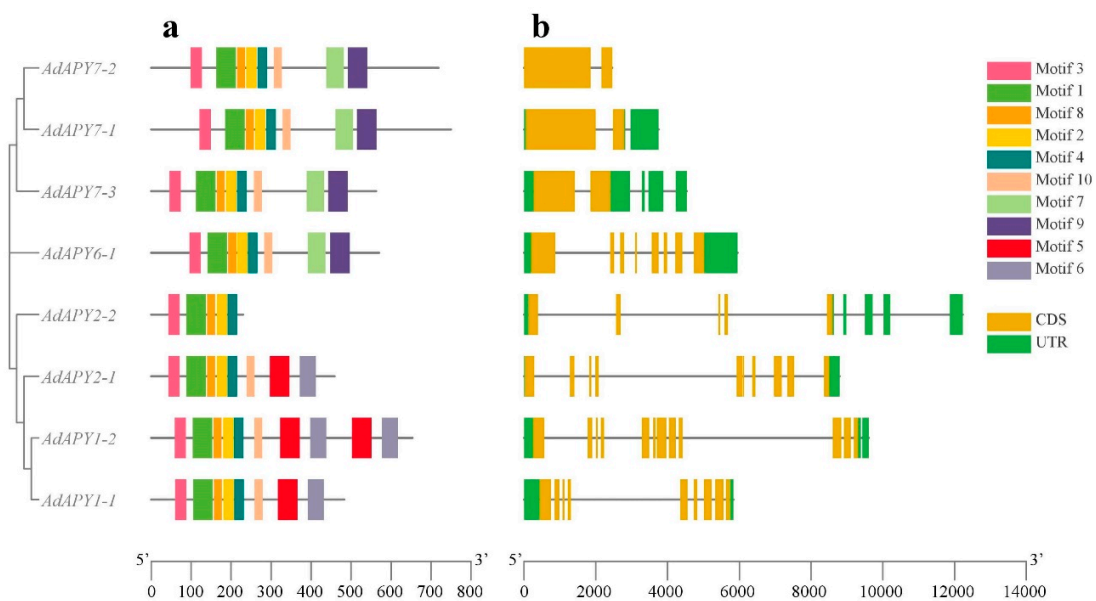
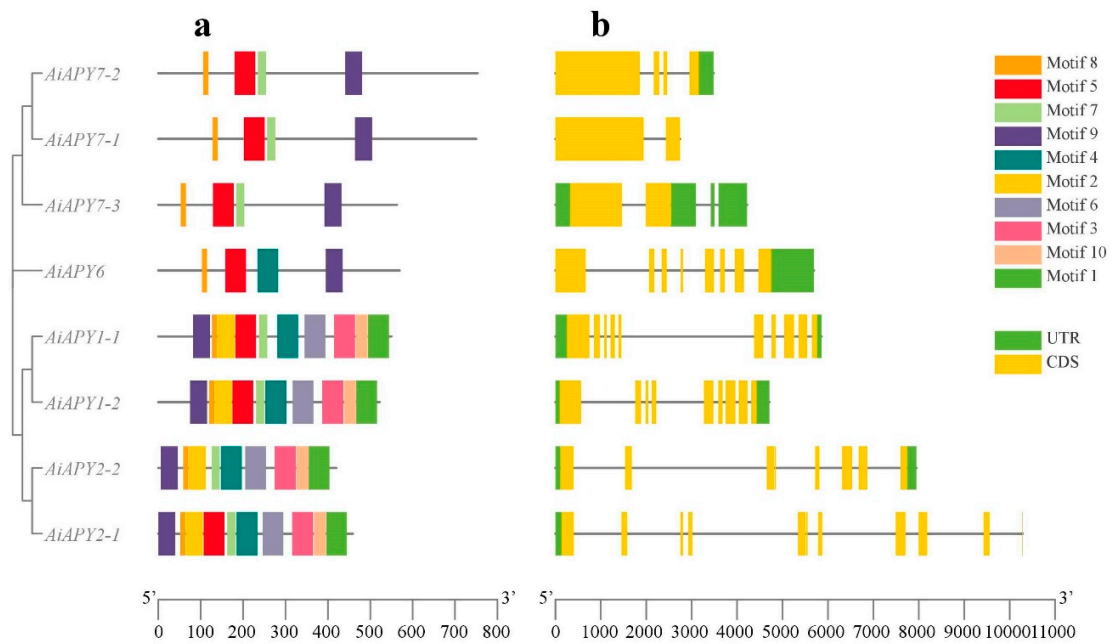


