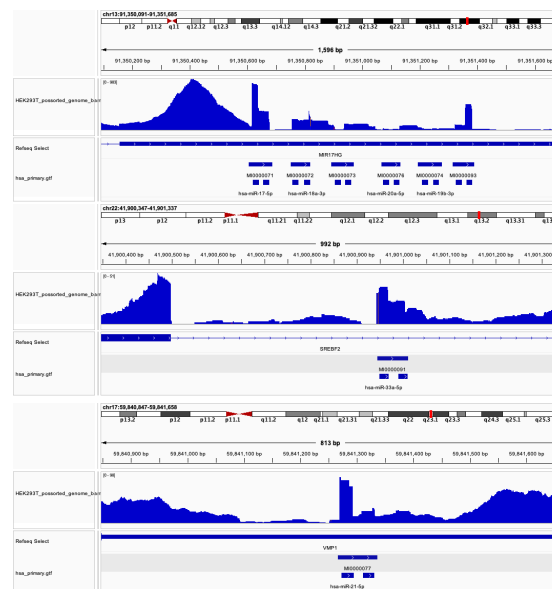
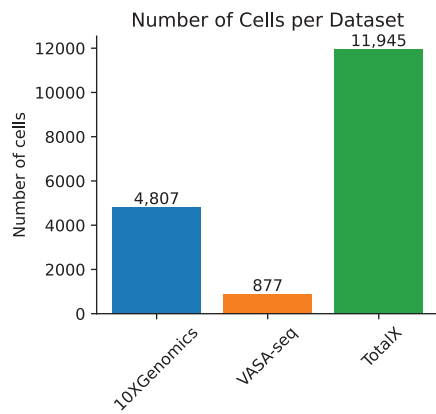


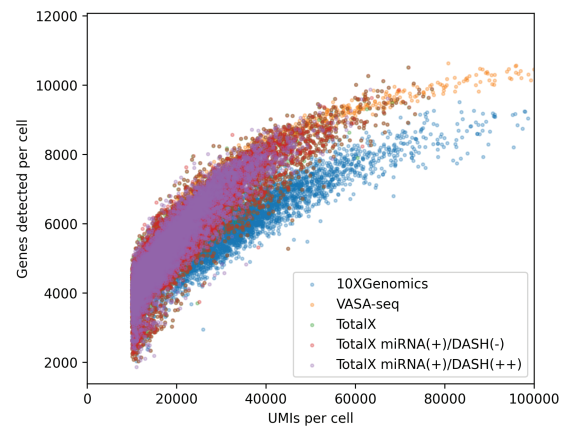
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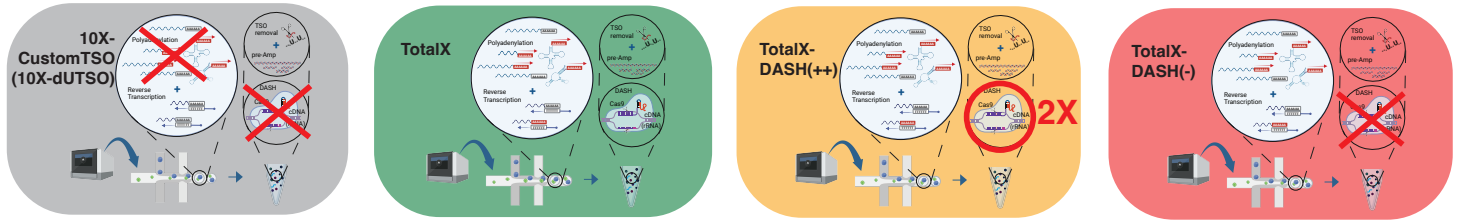
a Extended figure 2



b

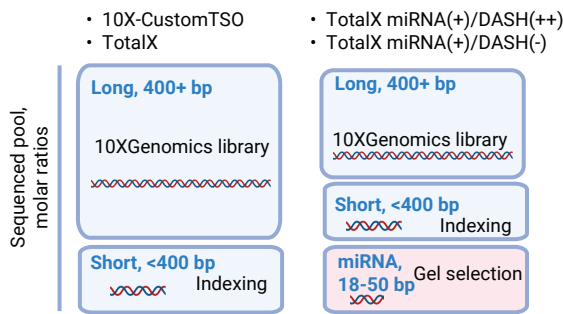


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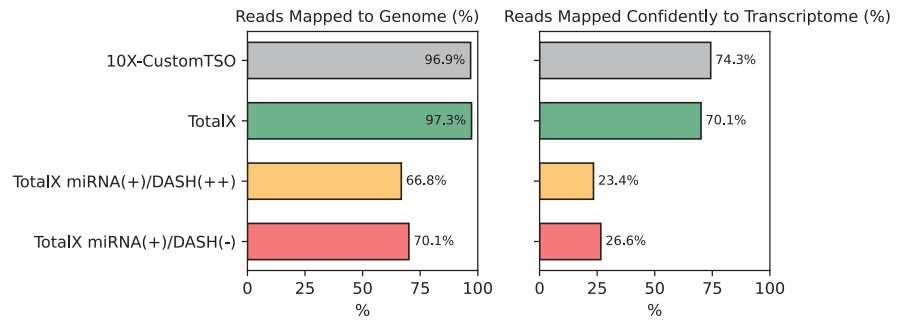


d

Sequencing library:

