

**Supplementary Table S1. Primers for the qPCR expression analyses**

<b>bZIP transcription factor primers and actin primers</b>			
<b>bZIP TF</b>	<b>Gene</b>	<b>Forward Primer (5'-3')</b>	<b>Reverse Primer (5'-3')</b>
ABF2	TraesCS5D02G244500	GGACCTGAACGAGGAACTGG	CCGTCCGAACTGATCCTTCA
ABF4	TraesCS5A02G237200	ACTGGTGAGGAAACAGGCAG	CCGTCCGAACTGATCCTTCA
ABI5	TraesCS1A02G306300	GAGCGCATTGGTTACAGCAG	TGGCTGAGGACCCAAATGAC
EMBP-1	TraesCS2B02G269600	TGAGAAGGGCAGTTCTGCTG	TCTCGTGTCTGAGGACTCGT
VIP1	TraesCS5B02G124200	GCCACTACGCTATCAGCACA	CTCCATGGACTGCAACCGAA
Actin	TraesCS1A02G274400	TCTATTTTGGCCTCTCTTAGCAC	TTTCCTGTACCCCTTATTCCTC

<b>bZIP target gene primers</b>			
<b>bZIP TF</b>	<b>Target gene</b>	<b>Forward Primer (5'-3')</b>	<b>Reverse Primer (5'-3')</b>
ABF2	TraesCS7D02G060400	CCATCCCTTCCACACTGTCC	CTTGGGATGTCGCCTGTGAG
	TraesCS3B02G439600	ATCATGCACGAGTACCGCC	CACAGCACCCAGTCATCCAA
ABF4	TraesCS6D02G333600	ACGAGAGAGGAGCACAAGGC	CCCATGCCATCATCCTCAGAC
ABI5	TraesCS3A02G242100	CCCCAAGGATAGACCAACGG	GGCAGGATGGTTCTCTCTCT
	TraesCS2A02G456100	ATTTCGGCCTCTCCGTCTTC	CAGCACTTCTGGGGCTACAT
EMBP-1	TraesCS5B02G490600	CATCAAGGAGCGGAAGCGT	CATCTCGAACCCCAGCCC
VIP1	TraesCS2B02G372900	ATGCTCCTGCTCACCATTCC	TCCCACGGGAGTACTTCACA
	TraesCS3A02G289300	CGTGTCCGAAGCTGGGTATT	GCACACGTTTGCCACTCATC

**Supplementary Table S2.** The phylogentic tree was constructed using 258, 83, 45 protein sequences in the wheat, rice, and Arabidopsis genome, respectively.

*Triticum aestivum* (wheat)

Name	Gene ID	Name	Gene ID
bZIP_1	TraesCSU02G019200.1 248 -310	TraesCSU02G019200.1 248 -310	Grp G
bZIP_2	TraesCS5D02G415300.1 63 - 113	TraesCS5D02G415300.1 63 - 113	Grp S
bZIP_3	TraesCS5D02G473000.2 255 -318	TraesCS5D02G473000.2 255 -318	Grp G
bZIP_4	TraesCS6A02G087400.1 220 -282	TraesCS6A02G087400.1 220 -282	Grp G
bZIP_5	TraesCS6A02G087400.2 251 -313	TraesCS6A02G087400.2 251 -313	Grp G
bZIP_6	TraesCS5B02G410000.1 62 - 114	TraesCS5B02G410000.1 62 - 114	Grp S
bZIP_7	TraesCS5B02G470600.1 251 -314	TraesCS5B02G470600.1 251 -314	Grp G
bZIP_8	TraesCS4A02G198100.1 127 -189	TraesCS4A02G198100.1 127 -189	Grp H
bZIP_9	TraesCS2A02G245700.1 258 -320	TraesCS2A02G245700.1 258 -320	Grp G
bZIP_10	TraesCS1B02G439800.1 263 -325	TraesCS1B02G439800.1 263 -325	Grp G
bZIP_11	TraesCS1D02G417100.1 263 -325	TraesCS1D02G417100.1 263 -325	Grp G
bZIP_12	TraesCS5D02G124600.1 291 -353	TraesCS5D02G124600.1 291 -353	Grp G
bZIP_13	TraesCS4D02G230200.1 280 -342	TraesCS4D02G230200.1 280 -342	Grp G
bZIP_14	TraesCS5D02G134100.1 114 -176	TraesCS5D02G134100.1 114 -176	Grp H
bZIP_15	TraesCS6B02G110100.1 250 -312	TraesCS6B02G110100.1 250 -312	Grp G
bZIP_16	TraesCS2B02G269600.1 259 -321	TraesCS2B02G269600.1 259 -321	Grp G
bZIP_17	TraesCS5A02G460800.1 249 -312	TraesCS5A02G460800.1 249 -312	Grp G
bZIP_18	TraesCS4B02G117400.1 128 -190	TraesCS4B02G117400.1 128 -190	Grp H
bZIP_19	TraesCS4B02G117400.2 221 -283	TraesCS4B02G117400.2 221 -283	Grp H
bZIP_20	TraesCS5A02G126600.1 114 -176	TraesCS5A02G126600.1 114 -176	Grp G
bZIP_21	TraesCS5B02G122000.1 269 -331	TraesCS5B02G122000.1 269 -331	Grp G
bZIP_22	TraesCS5B02G125800.1 114 -176	TraesCS5B02G125800.1 114 -176	Grp G
bZIP_23	TraesCS2D02G236200.1 258 -320	TraesCS2D02G236200.1 258 -320	Grp G
bZIP_24	TraesCS4B02G229100.2 323 -385	TraesCS4B02G229100.2 323 -385	Grp G
bZIP_25	TraesCS7D02G349300.1 128 -189	TraesCS7D02G349300.1 128 -189	GrpB
bZIP_26	TraesCS5D02G258000.1 89 - 144	TraesCS5D02G258000.1 89 - 144	Grp S
bZIP_27	TraesCS5D02G273500.1 206 -237	TraesCS6A02G175800.1 81 - 142	GrpB
bZIP_28	TraesCS6A02G175800.1 81 - 142	TraesCS7D02G182900.1 105 -154	Grp S
bZIP_29	TraesCS7D02G182900.1 105 -154	TraesCS7A02G181100.1 106 -156	Grp S
bZIP_30	TraesCS7A02G181100.1 106 -156	TraesCS7A02G373800.1 83 - 144	GrpB
bZIP_31	TraesCS7A02G373800.1 83 - 144	TraesCS6B02G209600.1 81 - 142	Grp H
bZIP_32	TraesCS6B02G209600.1 81 - 142	TraesCS7B02G086100.1 105 -154	Grp S
bZIP_33	TraesCS7B02G086100.1 105 -154	TraesCS3A02G128900.1 88 - 149	Grp H
bZIP_34	TraesCS3A02G128900.1 88 - 149	TraesCS5A02G250400.1 90 - 145	Grp S
bZIP_35	TraesCS5A02G250400.1 90 - 145	TraesCS6D02G167800.1 81 - 142	Grp H
bZIP_36	TraesCS5A02G265600.1 207 -238	TraesCS5B02G248400.1 90 - 145	Grp S
bZIP_37	TraesCS6D02G167800.1 81 - 142	TraesCS7B02G293900.1 72 - 122	Grp S
bZIP_38	TraesCS5B02G248400.1 90 - 145	TraesCS6D02G270000.1 103 -160	Grp S
bZIP_39	TraesCS5B02G265300.1 214 -245	TraesCS7D02G213200.1 86 - 134	Grp S
bZIP_40	TraesCS5B02G265300.2 214 -245	TraesCS6A02G288900.1 101 -152	Grp S
bZIP_41	TraesCS7B02G293900.1 72 - 122	TraesCS1B02G268500.1 174 -234	GrpB
bZIP_42	TraesCS6D02G270000.1 103 -160	TraesCS1B02G282800.1 170 -229	Grp A

