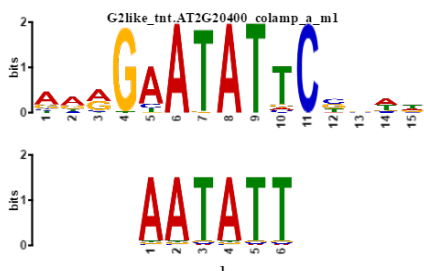


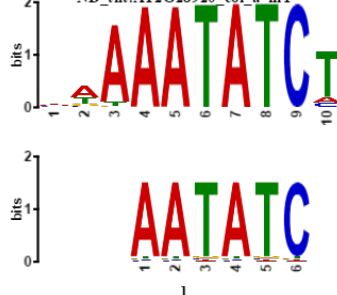
Fig. S1. Significant matches (e-value<0.05) of auxin-associated cis-regulatory elements with transcription factor binding sites identified by Tomtom tool (Gupta et al., 2007).

For each element alignment of two logos are presented: a transcription factor binding site sequence (above) and a hexamer sequence (below).

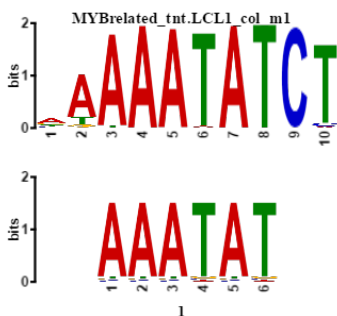
AATATT | AATATT



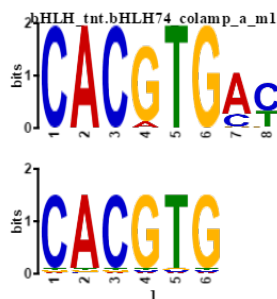
AATATC | GATATT



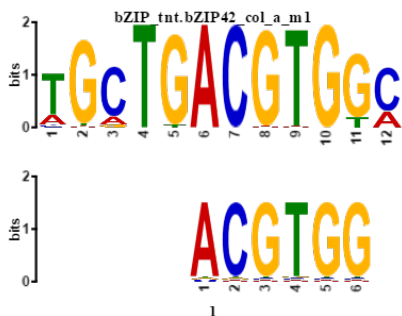
AAATAT | ATATTT



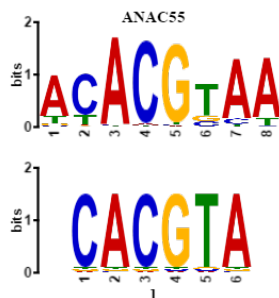
CACGTG | CACGTG



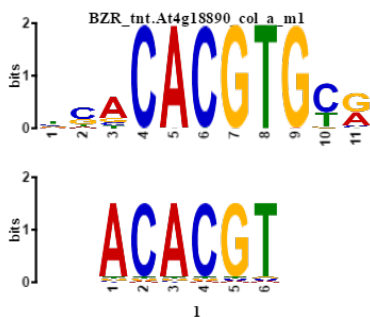
ACGTGG | CCACGT



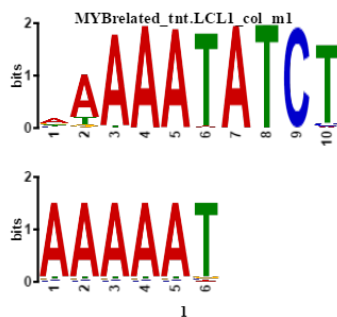
CACGTA | TACGTG



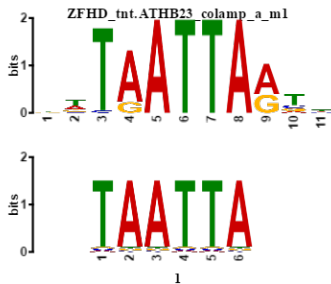
