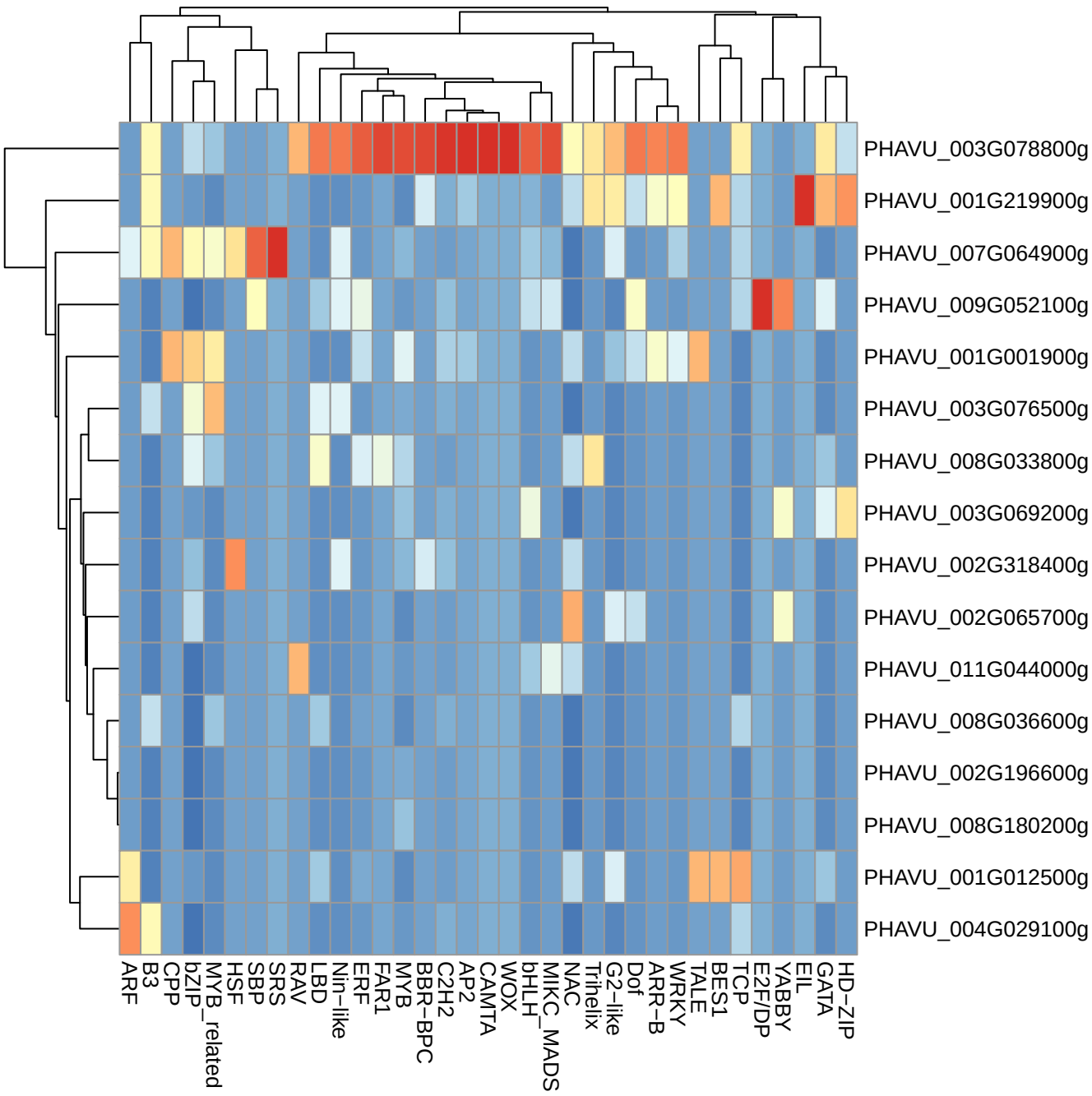
Presence of Conserved Motifs on Gene Promoters

Heatmap of motif presence on gene promoters

The heatmap shows the presence or absence of conserved motifs on gene promoters.
Each row represents a gene, and each column represents motifs.
Motifs are grouped by transcription factor family.
Red boxes indicate relatively high number of motifs on a promoter.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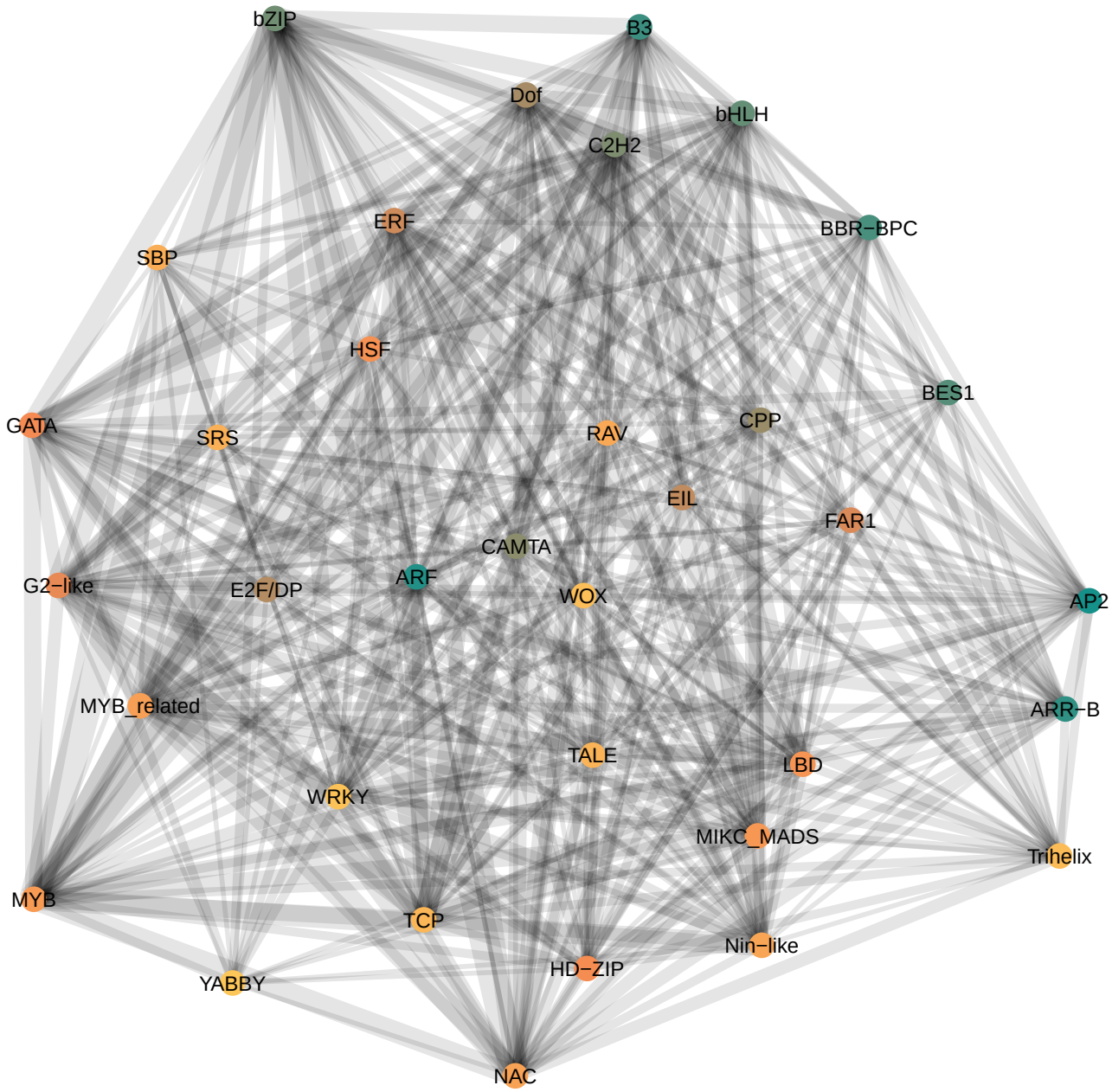
ARF
B3
CPP
bZIP_
MYB_related
HSF
SBP
SRS
RAV
LBD
Nin−like
ERF
FAR1
MYB
BBR−BPC
C2H2
AP2
CAMTA
WOX
bHLH_
MIKC_MADS
NAC
Trihelix
G2−like
Dof
ARR−B
WRKY
TALE
BES1
TCP
E2F/DP
YABBY
EIL
GATA
HD−ZIP

Network plot of transcription factor families

The network plot shows the relationships between transcription factor families based on their co−occurrence on gene promoters.
