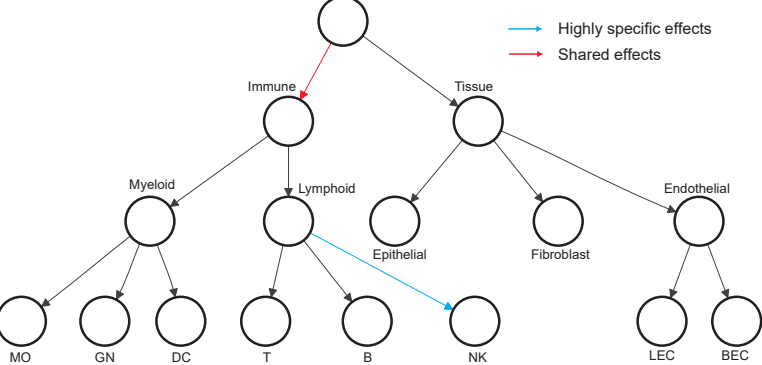
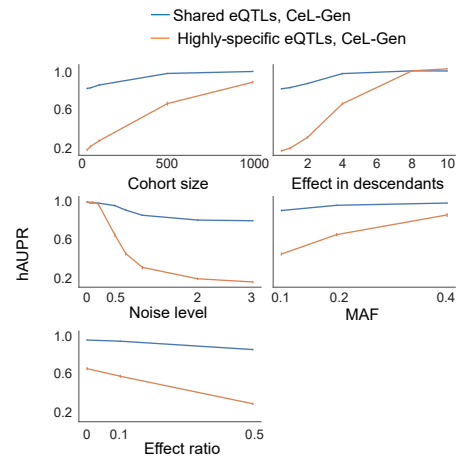


Supp. Figure 1

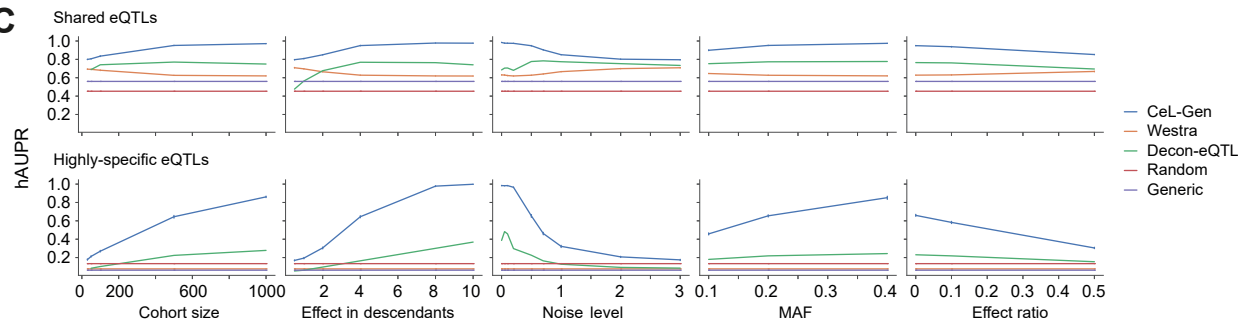
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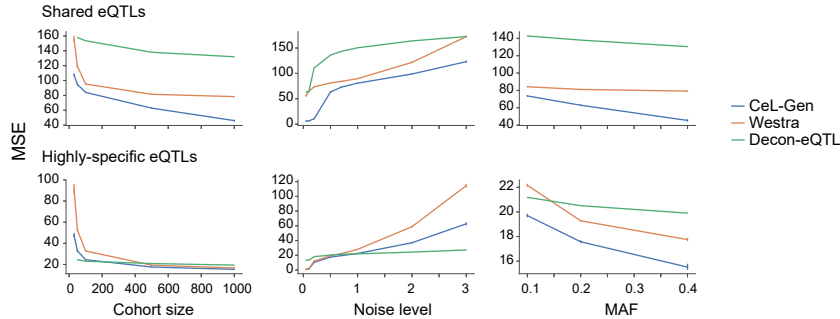
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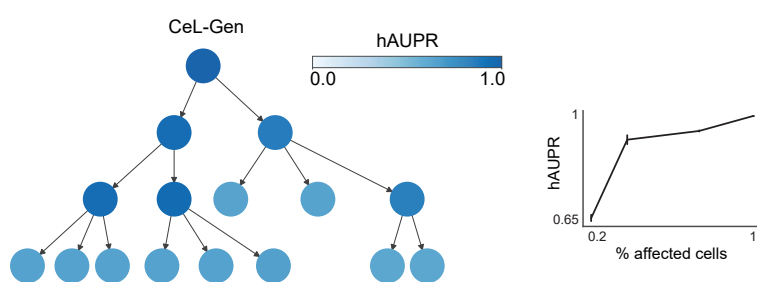
C



D



E



F

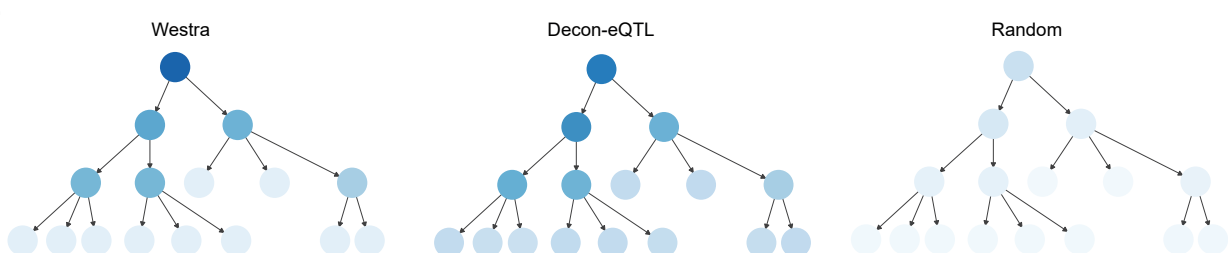


Figure S1: Benchmarking using synthetic data, using the known cell-type composition as input. (A) The lineage tree used as input in all simulations. (B) Hierarchical AUPR across different parameters, for highly-specific (orange) and shared (blue) eQTLs. (C) Analysis of the ability to identify the correct branch of alteration. Shown is the area under the hierarchical precision and recall curve (hAUPR, y axis), for different prediction methods (color coded) and across data parameter values (x axis). In all cases, the known cell-type composition was used as input. Results are shown for synthetic datasets of shared (top) and highly-specific (bottom) eQTLs. (D) Analysis of the ability to identify the correct effect size. Shown is the mean squared error between the simulated and predicted effect size (MSE, y axis) for different methods (color coding) across data parameter values (x axis). MSE was calculated as detailed in **Methods**. In all cases the known cell-type composition was used as input. Results are shown for synthetic datasets of shared (top) and highly-specific (bottom) eQTLs. (E) Performance of CeL-Gen positively correlated with the abundance of eQTL-affected cells. Plots are shown as in **Figure 3E**, but using the known cell-type composition as input. (F) Performance of compared methods for different branches of alterations. Results are shown as in **Figure 3E** (left) but for three compared methods (indicated on top). As in E, the known cell-type composition was used as input.