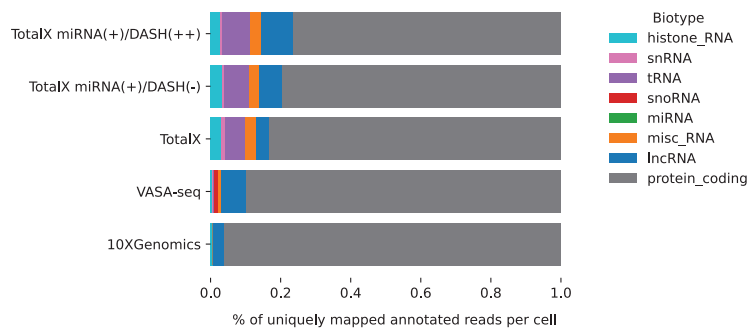


e



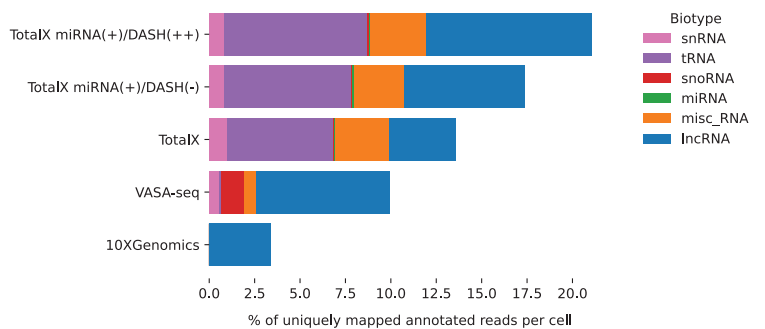
f

% of Uniquely mapped Annotated Reads



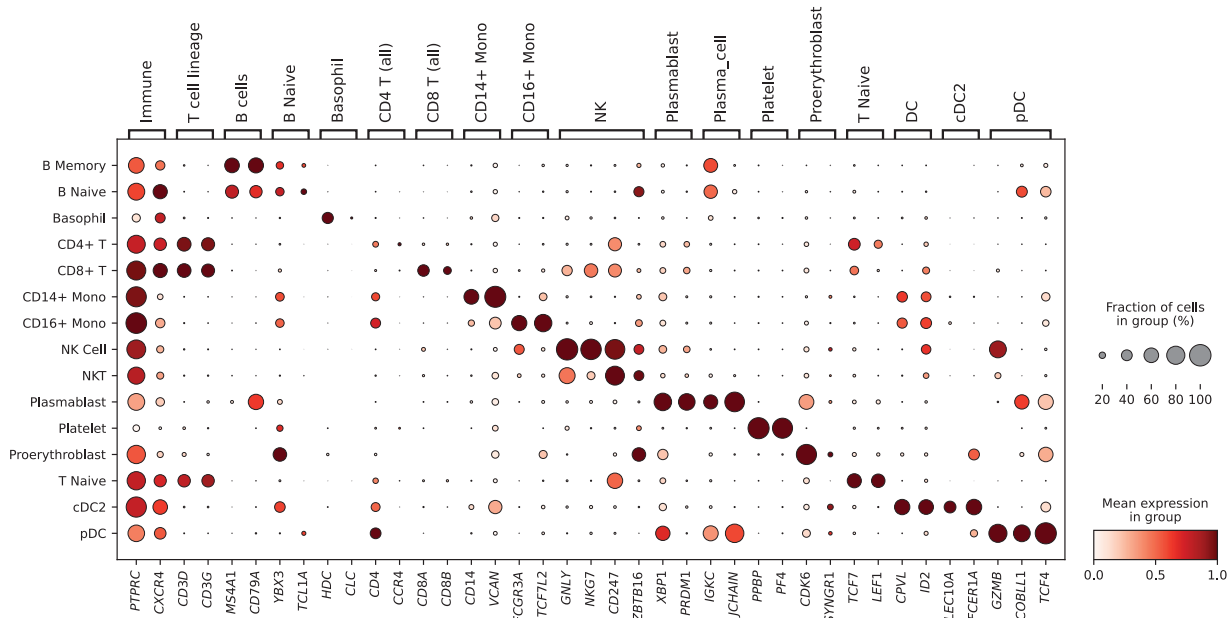
g

Non-coding Biotypes (% of Uniquely mapped Reads per cell)

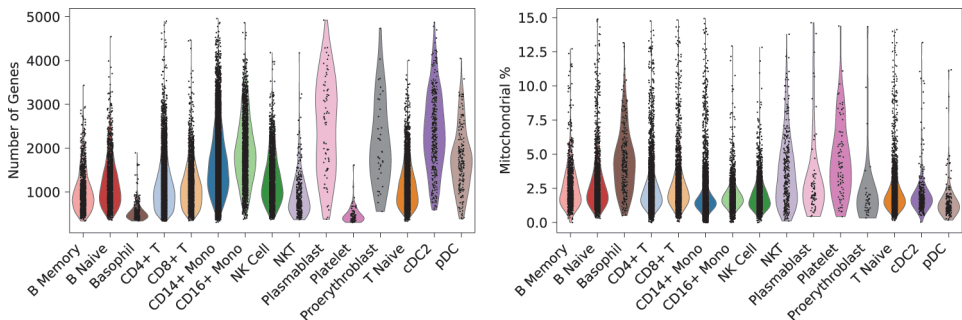


Extended figure 3

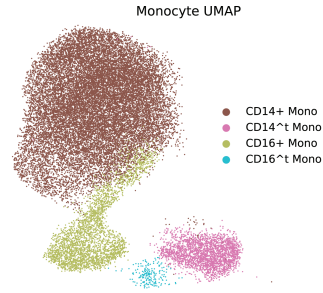
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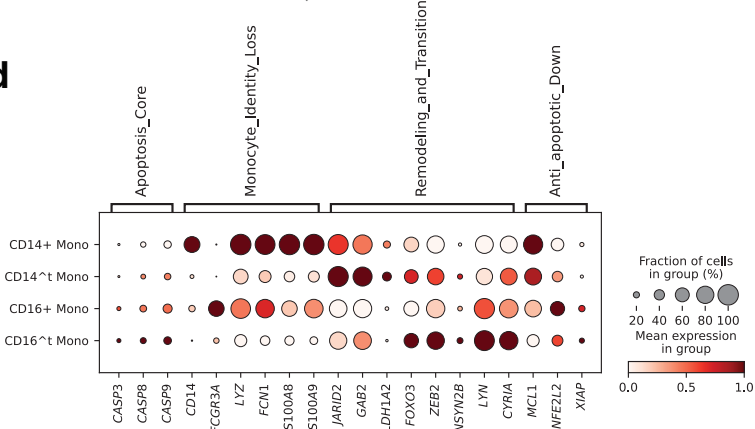
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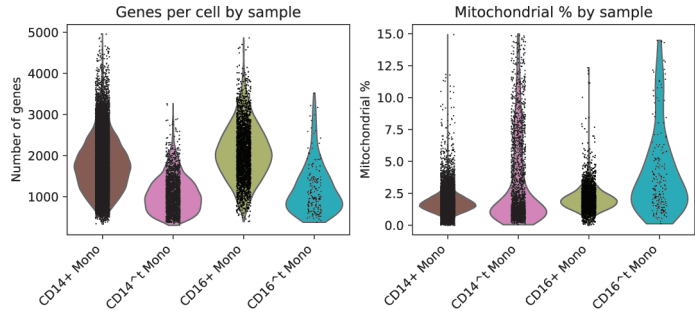
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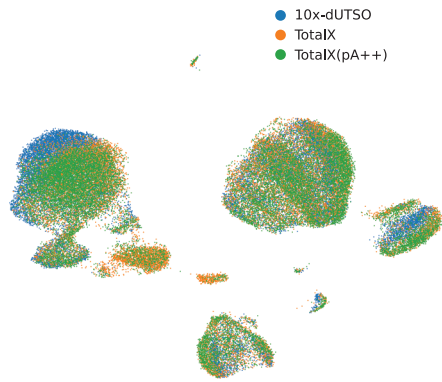
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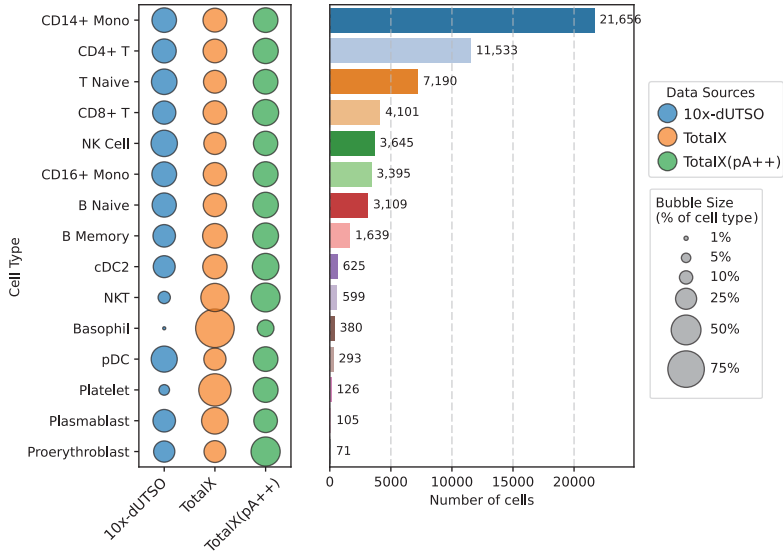
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f

