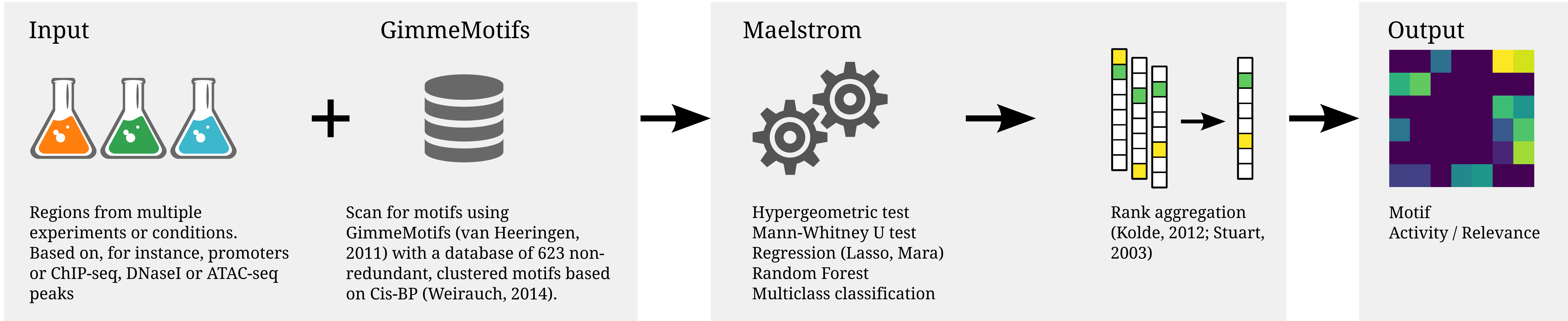


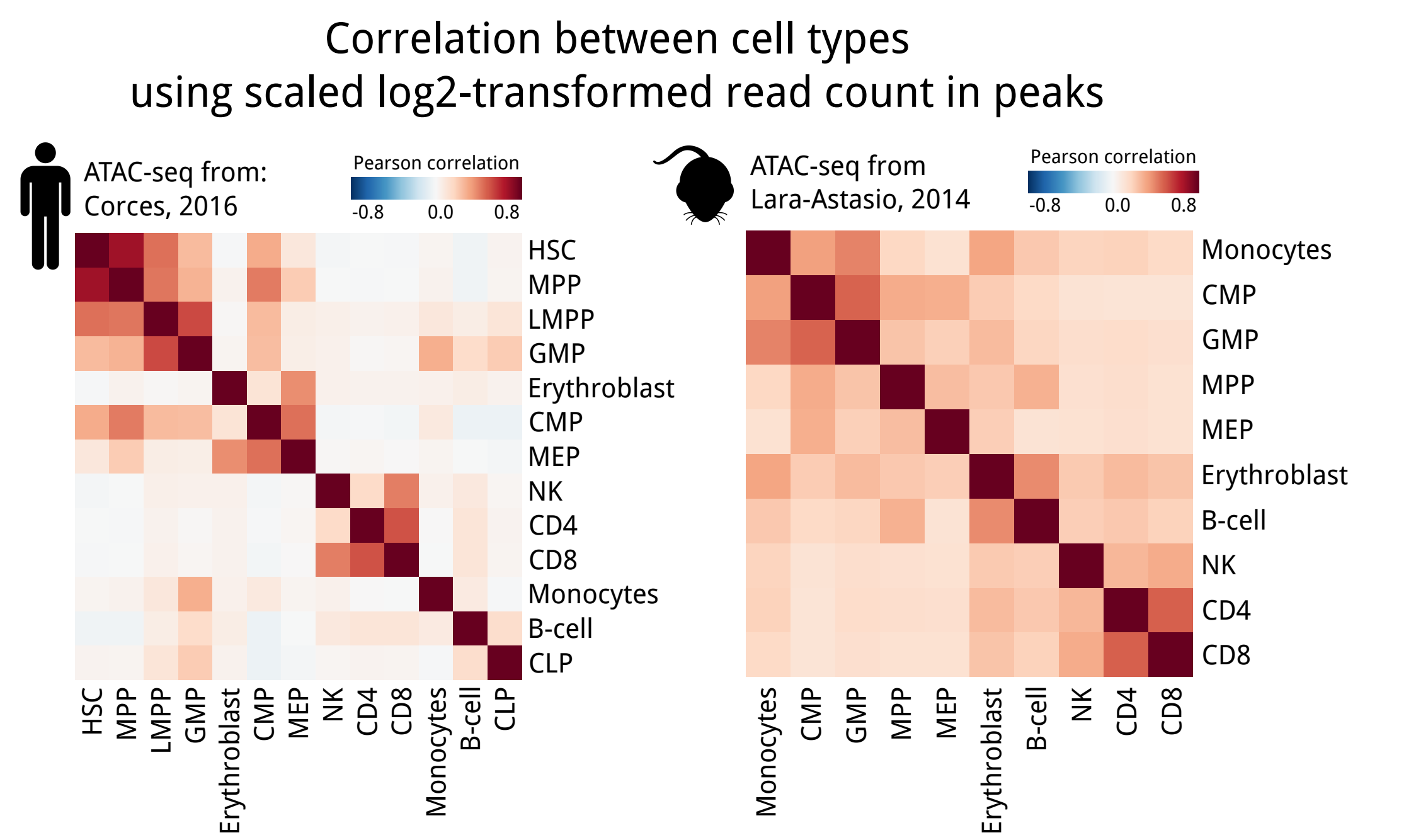
# Motif activity by ensemble learning for multi-experimental transcription factor motif analysis