bZIP_43	TraesCS7D02G213200.1 86 - 134	TraesCS1D02G257400.1 177 -237	GrpB
bZIP_44	TraesCS6A02G288900.1 101 -152	TraesCS2A02G142800.1 125 -185	Grp A
bZIP_45	TraesCS1B02G268500.1 174 -234	TraesCS1D02G273100.1 170 -229	Grp A
bZIP_46	TraesCS1B02G282800.1 170 -229	TraesCS7A02G211500.1 87 - 135	Grp S
bZIP_47	TraesCS1D02G257400.1 177 -237	TraesCS3A02G330800.1 70 - 118	Grp F
bZIP_48	TraesCS2A02G142800.1 125 -185	TraesCS5D02G068800.1 106 -160	Grp C
bZIP_49	TraesCS1D02G273100.1 170 -229	TraesCS3A02G378700.1 175 -235	Grp A
bZIP_50	TraesCS7A02G211500.1 87 - 135	TraesCS2B02G167900.1 122 -182	GrpB
bZIP_51	TraesCS3A02G330800.1 70 - 118	TraesCS7A02G391800.1 147 -198	Grp S
bZIP_52	TraesCS5D02G068800.1 106 -160	TraesCS5D02G150700.1 241 -289	Grp A
bZIP_53	TraesCS3A02G378700.1 175 -235	TraesCS5D02G150700.2 241 -287	Grp A
bZIP_54	TraesCS2B02G167900.1 122 -182	TraesCS1A02G273000.2 117 -176	Grp A
bZIP_55	TraesCS7A02G391800.1 147 -198	TraesCS6B02G318700.1 104 -161	Grp S
bZIP_56	TraesCS5D02G150700.1 241 -289	TraesCS5A02G057500.1 106 -160	Grp C
bZIP_57	TraesCS5D02G150700.2 241 -287	TraesCS2D02G146100.1 123 -183	Grp A
bZIP_58	TraesCS1A02G273000.2 117 -176	TraesCS5B02G059200.1 106 -160	Grp C
bZIP_59	TraesCS6B02G318700.1 104 -161	TraesCS7B02G118500.1 86 - 134	Grp S
bZIP_60	TraesCS5A02G057500.1 106 -160	TraesCS5A02G141500.1 241 -287	Grp A
bZIP_61	TraesCS2D02G146100.1 123 -183	TraesCS5B02G139800.1 241 -287	Grp A
bZIP_62	TraesCS5B02G059200.1 106 -160	TraesCS3D02G324200.1 71 - 119	Grp F
bZIP_63	TraesCS7B02G118500.1 86 - 134	TraesCS3D02G371900.1 168 -228	Grp A
bZIP_64	TraesCS5A02G141500.1 241 -287	TraesCS7D02G475100.1 143 -194	Grp C
bZIP_65	TraesCS5B02G139800.1 241 -287	TraesCS5D02G338000.1 129 -182	Grp A
bZIP_66	TraesCS3D02G324200.1 71 - 119	TraesCS7B02G391800.1 144 -195	Grp C
bZIP_67	TraesCS3D02G371900.1 168 -228	TraesCS7B02G464700.1 94 - 149	Grp A
bZIP_68	TraesCS7D02G475100.1 143 -194	TraesCS6A02G154600.1 137 -188	Grp C
bZIP_69	TraesCS5D02G338000.1 129 -182	TraesCS5B02G332300.1 129 -182	Grp A
bZIP_70	TraesCS7B02G391800.1 144 -195	TraesCS4A02G291200.1 55 - 102	Grp S
bZIP_71	TraesCS7B02G464700.1 94 - 149	TraesCS5A02G332000.1 134 -187	Grp A
bZIP_72	TraesCS6A02G154600.1 137 -188	TraesCS7A02G488600.1 146 -197	Grp C
bZIP_73	TraesCS6A02G165800.1 160 -200	TraesCS6B02G182500.1 136 -187	Grp C
bZIP_74	TraesCS5B02G332300.1 129 -182	TraesCS2D02G536700.1 106 -150	Grp A
bZIP_75	TraesCS4A02G291200.1 55 - 102	TraesCS6D02G144400.1 135 -186	Grp C
bZIP_76	TraesCS3A02G372400.3 244 -279	TraesCS7D02G268400.1 174 -232	Grp I
bZIP_77	TraesCS5A02G332000.1 134 -187	TraesCS7D02G269300.1 318 -367	Grp I
bZIP_78	TraesCS2B02G556600.1 133 -173	TraesCS7D02G392800.1 143 -199	GrpB
bZIP_79	TraesCS7A02G488600.1 146 -197	TraesCS5D02G244500.2 274 -324	Grp A
bZIP_80	TraesCS6B02G182500.1 136 -187	TraesCS7B02G299200.1 143 -199	GrpB
bZIP_81	TraesCS6B02G193200.1 151 -182	TraesCS5D02G308600.1 177 -235	Grp I
bZIP_82	TraesCS2D02G529000.1 124 -164	TraesCS5D02G315400.1 329 -383	Grp E
bZIP_83	TraesCS2D02G536700.1 106 -150	TraesCS5D02G447500.1 219 -269	Grp C
bZIP_84	TraesCS2A02G526300.1 122 -162	TraesCS6D02G312800.1 281 -326	Grp A
bZIP_85	TraesCS3D02G365200.2 251 -286	TraesCS6A02G170600.1 82 - 128	Grp S
bZIP_86	TraesCS6D02G144400.1 135 -186	TraesCS5B02G301900.1 177 -235	Grp I
bZIP_87	TraesCS6D02G154400.1 160 -200	TraesCS5B02G308800.1 329 -383	Grp E
bZIP_88	TraesCS7D02G268400.1 174 -232	TraesCS1B02G193800.1 243 -298	Grp I
bZIP_89	TraesCS7D02G269300.1 318 -367	TraesCS7D02G171300.1 265 -316	Grp A
bZIP_90	TraesCS7D02G392800.1 143 -199	TraesCS4A02G128900.1 155 -197	Grp A