Nodes represent transcription factor families,
and edges represent co−occurrence.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Dof
bHLH
C2H2
ERF
BBR−BPC
SBP
HSF
BES1
GATA
SRS
RAV
CPP
EIL
FAR1
CAMTA
G2−like
E2F/DP
ARF
WOX
AP2
MYB_related
ARR−B
TALE
LBD
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MYB
TCP
Nin−like
HD−ZIP
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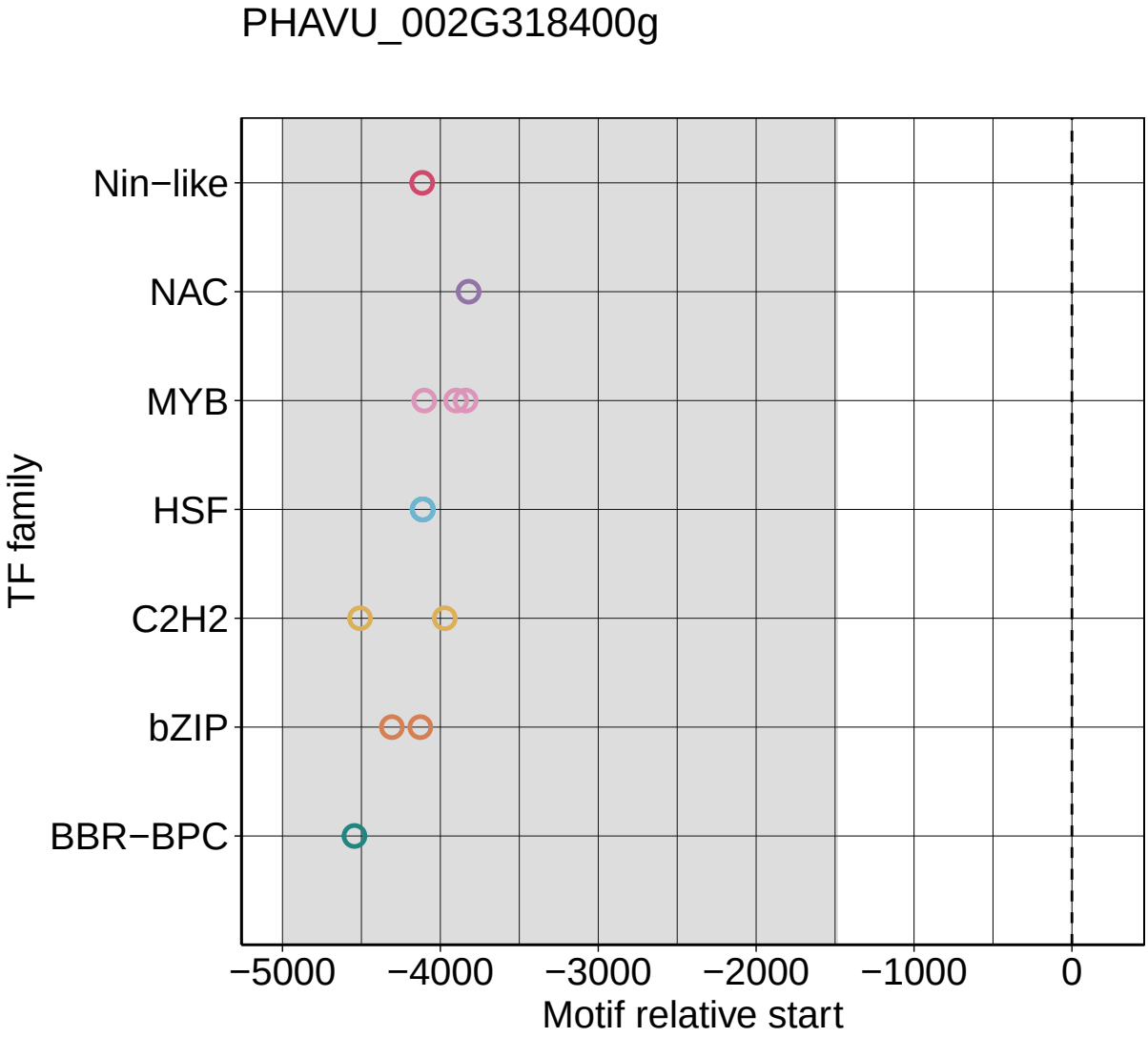
NAC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NAC
MYB
HSF
C2H2
bZIP
BBR−BPC
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
BBR−BPC	1	0.1444448957	PHAVU_002G318400g
bZIP	2	0.1344271335	PHAVU_002G318400g
C2H2	2	0.2410077107	PHAVU_002G318400g
HSF	4	0.0000932139	PHAVU_002G318400g
MYB	3	0.1724719316	PHAVU_002G318400g
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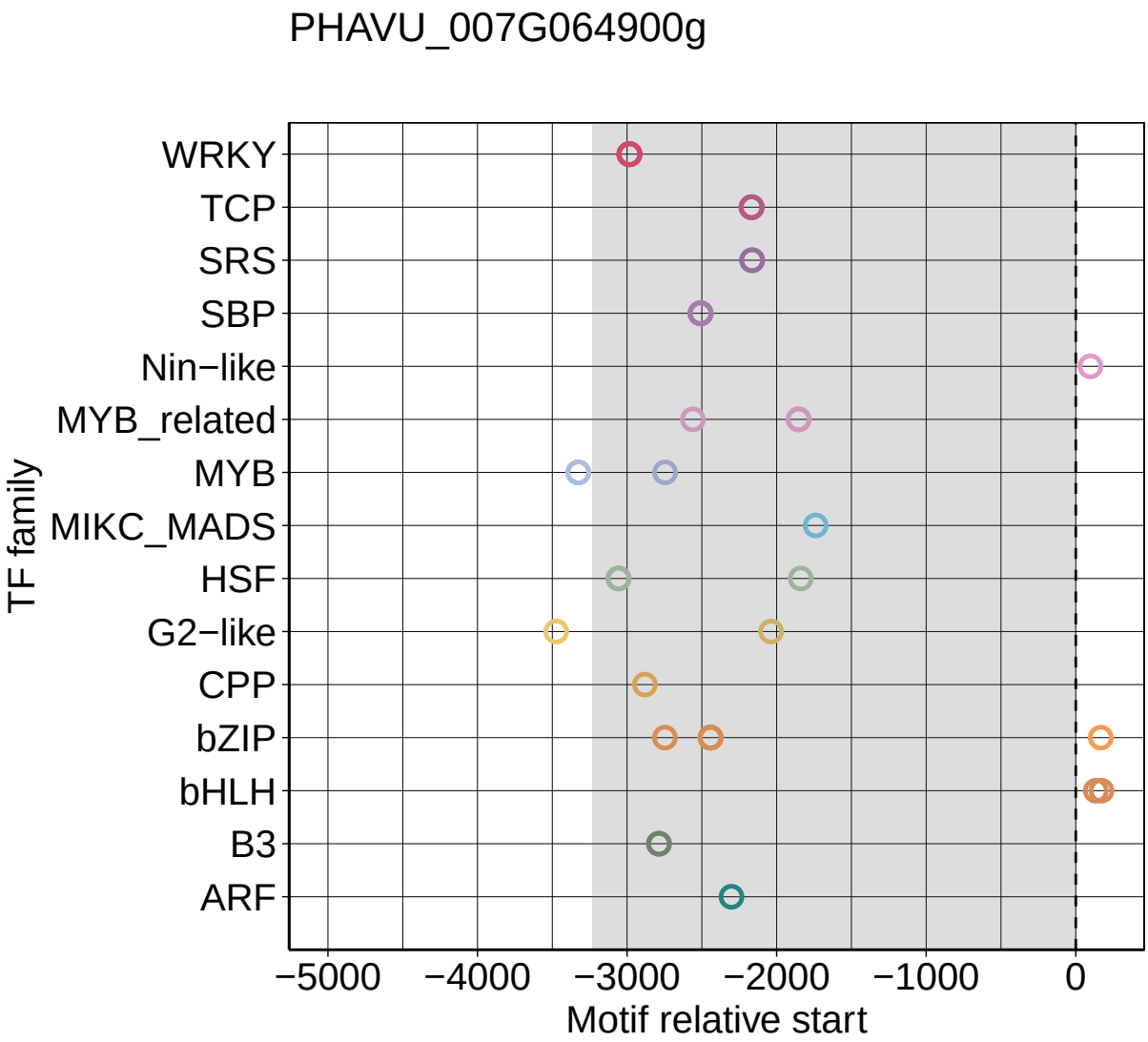
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TCP
SRS
SBP
Nin−like
MYB_related
MYB
MIKC_MADS
HSF
G2−like
CPP
bZIP
bHLH
B3
ARF
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
ARF	1	0.4070182797	PHAVU_007G064900g
B3	2	0.2337011816	PHAVU_007G064900g
bHLH	2	0.7383666298	PHAVU_007G064900g
bZIP	6	0.0085061630	PHAVU_007G064900g
CPP	1	0.3139134735	PHAVU_007G064900g
G2−like	2	0.2566068140	PHAVU_007G064900g
HSF	3	0.0334807693	PHAVU_007G064900g
