**Genome-wide identification and expression profile of the YABBY genes in *Averrhoa carambola***

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Supporting Materials

**Figure S1.** Sample preparations. A: flower bracts; B: inflorescences; C and D: anatomical and front views of the fruits, respectively. (Scale bar: C and D, 2 cm)

**Figure S2.** Domain of YABBY genes in star fruit.

**Figure S3.** Conserved motifs of YABBY genes in *A. thaliana* and star fruit were predicted by MEME. Grey lines represent the non-conserved sequences, and four conserved motifs are indicated by different colors with numbered boxes.

**Figure S4.** Chromosomal locations of *AcYABBYs*. A total of five chromosomes of star fruit were labeled with their names, Chr.02, Chr.04, Chr.06, Chr.08, and Chr.09, which are indicated at the top of each bar. The position of *AcYABBYs* on the chromosome was drawn by online software MG2C (<http://mg2c.iask.in/mg2c_v2.0/>) based on GFF file.

**Figure S5.** Gene structure of the *AcYABBYs* in star fruit. Exons and introns are represented by yellow rectangle and black lines, respectively. The lengths of exons and introns for each *AcYABBY* gene are shown proportionally.

**Figure S6.** The analysis of YABBY protein secondary structures. Different color blocks represent different secondary structures.

**Figure S7.** Cis-acting elements of *AcYABBYs* in promoter regions. *Note:* The numbers of different cis-elements are presented in the form of bar graphs and similar cis-elements are exhibited with the same colors.

**Table S1.** The primers of *AcYABBYs* and reference genes

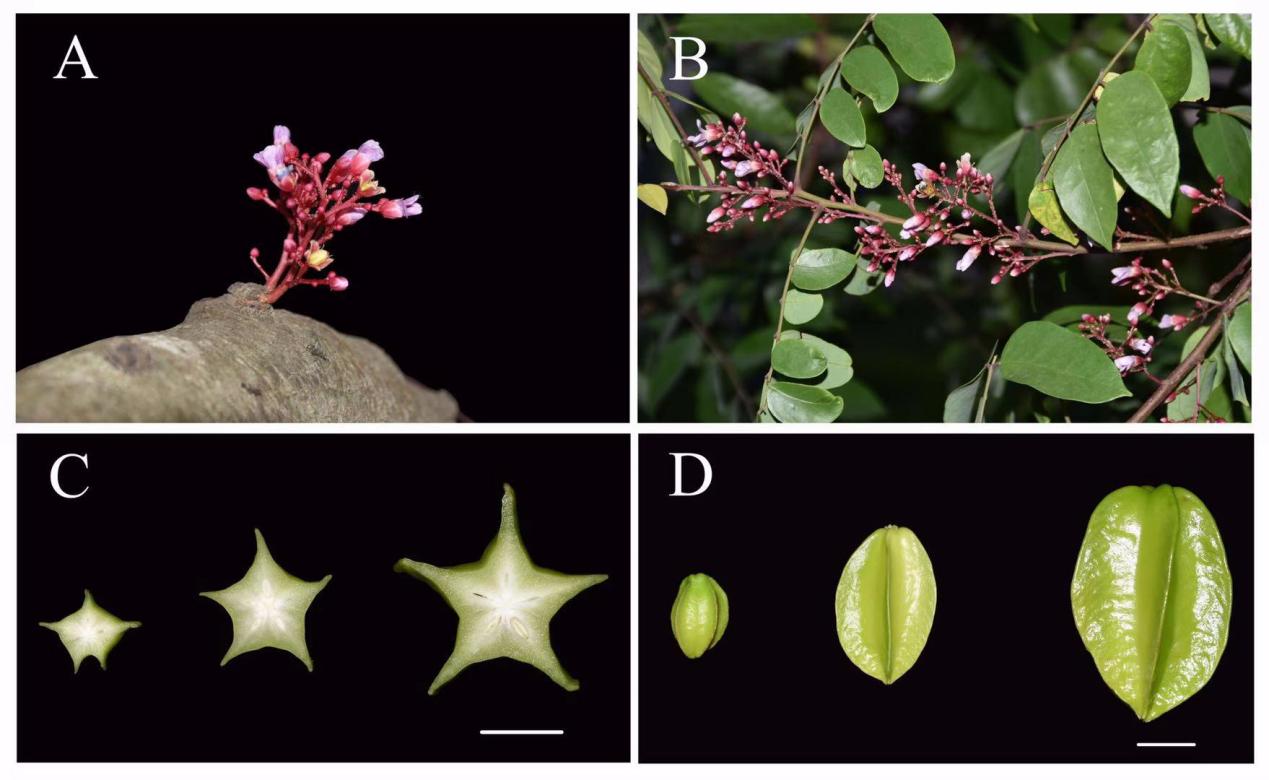
**Table S2.** The basic information of YABBY family members in *Ave. carambola*.

