Appendix D Information of Partial nsLTP in Wheat

Name	Locus ID	Len	MW	pI	atoms number	stability	GRAVY	Signal peptide(aa)	Subcellular localization	GPI-anchor
Type 1										no
TaLTP1.1	TraesCS1A01G300300.1	128	12633.88	9.75	1792	unstable	0.48	36	Cell membrane. Cell wall.	no
TaLTP1.2	TraesCS1B01G310400.1	125	12605.88	10.12	1787	unstable	0.413	33	Cell membrane. Cell wall.	no
TaLTP1.4	TraesCS2A01G477700.1	118	11659.6	9.32	1632	stable	0.436	24	Cell membrane. Cell wall.	no
TaLTP1.5	TraesCS2B01G500700.1	117	11602.29	8.73	1601	stable	0.411	19	Cell membrane. Cell wall.	no
TaLTP1.9	TraesCS2D01G476800.1	117	11619.37	8.16	1604	stable	0.462	19	Cell membrane. Cell wall.	no
TaLTP1.11	TraesCS3A01G053000.1	115	11507.41	9.38	1626	stable	0.444	25	Cell wall.	yes
TaLTP1.12	TraesCS3A01G053100.1	115	11488.41	9.38	1624	stable	0.449	25	Cell wall.	yes
TaLTP1.16	TraesCS3B01G062600.1	98	9500.93	9.2	1326	unstable	0.349	-	Cell membrane. Cell wall.	no
TaLTP1.17	TraesCS3B01G062700.1	150	15011.3	8.87	2109	unstable	0.401	-	Cell membrane.	no
TaLTP1.23	TraesCS3B01G063300.1	98	9777.17	7.48	1355	stable	0.427	-	Cell wall.	no
TaLTP1.28	TraesCS3B01G063800.1	98	9686	5.93	1328	unstable	0.38	-	Cell wall.	no
TaLTP1.37	TraesCS3D01G051900.1	106	10725.42	9.2	1495	unstable	0.209	16	Cell wall.	no
TaLTP1.38	TraesCS3D01G052100.1	150	15037.32	9.07	2101	unstable	0.22	-	Cell membrane. Cell wall.	no
TaLTP1.42	TraesCS4A01G194400.1	124	12127.2	9.35	1708	stable	0.44	30	Cell wall.	no
TaLTP1.43	TraesCS4B01G120900.1	124	12226.33	9.35	1724	stable	0.419	30	Cell wall.	no
TaLTP1.45	TraesCS4B01G382200.1	116	11887.2	10.1	1696	unstable	0.43	29	Cell membrane. Cell wall.	no
TaLTP1.48	TraesCS5A01G147400.1	115	12286.33	8.89	1716	unstable	0.063	26	Cell wall.	no
TaLTP1.51	TraesCS5B01G146000.1	116	12257.24	8.72	1710	unstable	0.085	26	Cell membrane. Cell wall.	no
TaLTP1.52	TraesCS5B01G475500.1	149	15013.36	7.54	2098	unstable	0.321	-	Cell wall.	no
TaLTP1.54	TraesCS5B01G475900.1	149	15095.53	7.54	2123	unstable	0.452	-	Cell wall.	no
TaLTP1.56	TraesCS5D01G145300.1	121	12378.59	9.43	1750	stable	0.313	29	Cell wall.	no
TaLTP1.58	TraesCS7A01G345900.1	122	12421.91	3.81	1698	unstable	0.21	28	Cell wall.	no
TaLTP1.59	TraesCS7B01G012800.1	128	13722.02	9.06	1921	stable	0.099	28	Cell wall.	no
TaLTP1.62	TraesCS7D01G333300.1	122	12440.97	3.7	1699	unstable	0.269	28	Cell wall.	no
TaLTP1.63	TraesCSU01G056600.1	98	9575.1	9.2	1342	unstable	0.302	-	Cell membrane. Cell wall.	no
TaLTP1.64	TraesCSU01G056700.1	150	14812.15	9.46	2084	unstable	0.338	-	Cell membrane. Cell wall.	no
TaLTP1.66	TraesCSU01G057000.1	98	9427.83	9.2	1314	unstable	0.309	-	Cell wall.	no
TaLTP1.67	TraesCSU01G057100.1	98	9427.83	9.2	1314	unstable	0.309	-	Cell wall.	no
