	IWGSC2	DArTSNP
2367	1064418	G/A	A	1A	67320414	-	IWGSC2	DArTSNP
2551	1201588	G/A	A	1A	533355277	+	IWGSC2	DArTSNP
2561	2276661	G/A	A	1A	593612483	+	IWGSC2	DArTSNP

2725	2277220	G/A	A	1A	484608929	+	IWGSC2	DArTSNP
2874	990431	G/A	A	1A	536786419	+	IWGSC2	DArTSNP
3136	1039623	G/A	A	1A	584754676	-	IWGSC2	DArTSNP
3311	1098073	G/A	A	1A	22584932	-	IWGSC2	DArTSNP
3357	1004470	G/A	A	1A	567485319	-	IWGSC2	DArTSNP
3421	1057186	G/A	A	1A	588937265	-	IWGSC2	DArTSNP
3452	1233560	G/A	A	1A	579978383	+	IWGSC2	DArTSNP
3687	1062584	G/A	A	1A	140403051	+	IWGSC2	DArTSNP
3732	1113827	G/A	A	1A	564999883	-	IWGSC2	DArTSNP
3818	2296159	G/A	A	1A	9612700	-	IWGSC2	DArTSNP
3834	1127911	G/A	A	1A	370224532	-	IWGSC2	DArTSNP
3841	2258419	G/A	A	1A	397916741	-	IWGSC2	DArTSNP
3875	38671649	G/A	A	1A	582573323	+	IWGSC2	DArTSNP
4000	49096166	G/A	A	1A	401155929	+	IWGSC2	DArTSNP
4107	1121737	G/A	A	1A	18186836	+	IWGSC2	DArTSNP
4306	2301669	G/A	A	1A	582649878	+	IWGSC2	DArTSNP
4344	1105542	G/A	A	1A	220045096	-	IWGSC2	DArTSNP
4489	1218061	G/A	A	1A	27654825	-	IWGSC2	DArTSNP
4628	1041189	G/A	A	1A	505611718	+	IWGSC2	DArTSNP
4734	1115856	G/A	A	1A	534204284	-	IWGSC2	DArTSNP
4750	7331599	G/A	A	1A	44424303	+	IWGSC2	DArTSNP
5058	3030753	G/A	A	1A	39766002	+	IWGSC2	DArTSNP
5103	3942623	G/A	A	1A	88921714	+	IWGSC2	DArTSNP
5352	1092374	G/A	A	1A	549179139	+	IWGSC2	DArTSNP
5377	1087232	G/A	A	1A	550930801	+	IWGSC2	DArTSNP
5568	1091718	G/A	A	1A	525837482	-	IWGSC2	DArTSNP
5947	3951873	G/A	A	1A	459703598	+	IWGSC2	DArTSNP
6092	3024889	G/A	A	1A	92437536	-	IWGSC2	DArTSNP
6134	3025228	G/A	A	1A	563328920	+	IWGSC2	DArTSNP
6580	1008201	G/A	A	1A	66184911	-	IWGSC2	DArTSNP
6971	1210851	G/A	A	1A	39784027	+	IWGSC2	DArTSNP
6991	1000008	G/A	A	1A	535984721	-	IWGSC2	DArTSNP
7240	3935863	G/A	A	1A	32266865	-	IWGSC2	DArTSNP
7504	1862516	G/A	A	1A	101987602	-	IWGSC2	DArTSNP
7944	1011702	G/A	A	1A	579561857	+	IWGSC2	DArTSNP
8146	10993005	G/A	A	1A	8635059	+	IWGSC2	DArTSNP
8263	1099870	G/A	A	1A	554190058	+	IWGSC2	DArTSNP
8286	1120034	G/A	A	1A	258837991	+	IWGSC2	DArTSNP
8381	1004030	G/A	A	1A	535751125	-	IWGSC2	DArTSNP
8589	2277497	G/A	A	1A	500043610	+	IWGSC2	DArTSNP
8600	991850	G/A	A	1A	42750994	+	IWGSC2	DArTSNP
8736	1030075	G/A	A	1A	578952072	-	IWGSC2	DArTSNP
8745	1082710	G/A	A	1A	29893859	+	IWGSC2	DArTSNP
8905	979259	G/A	A	1A	522302328	-	IWGSC2	DArTSNP
8907	1215529	G/A	A	1A	179455693	+	IWGSC2	DArTSNP
8950	3953998	G/A	A	1A	392314410	-	IWGSC2	DArTSNP
9092	1024648	G/A	A	1A	43418516	+	IWGSC2	DArTSNP
9231	1218722	G/A	A	1A	54768385	+	IWGSC2	DArTSNP
9297	1159673	G/A	A	1A	17361854	+	IWGSC2	DArTSNP
9358	1695042	G/A	A	1A	538349819	-	IWGSC2	DArTSNP

9432	2282159	G/A	A	1A	50015244	-	IWGSC2	DArTSNP
9446	1097536	G/A	A	1A	20323253	-	IWGSC2	DArTSNP
9678	1089641	G/A	A	1A	480063293	+	IWGSC2	DArTSNP
9680	1351058	G/A	A	1A	0	-	IWGSC2	DArTSNP
9814	1082152	G/A	A	1A	19114712	-	IWGSC2	DArTSNP
10079	2289282	G/A	A	1A	367715619	+	IWGSC2	DArTSNP
10168	1217318	G/A	A	1A	509681391	-	IWGSC2	DArTSNP
10350	1138661	G/A	A	1A	544804330	-	IWGSC2	DArTSNP
10466	38671658	G/A	A	1A	66975493	+	IWGSC2	DArTSNP
10606	1129025	G/A	A	1A	342652689	-	IWGSC2	DArTSNP
10670	1028725	G/A	A	1A	533237156	-	IWGSC2	DArTSNP
10733	1090380	G/A	A	1A	526086267	+	IWGSC2	DArTSNP
11240	1090990	G/A	A	1A	501567652	-	IWGSC2	DArTSNP
11408	999238	G/A	A	1A	507979108	-	IWGSC2	DArTSNP
11771	4260772	G/A	A	1A	544912101	+	IWGSC2	DArTSNP
11950	1059739	G/A	A	1A	55976346	-	IWGSC2	DArTSNP
12022	980023	G/A	A	1A	56966413	-	IWGSC2	DArTSNP
12359	1108901	G/A	A	1A	11583170	-	IWGSC2	DArTSNP
12428	1129006	G/A	A	1A	590913653	+	IWGSC2	DArTSNP
12711	1094943	G/A	A	1A	559956401	+	IWGSC2	DArTSNP
13021	2261995	G/A	A	1A	47826221	-	IWGSC2	DArTSNP
13461	1284549	G/A	A	1A	412082205	+	IWGSC2	DArTSNP
13672	1166905	G/A	A	1A	484270788	-	IWGSC2	DArTSNP
13900	3940559	G/A	A	1A	531863633	-	IWGSC2	DArTSNP
13965	3937866	G/A	A	1A	65509226	+	IWGSC2	DArTSNP
14264	5569907	G/A	A	1A	367685717	+	IWGSC2	DArTSNP
14508	1126925	G/A	A	1A	41907428	-	IWGSC2	DArTSNP
15075	3570055	G/A	A	1A	470495097	+	IWGSC2	DArTSNP
15401	5348584	G/A	A	1A	53238754	+	IWGSC2	DArTSNP
15535	4733781	G/A	A	1A	123339235	+	IWGSC2	DArTSNP
15590	1089977	G/A	A	1A	17212001	-	IWGSC2	DArTSNP
15601	1245046	G/A	A	1A	13939989	-	IWGSC2	DArTSNP
15665	3020545	G/A	A	1A	44365625	-	IWGSC2	DArTSNP
15780	1127622	G/A	A	1A	221318127	+	IWGSC2	DArTSNP
16065	1123593	G/A	A	1A	346715488	-	IWGSC2	DArTSNP
16447	984465	G/A	A	1A	448902098	-	IWGSC2	DArTSNP
16468	2304134	G/A	A	1A	534461387	-	IWGSC2	DArTSNP
16569	5368847	G/A	A	1A	16042820	+	IWGSC2	DArTSNP
17041	1243497	G/A	A	1A	594705252	-	IWGSC2	DArTSNP
17240	1064767	G/A	A	1A	582075267	+	IWGSC2	DArTSNP
17326	2255954	G/A	A	1A	21828199	+	IWGSC2	DArTSNP
17922	1201384	G/A	A	1A	389448659	+	IWGSC2	DArTSNP
17932	1097167	G/A	A	1A	571192708	-	IWGSC2	DArTSNP
18244	2255603	G/A	A	1A	425870359	-	IWGSC2	DArTSNP
18355	1043336	G/A	A	1A	1235959	+	IWGSC2	DArTSNP
18596	2303040	G/A	A	1A	73038824	+	IWGSC2	DArTSNP
18740	24505028	G/A	A	1A	521417724	-	IWGSC2	DArTSNP
18741	39632434	G/A	A	1A	521374413	-	IWGSC2	DArTSNP
18848	1E+08	G/A	A	1A	328603162	-	IWGSC2	DArTSNP
19105	1667138	G/A	A	1A	97307999	+	IWGSC2	DArTSNP

19138	2275330	G/A	A	1A	63342417	+	IWGSC2	DArTSNP
19207	1087379	G/A	A	1A	375961178	+	IWGSC2	DArTSNP
19226	1049250	G/A	A	1A	508507445	+	IWGSC2	DArTSNP
19257	5341737	G/A	A	1A	581250874	+	IWGSC2	DArTSNP
19357	993464	G/A	A	1A	356143738	+	IWGSC2	DArTSNP
19365	1246898	G/A	A	1A	565471936	+	IWGSC2	DArTSNP
19503	1094290	G/A	A	1A	149181699	+	IWGSC2	DArTSNP
19575	1E+08	G/A	A	1A	32910034	+	IWGSC2	DArTSNP
19753	1091533	G/A	A	1A	208288200	+	IWGSC2	DArTSNP
19997	1107683	G/A	A	1A	469902071	+	IWGSC2	DArTSNP
20571	5577242	G/A	A	1A	39103321	+	IWGSC2	DArTSNP
20579	2282236	G/A	A	1A	581554314	-	IWGSC2	DArTSNP
20707	1109747	G/A	A	1A	64705602	-	IWGSC2	DArTSNP
20870	2281423	G/A	A	1A	26306325	-	IWGSC2	DArTSNP
21275	1307211	G/A	A	1A	277569002	+	IWGSC2	DArTSNP
21293	1243691	G/A	A	1A	56966678	+	IWGSC2	DArTSNP
21482	1E+08	G/A	A	1A	16055506	-	IWGSC2	DArTSNP
22233	3023381	G/A	A	1A	501295808	-	IWGSC2	DArTSNP
22254	4408183	G/A	A	1A	41769635	-	IWGSC2	DArTSNP
22921	3064373	G/A	A	1A	5548650	+	IWGSC2	DArTSNP
23026	2294598	G/A	A	1A	543746511	-	IWGSC2	DArTSNP
23414	1228243	G/A	A	1A	63591116	-	IWGSC2	DArTSNP
23579	1092284	G/A	A	1A	534055249	-	IWGSC2	DArTSNP
23785	1038571	G/A	A	1A	0	-	IWGSC2	DArTSNP
24048	1E+08	G/A	A	1A	54359140	-	IWGSC2	DArTSNP
24108	3942183	G/A	A	1A	17404571	+	IWGSC2	DArTSNP
24137	978429	G/A	A	1A	427114392	+	IWGSC2	DArTSNP
24269	1187451	G/A	A	1A	497996114	+	IWGSC2	DArTSNP
24279	7336092	G/A	A	1A	11341749	+	IWGSC2	DArTSNP
24453	1011310	G/A	A	1A	594066670	-	IWGSC2	DArTSNP
24801	4911085	G/A	A	1A	578068905	+	IWGSC2	DArTSNP
24813	1107489	G/A	A	1A	587795947	-	IWGSC2	DArTSNP
25488	1111973	G/A	A	1A	575983529	-	IWGSC2	DArTSNP
25686	1239767	G/A	A	1A	565531057	+	IWGSC2	DArTSNP
25687	1239767	G/A	A	1A	565531059	+	IWGSC2	DArTSNP
25747	1276808	G/A	A	1A	483676041	+	IWGSC2	DArTSNP
25776	7918926	G/A	A	1A	485511735	-	IWGSC2	DArTSNP
25784	1008166	G/A	A	1A	407512833	+	IWGSC2	DArTSNP
25785	1008166	G/A	A	1A	407512877	+	IWGSC2	DArTSNP
25821	3956968	G/A	A	1A	44416485	+	IWGSC2	DArTSNP
25829	1104672	G/A	A	1A	192031913	+	IWGSC2	DArTSNP
26102	2322723	G/A	A	1A	590694991	+	IWGSC2	DArTSNP
26241	9723908	G/A	A	1A	53309096	-	IWGSC2	DArTSNP
26635	1E+08	G/A	A	1A	543739012	+	IWGSC2	DArTSNP
26938	1198074	G/A	A	1A	592946965	-	IWGSC2	DArTSNP
27025	1209801	G/A	A	1A	92446686	+	IWGSC2	DArTSNP
27057	1211261	G/A	A	1A	514668640	-	IWGSC2	DArTSNP
27066	23884247	G/A	A	1A	597313325	+	IWGSC2	DArTSNP
27135	1038264	G/A	A	1A	545815039	-	IWGSC2	DArTSNP
27191	1286528	G/A	A	1A	589168298	-	IWGSC2	DArTSNP

Tabela S1.6. Markery SNP isotnie ($p<0.001$) zasocjowane (FarmCPU) z badanymi cechami plonotwoczymi i jakościowymi

SNP_Nr	Chromosome	Position CS 2.1	P.value	maf	nobs	effect	Cecha
375	1A	518418963	5.65187E-06	0.194117647	170	-1.25557	Mean_A2
898	1B	506828567	3.23508E-07	0.144117647	170	-1.39001	Mean_A2
1684	2A	8299277	4.18422E-05	0.476470588	170	-0.72853	Mean_A2
4811	3B	24071831	0.000404998	0.264705882	170	-0.61131	Mean_A2
6368	4A	655324479	3.13592E-10	0.264705882	170	-2.0686	Mean_A2
6925	4B	641805214	5.08847E-09	0.376470588	170	1.13335	Mean_A2
7404	5A	473258150	1.33296E-06	0.341176471	170	-0.8375	Mean_A2
8108	5B	421200748	3.5858E-10	0.329411765	170	1.1798	Mean_A2
8367	5B	574152649	6.86918E-08	0.397058824	170	-1.00535	Mean_A2
8269	5B	531915779	0.000586652	0.317647059	170	-0.67443	Mean_A2
8386	5B	584282294	0.000762067	0.408823529	170	0.72571	Mean_A2
8748	5D	348996825	0.000181576	0.188235294	170	0.996	Mean_A2
10853	7A	17857128	1.93341E-05	0.382352941	170	-0.80474	Mean_A2
12882	7D	519381909	9.27846E-10	0.338235294	170	1.34512	Mean_A2
12757	7D	65665757	4.52966E-06	0.191176471	170	-1.3904	Mean_A2
12680	7D	16377374	0.000517796	0.247058824	170	-1.10344	Mean_A2
12610	7D	5174601	0.000583973	0.135294118	170	1.13095	Mean_A2
12828	7D	192021471	0.000763774	0.141176471	170	-1.18244	Mean_A2
14583	Un2	1636	7.25542E-06	0.108823529	170	-1.8535	Mean_A2
16746	Un2	3860	0.000574456	0.435294118	170	0.65807	Mean_A2
17266	Un2	4399	0.000778418	0.214705882	170	0.77594	Mean_A2
1561	1D	446245591	0.000515285	0.097058824	170	0.40327	STD_A2
1684	2A	8299277	0.000334553	0.476470588	170	-1.42181	STD_A2
2703	2B	66327248	0.00039595	0.294117647	170	0.25404	STD_A2
2577	2B	21706687	0.000787068	0.335294118	170	-0.74385	STD_A2
3567	2D	392509	0.000824859	0.314705882	170	-4.11099	STD_A2
6368	4A	655324479	0.000869868	0.264705882	170	-2.03467	STD_A2
7404	5A	473258150	0.000679579	0.341176471	170	-1.17454	STD_A2
8319	5B	541839052	0.000703497	0.238235294	170	-0.29036	STD_A2
9133	6A	18633992	0.000393737	0.15	170	0.39472	STD_A2
9696	6B	29594346	3.74205E-05	0.144117647	170	0.48912	STD_A2
9672	6B	24296831	0.000891594	0.202941176	170	-0.39171	STD_A2
11478	7A	643794039	0.000517572	0.329411765	170	-0.23891	STD_A2
12035	7B	286808036	0.000719665	0.073529412	170	3.01878	STD_A2
12882	7D	519381909	0.000186091	0.338235294	170	1.32069	STD_A2
12757	7D	65665757	0.000325608	0.191176471	170	-2.08386	STD_A2
12880	7D	519100791	0.000770706	0.352941176	170	1.19568	STD_A2
12847	7D	372469830	0.000771101	0.144117647	170	1.56599	STD_A2
12881	7D	519220612	0.000846444	0.355882353	170	1.19208	STD_A2
13376	Un2	255	0.000208181	0.147058824	170	-0.50074	STD_A2
16707	Un2	3820	0.000209818	0.420588235	170	-0.46894	STD_A2
17524	Un2	4688	0.000582537	0.147058824	170	0.36319	STD_A2
13622	Un2	544	0.000611153	0.258823529	170	0.38253	STD_A2
16198	Un2	3293	0.000712466	0.397058824	170	0.22522	STD_A2
14129	Un2	1137	0.000835717	0.3	170	-0.27034	STD_A2
351	1A	510068399	7.58245E-06	0.313043478	115	3.05643	KBP_A2
350	1A	510068396	9.78924E-05	0.330434783	115	-2.60756	KBP_A2
353	1A	511337488	0.000200291	0.47826087	115	-2.62719	KBP_A2
1649	1D	498411490	0.000251602	0.12173913	115	-3.34548	KBP_A2
4811	3B	24071831	0.000470501	0.230434783	115	-2.56177	KBP_A2
6908	4B	618506374	0.000568793	0.430434783	115	-2.2438	KBP_A2