**Table S3.** Subcellular localization prediction using three protein subcellular location prediction tools

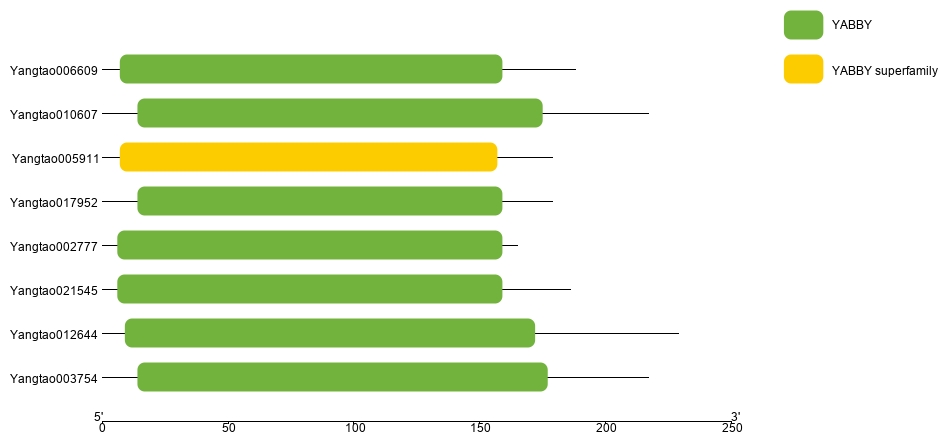
**Table S4.** *YABBY* genes in *A. thaliana*, *O. sativa*, *S. lycopersicum*, *V. vinifera*, *Z. mays*, and *Ave. carambola*.

**Table S5.** Selective pressure analysis of *AcYABBYs*.

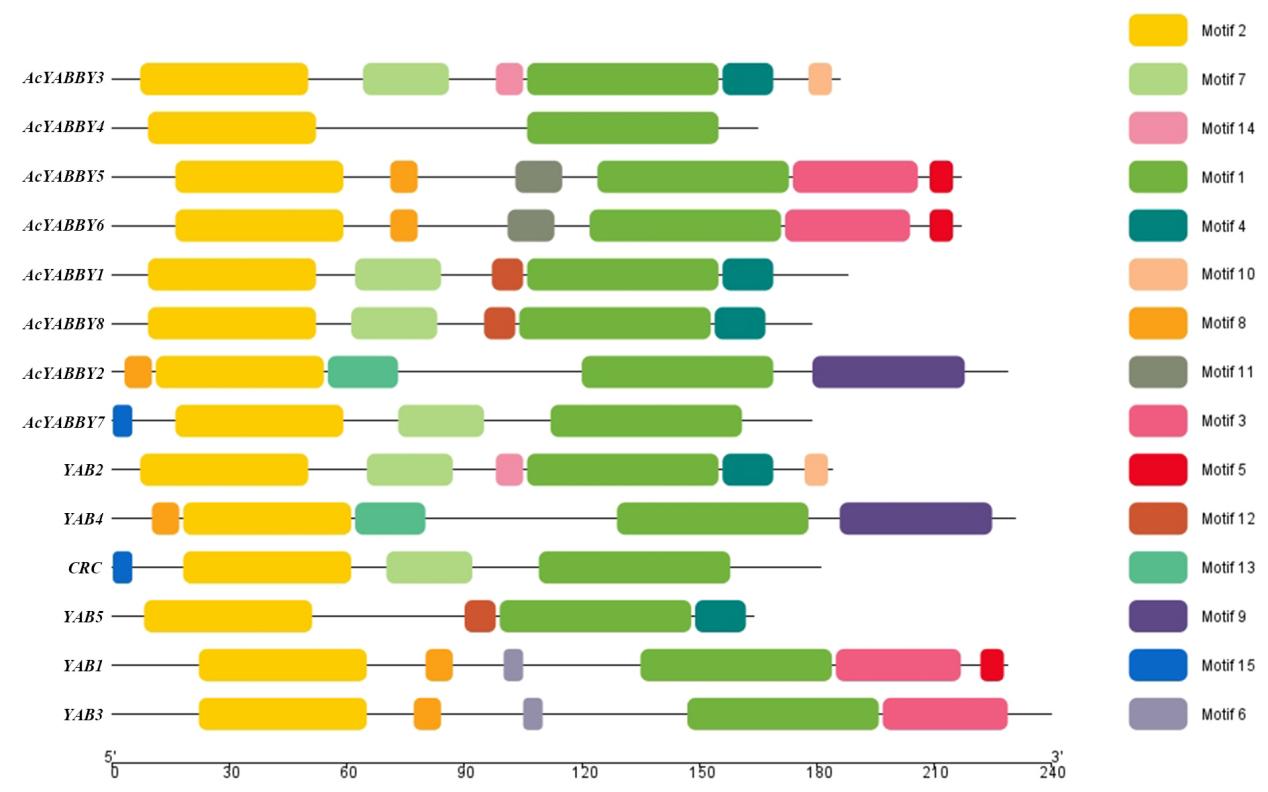
**Data S1.** The sequence of eight *AcYABBYs*.

