

Evolutionary optimization of transcription factor binding motif detection

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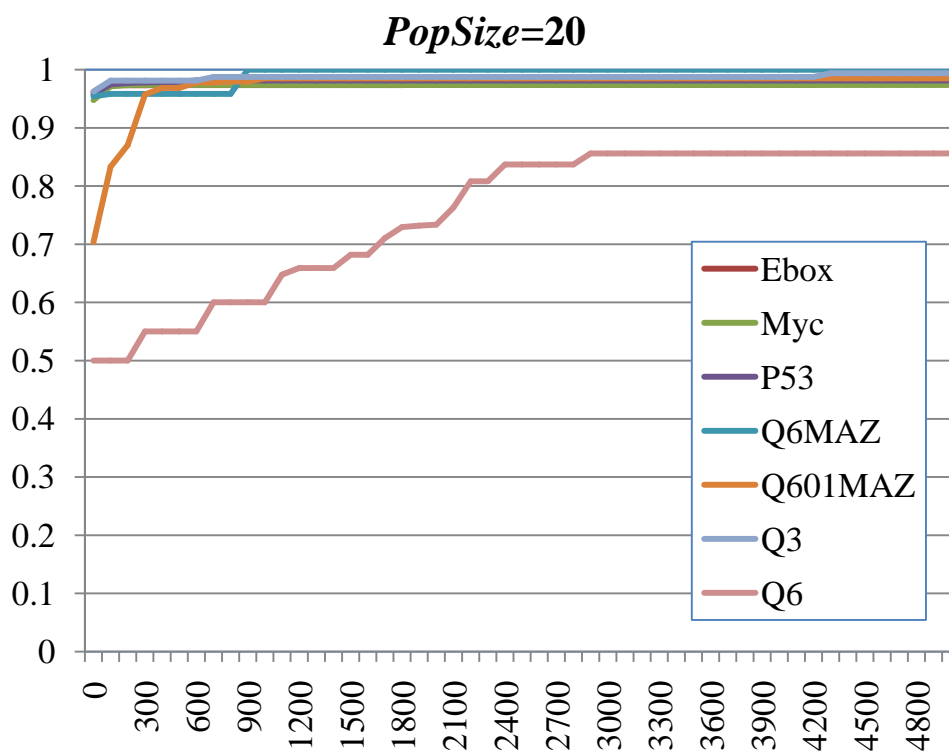
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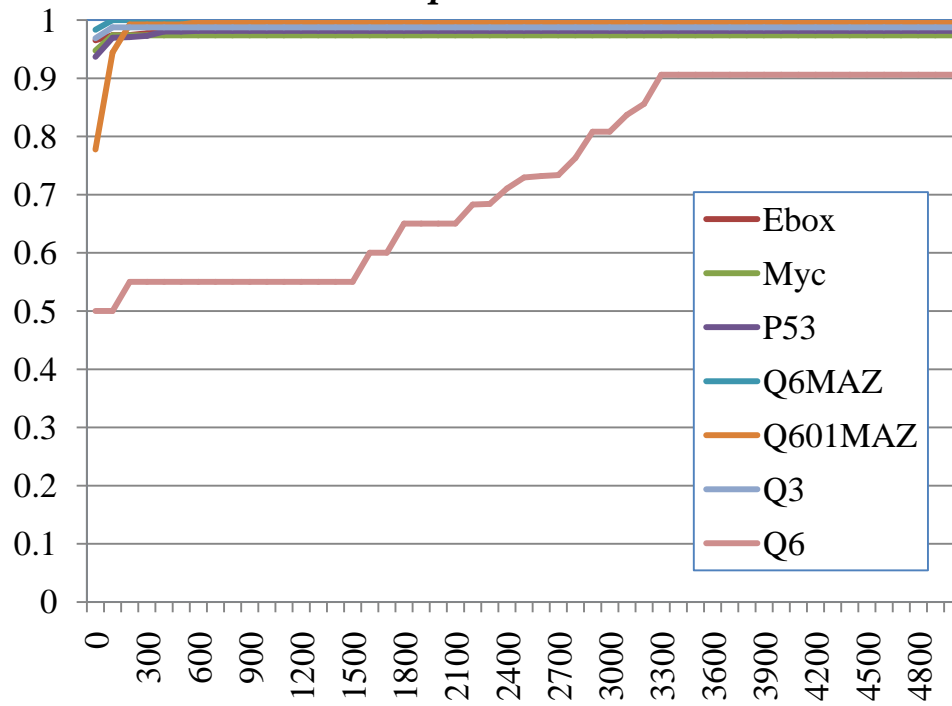
Supplementary Figure S1