bZIP_91	TraesCS5D02G244500.2 274 -324	TraesCS4A02G135600.2 160 -214	Grp I
bZIP_92	TraesCS7B02G299200.1 143 -199	TraesCS1D02G191000.1 242 -297	Grp I
bZIP_93	TraesCS5D02G308600.1 177 -235	TraesCS5B02G444100.2 212 -262	Grp C
bZIP_94	TraesCS5D02G315400.1 329 -383	TraesCS4A02G183400.1 234 -270	Grp F
bZIP_95	TraesCS5D02G447500.1 219 -269	TraesCS1B02G285800.2 215 -243	Grp D
bZIP_96	TraesCS6D02G312800.1 281 -326	TraesCS6A02G333600.1 271 -316	Grp A
bZIP_97	TraesCS6A02G170600.1 82 - 128	TraesCS7A02G170600.1 263 -314	Grp A
bZIP_98	TraesCS5B02G301900.1 177 -235	TraesCS4A02G209900.1 168 -222	Grp E
bZIP_99	TraesCS5B02G308800.1 329 -383	TraesCS1B02G317100.1 252 -295	Grp A
bZIP_100	TraesCS1B02G193800.1 243 -298	TraesCS1D02G276100.1 215 -243	Grp D
bZIP_101	TraesCS7D02G171300.1 265 -316	TraesCS3A02G293700.1 139 -184	Grp E
bZIP_102	TraesCS4A02G128900.1 155 -197	TraesCS7A02G207100.1 159 -200	Grp F
bZIP_103	TraesCS4A02G135600.2 160 -214	TraesCS1B02G343500.1 211 -256	Grp C
bZIP_104	TraesCS1D02G191000.1 242 -297	TraesCS1D02G306000.1 257 -300	Grp A
bZIP_105	TraesCS5B02G444100.2 212 -262	TraesCS3A02G334100.1 190 -230	Grp F
bZIP_106	TraesCS4A02G183400.1 234 -270	TraesCS2B02G115700.1 179 -225	Grp A
bZIP_107	TraesCS1B02G285800.2 215 -243	TraesCS1D02G332200.1 206 -252	Grp C
bZIP_108	TraesCS6A02G333600.1 271 -316	TraesCS2B02G122700.1 165 -209	Grp I
bZIP_109	TraesCS7A02G170600.1 263 -314	TraesCS7A02G266400.1 171 -229	Grp I
bZIP_110	TraesCS4A02G209900.1 168 -222	TraesCS7A02G268700.1 318 -367	Grp I
bZIP_111	TraesCS1B02G317100.1 252 -295	TraesCS3A02G371800.1 307 -355	Grp A
bZIP_112	TraesCS1D02G276100.1 215 -243	TraesCS3A02G372000.1 298 -344	Grp A
bZIP_113	TraesCS3A02G293700.1 139 -184	TraesCS3A02G372200.1 298 -345	Grp A
bZIP_114	TraesCS7A02G207100.1 159 -200	TraesCS3A02G372400.2 261 -295	Grp S
bZIP_115	TraesCS1B02G343500.1 211 -256	TraesCS2B02G165700.1 177 -227	Grp D
bZIP_116	TraesCS1D02G306000.1 257 -300	TraesCS7A02G398400.1 143 -199	GrpB
bZIP_117	TraesCS3A02G334100.1 190 -230	TraesCS5D02G132300.1 163 -221	Grp E
bZIP_118	TraesCS2B02G115700.1 179 -225	TraesCS2B02G523600.1 95 - 140	Grp A
bZIP_119	TraesCS1D02G332200.1 206 -252	TraesCS5D02G148700.1 112 -160	Grp E
bZIP_120	TraesCS2B02G122700.1 165 -209	TraesCS1A02G186000.1 246 -301	Grp I
bZIP_121	TraesCS7A02G266400.1 171 -229	TraesCS2B02G564900.1 106 -149	Grp A
bZIP_122	TraesCS7A02G268700.1 318 -367	TraesCS2A02G352100.1 168 -224	Grp I
bZIP_123	TraesCS3A02G371800.1 307 -355	TraesCS5A02G440400.1 204 -254	Grp C
bZIP_124	TraesCS3A02G372000.1 298 -344	TraesCS4D02G316900.1 110 -164	Grp I
bZIP_125	TraesCS3A02G372200.1 298 -345	TraesCS6B02G198700.1 82 - 128	Grp S
bZIP_126	TraesCS3A02G372400.2 261 -295	TraesCS2A02G099400.1 179 -225	Grp A
bZIP_127	TraesCS2B02G165700.1 177 -227	TraesCS3D02G148200.1 175 -225	Grp D
bZIP_128	TraesCS7A02G398400.1 143 -199	TraesCS2A02G105700.1 163 -207	Grp I
bZIP_129	TraesCS5D02G132300.1 163 -221	TraesCS5A02G491600.1 102 -156	Grp I
bZIP_130	TraesCS2B02G523600.1 95 - 140	TraesCS1A02G306300.1 254 -297	Grp A
bZIP_131	TraesCS5D02G148700.1 112 -160	TraesCS2D02G495700.1 111 -156	Grp A
bZIP_132	TraesCS1A02G186000.1 246 -301	TraesCS1A02G329900.1 211 -249	Grp C
bZIP_133	TraesCS2B02G564900.1 106 -149	TraesCS2D02G098700.1 179 -225	Grp A
bZIP_134	TraesCS5D02G178800.1 179 -207	TraesCS2D02G105400.1 163 -207	Grp E
bZIP_135	TraesCS2A02G352100.1 168 -224	TraesCS2D02G105400.2 163 -207	Grp I
bZIP_136	TraesCS5A02G440400.1 204 -254	TraesCS6B02G364000.1 272 -317	Grp A
bZIP_137	TraesCS4D02G316900.1 110 -164	TraesCS2D02G536800.1 109 -152	Grp A
bZIP_138	TraesCS6B02G198700.1 82 - 128	TraesCS2A02G495400.1 111 -156	Grp A