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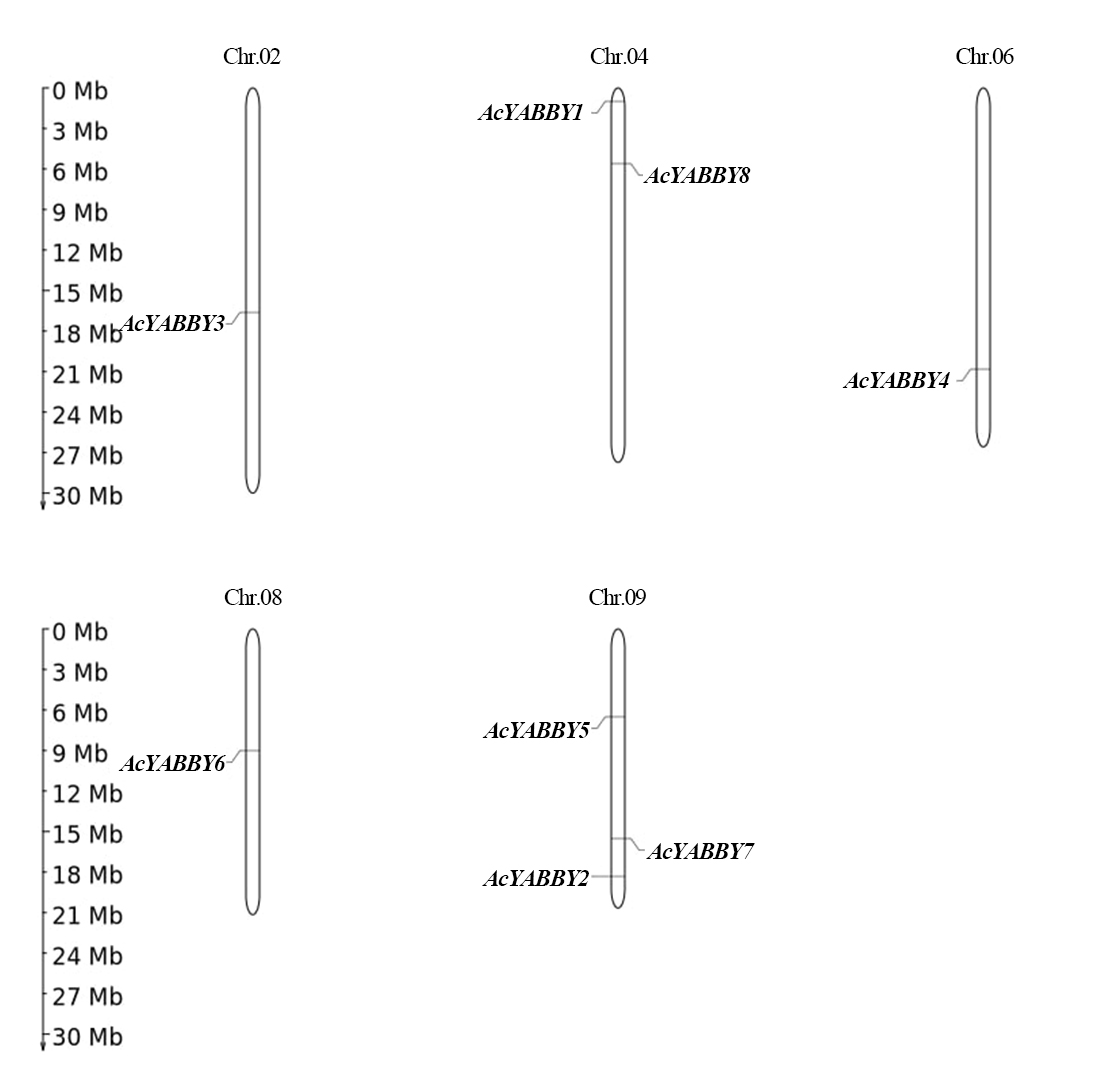
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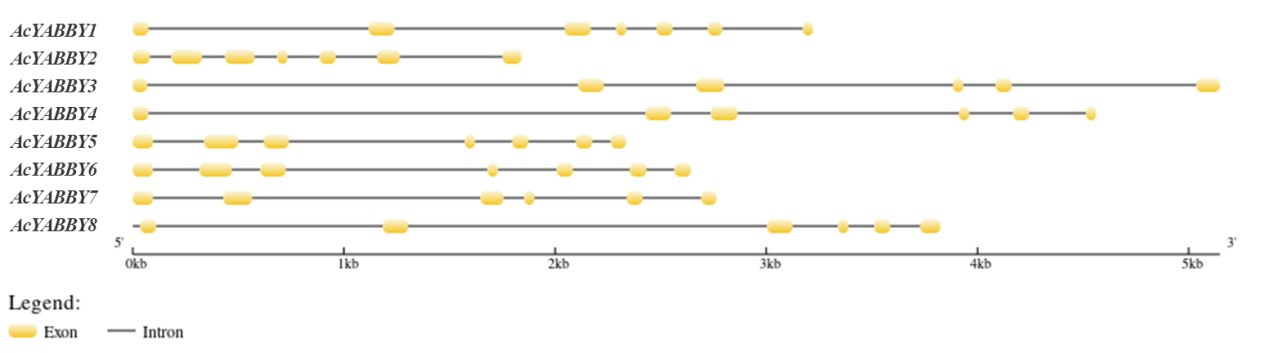
