

Table 3. Basic information of the PgMYB gene family.

Gene ID	Name	No. of Amino Acids	Mol. wt (kDa)	Isoelectric Point	Instability Index	Aliphatic Index	Grand Average of Hydropathicity	Subcellular Localization
XP_031371385.1	PgMYB1	356	39.91	6.12	55.2	73.46	-0.515	4
XP_031371476.1	PgMYB2	280	32.67	6.68	73.97	53.64	-1.163	4
XP_031371487.1	PgMYB3	270	30.69	6.61	51.37	80.63	-0.667	4
XP_031371488.1	PgMYB4	268	30.55	6.61	51.68	80.49	-0.685	4
XP_031371489.1	PgMYB5	267	30.21	5.82	59.34	79.33	-0.750	4
XP_031371490.1	PgMYB6	267	30.21	5.82	59.34	79.33	-0.750	4
XP_031371491.1	PgMYB7	267	30.21	5.82	59.34	79.33	-0.750	4
XP_031371585.1	PgMYB8	264	29.70	8.08	39.37	81.67	-0.597	4
XP_031371693.1	PgMYB9	257	28.89	7.62	48.25	87.24	-0.525	4
XP_031371757.1	PgMYB10	263	29.74	6.05	70.82	68.63	-0.833	4
XP_031371778.1	PgMYB11	235	26.61	5.40	45.40	78.85	-0.627	4
XP_031371802.1	PgMYB12	298	32.45	6.74	47.21	67.79	-0.505	4
XP_031371883.1	PgMYB13	272	31.45	8.80	50.53	74.60	-0.760	4
XP_031371924.1	PgMYB14	270	30.81	8.02	58.45	64.00	-0.859	4
XP_031372003.1	PgMYB15	310	35.36	5.55	57.77	63.84	-0.769	1 2 4
XP_031372004.1	PgMYB16	309	35.29	5.55	57.93	63.72	-0.776	4
XP_031372474.1	PgMYB17	1042	114.47	5.05	63.1	65.92	-0.673	4
XP_031372475.1	PgMYB18	1042	114.47	5.05	63.1	65.92	-0.673	4
XP_031372476.1	PgMYB19	1039	114.10	5.03	62.7	65.74	-0.676	4
XP_031372736.1	PgMYB20	128	15.15	9.96	65.69	68.67	-1.077	4
XP_031372772.1	PgMYB21	1218	138.39	8.16	42.35	88.52	-0.381	1
XP_031372773.1	PgMYB22	1158	131.56	7.72	42.62	90.16	-0.355	4
XP_031372774.1	PgMYB23	1019	115.37	7.16	41.64	89.55	-0.356	1 3 4
XP_031372985.1	PgMYB24	297	33.13	5.84	60.93	74.92	-0.562	4
XP_031373258.1	PgMYB25	274	30.16	5.3	69.96	70.15	-0.785	1 4
XP_031373439.1	PgMYB26	347	38.08	6.14	59.4	63.03	-0.583	4
XP_031374787.1	PgMYB27	312	34.89	8.12	59.94	65.71	-0.648	4
XP_031374796.1	PgMYB28	309	34.52	8.42	60.42	66.34	-0.650	4
XP_031375263.1	PgMYB29	344	38.86	5.44	64.67	69.51	-0.838	4
XP_031375310.1	PgMYB30	339	38.34	5.79	50.69	76.81	-0.653	4
XP_031375741.1	PgMYB31	313	35.39	5.74	45.06	68.18	-0.629	4
XP_031376297.1	PgMYB32	285	31.99	5.14	51.12	71.47	-0.695	4
XP_031376514.1	PgMYB33	213	24.46	9.02	62.22	62.3	-1.102	4
XP_031376586.1	PgMYB34	366	41.90	5.50	56.31	56.28	-1.065	4
XP_031376587.1	PgMYB35	334	38.03	5.14	58.2	54.37	-1.080	4
