

Table S1. Copy number of *ATG8* genes in *Arabidopsis* and *Brassica* crops.

| Gene name | <i>Arabidopsis thaliana</i> (125 Mb) | <i>Brassica rapa</i> (465 Mb) | <i>Brassica oleracea</i> (485 Mb) | <i>Brassica napus</i> (1,130 Mb) |
|----------------------|---|--|--|---|
| <i>ATG8A</i> | 1 | 4 | 6 | 8 |
| <i>ATG8B</i> | 1 | 0 | 1 | 0 |
| <i>ATG8C</i> | 1 | 2 | 2 | 2 |
| <i>ATG8D</i> | 1 | 0 | 0 | 2 |
| <i>ATG8E</i> | 1 | 2 | 2 | 5 |
| <i>ATG8F</i> | 1 | 2 | 3 | 6 |
| <i>ATG8G</i> | 1 | 0 | 0 | 0 |
| <i>ATG8H</i> | 1 | 2 | 2 | 4 |
| <i>ATG8I</i> | 1 | 1 | 1 | 2 |
| Total | 9 | 13 | 17 | 29 |

Table S2. Molecular characterization of autophagy-related 8 genes in *Arabidopsis* and rapeseed

| Gene ID | Gene name | Chromosome | MW (kDa) | PI | II | AI | GRAVY | Subcellular localization |
|------------------|--------------------|------------|----------|------|-------|-------|-------|--------------------------|
| AT4G21980 | <i>AtATG8A</i> | | 13.69 | 8.78 | 39.51 | 85.49 | -0.24 | cyto |
| BnaA01T004000WE | <i>BnaA1.ATG8A</i> | chrA1 | 13.78 | 6.59 | 32.1 | 84.67 | -0.23 | cyto |
| BnaA02T0252700WE | <i>BnaA2.ATG8A</i> | chrA2 | 14.12 | 8.78 | 37.87 | 86.67 | -0.25 | cyto |
| BnaA03T0470100WE | <i>BnaA3.ATG8A</i> | chrA3 | 15.46 | 8.61 | 36.32 | 84.01 | -0.08 | cyto |
| BnaA09T0224000WE | <i>BnaA9.ATG8A</i> | chrA9 | 13.64 | 7.78 | 40.87 | 83.67 | -0.31 | cyto |
| BnaC01T0120100WE | <i>BnaC1.ATG8A</i> | chrC1 | 15.48 | 6.59 | 35.15 | 86.13 | -0.12 | cyto |
| BnaC03T0624600WE | <i>BnaC2.ATG8A</i> | chrC2 | 15.48 | 9.06 | 38.95 | 83.85 | -0.25 | cyto |
| BnaC07T0384500WE | <i>BnaC3.ATG8A</i> | chrC3 | 15.42 | 8.95 | 34.19 | 84.74 | -0.14 | cyto |
| BnaC09T0256400WE | <i>BnaC9.ATG8A</i> | chrC9 | 13.65 | 7.78 | 36.18 | 86.08 | -0.32 | cyto |
| AT4G04620 | <i>AtATG8B</i> | | 13.88 | 8.61 | 37.83 | 79.1 | -0.29 | cyto |
| AT1G62040 | <i>AtATG8C</i> | | 13.73 | 8.83 | 49.75 | 85.97 | -0.39 | cyto |
| BnaA03T0589400WE | <i>BnaA3.ATG8C</i> | chrA3 | 7.70 | 9.45 | 32.78 | 90 | -0.38 | cyto |
| BnaC04T0234400WE | <i>BnaC4.ATG8C</i> | chrA4 | 13.62 | 7.92 | 46.54 | 89.24 | -0.29 | cyto |
| AT2G05630 | <i>AtATG8D</i> | | 13.91 | 7.93 | 45.72 | 88.58 | -0.29 | cyto |
| BnaA03T0399000WE | <i>BnaA3.ATG8D</i> | chrA3 | 13.72 | 7.9 | 50.46 | 88.49 | -0.33 | cyto |