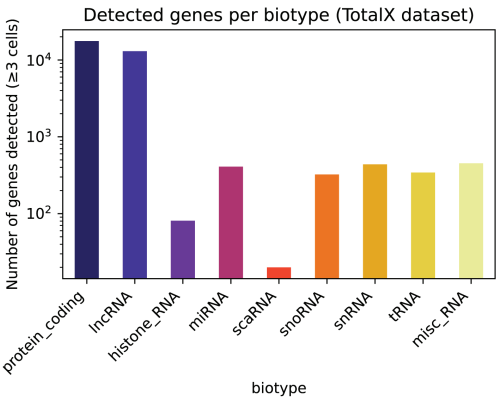


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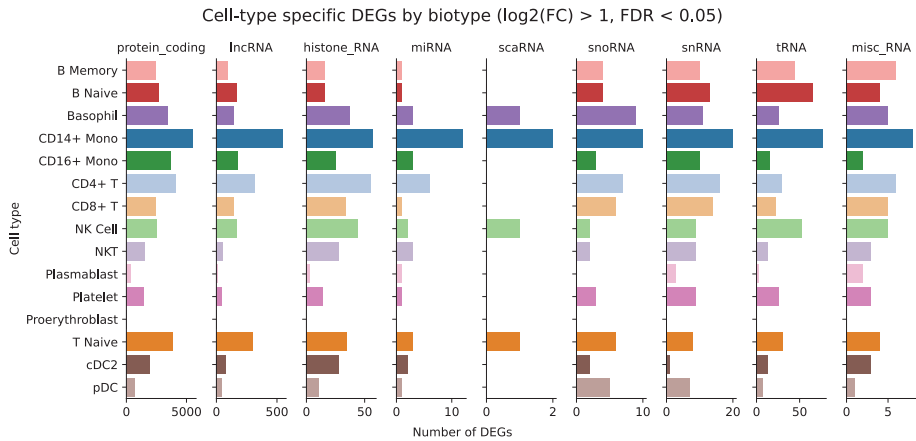