Distributions of overall classification accuracy, A_c , for different generation numbers. The population sizes $PopSize$ are fixed to (a) 20, (b) 40, (c) 60, (d) 80, (e) 100, (f) 120, (g) 140, (h) 160, (i) 180, and (j) 200, respectively.



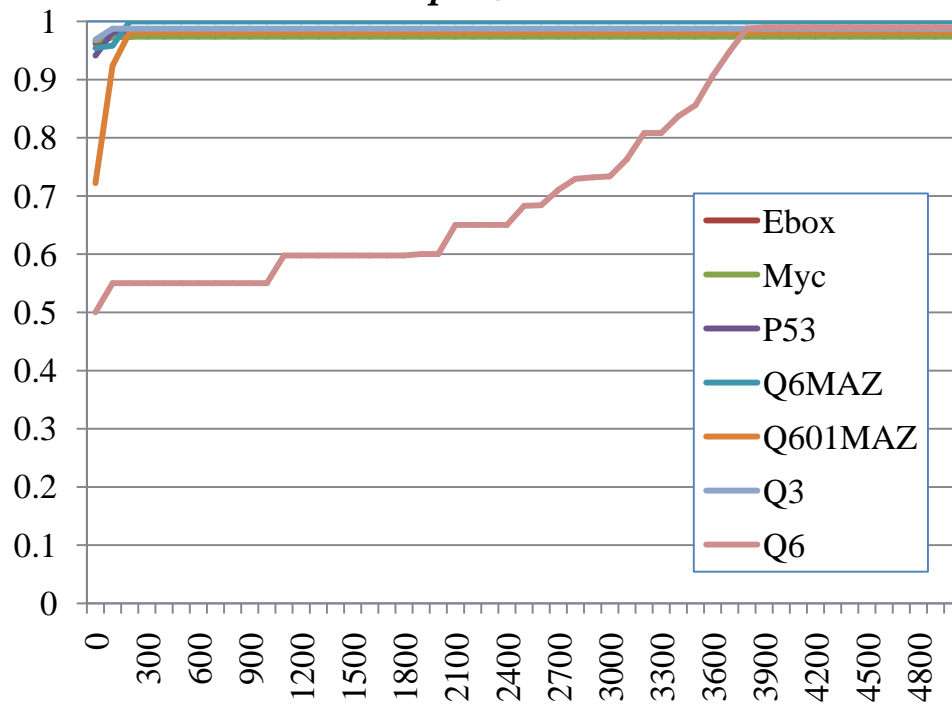
(a)