TaLTP1.68	TraesCSU01G057200.1	98	9427.83	9.2	1314	unstable	0.309	-	Cell wall.	no

TaLTP1.69	TraesCSU01G057300.1	98	9427.83	9.2	1314	unstable	1.309	-	Cell wall.	no
TaLTP1.74	TraesCSU01G176300.1	98	9776.07	5.93	1342	unstable	0.337	-	Cell wall.	no
TaLTP1.79	TraesCSU01G258000.1	117	11384.36	9.32	1608	unstable	0.52	25	Cell wall.	no
Type 2										
TaLTP2.2	TraesCS1A01G175200.1	85	8676.15	9.25	1206	stable	0.319	19	Cell membrane.	no
TaLTP2.8	TraesCS1B01G189400.1	91	9160.76	9.35	1278	stable	0.408	24	Cell membrane.	no
TaLTP2.13	TraesCS1B01G394600.1	144	15026.3	9.56	2092	unstable	-0.246	-	Cell membrane.	no
TaLTP2.17	TraesCS1D01G380800.1	96	9949.86	8.67	1396	unstable	0.382	28	Cell membrane.	no
TaLTP2.22	TraesCS2A01G534000.1	103	11155.37	8.08	1575	unstable	0.531	23	Cell membrane.	no
TaLTP2.24	TraesCS2B01G564300.1	104	11249.45	7.44	1579	unstable	0.468	21	Cell membrane.	no
TaLTP2.25	TraesCS2D01G510800.1	100	10786.63	8.13	1512	stable	0.058	23	Cell membrane.	no
TaLTP2.27	TraesCS3A01G261600.1	95	10370.25	9.53	1448	unstable	0.084	21	Cell membrane.	no
TaLTP2.28	TraesCS3B01G022200.1	98	10028.88	9.08	1399	unstable	0.576	30	Cell membrane.	no
TaLTP2.31	TraesCS3D01G261600.1	95	10401.35	9.57	1459	unstable	0.033	21	Cell membrane. Cell wall.	no
TaLTP2.34	TraesCS4B01G393400.1	94	9919.7	8.47	1382	unstable	0.262	27	Cell membrane.	no
TaLTP2.36	TraesCS5A01G554400.1	64	6701.8	8.57	920	unstable	0.072	-	Cell membrane.	no
TaLTP2.38	TraesCS5B01G531200.1	98	10064.72	9.05	1396	unstable	0.12	31	Cell membrane.	no
TaLTP2.41	TraesCSU01G033000.1	91	9331.11	9.01	1313	unstable	0.514	24	Cell membrane.	yes
TaLTP2.42	TraesCSU01G033100.1	81	8208.69	8.16	1139	unstable	0.506	-	Cell membrane.	no
Type c										
TaLTPc.1	TraesCS5A01G313100.1	103	10276.15	7.49	1461	unstable	0.544	32	Cell membrane.	no
TaLTPc.2	TraesCS5B01G314000.1	111	11174.2	8.74	1586	unstable	0.345	32	Cell membrane.	no
TaLTPc.3	TraesCS5D01G319800.1	102	10262.12	5.99	1455	unstable	0.521	31	Cell membrane.	no
TaLTPc.4	TraesCS7A01G269700.1	95	9601.24	8.18	1346	unstable	0.533	29	Cell membrane.	no
TaLTPc.5	TraesCS7B01G167900.1	95	9482.12	8.18	1332	unstable	0.587	29	Cell membrane.	no
TaLTPc.6	TraesCS7D01G270200.1	144	15906.32	11.75	2219	unstable	-0.46	-	Nucleus.	no
Type d1										
TaLTPd1.2	TraesCS2A01G440400.1	84	9064.83	8.61	1282	unstable	0.543	21	Cell membrane. Nucleus.	no
TaLTPd1.5	TraesCS2B01G460400.1	105	11189.13	7.59	1558	unstable	0.233	27	Cell membrane.	no
TaLTPd1.11	TraesCS2B01G461000.1	91	9548.23	8.14	1321	unstable	0.191	-	Cell membrane.	no
TaLTPd1.16	TraesCS2D01G438500.1	105	10914.89	8.77	1530	unstable	0.358	27	Cell membrane.	no