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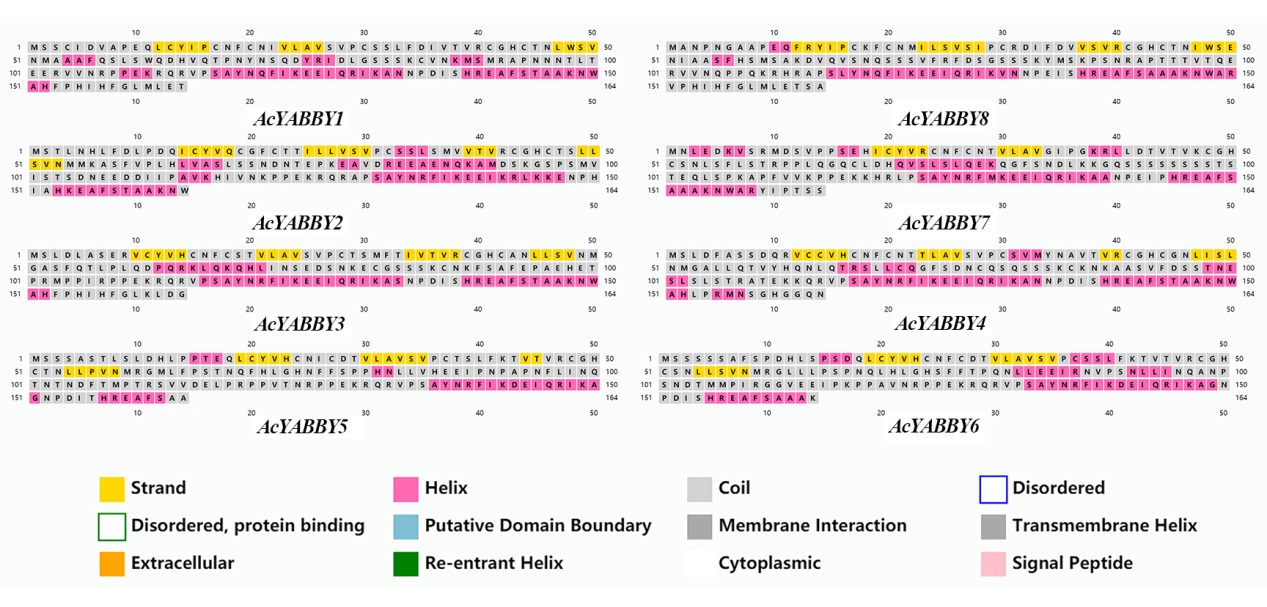
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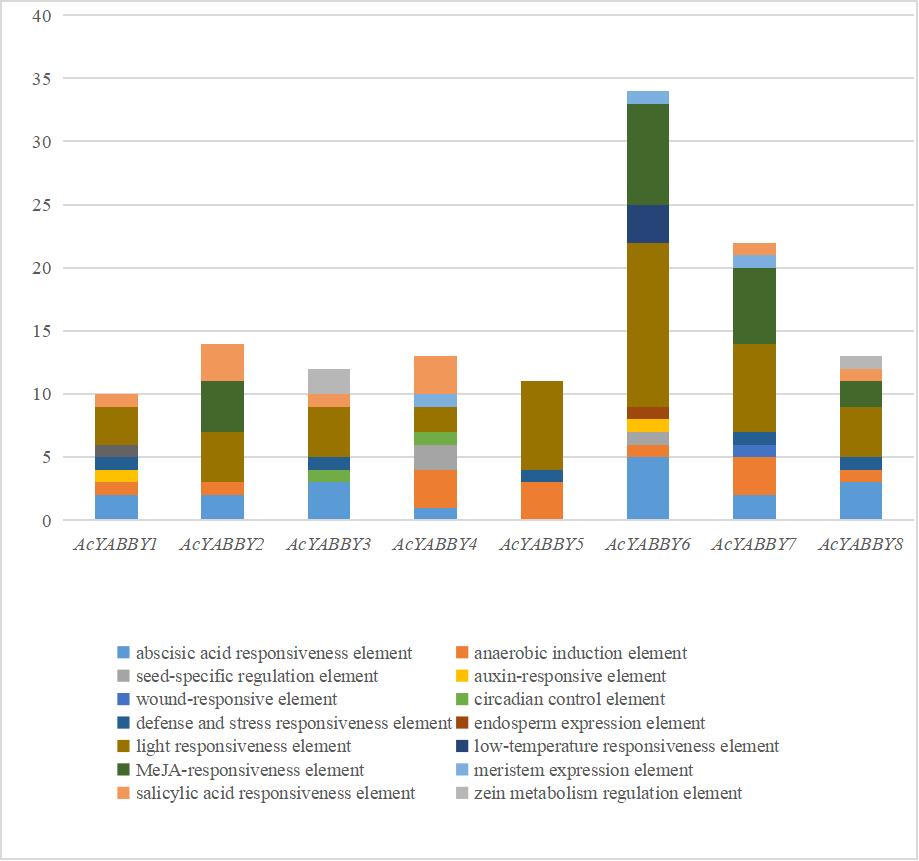
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**Figure S5.** Gene structure of the *AcYABBYs* in star fruit. Exons and introns are represented by yellow rectangle and black lines, respectively. The lengths of exons and introns for each *AcYABBY* gene are shown proportionally.