MIKC_MADS	1	0.6706708979	PHAVU_007G064900g
MYB	3	0.7862143470	PHAVU_007G064900g
MYB_related	3	0.1484153585	PHAVU_007G064900g
Nin−like	1	0.3393749026	PHAVU_007G064900g
SBP	4	0.0001559477	PHAVU_007G064900g
SRS	2	0.0024544560	PHAVU_007G064900g
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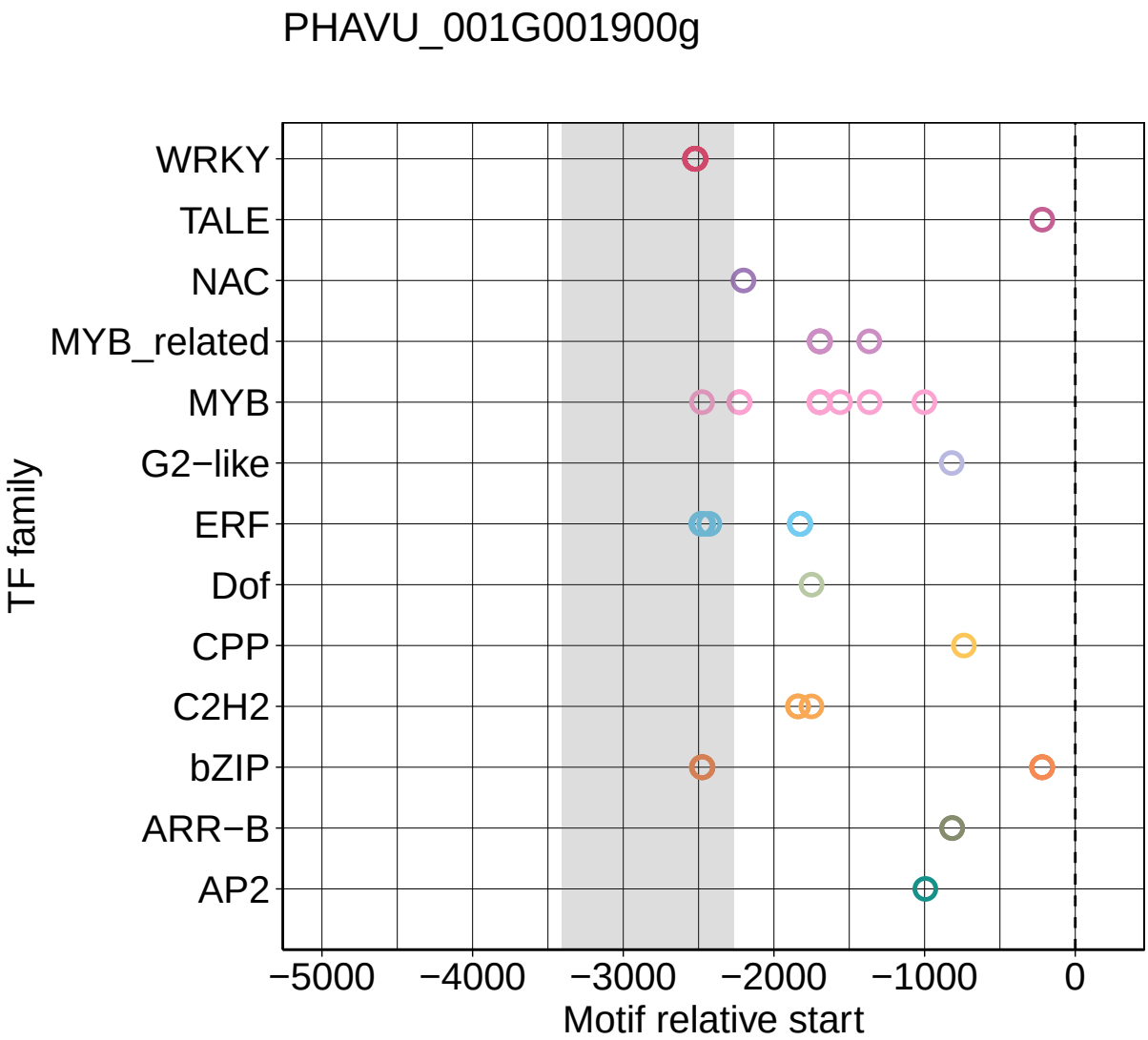
WRKY	5	0.0383312267	PHAVU_007G064900g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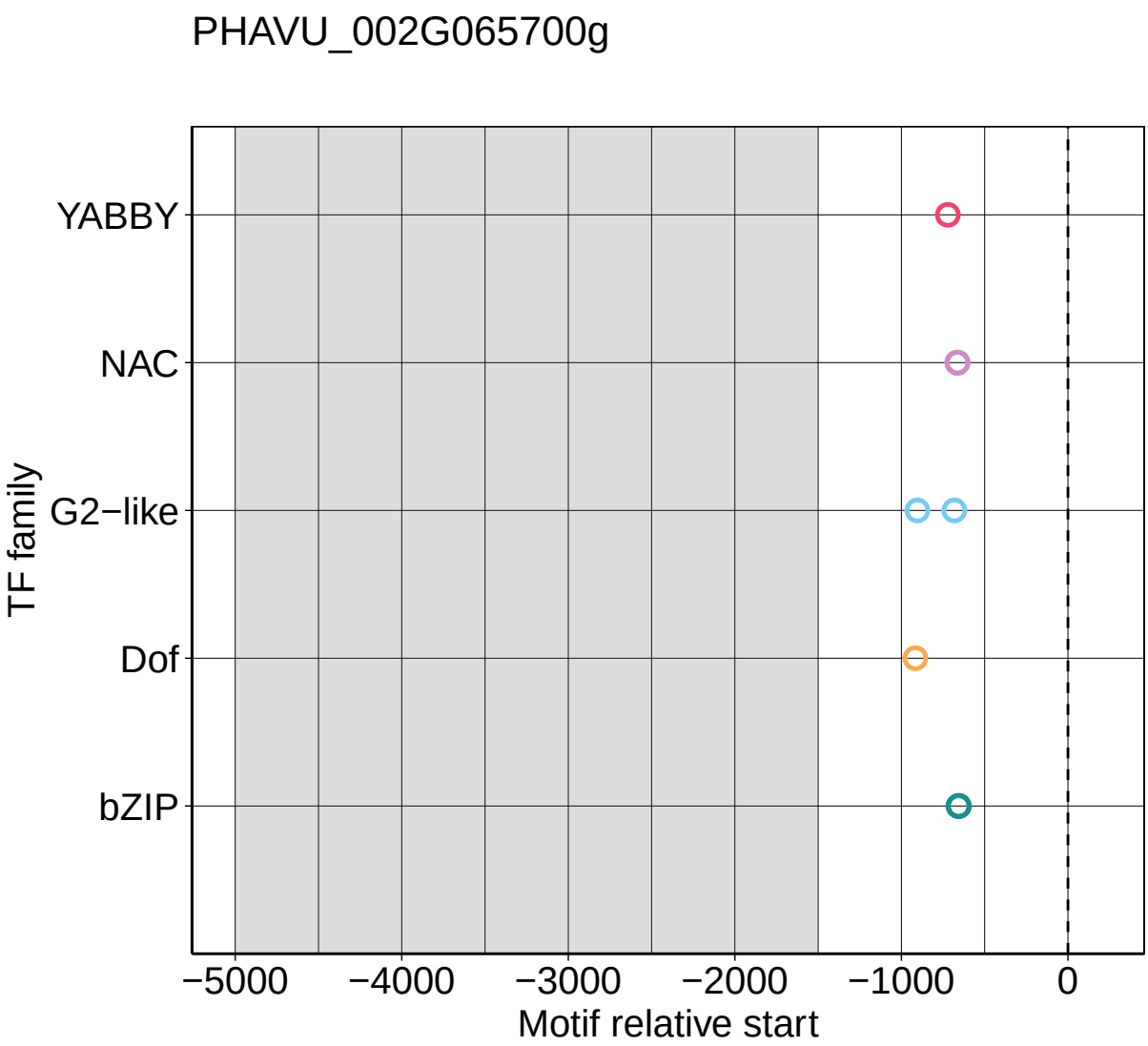
TALE
NAC
MYB_related
MYB
G2−like
ERF
Dof
CPP
C2H2
bZIP
ARR−B
AP2
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
AP2	1	0.5511962778	PHAVU_001G001900g
ARR−B	2	0.0125292784	PHAVU_001G001900g
bZIP	8	0.0019483503	PHAVU_001G001900g
C2H2	3	0.6607291178	PHAVU_001G001900g
CPP	1	0.3830792939	PHAVU_001G001900g
Dof	1	0.8239391309	PHAVU_001G001900g
ERF	9	0.6040631862	PHAVU_001G001900g
G2−like	1	0.7196988523	PHAVU_001G001900g
MYB	9	0.0708931591	PHAVU_001G001900g
MYB_related	4	0.0916358536	PHAVU_001G001900g
NAC	1	0.9477407044	PHAVU_001G001900g
TALE	1	0.1193363660	PHAVU_001G001900g
WRKY	9	0.0005820015	PHAVU_001G001900g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NAC
G2−like
Dof
bZIP
TF family
−5000
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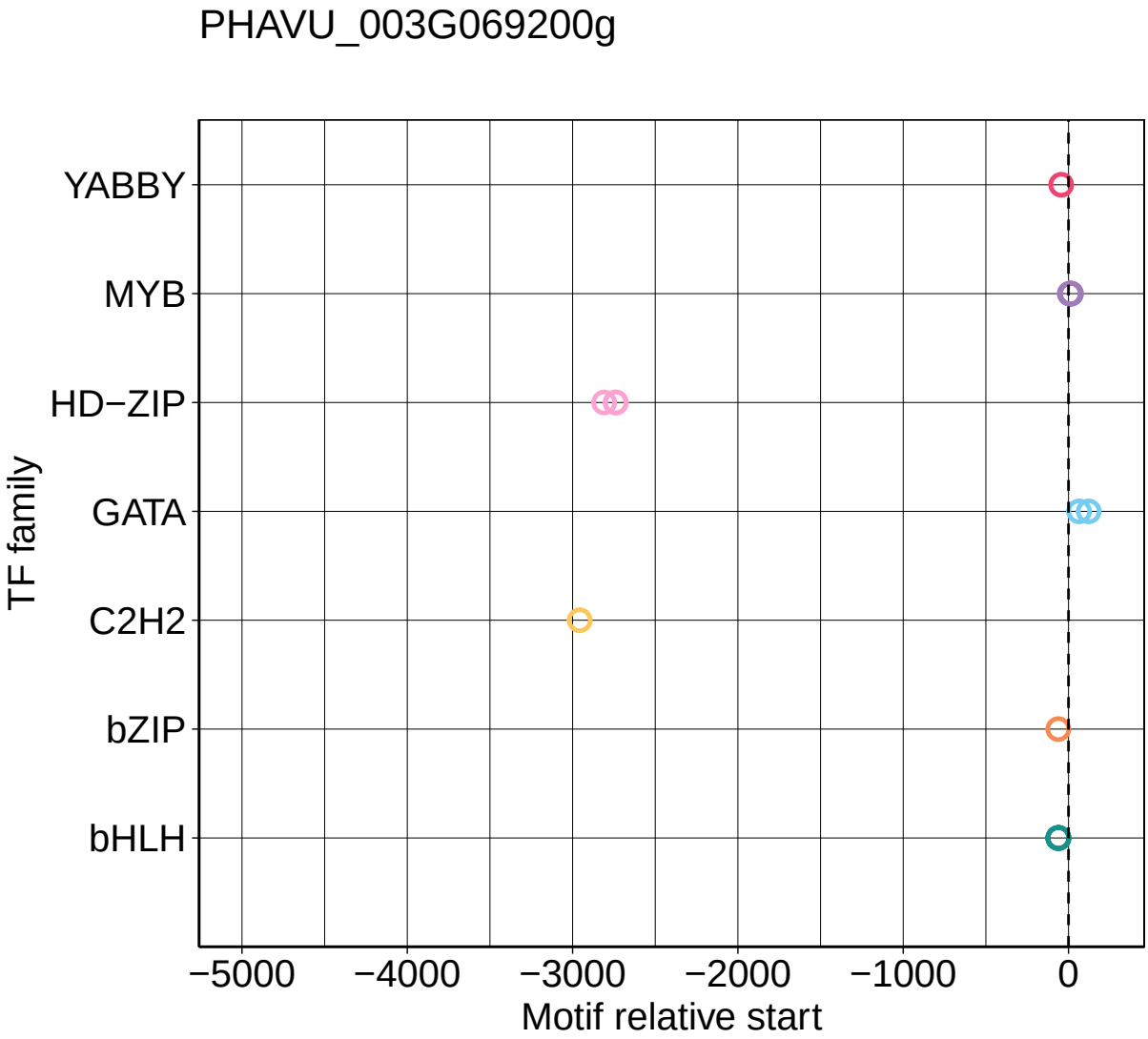
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
bZIP	3	0.009244319	PHAVU_002G065700g