bZIP_139	TraesCS2A02G099400.1	179 -225	TraesCS7B02G075600.1	260 -311	Grp A
bZIP_140	TraesCS3D02G148200.1	175 -225	TraesCS2D02G144300.1	177 -227	Grp D
bZIP_141	TraesCS2A02G105700.1	163 -207	TraesCS2A02G534200.1	107 -150	Grp A
bZIP_142	TraesCS1A02G276600.1	215 -243	TraesCS2A02G534300.1	94 - 137	Grp A
bZIP_143	TraesCS5A02G491600.1	102 -156	TraesCS4B02G113400.1	168 -222	Grp E
bZIP_144	TraesCS1A02G306300.1	254 -297	TraesCS7B02G114300.1	164 -205	Grp D
bZIP_145	TraesCS2D02G495700.1	111 -156	TraesCS3B02G167500.1	163 -212	Grp D
bZIP_146	TraesCS1A02G329900.1	211 -249	TraesCS5A02G124600.1	163 -221	Grp E
bZIP_147	TraesCS2D02G098700.1	179 -225	TraesCS5A02G143300.1	112 -160	Grp E
bZIP_148	TraesCS2D02G105400.1	163 -207	TraesCS4B02G169600.1	160 -214	Grp I
bZIP_149	TraesCS2D02G105400.2	163 -207	TraesCS3D02G293500.1	144 -189	Grp D
bZIP_150	TraesCS6B02G364000.1	272 -317	TraesCS7B02G166100.1	175 -233	Grp I
bZIP_151	TraesCS2D02G536800.1	109 -152	TraesCS4B02G175800.1	155 -197	Grp A
bZIP_152	TraesCS2A02G495400.1	111 -156	TraesCS5B02G124200.1	163 -221	Grp E
bZIP_153	TraesCS7B02G075600.1	260 -311	TraesCS5B02G142200.1	112 -160	Grp D
bZIP_154	TraesCS2D02G144300.1	177 -227	TraesCS3D02G327600.1	192 -232	Grp D
bZIP_155	TraesCS2A02G534200.1	107 -150	TraesCS3D02G330300.1	267 -311	Grp A
bZIP_156	TraesCS2A02G534300.1	94 - 137	TraesCS3A02G131900.1	175 -209	Grp D
bZIP_157	TraesCS4B02G113400.1	168 -222	TraesCS5A02G237200.2	289 -335	Grp A
bZIP_158	TraesCS7B02G114300.1	164 -205	TraesCS3D02G364900.1	306 -354	Grp A
bZIP_159	TraesCS3B02G167500.1	163 -212	TraesCS5A02G299400.1	177 -235	Grp I
bZIP_160	TraesCS5A02G124600.1	163 -221	TraesCS4B02G320400.1	245 -299	Grp I
bZIP_161	TraesCS4B02G135000.1	260 -296	TraesCS5A02G308400.1	372 -426	Grp E
bZIP_162	TraesCS5A02G143300.1	112 -160	TraesCS6D02G160200.1	81 - 127	Grp S
bZIP_163	TraesCS4B02G169600.1	160 -214	TraesCS5B02G235600.1	287 -337	Grp A
bZIP_164	TraesCS3D02G293500.1	144 -189	TraesCS7D02G527500.1	95 - 148	Grp A
bZIP_165	TraesCS7B02G166100.1	175 -233	TraesCS1B02G323600.1	74 - 119	Grp F
bZIP_166	TraesCS4B02G175800.1	155 -197	TraesCS1D02G312200.1	74 - 119	Grp D
bZIP_167	TraesCS5B02G124200.1	163 -221	TraesCS3A02G371900.1	299 -345	Grp A
bZIP_168	TraesCS5A02G174200.1	180 -208	TraesCS4D02G335000.1	109 -158	Grp A
bZIP_169	TraesCS5B02G142200.1	112 -160	TraesCS7A02G542700.1	95 - 148	Grp A
bZIP_170	TraesCS3D02G327600.1	192 -232	TraesCS5A02G508600.1	109 -158	Grp A
bZIP_171	TraesCS3D02G330300.1	267 -311	TraesCS1A02G311900.1	73 - 118	Grp D
bZIP_172	TraesCS3A02G131900.1	175 -209	TraesCS5B02G017700.1	88 - 134	Grp D
bZIP_173	TraesCS5A02G237200.2	289 -335	TraesCS2B02G489900.1	60 - 115	Grp A
bZIP_174	TraesCS3D02G364900.1	306 -354	TraesCS4B02G338700.1	109 -158	Grp A
bZIP_175	TraesCS3D02G365200.3	268 -302	TraesCS2A02G140900.1	179 -227	Grp D
bZIP_176	TraesCS3D02G365200.5	265 -299	TraesCS5D02G025800.1	90 - 135	Grp D
bZIP_177	TraesCS5A02G299400.1	177 -235	TraesCS5A02G020700.1	117 -161	Grp D
bZIP_178	TraesCS4B02G320400.1	245 -299	TraesCS3D02G365500.1	301 -347	Grp A
bZIP_179	TraesCS5A02G308400.1	372 -426	TraesCS7D02G518100.1	93 - 136	Grp D
bZIP_180	TraesCS6D02G160200.1	81 - 127	TraesCS7B02G447900.1	98 - 141	Grp S
bZIP_181	TraesCS5B02G235600.1	287 -337	TraesCS7A02G420400.1	158 -201	Grp S
bZIP_182	TraesCS7D02G527500.1	95 - 148	TraesCS7A02G530300.1	96 - 139	Grp F
bZIP_183	TraesCS1B02G323600.1	74 - 119	TraesCS3D02G365000.1	315 -359	Grp A
bZIP_184	TraesCS1D02G312200.1	74 - 119	TraesCS5D02G447500.2	160 -206	Grp C
bZIP_185	TraesCS3A02G371900.1	299 -345	TraesCS5B02G444100.1	159 -205	Grp C
bZIP_186	TraesCS4D02G335000.1	109 -158	TraesCS3A02G293700.2	178 -219	Grp D