**Figure S6.** The analysis of YABBY protein secondary structures. Different color blocks represent different secondary structures.



**Figure S7.** Cis-acting elements of *AcYABBYs* in promoter regions. *Note:* The numbers of different cis-elements are presented in the form of bar graphs and similar cis-elements are exhibited with the same colors.

**Table S1.** The primers of *AcYABBYs* and reference genes

|  |  |  |
| --- | --- | --- |
| Genes | （5′–3′）Forward primer | （5′–3′）Reverse primer |
| *AcYABBY1* | CAACTCTGCTACATCCCTTGC | GATCTTGCCATGAAAGTGACTG |
| *AcYABBY2* | ACGTGCAATGTGGTTTCTG | TGACTGAGAGAAGACTTGTGCAG |
| *AcYABBY3* | GAGAGAGTTTGTTATGTTCACTGCA | GAGGAAGTGTTTGAAATGAAGCTC |
| *AcYABBY4* | CTCGACTTTGCTTCTTCTGATC | CTTTGTTGCAGACTGTCTATCATC |
| *AcYABBY5* | CTCCTCAGCTTCTACCTTGTCTTT | GCATATTCACAGGCAGGAGAT |
| *AcYABBY6* | TCATCTGCTTTTTCACCGG | GCAGTCCACGCATGTTAACT |
| *AcYABBY7* | CACCATCCGAGCACATCT | AGTGGATCTGGTGCTGAGAAA |
| *AcYABBY8* | GCACCTGAGCAATTTCGC | GTTGGAGACCTGGACATCC |
| *ACTB* | CAGTGTCTGGATTGGAGGA | ATCTGTTGGAAGGTGCTGA |

**Table S2.** The basic information of YABBY family members in *Ave. carambola*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Nomenclature | Gene ID | Subfamily | Acession ID | Length of protein | MW (Da) | PI | Subcellular location |
| Yangtao006609 | *AcYABBY1* | YAB5 | MW014334 | 194 | 21287.25 | 8.13 | Nuclear |
| Yangtao012644 | *AcYABBY2* | INO | MW014336 | 235 | 25197.26 | 5.22 | Nuclear |
| Yangtao021545 | *AcYABBY3* | YAB2 | MW014333 | 192 | 20881.77 | 8.81 | Nuclear |
| Yangtao002777 | *AcYABBY4* | YAB2 | MW014337 | 169 | 18053.34 | 9.00 | Nuclear |
| Yangtao003754 | *AcYABBY5* | FIL/YAB3 | MW014335 | 223 | 24246.62 | 7.72 | Nuclear |
| Yangtao010607 | *AcYABBY6* | FIL/YAB3 | MW014332 | 223 | 23901.23 | 8.25 | Nuclear |
| Yangtao017952 | *AcYABBY7* | CRC | MW014338 | 183 | 19689.35 | 9.56 | Nuclear |
| Yangtao005911 | *AcYABBY8* | YAB5 | MW014339 | 183 | 19886.57 | 9.37 | Nuclear |

**Table S3.** Subcellular localization prediction using three protein subcellular location prediction tools

|  |  |  |  |
| --- | --- | --- | --- |
| Proteins | LocTree3 (confidence%) | PSORT (confidence%) | Softberry (score) |
| *AcYABBY3* | 89%: nucleus | 69.6 %: nuclear | Nuclear: 9.1 |
| *AcYABBY4* | 91%: nucleus | 78.3 %: nuclear | Nuclear: 9 |
| *AcYABBY5* | 87%: nucleus | 69.6 %: nuclear | Nuclear: 9.1 |
| *AcYABBY6* | 89%: nucleus | 73.9 %: nuclear | Nuclear: 9.1 |
| *AcYABBY1* | 94%: nucleus | 69.6 %: nuclear | Nuclear: 9 |
| *AcYABBY8* | 92%: nucleus | 78.3 %: nuclear | Nuclear: 9 |
| *AcYABBY2* | 88%: nucleus | 82.6 %: nuclear | Nuclear: 8.8 |
| *AcYABBY7* | 89%: nucleus | 82.6 %: nuclear | Nuclear: 8.9 |