Dof	1	0.293466810	PHAVU_002G065700g
G2−like	2	0.024826884	PHAVU_002G065700g
NAC	3	0.016665056	PHAVU_002G065700g
YABBY	1	0.060548621	PHAVU_002G065700g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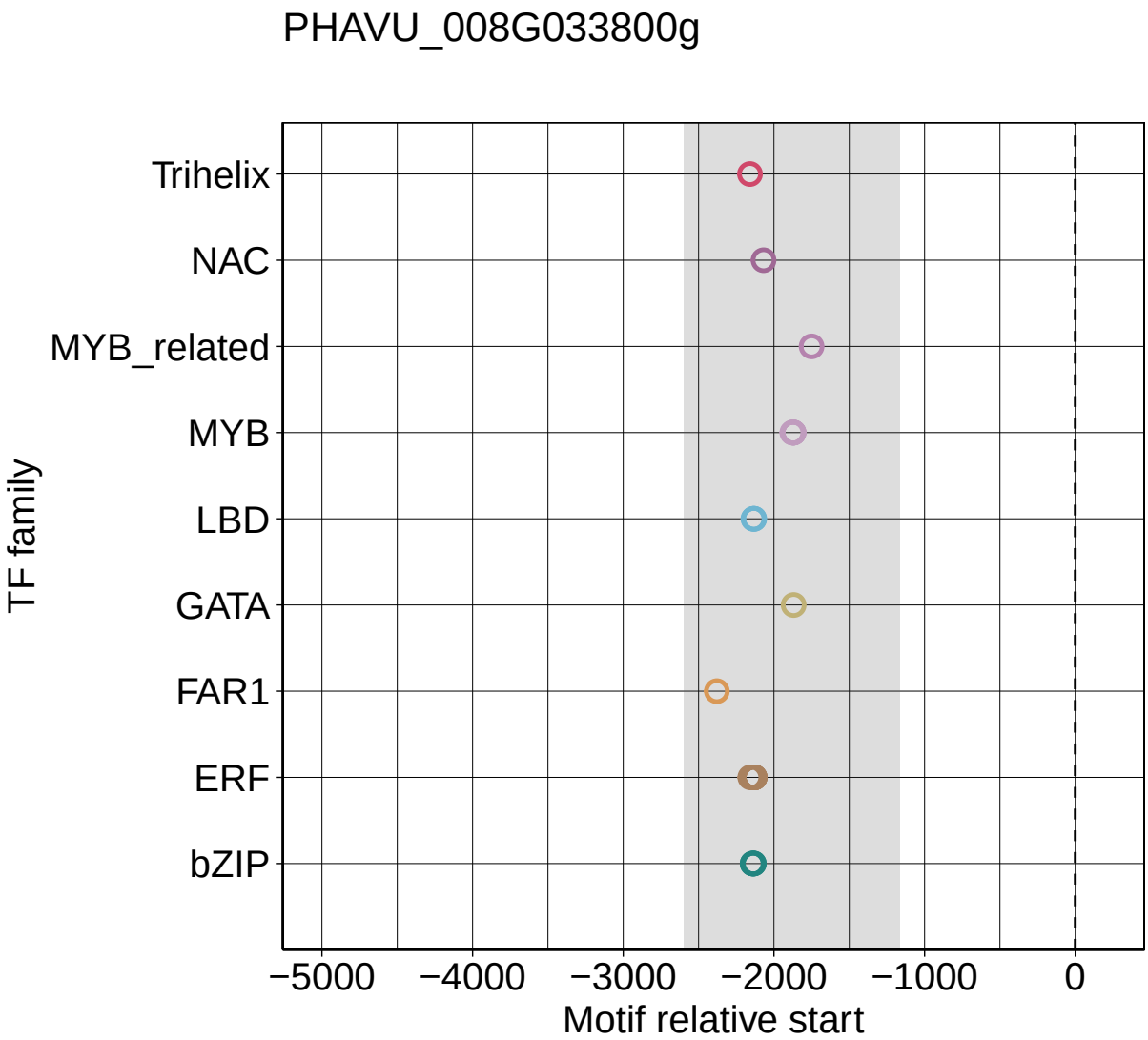
YABBY
MYB
HD−ZIP
GATA
C2H2
bZIP
bHLH
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
bHLH	5	0.003967637	PHAVU_003G069200g
bZIP	1	0.552266710	PHAVU_003G069200g
C2H2	1	0.692948317	PHAVU_003G069200g
GATA	2	0.082073374	PHAVU_003G069200g
HD−ZIP	3	0.007776773	PHAVU_003G069200g
MYB	4	0.092762637	PHAVU_003G069200g
YABBY	1	0.100737830	PHAVU_003G069200g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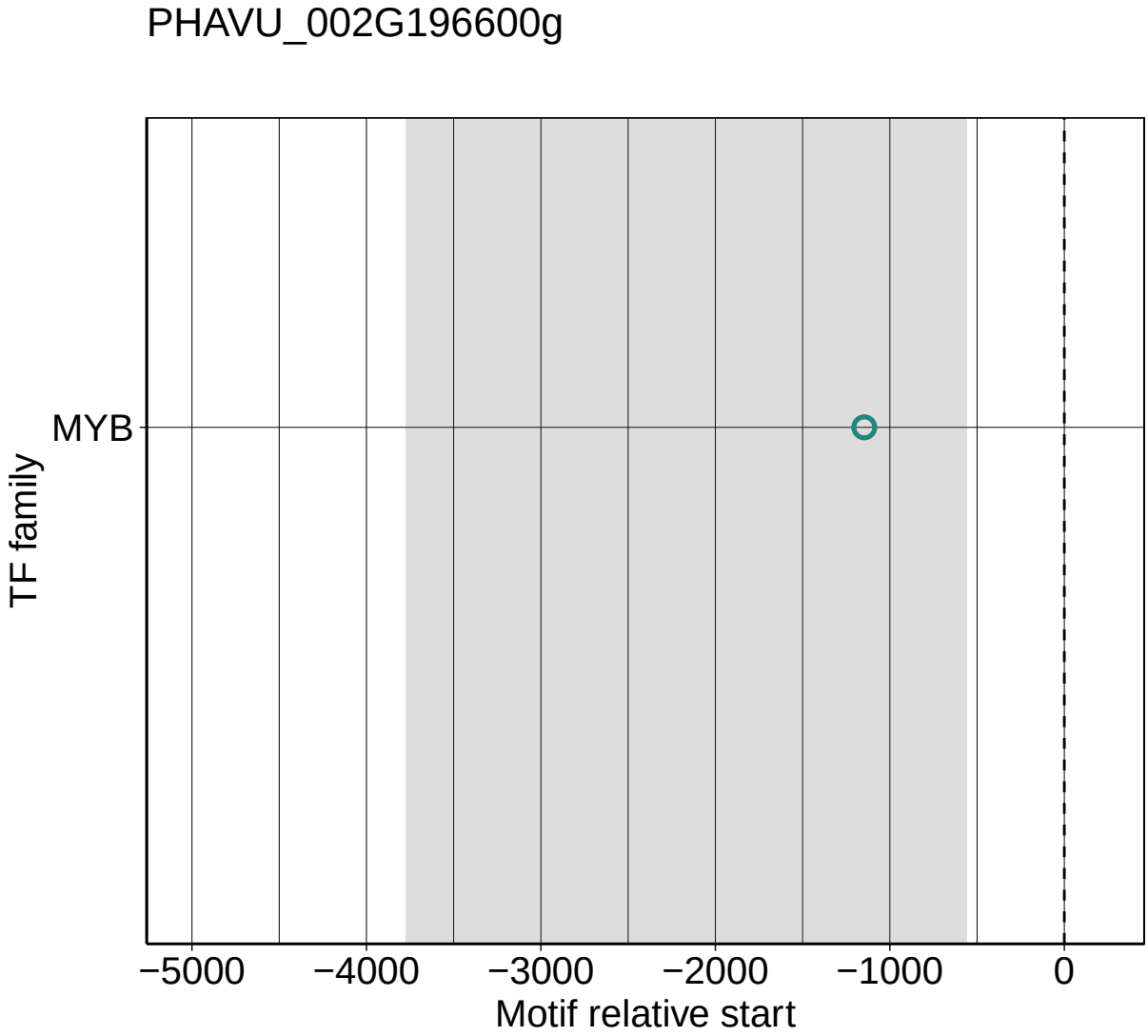
Trihelix
NAC
MYB_related
MYB
LBD
GATA
FAR1
ERF
bZIP
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
bZIP	4	0.04294770	PHAVU_008G033800g
ERF	11	0.01185825	PHAVU_008G033800g
FAR1	1	0.13706295	PHAVU_008G033800g
GATA	1	0.56457869	PHAVU_008G033800g
LBD	3	0.02209318	PHAVU_008G033800g
MYB	6	0.07447207	PHAVU_008G033800g
MYB_related	1	0.63600650	PHAVU_008G033800g
NAC	1	0.81947604	PHAVU_008G033800g
Trihelix	1	0.33633667	PHAVU_008G033800g


PHAVU_002G196600g
MYB
TF family
−5000
−4000
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Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