PopSize=40

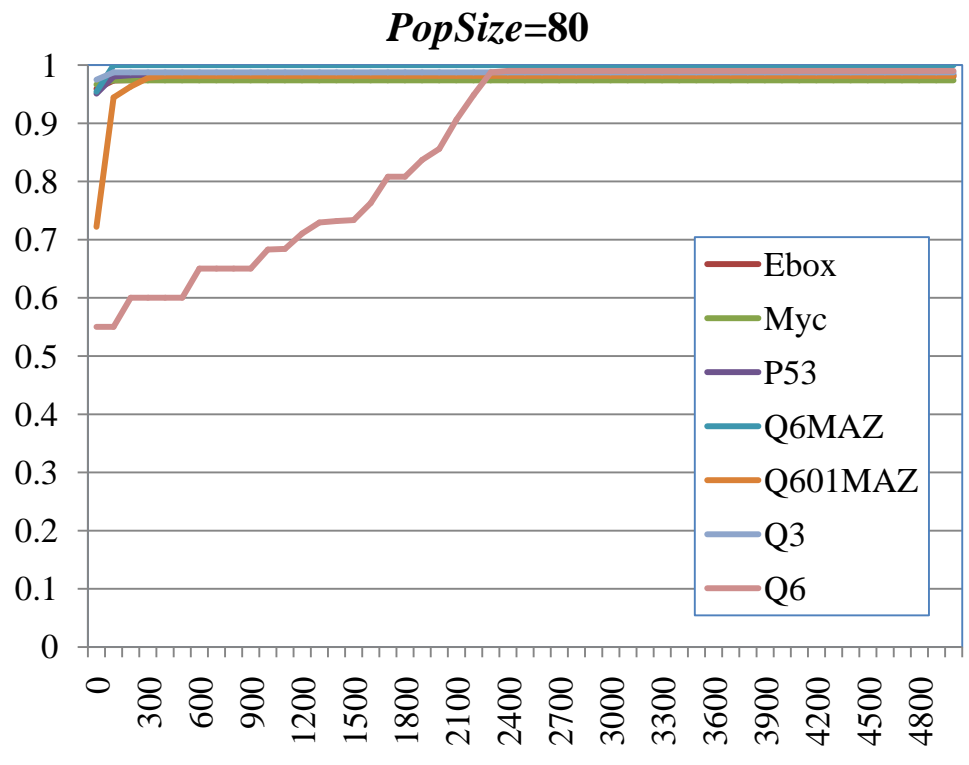


(b)

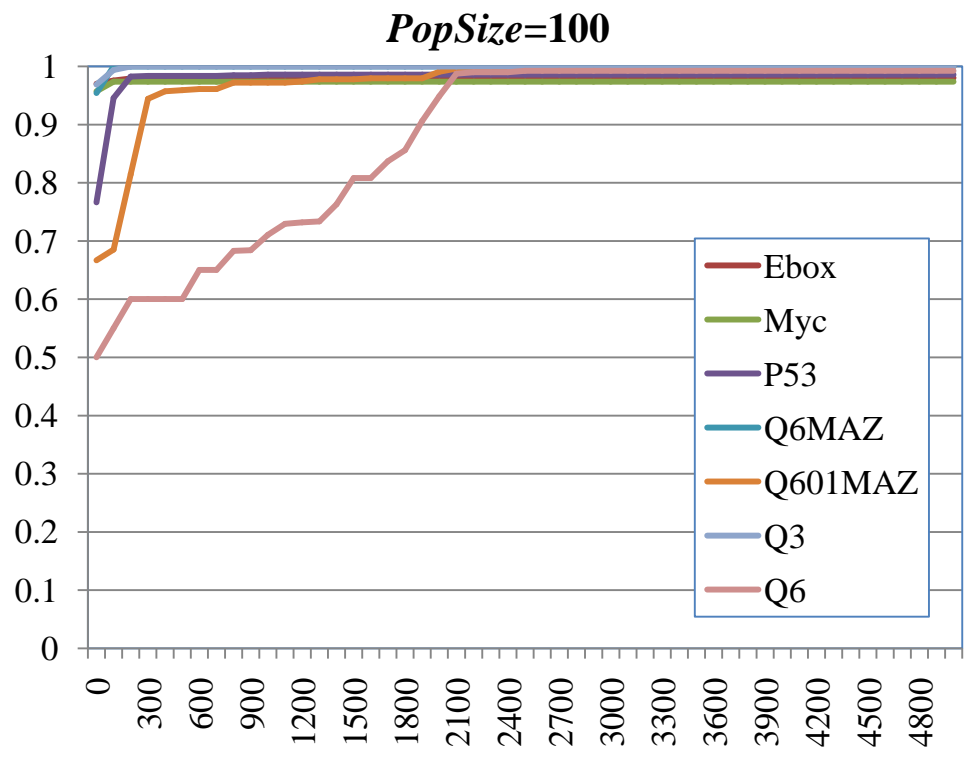
PopSize=60



(c)

