



Conservation of Gene Orientation in Fungi



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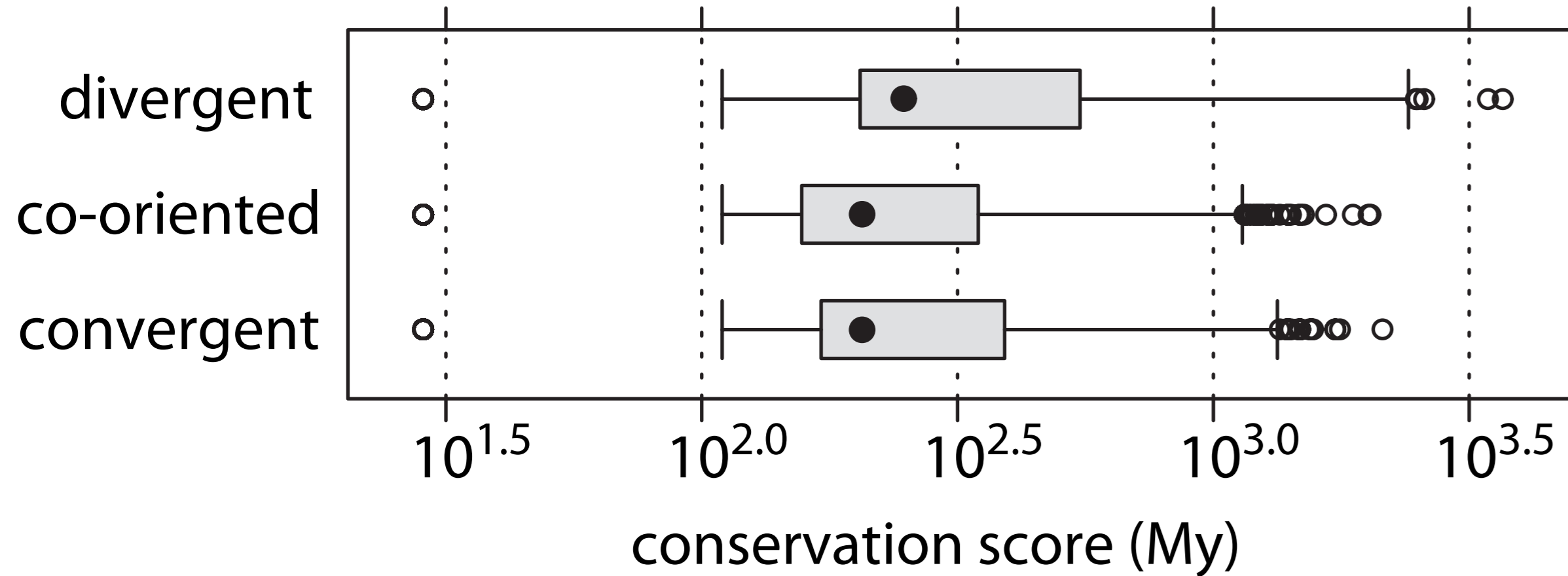