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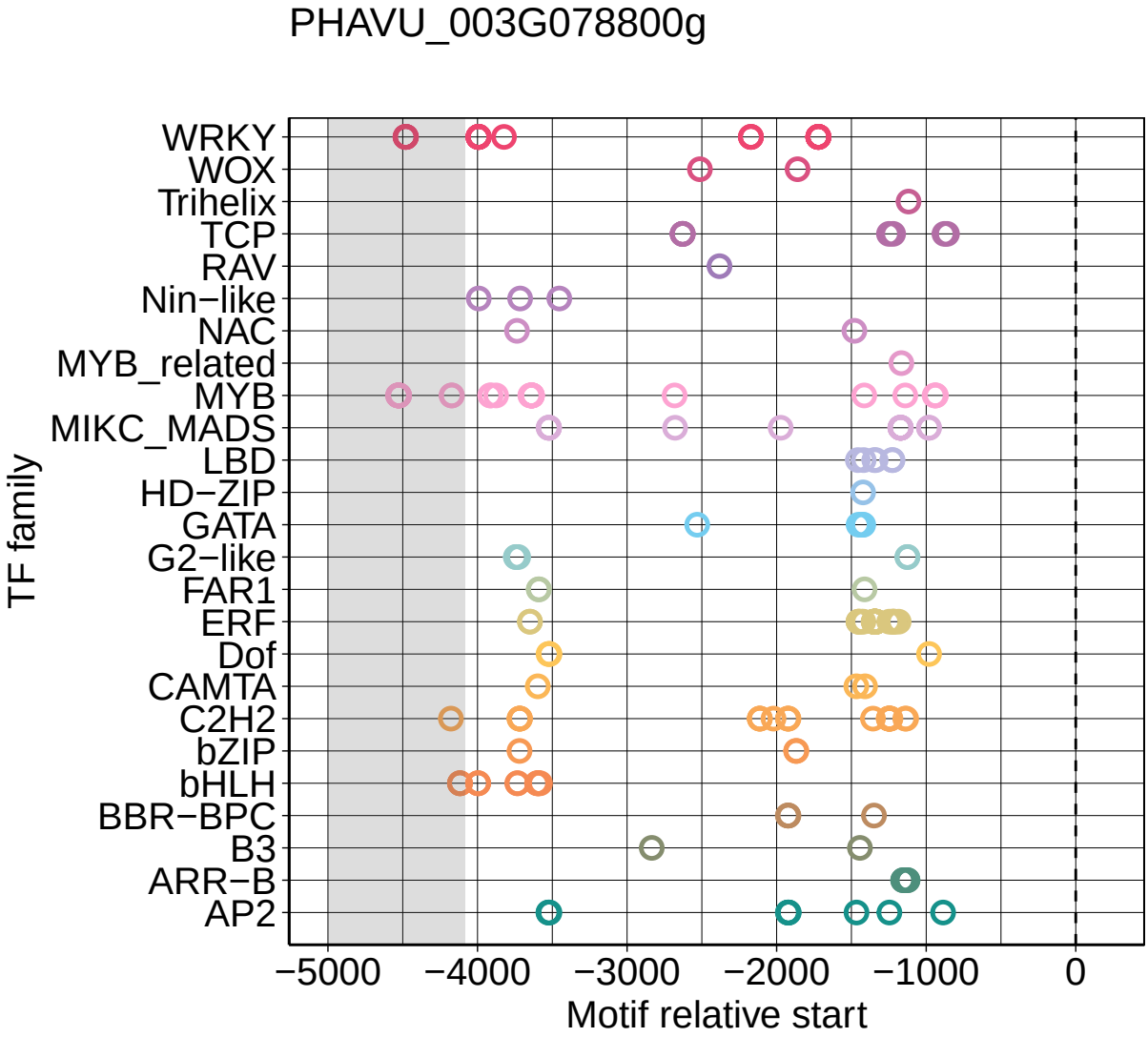
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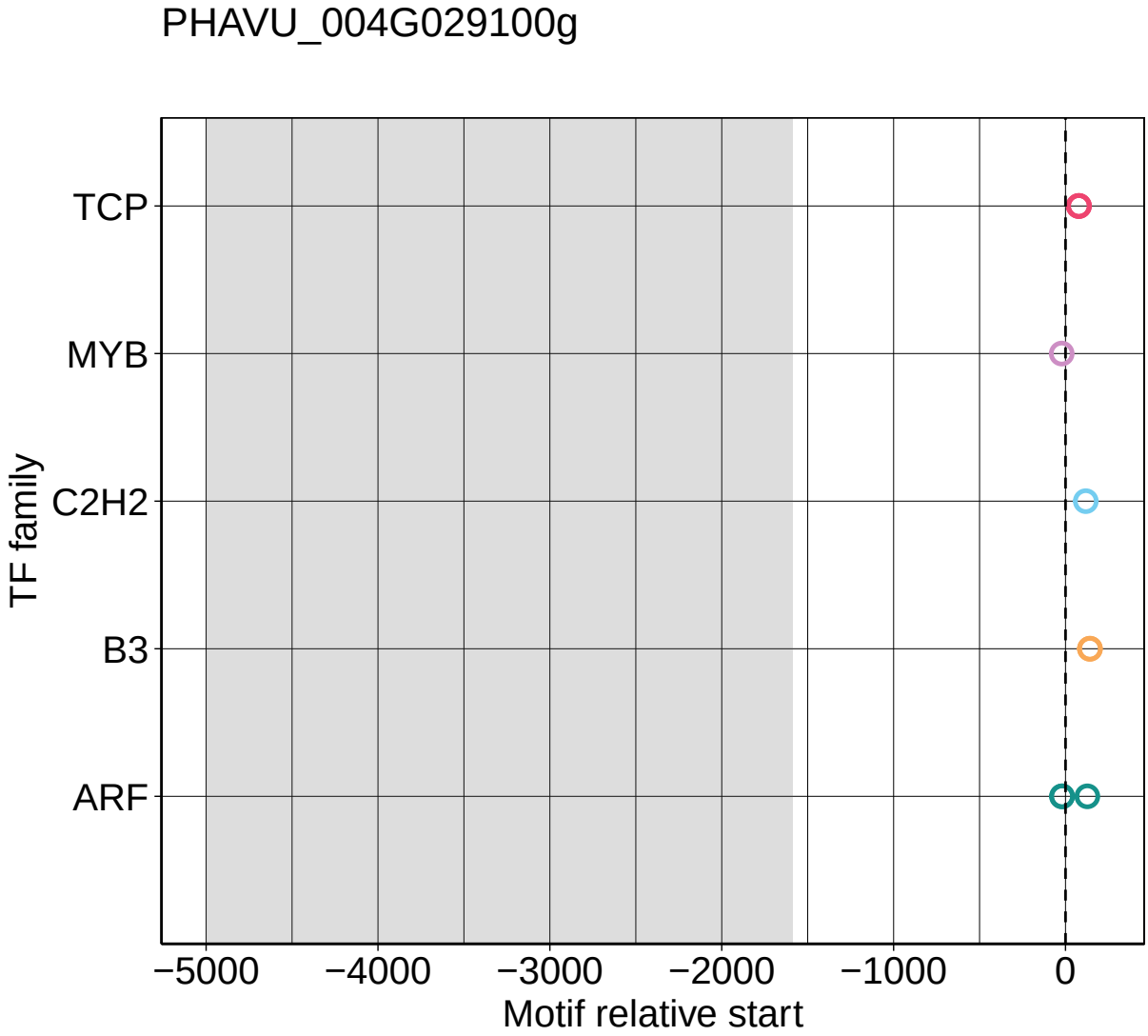
WOX
Trihelix
TCP
RAV
Nin−like
NAC
MYB_related
MYB
MIKC_MADS
LBD
HD−ZIP
GATA
G2−like
FAR1
ERF
Dof
CAMTA
C2H2
bZIP
bHLH
BBR−BPC
B3
ARR−B
AP2
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
AP2	10	2.312287e−03	PHAVU_003G078800g
ARR−B	4	6.086959e−03	PHAVU_003G078800g
B3	2	9.608145e−01	PHAVU_003G078800g
BBR−BPC	4	2.099855e−01	PHAVU_003G078800g
bHLH	13	6.484062e−01	PHAVU_003G078800g
bZIP	3	9.971694e−01	PHAVU_003G078800g
C2H2	22	2.854156e−02	PHAVU_003G078800g
CAMTA	3	8.150365e−02	PHAVU_003G078800g
Dof	4	9.331265e−01	PHAVU_003G078800g
ERF	38	6.344688e−01	PHAVU_003G078800g
FAR1	3	9.411847e−02	PHAVU_003G078800g
G2−like	5	6.172919e−01	PHAVU_003G078800g
GATA	4	8.518858e−01	PHAVU_003G078800g
HD−ZIP	1	9.948584e−01	PHAVU_003G078800g
LBD	6	2.822547e−01	PHAVU_003G078800g
MIKC_MADS	16	3.701959e−04	PHAVU_003G078800g
MYB	28	1.127898e−01	PHAVU_003G078800g
MYB_related	1	9.993814e−01	PHAVU_003G078800g
NAC	2	9.999490e−01	PHAVU_003G078800g
Nin−like	3	3.887650e−01	PHAVU_003G078800g
RAV	1	6.070469e−01	PHAVU_003G078800g
TCP	8	7.381951e−01	PHAVU_003G078800g
Trihelix	1	9.500682e−01	PHAVU_003G078800g
WOX	2	4.623267e−01	PHAVU_003G078800g