6906	4B	618437388	0.000619985	0.434782609	115	-2.17027	KBP_A2
7090	4D	485793283	0.000164663	0.313043478	115	-4.47404	KBP_A2
7095	4D	486286955	0.0005323	0.465217391	115	-2.38154	KBP_A2
7092	4D	485873210	0.000694692	0.295652174	115	-3.99271	KBP_A2
7654	5A	587054822	0.000378631	0.256521739	115	2.61126	KBP_A2
7740	5A	668091984	0.000636889	0.439130435	115	-2.32966	KBP_A2
7347	5A	445442364	0.000687782	0.32173913	115	-2.30992	KBP_A2
7435	5A	480567285	0.000955383	0.434782609	115	-2.00031	KBP_A2
12966	7D	605387134	0.00025657	0.191304348	115	3.01176	KBP_A2
12975	7D	608492250	0.000362144	0.169565217	115	-2.82848	KBP_A2
13678	Un2	611	0.00055331	0.286956522	115	-3.81698	KBP_A2
234	1A	345078440	0.000233929	0.182352941	170	-3.00751	KOH_A2
1236	1B	682423985	0.000790289	0.229411765	170	-2.67474	KOH_A2
1237	1B	682423988	0.000944204	0.223529412	170	-2.69827	KOH_A2
1684	2A	8299277	0.000308504	0.476470588	170	-2.78587	KOH_A2
4174	3A	12542514	0.000421115	0.158823529	170	3.6285	KOH_A2
4447	3A	597344510	0.000436241	0.2	170	-2.75413	KOH_A2
5731	3D	7789684	0.000144018	0.432352941	170	2.69593	KOH_A2
6070	3D	606953398	0.000589725	0.173529412	170	4.87648	KOH_A2
9919	6B	155405487	0.000582836	0.194117647	170	-2.74596	KOH_A2
10677	6D	483753108	0.00079247	0.073529412	170	-6.05756	KOH_A2
12166	7B	636006610	0.000300975	0.120588235	170	-3.73417	KOH_A2
12150	7B	619969469	0.000626397	0.170588235	170	-2.793	KOH_A2
15931	Un2	3017	0.000394085	0.217647059	170	-2.69204	KOH_A2
17497	Un2	4657	0.000752927	0.135294118	170	-4.57681	KOH_A2
898	1B	506828567	0.00053403	0.144117647	170	-3.71496	KRZ_A2
4969	3B	125722078	0.000889723	0.158823529	170	3.58494	KRZ_A2
16026	Un2	3117	0.000295925	0.364705882	170	2.65699	KRZ_A2
307	1A	485886649	0.00038365	0.367647059	170	2.59528	MOB_A2
1710	2A	13868030	0.000799206	0.191176471	170	-2.76079	MOB_A2
2625	2B	30008047	0.000635292	0.397058824	170	-2.29733	MOB_A2
2489	2B	5424879	0.000731096	0.364705882	170	2.45046	MOB_A2
3804	2D	81089710	0.000186074	0.411764706	170	2.63646	MOB_A2
3650	2D	14905082	0.000591847	0.5	170	-2.3394	MOB_A2
3608	2D	11306315	0.00061727	0.344117647	170	-2.53989	MOB_A2
3598	2D	10334188	0.000635142	0.338235294	170	-2.36075	MOB_A2
3655	2D	15154383	0.000832339	0.447058824	170	-2.25588	MOB_A2
3606	2D	11283040	0.000874479	0.276470588	170	-2.79231	MOB_A2
3623	2D	13579074	0.000999426	0.279411765	170	-2.61805	MOB_A2
4584	3A	705367362	7.78E-05	0.067647059	170	-7.19606	MOB_A2
7040	4D	344443075	0.000637322	0.185294118	170	-4.52748	MOB_A2
9349	6A	423990056	0.000969703	0.097058824	170	3.99149	MOB_A2
9856	6B	103102726	0.000631551	0.191176471	170	-3.57775	MOB_A2
10466	6D	23997843	0.000270923	0.158823529	170	-3.25518	MOB_A2
11088	7A	98133246	0.000363185	0.079411765	170	4.84172	MOB_A2
12757	7D	65665757	0.000881616	0.191176471	170	-3.96308	MOB_A2
17642	Un1	23369594	0.000324803	0.258823529	170	-2.77555	MOB_A2
14069	Un2	1069	0.000147667	0.323529412	170	4.39303	MOB_A2
16214	Un2	3309	0.000344315	0.423529412	170	-2.3952	MOB_A2
16222	Un2	3317	0.000380896	0.432352941	170	-2.37656	MOB_A2
16217	Un2	3312	0.000555287	0.426470588	170	-2.33449	MOB_A2
15731	Un2	2810	0.000673738	0.276470588	170	2.58172	MOB_A2
15661	Un2	2737	0.00067828	0.258823529	170	-2.72262	MOB_A2
16205	Un2	3300	0.00073448	0.426470588	170	-2.2106	MOB_A2
16839	Un2	3954	0.000736307	0.402941176	170	-4.63925	MOB_A2

319	1A	495464475	0.000834508	0.420588235	170	1.55226	RAH_A2
307	1A	485886649	0.000837628	0.367647059	170	1.58273	RAH_A2
4095	2D	651077880	0.000207046	0.220588235	170	-2.82965	RAH_A2
6483	4A	722833544	0.000237997	0.326470588	170	-2.67126	RAH_A2
6368	4A	655324479	0.000946511	0.264705882	170	-2.66042	RAH_A2
6890	4B	608373082	0.000545657	0.061764706	170	-3.53116	RAH_A2
7404	5A	473258150	0.000534748	0.341176471	170	-1.57371	RAH_A2
8855	5D	442081935	0.00017852	0.264705882	170	2.95083	RAH_A2
11565	7A	679790859	0.000311381	0.461764706	170	-1.58553	RAH_A2
11498	7A	655829103	0.000516821	0.376470588	170	-1.62378	RAH_A2
15799	Un2	2880	0.000492391	0.267647059	170	-3.25834	RAH_A2
14026	Un2	1023	0.000657788	0.379411765	170	-2.40089	RAH_A2
15731	Un2	2810	0.000697691	0.276470588	170	1.66172	RAH_A2
15812	Un2	2893	0.000863718	0.258823529	170	-3.13607	RAH_A2
344	1A	508175818	0.000343455	0.168639053	169	0.28481	Skrobia
342	1A	507766319	0.000497813	0.218934911	169	0.24974	Skrobia
2137	2A	697697076	0.000348763	0.349112426	169	0.25156	Skrobia
1894	2A	74914866	0.000590688	0.396449704	169	-0.20028	Skrobia
4122	3A	195665	1.59E-05	0.378698225	169	-0.25057	Skrobia
4590	3A	707968534	0.000273363	0.399408284	169	0.21686	Skrobia
4168	3A	10504144	0.000291368	0.088757396	169	0.48923	Skrobia
4123	3A	403054	0.000384869	0.349112426	169	-0.21406	Skrobia
4589	3A	707968533	0.000506372	0.414201183	169	0.20688	Skrobia
4126	3A	1101437	0.000538862	0.387573964	169	-0.19914	Skrobia
4562	3A	695233715	0.000851678	0.156804734	169	-0.29123	Skrobia
4207	3A	17975746	0.000959053	0.431952663	169	-0.19796	Skrobia
6406	4A	691923499	0.000436543	0.139053254	169	0.40205	Skrobia
7064	4D	452115882	0.000307996	0.25443787	169	0.24749	Skrobia
6979	4D	3409054	0.000773527	0.094674556	169	-0.35444	Skrobia
7512	5A	530376015	0.000612888	0.360946746	169	-0.28356	Skrobia
12526	7B	752525602	0.000945318	0.452662722	169	-0.21166	Skrobia
16055	Un2	3146	0.00033604	0.360946746	169	0.20669	Skrobia
150	1A	39783995	6.785E-04	0.337278107	169	1.96425	Twardość
134	1A	29468863	9.634E-04	0.298816568	169	2.24512	Twardość
3907	2D	505056768	9.802E-04	0.25443787	169	3.58348	Twardość
4309	3A	64879979	5.986E-05	0.381656805	169	3.72119	Twardość
4307	3A	61671004	2.114E-04	0.375739645	169	-2.11595	Twardość
4308	3A	61671007	3.701E-04	0.381656805	169	-2.05498	Twardość
4303	3A	59815608	7.236E-04	0.097633136	169	3.21635	Twardość
7069	4D	456459853	2.678E-04	0.286982249	169	-2.56353	Twardość
7760	5A	678684529	3.593E-04	0.26035503	169	-2.2988	Twardość
10912	7A	27249495	5.323E-04	0.387573964	169	1.93677	Twardość
11526	7A	669419209	6.462E-04	0.328402367	169	1.93592	Twardość
12934	7D	577646296	3.043E-04	0.402366864	169	-2.03246	Twardość
12664	7D	14158912	5.604E-04	0.198224852	169	2.4084	Twardość
12933	7D	577338155	9.849E-04	0.402366864	169	-1.89727	Twardość
16838	Un2	3953	3.566E-04	0.431952663	169	2.59814	Twardość
15247	Un2	2310	4.351E-04	0.180473373	169	2.51048	Twardość
17386	Un2	4531	4.907E-04	0.174556213	169	2.52905	Twardość
16978	Un2	4100	5.175E-04	0.375739645	169	-1.94308	Twardość
926	1B	535000910	2.920E-04	0.088757396	169	-1.12568	Wodochłonność
928	1B	535921570	3.332E-04	0.103550296	169	-1.13536	Wodochłonność
1436	1D	237620657	9.232E-04	0.177514793	169	0.83626	Wodochłonność
4766	3B	15362245	6.213E-04	0.204142012	169	-1.14124	Wodochłonność
4764	3B	15047302	9.561E-04	0.284023669	169	0.70739	Wodochłonność

5967	3D	569310538	4.113E-04	0.215976331	169	1.11648	Wodochłonność
7302	5A	383659449	1.850E-04	0.059171598	169	1.95832	Wodochłonność
8053	5B	334784330	8.060E-05	0.130177515	169	1.01341	Wodochłonność
8054	5B	335490084	1.476E-04	0.142011834	169	1.00044	Wodochłonność
8115	5B	426213075	2.200E-04	0.150887574	169	1.01317	Wodochłonność
8060	5B	359794278	2.679E-04	0.109467456	169	1.03205	Wodochłonność
8381	5B	580383571	7.793E-04	0.470414201	169	0.7365	Wodochłonność
13390	Un2	269	7.279E-04	0.112426036	169	1.29937	Wodochłonność
13421	Un2	303	7.916E-04	0.156804734	169	1.48592	Wodochłonność
488	1A	582561156	0.000830059	0.289940828	169	0.2971	Białko
645	1B	25242425	0.000120102	0.210059172	169	0.25834	Białko
663	1B	33634008	0.000471142	0.221893491	169	0.20025	Białko
576	1B	11079353	0.000725366	0.189349112	169	-0.27878	Białko
647	1B	25754513	0.000773913	0.390532544	169	0.16795	Białko
3236	2B	735674960	0.000914766	0.372781065	169	0.25832	Białko
3907	2D	505056768	0.000404182	0.25443787	169	0.34862	Białko
3707	2D	30529730	0.000834632	0.227810651	169	-0.21393	Białko
4168	3A	10504144	2.41E-05	0.088757396	169	-0.48276	Białko
4195	3A	15770410	0.000279148	0.396449704	169	0.1833	Białko
4123	3A	403054	0.000741789	0.349112426	169	0.17377	Białko
4151	3A	8320326	0.000809985	0.183431953	169	-0.23794	Białko
6936	4B	652993345	0.000297351	0.121301775	169	-0.28275	Białko
6941	4B	657401585	0.000389501	0.171597633	169	-0.24731	Białko
6940	4B	657086512	0.000393664	0.103550296	169	-0.29837	Białko
8381	5B	580383571	8.27E-05	0.470414201	169	0.22603	Białko
8053	5B	334784330	0.000301316	0.130177515	169	0.24699	Białko
8054	5B	335490084	0.00034536	0.142011834	169	0.25022	Białko
8060	5B	359794278	0.000664087	0.109467456	169	0.25545	Białko
9662	6B	21028081	7.09E-05	0.133136095	169	0.39167	Białko
10524	6D	118684843	0.00061654	0.136094675	169	0.27238	Białko
12934	7D	577646296	9.52E-05	0.402366864	169	-0.19933	Białko
15662	Un2	2738	6.10E-05	0.233727811	169	-0.22008	Białko
14308	Un2	1336	0.000127773	0.195266272	169	0.351	Białko
17155	Un2	4283	0.000227331	0.289940828	169	0.20566	Białko
17548	Un2	4717	0.00043173	0.133136095	169	-0.28651	Białko
16978	Un2	4100	0.000657828	0.375739645	169	-0.17364	Białko
407	1A	537993055	0.000497391	0.393491124	169	-0.46764	Gluten
406	1A	537560105	0.000847826	0.328402367	169	-0.48194	Gluten
576	1B	11079353	0.000855202	0.189349112	169	-0.74684	Gluten
663	1B	33634008	0.000973719	0.221893491	169	0.51375	Gluten
3236	2B	735674960	0.000183267	0.372781065	169	0.78717	Gluten
3555	2B	810116249	0.000503145	0.340236686	169	-0.50008	Gluten
4168	3A	10504144	1.72E-05	0.088757396	169	-1.33164	Gluten
4151	3A	8320326	0.000292871	0.183431953	169	-0.69608	Gluten
6177	4A	80606865	0.000483712	0.470414201	169	0.50774	Gluten
6158	4A	11922975	0.000879465	0.136094675	169	-0.62522	Gluten
7302	5A	383659449	0.000510468	0.059171598	169	1.31052	Gluten
8054	5B	335490084	3.03E-05	0.142011834	169	0.7856	Gluten
8053	5B	334784330	0.000126448	0.130177515	169	0.70902	Gluten
8060	5B	359794278	0.000201149	0.109467456	169	0.75438	Gluten
8052	5B	333256433	0.000636752	0.115384615	169	0.68468	Gluten
9662	6B	21028081	0.000212989	0.133136095	169	0.99395	Gluten
17860	Un1	228749243	0.000921388	0.275147929	169	0.78469	Gluten
13770	Un2	719	0.000634682	0.301775148	169	0.53263	Gluten

Tabela S2. Wybrane cechy plonowania badanych odmian pszenicy uzyskane w ramach projektu w 2023 roku. Wartości KOH, KRZ, MOB, RAH, KBP uzyskano z doświadczeń prowadzonych odpowiednio w miejscowościach Kończewice, Krzemlin, Modzurów, Radzików i Kobierzyce.

