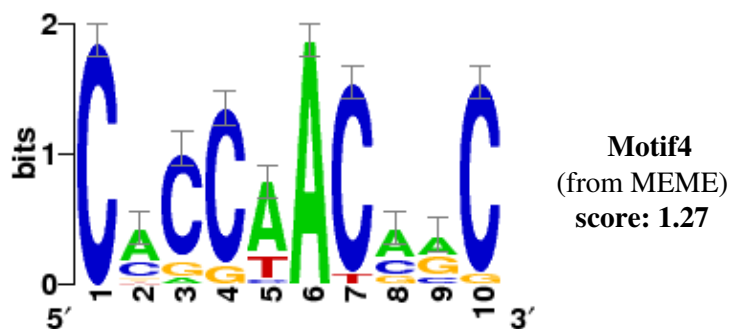
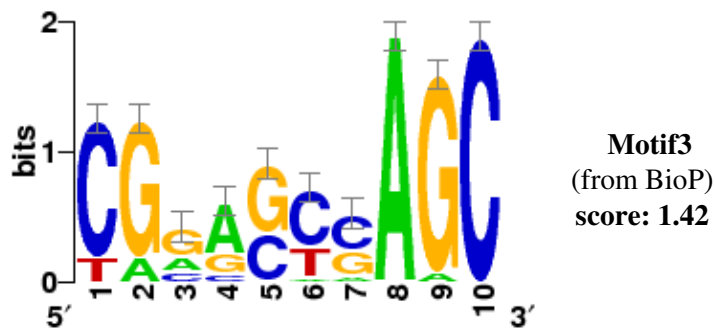
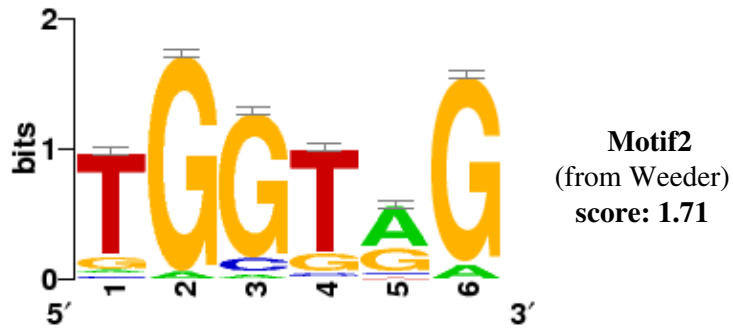


[Home](#)