Extended figure 4

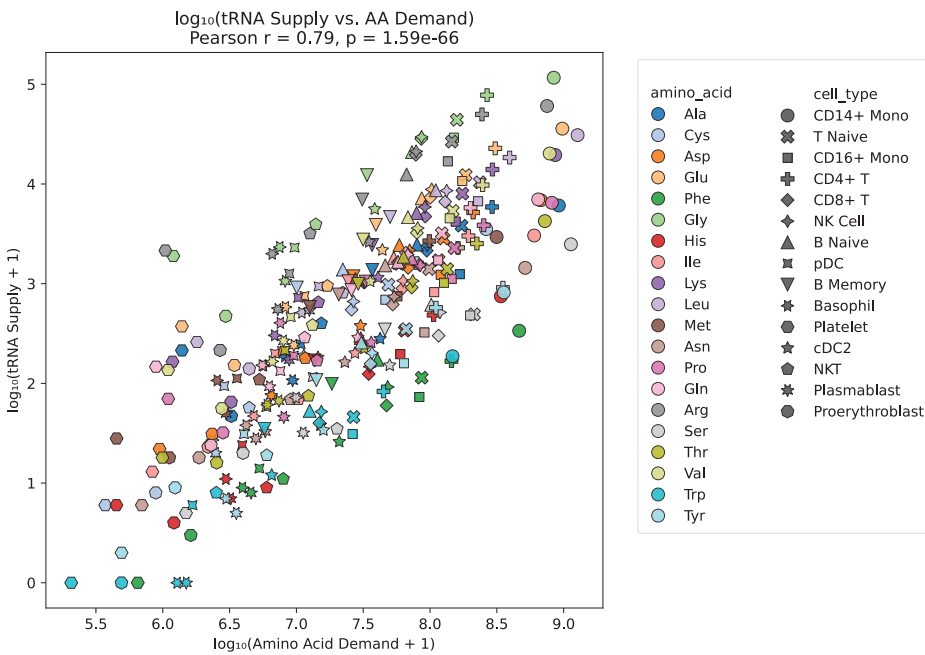
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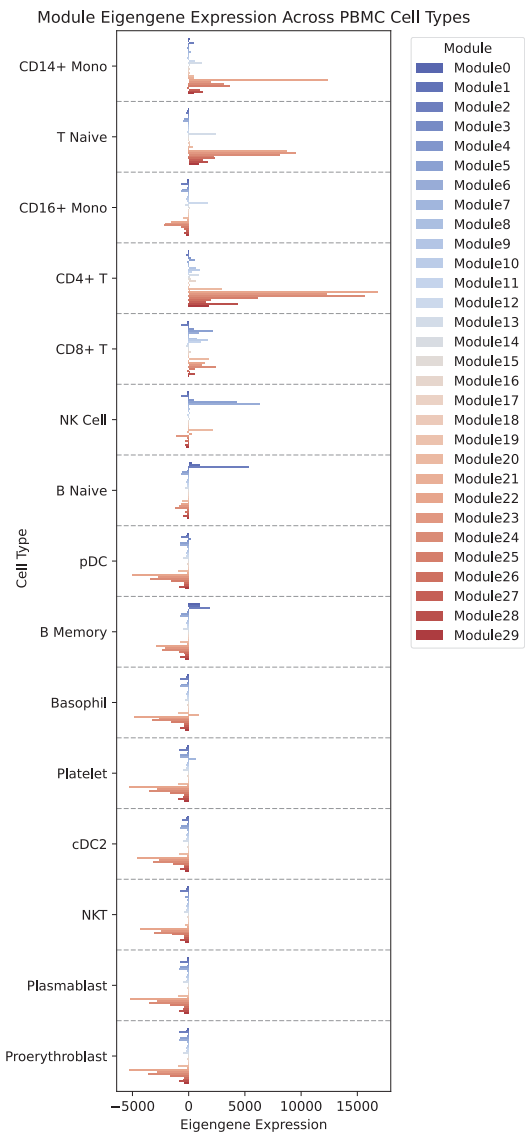
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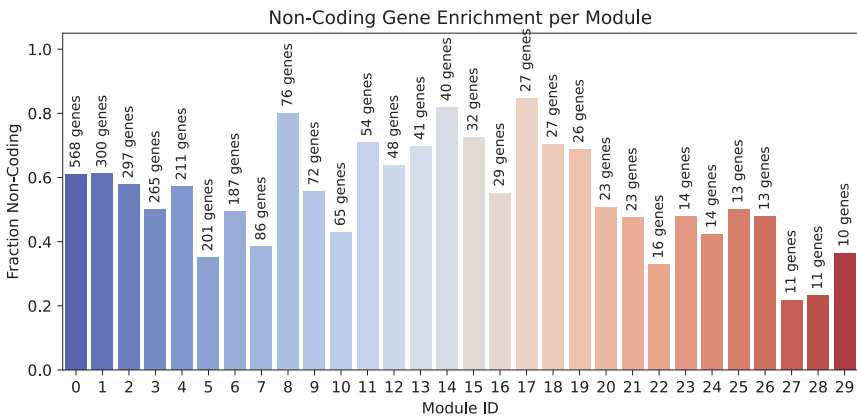
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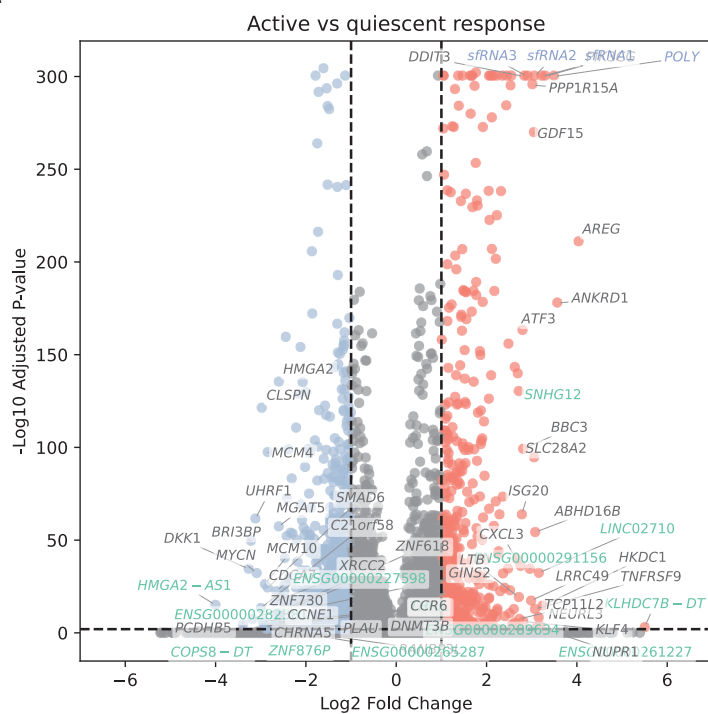
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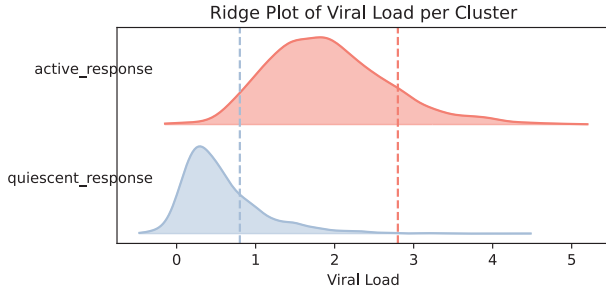


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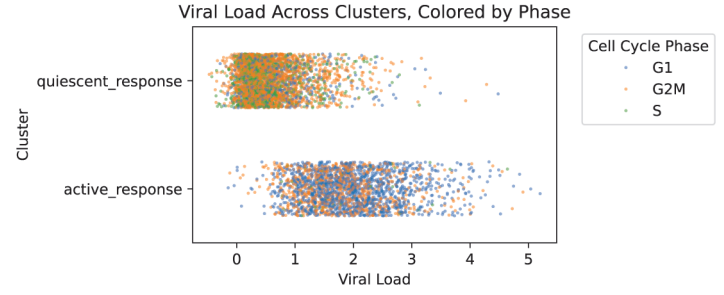