TaLTPd1.18	TraesCS3A01G419800.1	107	10682.4	8.95	1475	stable	0.347	33	Cell membrane.	no
TaLTPd1.19	TraesCS3B01G454900.1	110	11123.22	9.61	1553	stable	0.369	28	Cell membrane.	no

TaLTPd1.24	TraesCS3D01G415400.1	107	10621.31	8.94	1469	stable	0.358	33	Cell membrane.	no
TaLTPd1.25	TraesCS4B01G323400.1	103	10734.46	4.39	1483	unstable	0.225	27	Cell membrane.	no
TaLTPd1.26	TraesCS4D01G319600.1	87	9182.6	4.34	1257	unstable	0.028	-	Cell membrane.	no
TaLTPd1.28	TraesCS5A01G070300.1	105	11041.01	7.53	1543	stable	0.37	21	Cell membrane.	no
TaLTPd1.31	TraesCS5B01G076000.1	105	10995.01	6.68	1544	unstable	0.53	27	Cell membrane.	no
TaLTPd1.34	TraesCS5D01G082100.1	112	11870.93	6.24	1668	unstable	0.408	27	Cell membrane.	no
TaLTPd1.36	TraesCS7A01G126800.1	103	10579.59	9.06	1484	unstable	0.492	26	Cell membrane.	no
TaLTPd1.37	TraesCS7B01G026200.1	103	10602.67	9.04	1491	stable	0.527	26	Cell membrane.	no
TaLTPd1.40	TraesCSU01G187200.1	105	10915.88	8.46	1527	unstable	0.328	27	Cell membrane.	no
Type d2										
TaLTPd2.1	TraesCS1A01G062600.1	107	11930.16	8.56	1667	stable	0.007	20	Cell membrane. Nucleus.	no
TaLTPd2.5	TraesCS1B01G421200.1	107	12124.54	8.89	1711	unstable	0.059	20	Cell membrane. Nucleus.	no
TaLTPd2.6	TraesCS1D01G159700.1	201	20995.76	8.83	2901	unstable	-0.339	-	Cell membrane. Nucleus.	no
TaLTPd2.7	TraesCS2A01G449600.1	121	13164.51	9.19	1860	unstable	0.011	29	Nucleus.	no
TaLTPd2.9	TraesCS3A01G329900.1	107	11629.88	8.58	1642	unstable	0.293	19	Cell membrane.	no
TaLTPd2.10	TraesCS3B01G359900.1	129	13678.55	6.07	1905	unstable	0.579	20	Cell membrane.	no
TaLTPd2.13	TraesCS3D01G323300.1	107	11599.81	8.06	1634	stable	0.359	19	Cell membrane.	no
TaLTPd2.14	TraesCS5A01G422900.1	68	7609.11	9.05	1060	stable	-0.243	-	Golgi apparatus.	no
Type d3										
TaLTPd3.1	TraesCS2A01G297100.1	119	11928.16	9.18	1681	unstable	0.25	20	Cell membrane.	no
TaLTPd3.5	TraesCS2B01G313400.1	125	13094.43	8.65	1867	unstable	0.114	27	Cell membrane.	no
TaLTPd3.8	TraesCS2D01G295100.1	125	13016.32	8.44	1855	unstable	0.145	27	Cell membrane.	no
TaLTPd3.9	TraesCS3A01G364300.1	116	11845.28	9.83	1681	unstable	0.365	25	Cell membrane.	no
TaLTPd3.10	TraesCS3B01G396400.1	116	11916.42	9.91	1690	unstable	0.285	25	Cell membrane.	no
TaLTPd3.11	TraesCS3D01G357700.1	116	11783.25	9.78	1675	stable	0.366	25	Cell membrane.	no
TaLTPd3.12	TraesCS6B01G028400.1	117	11799.87	8.95	1662	unstable	0.235	25	Cell membrane.	no
TaLTPd3.13	TraesCS7A01G452100.1	118	11925.05	8.47	1666	unstable	0.297	25	Cell membrane.	no
TaLTPd3.14	TraesCS7B01G351900.1	118	11819.89	8.15	1653	unstable	0.377	21	Cell membrane.	no
TaLTPd3.15	TraesCS7D01G441100.1	118	11825.91	8.14	1650	unstable	0.338	21	Cell membrane.	no
Type g1										