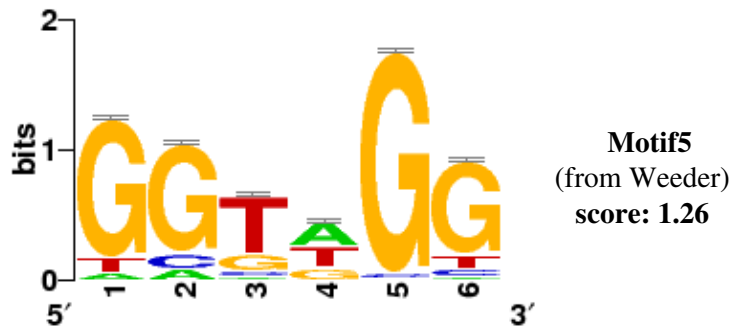
Results Summary

./input/anthocyanin_pathway.fas

Promzea - 00000496



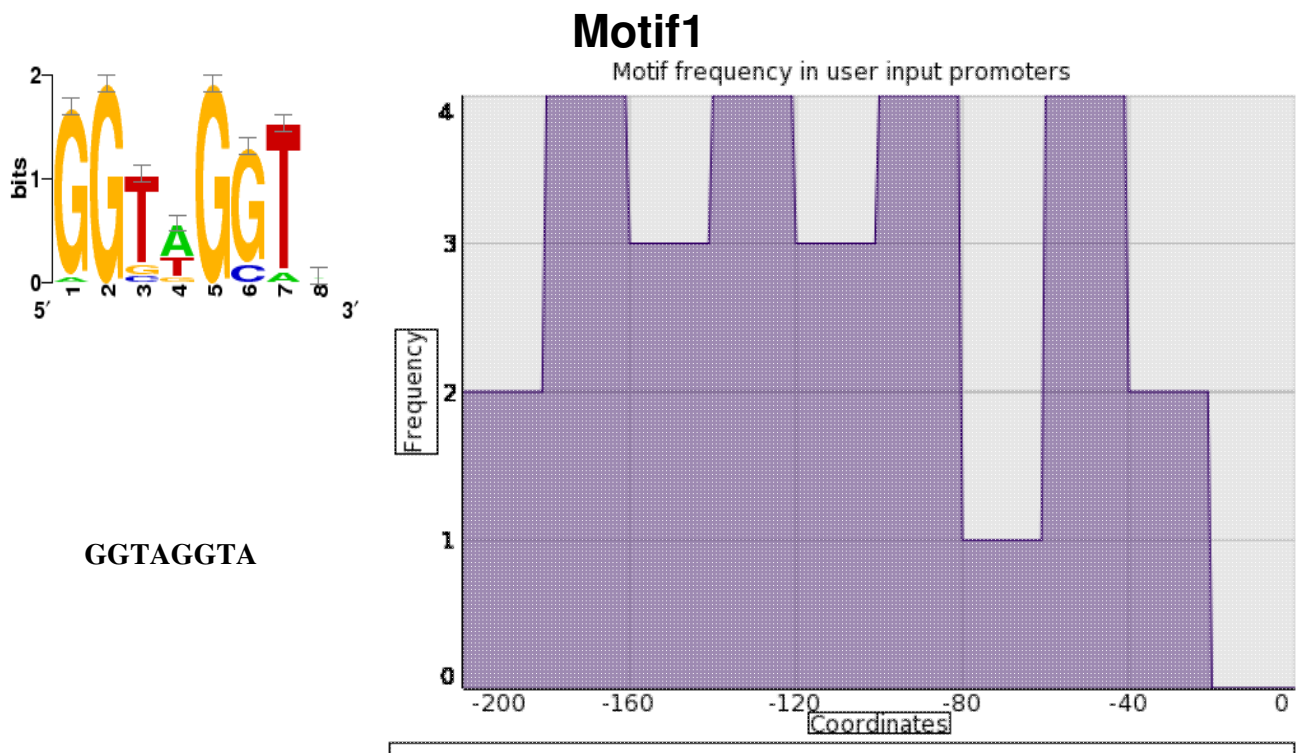
results - 00000496



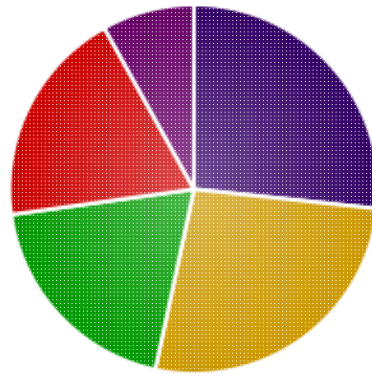
Compare your motifs to known promoter motif databases using STAMP website [motif file to copy in STAMP website](#)

Open the above link, copy content of the newly open file and paste in STAMP program link below In STAMP, under "Similarity Matching", we suggest selecting the plant motif databases: Athamap, AGRIS, PLACE, TRANSFAC; then submit

[STAMP website](#)



Motif1 annotation in the genome



Annotation	p-value
GO:0009081	1.51e-04
GO:0004084	1.51e-04
GO:0006351	1.65e-03
GO:0016459	1.83e-03
others	8.43e-03

Annotation complete description

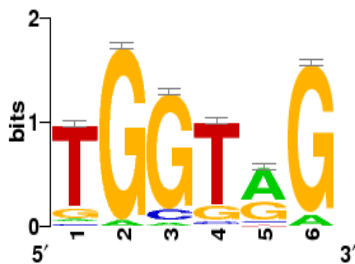
GO:0009081 => branched chain family amino acid metabolic process GO:0004084 => branched-chain-amino-acid transaminase activity GO:0006351 => transcription, DNA-dependent GO:0016459 => myosin complex GO:0003774 => motor activity GO:0016655 => oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor GO:0005971 => ribonucleoside-diphosphate reductase complex