Introduction

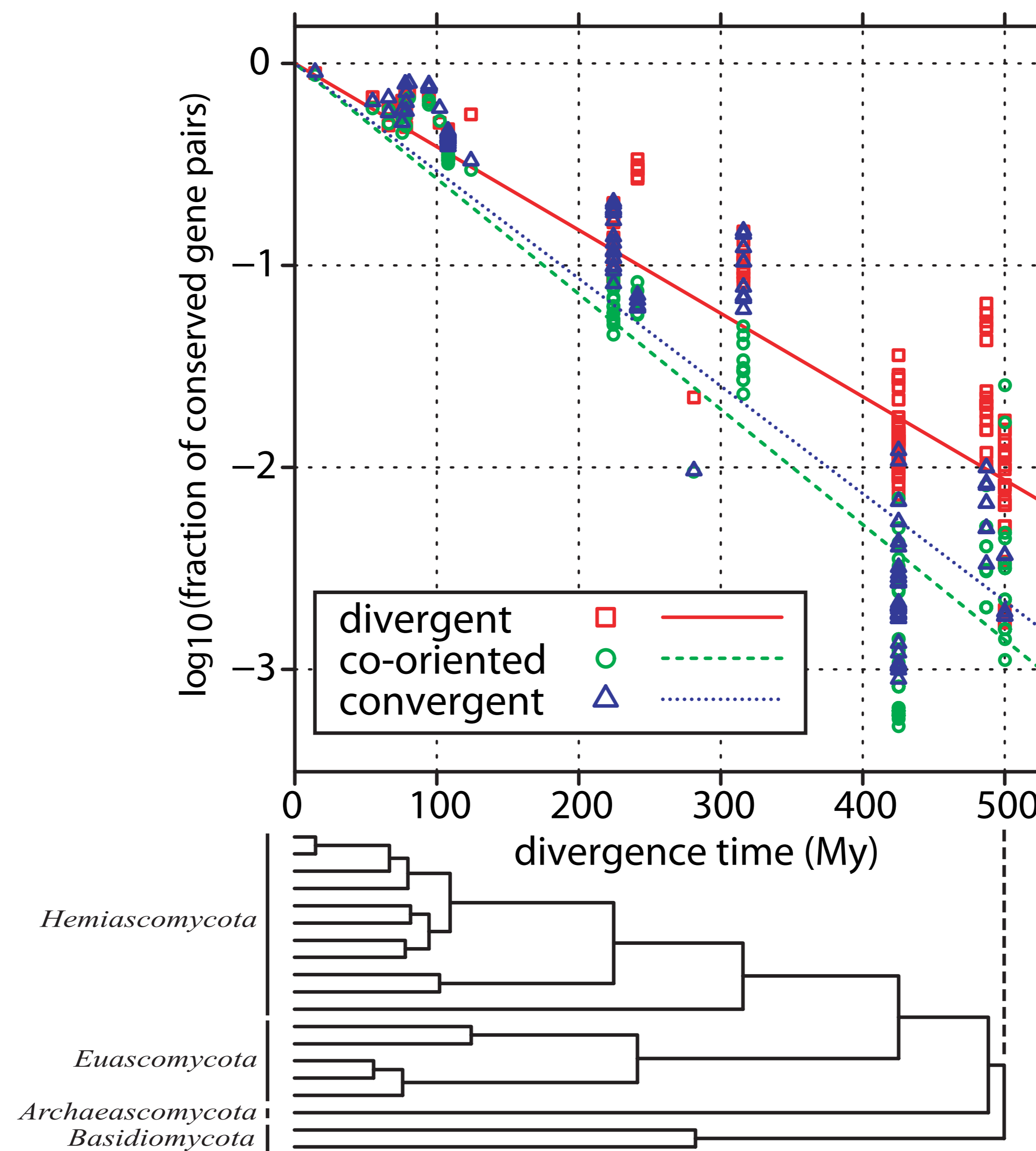
We quantified the conservation of divergent ($\leftarrow\rightarrow$), co-oriented ($\rightarrow\rightarrow$) and convergent ($\rightarrow\leftarrow$) genes in the genomes of 19 asco- and basidiomyceteous fungi.