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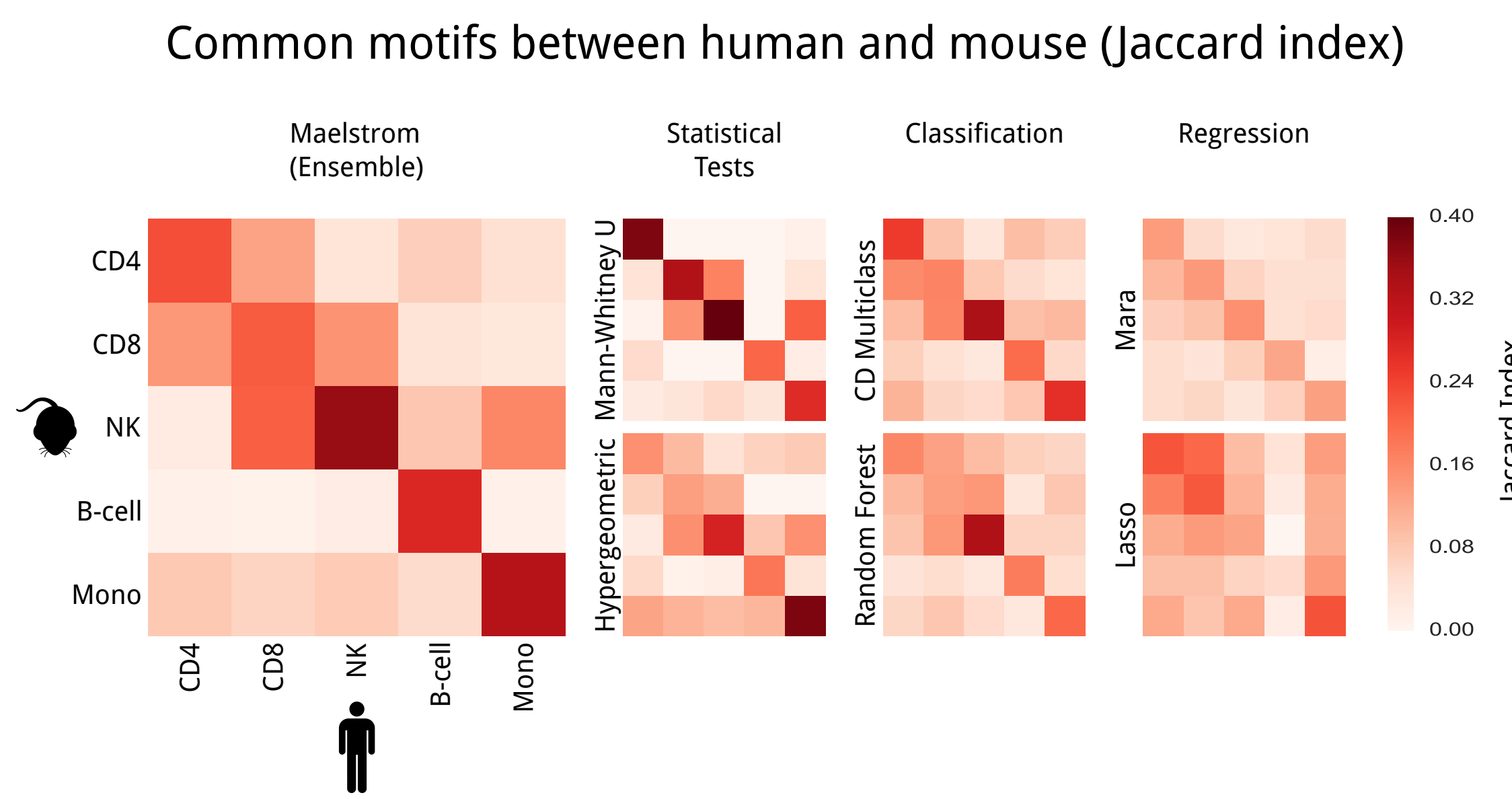
Maelstrom: an ensemble method to reliably predict relevant regulatory motifs