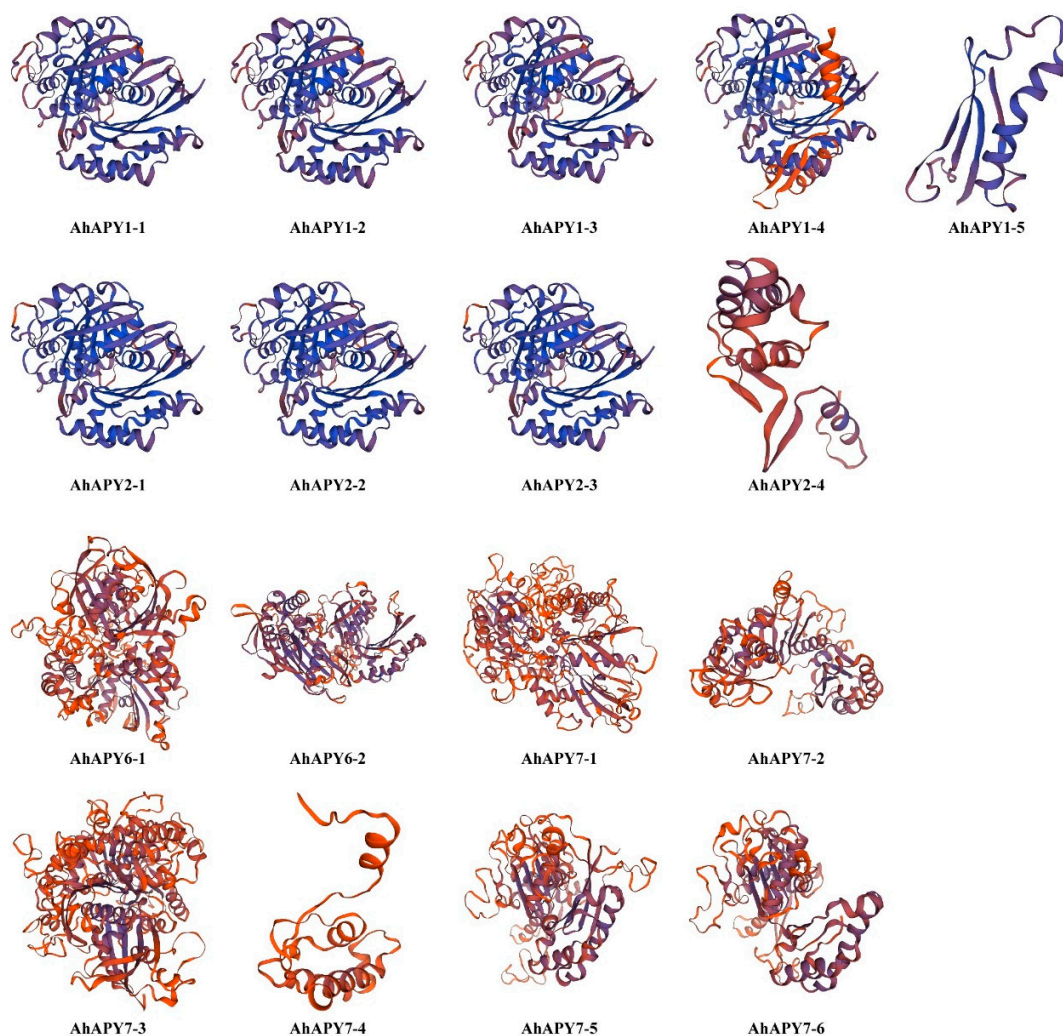
**Figure S1.** Chromosomal distribution of diploid peanut species. (a) Chromosomal distribution of *Arachis duranensis* APYs. (b) Chromosomal distribution of *Arachis ipaensis* APYs.



