Figure S1

![Image of gel electrophoresis with bands labeled 1, 2, and 3 for Ugp1 and rRNA, with Co27HT, H1493, and Co27LT samples]
Figure S2

This figure shows the gene expression levels for various GO-Terms between two clusters. The blue bars represent genes down-regulated in cluster 10, while the red bars represent genes up-regulated in cluster 15. The categories include:

- response to stress
- response to endogenous stimulus
- response to abiotic stimulus
- oxidation-reduction process
- response to salt stress
- carbohydrate metabolic process
- response to cold
- response to oxidative stress
- response to water deprivation
- lipid transport
- hydrogen peroxide catabolic process
- response to light stimulus
- response to osmotic stress
- chlorophyll catabolic process
- response to light intensity

The y-axis represents the GO-Terms, and the x-axis represents the number of genes.
Figure S4

![Image showing a gel electrophoresis with bands for different samples and genes](image-url)
SUPPLEMENTAL FIGURE LEGENDS

Figure S1. RNA gel blot analysis of *Ugp1* transcript levels in meiosis-stage florets.

The RNA gel blot was hybridized with corresponding *Ugp1* probes. Arrowheads indicate: (1) the unprocessed longer-than-full-length transcript; (2) endogenous *Ugp1* mRNA; (3) silencing-related RNA degradation intermediates. Loading of equal amounts of RNA was confirmed by ethidium bromide staining. H1493 refers to a mixture (in equal proportions) of total RNAs from H1493 plants grown at high temperature and low temperature. Co27HT and Co27LT refer to TGMS-Co27 plants grown at high temperature and low temperature, respectively.

Figure S2. GO slimes of functional categorization of DEGs related to stress responses.

The abscissa represents the number of corresponding genes in clusters 10 and 15 (genes down-regulated and up-regulated by different environmental conditions).

Figure S3. Heatmap of the expression of TGMS-related genes in the four sample types.

H1493HT and H1493LT refer to H1493 plants grown at high temperature and low temperature, respectively. Co27HT and Co27LT refer to TGMS-Co27 plants grown at high temperature and low temperature, respectively.

Figure S4. Semi-quantitative RT-PCR analysis of the expression and splicing patterns of selected serine/arginine-rich (*SR*) genes.

The names of the genes are shown on the left of each panel. An equal quantity of template in each reaction was verified by amplifying a constitutively expressed actin.
Table S1. Pollen development-related genes that were repressed in TGMS-Co27 plants at high temperature.

<table>
<thead>
<tr>
<th>QuerySymbol</th>
<th>probeID</th>
<th>Description</th>
<th>E-Value</th>
<th>SubjectSymbol</th>
<th>logFC_ Co27H/ Co27L/ HL/HH</th>
</tr>
</thead>
<tbody>
<tr>
<td>LOC_Os01g03670</td>
<td>Os.20305.1.S 1_at</td>
<td>dihydroflavonol-4-reductase, putative, expressed</td>
<td>1.00E-116</td>
<td>AT1G68540.2</td>
<td><strong>-1.87</strong> -1.63 -1.39</td>
</tr>
<tr>
<td>LOC_Os01g48440</td>
<td>Os.19374.1.S 1_at</td>
<td>glycosyltransferase family 43 protein, putative, expressed</td>
<td>3.00E-62</td>
<td>AT1G27600.2</td>
<td><strong>-1.53</strong> -0.24 <strong>1.46</strong></td>
</tr>
<tr>
<td>LOC_Os02g02560</td>
<td>Os.2370.1.S1 _at</td>
<td>uridylyltransferase, putative, expressed</td>
<td>0</td>
<td>AT5G17310.2</td>
<td><strong>-1.39</strong> -0.42 -0.44</td>
</tr>
<tr>
<td>LOC_Os06g08380</td>
<td>OsAffx.27509.1.S2_at</td>
<td>component domain containing protein, expressed</td>
<td>0</td>
<td>AT2G13680.1</td>
<td><strong>-2.59</strong> -1.44 -0.54</td>
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<tr>
<td>LOC_Os07g22850</td>
<td>OsAffx.28544.2.S1_x_at</td>
<td>chalcone and stilbene synthases, putative, expressed</td>
<td>1.00E-156</td>
<td>AT4G34850.1</td>
<td><strong>-3.4</strong> 0.41 <strong>-4.05</strong></td>
</tr>
<tr>
<td>LOC_Os09g38030</td>
<td>Os.10118.1.S 1_at</td>
<td>uridylyltransferase, putative, expressed</td>
<td>0</td>
<td>AT5G17310.2</td>
<td><strong>-2.01</strong> -0.73 0.21</td>
</tr>
</tbody>
</table>

HH and HL refer to H1493 plants grown at high temperature and low temperature, respectively, while Co27H and Co27L refer to TGMS-Co27 plants grown at high temperature and low temperature, respectively. Significant changes (p < 0.05; fold change ≥ 2) are indicated by boldface.