

Table S1 Features of rapeseed ATG proteins

Gene Name	Locus	Chromosome	Start	End	Strand	Length	MW	pI
ATG1/13 kinase complex								
BnATG1a	GSBRNA2T001248960	chrA03	8190848	8194622	+	716	79.13	6.4
BnATG1b	GSBRNA2T001264890	chrA04	3297987	3302544	-	713	79.2	8.3
BnATG1c	GSBRNA2T000990710	chrA07	15415971	15419120	-	606	67.28	6.4
BnATG1d	GSBRNA2T000910670	chrA08	2278450	2280614	+	268	30.62	7.7
BnATG1e	GSBRNA2T000494460	chrA09	28022400	28025991	-	587	65.22	6.2
BnATG1f	GSBRNA2T000261800	chrC03_random	514077	517856	+	722	80.02	6.4
BnATG1g	GSBRNA2T000710150	chrC04	28104206	28108211	-	711	79.01	8.3
BnATG1h	GSBRNA2T000329910	chrC05	20516040	20517603	-	265	30.29	7.2
BnATG1i	GSBRNA2T000289370	chrC06	20655750	20658951	-	606	67.29	6.1
BnATG1j	GSBRNA2T001279690	chrC08	2713063	2714635	+	265	30.29	7.2
BnATG1k	GSBRNA2T001270520	chrC08	31130379	31134129	-	586	65.43	6.4
BnATG13a	GSBRNA2T000055690	chrA01	18588167	18590675	+	586	64.62	9.2
BnATG13b	GSBRNA2T001097490	chrA06	14662493	14664903	+	559	61.58	9.7
BnATG13c	GSBRNA2T000455170	chrC01_random	3490892	3493438	+	592	65.25	9.2
BnATG13d	GSBRNA2T001457910	chrC03	37151076	37153562	-	562	62.31	9.2
BnATG20a	GSBRNA2T000296010	chrA10_random	2220274	2223395	-	390	44.99	7.1
BnATG20b	GSBRNA2T001070120	chrC09	47756555	47759649	+	390	45.03	7.1
BnTORa	GSBRNA2T000428950	chrA05	10560179	10577534	+	2464	277	6.3
BnTORb	GSBRNA2T000978550	chrA06_random	116528	139079	-	2444	274.7	6.7
BnTORc	GSBRNA2T000391060	chrC06	3757429	3775055	-	2478	278.5	6.2
BnATG101a	GSBRNA2T0011245700	chrA07	11189080	11190783	-	213	25.02	5.9
BnATG101b	GSBRNA2T0000568900	chrA09	3757694	3759363	-	217	25.29	5.9
BnATG101c	GSBRNA2T0007685000	chrC02	12077876	12079356	+	221	25.9	7.6
BnATG101d	GSBRNA2T0007039700	chrC07	22423673	22425267	-	213	25.03	5.9
BnATG101e	GSBRNA2T0013490300	chrC09	4757662	4759553	-	218	25.38	5.8
BnATG11a	GSBRNA2T0003994100	chrA01	2923421	2927356	+	1114	125.3	5.6
BnATG11b	GSBRNA2T0006746600	chrA03	26214555	26219552	-	1082	122.2	5.5
BnATG11c	GSBRNA2T0002181600	chrA08	11327438	11331707	+	1135	127.5	5.7
BnATG11d	GSBRNA2T0013037200	chrC01	3980448	3984505	+	1109	125	5.6
BnATG11e	GSBRNA2T0006212500	chrC03	57497005	57502324	-	1135	127.7	5.8
BnATG11f	GSBRNA2T0009974100	chrC07	42189856	42193884	-	1081	122.1	5.6
PI3K complex								
BnVPS15a	GSBRNA2T0007677900	chrA01	3479335	3485604	-	1410	159.2	7.6
BnVPS15b	GSBRNA2T0012305400	chrC01	5168427	5175016	-	1463	164.8	7.8
BnVPS34a	GSBRNA2T0000846500	chrA09	8090239	8094815	+	813	93.17	6.3
BnVPS34b	GSBRNA2T0008693500	chrC09	11273995	11278566	+	813	93.21	6.2
BnATG6a	GSBRNA2T0009905800	chrA07	15358890	15362175	-	521	58.86	5.9
BnATG6b	GSBRNA2T0002889600	chrC06	20457827	20461867	-	524	59.21	6
BnATG6c	GSBRNA2T0002891100	chrC06	20527493	20529612	-	383	43.32	5.7
BnATG6d	GSBRNA2T0000390100	chrC06_random	2466729	2469463	-	528	59.69	5.9
BnATG14a	GSBRNA2T0014648300	chrA07	23100379	23103301	+	449	50.71	8.9
BnATG14b	GSBRNA2T0006008600	chrAnn_random	4798793	4802258	+	474	53.23	9.4
BnATG14c	GSBRNA2T0014792900	chrC06	35997462	36000487	-	432	48.54	9.1
BnATG14d	GSBRNA2T0014793000	chrC06	36001318	36004617	+	449	50.68	8.8
BnATG14e	GSBRNA2T0011894500	chrC09	24700466	24703195	-	474	53.28	9.3
ATG9/2/18 complex								
BnATG9a	GSBRNA2T0000634300	chrA04	14599557	14604404	-	993	113.9	8.5