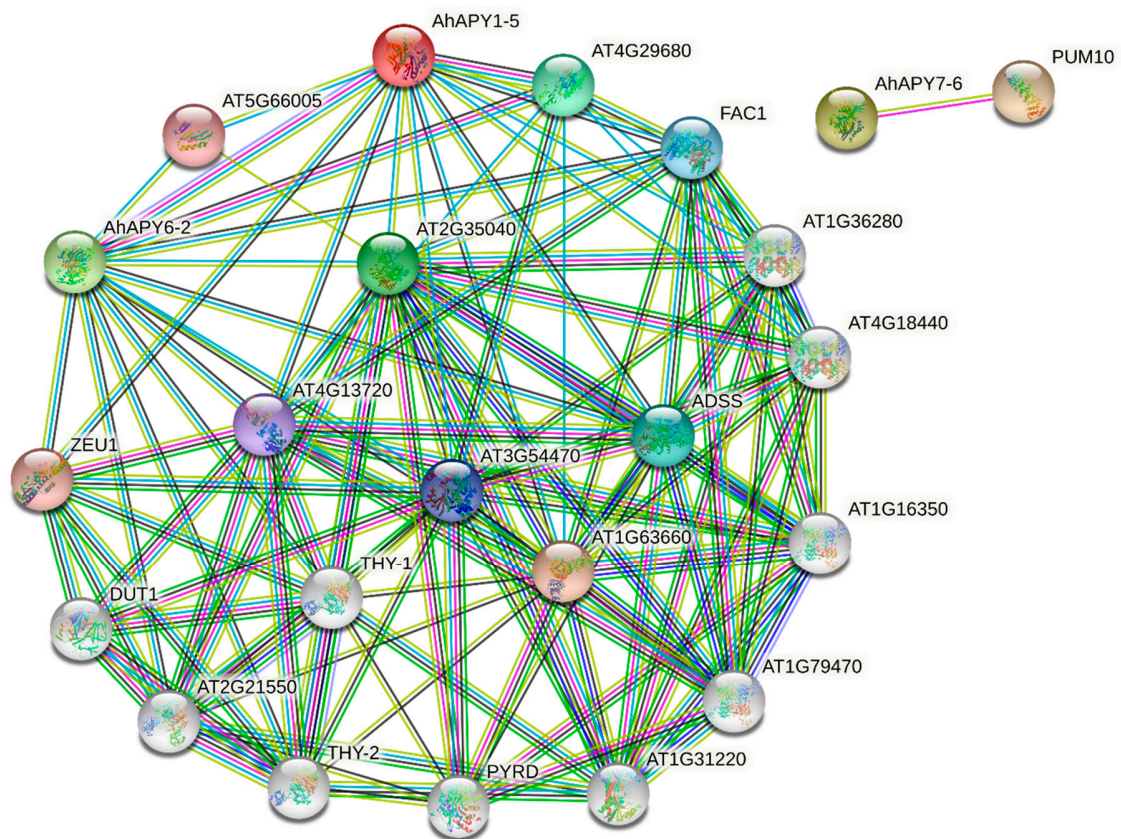
**Figure S2.** Conserved motifs and gene structure analysis of *AdAPYs*. (a) Top 10 conserved motifs of *AdAPYs* predicted by MEME suite. (b) Exon-intron distribution patterns of *AdAPYs*. The legends are given on right side.



**Figure S3.** Conserved motifs and gene structure analysis of *AiAPYs*. (a) Top 10 conserved motifs of *AiAPYs* predicted by MEME suite. (b) Exon-intron distribution patterns of *AiAPYs*. The legends are given on the right side.



**Figure S4.** Simulation of 3D models of protein tertiary structures. The 3D models are simulated by Swiss-Model using the default parameters. As the proteins of the first and second group perform similar functions, 3D structures also showed similar simulations and proteins of group six and seven perform similar functions, so their 3D structural simulations are almost similar.



**Figure S5.** Prediction of protein-protein interaction network of *AhAPYs*. The interaction network showed that *AhAPYs* showed closely related functions with their homologs of Arabidopsis.



# AhAPY2-1P

-2044 GATGAAC TTT GTAATGGTCT GCGAGACAAC TTTTACATGA TGCAAAAGTG **GAGCT**AGAGG CGCGTCTAAA 1  
 ABRE unnamed\_4(-) TATC-box

-1974 GAGGTAGGGA ACATGTGATA TATCCTGAAA ATG**ACGTGAG** AATTATTTTA AGCGGACGAT ATA**TATCCCA** 2

-1904 AACTAGATAC AATTATTTTC AATAAATTAA TCTTTTGATA TACAATATTC GTGAAAATGA ATTGTGTTTT 3

-1834 TATTCATCAT ACATAAGATC TGTTTGTTAA ATAAAATAAA ATTGTTTTTTT AATAAACATA AGTCATACAA 4  
 ERE BOX 4

-1764 ATATTATTG ATAAAATTAT TCTTAAAA**TT TAAAA**TGAT **TAATAGTGAA** ATTCGTTCTT TAAAAATAAT 5  
 GATA-motif

-1694 TTATTTTTTA AATTAGTTTT TAAAAAATTA AATTAGTCAT ATTAGTTCTT **AAAAGATAAG ATA**TAAGTCA 6  
 CGTCA-motif ARE G-Box ABRE

-1624 AATTGGCCTT TCTATTAGTC AGATAATGAC GTGTCA**TATG** **AAATGC****CACG** **TGTCATGATG** **ACGTG**GTAGA 7  
 BOX 4 unnamed\_1 G-Box(-) o2-site(-)

