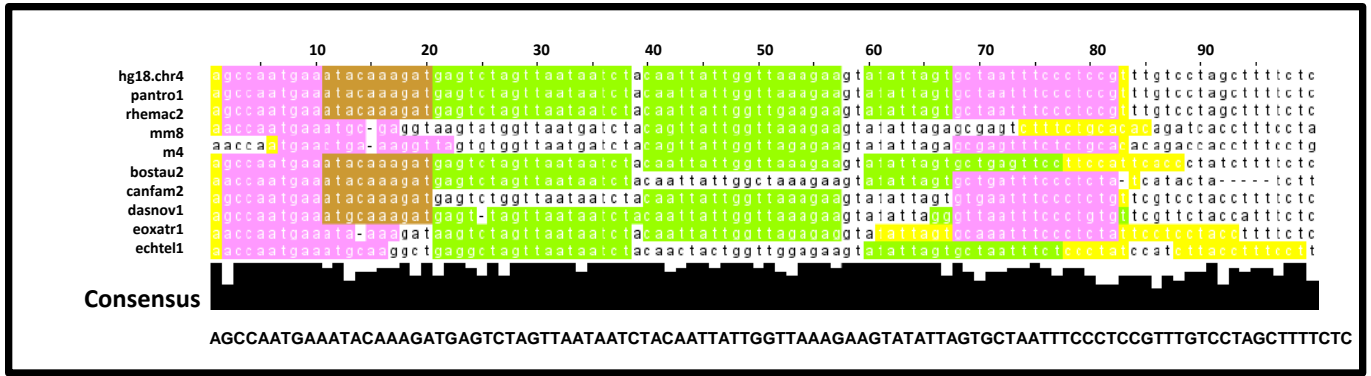
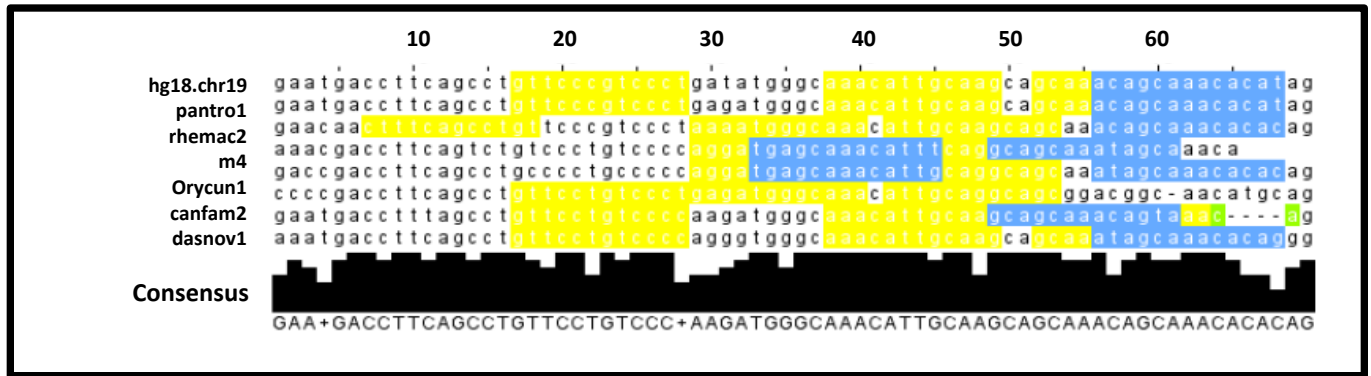


Supplementary Figure 1.