TaLTPg1.1	TraesCS4A01G021300.1	196	19752.77	6.05	2773	unstable	0.308	21	Cell membrane.	yes
TaLTPg1.2	TraesCS4B01G282200.1	196	19717.75	6.68	2775	unstable	0.297	26	Cell membrane.	yes
TaLTPg1.3	TraesCS4D01G280900.1	196	19576.53	6.04	2750	stable	0.305	26	Cell membrane.	yes

TaLTPg1.4	TraesCS5A01G452600.1	191	19666.77	8.66	2769	stable	0.306	26	Cell membrane.	yes
TaLTPg1.5	TraesCS5A01G452700.1	215	21842.28	8.33	3068	unstable	0.339	23	Cell membrane.	yes
TaLTPg1.6	TraesCS5B01G461500.1	192	19781.95	8.99	2790	unstable	0.287	28	Cell membrane.	yes
TaLTPg1.7	TraesCS5B01G461600.1	183	18642.57	8.44	2622	stable	0.328	23	Cell membrane.	yes
TaLTPg1.8	TraesCS5D01G463000.1	194	19821.94	8.66	2784	stable	0.29	29	Cell membrane.	yes
TaLTPg1.9	TraesCS5D01G463100.1	185	18808.84	8.44	2652	stable	0.409	26	Cell membrane.	yes
TaLTPg1.10	TraesCS6A01G260600.1	188	19044.08	8.46	2698	unstable	0.353	21	Cell membrane.	yes
TaLTPg1.11	TraesCS6B01G287900.1	184	18802.83	8.88	2666	unstable	0.315	21	Cell membrane.	yes
TaLTPg1.12	TraesCS6D01G241400.1	184	18791.86	8.69	2663	unstable	0.334	21	Cell membrane.	yes
TaLTPg1.13	TraesCS7A01G261900.1	153	15999.29	5.82	2225	unstable	0.193	23	Cell membrane.	yes
TaLTPg1.14	TraesCS7B01G159400.1	173	18203.76	5.71	2535	unstable	0.11	23	Cell membrane.	yes
TaLTPg1.15	TraesCS7D01G262500.1	173	18183.77	5.72	2537	unstable	0.117	23	Cell membrane.	yes
Type g2										
TaLTPg2.3	TraesCS6A01G098200.1	225	22626.37	8.34	3214	unstable	0.363	23	Cell membrane.	no
TaLTPg2.4	TraesCS6B01G126200.1	168	16972.91	8.58	2410	unstable	0.414	24	Cell membrane.	no
TaLTPg2.6	TraesCS6D01G082700.1	148	15131.57	4.13	2116	unstable	0.53	21	Cell membrane.	no
Type g3										
TaLTPg3.1	TraesCS1A01G048700.1	170	16276.6	8.14	2279	unstable	0.422	24	Cell membrane.	yes
TaLTPg3.2	TraesCS1B01G063600.1	172	16449.84	8.15	2312	unstable	0.513	27	Cell membrane.	yes
TaLTPg3.3	TraesCS1B01G063700.1	171	16336.68	8.15	2293	unstable	0.494	27	Cell membrane.	yes
TaLTPg3.4	TraesCS1B01G063800.1	184	17712.11	7.48	2471	unstable	0.418	21	Cell membrane.	yes
TaLTPg3.5	TraesCS1D01G050000.1	172	16362.69	8.14	2291	unstable	0.462	27	Cell membrane.	yes
TaLTPg3.6	TraesCS2B01G258900.1	164	16977.76	4.94	2382	unstable	0.373	20	Cell membrane.	yes
TaLTPg3.7	TraesCS2D01G245300.1	164	16870.61	4.94	2362	unstable	0.336	18	Cell membrane.	yes
TaLTPg3.8	TraesCS4A01G038400.1	197	19144.02	5.52	2693	unstable	0.493	22	Cell membrane.	yes
TaLTPg3.9	TraesCS4B01G267300.1	195	19121.79	5.2	2675	unstable	0.318	24	Cell membrane.	yes
TaLTPg3.10	TraesCS4D01G266900.1	193	18980.72	6.05	2657	unstable	0.318	30	Cell membrane.	yes
TaLTPg3.11	TraesCS5A01G432700.1	172	16674.92	8.14	2324	unstable	0.315	28	Cell membrane.	yes