ACACGT | ACGTGT



AAAAAT | ATTTTT

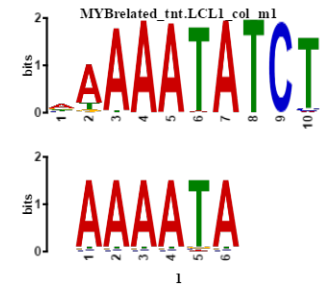


TAATTA | TAATTA



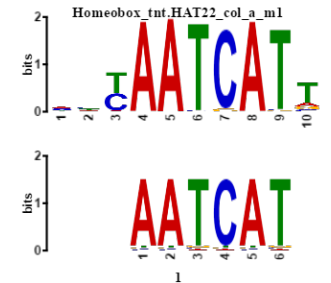
e-value =  
1.11e-02

AAAATA | TATTTT



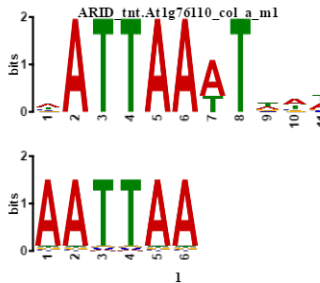
e-value =  
9.29e-03

AATCAT | ATGATT



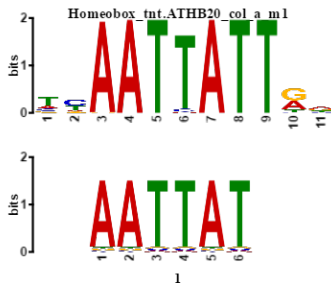
e-value =  
2.50e-02

AATTA | TTAATT



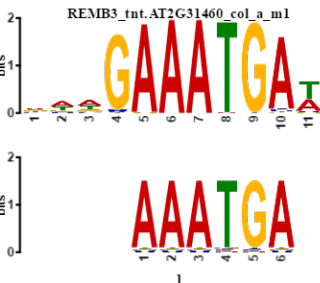
e-value =  
3.67e-02

AATTAT | ATAATT



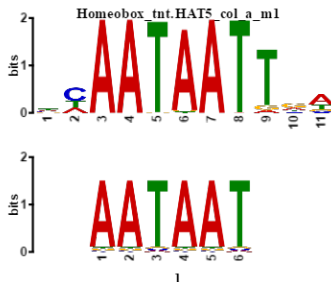
e-value =  
1.11e-02

AAATGA | TCATTT



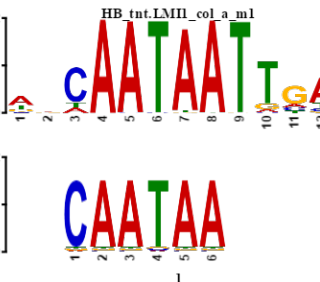
e-value =  
3.50e-02

AATAAT | ATTATT



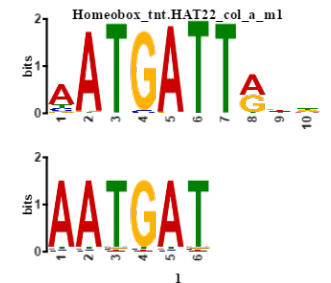
e-value =  
1.68e-03

CAATAA | TTATTG



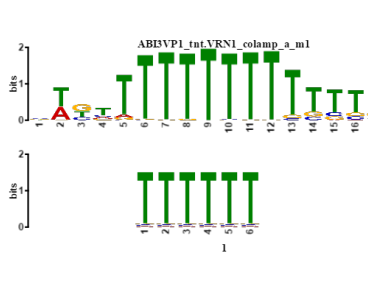
e-value =  
4.00e-02

AATGAT | ATCATT



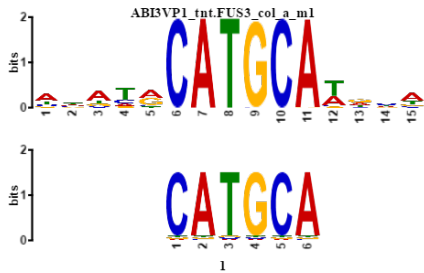
e-value =  
2.50e-02

