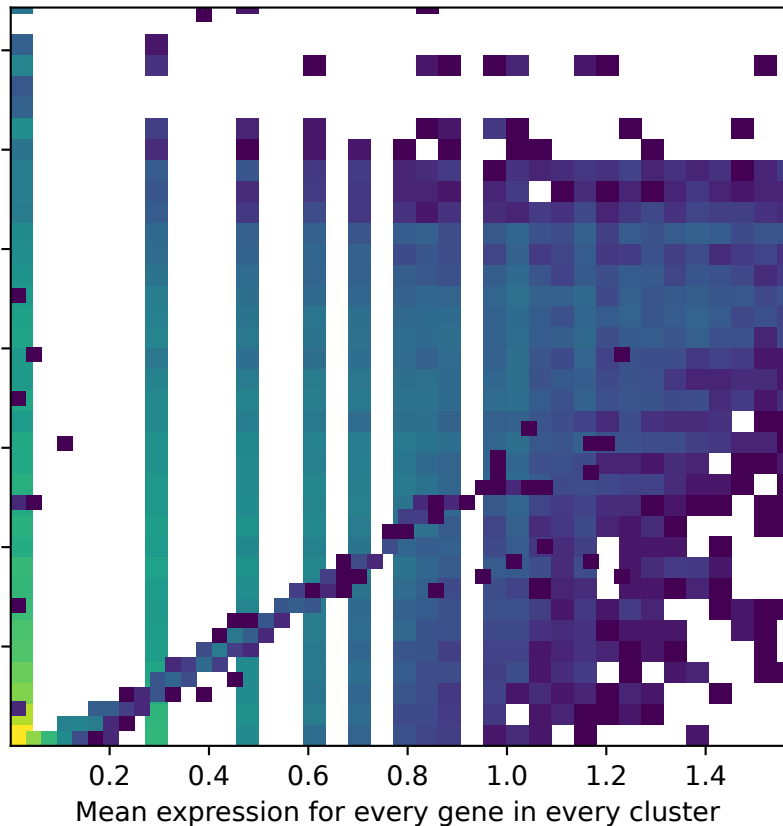


Reconstruction accuracy

Estimated expression for every gene in every cluster



Mean expression for every gene in every cluster