Extended figure 6

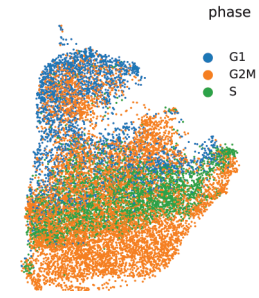
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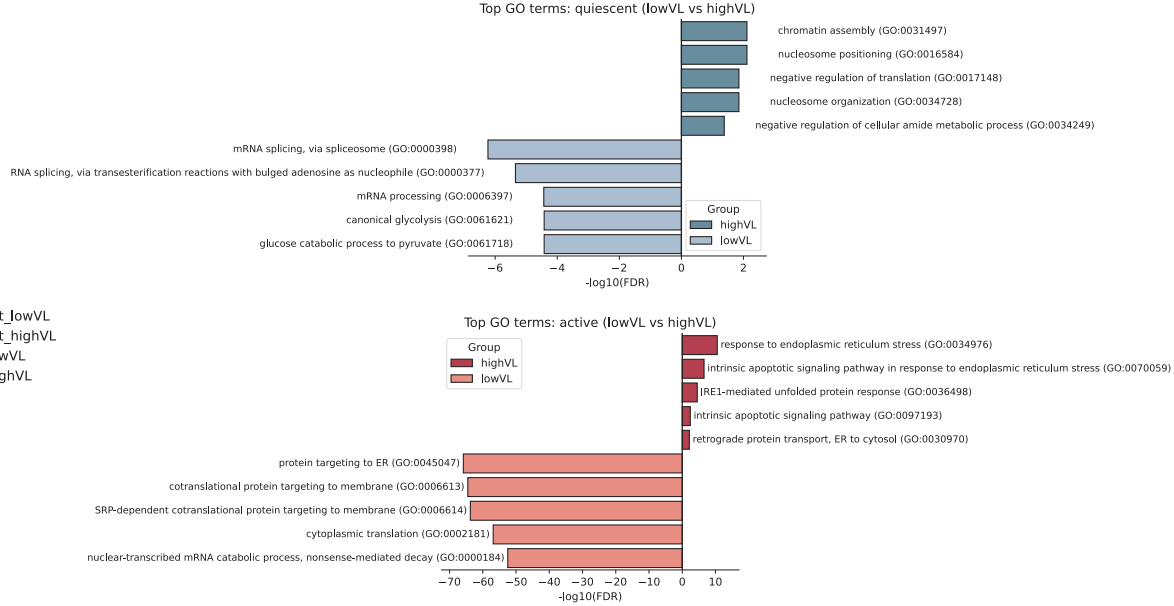
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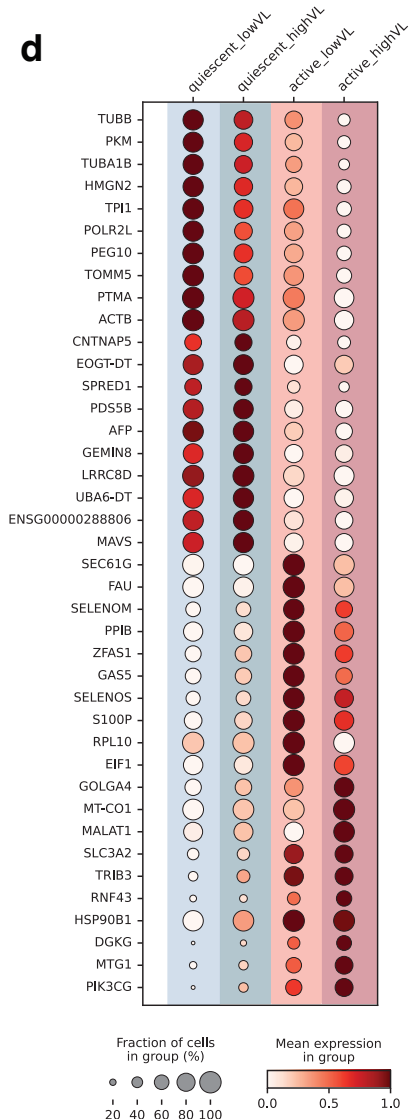
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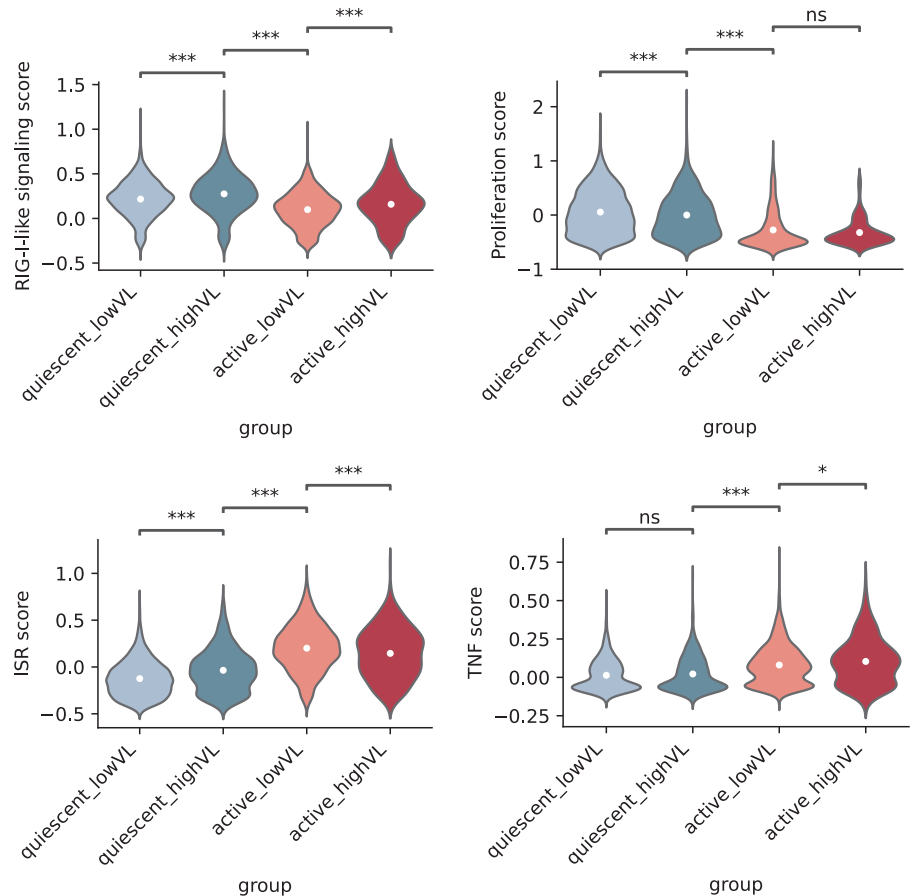
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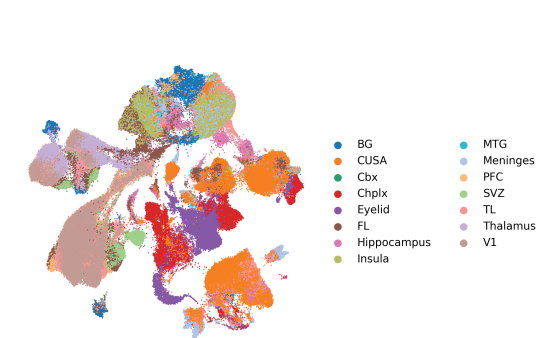


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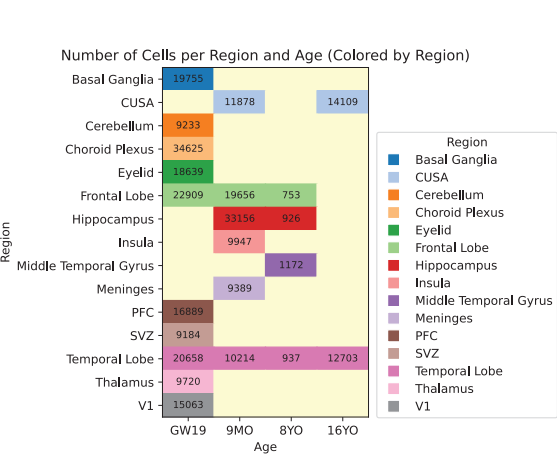