| BnaC03T0408800WE | <i>BnaC3.ATG8D</i> | chrC3 | 13.71 | 7.9 | 50.34 | 88.49 | -0.33 | cyto |
| AT2G45170 | <i>AtATG8E</i> | | 13.95 | 7.82 | 31.25 | 83.03 | -0.42 | nucl |
| BnaA03T0231500WE | <i>BnaA3.ATG8E</i> | chrA3 | 13.93 | 8.69 | 29.43 | 83.85 | -0.52 | nucl |
| BnaA04T0272200WE | <i>BnaA4.ATG8E</i> | chrA4 | 11.74 | 5.46 | 40.75 | 94.66 | -0.42 | nucl |
| BnaA07T0195100WE | <i>BnaA7.ATG8E</i> | chrA7 | 13.87 | 6.33 | 26.79 | 87.05 | -0.41 | nucl |
| BnaC03T0195700WE | <i>BnaC3.ATG8E</i> | chrC3 | 13.91 | 8.69 | 30.28 | 84.67 | -0.49 | nucl |
| BnaC04T0588400WE | <i>BnaC4.ATG8E</i> | chrC4 | 12.41 | 5.5 | 41.81 | 84.81 | -0.54 | nucl |
| AT4G16520 | <i>AtATG8F</i> | | 13.76 | 8.73 | 35.08 | 83.8 | -0.41 | cyto |
| BnaA01T0105500WE | <i>BnaA1.ATG8F</i> | chrA1 | 11.79 | 5.4 | 27.59 | 86.38 | -0.24 | cyto |
| BnaA03T0443400WE | <i>BnaA3.ATG8F</i> | chrA3 | 19.96 | 7.73 | 46.58 | 83.64 | -0.28 | cyto |
| BnaA08T0093200WE | <i>BnaA8.ATG8F</i> | chrA8 | 13.52 | 7.84 | 29.97 | 85.93 | -0.18 | cyto |
| BnaC01T0182300WE | <i>BnaC1.ATG8F</i> | chrC1 | 13.50 | 6.6 | 27.63 | 84.37 | -0.43 | cyto |
| BnaC06T0196800WE | <i>BnaC6.ATG8F</i> | chrC6 | 23.61 | 6.84 | 40.52 | 96.03 | 0.05 | cyto |
| BnaC08T0097700WE | <i>BnaC8.ATG8F</i> | chrC8 | 33.42 | 5.2 | 45.02 | 91.29 | -0.34 | cyto |
| AT3G60640 | <i>AtATG8G</i> | | 13.94 | 5.87 | 42.24 | 79.67 | -0.45 | cyto |
| AT3G06420 | <i>AtATG8H</i> | | 13.88 | 6.83 | 41.1 | 72.86 | -0.45 | nucl |
| BnaA03T0314100WE | <i>BnaA3.ATG8H</i> | chrA3 | 20.49 | 9.23 | 42.55 | 81.62 | -0.23 | nucl |
| BnaA05T0417300WE | <i>BnaA5.ATG8H</i> | chrA5 | 13.71 | 7.85 | 40.44 | 68.74 | -0.46 | nucl |
| BnaC03T0296700WE | <i>BnaC3.ATG8H</i> | chrC3 | 13.74 | 6.09 | 39.37 | 76.13 | -0.36 | nucl |
| BnaC05T0512100WE | <i>BnaC5.ATG8H</i> | chrC5 | 13.70 | 6.9 | 39.4 | 68.74 | -0.44 | nucl |
| AT3G15580 | <i>AtATG8I</i> | | 13.25 | 7.7 | 44.02 | 82.26 | -0.23 | cyto |
| BnaA05T0347900WE | <i>BnaA5.ATG8I</i> | chrA5 | 13.23 | 6.59 | 47.23 | 86.52 | -0.21 | cyto |
| BnaC05T0420900WE | <i>BnaC5.ATG8I</i> | chrC5 | 14.98 | 8.5 | 37.98 | 96.09 | -0.15 | cyto |

Note: GRAVY, grand average of hydropathy; II, instability index; MW, molecular weight; pI, isoelectric point; PM, plasma membrane; TM, transmembrane; Vac, vacuole; Endo, endosome