Genome-wide Motif1 search results

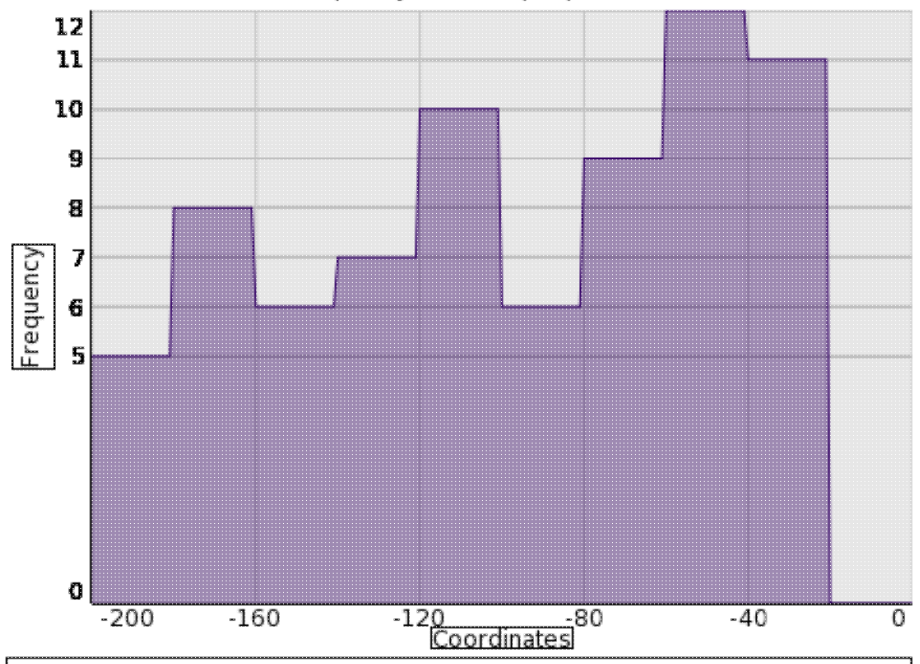
Motif1 gene list of over-represented annotation(s)

Motif2

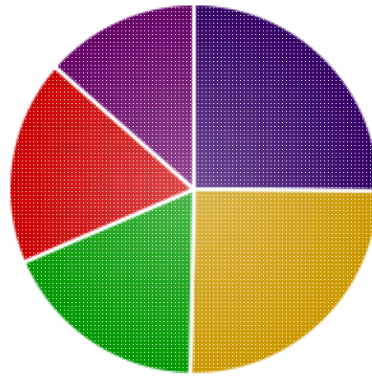
Motif frequency in user input promoters



TGGTAG



Motif2 annotation in the genome



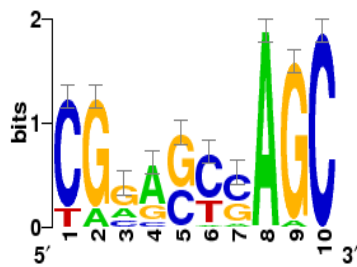
Annotation	p-value
GO:0009081	1.70e-04
GO:0004084	1.70e-04
GO:0006351	1.86e-03
GO:0016459	2.06e-03
GO:0003774	9.45e-03

Annotation complete description

GO:0009081 => branched chain family amino acid metabolic process
 GO:0004084 => branched-chain-amino-acid transaminase activity
 GO:0006351 => transcription, DNA-dependent
 GO:0016459 => myosin complex
 GO:0003774 => motor activity

Genome-wide Motif2 search results

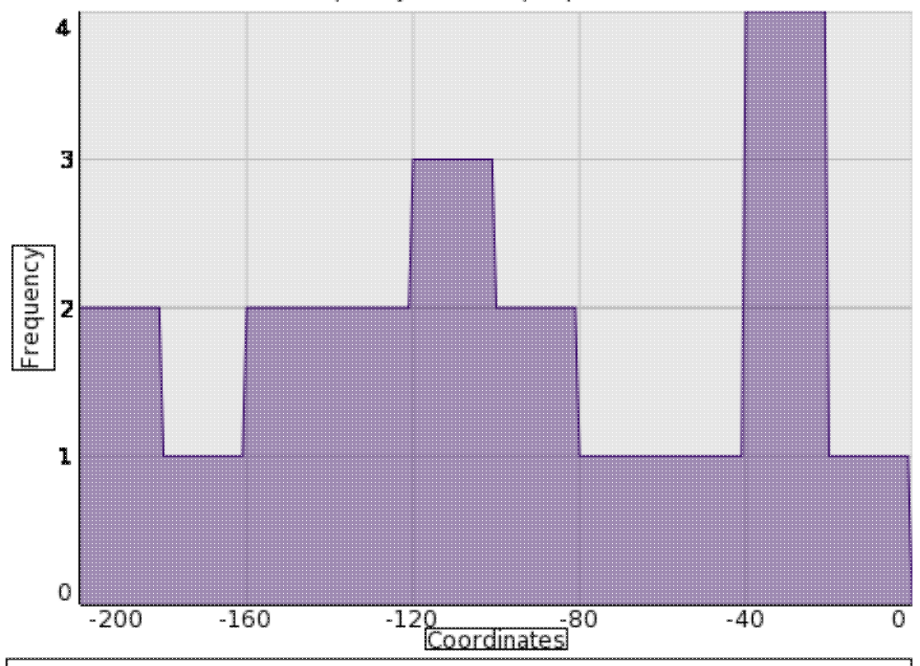
Motif2 gene list of over-represented annotation(s)



