Figure S1. Chrysanthemum sequences acquired by RNA-Seq. (A) Homology of chrysanthemum unigenes to those represented in the Nr database. (B) Similarity distribution of the result against Nr database. (C) The match between differentially transcribed chrysanthemum unigenes and sequences derived from other plant species.
Figure S2 COG and GO classification of differentially transcribed chrysanthemum unigenes. (A) COG-based functional classification of differentially transcribed chrysanthemum unigenes. (B) GO classification of differentially transcribed chrysanthemum unigenes.
Figure S3 reads per kilobase per million mapped reads. FDR: false discovery rate. The axes indicate the frequency of recovery of each sequence. WT-SD represents wild type plants under short day conditions, WT-LD represents wild type plants under long day conditions, M-SD represents mutant plants under short day conditions, M-LD represents mutant plants under long day conditions. (Red: up-regulated, green: down-regulated, blue: not differentially transcribed).

Figure S4 Venn diagram to classify differentially expressed genes in ‘Jinba’ WT and M plants under SD and LD.
Table S1. List of assembled transcripts up-regulated or down-regulated (> or < 2.0 fold) in WT and M chrysanthemum plant under SD and LD

<table>
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<th>WT-SD ratio</th>
<th>FDR</th>
<th>WT-SD ratio</th>
<th>P value</th>
<th>M-SD/M-LD ratio</th>
<th>FDR</th>
<th>M-LD/WT-LD ratio</th>
<th>P value</th>
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GA biosynthesis and signaling

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| Unigene27 395_All | 2.36 | 3.36 | 0.7 | **0.0121** | 0.05 | 3.36 | 3.19 | **1.05** | 0.705 | 0.813 | 2.36 | 8.18 | 0.29 | 5E-28 | 1E-26 | 8.18 | 3.19 | 2.56 | 1E-18 | 0 | Gibberellin receptor GID1
| Unigene27 740_All | 12.22 | 14.43 | 0.85 | **0.0011** | 0.007 | 14.43 | 45.74 | 0.32 | 12.22 | 23.59 | 0.52 | 2E-47 | 1E-45 | 23.59 | 45.74 | 0.5 | 6E-89 | 0 | DELLA protein GAI

**Flowering integrators**

| CL1484.Contig1_All | 0.41 | 0.39 | 0.93 | **0.8889** | 0.951 | 0.39 | 12.17 | 0.03 | 6E-72 | 4E-70 | 0.41 | 12.12 | 0.03 | 3E-72 | 2E-70 | 12.12 | 12.17 | **1.23** | 0.967 | 0.97 | flowering locus T-Like 1 protein [Chrysanthemum x morifolium]
| CL1484.Contig2_All | 31.81 | 16.88 | 1.88 | 6E-51 | 7E-49 | 16.88 | 1.68 | 3.94 | 31.81 | 2.08 | 15.32 | 0 | 0 | 2.08 | 1.68 | **1.23** | 0.169 | 0.31 | flowering locus T-Like 3 protein [Chrysanthemum x morifolium] MADS-box protein SOC1
| Unigene40 592_All | 17.65 | 8.68 | 2.03 | 2E-21 | 1E-19 | 8.68 | 3.6 | 2.41 | 9E-15 | 2E-13 | 17.65 | 16.82 | **1.05** | 0.455 | 0.576 | 16.82 | 3.6 | 4.67 | 5E-57 | 0 | Chrysanthemum x morifolium FLO/LFY-like protein gene APETALA1 and FRUITFULL like protein [Chrysanthemum seticuspe f. boreale]
| Unigene25 380_All | 0.57 | 0.75 | 0.76 | **0.3343** | 0.524 | 0.75 | 1.28 | 0.02 | 0.066 | 0.57 | 8.5 | 0.07 | 1E-71 | 8E-70 | 8.5 | 1.28 | 6.66 | 2E-50 | 0 |
| Unigene23 898_All | 76.84 | 47.87 | 1.61 | 1E-56 | 2E-54 | 47.87 | 1.54 | 31.12 | 0 | 0 | 76.84 | 2.03 | 37.89 | 0 | 0 | 2.03 | 1.54 | 1.32 | 0.126 | 0.25 |

**Aging, ambient temperature and autonomous pathway**

| Unigene29 044_All | 0.4 | 1.3 | 0.33 | **0.0024** | 0.014 | 1.3 | 9.51 | 0.14 | 2E-33 | 7E-32 | 0.4 | 7.11 | 0.06 | 2E-33 | 0.03 | 7.11 | 9.51 | **0.75** | 0.008 | 0.03 | Squamosa promoter-binding-like protein 5
| CL14613.Contig14_All | 2.96 | 1.01 | 2.93 | 1E-07 | 2E-06 | 1.01 | 1.59 | **0.63** | 0.056 | 0.144 | 2.96 | 1.6 | 1.85 | 8E-04 | 0.994 | 1.6 | 1.59 | 1 | 0.992 | 0.99 | FLC-like
| CL8773.Contig1_All | 1.7 | 1.03 | 1.92 | 4E-05 | 4E-04 | 1.03 | 0.89 | **0.86** | 0.396 | 0.568 | 1.7 | 0.63 | 2.7 | 1E-08 | 0.044 | 0.63 | 0.89 | **0.61** | 0.013 | 0.04 | Protein FRIGIDA
| Unigene20 776_All | 23.5 | 42.08 | 0.56 | 2E-45 | 2E-43 | 42.08 | 308.8 | 0.14 | 0 | 0 | 23.5 | 167.5 | 0.14 | 0 | 0 | 167.5 | 308.8 | 0.54 | 0 | MADS-box protein SVP

The bold repeat those genes are not differentially expressed and P>0.001.
Table S2: Transcription factor genes, arranged by family, which were differentially transcribed in WT and M chrysanthemum plants grown under SD and LD.

<table>
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<tr>
<th>unigene</th>
<th>WT-SD / WT-LD</th>
<th>WT-SD</th>
<th>WT-LD</th>
<th>ratio</th>
<th>P-value</th>
<th>Nr Annotation</th>
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<tr>
<td>Unigene2122_All</td>
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<td>6.3949</td>
<td>3.294532</td>
<td>1.6812E-75</td>
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<td>7.39666E-06</td>
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<tr>
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List of difference expression MYB family (> 2 fold or < 0.5, p<0.001) in M-SD /WT-SD chrysanthemum plants

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**Table S3.** qRT-PCR primer combinations used for quantifying the transcription of WT and M plants.