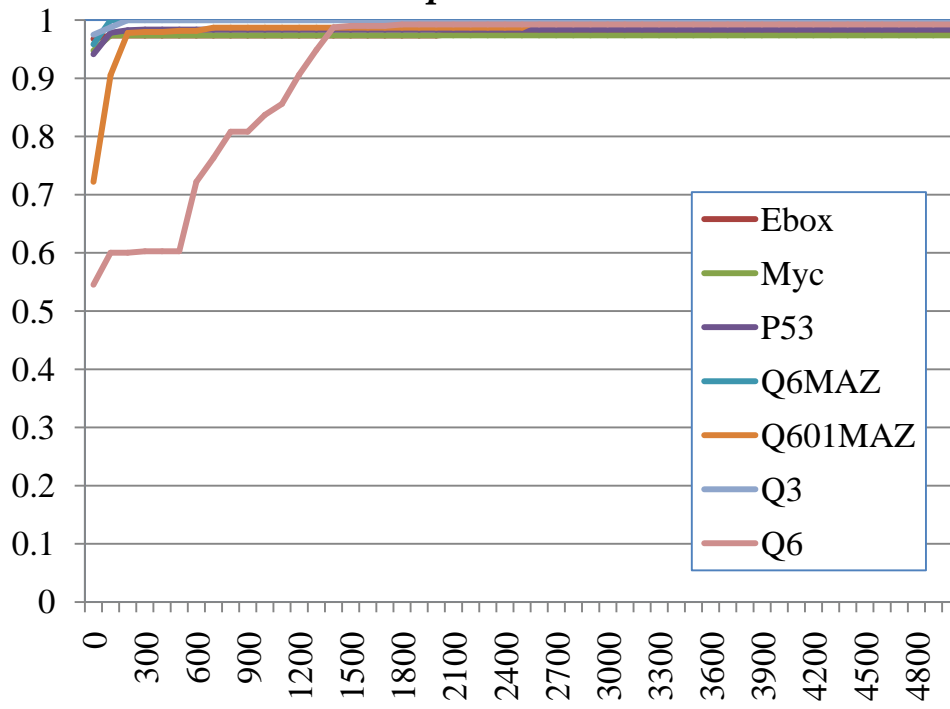


(d)



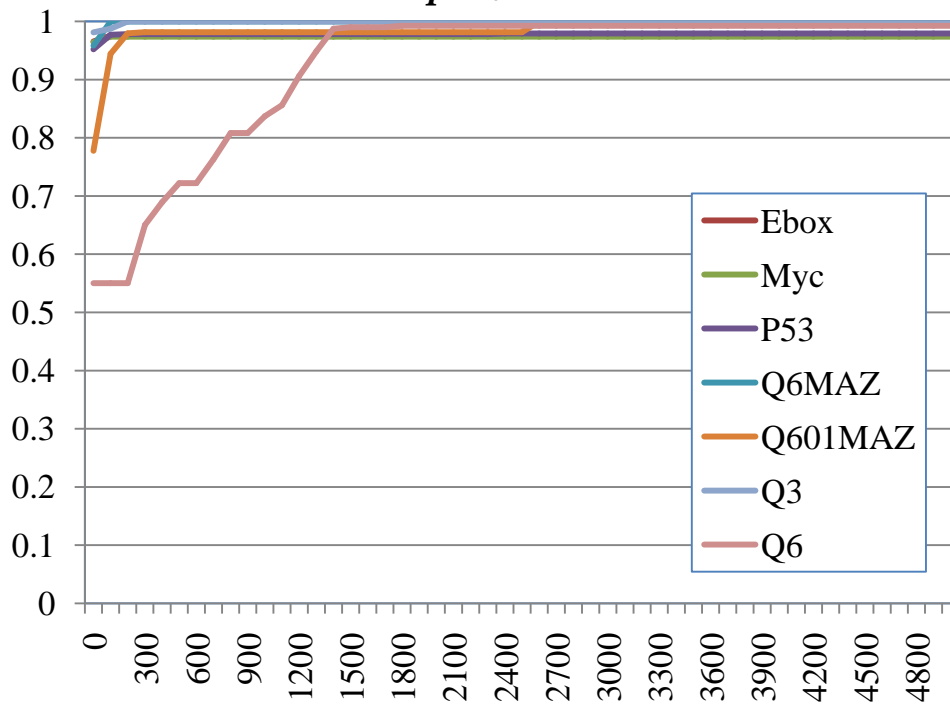
(e)