Num	Variety	Seria	Stability_A2	KBPS1_A2	KOHS1_A2	KRZS1_A2	MOBS1_A2	RAHS1_A2	Mean_A2	%standard_A2
1	AND 19057	S1	1.59	138.75	139.58	105.07	156.45	138.97	135.76	102.83
2	AND 19068	S1	2.09	126.85	140.72	103.51	162.12	140.06	134.65	101.99
3	AND 19249	S1	0.37	128.86	136.17	104.89	150.66	128.13	129.74	98.27
4	AND 19569	S1	1.51	139.76	140.64	101.34	158.08	132.52	134.47	101.85
5	AND 19791	S1	0.71	140.21	140.12	108.93	158.36	134.34	136.39	103.31
6	AND 19797	S1	1.46	124.58	137.47	101.51	152.79	128.96	129.06	97.75
7	ARTIST w1	S1	1.42	130.23	138.23	106.71	153.85	128.33	131.47	99.58
8	C 19 104	S1	5.00	131.42	126.09	79.78	146.50	133.91	123.54	93.57
9	C 19 573	S1	2.07	133.50	138.88	105.02	153.57	128.65	131.92	99.92
10	C2738/14-14	S1	0.71	140.02	141.97	110.53	161.34	142.85	139.34	105.54
11	DD 197/19	S1	0.85	144.33	142.14	105.13	162.45	134.54	137.72	104.31
12	DD 531/19	S1	1.27	133.53	139.65	107.15	156.87	135.44	134.53	101.90
13	DD 559/19	S1	1.27	136.55	138.86	101.90	152.98	132.46	132.55	100.40
14	DD 868/19	S1	2.58	136.22	139.78	100.34	157.74	136.80	134.18	101.63
15	DI 2/38	S1	1.55	125.04	136.99	100.70	153.71	130.91	129.47	98.06
16	DL 1027/19	S1	1.61	139.13	139.32	102.34	154.94	134.82	134.11	101.58
17	DL 1028/19	S1	0.54	128.65	137.13	97.61	155.63	130.26	129.86	98.36
18	DL 1091/19	S1	0.55	143.78	141.43	111.94	160.80	137.37	139.06	105.33
19	DL 1095/19	S1	1.36	127.55	136.52	104.40	153.69	122.94	129.02	97.72
20	KBP 21.16	S1	1.46	135.68	142.45	110.29	162.91	137.83	137.83	104.40
21	KBP 21.25	S1	2.16	132.65	138.53	105.85	154.78	135.36	133.43	101.07
22	KBP 21.28	S1	1.25	129.22	139.61	98.81	157.49	134.88	132.00	99.98
23	KBP 21.41	S1	0.88	133.47	138.85	102.56	156.15	135.94	133.39	101.04
24	KBP 21.47	S1	1.60	135.16	137.89	105.26	155.97	130.27	132.91	100.67
25	KILIMANJARO w2	S1	0.35	132.48	138.46	99.85	155.23	129.45	131.09	99.29
26	MIB 0245	S1	2.29	141.32	138.56	105.46	153.66	125.80	132.96	100.71
27	MIB 0534	S1	2.20	138.09	140.13	109.47	158.12	134.15	135.99	103.00
28	NAD_Z190674	S1	1.44	141.26	139.71	105.83	158.49	134.28	135.91	102.94
29	NAD_Z190702	S1	4.83	124.91	140.19	94.70	162.50	141.40	132.74	100.54
30	NAD_Z_19008	S1	0.56	131.43	137.57	99.58	154.42	128.18	130.23	98.64
31	NAD_Z_19040	S1	1.20	134.71	138.88	102.69	155.01	135.15	133.29	100.96
32	NAD_Z_19581	S1	2.16	139.20	140.37	103.08	156.99	139.62	135.85	102.90
33	NAD_Z_19647	S1	1.01	131.18	138.86	105.00	156.12	134.25	133.08	100.80
34	POB 0122	S1	1.03	132.02	136.13	99.00	154.16	132.16	130.69	98.99
35	POB 0222	S1	4.85	123.04	126.47	84.97	151.27	131.81	123.51	93.55
36	POB 0322	S1	0.92	136.10	140.82	101.49	158.55	133.66	134.12	101.59
37	SMH 497	S1	2.69	128.28	136.31	103.56	149.49	124.30	128.39	97.24
38	SMH 524	S1	2.99	129.45	139.61	109.75	160.42	127.12	133.27	100.94
39	SMH 553	S1	1.11	135.03	139.78	102.00	157.42	128.60	132.57	100.41
40	SMH 576	S1	0.91	133.33	136.91	104.93	154.59	129.21	131.80	99.83
41	SMH 578	S1	0.36	139.67	140.55	106.04	156.59	135.16	135.60	102.71
42	SMH 643	S1	0.86	138.70	139.89	104.75	156.05	135.25	134.93	102.20
43	SMH 710	S1	0.43	128.99	138.08	100.51	153.82	128.81	130.04	98.50
44	SMH 761	S1	1.56	138.92	139.81	106.53	156.89	129.44	134.32	101.74
45	SMH 796	S1	1.95	137.24	138.67	99.83	155.43	131.72	132.58	100.42
46	SMH 804	S1	0.25	132.36	138.71	102.43	156.41	135.09	133.00	100.74
47	SMH 825	S1	1.44	137.41	137.81	101.35	152.48	128.20	131.45	99.56
48	STH 0244L1	S1	1.15	142.47	140.05	107.61	161.39	133.34	136.97	103.75
49	STH 0244L2	S1	0.74	138.43	139.28	102.83	157.69	130.72	133.79	101.34
50	STH 0307	S1	1.18	135.54	137.22	104.17	153.57	127.63	131.63	99.70
51	STHD 0411	S1	3.15	119.96	142.01	112.03	162.60	139.04	135.13	102.35
52	STHD 0424	S1	2.36	134.74	139.12	106.44	155.20	127.77	132.65	100.48
53	STHD 0430	S1	0.52	128.74	137.04	102.77	153.86	126.09	129.70	98.24
54	STHD 0441	S1	0.93	128.81	139.89	107.02	159.06	129.08	132.77	100.56
55	STHD 0549	S1	1.35	141.20	139.79	107.49	153.68	134.52	135.34	102.51
56	STHD 1121	S1	1.69	133.99	138.40	106.76	154.92	133.71	133.56	101.16
57	STHD 1126	S1	1.53	125.46	138.37	103.11	155.10	137.06	131.82	99.84
58	STHD 1438	S1	1.63	141.70	140.29	110.74	156.83	136.99	137.31	104.00
59	STHD 1447	S1	3.68	127.24	136.65	95.55	157.04	138.05	130.91	99.15
60	SYMETRIA w3	S1	2.27	128.12	139.92	104.93	159.45	135.14	133.51	101.13
61	AND 19073	S2	1.43	127.92	138.51	117.90	159.43	130.21	134.79	101.91
62	AND 191003	S2	1.96	132.50	136.42	119.57	148.09	126.77	132.67	100.30
63	AND 191004	S2	3.25	138.44	139.71	114.84	164.39	133.40	138.16	104.45
64	AND 191009	S2	0.68	133.61	138.46	119.92	157.03	128.06	135.42	102.38
65	AND 19799	S2	1.94	129.81	136.75	110.90	149.69	126.96	130.82	98.91
66	AND 19829	S2	1.32	127.39	137.33	117.33	154.47	126.79	132.66	100.30
67	AND 19862	S2	3.04	129.15	137.26	126.77	157.78	128.55	135.90	102.75
68	ARTIST w1	S2	2.14	134.55	137.58	111.34	150.39	125.39	131.85	99.69
69	C 16 397	S2	3.27	133.64	140.19	135.21	151.47	131.46	138.39	104.63
70	C 17 263	S2	2.92	135.35	137.76	132.72	155.90	119.20	136.19	102.96
71	C 19 186	S2	2.43	136.73	137.39	113.10	154.69	127.76	133.93	101.26
72	C 3279/16os	S2	0.62	128.45	134.67	113.41	151.03	122.89	130.09	98.35
73	DD 198/19	S2	2.59	138.96	141.42	117.11	162.00	134.39	138.77	104.92

74	DD 530/19	S2	2.14	127.18	136.38	124.84	147.88	126.84	132.63	100.27
75	DD 561/19	S2	2.06	138.28	137.36	119.56	154.40	124.66	134.85	101.95
76	DD 909/19	S2	1.24	131.74	137.29	120.58	152.86	128.09	134.11	101.40
77	DL 1102/19	S2	1.20	133.14	138.21	112.81	153.11	132.46	133.94	101.27
78	DL 1121/19	S2	0.61	131.72	137.07	115.15	149.65	125.18	131.75	99.61
79	DL 1156/19	S2	2.80	124.57	136.27	120.68	148.27	125.23	131.00	99.05
80	DL 1175/19	S2	1.77	127.45	136.60	108.47	146.68	126.79	129.20	97.68
81	DL 1220/19	S2	2.56	130.01	139.29	131.18	156.75	129.29	137.30	103.81
82	KBP 21.17	S2	1.21	135.36	139.06	125.75	153.87	128.75	136.56	103.25
83	KBP 21.32	S2	1.16	128.54	135.54	110.53	157.27	119.19	130.21	98.45
84	KBP 21.42	S2	2.75	130.52	136.97	107.20	149.52	131.42	131.13	99.14
85	KBP 21.43	S2	1.03	127.84	131.53	112.71	143.86	121.56	127.50	96.40
86	KBP 21.50	S2	2.92	131.83	135.48	107.74	150.89	124.44	130.07	98.34
87	KBP 21.9	S2	2.58	135.88	136.95	108.93	152.50	127.59	132.37	100.08
88	KILIMANJARO w2	S2	0.84	126.33	135.75	113.34	150.92	124.26	130.12	98.38
89	MIB 01007	S2	1.38	136.60	139.10	115.51	152.99	131.54	135.15	102.18
90	NAD_Z_191004	S2	2.75	129.99	138.10	130.66	154.59	127.86	136.24	103.00
91	NAD_Z_191036	S2	3.20	139.88	141.54	138.86	158.81	131.51	142.12	107.45
92	NAD_Z_191090	S2	1.66	143.89	142.71	123.05	162.19	135.90	141.55	107.02
93	NAD_Z_19377	S2	1.90	128.40	139.14	125.25	156.56	129.64	135.80	102.67
94	NAD_Z_19796	S2	2.91	127.62	136.78	124.66	151.26	126.90	133.44	100.89
95	POB 0422	S2	2.81	128.03	135.23	102.70	149.94	121.59	127.50	96.39
96	POB 0522	S2	1.29	120.56	131.81	103.81	146.66	117.39	124.05	93.79
97	POB 0622	S2	2.40	130.45	133.29	104.26	150.98	129.95	129.79	98.12
98	SMH 520	S2	2.42	130.03	136.83	126.99	151.22	128.19	134.65	101.80
99	SMH 530	S2	0.44	129.14	136.95	118.67	149.76	128.21	132.55	100.21
100	SMH 574	S2	0.39	132.97	136.65	117.82	153.13	124.49	133.01	100.56
101	SMH 592	S2	2.71	134.40	136.07	125.05	142.20	125.79	132.70	100.33
102	SMH 644	S2	1.21	132.80	137.22	122.68	151.95	125.17	133.96	101.28
103	SMH 733	S2	2.68	131.56	138.44	129.69	153.04	128.56	136.26	103.02
104	SMH 786	S2	1.15	130.27	138.35	114.68	152.15	130.80	133.25	100.74
105	SMH 797	S2	0.83	133.91	137.42	117.93	152.33	128.22	133.96	101.28
106	SMH 816	S2	2.52	137.15	137.55	126.23	151.80	124.11	135.37	102.34
107	SMH 829	S2	2.76	129.63	137.95	111.48	158.25	127.46	132.95	100.52
108	SMH 840	S2	0.77	138.72	138.28	121.42	151.74	129.20	135.87	102.72
109	STHD 1461	S2	3.50	119.32	137.26	125.05	151.93	130.77	132.87	100.45
110	STHD 1464	S2	2.41	125.60	138.42	122.92	155.59	132.91	135.09	102.13
111	STHD 1468	S2	2.09	138.86	140.65	118.91	159.97	132.21	138.12	104.43
112	STHD 1471	S2	0.44	139.73	139.46	121.21	156.46	134.44	138.26	104.53
113	STHD 1472	S2	1.56	138.20	139.14	117.68	153.85	133.23	136.42	103.14
114	STHD 1474	S2	2.50	136.71	140.42	134.22	154.50	132.48	139.67	105.59
115	STHD 1475	S2	1.34	140.89	143.20	131.37	164.88	135.25	143.12	108.20
116	STHD 1476	S2	1.38	127.42	139.21	120.30	158.43	131.47	135.37	102.34
117	STHD 1477	S2	1.93	139.62	139.55	115.05	157.75	130.44	136.48	103.19
118	STHD 1479	S2	2.59	134.67	134.32	108.81	147.39	121.47	129.33	97.78
119	STHD 2001	S2	4.26	125.92	137.96	106.56	163.95	123.88	131.65	99.54
120	SYMETRIA w3	S2	3.82	123.07	136.94	128.04	158.86	127.23	134.83	101.94
121	AND 19019	S3	2.91	146.32	146.64	123.97	164.14	131.21	142.46	106.72
122	AND 19026	S3	1.38	139.66	141.42	122.09	154.52	122.20	135.98	101.87
123	AND 19337	S3	0.95	140.14	145.01	121.71	157.21	124.33	137.68	103.14
124	AND 19803	S3	2.03	136.87	141.61	113.88	156.57	119.95	133.78	100.22
125	AND 267/16	S3	2.47	130.04	139.10	121.15	155.66	122.55	133.70	100.16
126	AND 27/16	S3	2.23	143.43	149.78	121.53	162.60	128.15	141.10	105.70
127	AND 33/16	S3	0.37	142.27	142.13	127.28	157.85	127.21	139.35	104.39
128	ARTIST w1	S3	0.96	134.44	138.92	117.30	152.15	119.17	132.40	99.18
129	C 18 238	S3	2.06	137.84	139.67	124.24	154.13	120.03	135.18	101.27
130	C 1854/17-4	S3	1.10	123.68	135.35	108.51	146.85	113.20	125.52	94.03
131	C 19 318	S3	0.78	139.37	137.76	115.97	153.60	119.57	133.25	99.82
132	C2815/15-21	S3	3.57	126.04	140.72	127.21	146.94	114.83	131.15	98.25
133	DD 470/19	S3	1.23	140.29	142.42	119.15	156.32	121.96	136.03	101.90
134	DD 522/19	S3	1.16	128.59	137.26	121.83	155.21	119.33	132.44	99.22
135	DD 800/19	S3	1.20	142.42	146.07	122.60	160.54	124.95	139.32	104.37
136	DD 910/19	S3	0.94	135.95	143.30	122.17	153.96	121.08	135.29	101.35
137	DL 1278/19	S3	0.94	141.12	140.14	118.35	154.17	121.67	135.09	101.20
138	DL 1348/19	S3	1.34	139.45	142.48	116.51	156.42	122.35	135.44	101.46
139	DL 1359/19	S3	0.64	141.73	143.62	125.12	155.86	121.76	137.62	103.09
140	DL 1410/19	S3	1.15	133.43	139.98	115.23	156.36	118.23	132.65	99.37
141	DL 1552/19	S3	1.85	140.34	142.10	125.69	156.97	122.46	137.51	103.01
142	KBP 21.10	S3	1.32	133.72	125.94	121.25	150.78	117.67	129.87	97.29
143	KBP 21.19	S3	1.40	136.41	139.34	115.98	152.56	120.45	132.95	99.60
144	KBP 21.20	S3	0.79	136.58	138.16	115.66	150.31	115.95	131.33	98.38
145	KBP 21.33	S3	2.18	132.81	139.42	112.93	150.48	117.68	130.67	97.89
146	KBP 21.56	S3	2.08	140.27	146.78	114.46	155.54	124.45	136.30	102.11
147	KILIMANJARO w2	S3	1.40	134.22	141.62	113.14	151.55	118.32	131.77	98.71
148	KOH 03221	S3	0.94	133.05	139.72	115.47	149.98	117.49	131.14	98.24
149	KOH 12020	S3	0.94	137.33	140.31	119.63	151.64	121.50	134.08	100.44
150	KOH 18619	S3	0.57	143.40	145.82	121.65	158.47	122.65	138.40	103.68

