Table S1: Evolutionary models for gene regulatory sequence (S), gene expression (E) and using phylogenetic information (P).

Model	Components			Applications	Species
MAFIA[1]	P	S	-	Evolution of binding sites	Drosophila
EMMA[2]	P*	S	-	CRM alignment and prediction	Drosophila
Kimono[3]	-	S	E	Clustering of promoter and expression	Simulation
MODEM[4]	-	S	E	Identifying target genes of a transcription factor	Yeast
REDUCE[5]	-	S	E	Motif prediction	Yeast
DCA[6]	P	-	E	Identifying conserved and diverged co-expression patterns	Yeasts
SCSC[7]	P*	-	E	Identifying conserved and diverged co-expression patterns	Mammals
Khaitovich[8]	P	-	E	Neutral evolution of gene expression	Primates
Xie [this paper]	P	S	E	Evolution of gene regulatory networks	Yeasts, Mammals

* Only applied to two species.

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