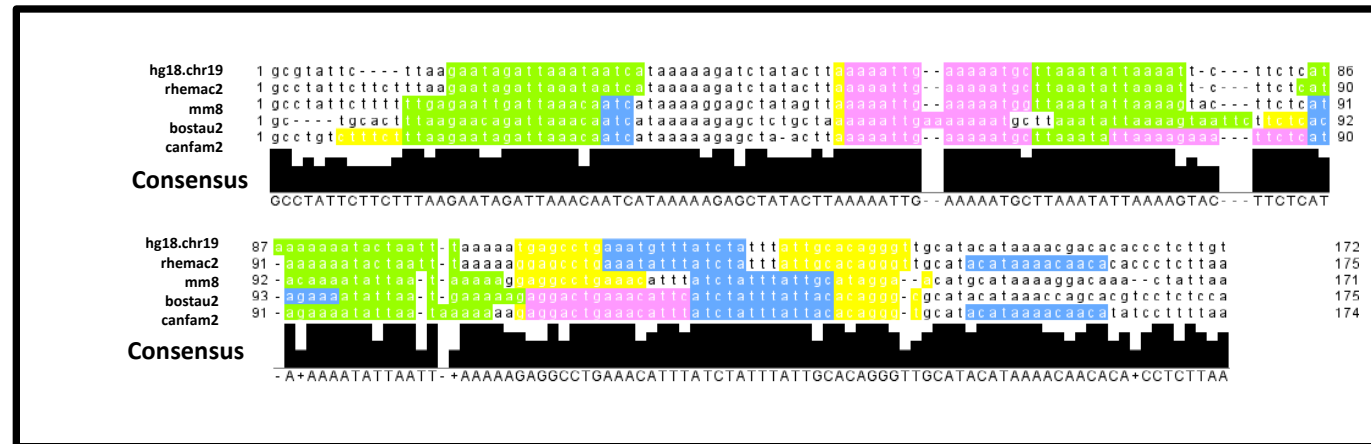
a. HS-CRM1 (Alb gene)



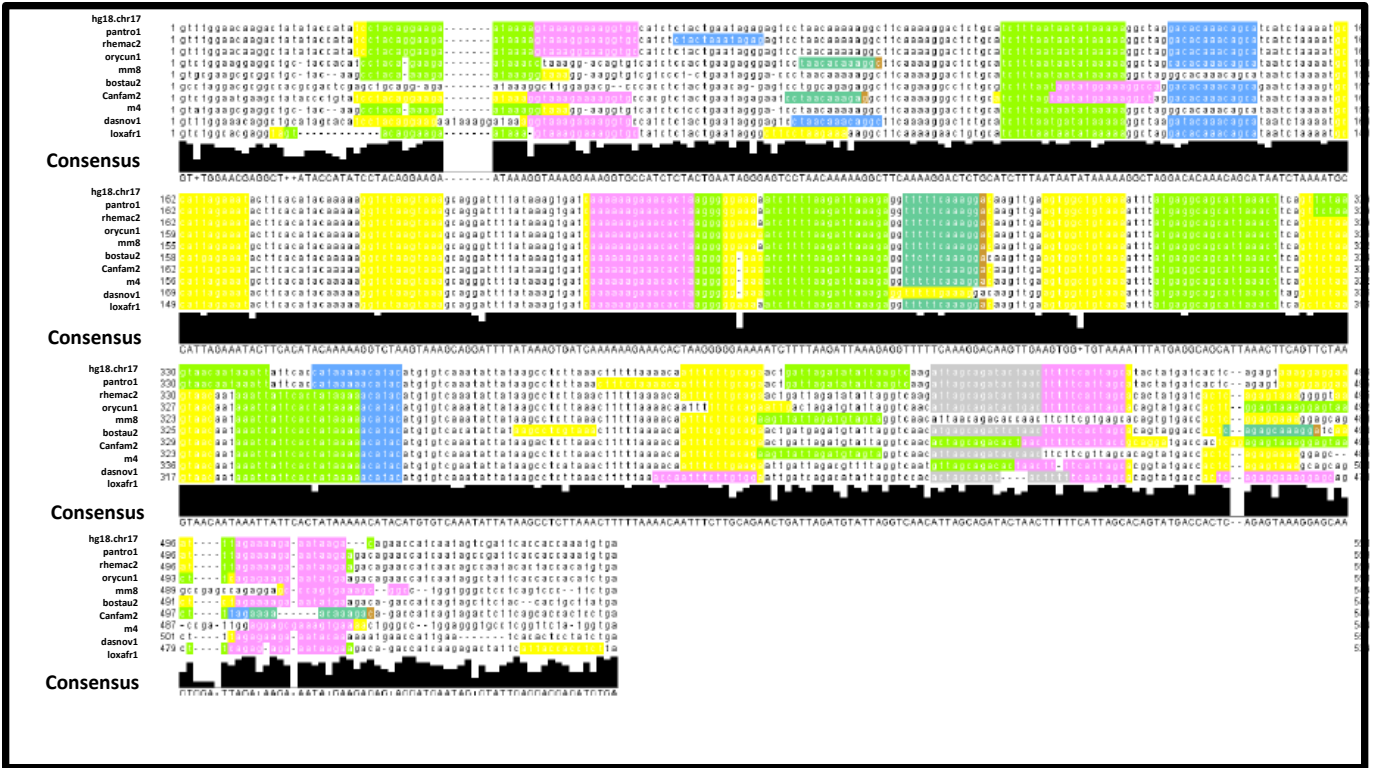
b. HS-CRM2 (Apoc4 gene)