151	MIB 01152	S3	0.63	141.69	147.13	119.56	155.75	119.79	136.78	102.47
152	NAD_Z190876	S3	2.53	149.18	152.58	125.64	166.77	131.57	145.15	108.73
153	NAD_Z_19110	S3	1.92	138.45	146.60	130.60	158.27	124.30	139.65	104.61
154	NAD_Z_19565	S3	2.51	140.19	143.56	117.72	154.22	123.63	135.86	101.78
155	NAD_Z_19628	S3	0.64	138.37	143.05	119.72	155.88	119.92	135.39	101.42
156	NAD_Z_19649	S3	0.81	138.95	145.30	123.68	157.52	123.37	137.76	103.20
157	POB 0722	S3	3.34	141.91	138.04	113.02	161.32	123.90	135.64	101.61
158	POB 0822	S3	0.94	127.83	137.32	110.26	150.36	114.15	127.98	95.87
159	POB 0922	S3	1.32	122.12	137.95	112.29	149.56	114.69	127.32	95.38
160	POB 1022	S3	1.48	131.71	137.87	116.21	152.00	117.38	131.04	98.16
161	SMH 521	S3	1.57	135.63	141.07	123.17	150.95	120.28	134.22	100.55
162	SMH 533	S3	1.04	134.04	144.49	118.61	150.85	121.20	133.84	100.26
163	SMH 575	S3	1.39	139.28	142.20	121.73	155.96	120.88	136.01	101.89
164	SMH 577	S3	0.51	139.22	137.95	121.95	151.58	119.17	133.97	100.36
165	SMH 633	S3	2.40	133.66	140.37	123.79	151.88	118.53	133.64	100.12
166	SMH 652	S3	2.74	132.22	133.98	117.78	146.20	114.01	128.84	96.52
167	SMH 754	S3	1.71	135.46	139.99	119.98	153.69	119.04	133.63	100.11
168	SMH 798	S3	1.72	130.61	136.38	117.50	149.01	114.14	129.53	97.03
169	SMH 820	S3	1.98	135.35	137.79	124.96	148.41	117.79	132.86	99.53
170	SMH 839	S3	1.33	140.20	139.57	115.16	152.66	119.70	133.46	99.98
171	STH 2008	S3	1.82	135.89	147.91	122.06	157.60	125.23	137.74	103.18
172	STH 2009	S3	1.28	132.94	139.85	123.66	155.97	121.75	134.84	101.01
173	STH 2010	S3	1.12	139.75	143.99	128.51	154.09	122.20	137.71	103.16
174	STHD 2002	S3	2.37	143.65	128.46	122.21	152.35	117.69	132.87	99.54
175	STHD 2003	S3	0.73	140.73	140.46	125.07	155.74	123.56	137.11	102.72
176	STHD 2004	S3	0.77	148.37	149.07	124.52	160.18	126.00	141.63	106.10
177	STHD 2005	S3	0.89	138.65	142.50	121.21	157.37	123.99	136.74	102.44
178	STHD 2006	S3	3.17	136.36	137.67	108.10	154.99	121.05	131.63	98.61
179	STHD 2007	S3	2.13	137.96	140.45	120.12	156.68	121.61	135.36	101.40
180	SYMETRIA w3	S3	2.61	131.90	143.59	125.08	157.31	123.61	136.30	102.10

Tabela S4.1. Lista wybranych 94 genotypów pszenicy zwyczajnej badanych w ramach konwersji markerów DArTseq i segregacje wybranych markerów z rejonów QTL. DPW - doświadczenie przedwstępne, DW - doświadczenie wstępne

								Segregacje wybranych markerów DArTseq																				
							CloneID (DATrSeq)	984529	1024562	1064047	1067378	1088387	1092495	1110071	1119844	1208957	1218808	1695128	2252258	2278048	2327344	3955009	3955557	4394207	5324794	1.5E+07	3.3E+07	3.9E+07
							Docelowy QTL	QGY1	QGY1	QS1	QS1	QGY5	QGY5	QGY2	QGY2	QGY3	QGY3	QGY3	QGY3	QGY4	QGY4	QGY6	QGY6	QGY7	QGY7	QGY8	QGY9	QGY9
							Chromosome	2A	2A	2B	2B	3B	3B	3D	3D	5A	5A	5A	5A	5A	5A	5B	5B	6A	6A	6A	7D	7D
Nr DNA	Symbol linii	Populacja	Pochodzen	Stężenie	Płytka	Pozycja	Pozycja (IWGMI 2.1)	36216026	39201857	643625410	644612105	802550967	803229423	18936183	19197634	464270897	473807772	476894853	543698374	691649147	691655672	433164266	436384186	587432118	587965598	598415823	4215386	5670027
1	SMH13722	DPW	SMH	373	P2	1	SMH13722	0	0	1	0	0	1	1	0	1	1	0	2	1	1	2	0	1	1	1	-	1
2	SMH13822	DPW	SMH	555	P2	2	SMH13822	0	0	1	-	0	-	1	-	0	-	-	2	1	1	1	0	1	-	1	0	1
3	SMH13922	DPW	SMH	337	P2	3	SMH13922	0	-	-	0	1	-	-	0	0	0	-	0	1	1	0	-	1	0	1	-	-
4	SMH14122	DPW	SMH	587	P2	4	SMH14122	0	0	1	0	1	0	1	0	0	0	0	2	1	1	0	1	1	2	1	0	-
5	SMH14422	DPW	SMH	571	P2	5	SMH14422	2	0	1	0	0	1	1	0	0	0	1	0	1	1	0	1	1	0	1	0	-
6	SMH14522	DPW	SMH	793	P2	6	SMH14522	0	2	1	0	1	0	1	0	0	0	1	0	1	1	0	1	1	0	1	0	-
7	C19104	DW	DANKO	417	P2	7	C19104	0	1	1	0	1	0	1	2	0	0	1	0	1	1	0	1	1	0	1	1	0
8	C19573	DW	DANKO	451	P2	8	C19573	2	1	1	0	-	0	1	2	0	0	1	0	1	1	0	1	1	0	1	0	-
9	DI238	DW	DANKO	719	P2	9	DI238	0	-	1	-	1	0	1	2	0	0	1	2	1	1	0	1	-	1	1	1	0
10	C273814-14	DW	DANKO	563	P2	10	C273814-14	0	0	1	0	1	0	1	0	0	0	1	0	1	1	0	1	-	0	0	-	0
11	DD19719	DW	DANKO	516	P2	11	DD19719	2	1	1	0	1	0	0	1	0	0	1	2	0	0	0	1	1	1	1	0	1
12	DD53119	DW	DANKO	687	P2	12	DD53119	0	2	1	0	-	0	1	0	0	0	1	0	1	1	0	1	-	0	0	0	1
13	DD55919	DW	DANKO	749	P2	13	DD55919	0	2	1	0	1	0	1	0	0	0	1	2	1	1	0	1	1	0	1	0	1
14	DD86819	DW	DANKO	527	P2	14	DD86819	0	0	1	0	1	0	-	0	0	0	0	2	0	0	0	1	1	1	1	0	1
15	DL102719	DW	DANKO	676	P2	15	DL102719	0	0	1	0	1	0	1	0	0	0	0	0	1	1	0	1	1	-	1	1	0
16	DL102819	DW	DANKO	479	P2	16	DL102819	0	0	1	0	1	0	1	0	0	0	0	2	1	1	0	1	1	0	1	1	0
17	DL109119	DW	DANKO	702	P2	17	DL109119	2	0	-	0	0	1	1	0	0	0	1	0	1	1	0	1	1	0	1	0	1
18	DL109519	DW	DANKO	428	P2	18	DL109519	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	MIB0245	DW	MHR	854	P2	19	MIB0245	0	0	1	0	1	0	0	1	1	1	0	0	1	1	0	1	1	-	1	0	1
20	MIB0534	DW	MHR	781	P2	20	MIB0534	0	0	0	1	1	0	-	0	1	1	0	2	1	1	0	1	1	1	1	0	-
21	POIB0122	DW	MHR	750	P2	21	POIB0122	0	0	1	0	2	0	1	0	0	0	1	0	-	0	0	1	1	0	1	0	1
22	POIB0222	DW	MHR	626	P2	22	POIB0222	2	1	1	0	0	1	1	0	1	1	0	0	1	1	0	1	1	0	1	0	1
23	POB0322	DW	MHR	880	P2	23	POB0322	0	0	1	0	1	0	1	0	1	1	0	2	1	1	0	1	1	1	1	-	-
24	KBP21.25	DW	MHR	895	P2	24	KBP21.25	2	1	1	0	1	0	1	-	0	0	1	0	-	1	0	1	1	0	1	0	-
25	KBP21.16	DW	MHR	913	P2	25	KBP21.16	0	0	1	0	1	0	1	0	0	0	1	0	-	1	0	1	1	0	1	0	-
26	KBP21.41	DW	MHR	674	P2	26	KBP21.41	0	0	1	0	1	0	1	-	0	0	1	2	0	0	0	1	1	1	1	0	1
27	KBP21.28	DW	MHR	791	P2	27	KBP21.28	0	0	1	0	2	1	1	0	0	0	1	0	0	0	0	1	1	0	1	0	1
28	KBP21.47	DW	MHR	977	P2	28	KBP21.47	0	0	1	-	1	0	1	0	0	0	1	0	1	1	0	1	1	0	1	0	1
29	AND19057	DW	PHR	1150	P2	29	AND19057	0	0	1	0	2	-	1	0	0	0	1	0	1	1	0	1	0	0	1	0	-
30	AND19068	DW	PHR	951	P2	30	AND19068	0	0	1	0	1	0	0	-	0	0	1	0	0	0	0	1	1	0	1	0	1
31	AND10249	DW	PHR	872	P2	31	AND10249	0	0	1	0	1	0	1	0	0	0	1	2	1	1	0	1	1	1	1	0	1
32	AND19569	DW	PHR	790	P2	32	AND19569	0	0	1	-	1	0	1	0	0	0	1	0	-	0	0	1	1	0	1	0	1
33	AND19791	DW	PHR	981	P2	33	AND19791	0	0	0	2	1	0	1	-	0	0	1	0	1	1	0	-	1	0	1	0	1
34	AND19797	DW	PHR	822	P2	34	AND19797	0	0	1	0	-	0	1	0	1	0	0	0	1	1	0	1	1	0	1	0	-
35	NADZ190702	DW	PHR	579	P2	35	NADZ190702	0	0	1	0	1	0	-	0	0	0	1	2	1	1	0	1	1	1	1	1	0
36	NADZ19008	DW	PHR	819	P2	36	NADZ19008	2	1	-	0	1	0	0	1	1	-	-	2	0	0	0	1	1	0	1	0	1
37	NADZ19040	DW	PHR	1070	P2	37	NADZ19040	0	0	1	0	1	0	1	0	0	0	1	0	1	1	0	1	1	0	1	1	0
38	NADZ190674	DW	PHR	885	P2	38	NADZ190674	0	0	1	0	1	0	1	0	0	0	1	0	1	1	0	1	0	0	1	0	1
39	NADZ19581	DW	PHR	869	P2	39	NADZ19581	0	0	-	0	0	1	-	1	0	0	1	2	0	0	0	1	1	-	1	0	1
40	NADZ19647	DW	PHR	875	P2	40	NADZ19647	0	0	1	0	-	0	1	-	0	0	1	0	1	1	0	1	1	0	1	0	1
41	STHD0424	DW	STH	890	P2	41	STHD0424	0	0	1	0	1	0	1	0	1	1	0	0	0	0	0	1	1	0	1	0	-
42	STHD0430	DW	STH	1090	P2	42	STHD0430	0	0	0	1	-	0	1	0	0	0	1	0	1	1	0	1	1	-	1	0	1
43	STH0244L1	DW	STH	868	P2	43	STH0244L1	0	0	1	0	1	0	1	-	0	0	1	0	1	1	0	1	1	-	1	0	1
44	STH0244L2	DW	STH	976	P2	44	STH0244L2	0	0	1	-	1	0	1	-	0	0	1	0	1	1	0	1	1	0	1	0	1
45	STH0307	DW	STH	1130	P2	45	STH0307	0	0	1	0	1	0	1	-	1	1	-	0	1	1	0	1	1	0	1	0	1
46	STHD0411	DW	STH	947	P2	46	STHD0411	0	0	-	-	-	0	1	0	0	0	1	2	0	0	0	1	1	1	1	0	-
47	STHD0441	DW	STH	938	P2	47	STHD0441	0	0	0	1	1	0	1	-	0	0	1	0	1	1	0	1	1	0	1	0	1
48	STHD0549	DW	STH	1260	P2	48	STHD0549	0	0	1	0	1	0	1	0	0	0	0	0	1	1	0	1	1	0	1	0	1
49	STHD1121	DW	STH	837	P2	49	STHD1121	0	0	1	0	0	1	1	0	0	0	1	0	0	0	0	1	1	0	1	0	1
50	STHD1126	DW	STH	1000	P2	50	STHD1126	0	0	1	0	0	1	1	-	0	0	1	0	0	0	0	1	0	-	1	-	-
51	STHD1438	DW	STH	596	P2	51	STHD1438	0	0	1	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0	1	0	-
52	STHD1447	DW	STH	1100	P2	52	STHD1447	0	0	0	1	1	0	1	0	0	0	1	2	1	1	0	1	1	1	1	1	0
53	ARTIST	DW	WZ1	704	P2	53	Artist	0	0	0	1	-	0	1	-	0	0	1	0	1	1	0	1	1	0	1	0	1
54	KILIMANJARO	DW	WZ2	552	P2	54	KILIMANJARO	0	0	-	0	1	0	1	0	0	0	1	0	1	1	0	1	1	0	1	1	0
55	SYMETRIA	DW	WZ3	812	P2	55	SYMETRIA	2	1	1	0	1	0	1	0	0	0	1	2	0	0	1	0	1	1	1	0	1
56	C19186	DW	DANKO	639	P2	56	C19186	0	0	1	0	1	0	1	-	0	1	0	0	0	0	0	1	1	0	1	-	1
57	C327916-1ost	DW	DANKO	800	P2	57	C327916-1ost	0	0	1	0	1	0	1	0	-	0	1	2	0	0	0	-	1	1	1	0	-
58	C17263	DW	DANKO	884	P2	58	C17263	0	0	1	0	1	0	1	0	0	0	1	0	-	0	0	1	1	0	0	0	1
59	C16397	DW	DANKO	770	P2	59	C16397	0	0	1	0	-	0	1	0	0	0	1	2	-	0	0	1	-	1	1	0	1
60	DD19819	DW	DANKO	767	P2	60	DD19819	2	1	-	0	1	0	-	1	0	0	1	2	-	0	0	1	1	1	1	0	1
61	DD53019	DW	DANKO	767	P2	61	DD53019	0	0	1	0	-	0	-	0	0	0	1	0	1	1	0	1	-	0	0	-	1
62	DD56119	DW	DANKO	701	P2	62	DD56119	0	0	1	0	1	0	1	-	0	-	1	0	1	1	0	1	1	0	1	0	1
63	DD90919	DW	DANKO	614	P2	63	DD90919	0	0	1	0	-	0	1	0	0	0	1	0	1	1	0	1	1	0	0	0	1
64	DL110219	DW	DANKO	796	P2	64	DL110219	0	0	1	1	1	0	1	0	0	0	1	0	1	1	0	1	1	0	1	-	2
65	DL112119	DW	DANKO	624	P2	65	DL112119	0	0	1	0	1	0	1	0	-	0	1	0	1	2	2	2	1	0	1	0	1
66	DL115619	DW	DANKO	776	P2	66	DL115619	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
67	DL117519	DW	DANKO	627	P2	67	DL117519	0	0	1	0	1	0	1	0	0	0	0	2	1	1	0	-	1	2	1	0	-
68	DL122019	DW	DANKO	790	P2	68	DL122019	0	2	1	0	-	0	1	0	1	0	0	2	1	1	0	-	1	1	1	0	1
69	MIB01007	DW	MHR	685	P2	69	MIB01007	0	0	0	1	-	0	1	0	0	0	0	0	1	1	0	1	-	2	1	0	1