XP_031376795.1	PgMYB36	282	30.55	6.45	57.83	54.82	-0.651	4
XP_031376962.1	PgMYB37	326	36.60	5.82	49.46	63.16	-0.924	4
XP_031377075.1	PgMYB38	563	61.60	5.55	52.64	61.17	-0.706	4
XP_031377076.1	PgMYB39	563	61.60	5.55	52.64	61.17	-0.706	4
XP_031377077.1	PgMYB40	563	61.60	5.55	52.64	61.17	-0.706	4
XP_031377078.1	PgMYB41	563	61.60	5.55	52.64	61.17	-0.706	4
XP_031377086.1	PgMYB42	405	43.47	5.42	41.44	65.78	-0.536	4
XP_031377218.1	PgMYB43	548	60.07	6.82	66.51	67.48	-0.653	4
XP_031377227.1	PgMYB44	466	51.02	9.17	68.58	64.7	-0.653	4
XP_031377496.1	PgMYB45	309	34.67	7.58	50.3	62.56	-0.800	4
XP_031377704.1	PgMYB46	362	40.03	8.60	58.24	67.90	-0.537	4
XP_031377709.1	PgMYB47	320	35.37	8.94	57.24	70.72	-0.552	4
XP_031377882.1	PgMYB48	280	31.49	5.82	47.9	82.57	-0.520	4
XP_031378012.1	PgMYB49	268	30.02	6.76	47.02	72.09	-0.744	4
XP_031378029.1	PgMYB50	335	36.71	6.24	67.68	70.45	-0.740	4
XP_031378316.1	PgMYB51	272	30.50	9.45	51.19	74.19	-0.780	4
XP_031378328.1	PgMYB52	321	36.41	5.83	58.11	60.22	-0.756	1 4
XP_031378550.1	PgMYB53	316	35.63	7.59	51.74	77.82	-0.593	1 4
XP_031378551.1	PgMYB54	277	31.30	7.07	51.75	69.42	-0.837	4
XP_031378772.1	PgMYB55	225	25.93	9.08	55.42	71.11	-0.836	4
XP_031378943.1	PgMYB56	269	30.33	5.25	42.51	70.33	-0.606	4
XP_031379312.1	PgMYB57	322	34.99	6.39	65.69	66.68	-0.428	4
XP_031379372.1	PgMYB58	339	37.58	8.12	57.93	71.18	-0.641	4

XP_031379656.1	PgMYB59	313	35.17	6.51	49.07	69.20	-0.705	4
XP_031379750.1	PgMYB60	384	42.95	6.27	68.42	72.68	-0.661	4
XP_031379785.1	PgMYB61	546	62.47	6.21	42.35	52.03	-1.165	4
XP_031379786.1	PgMYB62	521	59.21	6.23	42.84	50.98	-1.202	4
XP_031379915.1	PgMYB63	199	22.84	9.48	65.69	66.73	-0.917	4
XP_031380057.1	PgMYB64	283	32.69	7.62	62.82	63.75	-0.855	4
XP_031380854.1	PgMYB65	263	29.56	9.07	50.44	72.4	-0.718	4
XP_031380977.1	PgMYB66	359	39.77	5.43	50.01	64.15	-0.573	4
XP_031381006.1	PgMYB67	534	58.16	5.89	64.56	66.22	-0.689	4
XP_031381106.1	PgMYB68	274	30.86	5.47	59.81	62.30	-0.725	4
XP_031381905.1	PgMYB69	255	27.65	6.10	54.28	63.14	-0.733	1 4
XP_031382083.1	PgMYB70	279	31.88	8.56	44.92	70.25	-0.795	4
XP_031382504.1	PgMYB71	200	23.09	6.44	49.86	69.30	-0.784	4
XP_031382573.1	PgMYB72	314	33.93	9.42	57.29	67.13	-0.540	4
XP_031382691.1	PgMYB73	440	48.71	9.28	59.42	64.73	-0.547	4