PopSize=120



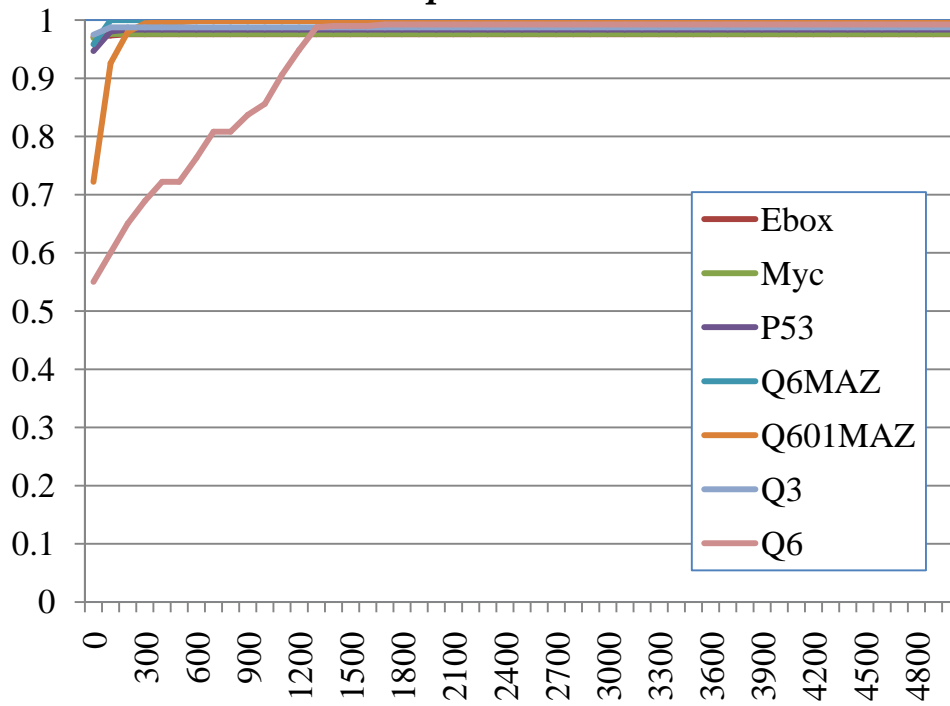
(f)