BnATG9b	GSBRNA2T0004861600	chrA05	6489894	6493395	-	542	63.09	6.7
BnATG9c	GSBRNA2T0008572100	chrC04	42792495	42797397	-	909	103.6	6
BnATG18a	GSBRNA2T0007229500	chrA02	20664730	20667820	-	704	75.96	5.4
BnATG18b	GSBRNA2T0007585000	chrA03	5270163	5273670	+	760	82.57	5.6
BnATG18c	GSBRNA2T0006742800	chrA03	26066335	26068574	-	367	39.72	8.2
BnATG18d	GSBRNA2T0000496500	chrA03_random	199354	200899	-	377	41.89	8.7
BnATG18e	GSBRNA2T0014929700	chrA04	228394	230197	+	415	45.53	7.6
BnATG18f	GSBRNA2T0012326300	chrA04	17470624	17473236	+	408	45.12	6.1
BnATG18g	GSBRNA2T0009910900	chrA07	15539494	15541534	-	404	44.32	7.2
BnATG18h	GSBRNA2T0007345600	chrA09	9120968	9124740	+	903	98.33	5.5
BnATG18i	GSBRNA2T0003708500	chrA09	26114728	26117472	+	387	43.16	7.2
BnATG18j	GSBRNA2T0004951500	chrA09	28255018	28256871	-	432	47.8	7.6
BnATG18k	GSBRNA2T0007490500	chrA10	7250254	7253233	-	741	81.04	5.9
BnATG18l	GSBRNA2T0008937700	chrAnn_random	10242374	10246172	-	856	92.33	5.9
BnATG18m	GSBRNA2T0000172800	chrC01	24215618	24219547	-	860	93.04	6
BnATG18n	GSBRNA2T0013436500	chrC03	959475	961043	-	377	41.8	8.8
BnATG18o	GSBRNA2T0015680000	chrC04	22106993	22109095	+	419	46.23	7.6
BnATG18p	GSBRNA2T0008459300	chrC04	46413606	46415588	+	408	45.09	6
BnATG18q	GSBRNA2T0000269300	chrC05	933342	938207	+	989	107.5	6.1
BnATG18r	GSBRNA2T0002899100	chrC06	20941852	20943989	-	429	47	7.2
BnATG18s	GSBRNA2T0009971600	chrC07	42072801	42075076	-	367	39.73	8.2
BnATG18t	GSBRNA2T0015595400	chrC08	28400737	28403541	+	387	43.24	7.7
BnATG18u	GSBRNA2T0015595300	chrC08	28406147	28408220	-	387	43.24	7.7
BnATG18v	GSBRNA2T0012713400	chrC08	31398523	31400239	-	424	46.83	7.6
BnATG18w	GSBRNA2T0008748700	chrC09	34134208	34137263	-	742	81.32	5.6
BnATG18x	GSBRNA2T0004098800	chrC09_random	826812	830645	-	968	105.8	6

Ubiquitin-like ATG8 and PE conjugation pathway

BnATG3a	GSBRNA2T0011353500	chrA03	20141348	20143370	-	309	35.09	4.6
BnATG3b	GSBRNA2T0007168100	chrAnn_random	6281135	6282803	-	306	34.46	4.6
BnATG3c	GSBRNA2T0007856100	chrC02	620736	622664	-	309	35.09	4.6
BnATG3d	GSBRNA2T0002153000	chrC07	35439467	35441608	-	310	35.15	4.6
BnATG4a	GSBRNA2T0014915800	chrA04	954503	957505	+	425	46.74	4.9
BnATG4b	GSBRNA2T0013260700	chrA05	2015984	2018064	-	456	50.52	5.1
BnATG4c	GSBRNA2T0007260400	chrA09	27341547	27344526	-	447	49.08	4.8
BnATG4d	GSBRNA2T0000222100	chrC04	2405691	2407814	-	454	50.12	5
BnATG4e	GSBRNA2T0008269700	chrC04	23602645	23605673	+	427	46.82	4.8
BnATG7a	GSBRNA2T0009686800	chrA02	17485495	17488861	+	697	76.56	5
BnATG7b	GSBRNA2T0014682700	chrC02	34351353	34354697	+	696	76.37	5
BnATG8a	GSBRNA2T0013166200	chrA01	5911222	5912383	+	122	13.78	6.6
BnATG8b	GSBRNA2T0005171100	chrA01	9045173	9046211	+	122	13.6	8.7
BnATG8c	GSBRNA2T0013896500	chrA03	9986572	9987768	+	122	13.93	8.7
BnATG8d	GSBRNA2T0011185900	chrA03	14313506	14314879	-	119	13.75	6.1
BnATG8e	GSBRNA2T0015499800	chrA03	18927952	18929424	-	119	13.72	7.9
BnATG8f	GSBRNA2T0015114100	chrA03	21395483	21397007	-	183	20.66	8.4
BnATG8g	GSBRNA2T0010679200	chrA03	22894369	22895827	+	124	13.92	8.8
BnATG8h	GSBRNA2T0010493000	chrA05	18019583	18020612	+	115	13.22	6.6
BnATG8i	GSBRNA2T0002707700	chrA05	21421292	21422730	+	119	13.71	7.9
BnATG8j	GSBRNA2T0001801300	chrA07_random	1406643	1408048	+	122	13.87	6.3
BnATG8k	GSBRNA2T0009449400	chrA09	13236987	13238417	+	120	13.64	7.8
BnATG8l	GSBRNA2T0007537900	chrAnn_random	31521868	31523203	+	118	13.52	7.8