Conservation based on Dollo parsimony

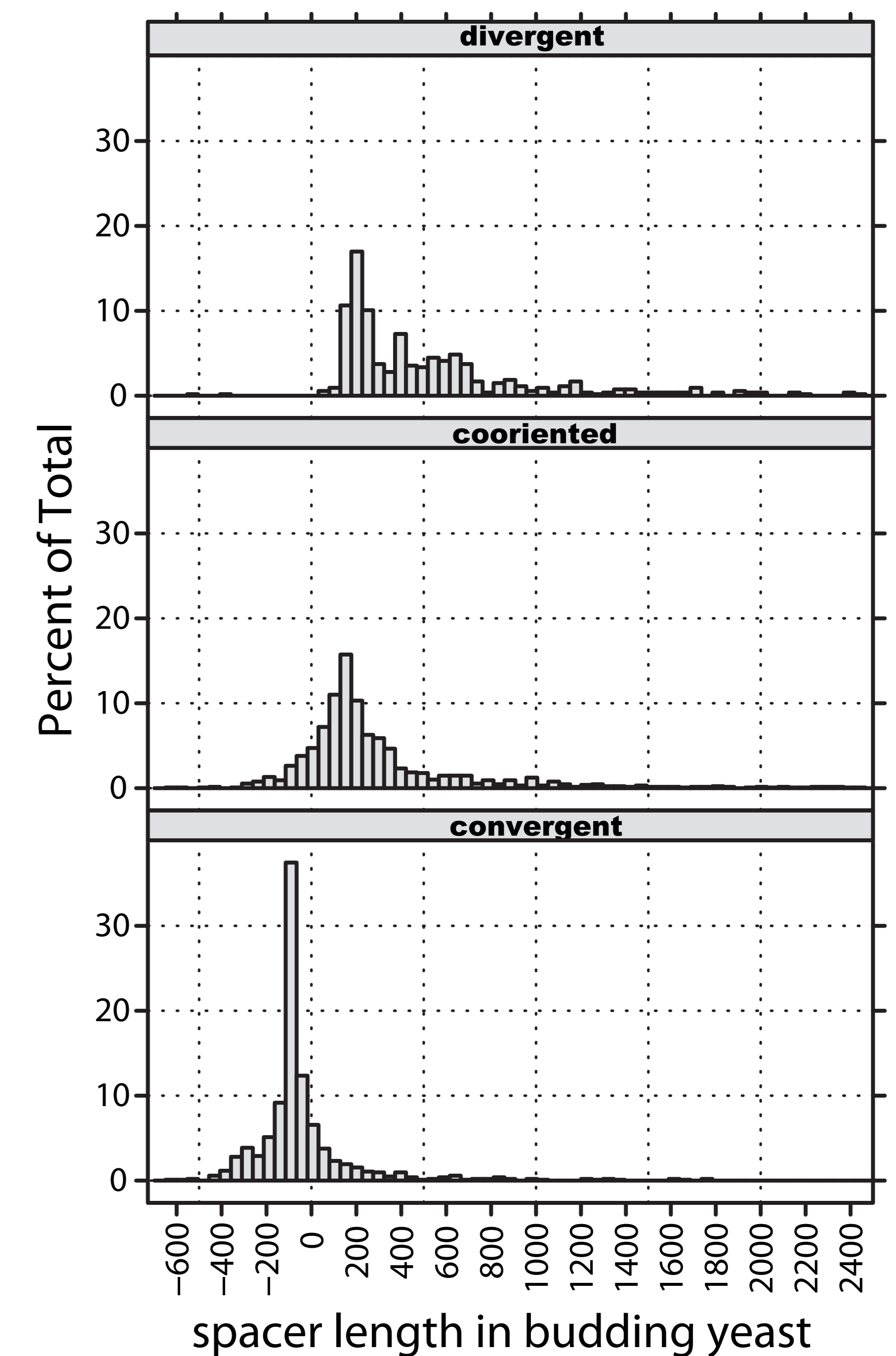
Divergently transcribed gene pairs are on average 61 million years longer conserved than co-oriented gene pairs, leading to a 3-fold higher probability of conservation of divergent gene orientation at a score cutoff of 1000 million years.