**Table S4.** *YABBY* genes in *A. thaliana*, *O. sativa*, *S. lycopersicum*, *V. vinifera*, *Z. mays*, and *Ave. carambola*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Subfamilies | *A. thaliana* | *O. sativa* | *S. lycopersicum* | *V. vinifera* | *Z. mays* | *Ave. carambola* |
| YAB3/FIL | 1 | 3 | 2 | 2 | 5 | 2 |
| YAB2 | 1 | 3 | 2 | 2 | 5 | 2 |
| YAB5 | 1 | 0 | 2 | 1 | 0 | 2 |
| INO | 1 | 1 | 1 | 1 | 1 | 1 |
| CRC | 1 | 1 | 2 | 1 | 2 | 1 |
| Total | 6 | 8 | 9 | 7 | 13 | 8 |

**Table S5.** Selective pressure analysis of *AcYABBYs*.

|  |  |  |  |
| --- | --- | --- | --- |
| Gene pairs | Ka | Ks | Ka/Ks |
| *AcYABBY1*-*AcYABBY2* | 0.480962 | 2.66364 | 0.180566 |
| *AcYABBY1*-*AcYABBY7* | 0.479474 | 2.65874 | 0.180338 |
| *AcYABBY1*-*AcYABBY8* | 0.241087 | 0.877205 | 0.274836 |
| *AcYABBY2*-*AcYABBY7* | 0.653473 | 2.08623 | 0.313231 |
| *AcYABBY3*-*AcYABBY1* | 0.253378 | 3.51706 | 0.072043 |
| *AcYABBY3*-*AcYABBY2* | 0.43698 | 2.87199 | 0.152152 |
| *AcYABBY3*-*AcYABBY4* | 0.28933 | 2.13382 | 0.135593 |
| *AcYABBY3*-*AcYABBY5* | 0.339389 | 3.17847 | 0.106777 |
| *AcYABBY3*-*AcYABBY6* | 0.338746 | 3.2288 | 0.104914 |
| *AcYABBY3*-*AcYABBY7* | 0.479383 | 2.58086 | 0.185745 |
| *AcYABBY3*-*AcYABBY8* | 0.422429 | 2.82667 | 0.149444 |
| *AcYABBY4*-*AcYABBY1* | 0.383274 | 3.1167 | 0.122974 |
| *AcYABBY4*-*AcYABBY2* | 0.498694 | 2.64518 | 0.188529 |
| *AcYABBY4*-*AcYABBY5* | 0.475185 | 2.76021 | 0.172155 |
| *AcYABBY4*-*AcYABBY6* | 0.441681 | 2.87623 | 0.153562 |
| *AcYABBY4*-*AcYABBY7* | 0.54048 | 2.45434 | 0.220214 |
| *AcYABBY4*-*AcYABBY8* | 0.471921 | 2.82097 | 0.16729 |
| *AcYABBY5*-*AcYABBY1* | 0.444926 | 2.91518 | 0.152624 |
| *AcYABBY5*-*AcYABBY2* | 0.591704 | 2.33286 | 0.253639 |
| *AcYABBY5*-*AcYABBY6* | 0.14116 | 1.00591 | 0.140331 |
| *AcYABBY5*-*AcYABBY7* | 0.556525 | 2.34785 | 0.237036 |
| *AcYABBY5*-*AcYABBY8* | 0.56551 | 2.42067 | 0.233617 |
| *AcYABBY6*-*AcYABBY1* | 0.428934 | 2.92835 | 0.146477 |
| *AcYABBY6*-*AcYABBY2* | 0.59031 | 2.29868 | 0.256804 |
| *AcYABBY6*-*AcYABBY7* | 0.54795 | 2.36836 | 0.231362 |
| *AcYABBY6*-*AcYABBY8* | 0.535098 | 2.47645 | 0.216075 |
| *AcYABBY8*-*AcYABBY2* | 0.533001 | 2.49644 | 0.213504 |
| *AcYABBY8*-*AcYABBY7* | 0.554948 | 2.3545 | 0.235696 |

*Note:* Ka indicates the number of [nonsynonymous substitutions](https://en.wikipedia.org/wiki/Nonsynonymous_substitution) per non-synonymous site; Ks indicates the number of [synonymous substitutions](https://en.wikipedia.org/wiki/Synonymous_substitution) per synonymous site. 0< Ka/Ks <1, negative selection; Ka/Ks =1, neutral selection; Ka/Ks >1, positive selection.