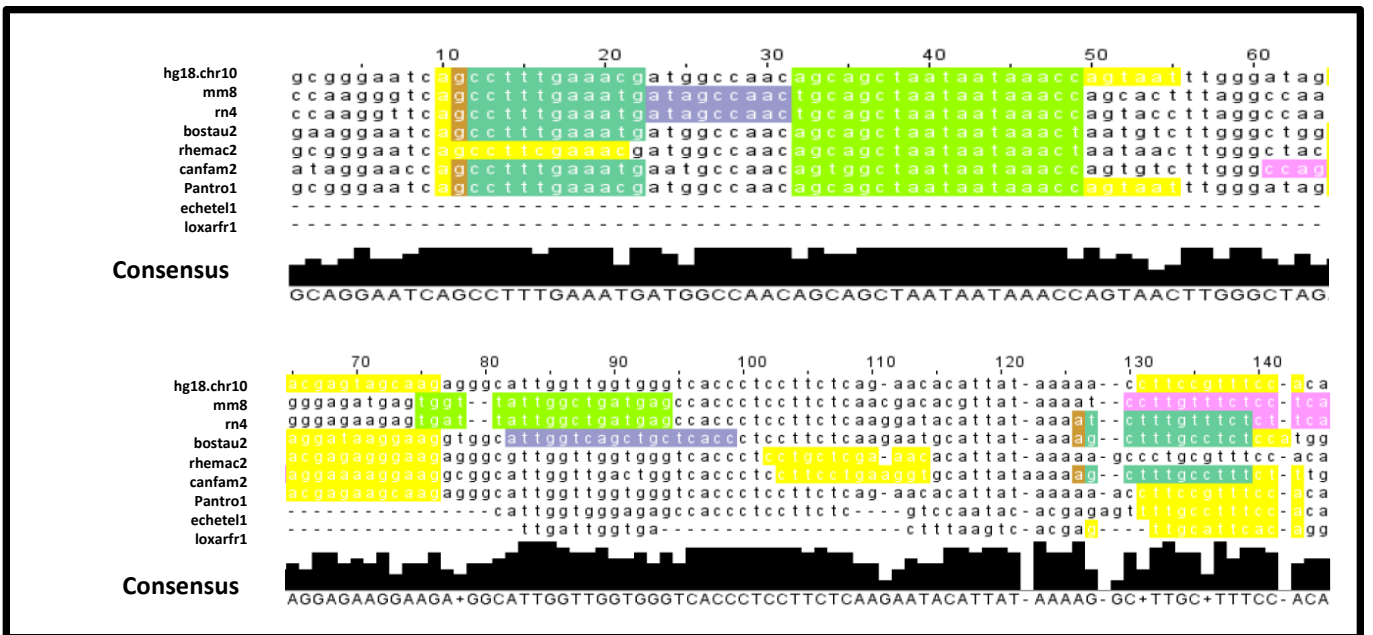
c. HS-CRM3 (Apo^ha gene)