WRKY	28	1.535407e−06	PHAVU_003G078800g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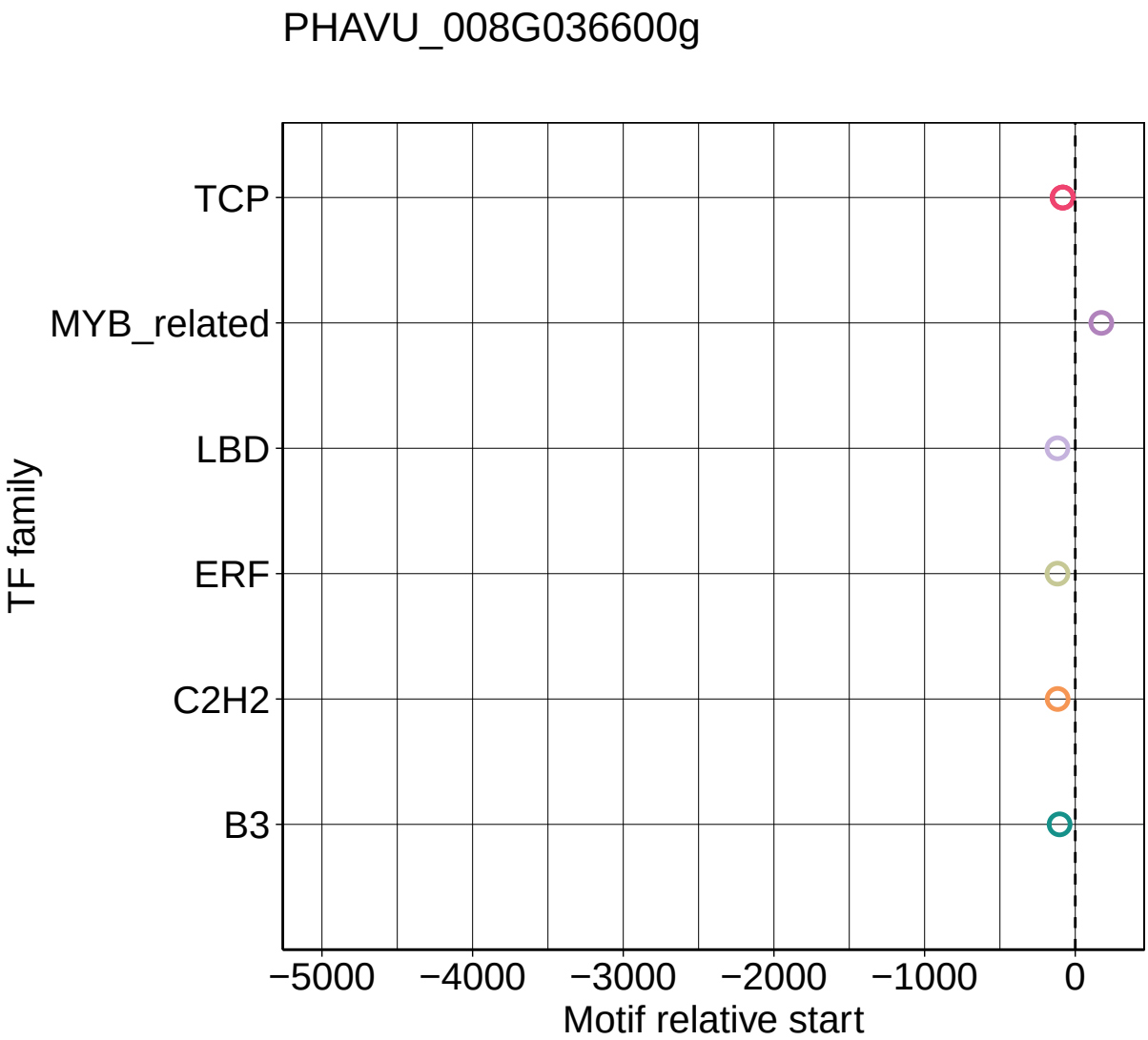
TCP
MYB
C2H2
B3
ARF
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
ARF	3	0.0002638255	PHAVU_004G029100g
B3	2	0.0219853149	PHAVU_004G029100g
C2H2	1	0.5007021510	PHAVU_004G029100g
MYB	1	0.6667198472	PHAVU_004G029100g
TCP	3	0.0085360082	PHAVU_004G029100g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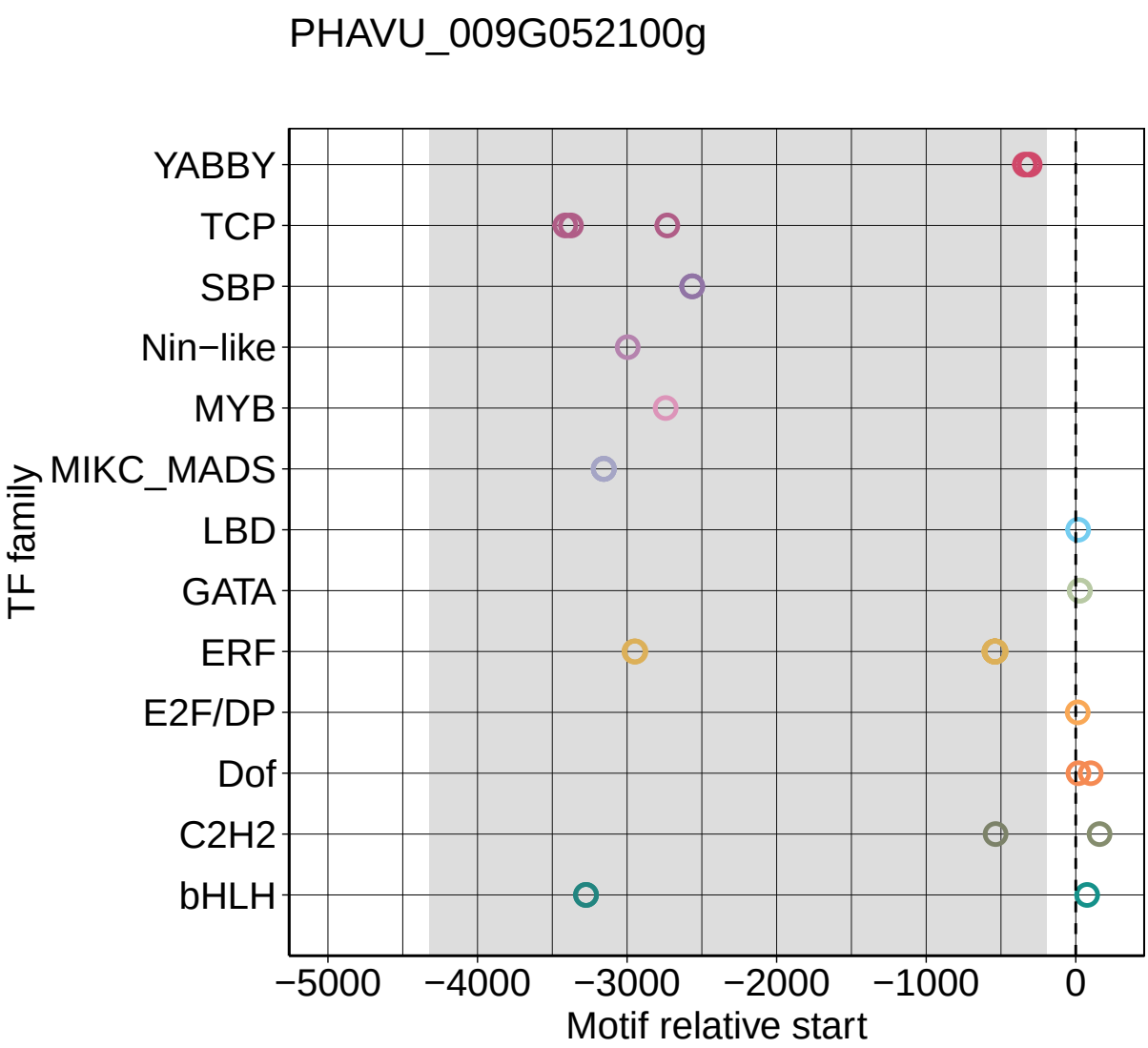
TF family
TCP
MYB_related
LBD
ERF
C2H2
B3
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
B3	1	0.173489242	PHAVU_008G036600g
C2H2	1	0.426296161	PHAVU_008G036600g
ERF	1	0.808229689	PHAVU_008G036600g
LBD	1	0.155083982	PHAVU_008G036600g
MYB_related	1	0.243302357	PHAVU_008G036600g
TCP	3	0.004261775	PHAVU_008G036600g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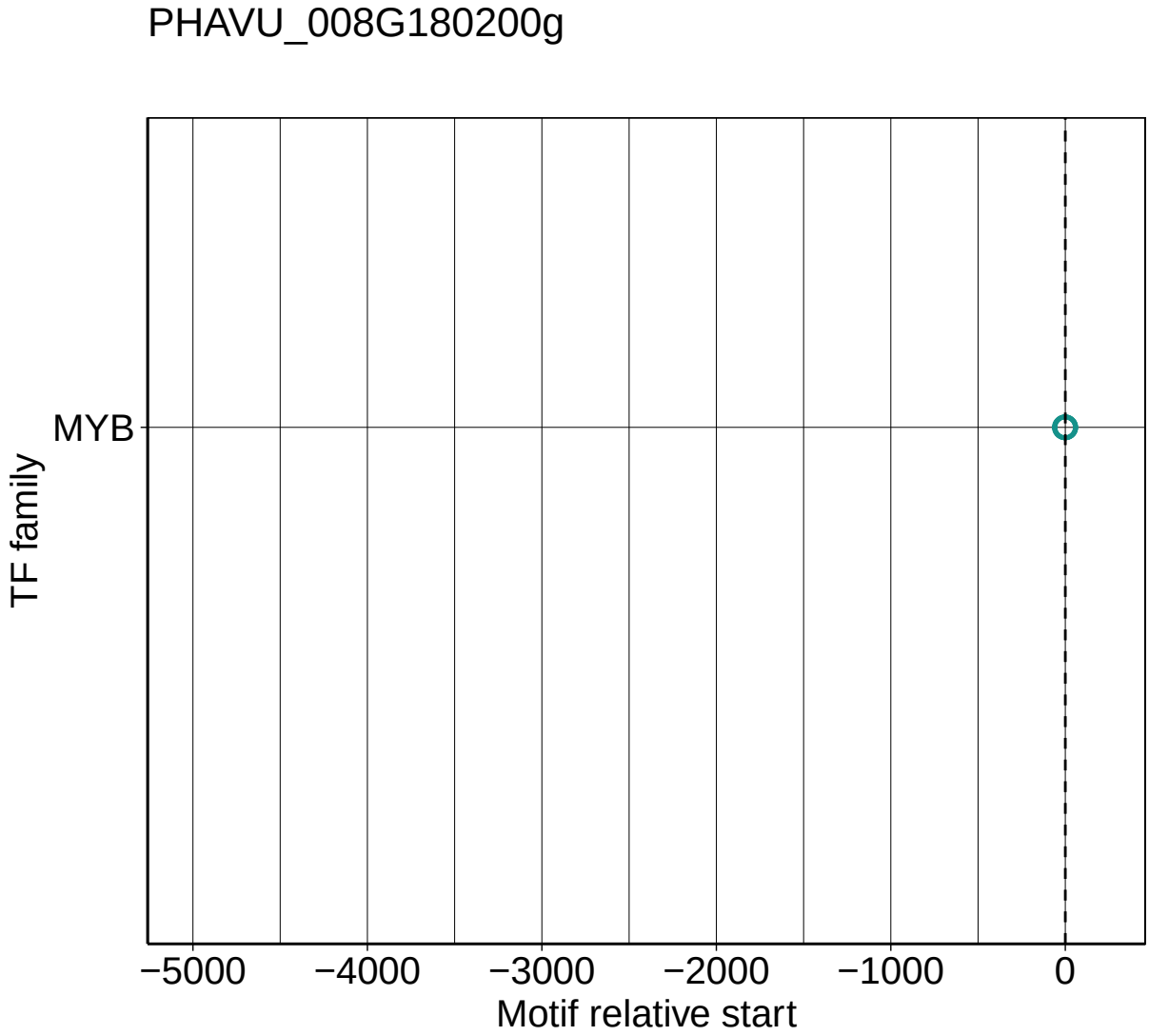
YABBY
TCP
SBP
Nin−like
MYB
MIKC_MADS
LBD
GATA
ERF
E2F/DP
Dof
C2H2
bHLH
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
bHLH	3	0.463090290	PHAVU_009G052100g
C2H2	2	0.733413440	PHAVU_009G052100g
Dof	2	0.374072279	PHAVU_009G052100g
E2F/DP	1	0.124538261	PHAVU_009G052100g
ERF	14	0.006461023	PHAVU_009G052100g
GATA	2	0.291810698	PHAVU_009G052100g
LBD	1	0.550877997	PHAVU_009G052100g
MIKC_MADS	4	0.021467250	PHAVU_009G052100g
MYB	1	0.984629927	PHAVU_009G052100g