bZIP_187	TraesCS7A02G542700.1 95 - 148	TraesCS5A02G440400.2 153 -199	Grp C
bZIP_188	TraesCS5A02G508600.1 109 -158	TraesCS5A02G405200.1 48 - 98	Grp S
bZIP_189	TraesCS1A02G311900.1 73 - 118	TraesCS4A02G120500.1 23 - 83	Grp S
bZIP_190	TraesCS5B02G017700.1 88 - 134	TraesCS5D02G183500.1 30 - 78	Grp S
bZIP_191	TraesCS2B02G489900.1 60 - 115	TraesCS4B02G184500.1 23 - 83	Grp S
bZIP_192	TraesCS4B02G338700.1 109 -158	TraesCS5A02G179000.1 30 - 78	Grp S
bZIP_193	TraesCS2A02G140900.1 179 -227	TraesCS5B02G176700.1 30 - 80	Grp C
bZIP_194	TraesCS5D02G025800.1 90 - 135	TraesCS6A02G096300.1 37 - 78	Grp S
bZIP_195	TraesCS5A02G020700.1 117 -161	TraesCS6B02G124700.1 38 - 79	Grp S
bZIP_196	TraesCS3D02G365500.1 301 -347	TraesCS3D02G203300.1 32 - 85	Grp S
bZIP_197	TraesCS7D02G518100.1 93 - 136	TraesCS3B02G226200.1 27 - 79	Grp S
bZIP_198	TraesCS7B02G447900.1 98 - 141	TraesCS6D02G087400.1 39 - 80	Grp S
bZIP_199	TraesCS7A02G420400.1 158 -201	TraesCS1B02G091500.1 28 - 81	Grp S
bZIP_200	TraesCS7A02G530300.1 96 - 139	TraesCS1D02G075500.1 28 - 81	Grp S
bZIP_201	TraesCS3D02G365000.1 315 -359	TraesCS1B02G127400.1 48 - 77	Grp S
bZIP_202	TraesCS5D02G447500.2 160 -206	TraesCS1D02G105300.1 48 - 86	Grp S
bZIP_203	TraesCS5B02G444100.1 159 -205	TraesCS4A02G126300.1 50 - 91	Grp D
bZIP_204	TraesCS3A02G293700.2 178 -219	TraesCS1A02G072600.1 28 - 81	Grp S
bZIP_205	TraesCS5A02G440400.2 153 -199	TraesCS2B02G113200.2 51 - 92	Grp F
bZIP_206	TraesCS5A02G405200.1 48 - 98	TraesCS1A02G096300.1 49 - 78	Grp S
bZIP_207	TraesCS4A02G120500.1 23 - 83	TraesCS5D02G100700.1 30 - 78	Grp S
bZIP_208	TraesCS5D02G183500.1 30 - 78	TraesCS4D02G316900.2 19 - 66	Grp I
bZIP_209	TraesCS4B02G184500.1 23 - 83	TraesCS2A02G097500.1 48 - 89	Grp F
bZIP_210	TraesCS5A02G179000.1 30 - 78	TraesCS3D02G194800.1 46 - 86	Grp D
bZIP_211	TraesCS5B02G176700.1 30 - 80	TraesCS2D02G096800.1 48 - 89	Grp F
bZIP_212	TraesCS6A02G096300.1 37 - 78	TraesCS5A02G088300.1 30 - 78	Grp S
bZIP_213	TraesCS6B02G124700.1 38 - 79	TraesCS5B02G094300.1 30 - 78	Grp S
bZIP_214	TraesCS3D02G203300.1 32 - 85	TraesCS3B02G220400.1 46 - 86	Grp D
bZIP_215	TraesCS3B02G226200.1 27 - 79	TraesCS4B02G178600.1 50 - 91	Grp D
bZIP_216	TraesCS6D02G087400.1 39 - 80	TraesCS3A02G190700.1 46 - 86	Grp D
bZIP_217	TraesCS1B02G091500.1 28 - 81	TraesCS3A02G200600.1 33 - 79	Grp S
bZIP_218	TraesCS1D02G075500.1 28 - 81	TraesCS4A02G126300.2 53 - 92	Grp D
bZIP_219	TraesCS1B02G127400.1 48 - 77	TraesCS4D02G115200.1 127- 189	Grp G
bZIP_220	TraesCS1D02G105300.1 48 - 86	TraesCS3D02G129800.1 88 - 149	Grp H
bZIP_221	TraesCS4A02G126300.1 50 - 91	TraesCS4D02G185500.1 23 - 83	Grp S
bZIP_222	TraesCS1A02G072600.1 28 - 81	TraesCS3B02G360900.1 109- 157	Grp D
bZIP_223	TraesCS2B02G113200.2 51 - 92	TraesCS3B02G411300.1 168- 227	Grp A
bZIP_224	TraesCS1A02G096300.1 49 - 78	TraesCS4D02G020600.1 55 - 99	Grp C
bZIP_225	TraesCS5D02G100700.1 30 - 78	TraesCS4D02G110900.1 167- 221	Grp E
bZIP_226	TraesCS4D02G316900.2 19 - 66	TraesCS4D02G171700.2 160- 214	Grp I
bZIP_227	TraesCS2A02G097500.1 48 - 89	TraesCS4D02G177700.1 153- 195	Grp A
bZIP_228	TraesCS3D02G194800.1 46 - 86	TraesCS4D02G180200.1 50 - 91	Grp D
bZIP_229	TraesCS2D02G096800.1 48 - 89	TraesCS3B02G328400.1 144- 189	Grp D
bZIP_230	TraesCS5A02G088300.1 30 - 78	TraesCS3B02G365100.1 192- 232	Grp D
bZIP_231	TraesCS5B02G094300.1 30 - 78	TraesCS3B02G368300.1 273- 317	Grp A
bZIP_232	TraesCS3B02G220400.1 46 - 86	TraesCS3B02G404200.1 306- 362	Grp A
bZIP_233	TraesCS4B02G178600.1 50 - 91	TraesCS3B02G404300.1 307- 355	Grp A
bZIP_234	TraesCS3A02G190700.1 46 - 86	TraesCS3B02G404400.1 307- 351	Grp A