TaLTPg3.13	TraesCS5A01G432900.1	172	16570.81	8.46	2312	unstable	0.291	28	Cell membrane.	yes
TaLTPg3.14	TraesCS5A01G433100.1	182	17354.78	8.69	2432	unstable	0.546	34	Cell membrane.	yes
TaLTPg3.15	TraesCS5A01G433500.1	212	21001.24	5.8	2907	unstable	0.469	19	Cell membrane.	yes
TaLTPg3.16	TraesCS5A01G433800.1	184	17962.74	8.38	2499	unstable	0.359	19	Cell membrane.	yes
TaLTPg3.17	TraesCS5B01G435500.1	170	16481.74	8.12	2291	unstable	0.335	28	Cell membrane.	yes

TaLTPg3.18	TraesCS5B01G435600.1	172	16696.96	8.13	2334	unstable	0.277	28	Cell membrane.	yes
TaLTPg3.19	TraesCS5B01G435800.1	169	16239.4	8.89	2263	unstable	0.311	34	Cell membrane.	yes
TaLTPg3.20	TraesCS5B01G435900.1	182	17485.9	9.18	2452	unstable	0.361	34	Cell membrane.	yes
TaLTPg3.21	TraesCS5B01G436000.1	212	20790.93	8.72	2921	unstable	0.54	34	Cell membrane.	yes
TaLTPg3.22	TraesCS5B01G436100.1	177	16863.25	8.69	2359	unstable	0.466	34	Cell membrane.	yes
TaLTPg3.23	TraesCS5B01G436700.1	186	17945.67	8.38	2491	unstable	0.38	30	Cell membrane.	yes
TaLTPg3.24	TraesCS5D01G440800.1	172	16606.86	8.46	2310	unstable	0.295	28	Cell membrane.	yes
TaLTPg3.25	TraesCS5D01G441000.1	172	16414.65	8.47	2295	unstable	0.417	24	Cell membrane.	yes
TaLTPg3.26	TraesCS5D01G441100.1	182	17333.76	8.88	2428	unstable	0.473	34	Cell membrane.	yes
TaLTPg3.27	TraesCS5D01G441200.1	168	16215.48	8.89	2264	unstable	0.395	34	Cell membrane.	yes
TaLTPg3.28	TraesCS5D01G441300.1	172	16670.88	8.13	2323	unstable	0.252	28	Cell membrane.	yes
TaLTPg3.29	TraesCS5D01G441700.1	188	18165.89	7.46	2522	unstable	0.35	28	Cell membrane.	yes
Type g4										
TaLTPg4.1	TraesCS1A01G010900.1	156	17557.82	7.67	2430	unstable	-0.522	-	Vacuole.	no
TaLTPg4.2	TraesCS1B01G010700.1	123	13739.65	5.8	1916	unstable	-0.352	-	Vacuole.	no
TaLTPg4.3	TraesCS2A01G419000.1	189	19120.33	7.49	2698	unstable	0.419	24	Cell membrane.	yes
TaLTPg4.4	TraesCS2B01G437700.1	189	19100.34	7.49	2700	unstable	0.422	24	Cell membrane.	yes
TaLTPg4.5	TraesCS2D01G415900.1	191	19330.55	7.49	2735	unstable	0.407	24	Cell membrane.	yes
TaLTPg4.6	TraesCS6A01G048900.1	318	36532.05	6.73	5088	unstable	-0.874	20	Cytoplasm. Nucleus.	yes
TaLTPg4.7	TraesCS6A01G049100.1	283	32551.82	7.66	4542	unstable	-0.757	20	Cytoplasm. Nucleus.	yes
TaLTPg4.8	TraesCS6A01G049200.1	306	35524.91	6.98	4941	unstable	-0.937	20	Cytoplasm. Nucleus.	yes
TaLTPg4.9	TraesCS6A01G049400.1	284	32666.06	8.25	4565	unstable	-0.736	20	Cytoplasm.	yes
TaLTPg4.10	TraesCS6A01G049500.1	231	26931.36	7.74	3760	unstable	-0.921	20	Cytoplasm.	no
TaLTPg4.11	TraesCS6A01G049600.1	287	33079.46	7.64	4615	unstable	-0.8	20	Cytoplasm.	yes
TaLTPg4.12	TraesCS6A01G049700.1	297	34226.51	6.93	4768	unstable	-0.867	20	Cytoplasm.	yes