70	POB0422	DW	MHR	605	P2	78	POB0422	0	0	1	0	0	1	-	0	0	0	1	2	2	2	1	0	1	1	1	0	-
71	POB0522	DW	MHR	687	P2	71	POB0522	2	1	1	0	1	0	-	0	1	0	0	2	1	1	0	1	1	1	1	0	1
72	POB0622	DW	MHR	848	P2	72	POB0622	0	0	1	0	-	0	1	0	0	0	1	2	1	1	0	1	1	1	1	0	1
73	KBP21.9	DW	MHR	719	P2	73	KBP21.9	0	0	-	0	1	0	1	-	0	0	1	2	0	0	0	1	1	-	1	0	1
74	KBP21.17	DW	MHR	1020	P2	74	KBP21.17	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	KBP21.43	DW	MHR	833	P2	75	KBP21.43	0	0	1	0	2	1	-	0	0	0	1	0	1	1	0	1	1	0	-	0	1
76	KBP21.32	DW	MHR	1030	P2	76	KBP21.32	0	0	1	0	0	1	0	-	0	0	1	0	1	1	0	1	1	0	1	-	1
77	KBP21.50	DW	MHR	724	P2	77	KBP21.50	0	0	1	0	-	0	1	0	0	1	0	2	1	1	0	1	1	2	1	0	1
78	KBP21.42	DW	MHR	698	P2	70	KBP21.42	0	0	1	0	1	0	0	-	0	0	1	2	1	2	0	1	1	0	1	-	1
79	AND19073	DW	PHR	934	P2	79	AND19073	0	0	1	0	1	0	0	-	0	0	1	0	0	0	0	1	1	0	1	0	1
80	AND19799	DW	PHR	808	P2	80	AND19799	0	0	1	-	1	0	1	-	0	-	1	0	1	1	0	1	1	0	1	1	0
81	AND19829	DW	PHR	990	P2	81	AND19829	0	0	-	0	-	0	1	0	0	0	1	2	1	1	0	1	1	1	1	0	1
82	AND19862	DW	PHR	1020	P2	82	AND19862	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
83	AND191003	DW	PHR	977	P2	83	AND191003	0	0	1	0	1	0	1	-	1	0	1	0	1	1	0	1	1	0	1	0	1
84	AND191004	DW	PHR	988	P2	84	AND191004	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
85	AND191009	DW	PHR	927	P2	85	AND191009	0	0	1	0	0	1	0	1	0	0	1	0	-	1	0	1	1	0	1	0	1
86	NADZ191004	DW	PHR	925	P2	86	NADZ191004	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
87	NADZ191036	DW	PHR	485	P2	87	NADZ191036	0	0	1	0	1	0	1	0	0	0	1	0	1	1	1	0	1	0	1	0	1
88	NADZ191090	DW	PHR	1170	P2	88	NADZ191090	0	0	1	0	0	1	1	0	1	0	0	0	1	1	0	1	1	0	1	0	-
89	NADZ19377	DW	PHR	901	P2	89	NADZ19377	0	0	0	1	1	0	0	1	0	0	1	2	-	1	0	1	1	0	1	0	1
90	NADZ19796	DW	PHR	1470	P2	90	NADZ19796	0	0	1	0	-	0	1	0	0	0	1	2	0	0	0	1	1	1	1	0	-
91	STHD1461	DW	STH	1160	P2	91	STHD1461	2	1	1	0	1	0	1	0	0	0	1	2	0	0	1	0	1	1	1	-	1
92	STHD1464	DW	STH	1130	P2	92	STHD1464	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
93	STHD1468	DW	STH	941	P2	93	STHD1468	0	2	1	-	1	0	1	0	0	0	1	0	0	0	0	1	1	0	1	0	-
94	STHD2001	DW	STH	842	P2	94	STHD2001	0	0	1	0	-	0	-	-	1	1	0	2	1	1	0	1	1	-	1	0	-

Tabela S4.2. Wyniki wstępnego testowania 20 oznaczeń dla konwertowanych markerów DArTseq. Ref - segregacje markerów DArTseq, Mono - brak polimorfizmu

						segregacje												
Numer PCR	Starter1	Starter2	Starter3	DArTseq warunki PCR	dlugość DNA/Tm	1	2	3	4	5	6	7	8	9	10	11	12	uwagi
1	QGY1_2A _L	QGY1_2A _R	QGY1_2A _R2	36216026		0	0	0	0	2	0	0	2	0	0	0	0	Ref
				39201857		0	2	0	0	1	0	0	1	2	0	0	0	Ref
				Std	**200**	**0**	**1**	**1**	**1**	**0**	**1**	**1**	**0**	**1**	**1**	**1**	**0**	**zgodne z 3616026**
				Phire	350/650	1	1	1	1	1	1	1	1	1	1	1	1	Mono
2	QS1_2B _L	QS1_2B _R		643625410		1	1	1	1	1	1	0	1	0	1	1	1	Ref
				644612105		0	0	0	0	0	0	1	0	1	0	0	-	Ref
				Std	390	1	1	1	1	1	1	1	1	1	1	1	1	Mono
3	QGY5_3A _L	QGY5_3A _R		543698374		2	0	0	2	0	0	0	0	0	0	0	2	Ref
				Std	350	1	1	1	1	1	1	1	1	1	1	1	1	Mono
4	QS2_3B _L	QS2_3B _R	QS2_3B _R2	802550967		1	1	0	1	1	-	1	1	0	1	0	-	Ref
				803229423		0	0	1	0	0	0	0	0	1	0	0	0	Ref
				Std	80	0	0	0	0	0	0	0	0	0	0	0	0	Mono
				Phire	480	1	1	1	1	1	1	1	1	1	1	1	1	Mono
5	QGY2_3D _L	QGY2_3D _R		18936183		-	0	0	1	-	1	1	1	1	-	1	1	Ref
				19197634		0	1	1	0	0	-	0	0	0	0	-	0	Ref
					700	1	1	1	1	1	1	1	1	1	1	1	1	Mono
6	QGY3_5A _L	QGY3_5A _R		464270897		1	0	0	0	0	1	0	-	-	0	0	0	Ref
				Std	580	1	2	1	2	1	1	1	-	2	1	1	-	niezgodna z 464270897
				Phire	400/900	1	1	1	1	1	1	1	1	1	1	1	1	Mono
7	**QGY4_5A1_L**	**QGY4_5A1_R**	**QGY4_5A1_R2**	**473807772**		**0**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**0**	**-**	**0**	**-**	Ref
				Std	**1000**	**1**	**1**	**1**	**1**	**1**	**1**	**0**	**1**	**1**	**1**	**1**	**-**	**zgodne z 473807772**
8	QGY4_5A2_L	QGY4_5A2_R	QGY4_5A2_R2	476894853		1	0	0	1	1	1	1	1	0	1	1	-	Ref
				Std	260	1	1	1	1	1	1	1	1	1	1	1	-	Mono
9	QS3_L	QS3_R		691649147		1	0	1	0	1	1	0	-	1	1	1	0	Ref
				691655672		1	0	1	0	1	1	0	0	1	1	1	0	Ref
				Std	370	1	1	1	1	1	1	1	1	1	1	1	1	Mono
				Phire	350	1	1	1	1	1	1	1	1	1	1	1	1	Mono
10	QGY6_5B1_L	QGY6_5B1_R		433164266		2	0	0	0	0	0	0	0	2	0	0	0	Ref
				Std	820	1	1	0	1	1	1	0	1	1	1	1	1	niezgodna z 433164266
				Phire	350	1	1	1	1	1	1	1	1	1	1	1	1	Mono
11	QGY6_5B2_L	QGY6_5B2_R		436384186		0	1	0	1	1	1	1	1	0	0	0	1	Ref
				Std	650	1	1	1	1	1	1	1	1	1	1	1	1	Mono
12	QGY7_6A_L	QGY7_6A_R	QGY7_6A_R2	587432118		1	1	1	0	1	1	1	-	-	1	1	1	Ref
				587965598		0	0	0	0	0	0	0	0	2	2	0	0	Ref
				Std	180/2000	1	1	1	1	1	1	1	1	1	1	1	1	Mono
13	QGY8_6A _L	QGY8_6A _R		598415823		1	0	1	1	1	1	1	1	1	1	0	0	Ref
				Std	400	1	1	1	1	-	-	-	-	-	-	-	-	Mono
				Phire	380	0	1	0	0	1	0	0	1	1	0	0	0	niezgodna z 598415823
14	QGY9_7D_L	QGY9_7D_R	QGY9_7D_R2	4215386		0	0	0	0	0	0	1	0	0	-	0	0	Ref
				5670027		-	1	1	1	1	-	0	1	-	1	0	-	Ref
				Std	200	1	1	1	1	1	1	1	1	1	1	1	1	Mono
15	QGY1_2A2 _L	QGY1_2A2 _R	QGY1_2A2 _R2	36216026		0	0	0	0	2	0	0	2	0	0	0	0	Ref
				39201857		0	2	0	0	1	0	0	1	2	0	0	0	Ref
				Std	500	-	-	-	-	-	-	-	-	-	-	-	-	Mono
16	QGY3_5A2 _L	QGY3_5A2 _R	QGY3_5A2 _RC	464270897		0	0	1	0	0	0	0	0	1	0	0		Ref
				hrm	78.1/78.4	1	1	0	1	1	1	1	1	0	1	1	0	zgodne z 464270897
				hrm	78.7	0	0	1	0	0	1	0	0	1	0	0	0	zgodne z 464270897
				hrm	82	0	0	0	0	0	0	0	1	0	0	0	0	dodatkowy produkt
17	QGY4_5A3_L	QGY4_5A3_R		473807772	R7	0	0	1	0	0	0	0	0	0	0	0	-	Ref
				476894853		1	0	0	1	1	1	1	1	0	1	1	-	Ref
				Std	80	1	1	1	1	1	-	1	1	1	1	1	0	niezgodna z 598415823
18	QGY4_5A4_L	QGY4_5A4_R		473807772	R8	0	0	0	0	0	0	1	0	0	-	0	-	Ref
				476894853		1	0	1	1	1	0	0	1	1	1	0	-	Ref
				Std	500	1	1	1	1	1	1	1	1	1	1	1	0	niezgodna z 598415823
19	QGY6_5B3_L	QGY6_5B3_R		433164266	R5	0	0	0	0	0	0	0	0	0	0	0	0	Ref
				Std	200	1	1	1	1	1	1	1	1	1	1	1	1	Mono
20	QGY8_6A1_L	QGY8_6A1_RT	QGY8_6A1_RC	598415823	P2R6	1	1	1	1	1	1	1	1	1	1	0	1	Ref
				hrm	93.1	1	0	0	0	0	0	1	1	0	0	0	0	niezgodna z 598415823
					93.4	1	1	1	1	0	0	0	0	1	1	1	0	niezgodna z 598415823
					93.7	0	0	0	0	1	1	0	0	0	0	0	1	niezgodna z 598415823

Tabela S5.1. Zestaw 23283 markerów silicoDArT wykorzystywanych do przewidywania wartości hodowlanych w latach 2019/20, 2020/21, 2021/22 i 2022/23. Wartości 1 oznaczono jako A natomiast 0 jako C. Efekty na średni plon (BLUP) i względem standardu (STD).

Lp	Marker	chrom	pos	N(lat)	N(+)	N(-)	alleles	BLUP_23	STD_23	BLUP_22	STD_22	BLUP_21	STD_21	BLUP_20	STD_20
1	1025210	1A	1156301	2	2	2	A/C	0.0041	0.0040	-0.0075	-0.0067				
2	1089771	1A	1160153	3	4	2				-0.0008	-0.0005	0.0007	0.0005	0.0026	0.0021
3	1252727	1A	1160397	1	2	0	A/C	0.0013	0.0009						
4	4991245	1A	1311189	1	0	2	A/C	-0.0045	-0.0032						
5	1040965	1A	1631930	1	0	2				-0.0005	-0.0006				
6	4262489	1A	1632059	2	4	0	A/C	0.0005	0.0007	0.0017	0.0014				
7	1252654	1A	1810806	3	6	0	A/C	0.0040	0.0036			0.0001	0.0002	0.0008	0.0010
8	5370345	1A	1868201	1	2	0	A/C	0.0010	0.0010						
9	4991395	1A	1868819	1	2	0	A/C	0.0027	0.0030						
10	4999886	1A	1868819	1	2	0	A/C	0.0019	0.0023						
11	2261520	1A	1902482	1	2	0	A/C	0.0048	0.0034						
12	3937058	1A	1910079	1	0	2	A/C	-0.0044	-0.0037						
13	5323776	1A	1949719	1	2	0				0.0021	0.0010				
14	1110821	1A	2580229	1	2	0	A/C	0.0059	0.0036						
15	3939550	1A	2580229	4	6	2	A/C	0.0013	0.0017	-0.0077	-0.0048	0.0013	0.0011	0.0008	0.0009
16	3947465	1A	2580364	2	2	2	A/C	0.0034	0.0032	-0.0083	-0.0086				
17	1723678	1A	2584331	2	2	2	A/C	0.0012	0.0014	-0.0009	-0.0006				
18	3958152	1A	2584331	4	4	4	A/C	0.0027	0.0018	-0.0042	-0.0051	0.0014	0.0011	-0.0026	-0.0055
19	1251432	1A	3141591	4	4	4	A/C	-0.0010	-0.0002	-0.0084	-0.0067	0.0013	0.0011	0.0025	0.0020
20	1130983	1A	3181875	4	6	2	A/C	0.0022	0.0028	0.0015	0.0031	-0.0004	-0.0006	0.0051	0.0037
21	1688043	1A	3181875	1	2	0	A/C	0.0016	0.0016						
22	4009408	1A	3181875	3	4	2	A/C	0.0003	0.0007			0.0001	0.0000	-0.0005	0.0000
23	1102329	1A	3341067	1	0	2	A/C	-0.0020	-0.0017						
24	1032449	1A	3764863	4	3	5	A/C	-0.0093	-0.0065	-0.0027	-0.0026	0.0024	0.0018	0.0018	-0.0004
25	1221906	1A	3919892	1	0	2	A/C	-0.0022	-0.0017						
26	4439965	1A	4912787	2	4	0	A/C	0.0061	0.0057	0.0033	0.0022				
27	1093668	1A	4968120	2	4	0	A/C	0.0004	0.0010	0.0033	0.0026				
28	4395958	1A	4968391	3	6	0	A/C	0.0016	0.0016			0.0015	0.0013	0.0045	0.0042
29	3947128	1A	5197377	3	4	2	A/C	-0.0017	-0.0010			0.0025	0.0020	0.0068	0.0035
30	1068748	1A	5554758	2	1	3	A/C	-0.0086	-0.0081	0.0016	-0.0005				
31	1077302	1A	5595391	4	8	0	A/C	0.0071	0.0046	0.0014	0.0009	0.0005	0.0004	0.0030	0.0026
32	992113	1A	5686515	1	2	0	A/C	0.0065	0.0058						
33	1765789	1A	5849521	2	2	2	A/C	-0.0075	-0.0050	0.0028	0.0024				
34	2322317	1A	5849521	1	2	0				0.0155	0.0121				

Tabela S5.2. Zestaw 17979 markerów SNP wykorzystywanych do przewidywania wartości hodowlanych w latach 2019/20, 2020/21, 2021/22 i 2022/23.

Lp	rs	chrom	pos	N(lat)	N(+)	N(-)	alleles	BLUP_23	STD_23	BLUP_22	STD_22	BLUP_21	STD_21	BLUP_20	STD_20
1	1216560	1A	0	1	0	2	G/C	-0.0124	-0.0103						
2	1120440	1A	1195489	1	2	0	A/C	0.0035	0.0039						
3	1043336	1A	1235912	4	4	4	G/A	0.0037	0.0041	-0.0096	-0.0088	-0.0040	-0.0034	0.0016	0.0002
4	1212218	1A	1235915	3	5	1	A/G	0.0042	0.0050			0.0010	0.0004	0.0024	-0.0028
5	1076290	1A	1345408	2	0	4	A/G	-0.0021	-0.0004	-0.0075	-0.0057				
6	1040965	1A	1631957	1	1	1	C/T	-0.0007	0.0006						
7	4541348	1A	1745563	1	0	2	C/T			-0.0161	-0.0102				
8	1070663	1A	1868201	4	6	2	T/C	0.0037	0.0043	-0.0061	-0.0044	0.0036	0.0030	0.0006	0.0017
9	4991395	1A	1868819	4	5	3	C/G	0.0027	0.0039	-0.0106	-0.0072	0.0010	0.0010	0.0000	0.0008
10	3023688	1A	1947069	4	2	6	C/A	0.0009	0.0018	-0.0061	-0.0044	-0.0024	-0.0019	-0.0047	-0.0034
11	3575516	1A	1947072	2	0	4	G/T					0.0000	-0.0004	-0.0071	-0.0086
12	1279778	1A	4496500	1	0	2	T/G	-0.0081	-0.0068						
13	1256788	1A	4496543	1	2	0	A/G	0.0042	0.0041						
14	2266418	1A	4929734	1	0	2	T/C	-0.0040	-0.0027						
15	2325861	1A	4968262	1	0	2	A/G	-0.0060	-0.0078						
16	3064373	1A	5548650	1	0	2	G/A	-0.0013	-0.0007						
17	992113	1A	5686515	2	2	2	C/T	0.0015	0.0011	-0.0069	-0.0054				
18	3033029	1A	5704798	1	2	0	C/T	0.0036	0.0034						
19	7487803	1A	5857407	2	4	0	C/A	0.0021	0.0019	0.0193	0.0159				
20	993566	1A	6213314	1	1	1	C/T	-0.0002	0.0008						
21	3950972	1A	7054793	2	2	2	G/C					0.0018	0.0017	-0.0054	-0.0050
22	11914863	1A	7526878	1	0	2	A/G			-0.0079	-0.0055				
23	993293	1A	7528915	1	0	2	T/G	-0.0019	-0.0022						
24	3946763	1A	7528943	3	0	6	G/T			-0.0012	-0.0008	-0.0015	-0.0011	-0.0012	-0.0018
25	4911117	1A	7557797	1	2	0	C/T	0.0019	0.0031						
26	1059727	1A	7988319	4	5	3	C/T	0.0079	0.0061	-0.0060	-0.0054	0.0018	0.0012	-0.0009	0.0015
27	3021529	1A	8077230	1	2	0	T/C	0.0027	0.0018						
28	3021967	1A	8542962	4	8	0	C/A	0.0037	0.0043	0.0042	0.0037	0.0031	0.0025	0.0055	0.0030
29	2281925	1A	8619460	1	2	0	T/C	0.0020	0.0017						
30	10993005	1A	8635002	4	2	6	G/A	0.0018	0.0017	-0.0033	-0.0011	-0.0001	-0.0003	-0.0043	-0.0043
31	2334587	1A	8656388	1	2	0	C/A	0.0057	0.0062						
32	3032740	1A	9117622	1	2	0	T/C	0.0050	0.0053						
33	100142839	1A	9163987	1	2	0	A/G	0.0031	0.0032						
34	1020433	1A	9913160	3	4	2	C/G	0.0054	0.0048			0.0023	0.0015	-0.0098	-0.0040
35	2258784	1A	9970740	2	2	2	C/A			0.0045	0.0041			-0.0075	-0.0052

Tabela S5.3. Wartości hodowlane estymowane genetycznie dla materiałów badanych w latach 2019/20, 2020/21, 2021/22 i 2022/23. Wartości przewidywano oddzielnie dla markerów SNP i silicoDArT dla średniego plonu (BLUP) oraz dla plonu względem standardów (STD).