Nin−like	1	0.332315022	PHAVU_009G052100g
SBP	2	0.028596879	PHAVU_009G052100g
TCP	3	0.242067524	PHAVU_009G052100g
YABBY	2	0.023496494	PHAVU_009G052100g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MYB
TF family
−5000
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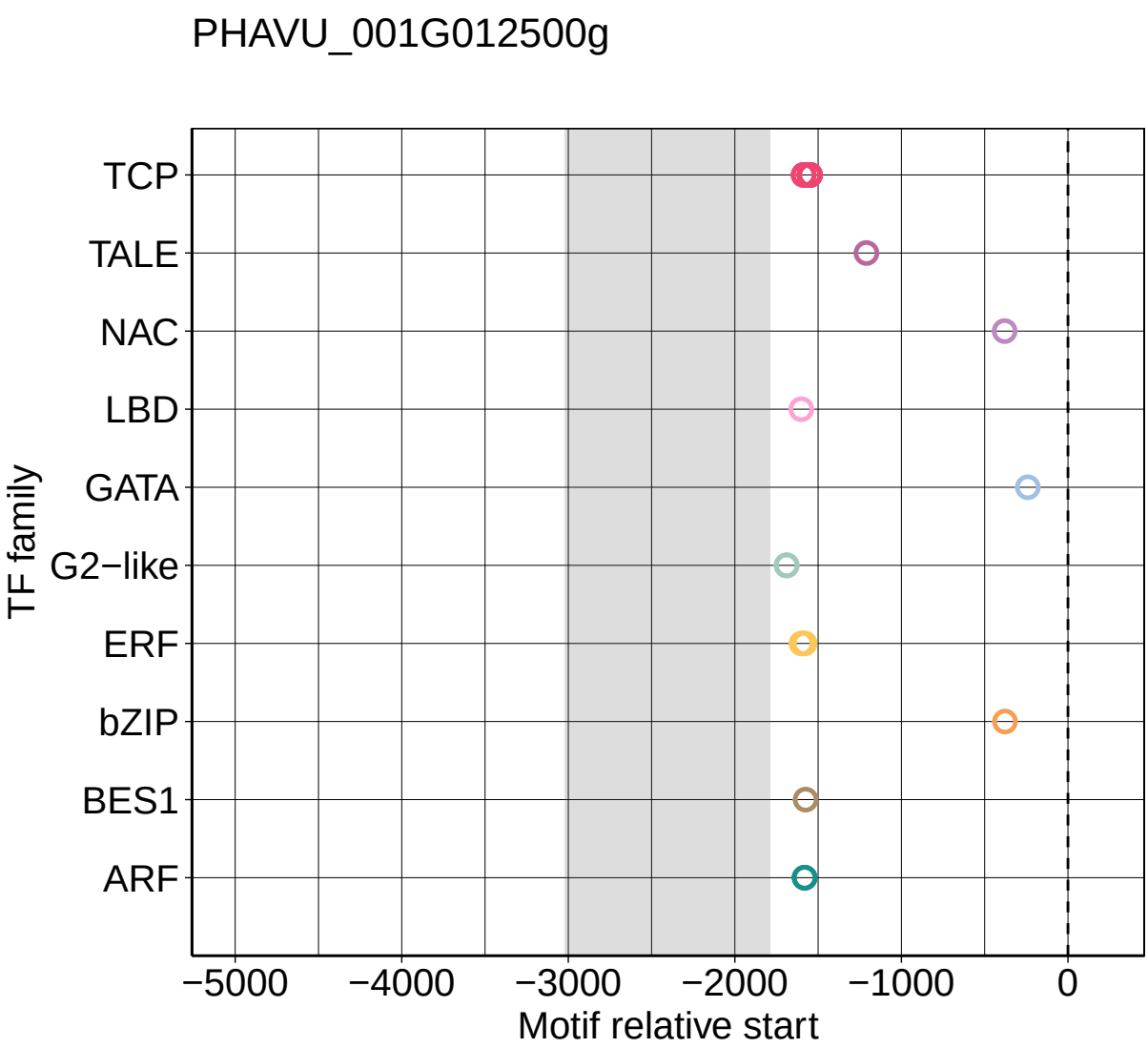
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
MYB	4	0.0001172373	PHAVU_008G180200g


PHAVU_001G012500g
TF family
TCP
TALE
NAC
LBD
GATA
G2−like
ERF
bZIP
BES1
ARF
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
ARF	2	3.725093e−02	PHAVU_001G012500g
BES1	1	2.211945e−01	PHAVU_001G012500g
bZIP	1	6.628294e−01	PHAVU_001G012500g
ERF	2	9.456113e−01	PHAVU_001G012500g
G2−like	2	1.128292e−01	PHAVU_001G012500g
GATA	1	4.828482e−01	PHAVU_001G012500g
LBD	1	3.839883e−01	PHAVU_001G012500g
NAC	1	7.427501e−01	PHAVU_001G012500g
TALE	1	5.678081e−02	PHAVU_001G012500g
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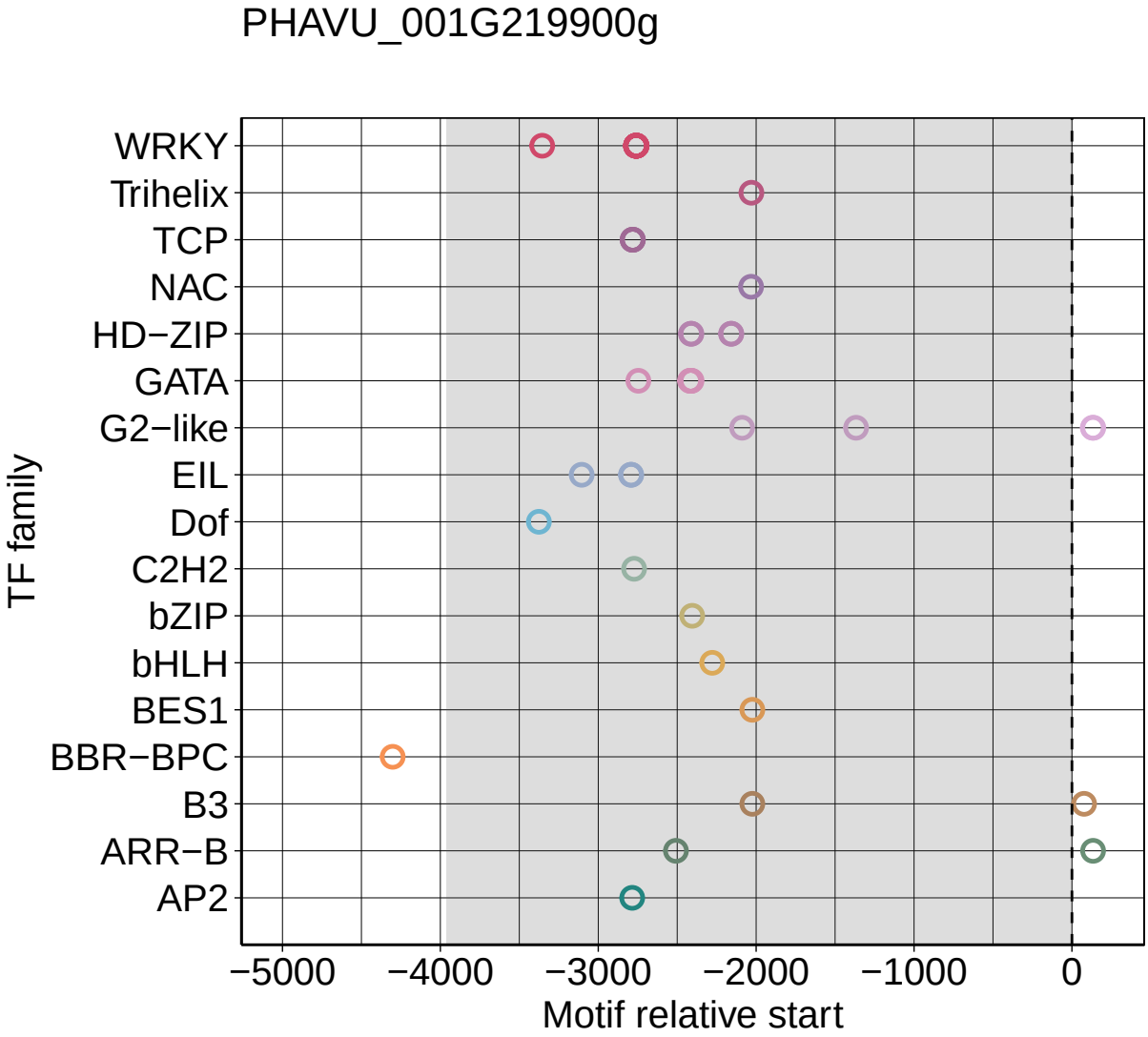
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WRKY
Trihelix
TCP
NAC
HD−ZIP
GATA
G2−like
EIL
Dof
C2H2
bZIP
bHLH
BES1
BBR−BPC
B3
ARR−B
AP2
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
AP2	1	5.290953e−01	PHAVU_001G219900g
ARR−B	2	1.113042e−02	PHAVU_001G219900g
B3	2	3.036939e−01	PHAVU_001G219900g
BBR−BPC	1	4.076931e−01	PHAVU_001G219900g