Extended Figure 7

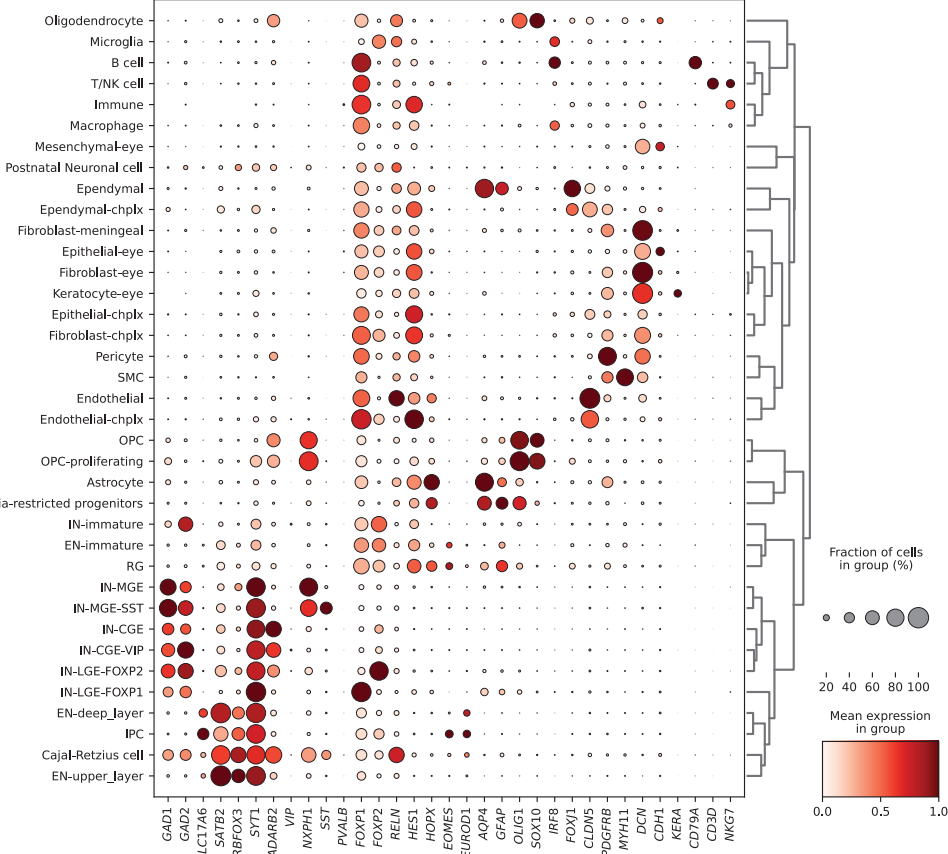
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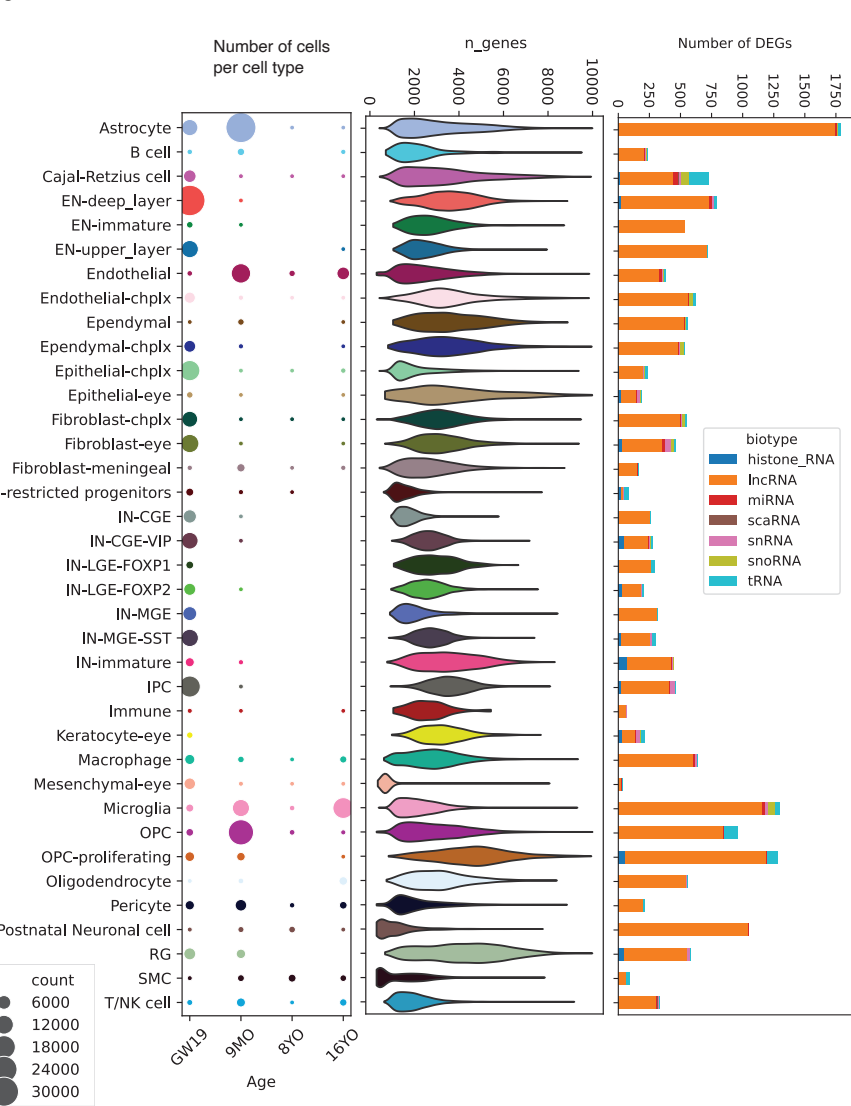
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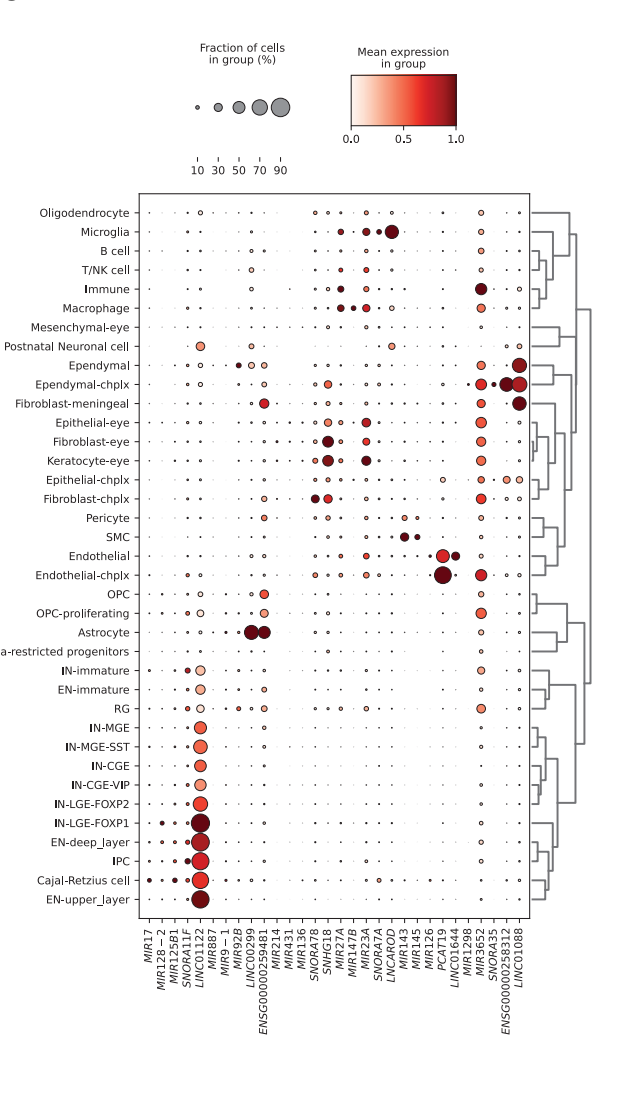
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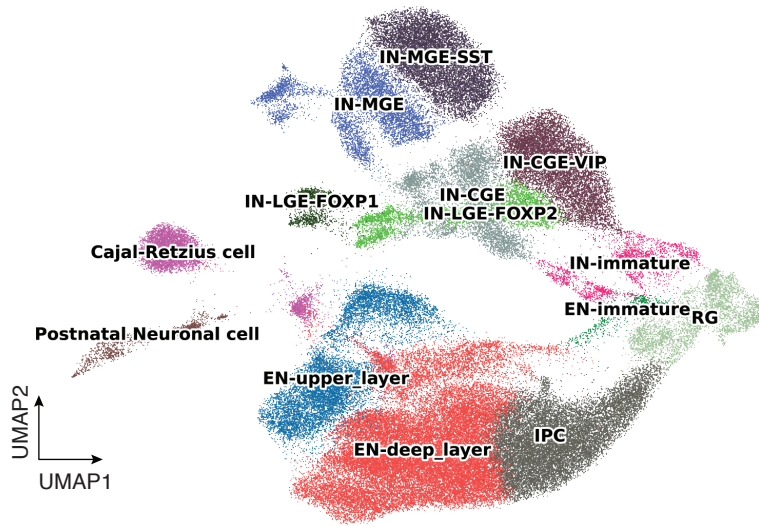