bZIP_235	TraesCS3A02G200600.1	33 - 79	TraesCS3B02G404600.1	307- 354	Grp A
bZIP_236	TraesCS4A02G126300.2	53 - 92	TraesCS3B02G404500.1	308- 351	Grp A
bZIP_237	TraesCS4D02G115200.1	127- 189	TraesCS4D02G180200.4	53 - 92	Grp D
bZIP_238	TraesCS3D02G129800.1	88 - 149			
bZIP_239	TraesCS4D02G185500.1	23 - 83			
bZIP_240	TraesCS3B02G360900.1	109- 157			
bZIP_241	TraesCS3B02G411300.1	168- 227			
bZIP_242	TraesCS3B02G404800.4	244- 279			
bZIP_243	TraesCS4D02G020600.1	55 - 99			
bZIP_244	TraesCS4D02G110900.1	167- 221			
bZIP_245	TraesCS4D02G129900.1	232- 268			
bZIP_246	TraesCS4D02G171700.2	160- 214			
bZIP_247	TraesCS4D02G177700.1	153- 195			
bZIP_248	TraesCS4D02G180200.1	50 - 91			
bZIP_249	TraesCS3B02G328400.1	144- 189			
bZIP_250	TraesCS3B02G365100.1	192- 232			
bZIP_251	TraesCS3B02G368300.1	273- 317			
bZIP_252	TraesCS3B02G404200.1	306- 362			
bZIP_253	TraesCS3B02G404300.1	307- 355			
bZIP_254	TraesCS3B02G404400.1	307- 351			
bZIP_255	TraesCS3B02G404600.1	307- 354			
bZIP_256	TraesCS3B02G404800.2	261- 295			
bZIP_257	TraesCS3B02G404500.1	308- 351			
bZIP_258	TraesCS4D02G180200.4	53 - 92			