BES1	1	4.000189e−01	PHAVU_001G219900g
bHLH	1	9.596930e−01	PHAVU_001G219900g
bZIP	1	8.915646e−01	PHAVU_001G219900g
C2H2	1	9.617800e−01	PHAVU_001G219900g
Dof	1	8.046007e−01	PHAVU_001G219900g
EIL	3	4.103402e−04	PHAVU_001G219900g
G2−like	4	3.015825e−02	PHAVU_001G219900g
GATA	5	1.032280e−02	PHAVU_001G219900g
HD−ZIP	4	2.807111e−02	PHAVU_001G219900g
NAC	1	9.376159e−01	PHAVU_001G219900g
TCP	3	3.531752e−01	PHAVU_001G219900g
Trihelix	1	4.854440e−01	PHAVU_001G219900g
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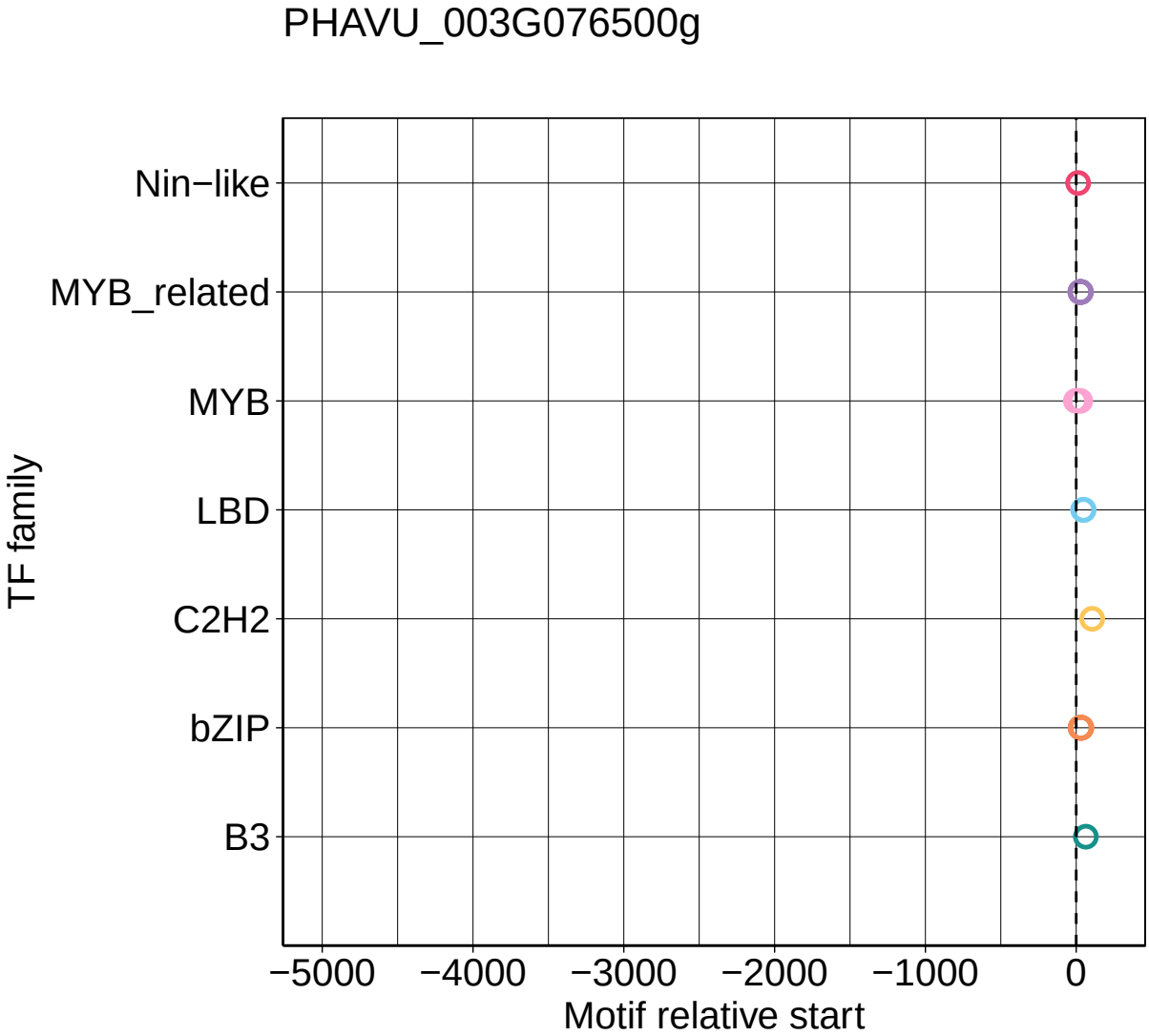
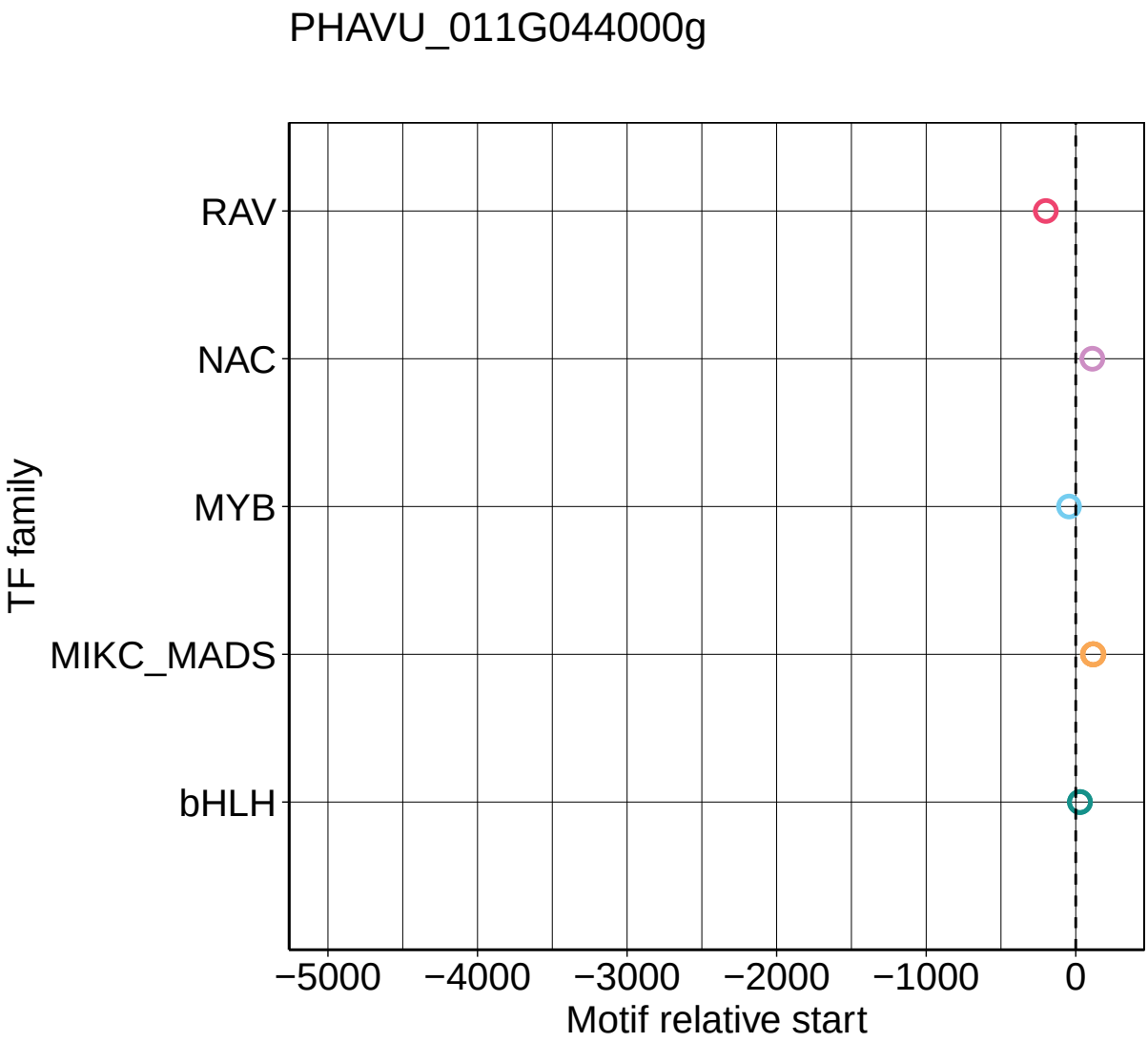

PHAVU_003G076500g
Nin−like
MYB_related
MYB
LBD
C2H2
bZIP
B3
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
B3	1	0.3329581459	PHAVU_003G076500g
bZIP	5	0.0008131161	PHAVU_003G076500g
C2H2	1	0.6929483173	PHAVU_003G076500g
LBD	2	0.0480289990	PHAVU_003G076500g
MYB	2	0.5406169588	PHAVU_003G076500g
MYB_related	5	0.0002063421	PHAVU_003G076500g
Nin−like	1	0.1653221742	PHAVU_003G076500g


PHAVU_011G044000g
RAV
NAC
MYB
MIKC_MADS
bHLH
TF family
−5000
−4000
−3000
−2000
−1000
0
Motif relative start

TF.family	Motifs.count	Binomial.statistics	Gene
bHLH	2	1.379410e−01	PHAVU_011G044000g
MIKC_MADS	5	3.907226e−06	PHAVU_011G044000g
MYB	1	6.667198e−01	PHAVU_011G044000g
NAC	1	4.458431e−01	PHAVU_011G044000g
RAV	1	4.310314e−02	PHAVU_011G044000g