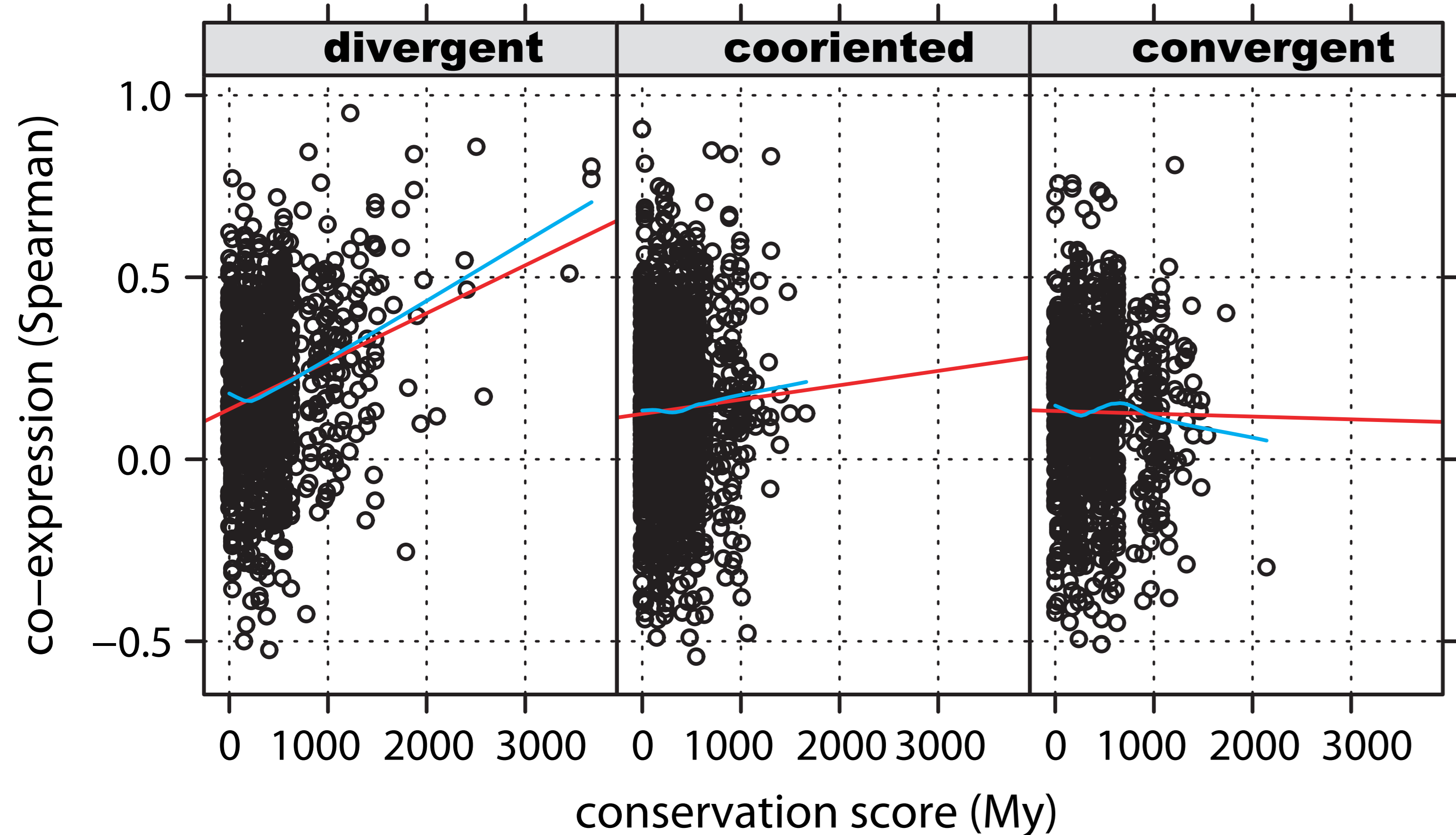
Divergent gene pairs are more conserved ...



... although they are more distant!