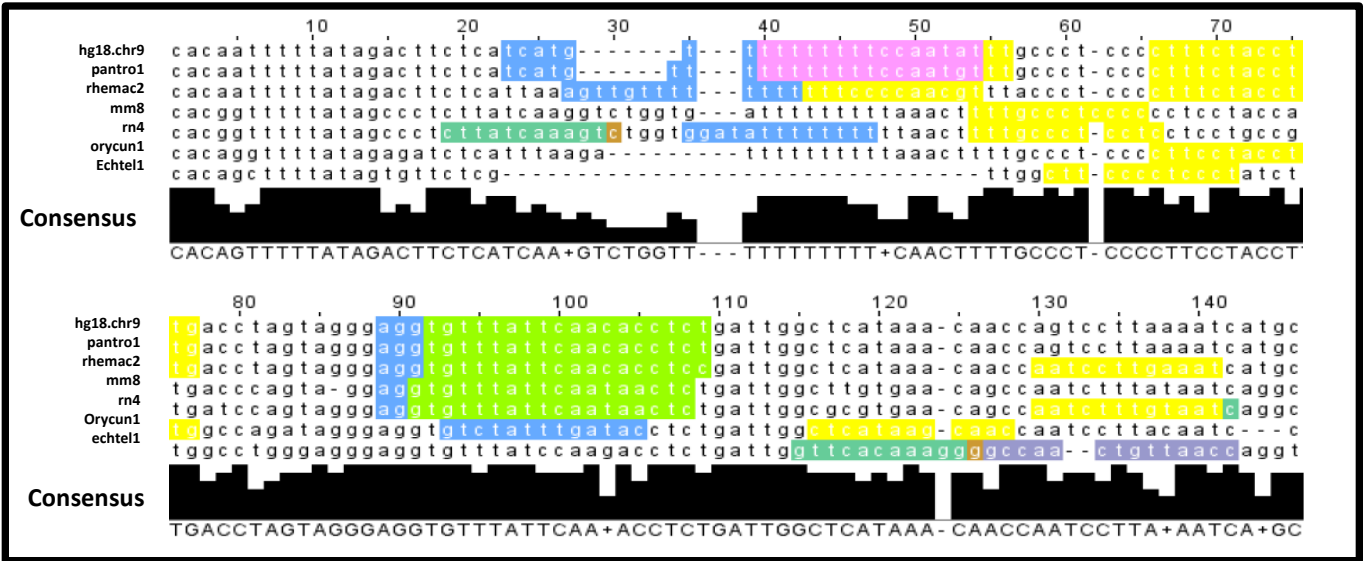
d. HS-CRM4 (ApoH^b gene)



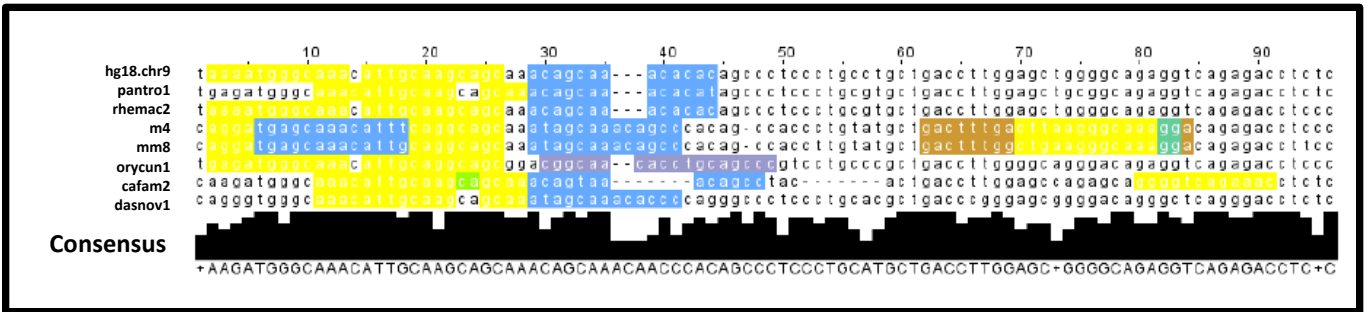
e HS-CRM5 (Cyp2 gene)



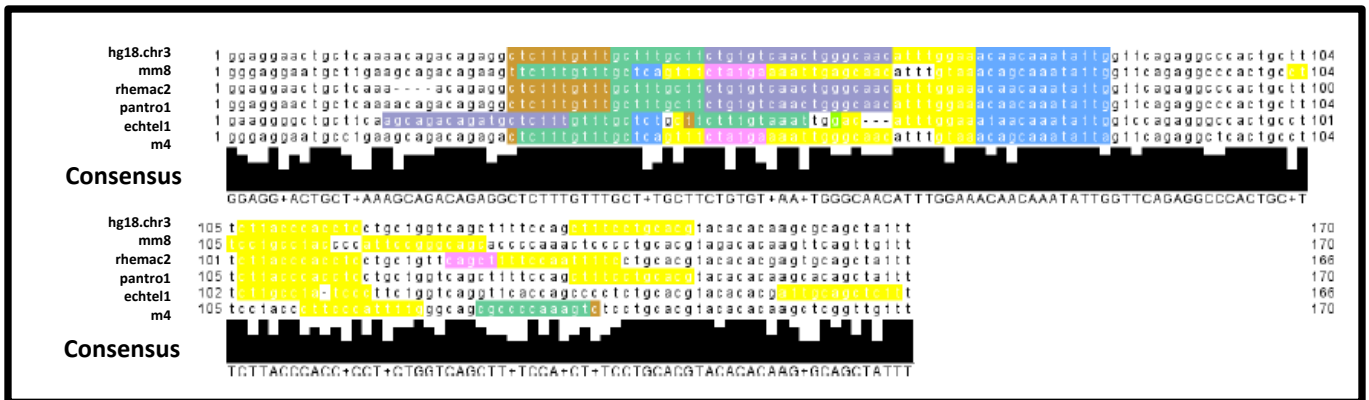
f. HS-CRM6 (Aldob gene)