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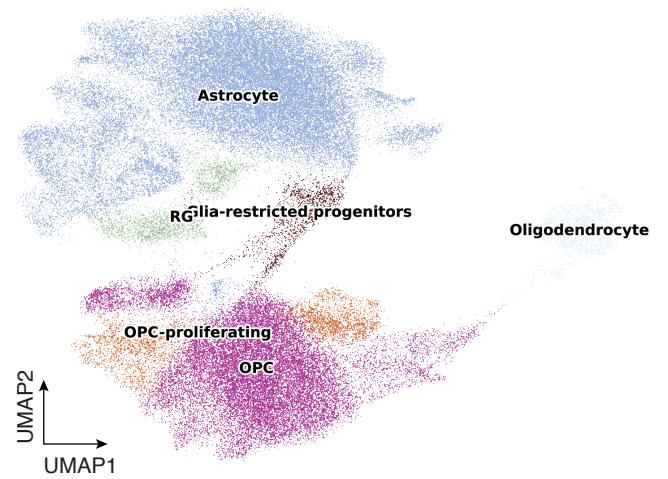


Extended figure 8

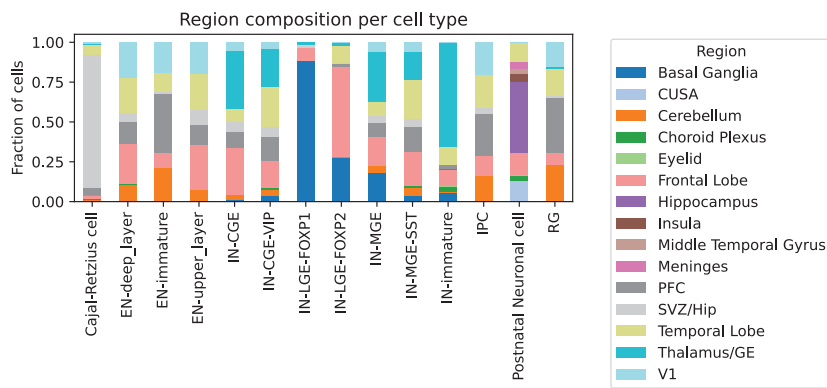
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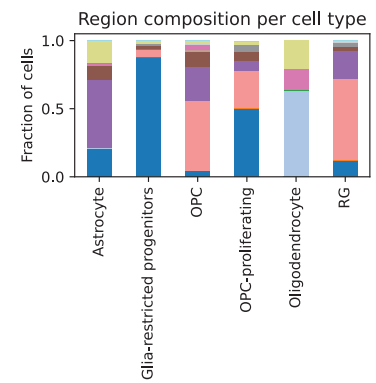
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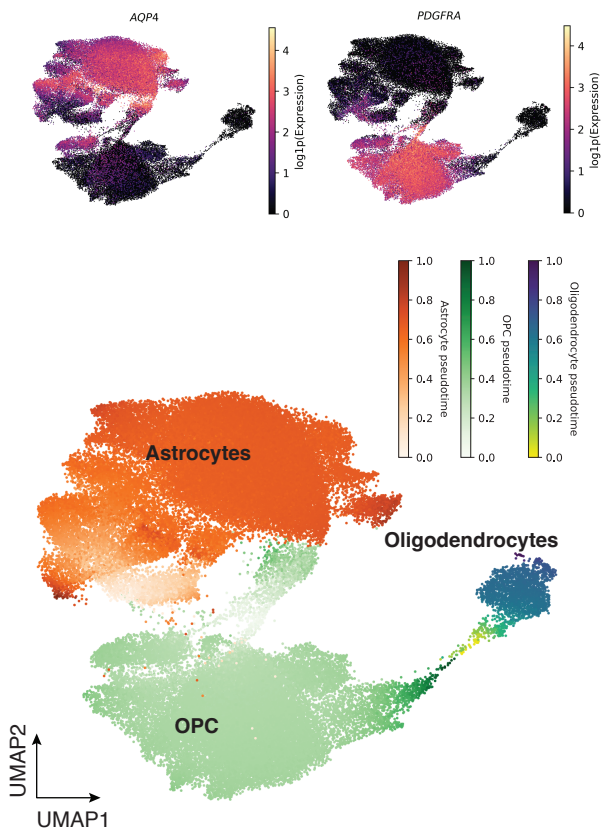
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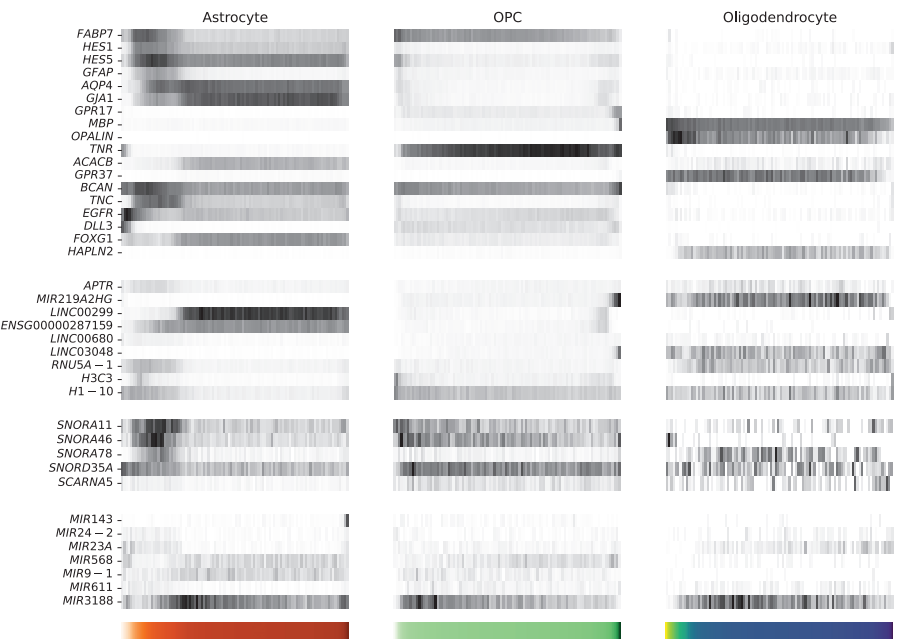