Table S3. Molecular characterization of autophagy-related 8 genes in *Arabidopsis* and rapeseed.

| Gene ID | Gene name | Block | Protein Length (aa) | CDS Length (bp) | Exon/intron | Ka | Ks | Ka/Ks | Divergent time (Mya) |
|------------------|--------------------|-------|---------------------|-----------------|-------------|-------|-------|-------|----------------------|
| AT4G21980 | <i>AtATG8A</i> | U | 122 | 369 | | | | | |
| BnaA01T0040000WE | <i>BnaA1.ATG8A</i> | U | 122 | 369 | 5 | 0.037 | 0.432 | 0.085 | 14.38 |
| BnaA02T0252700WE | <i>BnaA2.ATG8A</i> | U | 126 | 381 | 5 | 0.054 | 0.532 | 0.101 | 17.72 |
| BnaA03T0470100WE | <i>BnaA3.ATG8A</i> | U | 137 | 414 | 5 | 0.036 | 0.412 | 0.089 | 13.73 |
| BnaA09T0224000WE | <i>BnaA9.ATG8A</i> | U | 120 | 363 | 5 | 0.058 | 0.555 | 0.105 | 18.49 |
| BnaC01T0120100WE | <i>BnaC1.ATG8A</i> | U | 137 | 414 | 5 | 0.040 | 0.430 | 0.094 | 14.35 |
| BnaC03T0624600WE | <i>BnaC3.ATG8A</i> | U | 135 | 408 | 5 | 0.040 | 0.390 | 0.103 | 13.00 |
| BnaC07T0384500WE | <i>BnaC7.ATG8A</i> | U | 139 | 420 | 5 | 0.109 | 0.479 | 0.227 | 15.96 |
| BnaC09T0256400WE | <i>BnaC9.ATG8A</i> | U | 120 | 363 | 5 | 0.066 | 0.555 | 0.119 | 18.49 |
| AT4G04620 | <i>AtATG8B</i> | O | 122 | 369 | | | | | |
| AT1G62040 | <i>AtATG8C</i> | D | 119 | 360 | | | | | |
| BnaA03T0589400WE | <i>BnaA3.ATG8C</i> | D | 66 | 201 | 3 | 0.077 | 0.340 | 0.226 | 11.32 |
| BnaC04T0234400WE | <i>BnaC4.ATG8C</i> | D | 119 | 360 | 5 | 0.049 | 0.231 | 0.211 | 7.69 |
| AT2G05630 | <i>AtATG8D</i> | G | 120 | 363 | | | | | |
| BnaA03T0399000WE | <i>BnaA3.ATG8D</i> | G | 119 | 360 | 5 | 0.015 | 0.531 | 0.027 | 17.70 |
| BnaC03T0408800WE | <i>BnaC3.ATG8D</i> | G | 119 | 360 | 5 | 0.018 | 0.389 | 0.047 | 12.98 |
| AT2G45170 | <i>AtATG8E</i> | J | 122 | 369 | | | | | |
| BnaA03T0231500WE | <i>BnaA3.ATG8E</i> | J | 122 | 369 | 4 | 0.030 | 0.433 | 0.070 | 14.45 |
| BnaA04T0272200WE | <i>BnaA4.ATG8E</i> | J | 103 | 312 | 4 | 0.118 | 0.486 | 0.242 | 16.21 |
| BnaA07T0195100WE | <i>BnaA7.ATG8E</i> | J | 122 | 369 | 4 | 0.037 | 0.397 | 0.093 | 13.24 |
| BnaC03T0195700WE | <i>BnaC3.ATG8E</i> | J | 122 | 369 | 4 | 0.034 | 0.482 | 0.071 | 16.06 |
| BnaC04T0588400WE | <i>BnaC4.ATG8E</i> | J | 108 | 327 | 5 | 0.096 | 0.480 | 0.200 | 16.01 |