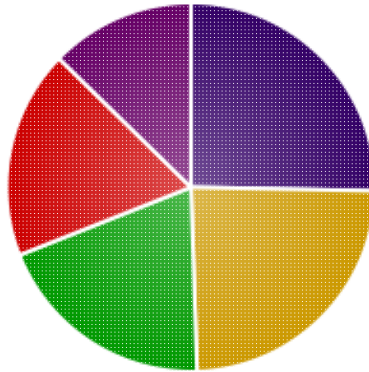
CGGAGCCAGC

Motif3

Motif frequency in user input promoters



Motif3 annotation in the genome



Annotation	p-value
GO:0008270	2.71e-04
GO:0016459	3.96e-04
GO:0003677	1.78e-03
GO:0003676	2.65e-03
others	4.63e-03

Annotation complete description

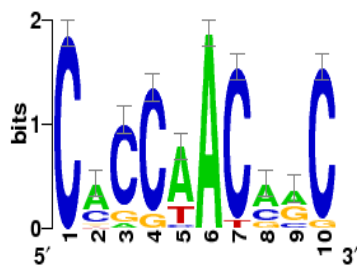
GO:0008270 => zinc ion binding GO:0016459 => myosin complex GO:0003677 => DNA binding GO:0003676 => nucleic acid binding GO:0009081 => branched chain family amino acid metabolic process GO:0004084 => branched-chain-amino-acid transaminase activity GO:0016987 => sigma factor activity

Genome-wide Motif3 search results

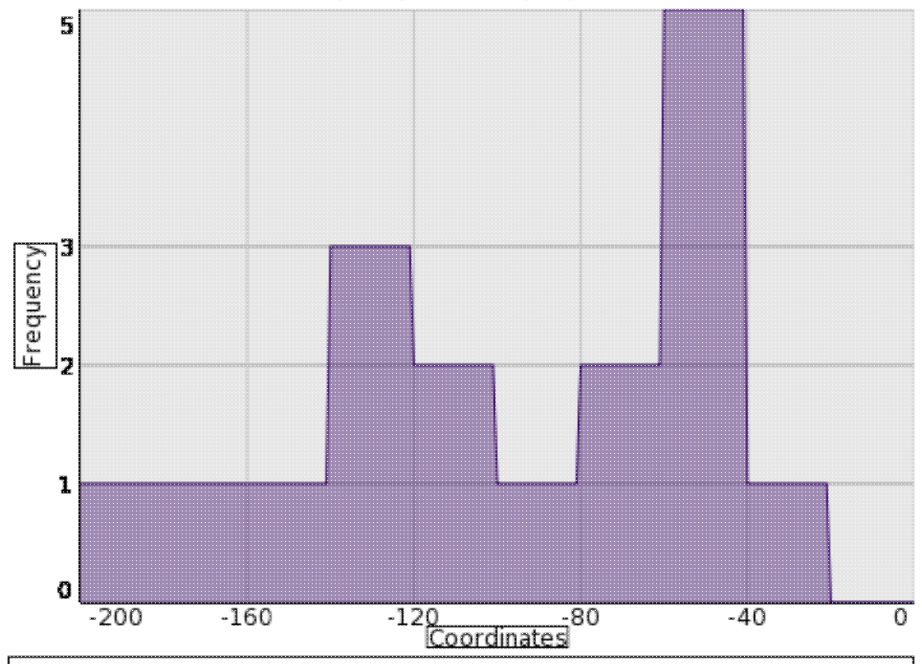
Motif3 gene list of over-represented annotation(s)