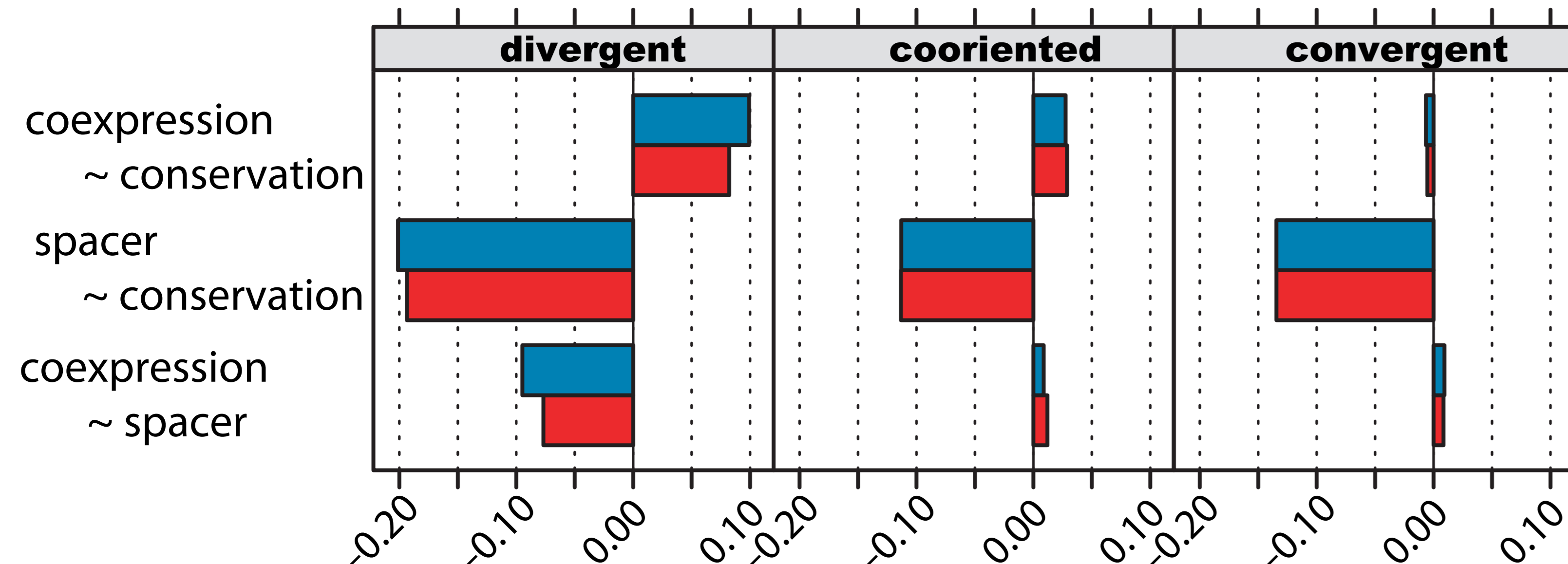


For divergent gene pairs the conservation correlates with co-expression ...

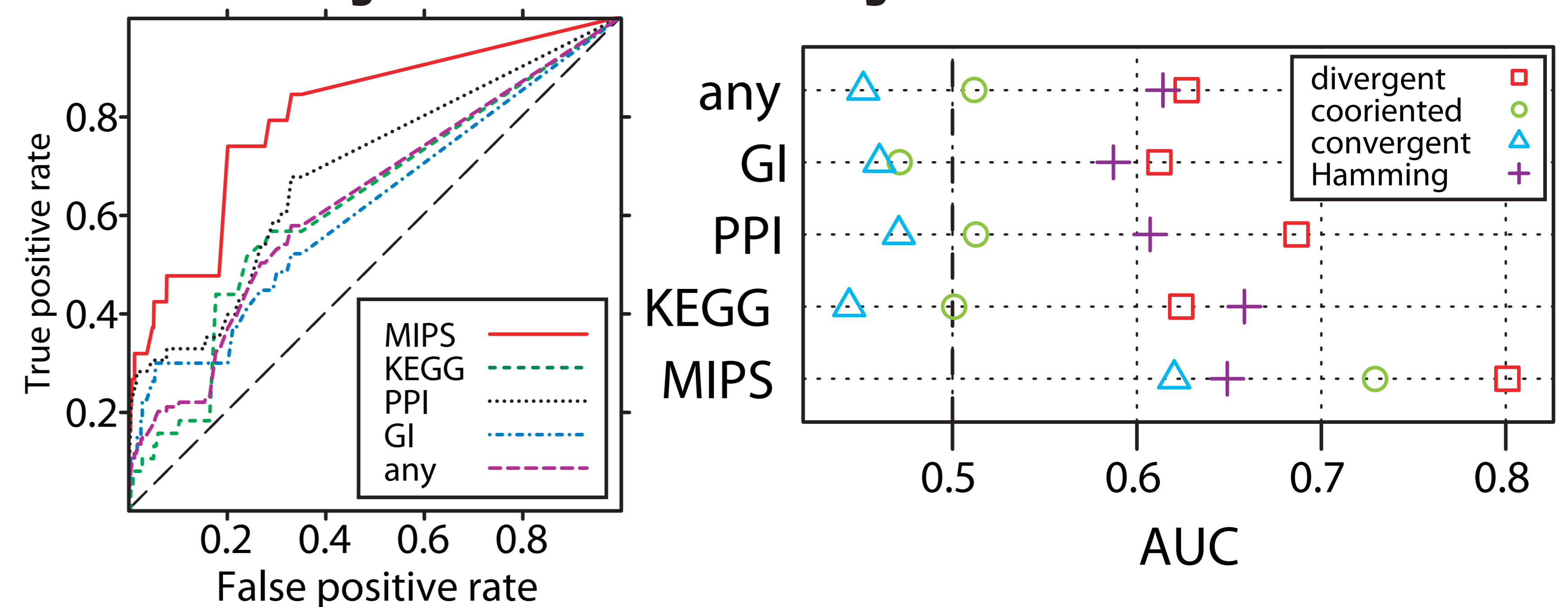


... independent of spacer length ...