| | | | | | | | | | |
|------------------|--------------------|---|-----|-----|---|-------|-------|-------|--------|
| AT4G16520 | <i>AtATG8F</i> | U | 121 | 366 | | | | | |
| BnaA01T0105500WE | <i>BnaA1.ATG8F</i> | U | 105 | 318 | 4 | 0.067 | 0.373 | 0.180 | 12.43 |
| BnaA03T0443400WE | <i>BnaA3.ATG8F</i> | U | 176 | 531 | 7 | 0.152 | 0.438 | 0.348 | 14.58 |
| BnaA08T0093200WE | <i>BnaA8.ATG8F</i> | U | 118 | 357 | 5 | 0.030 | 0.234 | 0.127 | 7.81 |
| BnaC01T0182300WE | <i>BnaC1.ATG8F</i> | U | 119 | 360 | 5 | 0.022 | 0.394 | 0.056 | 13.15 |
| BnaC06T0196800WE | <i>BnaC6.ATG8F</i> | U | 209 | 630 | 6 | 0.040 | 0.370 | 0.109 | 12.33 |
| BnaC08T0097700WE | <i>BnaC8.ATG8F</i> | U | 286 | 861 | 8 | 0.030 | 0.252 | 0.118 | 8.39 |
| AT3G60640 | <i>AtATG8G</i> | N | 121 | 366 | | | | | |
| AT3G06420 | <i>AtATG8H</i> | F | 119 | 360 | | | | | |
| BnaA03T0314100WE | <i>BnaA3.ATG8H</i> | F | 179 | 540 | 5 | 0.052 | 0.531 | 0.097 | 17.71 |
| BnaA05T0417300WE | <i>BnaA5.ATG8H</i> | F | 119 | 360 | 5 | 0.069 | 0.373 | 0.185 | 12.45 |
| BnaC03T0296700WE | <i>BnaC3.ATG8H</i> | F | 119 | 360 | 5 | 0.050 | 0.467 | 0.106 | 15.56 |
| BnaC05T0512100WE | <i>BnaC5.ATG8H</i> | F | 119 | 360 | 5 | 0.065 | 0.373 | 0.174 | 12.45 |
| AT3G15580 | <i>AtATG8I</i> | F | 115 | 348 | | | | | |
| BnaA05T0347900WE | <i>BnaA5.ATG8I</i> | F | 115 | 348 | 5 | 0.027 | 0.349 | 0.077 | 11.63 |
| BnaC05T0420900WE | <i>BnaC5.ATG8I</i> | F | 133 | 402 | 3 | 0.051 | 0.449 | 0.113 | 14.957 |

Note: CDS, coding sequence; Ka, non-synonymous nucleotide substitution rate; Ks, synonymous nucleotide substitution rate.

Table S4. Gene used to validate the transcriptome information and sequence of primers

| ggen | F sense primer | R anti-sense primer |
|----------------------|--------------------------------|-------------------------------|
| <i>BnaA8.ATG8F</i> | 5-TGCTCGGATCAGAGAGAAGTA-3 | 5-TGCCCCACTGTCAAATCAGCC-3 |
| <i>BnaC8.NRT2.1a</i> | 5-AAAGGTACTGAGGAGCACTATTATGG-3 | 5-GTATTCTGAGGCGGCGTAGC-3 |
| <i>BnaC2.NAR2.1</i> | 5-TCAAGAAGCTCCTTTTCGCG-3 | 5-TAAATTCAGGCTCCTTTGTAGCC-3 |
| <i>BnaC2.NRT1.7</i> | 5-GCTGGATCATCGGCTTTAGC -3 | 5-GAGCTTCATCTTTCGCTTCTTG -3 |
| <i>BnaA3.NRT1.8</i> | 5-GGGTATGGTGGTTATCAGCCC -3 | 5-CGAAAGGAGCGATCCGAGG -3 |
| <i>BnaEF1-α</i> | 5-GCCTGGTATGGTTGTGACCT -3 | 5- GAAGTTAGCAGCACCCCTTGG-3 |
| <i>BnaTublin</i> | 5-CAGCAATACAGTGCCTTGAGTG-3 | 5-CCTGTGTACCAATGAAGGAAAGCC -3 |