Lp	Linia/odmiana	BLUP_SIL	STD_SIL	BLUP_SNP	STD_SNP	ROK
1	AND19019	141.78	106.62	141.66	106.58	2023
2	AND19057	135.78	102.81	135.74	102.79	2023
3	AND19068	135.54	102.13	135.63	102.19	2023
4	AND19073	135.66	102.09	135.85	102.19	2023
5	AND191003	132.79	100.30	132.84	100.31	2023
6	AND191009	135.29	102.35	135.32	102.35	2023
7	AND19249	130.47	98.39	130.32	98.39	2023
8	AND19569	134.32	101.82	134.26	101.80	2023
9	AND19791	136.26	103.29	136.16	103.26	2023
10	AND19797	129.52	97.82	129.71	97.87	2023
11	AND19799	131.59	99.07	131.68	99.15	2023
12	AND19803	133.17	100.15	133.05	100.11	2023
13	AND19829	132.97	100.34	133.11	100.37	2023
14	AND26716	133.94	100.21	134.19	100.30	2023
15	AND2716	140.37	105.60	140.08	105.52	2023
16	AND3316	138.99	104.34	138.88	104.32	2023
17	Artist	132.19	99.51	132.21	99.51	2023
18	C16397	137.98	104.55	137.80	104.49	2023
19	C17263	135.96	102.91	135.87	102.88	2023
20	C185417-4	126.30	94.18	126.63	94.29	2023
21	C19104	124.54	93.74	124.99	93.88	2023
22	C19186	133.70	101.22	133.76	101.21	2023
23	C19573	132.36	99.98	132.61	100.06	2023
24	C273814-14	138.45	105.37	138.27	105.28	2023
25	C281515-21	131.47	98.32	131.61	98.38	2023
26	C327916-1ost	130.77	98.46	130.88	98.51	2023
27	DD19719	137.65	104.31	137.48	104.24	2023
28	DD19819	138.02	104.76	137.93	104.71	2023
29	DD47019	135.71	101.87	135.58	101.84	2023
30	DD53019	133.47	100.48	133.56	100.54	2023
31	DD53119	134.24	101.71	134.26	101.66	2023
32	DD55919	133.03	100.48	133.19	100.55	2023
33	DD56119	134.43	101.86	134.38	101.81	2023
34	DD80019	138.60	104.26	138.30	104.19	2023
35	DD86819	134.46	101.67	134.49	101.69	2023
36	DD90919	134.12	101.37	134.23	101.39	2023
37	DD91019	134.65	101.36	134.66	101.36	2023
38	DI238	129.70	98.09	129.81	98.11	2023
39	DL102719	133.78	101.52	133.57	101.44	2023
40	DL102819	130.40	98.44	130.47	98.46	2023
41	DL109119	138.30	105.18	138.00	105.05	2023
42	DL110219	134.01	101.29	133.98	101.29	2023
43	DL112119	131.62	99.58	131.67	99.57	2023
44	DL117519	129.83	97.78	130.23	97.91	2023
45	DL122019	137.01	103.75	136.83	103.68	2023
46	DL127819	135.01	101.20	135.11	101.24	2023
47	DL134819	135.60	101.53	135.63	101.59	2023
48	DL135919	137.11	103.02	136.88	102.96	2023
49	DL141019	132.77	99.40	132.80	99.43	2023
50	DL155219	136.83	102.92	136.61	102.87	2023
51	KBP21.10	130.41	97.39	130.68	97.50	2023
52	KBP21.16	137.75	104.37	137.65	104.33	2023

53	KBP21.19	132.89	99.62	132.75	99.61	2023
54	KBP21.20	131.52	98.43	131.62	98.47	2023
55	KBP21.25	133.50	101.07	133.45	101.05	2023
56	KBP21.28	131.83	99.94	131.88	99.94	2023
57	KBP21.32	130.38	98.46	130.51	98.49	2023
58	KBP21.33	130.56	97.89	130.40	97.84	2023
59	KBP21.41	133.78	101.08	133.80	101.08	2023
60	KBP21.42	131.54	99.20	131.65	99.24	2023
61	KBP21.43	127.99	96.47	128.39	96.57	2023
62	KBP21.47	132.93	100.65	132.88	100.62	2023
63	KBP21.50	130.58	98.43	130.91	98.53	2023
64	KBP21.56	135.97	102.07	135.90	102.06	2023
65	KBP21.9	132.67	100.12	132.84	100.18	2023
66	KILIMANJARO	131.71	98.98	131.73	99.05	2023
67	KOH03221	131.30	98.28	131.41	98.32	2023
68	KOH12020	134.11	100.46	134.27	100.52	2023
69	KOH18619	137.57	103.56	137.26	103.45	2023
70	MIB01007	134.80	102.12	135.07	102.16	2023
71	MIB01152	136.31	102.43	136.30	102.43	2023
72	MIB0245	133.13	100.72	133.12	100.71	2023
73	MIB0534	135.71	102.93	135.77	102.92	2023
74	NADZ19008	130.59	98.69	130.83	98.76	2023
75	NADZ19040	132.85	100.78	132.61	100.62	2023
76	NADZ190674	135.57	102.86	135.33	102.78	2023
77	NADZ190702	133.39	100.65	133.48	100.69	2023
78	NADZ190876	143.88	108.55	143.46	108.42	2023
79	NADZ191036	141.65	107.36	141.47	107.30	2023
80	NADZ191090	140.94	106.91	140.64	106.82	2023
81	NADZ19110	137.98	104.30	137.71	104.15	2023
82	NADZ19377	135.35	102.58	135.40	102.57	2023
83	NADZ19581	135.75	102.89	135.74	102.87	2023
84	NADZ19628	135.27	101.43	135.00	101.37	2023
85	NADZ19647	133.65	100.86	133.73	100.91	2023
86	NADZ19649	137.01	103.11	136.58	102.98	2023
87	NADZ19796	133.35	100.87	133.26	100.84	2023
88	POB0122	130.83	99.00	130.82	99.00	2023
89	POB0222	124.58	93.72	124.84	93.82	2023
90	POB0322	134.04	101.56	134.01	101.55	2023
91	POB0422	127.69	96.39	127.93	96.43	2023
92	POB0522	125.40	94.00	125.69	94.13	2023
93	POB0622	130.34	98.21	130.39	98.24	2023
94	POB0722	135.33	101.57	135.05	101.50	2023
95	POB0822	128.47	95.97	128.78	96.07	2023
96	POB0922	127.75	95.48	127.99	95.58	2023
97	POB1022	130.69	98.11	130.51	98.06	2023
98	SMH521	134.01	100.52	134.00	100.52	2023
99	SMH530	132.71	100.23	132.62	100.19	2023
100	SMH574	133.40	100.62	133.35	100.62	2023
101	SMH575	135.51	101.86	135.31	101.81	2023
102	SMH578	135.30	102.61	135.49	102.63	2023
103	SMH592	132.85	100.35	132.73	100.32	2023
104	SMH633	133.33	100.11	133.27	100.12	2023
105	SMH643	134.85	102.17	134.78	102.15	2023
106	SMH733	135.84	102.94	135.64	102.88	2023
107	SMH754	133.74	100.15	133.52	100.12	2023
108	SMH761	134.16	101.69	134.05	101.66	2023
109	SMH796	132.90	100.45	132.87	100.45	2023

110	SMH798	130.00	97.14	130.36	97.26	2023
111	SMH820	132.92	99.56	133.08	99.61	2023
112	SMH829	132.90	100.50	132.95	100.50	2023
113	SMH840	135.54	102.66	135.31	102.59	2023
114	STH0244L1	136.58	103.66	136.40	103.59	2023
115	STH0244L2	133.89	101.37	134.19	101.46	2023
116	STH0307	131.75	99.71	131.95	99.76	2023
117	STH2009	134.86	101.03	134.73	101.01	2023
118	STH2010	137.09	103.07	136.88	103.01	2023
119	STHD0411	135.15	102.35	134.93	102.28	2023
120	STHD0424	132.81	100.49	132.84	100.50	2023
121	STHD0430	129.92	98.26	130.17	98.31	2023
122	STHD0441	133.13	100.62	133.03	100.60	2023
123	STHD0549	135.13	102.46	135.08	102.42	2023
124	STHD1121	133.43	101.13	133.38	101.10	2023
125	STHD1126	132.12	99.88	132.26	99.92	2023
126	STHD1438	137.14	103.97	136.97	103.93	2023
127	STHD1447	130.61	99.07	130.80	99.08	2023
128	STHD1461	133.25	100.50	133.60	100.59	2023
129	STHD1468	137.63	104.34	137.44	104.28	2023
130	STHD1476	135.37	102.33	135.55	102.37	2023
131	STHD1477	136.26	103.15	136.28	103.15	2023
132	STHD1479	129.81	97.84	130.15	97.92	2023
133	STHD2001	131.99	99.59	132.06	99.63	2023
134	STHD2002	132.89	99.57	132.81	99.56	2023
135	STHD2003	137.12	102.74	136.96	102.72	2023
136	STHD2004	140.67	105.94	140.22	105.81	2023
137	STHD2005	136.74	102.46	136.78	102.48	2023
138	STHD2006	132.06	98.71	132.11	98.76	2023
139	STHD2007	135.15	101.38	135.04	101.35	2023
140	SYMETRIA	135.33	101.80	135.49	101.86	2023
141	AND_11_16	124.56	99.66	124.65	99.68	2022
142	AND_15_16	129.70	104.74	130.41	105.01	2022
143	AND_150_18	122.02	97.73	122.41	97.89	2022
144	AND_189_18	124.55	101.33	124.72	101.49	2022
145	AND_2_16	126.32	102.57	126.70	102.88	2022
146	AND_213_18	119.14	95.15	118.24	94.74	2022
147	AND_37_16	125.98	100.63	126.01	100.67	2022
148	AND_370_18	124.10	100.95	124.17	100.93	2022
149	AND_393_18	125.72	101.20	125.38	101.09	2022
150	AND_398_18	128.05	102.63	128.94	102.95	2022
151	AND_410_18	121.63	98.13	121.52	98.11	2022
152	AND_5_18	123.30	100.01	123.28	100.11	2022
153	AND_69_18	122.95	99.97	123.36	100.16	2022
154	AND_8_16	122.26	99.31	122.24	99.36	2022
155	AND_896_18	126.21	101.90	126.85	102.20	2022
156	AND_90_18	123.30	99.48	123.07	99.36	2022
157	Artist_wz1	126.03	101.83	126.24	101.91	2022
158	C18_025	122.89	99.65	122.32	99.41	2022
159	C18_061	122.21	99.33	122.46	99.47	2022
160	C18_141	119.42	96.93	119.04	96.95	2022
161	C18_199	120.06	97.47	119.83	97.45	2022
162	C18_307	126.28	101.20	127.42	101.73	2022
163	C18_406	124.26	100.23	123.98	100.06	2022
164	C18_487-5	123.56	98.95	124.06	99.22	2022
165	C18_542	127.24	101.90	127.85	102.06	2022
166	C18_720	123.55	99.76	123.54	99.68	2022

167	C2782_14-55	120.78	96.78	120.81	96.88	2022
168	C2805_14-75	124.83	100.73	124.92	100.82	2022
169	CDI_4_8	120.99	97.28	120.84	97.17	2022
170	DD_166_18	123.10	99.87	122.54	99.72	2022
171	DD_185_18	127.67	103.89	127.85	103.89	2022
172	DD_201_18	126.12	100.87	126.06	100.79	2022
173	DD_210_18	125.83	101.58	126.22	101.70	2022
174	DD_307_18	128.41	102.67	128.85	102.76	2022
175	DD_333_18-1	126.00	101.71	125.96	101.61	2022
176	DD_335_18	127.69	102.27	128.54	102.56	2022
177	DD_372_18	122.80	99.76	122.74	99.67	2022
178	DD_373_18	121.32	98.04	120.82	97.69	2022
179	DD_388_18	124.44	100.60	125.49	101.06	2022
180	DD_391_18	121.69	97.51	121.46	97.41	2022
181	DD_392_18	122.38	99.22	122.31	99.32	2022
182	DL_505_18	127.81	103.92	128.20	103.99	2022
183	DL_525_18	125.62	101.79	125.18	101.75	2022
184	DL_657_18	123.06	100.08	123.05	100.06	2022
185	DL_678_18	120.62	97.85	120.06	97.65	2022
186	DL_683_18	124.07	99.29	124.11	99.21	2022
187	DL_695_18	128.52	103.09	129.21	103.24	2022
188	DL_775_18	124.32	99.54	124.70	99.63	2022
189	DL_806_18	122.38	97.90	122.72	98.04	2022
190	DL_835_18	125.58	101.38	125.77	101.38	2022
191	DL_855_18	122.12	98.53	122.22	98.62	2022
192	DL_880_18	128.38	103.61	128.69	103.73	2022
193	DL_909_18	125.53	101.44	125.93	101.57	2022
194	DL_947_18	127.71	103.13	127.91	103.09	2022
195	Formacja_wz3	120.49	97.01	119.78	96.66	2022
196	KBP_19_13	119.67	97.14	119.72	97.37	2022
197	KBP_19_41	119.99	96.39	118.81	95.97	2022
198	KBP_20_1	119.23	95.13	117.82	94.46	2022
199	KBP_20_12	127.29	101.63	127.54	101.76	2022
200	KBP_20_13	121.60	97.50	121.80	97.47	2022
201	KBP_20_14	123.61	99.86	123.32	99.75	2022
202	KBP_20_15	124.96	101.42	125.35	101.68	2022
203	KBP_20_16	123.62	100.48	123.73	100.63	2022
204	KBP_20_19	122.04	97.55	122.09	97.62	2022
205	KBP_20_28	127.08	102.69	127.82	102.88	2022
206	KBP_20_3	118.76	94.82	118.00	94.43	2022
207	KBP_20_34	126.16	101.82	126.27	101.81	2022
208	KBP_20_39	122.28	97.71	122.20	97.64	2022
209	KBP_20_4	121.22	98.39	120.64	98.26	2022
210	KBP_20_49	121.70	97.90	120.58	97.43	2022
211	KBP_20_5	121.65	97.30	121.70	97.36	2022
212	KBP_20_51	126.20	102.00	127.10	102.47	2022
213	KBP_20_57	127.27	103.57	128.09	103.92	2022
214	KBP_20_8	123.08	99.28	122.98	99.35	2022
215	Kiliman.wz2	125.23	101.00	125.57	101.03	2022
216	KOH_03419	121.60	98.18	121.37	98.07	2022
217	KOH_13220	120.53	97.28	120.27	97.10	2022
218	KOH_20520	121.69	98.03	121.00	97.83	2022
219	MIB_9503	122.84	99.89	122.99	99.99	2022
220	MIB_9629	125.30	100.29	125.60	100.33	2022
221	MIB_9631	123.88	99.61	123.31	99.43	2022
222	NAD_190021	125.32	102.09	126.12	102.50	2022
223	NAD_190022	128.22	102.80	128.86	102.98	2022