Motif4

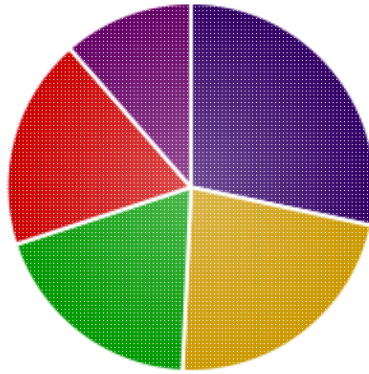
Motif frequency in user input promoters



CACCAACAAC



Motif4 annotation in the genome



Annotation	p-value
GO:0016459	7.62e-05
GO:0016021	5.54e-04
GO:0003774	1.61e-03
GO:0009081	1.98e-03
others	1.98e-03

Annotation complete description

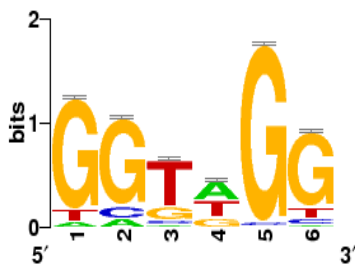
GO:0016459 => myosin complex GO:0016021 => integral to membrane GO:0003774 => motor activity
 GO:0009081 => branched chain family amino acid metabolic process GO:0004084 =>
 branched-chain-amino-acid transaminase activity GO:0008199 => ferric iron binding GO:0031072 => heat
 shock protein binding

Genome-wide Motif4 search results

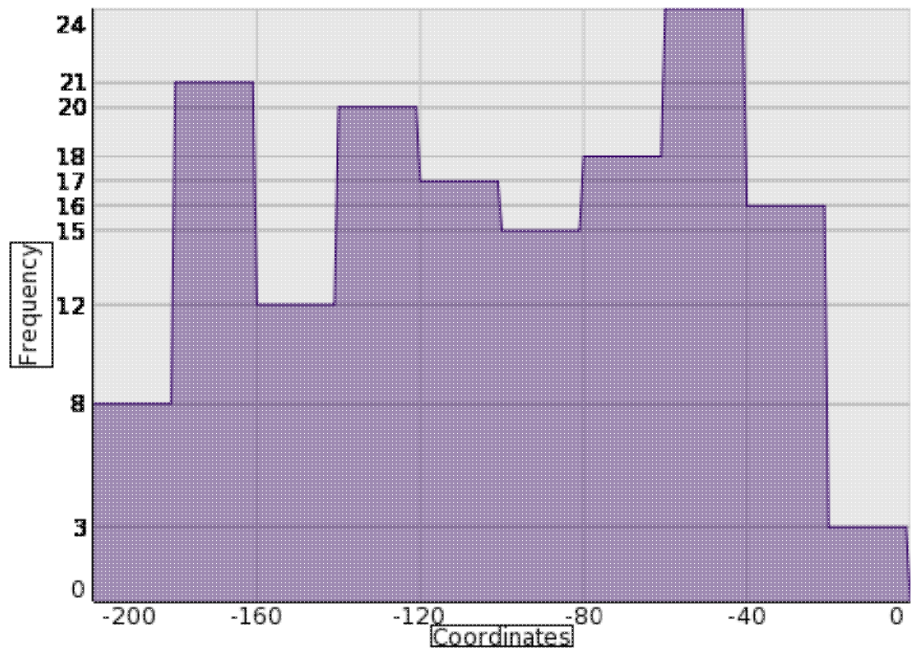
Motif4 gene list of over-represented annotation(s)

Motif5

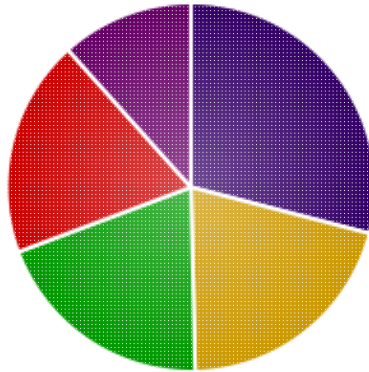
Motif frequency in user input promoters



GGTAGG



Motif5 annotation in the genome



Annotation	p-value
GO:0016459	8.07e-05
GO:0016021	1.25e-03
GO:0003774	1.70e-03
GO:0009081	2.04e-03
others	2.04e-03

Annotation complete description

GO:0016459 => myosin complex GO:0016021 => integral to membrane GO:0003774 => motor activity
GO:0009081 => branched chain family amino acid metabolic process GO:0004084 =>
branched-chain-amino-acid transaminase activity GO:0008199 => ferric iron binding GO:0031072 => heat
shock protein binding

Genome-wide Motif5 search results

Motif5 gene list of over-represented annotation(s)

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[Promzea program from the Raizada lab](#)