-1554 TTAATA**CCAC** **G**TAACATAAG ATGATTAGCC GATGTGTAT**C ACGTA**TTATC TAATATGTCA TAAATTTATT 8  
 BOX 4 Box III Box 4

-1484 TAAGTCAAA**T** **TAAT**TCTAAA AGTACACACG CAA**ATCATT** **TCATT**ATTAA AATTTTAAAA **ATTAAT**CAAA 9  
 unnamed\_6

-1414 TTAGTTCTTA **TATAAATCTC** **T**TTTATTTTT TTTATAATAT TAAATTTTAG ATAAATTCTA CTATACTCTT 10  
 WUN-motif

-1344 TTTAAAGTGA CATGTAATTG **TAAATTACTC** TGAGTGATCA TTTTATGATC GAATACTATC TTAATCATAA 11

-1274 TTAGGCCATT TTATAATTAA AAAATTATTT GAAAGGGTG AATGTATAAT TTAATAAAAT ATTAATAATT 12  
 MYB

-1204 GAATCCTATT TTTTTTTTCA AATCAATCTT TTAATAAATG TATCCTAACT CTCTTTAA**TG GTTG**TCGCTC 13  
 unnamed\_4 TGA-element LTR

-1134 CTTCT**CTAT**T CATTCTTT**GT** **CGTTG**CGCCT **CCGAAA**CATG ACCATTCCAT TGTGTGTTCT GATATTCGAA 14  
 circadian (-) unnamed\_2 GT1-motif

-1064 CTAGAAGTAG AATTTTTTGG CACAAATTTT TTGGCC**TATA** **TCTTTGCCAT** TGATGCTT**AA CTTAAGC**TG 15

-994 ATTGCACCTC TAAGCACGAT GTCAATGGTG GATACCTTTT GAAATACAAT TCGAGCGAAA AGAGACTGAT 16  
 unnamed\_4

-924 **GGTTT**GATGG GTGCTATACC TCC**TGCA**TGT ACAATACTTC AATGCAATCT CCATACGCTA TTGTCAAAAA 17  
 ARE (-) unnamed\_4 CGTCA-motif

-854 CTCTTTCTCT TTCACTTCC**C TCC**CCTCTCG TCCATTCTGT ATCCTTTTCGA AA**CGTC**ACA AACATCGTCC 18  
 ERE

-784 TTGTCTCGTC TCTGCGAAAA CACTTCACCA CCACCACCAC CGTAGTTCCT CTTATCC**ATT TTA**AAAAATT 19  
 AT1-motif

-714 ATTTAATTAT AAAATTGTCC TATTTTAATT AAAAAATTAA **TTTTTATTAG** ATTAAATTAA CTTAATTTAA 20  
 AT1-motif

-644 AAAGGAACAT TCCATTAAAA TGTATCATAT **CATAAAAAAT** **AATTTATATG** TTATTTAAAA AGAGTTGAAT 21

-574 AGAATTTATC TAAATTTTAA TATTTCTTAA TTCAACTAAT TTAAATATCA TCTTTTACAC TTTGAAAAAC 22  
 AT1-motif

-504 AATATTTTTT AAACAAAATA ATAAAAATAA TCAAATTATT **ACAAAATTAT** **TTTTTATTG** TATCTTTAGA 23

-434 TTTTATATTT TTGAATTCTA GTTCTGGTGA AATTTTTTCA TATAAATAAT TTTATCAAAT TATTTCTAAT 24

-364 TATATATTAC AAGTTTAAAT TTTCTGAATC TTATTATTTT TTAATTTTTT TATTTCTTAT GGTATTTTTT 25

-294 AACTCGACAA GATAAAGAT TAGTCAGCGG TATATTTTAA CTATATTCAA GAATTTGTCT AACTAATAAA 26  
 chs-CMA1a BOX 4

-224 TTGTTATATA CATAAAACAA AAATTTAAAC TTCCGATACT **TACTTAA**ACA AATAAATAAA **TTAATA**ACTA 27  
 MYB

-154 CTCTAA**TAAC CA**AATAAGTT AATCGACTAA TCCAAATTG TTTATTCCTT CTGTATTTAG TAAAGAACAA 28  
 TATA-box ABRE CAAT-box

-84 TGGCACCAT**A TATAA**TGGTG TATTTTCG**AC** **GTG**GGAGCTA ATTAAGTTAC TCGAG**CAAT**A ATATATAGAG 29  
 +1

-14 GTAGAGACTA CCGC**ATG** 30

**Figure S6.** *Cis*-regulatory elements in *AhAPY2-1P*, predicted by the PlantCARE database.