*Oryza sativa* (rice)

Gene ID	Group
LOC_Os02g03580	244-306 GrpG
LOC_Os02g58670	67-127 GrpA
LOC_Os03g13614	299-361 GrpG
LOC_Os03g56010	65-114 GrpS
LOC_Os03g59460	200-226 GrpG
LOC_Os05g49420	245-307 GrpG
LOC_Os07g03220	72-122 GrpS
LOC_Os07g10890	265-327 GrpG
LOC_Os11g05640	124-186 GrpG
LOC_Os12g13170	294-356 GrpG
LOC_Os12g43790	60-108 GrpS
LOC_Os01g07880	109-170 GrpH
LOC_Os01g46970	224-285 GrpG
LOC_Os02g10860	172-233 GrpH
LOC_Os03g19370	22-71 GrpS
LOC_Os06g39960	104-163 GrpH
LOC_Os07g08420	235-289 GrpC
LOC_Os08g38020	119-178 GrpS
LOC_Os09g29820	76-131 GrpS
LOC_Os09g31390	201-243 GrpD

*Arabidopsis thaliana* (Arabidopsis)

Gene ID	Group
AT_Q9C5Q2_192_234	GrpA
AT_Q9LES3_227_270	GrpA
AT_Q84JK2_216_265	GrpA
AT_Q7PCC6_164_213	GrpA
AT_Q9M7Q5_313_369	GrpA
AT_Q9M7Q3_374_430	GrpA
AT_Q9M7Q2_353_405	GrpA
AT_Q9SJN0_357_405	GrpA
AT_Q8RYD6_249_301	GrpA
AT_P42777_186_247	GrpA
AT_Q9FMM7_294_344	GrpD
AT_Q9SI15_31_82	GrpS
AT_O65683_26_67	GrpS
AT_C0Z2L5_41_81	GrpS
AT_Q9LZP8_25_83	GrpS
AT_Q9FMC2_72_118	GrpS
AT_Q9CA46_46_100	GrpS
AT_Q9FUD3_120_166	GrpC
AT_O22763_215_269	GrpC
AT_Q9M1G6_230_283	GrpC