AAAAAA | TTTTTT



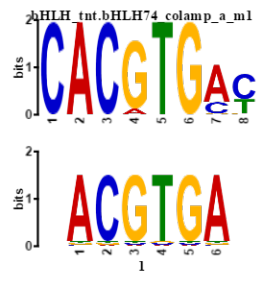
e-value =  
3.92e-03

CATGCA | TGCATG



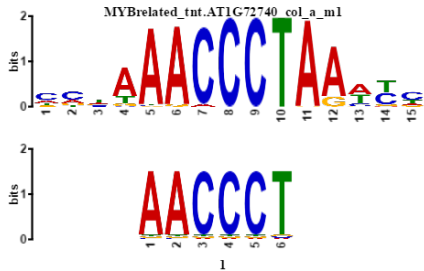
e-value =  
3.75e-02

ACGTTA | TCACCT



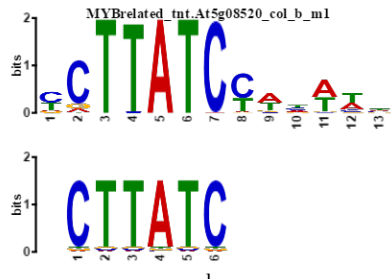
e-value =  
4.72e-02

AACCCT | AGGGTT



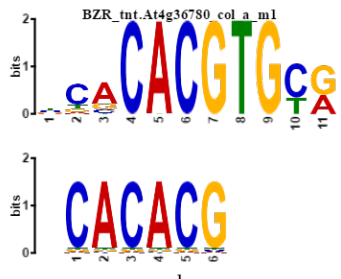
e-value =  
3.75e-02

CTTATC | GATAAG



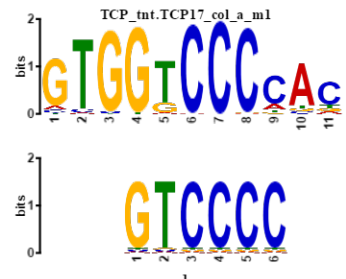
e-value =  
3.46e-02

CACACG | CGTGTG



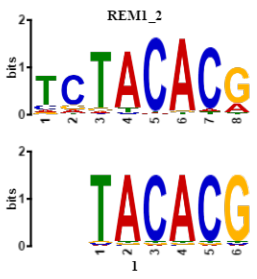
e-value =  
4.62e-02

GGGGAC | GTCCCC



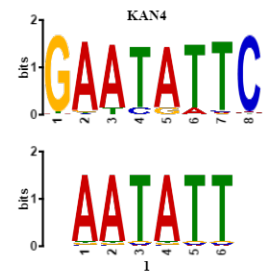
e-value =  
3.86e-02

CGTGTG | TACACG



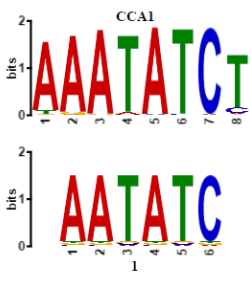
e-value =  
3.91e-02

AATATT | AATATT



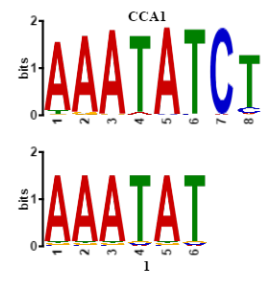
e-value =  
4.19e-02

AATATC | GATATT



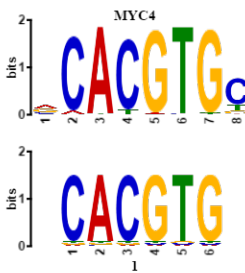
e-value =  