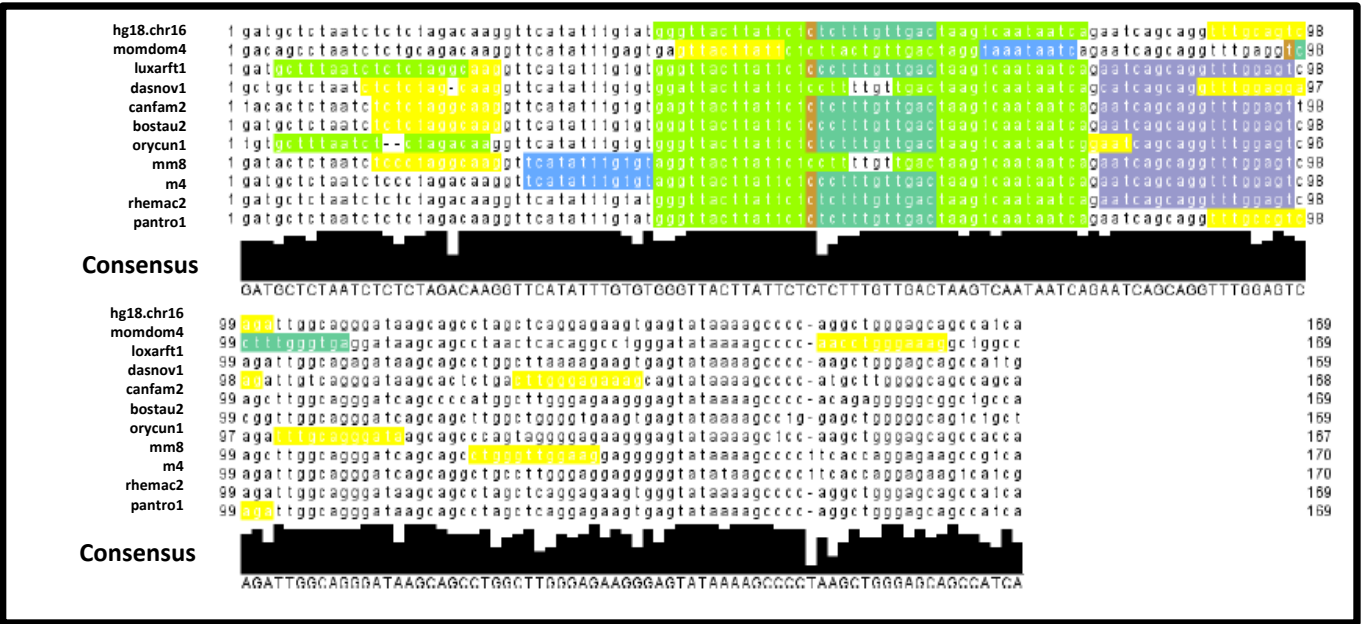
g. HS-CRM7 (Apoc1 gene)