LOC_Os01g64730 184-242	GrpA	AT_B9DGI8_152_199	GrpC
LOC_Os02g49560 78-132	GrpS	AT_Q9LQ65_49_96	GrpS
LOC_Os04g54474 104-144	GrpD	AT_Q501B2_304_365	GrpG
LOC_Os05g34050 172-232	GrpB	AT_Q84LG2_293_355	GrpG
LOC_Os05g36160 186-237	GrpA	AT_P42774_220_282	GrpG
LOC_Os05g41540 69-117	GrpF	AT_P42775_247_309	GrpG
LOC_Os06g45140 134-186	GrpC	AT_P42776_257_319	GrpG
LOC_Os07g44950 111-171	GrpB	AT_P43273_46_86	GrpD
LOC_Os08g07970 107-142	GrpD	AT_Q39163_46_86	GrpD
LOC_Os08g26880 36-95	GrpS	AT_Q39140_46_86	GrpD
LOC_Os09g13570 29-77	GrpS	AT_Q93XM6_177_218	GrpD
LOC_Os01g17260 44-85	GrpD	AT_E3VNM4_161_191	GrpD
LOC_Os01g64020 228-259	GrpD	AT_Q9SX27_166_206	GrpD
LOC_Os02g03960 36-78	GrpS	AT_Q93ZE2_92_134	GrpD
LOC_Os02g07840 123-172	GrpC	AT_Q39237_82_113	GrpD
LOC_Os02g10140 134-174	GrpD	AT_Q39162_78_108	GrpD
LOC_Os02g16680 142-191	GrpC	AT_Q9M2K4_204_248	GrpE
LOC_Os05g37170 230-260	GrpD	AT_O22873_150_208	GrpD
LOC_Os06g41770 210-267	GrpB	AT_Q04088_203_255	GrpD
LOC_Os06g42690 69-128	GrpS	AT_Q9MA75_196_254	GrpD
LOC_Os06g50480 96-143	GrpA	AT_O24646_86_147	GrpH
LOC_Os06g50600 96-152	GrpA	AT_Q8W191_77_136	GrpF
LOC_Os06g50830 96-152	GrpA	AT_O22208_227_288	GrpB
LOC_Os09g36910 125-178	GrpA	AT_Q9LXX4_172_231	GrpB
LOC_Os12g37410 25-84	GrpS	AT_Q9SG86_192_249	GrpB
LOC_Os12g40920 115-169	GrpC		
LOC_Os01g11350 190-240	GrpE		
LOC_Os01g36220 42-99	GrpS		
LOC_Os01g55150 139-184	GrpE		
LOC_Os01g59350 187-222	GrpD		
LOC_Os01g59760 265-308	GrpA		
LOC_Os01g64000 304-350	GrpA		
LOC_Os02g09830 74-120	GrpS		
LOC_Os02g14910 142-192	GrpE		
LOC_Os02g52780 277-327	GrpA		
LOC_Os03g03550 277-335	GrpI		
LOC_Os03g20310 49-79	GrpD		
LOC_Os03g20650 162-203	GrpA		
LOC_Os03g21800 134-180	GrpI		
LOC_Os03g47200 52-93	GrpS		
LOC_Os03g58250 234-285	GrpC		
LOC_Os04g41820 270-328	GrpI		
LOC_Os05g03860 25-79	GrpS		
LOC_Os05g41070 265-308	GrpA		
LOC_Os06g10880 244-296	GrpA		
LOC_Os06g15480 95-135	GrpD		
LOC_Os06g41100 149-177	GrpD		
LOC_Os07g48180 175-220	GrpI		

LOC_Os07g48660 183-225	GrpA
LOC_Os07g48820 50-91	GrpD
LOC_Os08g36790 243-295	GrpA
LOC_Os08g43090 322-380	GrpI
LOC_Os08g43600 72-122	GrpA
LOC_Os09g10840 189-218	GrpD
LOC_Os09g28310 297-347	GrpA
LOC_Os09g34060 183-241	GrpI
LOC_Os10g38820 248-306	GrpI
LOC_Os11g05480 180-209	GrpD
LOC_Os11g06170 162-209	GrpI
LOC_Os12g06520 164-221	GrpI
LOC_Os12g05680 184-212	GrpD
LOC_Os05g41280 24-63	GrpD
LOC_Os06g50310 97-142	GrpF

**Supplementary Table S3. bZIP transcription factor proteins - proposed functionalities, processes and cellular components based on Gene Ontology results.**

<b>bZIP</b>	<b>Gene</b>	<b>Functional name</b>	<b>Molecular function</b>	<b>Biological process</b>	<b>Cellular component</b>
ABF2	TraesCS5D02G244500	bZIP transcription factor TRAB1	transcription regulatory region sequence-specific DNA binding,  DNA-binding transcription factor activity	regulation of transcription, DNA-templated, abscisic acid-activated signalling pathway, positive regulation of transcription	nucleus
ABF4	TraesCS5A02G237200	bZIP transcription factor TRAB1	transcription regulatory region sequence-specific DNA binding  DNA-binding transcription factor activity	abscisic acid-activated signalling pathway  regulation of transcription, DNA-templated, positive regulation of transcription	nucleus
ABI5	TraesCS1A02G306300	ABSCISIC ACID-INSENSITIVE 5-like protein 2	DNA-binding transcription factor activity  DNA binding	positive regulation of transcription,  DNA-templated  response to abscisic acid, abscisic acid-activated signalling pathway	nucleus
EMBP-1	TraesCS2B02G269600	DNA-binding protein EMBP-1	DNA-binding transcription factor activity,  sequence-specific DNA binding	regulation of transcription, DNA-templated abscisic acid-activated signalling pathway	nucleus
VIP1	TraesCS5B02G124200	transcription factor VIP1	nucleic acid binding  mitogen-activated protein kinase binding  chromatin binding  DNA-binding transcription factor activity  sequence-specific DNA binding	defence response, thigmotropism response to osmotic stress, osmosensory signalling pathway,  sulphate transport, DNA mediated transformation  import into nucleus, negative regulation of cell differentiation	nucleus  cytosol

			protein self- association		
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