Fig. S2. Profiling of endothelial cells

a t-SNE plots showing EC marker gene expressions for unaligned clusters. **b** t-SNE plots showing unaligned or CCA aligned clusters colour-coded by sample origin (upper panels) and cancer type (low panels). **c** Fraction of cells for unaligned EC clusters per cancer type. **d** Fraction of singlet and doublet cells in each EC subcluster calculated by DoubletFinder. **e** Box plot showing number of detected genes for each EC subcluster. **f** Fraction of cells derived from normal (red) or tumour tissue (green) for each EC subcluster in each cancer type. **g** Violin plots of genes specifically expressed in tumour or normal tissue for each of the 5 EC subclusters. **h** Violin plot showing marker gene expressions for capillary EC subclusters. **i** Heatmap of differentially expressed genes between CRC, LC and OvC in the C3_TEC clusters. **j** Violin plot for metabolic activity for capillary EC subclusters scored by AUCell. **k**-**l** Differences in cancer hallmark pathway activities scored per cell by AUCell for all major EC subclusters (**k**) or subclusters of capillary ECs (**l**).