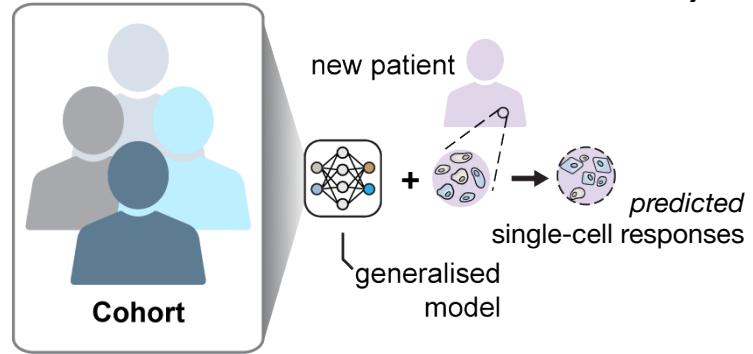
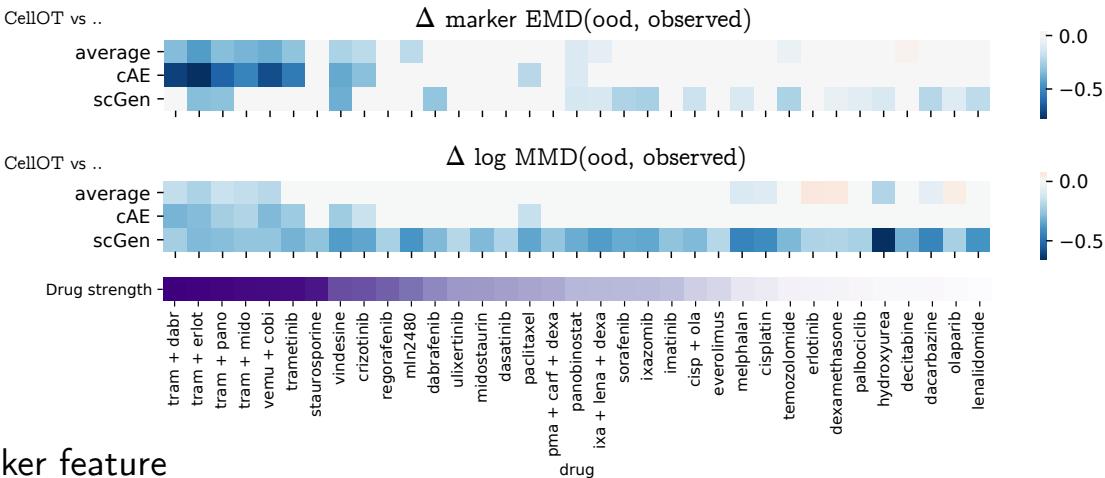
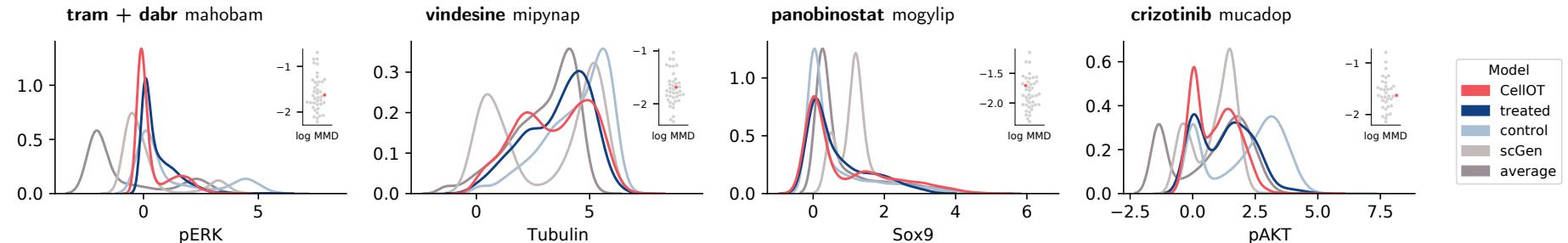


a)**b)**

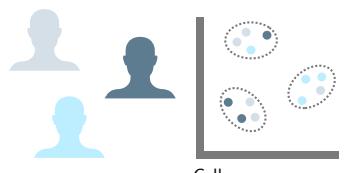
Predicting responses of unseen samples

**c)**

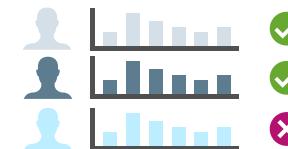
Selected marginals of holdout samples: marker feature

**d)**

1. Compute & cluster single-cell responses from observed samples



2. Classify progressed (✗) or healthy (✓) at 90 days with sample response profiles

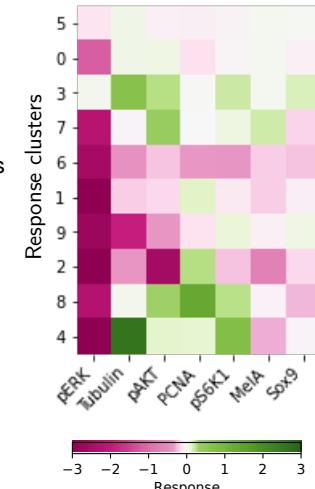


3. Classify incoming samples using predicted single-cell responses

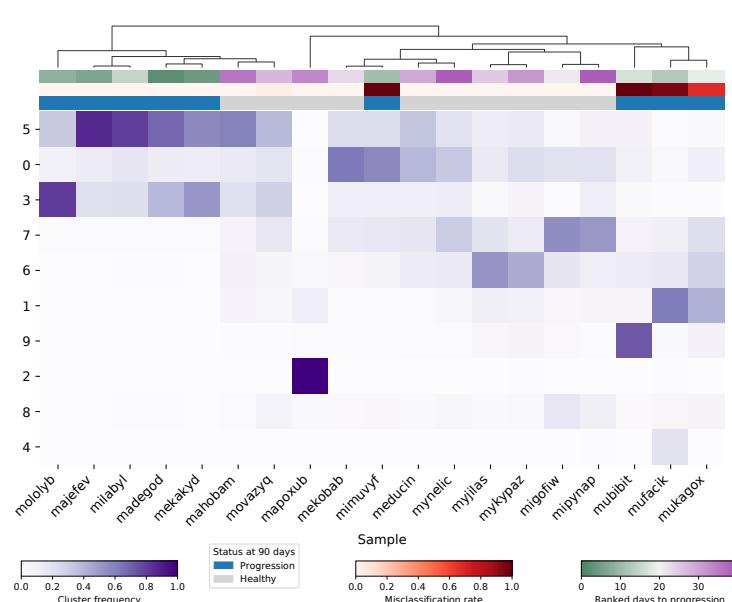
**e)**

Cluster centers

Marker intensities



Sample-level single-cell response profiles

**f)**

Predict progression within 90 days

Holdout accuracy

