Supplementary figure 2: **Benchmarking and threshold optimization:** Benchmarking based on the tissue dataset (above) and brain-subtypes (below) - a,d) Mean error rate based on 10 repeats of a 5-fold cross-validation over a range of POE thresholds. Error bars indicate +/- 1 std.dev. The black line indicates the ratio for the unthresholded POE matrix, and the red for the barcode, dashed lines indicate +/- 1 std.dev. b,d) Intra-cluster vs inter-cluster variance ratio, over a range of POE thresholds dashed line indicates the ratio for the unthresholded POE matrix. c,f) Mean average precision over a range of POE thresholds for the pathway fingerprint (black circles) and a fingerprint build on random gene sets of equivalent size distribution (blue circles). Solid lines indicate the mean average precision for Barcode (blue), Spearman correlation (green) and the unthresholded fingerprint (red) N.B. barcode or gene expression correlation data was not calculated for the brain-subtype dataset.