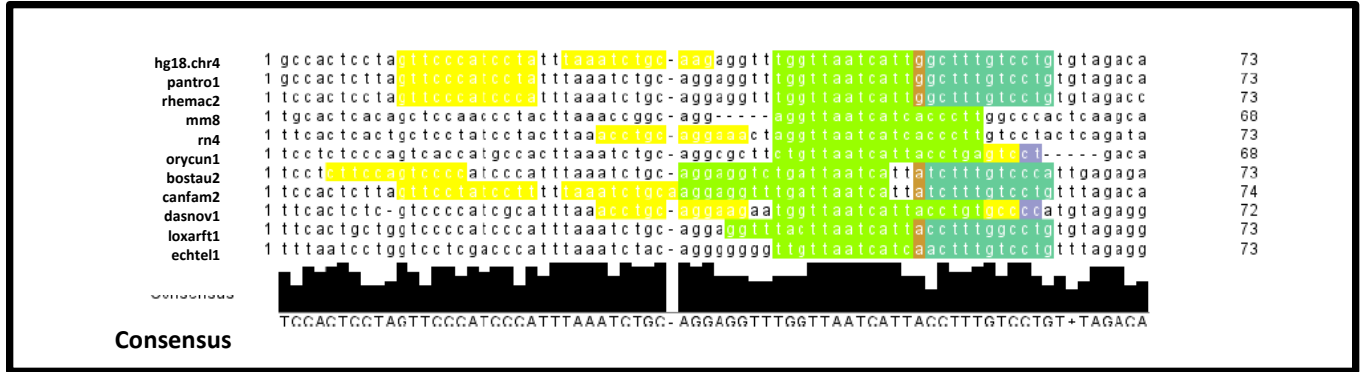
h. HS-CRM9 (Tf gene)



i. HS-CRM10 (Tr gene)



j. HS-CRM11 (Fga gene)



k. HS-CRM12 (HPR gene)

hg18.chr16 1 t c c t t c c c c t t c c a a g a c c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 pantro1 1 t c c t t c c c c t t c c a a g a c c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 rhemac2 1 t c t t t c c c c t t c c a a g a c c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 m4 1 t c t a c c c c c t t c c a a g a c c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a g t a 97
 orycun1 1 c c t a c c c c c t t t a a a g a c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
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 canfam2 1 t c t c t c a c c c t t c a a a g c c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 loxaf1 1 t c t c t c c t c t c c a a a d g c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 echtel1 1 t c t c t t c c c t t c c a a g c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t a t t a t g a c a a g c g g c t a c a a a t c a a t a 97
 momdom4 1 t c t c t c c c c c c t t g g a c c c c t g a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g g t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 96
 galgal2 1 t t t t c c c c c t c c t t t g a c a c c c t c a a t c c t a t c a a a a g c a c a t c t t c c a t t c a t t g c t t c c c g a t g t c a t t a t g a c a a g c g g c t a c a a a t c a a t a 95

Consensus

TCTCTCCCCTTCGAAGACCCCTGAATCCTATCAAAGACATCTTCCATTATTGCTTCCCCTGTCATTATGACAAGCGGCTACAAATCAATA

hg18.chr16 98 g a g a g g g a a a g g c a g a c c a c c g c a c t c a c c a a g t g a a a a g a t t c a c t c t c a g c c c c g a t t t g c t a a a l a g c c a a t a t a g c a g c c a t t g g c g c 194
 pantro1 98 g a g a g g g a a a g g c a g a c c a c c g c a c t c a c c a a g t g a a a a g a t t c a c t c t c a g c c c c g a t t t g c t a a a l a g c c a a t a t a g c a g c c a t t g g c g c 194
 rhemac2 98 g a g a g g g a a a g g c a g a c c a c c g t a c t c a c c a a g t g a a a a g a t t c a c t c t c a g c c c c g a t t t g c t a a a l a g c c a a t a a c a g c c a t t g g t g c 194
 m4 98 g a g a g g g a a a g g c a g a c c a g c c c g c a c t a c c a a g t g a a a a g a t t c a c t c t c a g c t c c g a t t t g c t a a a l a g c c a a t a a t a g c a g c c a t t g g c g c 194
 orycun1 98 g a g a g g g a a a g g c a g a c c a c c g c a c t a c c g a g t g a a a a g a t t c a c t c t c a g c c c c g a t t t g c t a a a l a g c c a a t a t a g c a g c c a t t g g c g c 194
 bostau2 98 g a g a g g g a a a g g c a g a c c a c c g c a c t c a c c a a g t g a a a a g a t t c a c t c t c a g c c t c g a t t t g c t a a a l a g c c a a t a t a g c a g c c a t t g g c g c 194
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 galgal2 96 g a g a g g c a a a g g c a g g c t c g c c c g c a c t c a c c a a g t g a a a a g a t t c a c t c t c a a c c c g a t t t g c t a a a l a g c a a t a t a g c a g c c a t t g g c g c 192

