**Fig. S4. Subclustering of dendritic cells**

**a** t-SNE plots showing marker gene expressions for unaligned DC clusters. **b** Violin plot showing marker gene expressions for both unaligned and CCA aligned DC clusters. **c** Ratio of relative percentage for DC subclusters between normal and tumour tissues. Less than 1 indicates tumour enrichment. Langerhans-like DCs were enriched in tumour (FDR=$1.5\times10^{-31}$). **d** Fraction of cells derived from normal (red) or tumour tissue (green) for each DC phenotype in each cancer type. **e** Differences in cancer-hallmark pathway activities scored per cell by AUCell for DC phenotypes. **f** Metabolic activity of each unaligned DC phenotype scored by AUCell. **g** t-SNEs of DCs colour-coded for marker genes: *CCL22* and *CCL17* (early activation markers of the C3_DC cluster), as well as *CCR7* and *LAMP3* (late activation markers of the C3_DC cluster). **h** Expression pattern of *CCL22*, *CCR7* and *LAMP3* along the trajectory pseudotime of the C2 to C3 trajectory. **i** Density plots for CRC, LC and OvC along the cDC2 trajectory. **j** Transcription factor inactivation dynamics during cDC2 to migratory cDC differentiation.