BnATG8m	GSBRNA2T0013826200	chrC01	8718492	8719455	+	124	14.06	5.8
BnATG8n	GSBRNA2T0013826400	chrC01	8727157	8728346	+	122	13.78	6.6
BnATG8o	GSBRNA2T0006985900	chrC01	13715805	13717527	-	119	13.5	6.6
BnATG8p	GSBRNA2T0005482500	chrC02	23318402	23319809	+	126	14.13	9.3
BnATG8q	GSBRNA2T0010151400	chrC03	14130299	14131524	+	122	13.9	8.7
BnATG8r	GSBRNA2T0012530500	chrC03	21062558	21064011	-	119	13.74	6.1
BnATG8s	GSBRNA2T0004770000	chrC03	53193127	53194365	+	135	15.48	9.1
BnATG8t	GSBRNA2T0009780500	chrC03_random	2372814	2374225	+	119	13.71	7.9
BnATG8u	GSBRNA2T0012404800	chrC04	19655525	19656812	+	119	13.58	7.9
BnATG8v	GSBRNA2T0012008600	chrC05	41321889	41323325	+	119	13.69	6.9
BnATG8w	GSBRNA2T0003135300	chrC07	36812177	36813774	-	185	20.89	7.7
BnATG8x	GSBRNA2T0015697300	chrC07	38904199	38905532	+	137	15.43	9
BnATG8y	GSBRNA2T0009759500	chrC08_random	2952337	2954834	+	286	33.41	5.2
BnATG8z	GSBRNA2T0015783000	chrC09	19977907	19979246	+	120	13.65	7.8
Ubiquitin-like ATG12 and ATG5 conjugation pathway								
BnATG5a	GSBRNA2T0014316100	chrA02	1548076	1550429	-	342	39.12	5
BnATG5b	GSBRNA2T0013535400	chrA10	12886050	12888645	+	335	38.08	5
BnATG5c	GSBRNA2T0011486700	chrC02	3805663	3808073	-	341	38.86	5
BnATG5d	GSBRNA2T0009486300	chrC09	43024453	43026863	+	334	37.79	4.9
BnATG10a	GSBRNA2T0005949300	chrA05	20867783	20869310	+	223	25.54	4.8
BnATG10b	GSBRNA2T0003898200	chrC05	40767187	40768319	+	223	25.56	4.8
BnATG12a	GSBRNA2T0010474300	chrA05	18837891	18839513	+	140	15.87	9.7
BnATG12b	GSBRNA2T0005372100	chrC06	7552550	7553786	+	93	10.3	6.7
BnATG12c	GSBRNA2T0001651400	chrCnn_random	26974218	26975566	-	94	10.29	8.8
BnATG16a	GSBRNA2T0012088900	chrA10	4588445	4592200	+	575	63.18	6.4
BnATG16b	GSBRNA2T0012088800	chrA10	4592738	4594835	+	502	55.49	6.1
SNARE								
BnVTI12a	GSBRNA2T0007948600	chrA02	8042492	8044013	+	222	25.12	8.8
BnVTI12b	GSBRNA2T0011432000	chrA04	8416636	8418470	+	221	34.73	9.7
BnVTI12c	GSBRNA2T0000982200	chrA09	1307902	1309529	-	221	24.96	9.6
BnVTI12d	GSBRNA2T0004049100	chrC02	15468897	15470211	+	222	25.16	8.8
BnVTI12e	GSBRNA2T0004488400	chrC04	33401654	33403360	+	221	24.72	9.7
BnVTI12f	GSBRNA2T0006319500	chrC06	15115209	15116665	-	221	24.63	9.7
BnVTI12g	GSBRNA2T0001272200	chrC07	17865912	17867672	+	222	25.13	8.4
BnVTI12h	GSBRNA2T0010959800	chrC09	1111364	1112971	-	221	24.98	9.6

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Cytoplasmic	Mitochondrial	
Nucleus	Cytoplasmic	
Mitochondrial	Cytoplasmic	Nucleus
Cytoplasmic	Nucleus	
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