2.01e-02

AAATAT | ATATTT



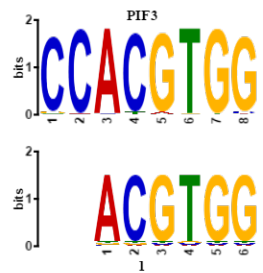
e-value =  
2.87e-03

CACGTG | CACGTG



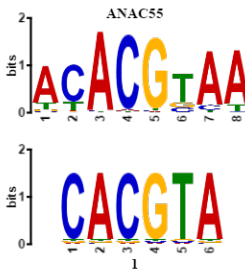
e-value = 2.40e-02

ACGTGG | CACGTG



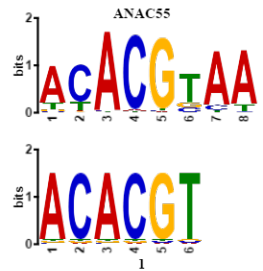
e-value = 2.40e-02

CACGTA | TACGTG



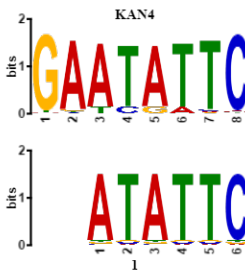
e-value = 3.91e-02

ACACGT | ACGTGG



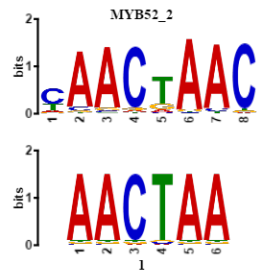
e-value = 3.91e-02

ATATTC | GAATAT



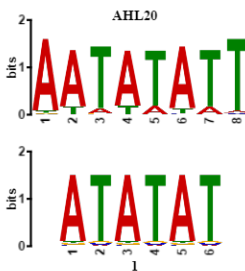
e-value = 2.01e-02

AACTAA | TTAGTT



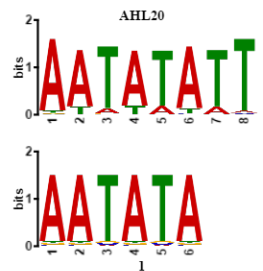
e-value = 2.01e-02

ATATAT | ATATAT



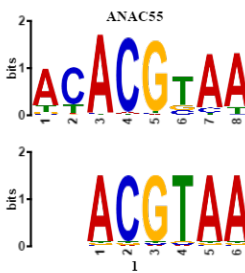
e-value = 4.19e-02

AATATA | TATATT



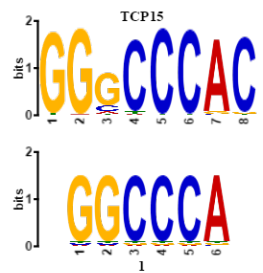
e-value = 3.15e-02

ACGTAA | TTACGT



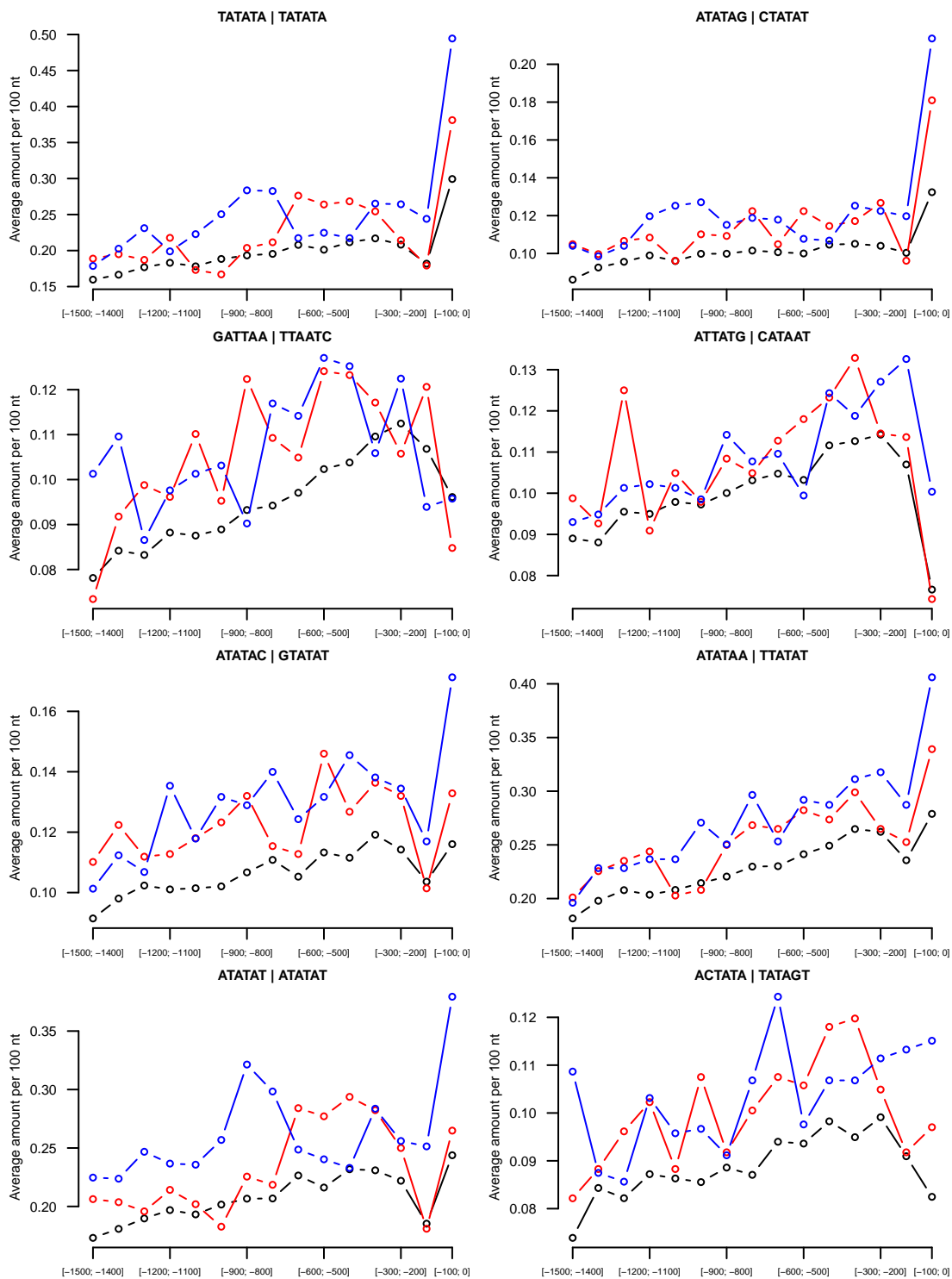
e-value = 2.13e-02

