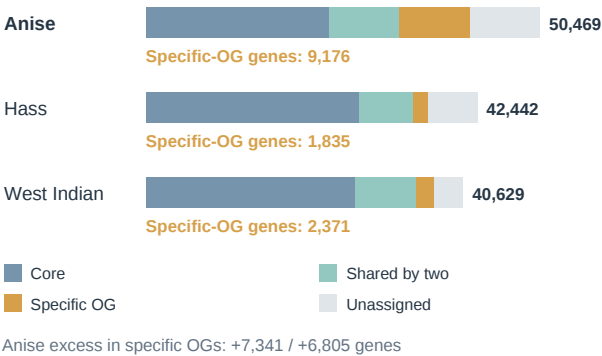


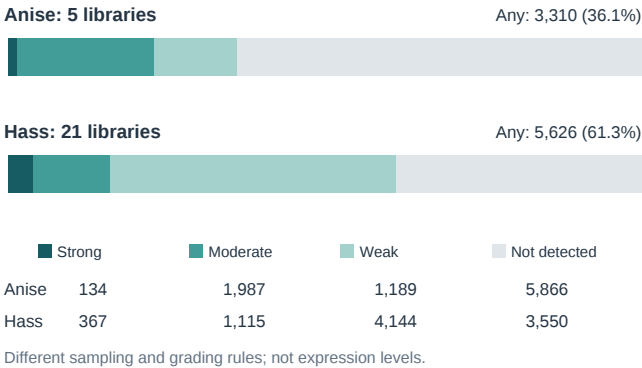
Reassessment of annotation-defined Anise-specific candidates

9,176 candidates | Direct Anise RNA evidence and cross-cultivar Hass RNA evidence

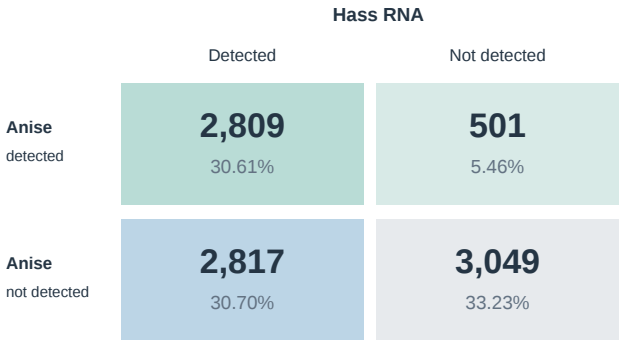
A Gene annotation and Orthogroup partition



B RNA support for the same 9,176 candidates



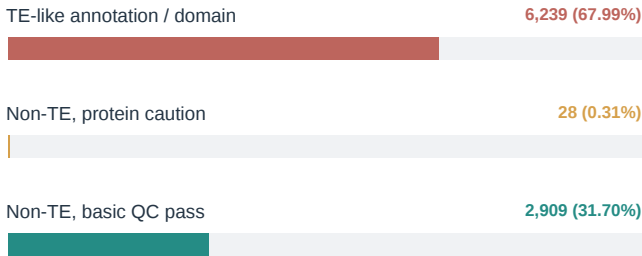
C Joint RNA evidence: overlapping sets



Either RNA source: 6,127 / 9,176 (66.77%)

Detected includes weak signals; non-detection is not absence.

D TE and protein-quality reassessment



TE-like and RNA-supported sets overlap:
4,098 TE-like candidates have at least one RNA signal.
Transcription alone does not establish a non-TE coding gene.

E Prioritization of 2,909 retained candidates

Tier1	RNA + structural evidence	21
Tier2	Anise RNA; Hass not detected	155
Tier2b	Anise RNA; weak Hass signal	685
Tier3	Strong/moderate Hass signal	380
Tier4	Limited RNA/structural evidence	1,066
Tier5	No RNA or strict structural support	602

Tier1 + Tier2 = 176 selected for deeper review
Priority classes do not establish genomic specificity.

F Follow-up of the 176 selected candidates