XP_031382705.1	PgMYB74	440	48.71	9.28	59.42	64.73	-0.547	4
XP_031382964.1	PgMYB75	275	31.42	5.58	50.36	72.69	-0.650	4
XP_031382966.1	PgMYB76	272	31.13	5.58	50.37	72.43	-0.679	4
XP_031383000.1	PgMYB77	283	32.32	6.55	67.6	64.13	-0.759	4
XP_031383445.1	PgMYB78	350	38.69	8.36	54.58	66.63	-0.665	4
XP_031384323.1	PgMYB79	395	43.75	7.51	64.5	65.27	-0.642	4
XP_031384680.1	PgMYB80	295	33.47	6.08	73.25	75.02	-0.709	4
XP_031384702.1	PgMYB81	515	57.34	6.19	44.63	58.37	-0.742	4
XP_031384703.1	PgMYB82	511	56.85	6.30	44.91	58.06	-0.745	4
XP_031384860.1	PgMYB83	292	32.92	5.32	59.74	75.14	-0.634	4
XP_031385396.1	PgMYB84	330	35.41	8.94	62.21	70.82	-0.401	1 4
XP_031385440.1	PgMYB85	364	41.09	6.59	59.19	68.63	-0.727	4
XP_031385441.1	PgMYB86	320	36.33	5.86	53.96	76.12	-0.651	4
XP_031385592.1	PgMYB87	328	36.54	6.07	44.15	67.53	-0.686	4
XP_031386277.1	PgMYB88	455	50.98	8.23	58.64	65.60	-0.811	1 4
XP_031386278.1	PgMYB89	455	50.98	8.23	58.64	65.60	-0.811	1 4
XP_031386279.1	PgMYB90	455	50.98	8.23	58.64	65.60	-0.811	1 4
XP_031386280.1	PgMYB91	455	51.01	8.23	57.68	64.75	-0.815	1 4
XP_031387342.1	PgMYB92	287	30.35	6.72	59.01	63.24	-0.648	4
XP_031387343.1	PgMYB93	287	30.35	6.72	59.01	63.24	-0.648	4
XP_031387344.1	PgMYB94	287	30.35	6.72	59.01	63.24	-0.648	4
XP_031387608.1	PgMYB95	261	29.84	5.45	62.44	56.40	-0.836	4
XP_031387609.1	PgMYB96	196	22.16	4.81	62.97	51.28	-0.867	4
XP_031387610.1	PgMYB97	267	30.42	5.45	60.63	56.59	-0.837	4
XP_031387948.1	PgMYB98	223	25.84	8.72	47.15	79.15	-0.757	4
XP_031387960.1	PgMYB99	306	34.39	8.94	55.61	66.96	-0.762	4
XP_031388462.1	PgMYB100	94	10.55	8.93	63.81	80.96	-0.528	4
XP_031388525.1	PgMYB101	253	28.38	5.57	61.64	64.55	-0.763	4
XP_031389116.1	PgMYB102	233	26.27	9.16	55.75	74.16	-0.562	4
XP_031389838.1	PgMYB103	283	31.74	5.13	53.11	78.59	-0.672	4
XP_031389861.1	PgMYB104	252	28.19	8.49	55.92	75.12	-0.683	4
XP_031389966.1	PgMYB105	261	29.70	8.24	45.33	71.80	-0.750	4
XP_031389987.1	PgMYB106	360	41.01	6.13	54.39	74.50	-0.761	4
XP_031390019.1	PgMYB107	395	43.50	9.42	46.15	62.00	-0.777	4
XP_031390085.1	PgMYB108	203	23.31	9.13	55.62	71.63	-0.924	4
XP_031390203.1	PgMYB109	331	36.47	6.50	55.42	83.38	-0.410	4
XP_031390243.1	PgMYB110	401	44.66	5.61	58.53	67.16	-0.615	4
XP_031390263.1	PgMYB111	496	54.88	9.13	64.58	59.13	-0.892	4