**Data S1.** The sequences of eight *AcYABBYs*.

>*AcYABBY3*

MSLDLASERVCYVHCNFCSTVLAVSVPCTSMFTIVTVRCGHCANLLSVNMGASFQTLPLQ

DPQRKLQKQHLINSEDSNKECGSSSKCNKFSAFEPAEHETPRMPPIRPPEKRQRVPSAYN

RFIKEEIQRIKASNPDISHREAFSTAAKNWAHFPHIHFGLKLDGNKQARMEQALEEGTQK

SNGFY\*

>*AcYABBY4*

MSLDFASSDQRVCCVHCNFCNTTLAVSVPCSVMYNAVTVRCGHCGNLISLNMGALLQTVY

HQNLQTRSLLCQGFSDNCQSQSSSKCKNKAASVFDSSTNESLSLSTRATEKKQRVPSAYN

RFIKEEIQRIKANNPDISHREAFSTAAKNWAHLPRMNSGHGGQN\*

>*AcYABBY5*

MSSSASTLSLDHLPPTEQLCYVHCNICDTVLAVSVPCTSLFKTVTVRCGHCTNLLPVNMR

GMLFPSTNQFHLGHNFFSPPHNLLVHEEIPNPAPNFLINQTNTNDFTMPTRSVVDELPRP

PVTNRPPEKRQRVPSAYNRFIKDEIQRIKAGNPDITHREAFSAAAKNWAHFPHIHFGLMP

DQTTVKKTNMRPQEGDDVLMKENGYFASANVGVSPY\*

>*AcYABBY6*

MSSSSSAFSPDHLSPSDQLCYVHCNFCDTVLAVSVPCSSLFKTVTVRCGHCSNLLSVNMR

GLLLPSPNQLHLGHSFFTPQNLLEEIRNVPSNLLINQANPSNDTMMPIRGGVEEIPKPPA

VNRPPEKRQRVPSAYNRFIKDEIQRIKAGNPDISHREAFSAAAKNWAHFPHIHFGLLPDH

QPVKKANVRQQEGEDVLMKDGFFTAPPATNVGVTPY\*

>*AcYABBY1*

MSSCIDVAPEQLCYIPCNFCNIVLAVSVPCSSLFDIVTVRCGHCTNLWSVNMAAAFQSLS

WQDHVQTPNYNSQDYRIDLGSSSKCVNKMSMRAPNNNTLTEERVVNRPPEKRQRVPSAYN

QFIKEEIQRIKANNPDISHREAFSTAAKNWAHFPHIHFGLMLETNNQPKMDDGPEKHLMP

RTALLHK\*

>*AcYABBY8*

MANPNGAAPEQFRYIPCKFCNMILSVSIPCRDIFDVVSVRCGHCTNIWSENIAASFHSMS

AKDVQVSNQSSSVFRFDSGSSSKYMSKPSNRAPTTTVTQERVVNQPPQKRHRAPSLYNQF

IKEEIQRIKVNNPEISHREAFSAAAKNWARVPHIHFGLMLETSANSTKLDDVSAIAVK\*

>*AcYABBY2*

MSTLNHLFDLPDQICYVQCGFCTTILLVSVPCSSLSMVVTVRCGHCTSLLSVNMMKASFV

PLHLVASLSSNDNTEPKEAVDREEAENQKAMDSKGSPSMVISTSDNEEDDIIPAVKHIVN

KPPEKRQRAPSAYNRFIKEEIKRLKKENPHIAHKEAFSTAAKNWAQNPPMQFNRDEESCG

QEVEEGEGEATWNPNAVEGVDIQGNGFRERKSPEGLDTGSKNNFSTVA\*

>*AcYABBY7*

MNLEDKVSRMDSVPPSEHICYVRCNFCNTVLAVGIPGKRLLDTVTVKCGHCSNLSFLSTR

PPLQGQCLDHQVSLSLQEKQGFSNDLKKGQSSSSSSSSTSTEQLSPKAPFVVKPPEKKHR

LPSAYNRFMKEEIQRIKAANPEIPHREAFSAAAKNWARYIPTSSNGSVSRTSNNVRNI\*