Complete USDA-GRIN database

Retained phenotypes for genotyped *M. domestica*

Phenotypes recoded

Clones averaged

Phenotypes averaged across years

Final data set

Removed phenotypes with an extremely skewed distribution

Removed phenotypes with no variability

Removed phenotypes with <100 samples

Removed categorical phenotypes
Fruit shape uniformity (N = 642)

Fruit size uniformity (N = 656)

Fruit stem length (N = 654)

Fruit stem thickness (N = 655)

Fruit texture (N = 650)

Fruit weight (N = 656)

Fruit width (N = 641)

Harvest season (N = 654)

Harvest uniformity (N = 406)
Fruit shape uniformity (N = 642)

Fruit size uniformity (N = 656)

Fruit stem length (N = 654)

Fruit stem thickness (N = 655)

Fruit texture (N = 650)

Fruit weight (N = 656)

Fruit width (N = 641)

Harvest season (N = 654)

Harvest uniformity (N = 406)
The diagram illustrates the proportion of variance explained (R²) for various phenotypic traits grouped under Floral, Inner Fruit, Outer Fruit, Phenology, and Vegetative categories. Each trait is represented by a bar, with the color indicating the principal component. The x-axis shows the proportion of variance explained, ranging from 0.00 to 0.30. The y-axis lists the specific traits, with each trait's bar indicating its contribution to the variance explained by each principal component.
calyx persistence (N = 641)

calyx basin (N = 653)

flower size (N = 192)
flower color (N = 290)

fruit flesh color (N = 612)

fruit flesh flavor (N = 645)
fruit length (N = 654)

fruit overcolor (N = 574)

fruit russet intensity (N = 590)
fruit russet location (N = 532)

fruit russet type (N = 533)

fruit shape uniformity (N = 642)
fruit size uniformity (N = 656)

fruit stem length (N = 654)

fruit stem thickness (N = 655)
fruit juiciness (N = 435)

fruit shape overall (N = 630)

fruit width (N = 641)
overcolor intensity (N = 630)

overcolor pattern (N = 640)

prebloom flower color (N = 217)
soluble solids (N = 650)

stem cavity (N = 653)

fruit shape top (N = 656)
tree bearing habit (N = 462)

- \log_{10} P

Chromosome

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tree vigor (N = 463)

- \log_{10} P

Chromosome

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young leaf color (N = 611)

- \log_{10} P

Chromosome
<table>
<thead>
<tr>
<th>Species</th>
<th>NAC Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apple derived (Malus domestica)</td>
<td>MECT YSS SAGS</td>
</tr>
<tr>
<td>Apple ancestral (Malus domestica)</td>
<td>MECT TDS SAGS</td>
</tr>
<tr>
<td>Pear (Pyrus bretschneideri)</td>
<td>MEST TDS SAGS</td>
</tr>
<tr>
<td>Grape (Vitis vinifera)</td>
<td>MEST TDS SSGS</td>
</tr>
<tr>
<td>Arabidopsis (Arabidopsis thaliana)</td>
<td>MEST TDS SGGP</td>
</tr>
<tr>
<td>Poplar (Populus euphratic)</td>
<td>MEGT I SSS G S G S</td>
</tr>
<tr>
<td>Kiwifruit (Actinidia arguta) NAC1</td>
<td>MEST D S S T G S</td>
</tr>
<tr>
<td>Kiwifruit (Actinidia arguta) NAC2</td>
<td>MESP D S S V G L</td>
</tr>
<tr>
<td>Rice (Oryza sativa Japonica Group)</td>
<td>MESP D S S G S G S</td>
</tr>
<tr>
<td>Wheat (Aegilops longissima)</td>
<td>MGSP D S S G S G S</td>
</tr>
</tbody>
</table>
Genomic prediction accuracy ($r$) $p = 1.141 \times 10^{-13}$ $r = 0.898$

Proportion of phenotypic variance explained by PCs 1 to 10 ($R^2$)