XP_031390345.1	PgMYB112	310	35.25	6.39	63.71	72.32	-0.679	4
XP_031390582.1	PgMYB113	499	55.01	6.52	51.33	70.30	-0.671	4
XP_031390583.1	PgMYB114	475	52.15	6.28	50.98	69.75	-0.637	4
XP_031390609.1	PgMYB115	326	36.60	8.67	62.34	50.89	-0.880	1
XP_031390705.1	PgMYB116	270	30.29	5.91	63.52	74.78	-0.663	4
XP_031390841.1	PgMYB117	494	54.66	6.25	51.31	67.00	-0.730	4
XP_031391498.1	PgMYB118	285	31.87	8.57	58.53	70.25	-0.664	4
XP_031391581.1	PgMYB119	499	55.40	7.47	62.26	82.73	-0.449	4
XP_031391582.1	PgMYB120	497	55.17	7.88	61.36	83.06	-0.449	4
XP_031391583.1	PgMYB121	472	52.41	7.92	62.13	77.33	-0.569	4

XP_031391584.1	PgMYB122	485	53.66	6.64	57.81	76.89	-0.552	4
XP_031391585.1	PgMYB123	483	53.42	7.00	56.86	77.20	-0.552	4
XP_031392303.1	PgMYB124	457	50.97	6.38	47.76	65.6	-0.841	1 4
XP_031393223.1	PgMYB125	337	37.89	5.61	48.29	77.86	-0.578	4
XP_031393246.1	PgMYB126	293	32.43	8.66	49.74	71.67	-0.457	4
XP_031393574.1	PgMYB127	318	35.62	8.55	52.03	68.99	-0.735	4
XP_031393752.1	PgMYB128	279	31.67	8.69	52.19	81.08	-0.653	4
XP_031393848.1	PgMYB129	311	34.84	7.17	46.36	74.37	-0.645	4
XP_031394004.1	PgMYB130	244	27.19	8.77	52.58	64.8	-0.833	4
XP_031394202.1	PgMYB131	273	30.88	6.15	57.46	69.71	-0.722	1 4
XP_031395231.1	PgMYB132	305	34.58	8.82	55.95	61.11	-0.873	4
XP_031395302.1	PgMYB133	310	34.96	5.22	61.92	66.71	-0.741	4
XP_031395457.1	PgMYB134	329	36.37	6.25	62.06	62.89	-0.683	4
XP_031395673.1	PgMYB135	338	37.64	6.45	59.01	73.93	-0.551	4
XP_031395723.1	PgMYB136	249	28.82	9.19	62.61	72.45	-0.772	4
XP_031395956.1	PgMYB137	284	32.26	9.32	43.41	77.61	-0.638	1 4
XP_031395988.1	PgMYB138	534	59.16	6.56	50.86	62.64	-0.671	4
XP_031396052.1	PgMYB139	379	42.43	5.95	50.74	71.27	-0.708	4
XP_031396691.1	PgMYB140	254	29.79	5.87	50.62	71.02	-0.880	4
XP_031396742.1	PgMYB141	383	42.33	8.17	58.9	69.32	-0.620	4
XP_031396760.1	PgMYB142	354	40.51	9.13	59.43	72.82	-0.856	4
XP_031396762.1	PgMYB143	354	40.51	9.13	59.43	72.82	-0.856	4
XP_031396896.1	PgMYB144	254	27.95	9.25	66.46	64.17	-0.703	4
XP_031398107.1	PgMYB145	234	26.95	6.15	68.07	77.91	-0.694	4
XP_031398278.1	PgMYB146	282	32.27	5.27	57.96	67.52	-0.741	4
XP_031398458.1	PgMYB147	289	32.92	9.06	42.35	76.54	-0.488	4
XP_031398997.1	PgMYB148	552	60.5	7.59	55.84	64.75	-0.808	4
XP_031398998.1	PgMYB149	552	60.5	7.59	55.84	64.75	-0.808	4