PopSize=140



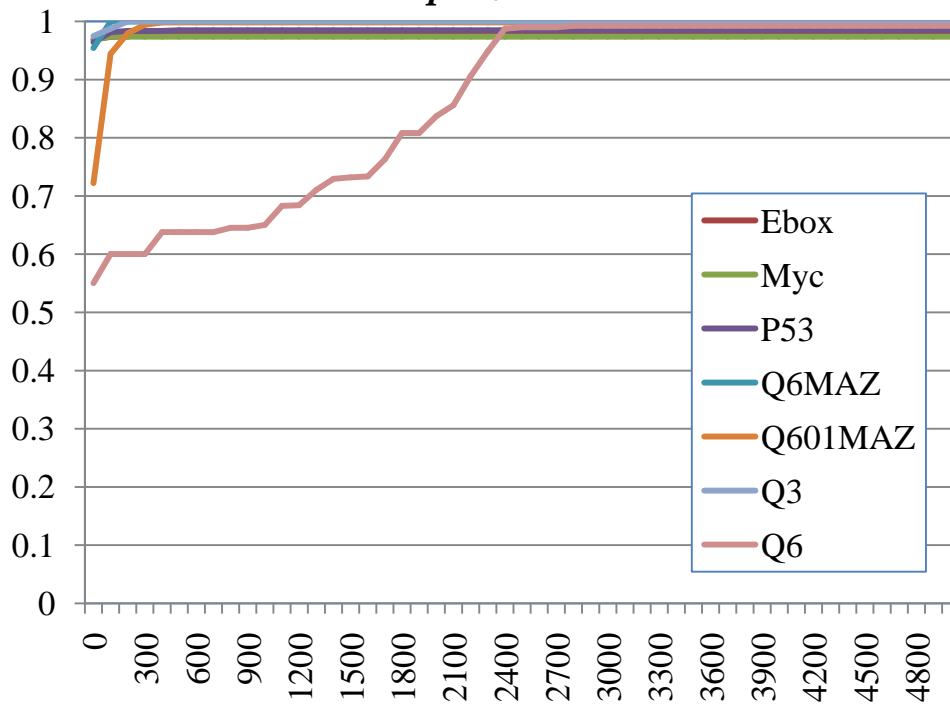
(g)

PopSize=160



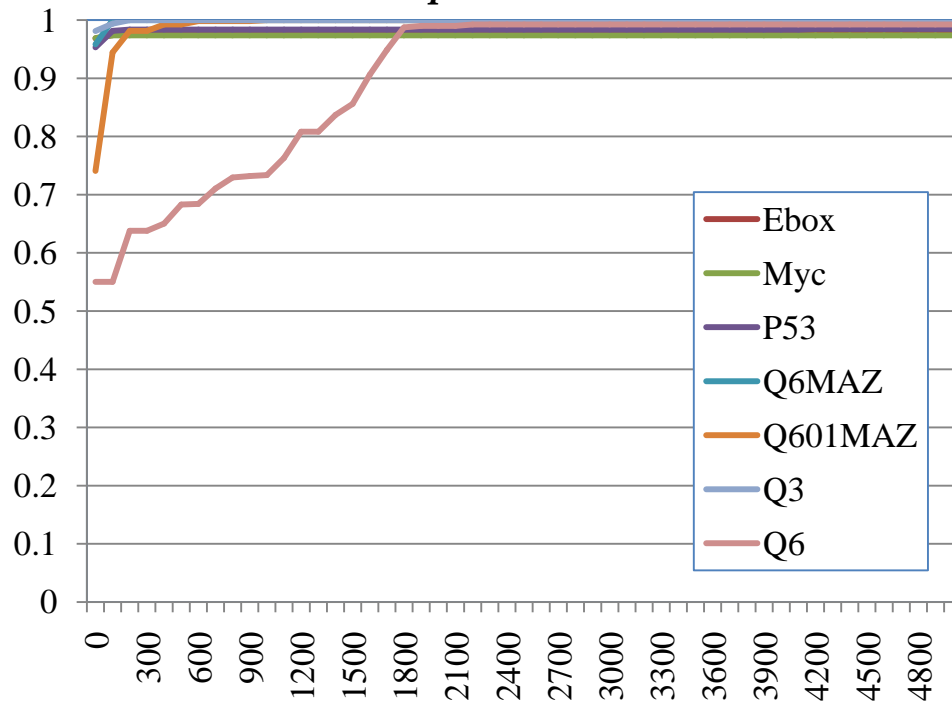
(h)

PopSize=180



(i)

PopSize=200



(j)