Consensus

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 pantro1 195 c c c g c a t t a a a t a t a c a t t t c a c t c t g c g t t t a t a a a c t c c t c a c c a a a t t g g a t t t t c t e g a t g t t c t a a t t t c c a c a t t 291
 rhemac2 195 c c t g c a t t a a a t a t a c a t t t c a c t t g c g t t t a t a a a c t c c t c a c c a a a t t g g a t t t t c t e g a t g t t c t a a t t t c c a c a t t 291
 m4 195 c c t g c a t t a a a t a t a c a t t t c a c t c t g c g t t t a t a a a c t c c t c a c c a a a t t g g a t t t t c t e g a t g t t c t a a t t t c c a c a t t 291
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 loxaf1 195 c c t g c a t t a a a t a t a c a t t t c a c t t g c g t t t a t a a a c t c c t c a c c a a a t t g g a t t t t c g t g a t g t t c t c t a a t t t c c a c a t t 291
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 galgal2 193 c c c g c a t t a a a t a t a c a t t t c a c t t g c g t t t a t a a a c t c c t c a c c a a a t t g g a t t t t c t e g a c g t t c t c t a a t t t c c a c a t t 289

Consensus

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 rhemac2 292 t a t c a t t t a a a t t a a a c c c t c t g t g g a a g g - - - - g g g a t a a a - - - a g a a a a g g t a g a g a g a g g c a g a c a g t a c t t a t t t t - - - - t c c 376
 m4 292 t a t c a t t t a a a t t a a a c c c g c t g t g g a g g - - - g g t g t g g g g t a g a g a - - - a g g a g a g g t a g a g a g a g g c a g a c a g t a g a t a t t t t - - - - t c c 379
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 bostau2 292 t a t c a t t t a a a t t a a a c c c t c t g t g g a g a d d - - - - g g g a a t a g a g a - - - a g a a g a a g t a g a a a a g g c c a g a a a t a c t g t t t t - - - - t t c 376
 canfam2 292 t a t c a t t t a a a t t a a a c c c t c t g t g g a g a g - - - - g g g a a t a g a g a a g g a g a g a a g g t a g a g a g a g g c c a a a a g a t g t a t t t t - - - - t t c 379
 loxaf1 292 t a t c a t t t a a a t t a a a c c c t c t g t g g a g a g - - - - g g g a a d a g a g a - - - a g a a a a a a a g l a g a g a g a g c c a a a c a g t t c t t a t t t t t c t t c 382
 echtel1 292 t a t c a t t t a a a t t a a a c c c t c t g t g g a g a g - - - - g g g a a t a g a g a - - - a g a a a a a a a g l a g a g a g a g c c a a a c a g t t c t t a t t t t t c t t c 383
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 galgal2 290 t a t c a t t t a a a t t a a a c c c t c a g t g g g g a g a - - - - g g g g g t t g g g a a - - - a g g g a a a g a g a a g a g a a g c c g t g c a g t t c t g t a t t t - - - - t c c 374