XP_031398999.1	PgMYB150	552	60.5	7.59	55.84	64.75	-0.808	4
XP_031399664.1	PgMYB151	395	43.71	5.31	47.61	62.73	-0.803	4
XP_031399925.1	PgMYB152	362	40.45	5.95	60.23	73.56	-0.459	4
XP_031399938.1	PgMYB153	302	33.69	5.47	46.15	74.93	-0.698	4
XP_031399944.1	PgMYB154	271	29.99	5.33	59.90	67.34	-0.832	4
XP_031399950.1	PgMYB155	221	25.13	9.49	55.05	64.07	-0.950	4
XP_031399951.1	PgMYB156	212	24.21	9.18	46.40	76.89	-0.738	4
XP_031400148.1	PgMYB157	321	36.16	8.44	55.15	68.38	-0.674	4
XP_031400370.1	PgMYB158	458	51.41	7.15	56.68	71.59	-0.721	4
XP_031400371.1	PgMYB159	457	51.34	7.15	56.78	71.53	-0.727	4
XP_031400372.1	PgMYB160	456	51.25	7.15	57.03	71.91	-0.722	4
XP_031400584.1	PgMYB161	339	37.34	6.60	58.21	67.96	-0.743	4
XP_031400585.1	PgMYB162	339	37.34	6.60	58.21	67.96	-0.743	4
XP_031401828.1	PgMYB163	255	29.51	5.76	59.27	55.45	-0.883	4
XP_031402493.1	PgMYB164	375	41.68	9.11	58.83	54.45	-0.718	1 4
XP_031402494.1	PgMYB165	358	39.76	9.38	58.21	55.95	-0.735	4
XP_031403013.1	PgMYB166	225	25.37	9.45	50.21	75.51	-0.789	4
XP_031403326.1	PgMYB167	188	21.50	9.69	47.62	74.15	-0.914	4
XP_031403532.1	PgMYB168	338	38.13	5.47	53.46	70.38	-0.615	4
XP_031403579.1	PgMYB169	277	31.40	8.85	46.78	67.22	-0.796	4
XP_031403580.1	PgMYB170	256	29.07	8.69	45.22	67.77	-0.844	4
XP_031403581.1	PgMYB171	194	21.78	6.60	49.69	71.86	-0.724	4
XP_031403583.1	PgMYB172	186	21.26	9.51	55.50	69.73	-0.823	4
XP_031403692.1	PgMYB173	364	40.56	8.02	60.47	67.62	-0.612	4
XP_031403914.1	PgMYB174	1516	169.43	5.38	41.51	78.99	-0.406	4
XP_031404042.1	PgMYB175	718	81.15	7.59	52.92	68.48	-0.704	4
XP_031404055.1	PgMYB176	391	43.47	8.46	49.19	71.10	-0.747	44
XP_031404282.1	PgMYB177	692	78.81	6.25	51.48	63.28	-0.759	4
XP_031404413.1	PgMYB178	429	49.16	5.49	54.94	63.17	-0.831	1 4
XP_031404432.1	PgMYB179	319	34.15	8.34	52.42	65.17	-0.579	4
XP_031406094.1	PgMYB180	819	92.26	6.35	54.71	68.27	-0.836	4
XP_031406209.1	PgMYB181	326	37.51	4.92	59.05	66.10	-0.672	4
XP_031406425.1	PgMYB182	219	25.31	8.94	47.05	70.27	-0.811	4
XP_031406969.1	PgMYB183	359	39.86	5.94	65.59	60.36	-0.723	4
XP_031407346.1	PgMYB184	398	43.2	6.24	54.32	58.89	-0.720	4

XP_031407492.1	PgMYB185	274	30.56	9.38	45.95	81.53	-0.555	4
XP_031407840.1	PgMYB186	299	33.93	7.00	53.39	64.95	-0.757	4

1: Cytoplasm, 2: Extracell, 3: Cell membance, 4: Nucleus.