Kendall's τ
partial Kendall's τ



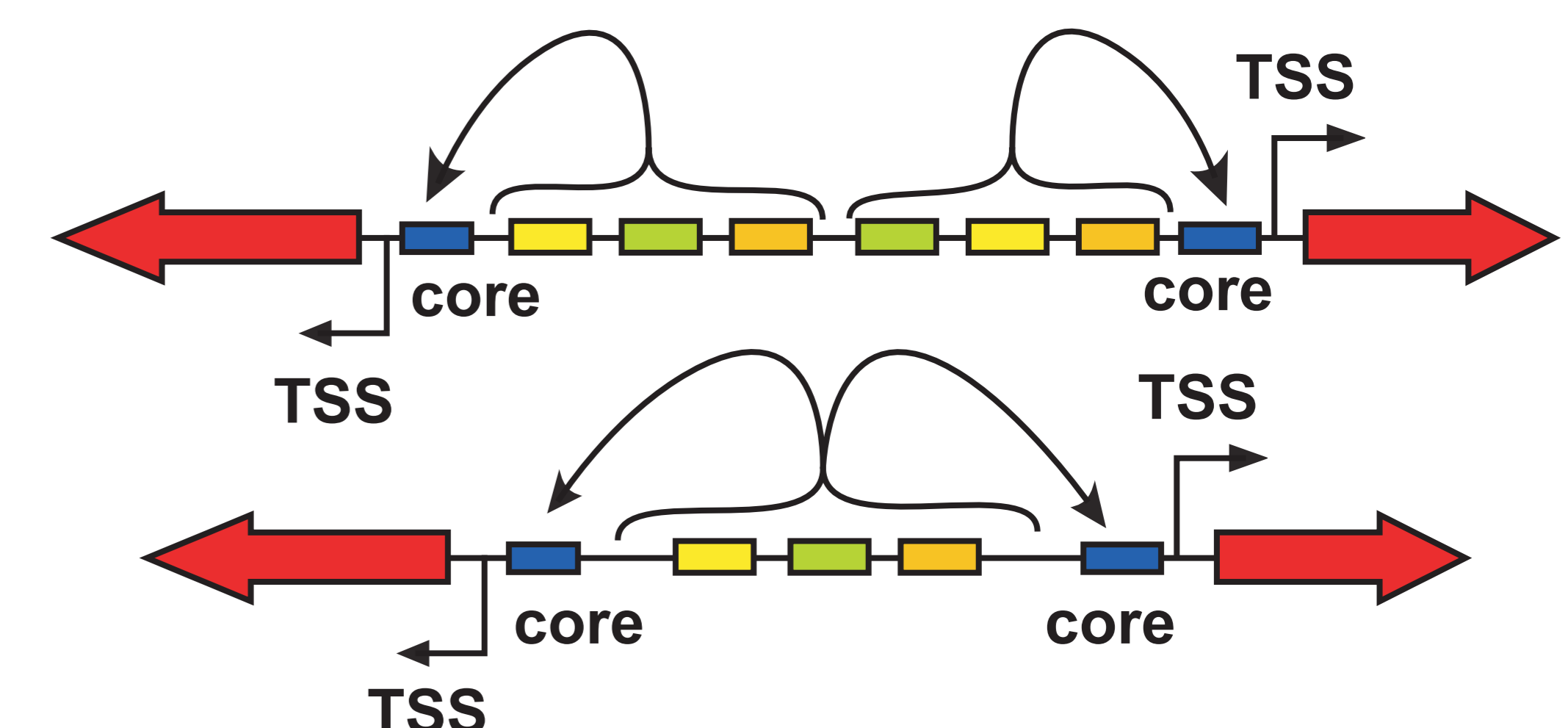
... and they are functionally related!



Shared TFs suggest bidirectional promoters between conserved divergent gene pairs

≤ 500 My
#TF(div.) > #TF(coor.)
 $p < 3.3 \times 10^{-8}$, $\Delta\text{means} = 0.50$

> 500 My
#TF(div.) \sim #TF(coo.)
 $p = 0.19$, $\Delta\text{means} = 0.07$



... even when controlling for spacer length
(≤ 500 My: $p < 2.4 \times 10^{-4}$; > 500 My: $p = 0.53$; one-sided U tests)

Acknowledgements

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