224	NAD_190034	128.58	103.02	128.48	102.90	2022
225	NAD_190050	129.57	104.50	130.11	104.66	2022
226	NAD_190051	127.49	102.73	127.10	102.56	2022
227	NAD_19019	128.11	104.22	128.77	104.65	2022
228	NAD_19022	125.12	100.09	125.35	100.08	2022
229	NAD_19024	127.81	103.87	128.56	104.30	2022
230	NAD_19031	124.63	100.60	124.74	100.59	2022
231	NAD_19040	123.70	99.84	123.75	99.80	2022
232	NAD_19072	127.73	102.85	128.23	103.14	2022
233	NAD_19089	122.62	99.57	122.50	99.61	2022
234	NAD_19090	125.22	100.23	125.10	100.04	2022
235	NAD_19093	128.20	103.62	128.76	103.76	2022
236	NAD_19116	125.20	101.79	125.44	101.93	2022
237	NAD_19117	127.36	102.20	128.21	102.49	2022
238	NAD_19130	127.93	102.69	128.41	102.70	2022
239	POB_0221	120.51	97.77	119.74	97.44	2022
240	POB_0321	118.48	96.25	118.31	96.38	2022
241	POB_0421	122.86	99.94	123.44	100.24	2022
242	POB_0521	127.66	102.28	128.43	102.48	2022
243	POB_0621	124.96	99.94	124.96	99.92	2022
244	POB_0721	124.60	99.74	124.54	99.52	2022
245	POB_0821	123.85	100.00	124.02	100.07	2022
246	POB_0921	126.08	101.92	126.96	102.31	2022
247	POB_1021	122.96	99.25	122.89	99.20	2022
248	SMH_323	119.51	96.80	119.23	96.67	2022
249	SMH_324	118.90	95.30	118.24	94.90	2022
250	SMH_331	118.45	95.62	118.03	95.43	2022
251	SMH_334	117.16	95.03	116.36	94.82	2022
252	SMH_340	117.95	94.34	117.90	94.30	2022
253	SMH_354	118.06	95.21	117.54	94.98	2022
254	SMH_361	120.08	97.42	119.79	97.46	2022
255	SMH_364	117.73	93.95	117.37	93.98	2022
256	SMH_370	120.80	97.46	120.48	97.37	2022
257	SMH_375	123.60	100.44	123.61	100.49	2022
258	SMH_376	119.07	95.36	120.04	95.88	2022
259	SMH_377	116.08	93.29	114.31	92.34	2022
260	SMH_378	115.30	93.56	114.94	93.61	2022
261	SMH_380	119.50	95.71	119.65	95.68	2022
262	SMH_394	121.14	97.60	120.79	97.49	2022
263	SMH_402	122.41	99.63	122.60	99.73	2022
264	SMH_411	116.72	93.22	116.39	93.08	2022
265	SMH_426	118.29	95.31	117.72	95.10	2022
266	SMH_427	119.63	97.17	119.83	97.44	2022
267	SMH_430	119.60	95.60	119.37	95.44	2022
268	SMH_431	116.56	94.00	116.07	93.83	2022
269	SMH_434	119.07	96.66	118.96	96.57	2022
270	SMH_436	119.42	95.43	118.88	95.15	2022
271	SMH_444	121.69	98.25	121.76	98.24	2022
272	SMH_446	120.78	98.04	120.63	98.00	2022
273	SMH_447	122.84	98.21	122.97	98.32	2022
274	SMH_458	116.39	93.63	115.68	93.43	2022
275	SMH_462	123.16	99.95	122.40	99.69	2022
276	SMH_478	117.34	93.80	117.19	93.75	2022
277	SMH_479	117.84	94.96	117.06	94.61	2022
278	SMH_486	119.15	96.75	118.70	96.56	2022
279	STH_0102	122.88	99.62	122.31	99.50	2022
280	STH_0208	124.61	99.79	124.67	99.69	2022

281	STH_0215	124.84	99.89	125.03	99.89	2022
282	STH_0217	117.74	93.90	116.57	93.36	2022
283	STH_0245	125.65	100.45	126.00	100.62	2022
284	STH_0308	127.82	102.43	128.56	102.58	2022
285	STH_0309	124.80	99.75	124.90	99.79	2022
286	STH_0330	130.08	104.21	131.26	104.57	2022
287	STH_0344	121.64	97.20	121.63	97.23	2022
288	STH_8211	128.32	103.71	128.68	103.75	2022
289	STH_9115L1	120.57	97.51	120.68	97.44	2022
290	STH_9441	119.09	96.71	118.56	96.52	2022
291	STHD_0119	121.81	99.00	122.15	99.26	2022
292	STHD_0121	121.13	98.38	121.14	98.54	2022
293	STHD_0123	123.67	100.60	123.55	100.46	2022
294	STHD_0126	128.02	104.22	128.13	104.12	2022
295	STHD_0127	127.97	104.18	128.31	104.33	2022
296	STHD_0129	128.08	104.32	128.61	104.53	2022
297	STHD_0132	122.35	97.69	121.96	97.57	2022
298	STHD_0133	122.82	98.32	122.90	98.21	2022
299	STHD_0142	129.43	103.80	130.60	104.18	2022
300	STHD_0144	121.51	97.17	121.41	97.03	2022
301	STHD_0414	122.14	98.46	121.85	98.34	2022
302	STHD_0443	122.61	98.89	122.22	98.73	2022
303	STHD_0472	122.08	98.60	121.77	98.37	2022
304	STHD_0503	119.87	96.77	119.69	96.64	2022
305	STHD_0504	118.37	95.48	117.68	95.19	2022
306	STHD_0519	118.58	95.44	117.30	94.93	2022
307	STHD_9310	124.04	100.77	124.37	101.03	2022
308	STHD_9403	122.42	99.57	122.75	99.79	2022
309	STHD_9404	121.66	98.51	120.95	98.44	2022
310	STHD_9563	123.80	100.39	123.71	100.55	2022
311	AND_13_15	117.54	99.94	118.24	100.56	2021
312	AND_15_15	117.94	100.14	118.09	100.42	2021
313	AND_23_15	117.66	100.23	117.74	100.42	2021
314	AND_29_14	117.30	99.78	117.54	99.97	2021
315	AND_3_14	117.63	100.22	118.21	100.81	2021
316	AND_361_17	117.80	100.32	117.85	100.44	2021
317	AND_42_15	118.02	100.47	118.27	100.75	2021
318	AND_471_17	117.20	99.59	117.49	99.93	2021
319	AND_50_15	117.45	99.91	117.82	100.22	2021
320	AND_560_17	116.24	99.03	115.68	98.49	2021
321	AND_582_17	116.10	98.99	115.48	98.35	2021
322	AND_657_17	117.12	99.92	117.28	100.12	2021
323	AND_659_17	117.86	100.38	118.17	100.68	2021
324	AND_660_17	117.91	100.21	118.27	100.53	2021
325	AND_678_17	117.66	100.02	117.86	100.21	2021
326	AND_791_17	116.90	99.59	117.11	99.79	2021
327	AND_793_17	116.99	99.61	117.17	99.79	2021
328	ARTIST	117.72	100.05	117.99	100.35	2021
329	DC_17_1051-5	117.12	99.68	117.22	99.70	2021
330	DC_17_1216_ost	117.45	100.17	117.53	100.34	2021
331	DC_17_132	116.61	99.46	116.87	99.68	2021
332	DC_17_673	117.49	99.87	117.93	100.20	2021
333	DC_17_698	117.48	100.07	117.79	100.34	2021
334	DC_17_704	116.18	99.13	115.99	99.03	2021
335	DC_17_705-2	116.43	99.21	116.13	99.00	2021
336	DC_17_959	117.31	100.05	117.80	100.50	2021
337	DC_17_962	117.65	100.05	118.42	100.70	2021

338	DC_2683_14-5	115.56	98.70	115.31	98.51	2021
339	DD_1035_17	115.34	98.28	115.40	98.28	2021
340	DD_1047_17	116.06	98.87	115.46	98.30	2021
341	DD_168_17	116.29	99.24	116.02	99.05	2021
342	DD_304_17	117.39	99.79	117.92	100.24	2021
343	DD_556_17	116.99	99.66	117.30	99.99	2021
344	DD_646_17	116.72	99.43	116.67	99.36	2021
345	DD_694_17	117.18	99.98	117.05	99.94	2021
346	DD_800_17	116.83	99.46	116.83	99.38	2021
347	DL_1081_17	117.03	99.76	117.28	100.02	2021
348	DL_1085_17	116.42	99.35	116.23	99.25	2021
349	DL_1089_17	116.41	99.35	116.08	99.13	2021
350	DL_1095_17	117.05	99.77	117.30	100.04	2021
351	DL_1096_17	117.02	99.67	117.28	99.93	2021
352	DL_1128_17	117.33	99.72	117.21	99.58	2021
353	DL_1141_17	116.41	99.11	116.23	98.95	2021
354	DL_1214_17	117.21	99.74	117.62	100.07	2021
355	DL_1274_17	117.73	100.01	117.92	100.13	2021
356	FORMACJA	116.06	98.85	116.10	98.85	2021
357	HRSM_937	117.56	100.08	117.91	100.37	2021
358	HRSM_940	117.76	100.22	118.11	100.52	2021
359	KBP_18_14B	115.71	98.87	115.40	98.62	2021
360	KBP_18_16	116.94	99.54	117.33	99.78	2021
361	KBP_19_1	116.99	99.78	116.97	99.74	2021
362	KBP_19_13	116.55	99.37	116.67	99.48	2021
363	KBP_19_18	115.91	98.66	115.86	98.59	2021
364	KBP_19_2	116.88	99.73	116.83	99.73	2021
365	KBP_19_26	116.73	99.39	116.73	99.38	2021
366	KBP_19_27	117.98	100.38	118.48	100.83	2021
367	KBP_19_3B	117.13	99.67	117.03	99.49	2021
368	KBP_19_41	116.95	99.72	116.97	99.77	2021
369	KBP_19_44	117.51	100.18	117.80	100.52	2021
370	KBP_19_6	116.49	99.42	116.56	99.58	2021
371	KBP_20_70	116.13	98.95	116.04	98.76	2021
372	KILI	116.33	99.07	116.53	99.22	2021
373	KOH_23419	117.12	99.91	117.18	100.05	2021
374	MIB_18203	117.19	99.95	116.96	99.86	2021
375	MIB_18265	115.56	98.74	115.05	98.30	2021
376	MIB_18624	116.36	99.09	116.14	98.84	2021
377	MIB_9168	116.31	99.00	116.33	99.00	2021
378	MIB_9187	117.04	99.60	116.99	99.60	2021
379	NAD_17036	116.92	99.63	116.82	99.57	2021
380	NAD_18001	116.71	99.25	116.74	99.19	2021
381	NAD_180015	117.57	100.06	118.36	100.78	2021
382	NAD_180020	117.73	100.16	118.14	100.48	2021
383	NAD_180036	117.89	100.24	118.22	100.52	2021
384	NAD_180061	116.47	99.35	116.38	99.28	2021
385	NAD_180062	116.90	99.54	116.24	98.92	2021
386	NAD_18016	117.91	100.11	117.95	100.30	2021
387	NAD_18020	116.46	99.32	116.14	99.05	2021
388	NAD_18034	116.24	99.05	116.12	98.82	2021
389	NAD_18055	117.58	100.16	117.60	100.24	2021
390	NAD_18070	118.21	100.47	118.80	100.92	2021
391	NAD_18095	116.85	99.65	116.80	99.67	2021
392	NAD_18106	116.53	99.24	116.50	99.13	2021
393	NAD_18109	116.91	99.60	116.84	99.48	2021
394	NAD_18117	117.26	99.86	117.34	99.99	2021

395	NAD_18119	116.32	99.07	115.96	98.68	2021
396	NAD_189007	118.72	100.86	119.30	101.47	2021
397	POB_0120	116.52	99.40	116.27	99.24	2021
398	POB_0220	115.67	98.73	115.41	98.45	2021
399	POB_0320	116.65	99.42	116.35	99.25	2021
400	POB_0420	116.29	99.28	115.65	98.71	2021
401	POB_0520	115.94	98.83	115.90	98.73	2021
402	POB_0620	115.81	98.69	115.51	98.25	2021
403	POB_0720	115.93	98.82	115.65	98.47	2021
404	POB_0820	116.54	99.36	115.93	98.87	2021
405	POB_0920	116.09	98.84	116.00	98.69	2021
406	POB_1120	115.70	98.53	115.76	98.57	2021
407	POB_1220	115.79	98.67	115.20	98.10	2021
408	SMH_140	116.44	99.15	116.34	99.01	2021
409	SMH_18	116.19	99.02	115.67	98.56	2021
410	SMH_201	117.45	100.08	117.62	100.33	2021
411	SMH_205	117.29	99.95	117.52	100.22	2021
412	SMH_206	115.91	99.02	115.43	98.66	2021
413	SMH_210	116.06	99.01	115.83	98.83	2021
414	SMH_213	115.95	98.91	115.63	98.66	2021
415	SMH_214	115.38	98.56	114.86	98.14	2021
416	SMH_216	115.28	98.44	114.81	98.08	2021
417	SMH_230	116.29	99.25	116.11	99.09	2021
418	SMH_232	116.43	99.32	116.13	99.14	2021
419	SMH_25	116.14	98.98	116.05	98.83	2021
420	SMH_250	117.38	100.01	117.96	100.54	2021
421	SMH_254	116.14	98.98	115.75	98.67	2021
422	SMH_264	116.60	99.30	116.50	99.18	2021
423	SMH_280	116.35	98.95	116.39	98.93	2021
424	SMH_284	116.07	98.87	115.83	98.55	2021
425	SMH_289	115.89	98.67	115.82	98.43	2021
426	SMH_29	116.70	99.36	116.57	99.21	2021
427	SMH_290	115.74	98.55	115.42	98.10	2021
428	SMH_291	115.95	98.73	116.09	98.69	2021
429	SMH_302	116.08	98.92	115.02	97.87	2021
430	SMH_312	116.82	99.31	116.87	99.30	2021
431	SMH_320	117.03	99.50	117.01	99.45	2021
432	SMH_487	116.70	99.40	116.59	99.23	2021
433	SMH_488	116.68	99.39	116.44	99.14	2021
434	SMH_489	116.40	99.31	116.21	99.14	2021
435	SMH_60	117.33	99.97	117.38	100.05	2021
436	STH_7307B	117.99	100.35	118.81	101.15	2021
437	STH_8210	117.79	100.38	118.18	100.88	2021
438	STH_8308_L1	116.58	99.50	116.56	99.56	2021
439	STH_8313	116.73	99.60	116.29	99.40	2021
440	STH_8355	116.28	99.20	116.11	98.99	2021
441	STH_8374_L1	117.72	100.32	117.98	100.70	2021
442	STH_8377	116.79	99.72	116.60	99.64	2021
443	STH_9240	116.70	99.30	116.76	99.33	2021
444	STHD_8435	117.97	100.43	118.46	101.00	2021
445	STHD_8583	117.11	99.88	117.30	100.13	2021
446	STHD_9115	117.96	100.25	118.42	100.59	2021
447	STHD_9119	118.44	100.48	118.58	100.74	2021
448	STHD_9124	117.45	100.19	117.78	100.55	2021
449	STHD_9126	117.96	100.08	118.18	100.34	2021
450	STHD_9321	117.06	99.66	116.87	99.41	2021
451	STHD_9325	116.32	98.99	116.17	98.80	2021