Consensus

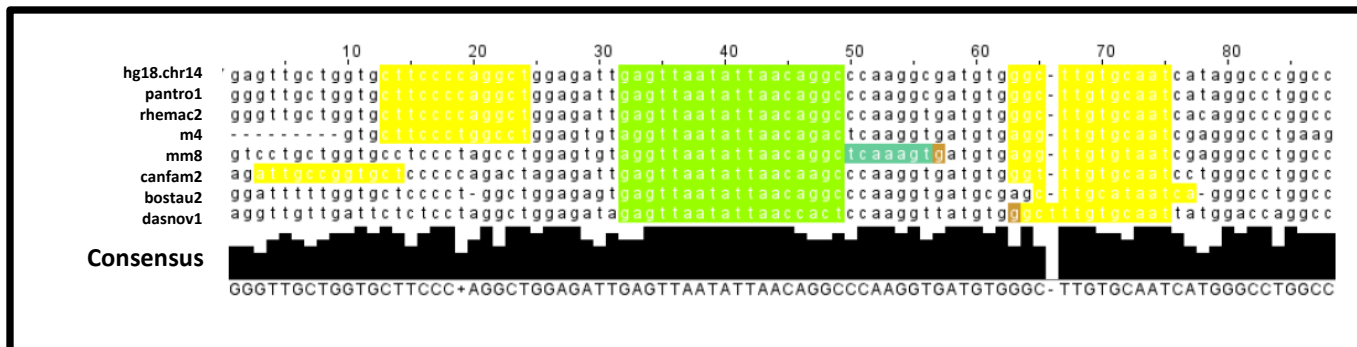
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 pantro1 374 t t t t - - - - g a t t c c - - - - c c c t t t a t g a a a c c c a t a a a t a a t a c a g g t a t c a c a g c t a a a g c a g c - - - - a g g 437
 rhemac2 377 t t t t - - - - g a t t c c - - - - c c c t t t a t g a a a c c c a t a a a t g a t a c a g g t a t c a c a g c t a t a a g c a g c - - - - a g a 440
 m4 380 t t t t - - - - g a t c c c - - - - t c c c t t t a t g a a a c c c a t a a a t a a a c a c a g g t a t c a a a g c t a - g c g c a g c - - - - t g t 443
 orycun1 382 t t t t - - - - g a t c c c - - - - t c c a t t t a t g a a a a c c t a a a a t a a t a c a g g t a t c a t a n c c a t a a g c a g c a g g g t g g c 451
 bostau2 377 t t t t a a g c c c c c c c t t t t t t a t g a a a c c c a t a a a t a a t a c a c a g g t a t c a c a g t t a t a a g c a g c - - - - a g g 446
 canfam2 380 t t t t - - - - g a c c c c c c c t t t t t a t g a a a c c c a t a a a t a a t a c a c a g g t a t c a t a n c c a t a a g c a g c - - - - a g g 446
 loxaf1 383 t t t t - - - - c t c c c c t a c c t t t t t a t g a a a c c c a t a a a t a a t g c a g g t a t g t a g c t a a a a t - - - - - a g 447
 echtel1 384 t t t t - - - - g a a c c c c a c c t t t t t a t g a a a a c c c a t a a a t a a t g c a g g t a t c a t a n c c t a c a a g c - - - - a g g 448
 momdom4 379 t t t t - - - - g a t t t t a t g a a a c c c a t a a a t a a t a c a g g t a t c g l a n c c a t c a g c a g t - - - - g g t 439
 galgal2 375 t t t t - - - - g a t t t t a t g a a a c c c a t a a a t a a t a c a c a g g t a t c a t a g c t a t a a g c a g c - - - - a g g 432

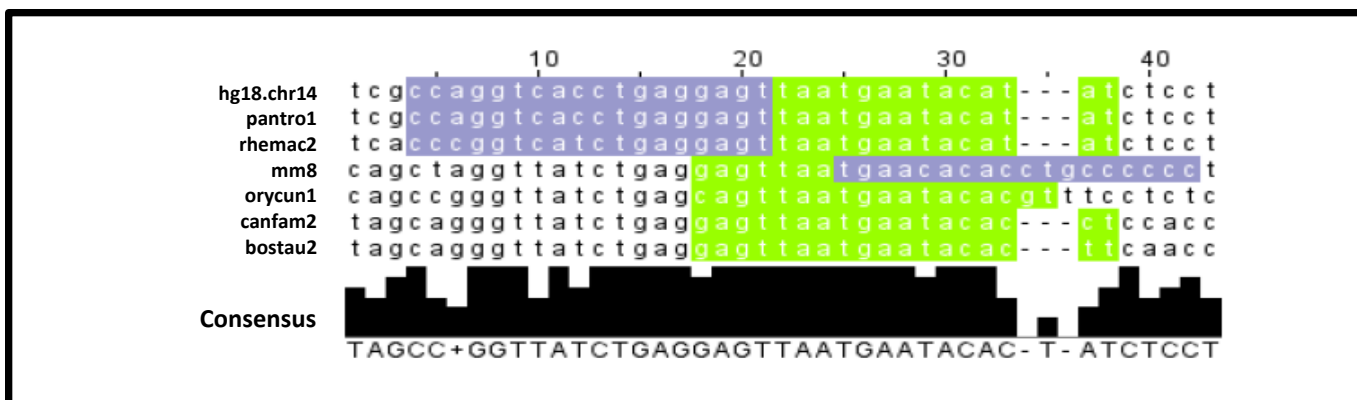
Consensus



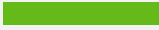




TTTT--CACC--TCCTTTTATGAAACCATAAATAATACCAGGTATCATAGCTATAAGCAGC-----AGG

I. HS-CRM13 (Serpina1^b gene)



m. HS-CRM14 (Serpina1^c gene)



TF identifier	Color code
LEF1/TCF1	
LEF1	
HNF1	
CEBP	
FOX	
TAL1/BETAE47	
IRF	
MYOD	