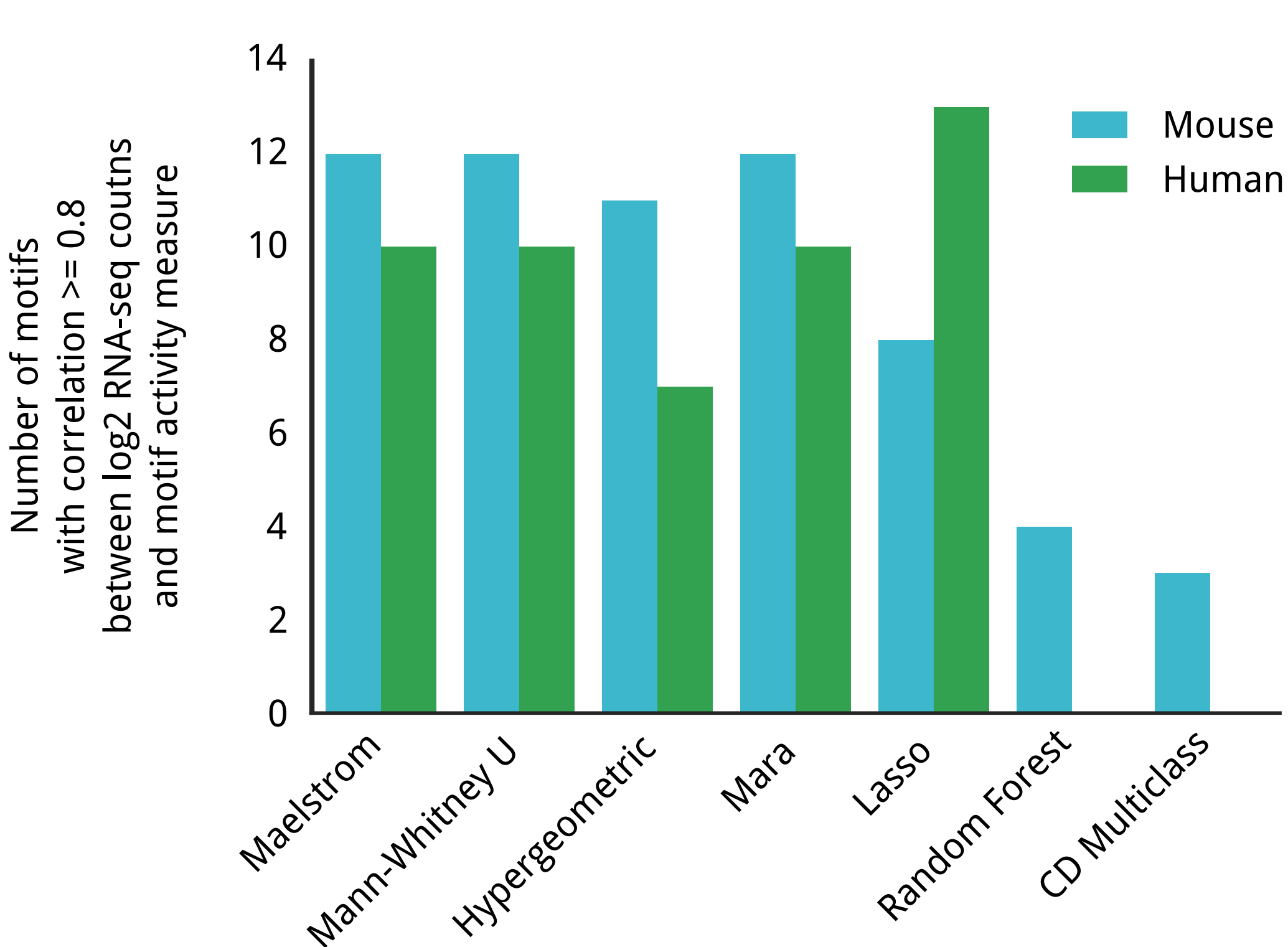
Example data: ATAC-seq in hematopoiesis



Motifs identified by maelstrom are conserved



Correlation of motifs with TF gene expression



Affiliations: Radboud University, Department of Molecular Developmental Biology, Faculty of Science, Nijmegen, The Netherlands. Funding: the Netherlands Organization of Scientific Research (NWO-ALW)

Try Maelstrom!  
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<http://github.com/simonvh/maelstrom-poster>

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Maelstrom output: heatmap of motif relevance or activity (-log10 p-value of rank aggregation)