GGCCCA | TGGGCC

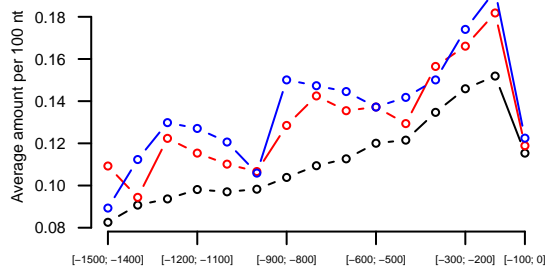


e-value = 2.54e-02

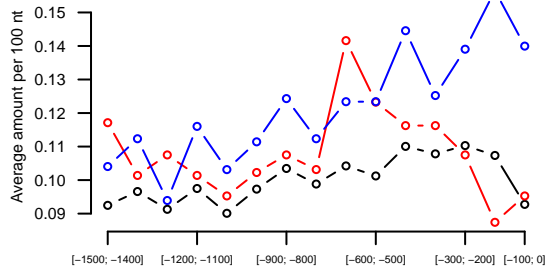
**Fig. S2. Distribution of AT-rich hexamers identified as associated with early auxin response along the upstream regions in Arabidopsis genes.** The hexamers amount was calculated per each 100 nt in [-1500; +1] upstream regions of all genes (black line), auxin up-regulated (red line) and auxin down-regulated genes (blue line).



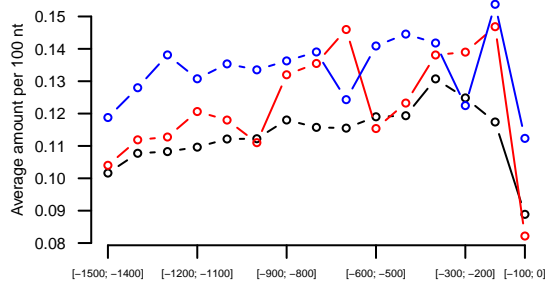
TAATTA | TAATTA



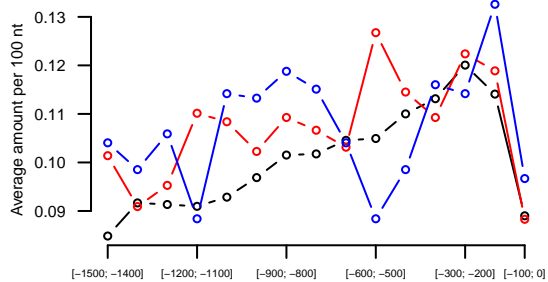
ATAATG | CATTAT



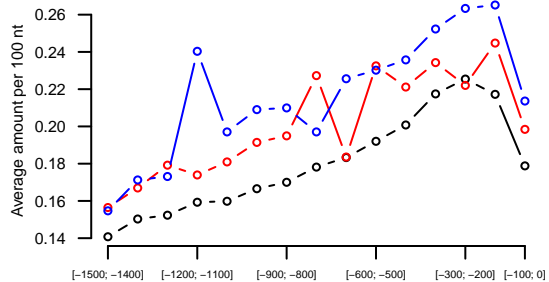
AATATG | CATATT



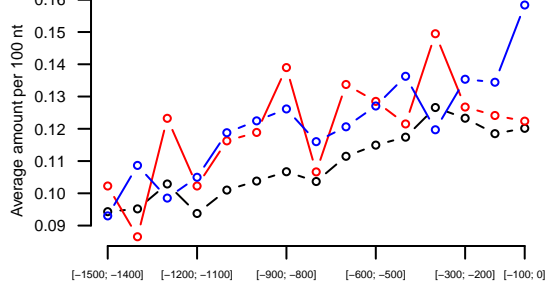
ATTAGA | TCTAAT



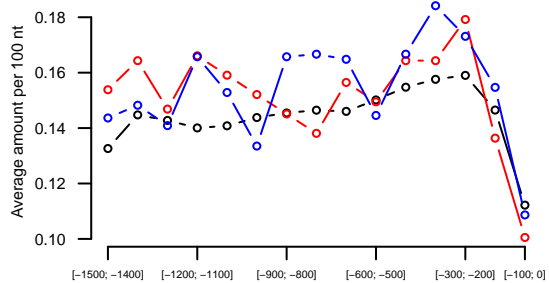
TATTA | TTAATA



AAATAC | GTATT



AACATT | AATGTT



TATAAA | TTTATA