TaLTPg4.13	TraesCS6A01G049800.1	279	32041.31	6.48	4476	unstable	-0.711	20	Cytoplasm.	yes
TaLTPg4.14	TraesCS6B01G065600.1	243	27660.01	7.71	3850	unstable	-0.953	20	Nucleus.	no
TaLTPg4.15	TraesCS6B01G065800.1	316	36529.06	8.58	5088	unstable	-0.944	17	Cytoplasm. Nucleus.	yes
TaLTPg4.16	TraesCS6B01G065900.1	129	14307.49	9.06	1983	unstable	-0.188	-	Cell membrane. Nucleus.	no
TaLTPg4.17	TraesCS6B01G066000.1	280	32284.41	7.66	4497	unstable	-0.829	20	Cytoplasm. Nucleus.	yes
TaLTPg4.19	TraesCS7A01G405800.1	183	17932.59	8.05	2492	stable	0.501	33	Cell membrane.	yes
TaLTPg4.20	TraesCS7A01G446700.1	154	15409.79	8.86	2151	unstable	0.193	24	Cell membrane.	yes
TaLTPg4.22	TraesCS7B01G305700.1	185	18005.58	7.45	2501	stable	0.476	33	Cell membrane.	yes

TaLTPg4.23	TraesCS7B01G346500.1	110	11470.13	8.61	1588	unstable	-0.128	-	Cell membrane.	no
TaLTPg4.25	TraesCS7D01G399700.1	185	17991.61	6.5	2494	unstable	0.502	27	Cell membrane.	yes
TaLTPg4.26	TraesCS7D01G435200.1	157	15686.12	8.67	2194	unstable	0.277	24	Cell membrane.	yes
TaLTPg4.27	TraesCSU01G108100.1	291	33587.84	7.1	4672	unstable	-0.812	20	Cytoplasm.	yes
TaLTPg4.28	TraesCSU01G108200.1	316	36342.89	7.58	5062	unstable	-0.88	20	Cytoplasm. Nucleus.	yes
TaLTPg4.29	TraesCSU01G108300.1	300	34531.92	6.93	4806	unstable	-0.83	20	Cytoplasm.	yes
TaLTPg4.30	TraesCSU01G108400.1	293	33647.97	6.98	4691	unstable	-0.8	20	Cytoplasm.	yes
TaLTPg4.31	TraesCSU01G108500.1	286	32867.23	7.67	4592	unstable	-0.756	20	Cytoplasm.	yes
TaLTPg4.32	TraesCSU01G108700.1	282	32206.16	6.68	4467	unstable	-0.82	20	Cytoplasm.	yes
TaLTPg4.33	TraesCSU01G153800.1	294	33501.73	6.63	4669	unstable	-0.768	20	Cytoplasm.	yes
TaLTPg4.34	TraesCSU01G160200.1	231	26743.33	7.04	3753	unstable	-0.801	20	Cytoplasm.	no
TaLTPg4.35	TraesCSU01G188800.1	307	35341.85	7.61	4930	unstable	-0.862	20	Cytoplasm.	yes
TaLTPg4.36	TraesCSU01G220200.1	297	34189.61	8.5	4764	unstable	-0.833	20	Cytoplasm.	yes
TaLTPg4.37	TraesCSU01G220600.1	290	33249.67	8.18	4641	unstable	-0.74	20	Cytoplasm.	yes
TaLTPg4.38	TraesCSU01G239000.1	308	35470.02	8.21	4951	unstable	-0.871	20	Cytoplasm.	yes
Type g5										
TaLTPg5.1	TraesCS1A01G306000.1	250	24681.85	8.57	3501	unstable	0.526	33	Cell membrane.	yes
TaLTPg5.2	TraesCS1B01G316700.1	214	20901.39	8.88	2946	unstable	0.413	33	Cell membrane.	yes
TaLTPg5.3	TraesCS1D01G305700.1	215	21131.57	8.81	2969	unstable	0.402	33	Cell membrane.	yes
TaLTPg5.4	TraesCS3A01G338000.1	189	18660.72	8.1	2618	unstable	0.395	26	Cell membrane.	yes
TaLTPg5.5	TraesCS3B01G369600.1	247	25086.09	9.14	3516	unstable	0.188	-	Cell membrane.	yes
TaLTPg5.6	TraesCS3D01G331400.1	190	18747.89	8.41	2637	unstable	0.371	26	Cell membrane.	yes