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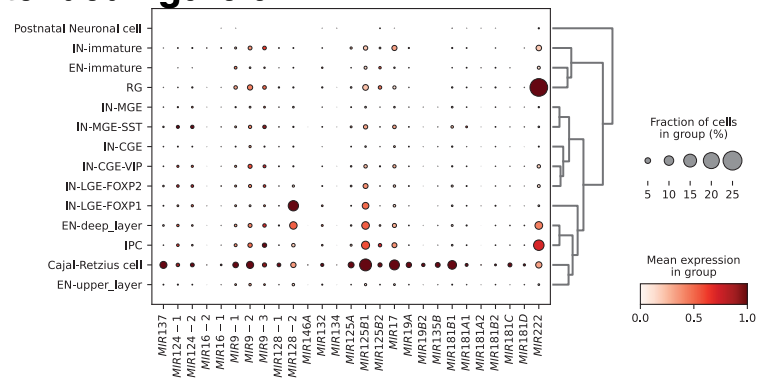


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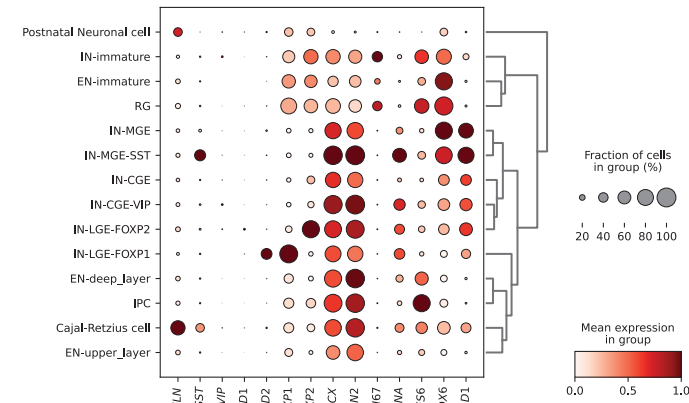


Extended figure 9

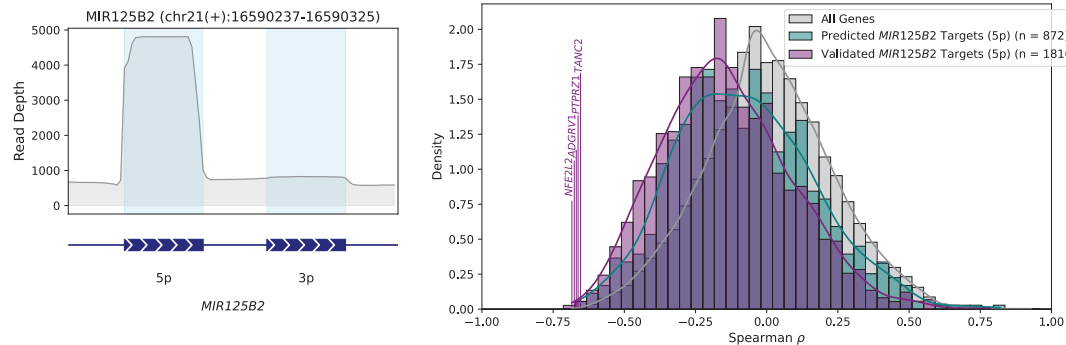
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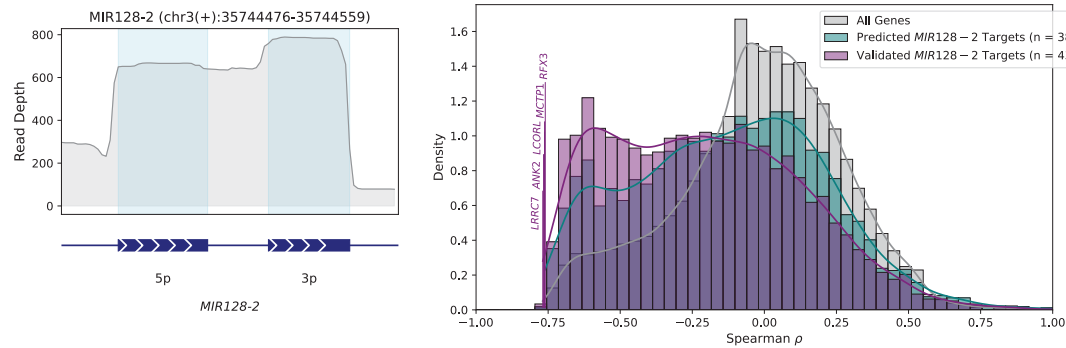
b



c



d



e