452	STHD_9337	116.93	99.35	117.05	99.45	2021
453	STHD_9410	116.16	98.81	116.15	98.79	2021
454	STHD_9433	115.87	98.60	115.48	98.09	2021
455	STHD_9437	115.79	98.55	115.29	97.96	2021
456	STHD_9440	116.44	99.06	116.29	98.83	2021
457	STHD_9449	117.28	99.76	117.41	99.82	2021
458	STHD_9470	117.07	99.57	117.41	99.84	2021
459	STHD_9482	115.58	98.48	115.32	98.16	2021
460	STHD_9501	116.60	99.31	116.63	99.29	2021
461	STHD_9508	116.23	99.13	115.74	98.74	2021
462	STHD_9511	116.77	99.43	116.99	99.55	2021
463	STHD_9545	117.66	100.11	118.03	100.50	2021
464	STHD_9560	116.39	99.14	116.30	99.03	2021
465	STHD_9564	116.40	99.22	115.97	98.80	2021
466	STHD_9565	115.71	98.72	115.26	98.28	2021
467	STHD_9566	117.11	99.65	117.38	99.88	2021
468	STHD_9567	117.24	99.68	117.32	99.77	2021
469	AND_1011_16	113.35	101.93	113.49	102.25	2020
470	AND_1113_16	108.72	98.17	108.15	97.84	2020
471	AND_1293_16	105.59	95.52	104.85	95.14	2020
472	AND_344_16	107.47	98.41	108.90	99.85	2020
473	AND_345_16	106.11	95.98	105.40	94.76	2020
474	AND_360_16	105.88	95.51	104.93	94.89	2020
475	AND_4015_18	108.79	98.26	109.09	98.56	2020
476	AND_466_16	104.27	95.57	103.51	94.96	2020
477	AND_5271_17	106.37	95.93	105.50	95.27	2020
478	AND_670_16	108.15	98.69	107.44	98.43	2020
479	AND_671_16	110.20	99.14	110.47	98.90	2020
480	AND_673_16	112.05	100.58	113.27	101.17	2020
481	AND_673_17	104.29	95.42	102.99	94.40	2020
482	AND_681_17	109.31	98.26	108.16	96.93	2020
483	AND_691_16	110.90	99.80	111.29	100.20	2020
484	AND_751_16	100.39	90.36	98.71	88.39	2020
485	AND_916_15	105.16	96.02	105.49	96.63	2020
486	AND_942_16	103.33	93.57	101.54	91.41	2020
487	ARTIST_wz1	111.74	101.27	112.02	101.38	2020
488	DC_16_047	111.46	101.81	112.42	102.97	2020
489	DC_16_162	114.29	102.36	115.62	103.17	2020
490	DC_16_239	104.72	96.06	105.21	96.85	2020
491	DC_16_246	109.73	98.46	110.80	99.03	2020
492	DC_16_397	109.41	100.13	109.26	100.32	2020
493	DC_16_508	109.25	98.14	110.15	98.41	2020
494	DC_16_684	106.28	96.32	105.59	95.81	2020
495	DC_1639_13-2	106.36	97.41	106.23	97.54	2020
496	DC_3176_15	109.04	98.51	109.38	98.89	2020
497	DC_3279_15	104.46	94.01	103.70	92.77	2020
498	DC_3496_15	108.05	98.74	108.32	99.27	2020
499	DC_3524_15	109.74	99.01	110.49	99.79	2020
500	DD_240_16	108.15	97.81	108.93	98.48	2020
501	DD_269_16	108.13	96.89	109.45	97.61	2020
502	DD_403_16	112.94	101.33	112.61	101.34	2020
503	DD_455_16	105.41	96.07	104.66	95.67	2020
504	DD_597_16	107.48	98.67	107.01	98.47	2020
505	DD_722_16	107.68	96.61	109.35	98.36	2020
506	DD_846_16	112.80	101.54	112.94	101.84	2020
507	DD_875_16	114.29	102.70	115.59	103.54	2020
508	DD_876_16	112.74	102.41	113.96	103.97	2020

509	DD_940_16	108.94	99.74	109.32	100.30	2020
510	DD_981_16	107.67	96.94	107.44	96.31	2020
511	DD_998_16	108.31	96.99	108.37	96.45	2020
512	DL_514_16	104.19	95.46	102.48	94.23	2020
513	DL_530_16	103.34	95.01	102.51	94.24	2020
514	DL_564_16	107.51	98.22	108.27	99.23	2020
515	DL_574_16	109.02	97.19	109.38	97.59	2020
516	DL_578_16	110.91	99.43	110.95	99.76	2020
517	DL_628_16	108.23	99.32	107.97	99.17	2020
518	DL_640_16	112.90	102.76	112.68	102.79	2020
519	DL_665_16	110.30	98.73	111.20	99.09	2020
520	DL_762_16	107.38	96.45	107.96	96.68	2020
521	DL_768_16	106.56	95.59	106.16	94.91	2020
522	DL_797_16	105.22	94.94	104.60	94.44	2020
523	DL_896_16	109.09	98.23	109.04	98.34	2020
524	DL_900_16	111.33	100.02	113.02	100.83	2020
525	DL_902_16	109.10	98.10	108.86	97.92	2020
526	DL_906_16	107.97	97.00	108.67	98.23	2020
527	KBP_18_14A	103.37	94.92	102.20	94.06	2020
528	KBP_18_15	102.40	94.12	100.62	92.63	2020
529	KBP_18_17	107.63	97.05	106.82	96.64	2020
530	KBP_18_28	106.38	97.16	105.82	96.74	2020
531	KBP_18_33	106.85	96.29	106.86	96.35	2020
532	KBP_18_42	102.57	93.97	102.08	93.84	2020
533	KBP_18_44	104.21	93.68	102.80	91.94	2020
534	KBP_18_47	107.15	96.76	108.00	96.96	2020
535	KBP_18_48	106.09	95.43	105.20	94.95	2020
536	KBP_18_51	109.20	98.26	109.26	98.47	2020
537	KBP_18_61	106.93	96.38	107.39	96.18	2020
538	KBP_19_3A	108.54	98.14	108.72	98.10	2020
539	KBP_19_4	109.54	98.43	110.49	98.54	2020
540	KBP_19_5	103.85	93.62	102.43	92.95	2020
541	KILIM_Wz2S1	108.37	98.85	108.57	98.80	2020
542	MIB_17228	109.88	100.40	110.76	101.37	2020
543	MIB_17305	110.04	100.64	109.95	100.78	2020
544	MIB_17376	106.66	96.02	106.58	95.29	2020
545	MIB_17445	106.48	95.81	105.94	95.42	2020
546	MIB_17456	105.36	95.31	104.93	95.10	2020
547	NAD_17008	112.13	101.29	113.29	101.77	2020
548	NAD_17011	112.34	101.34	112.15	101.27	2020
549	NAD_17012	110.91	101.08	112.04	102.38	2020
550	NAD_17013	111.80	101.81	112.42	102.47	2020
551	NAD_17015	111.95	101.06	112.77	101.44	2020
552	NAD_17017	112.98	101.77	112.83	101.96	2020
553	NAD_17019	112.17	101.97	112.32	102.28	2020
554	NAD_17034	112.49	102.87	113.49	103.87	2020
555	NAD_17035	109.75	100.23	110.07	100.84	2020
556	NAD_17038	112.73	101.55	113.14	102.08	2020
557	NAD_17053	111.46	100.23	112.46	100.74	2020
558	NAD_17055	111.88	100.34	111.78	100.46	2020
559	NAD_17063	106.56	97.44	105.47	96.54	2020
560	NAD_17067	108.91	97.84	108.44	97.86	2020
561	NAD_17076	111.81	101.48	113.37	102.95	2020
562	NAD_17079	113.43	101.44	114.52	102.40	2020
563	NAD_17082	107.14	96.85	105.53	95.57	2020
564	NAD_17084	111.17	99.43	111.95	99.85	2020
565	NAD_17108	108.21	96.88	109.78	97.92	2020

566	NAD_17168	107.68	96.58	107.53	96.26	2020
567	NAD_17172	111.98	100.63	112.21	101.22	2020
568	PATRAS_wz3	109.54	99.22	109.20	98.92	2020
569	POB_0119	105.23	96.46	104.25	95.86	2020
570	POB_0219	104.18	95.29	102.62	94.17	2020
571	POB_0319	108.26	98.89	108.51	99.46	2020
572	POB_0419	111.93	100.43	113.36	100.98	2020
573	POB_0519	99.03	89.33	97.04	86.95	2020
574	POB_0619	111.72	99.89	112.90	100.51	2020
575	POB_0719	109.62	98.09	109.05	97.17	2020
576	POB_0819	107.17	96.67	107.09	96.46	2020
577	POB_0919	106.54	96.06	106.41	96.00	2020
578	POB_1019	105.55	95.25	103.81	93.81	2020
579	SMH_107	113.23	100.68	114.33	101.51	2020
580	SMH_138	104.91	95.74	103.94	95.08	2020
581	SMH_148	109.91	97.83	109.33	97.73	2020
582	SMH_160	107.73	96.15	107.43	95.95	2020
583	SMH_163	105.44	96.05	104.27	95.30	2020
584	SMH_166	109.35	97.18	109.52	97.43	2020
585	SMH_19	109.97	97.89	109.86	97.69	2020
586	SMH_2	107.56	98.13	108.46	98.98	2020
587	SMH_3	108.33	97.21	108.12	96.96	2020
588	SMH_31	103.85	94.82	103.30	94.56	2020
589	SMH_32	104.79	93.43	104.89	93.41	2020
590	SMH_38	106.55	96.91	106.91	97.55	2020
591	SMH_39	109.25	99.68	110.04	100.78	2020
592	SMH_52	112.28	99.53	112.68	100.04	2020
593	SMH_6	110.69	101.04	111.17	101.78	2020
594	SMH_71	106.68	97.31	105.82	96.64	2020
595	SMH_80	103.04	94.33	101.98	93.28	2020
596	SMH_9714	103.65	94.78	102.49	94.00	2020
597	SMH_9817	105.38	94.46	105.12	94.05	2020
598	SMH_9901	108.50	97.35	107.99	96.67	2020
599	SMH_9903	105.58	94.44	105.01	93.83	2020
600	STH_6207	105.87	96.73	105.34	96.56	2020
601	STH_6527	109.58	100.30	110.13	100.80	2020
602	STH_7135	105.21	96.27	104.69	96.08	2020
603	STH_7263	107.44	98.35	107.20	98.23	2020
604	STH_7307	109.37	100.34	108.96	100.08	2020
605	STH_7324	110.79	101.28	110.71	101.40	2020
606	STH_7341	109.45	100.25	109.92	100.92	2020
607	STH_7420	109.10	99.95	108.78	100.07	2020
608	STH_7431	107.86	98.66	108.26	99.23	2020
609	STH_7506	109.47	97.41	109.28	96.95	2020
610	STH_8211	117.90	105.17	119.32	106.34	2020
611	STH_8214	113.72	100.95	114.30	101.52	2020
612	STH_8215	114.50	101.71	115.74	102.66	2020
613	STH_8220	107.37	95.84	106.86	95.29	2020
614	STH_8274	113.73	101.15	115.32	102.24	2020
615	STH_8280	111.62	99.24	111.51	99.22	2020
616	STH_8311	110.62	98.34	110.84	98.61	2020
617	STH_8325	109.29	97.42	109.86	97.84	2020
618	STHD_7234	105.11	96.13	104.11	95.35	2020
619	STHD_8102	109.79	97.55	109.95	97.62	2020
620	STHD_8483	107.80	96.85	108.44	97.64	2020
621	STHD_8506	110.89	99.80	111.01	99.96	2020
622	DD_489_16	105.14	95.35	103.55	93.93	2020

623	HRSM_930	107.46	97.08	107.56	97.32	2020
624	HRSM_931	108.37	97.79	108.72	98.25	2020
625	HRSM_932	108.63	98.02	109.01	98.09	2020
626	SMH_130	108.67	98.25	109.96	99.12	2020
627	SMH_161	108.36	97.75	108.33	97.43	2020
628	SMH_174	107.93	97.33	108.02	97.38	2020
629	SMH_182	108.52	97.74	108.80	97.97	2020
630	SMH_34	105.49	95.40	104.85	94.63	2020
631	SMH_75	106.74	96.19	107.11	96.40	2020
632	STH_8326	108.03	97.41	108.13	97.33	2020
633	STHD_8441	107.02	96.23	106.96	96.24	2020
634	STHD_8463	107.05	96.90	106.55	96.38	2020
635	STHD_8510	107.15	96.64	106.62	96.17	2020
636	STHD_8511	106.75	96.35	106.51	96.05	2020
637	STHD_8520	107.32	96.73	106.65	96.10	2020
638	STHD_8534	108.51	98.12	110.15	99.34	2020
639	STHD_8574	105.65	95.47	104.55	94.33	2020

Tabela S5.4. Efekty selekcyjne markerów na plon (GY) względem standartów (STD) lub wartości BLUP wybranych na podstawie analiz asocjacyjnych w 2023.

	Marker	chrom	pos	N(lat)	N(+)	N(-)	alleles	BLUP_23	STD_23	BLUP_22	STD_22	BLUP_21	STD_21	BLUP_20	STD_20	cecha i R2 w 2023 roku	R2 dla istotnych lokalizacji w 2023 roku
QGY1	3064473	2A	36353589	4	8	0	G/A	0.001	0.002	0.001	0.003	0.000	0.001	0.009	0.005	GY_STD (14.04)	NAD/SMH 11.8-13.7
QGY1	4393934	2A	37426995	3	6	0	C/A	0.002	0.002			0.003	0.002	0.005	0.005		
QGY1	3945141	2A	37858599	4	6	2	T/A	**-0.010**	**-0.010**	0.003	0.005	0.000	0.000	0.003	0.001		
QGY1	1119844	2A	39201843	4	4	4	G/A	**-0.015**	**-0.014**	**0.011**	**0.009**	-0.002	-0.002	0.003	0.003		
QGY2	1007916	3D	18952308	4	8	0	C/G	**0.007**	**0.006**	**0.006**	**0.006**	0.002	0.002	0.001	0.002		KOH 15.8-19.7
QGY2	1024777	3D	19158599	4	5	3	G/T	0.004	0.003	0.000	0.001	-0.001	-0.001	0.006	0.005		
QGY3	1088387	5A	464270888	4	4	4	G/A	**-0.007**	**-0.006**	**-0.018**	**-0.014**	0.000	0.001	0.000	0.001	GY_BLUP 15.5, GY_STD 16.6	NAD13.3-15.5
QGY4	3955009	5A	473807733	4	0	8	T/C	**-0.006**	**-0.006**	**-0.010**	**-0.007**	-0.001	-0.002	-0.004	-0.006	GY_BLUP 16.9, GY_STD 18.5	NAD12.7-15.3
QGY4	2253343	5A	474974899	4	3	5	G/C	0.003	0.004	0.001	0.000	-0.004	-0.003	-0.009	-0.007		
QGY4	988867	5A	475017306	3	2	4	G/A			-0.001	0.000	-0.002	-0.001	0.016	0.012		
QGY4	1037130	5A	475863114	3	1	5	A/G	-0.004	-0.003			0.000	0.000	-0.005	-0.002		
QGY4	5360863	5A	476089502	4	0	8	A/G	**-0.004**	**-0.003**	**-0.011**	**-0.007**	0.000	0.000	-0.011	-0.009		
QGY5	1208957	5A	543698356	2	0	4	A/G	**-0.011**	**-0.009**	**-0.008**	**-0.007**					GY_BLUP 13.4, GY_STD 19.7	KBP17.1-18.3
QGY6	1088869	5B	433342372	3	2	4	G/T	-0.005	-0.004	0.001	0.001			-0.005	-0.008		SMH12.5-16.8
QGY6	1091135	5B	434733713	4	3	5	A/G	0.003	0.006	-0.001	0.001	0.000	0.000	-0.004	-0.009		
QGY6	1218808	5B	436384166	4	4	4	C/A	-0.003	-0.004	**0.015**	**0.011**	0.000	0.000	**0.008**	**0.003**		
QGY7	1052322	6A	587644494	3	4	2	A/G	0.001	0.000			-0.001	-0.001	0.008	0.005		KBP 16.2-16.6
QGY7	1133638	6A	587843608	3	4	2	G/A	-0.015	-0.011			0.003	0.003	0.005	0.010		
QGY7	1092576	6A	587851201	4	3	5	C/T	**-0.012**	**-0.008**	-0.006	-0.001	0.003	0.003	-0.003	0.001		
QGY7	1076760	6A	587858102	4	3	5	T/C	**-0.012**	**-0.009**	0.000	0.004	0.004	0.003	-0.002	-0.001		
QGY7	984529	6A	587965586	3	4	2	A/G	-0.014	-0.010			0.007	0.006	0.014	0.009		
QGY8	1695128	6A	598415890	2	0	4	G/T	**-0.008**	**-0.006**	-0.001	0.000					GY_BLUP 11.2, GY_STD 17.3	STH14.4
QGY9	1073523	7D	4227000	3	1	5	C/G	-0.002	-0.002			-0.002	-0.002	0.002	0.000		RAH/KRZ15.3-18.03
QGY9	4910310	7D	4371634	3	1	5	A/T	-0.002	-0.001			-0.003	-0.003	0.002	-0.002		
QGY9	2247383	7D	4548389	4	4	4	T/C	-0.004	-0.003	**0.008**	**0.007**	-0.001	-0.001	0.005	0.002		
QGY9	2248056	7D	4553755	4	4	4	G/C	-0.003	-0.002	**0.011**	**0.008**	-0.002	-0.001	0.004	0.000		
QGY9	2264325	7D	4882841	3	3	3	C/G			0.001	0.000	0.001	0.001	-0.001	0.000		
QGY9	989214	7D	4989653	3	1	5	C/T	-0.002	-0.001			-0.002	-0.002	0.002	-0.002		
QGY9	1095172	7D	4989866	4	3	5	T/A	-0.001	-0.001	0.012	0.008	0.000	0.000	-0.007	-0.007		
QGY9	2243521	7D	5086419	3	0	6	A/T	-0.001	-0.001			-0.003	-0.002	-0.001	-0.003		
QGY9	23919601	7D	5488315	4	2	6	C/G	0.001	0.001	-0.005	-0.003	0.000	0.000	-0.001	0.000		