TaLTPg5.7	TraesCS4A01G129300.1	206	20717.03	8.83	2922	unstable	0.3	-	Cell membrane.	yes
TaLTPg5.8	TraesCS4B01G175200.1	185	18427.48	8.11	2605	unstable	0.462	25	Cell membrane.	yes
TaLTPg5.9	TraesCS4D01G177100.1	184	18251.21	7.49	2579	unstable	0.474	25	Cell membrane.	yes
Type g6										
TaLTPg6.1	TraesCS3A01G095600.1	154	16796.57	7.99	2331	stable	0.103	22	Endoplasmic reticulum	no
TaLTPg6.2	TraesCS3B01G111100.1	154	16482.26	5.77	2291	stable	0.292	22	Endoplasmic reticulum. Nucleus.	no
TaLTPg6.5	TraesCS3D01G096000.1	154	16614.32	6.06	2295	stable	0.18	22	Endoplasmic reticulum.	no
TaLTPg6.6	TraesCS5A01G003300.1	164	18170.81	6.27	2515	unstable	-0.256	19	Extracell.	no
TaLTPg6.7	TraesCS5B01G003500.1	164	18449.27	8.02	2557	unstable	-0.22	19	Extracell.	no
TaLTPg6.8	TraesCS5D01G004000.1	164	18195.91	8.33	2524	unstable	-0.209	19	Endoplasmic reticulum. Extracell.	no
TaLTPg6.11	TraesCS6B01G008200.1	145	15897.67	6.79	2189	stable	0.106	21	Endoplasmic reticulum.	no

TaLTPg6.12	TraesCS6D01G000200.1	151	16628.38	7.45	2304	stable	0.048	21	Extracell.	no
TaLTPg6.13	TraesCS7A01G514400.1	149	16578.39	9.03	2322	stable	-0.142	19	Endoplasmic reticulum. Extracell.	no
TaLTPg6.15	TraesCS7B01G431200.1	150	16901.81	9.29	2365	stable	-0.231	19	Endoplasmic reticulum. Extracell.	no
TaLTPg6.16	TraesCS7D01G504800.1	149	16582.39	9.13	2322	stable	-0.177	19	Endoplasmic reticulum. Extracell.	no
Type g7										
TaLTPg7.1	TraesCS2B01G004100.1	195	21485.02	8.75	3014	unstable	-0.155	-	Endoplasmic reticulum. Nucleus.	no
TaLTPg7.3	TraesCS4A01G055200.1	121	13843.25	9.37	1962	unstable	-0.193	24	Endoplasmic reticulum.	no
TaLTPg7.5	TraesCS4B01G066900.1	157	17249.12	9.3	2439	unstable	-0.066	23	Endoplasmic reticulum. Nucleus.	no
TaLTPg7.10	TraesCS4D01G065900.1	147	15670.44	8.06	2202	unstable	0.276	23	Endoplasmic reticulum.	yes
TaLTPg7.13	TraesCS4D01G325100.1	168	18318.5	7.44	2569	unstable	0.29	25	Endoplasmic reticulum. Nucleus.	yes
TaLTPg7.14	TraesCS6A01G260500.1	153	16518.21	8.11	2319	unstable	0.084	24	Endoplasmic reticulum.	no
TaLTPg7.15	TraesCS6B01G287800.1	154	16667.32	8.11	2333	unstable	0.038	24	Endoplasmic reticulum.	no
TaLTPg7.16	TraesCS6D01G241300.1	226	24966.72	7.96	3480	unstable	-0.227	-	Endoplasmic reticulum.	no
TaLTPg7.17	TraesCS7B01G072000.1	169	18232.01	8.33	2532	stable	-0.121	25	Endoplasmic reticulum.	no
TaLTPg7.18	TraesCS7D01G083700.1	143	15277.74	7.48	2121	unstable	0.158	24	Endoplasmic reticulum.	yes
TaLTPg7.19	TraesCS7D01G168000.1	145	15526.82	7.5	2152	stable	-0.037	25	Endoplasmic reticulum.	yes

Len, Length (aa); MW, molecular weight (kD); pI, Isoelectric point; GRAVY, Grand average of hydropathicit; GPI, glycosylphosphatidylinositol