Fig. S7. Profiling of monocytes, macrophages and neutrophils

a Barplot showing fraction of singlet and doublet cells predicted by DoubletFinder for unaligned myeloid clusters. **b** Number of detected genes in unaligned myeloid clusters. **c** t-SNE plot showing myeloid clusters after CCA alignment. **d** Heatmaps comparing marker gene expression signatures of common clusters generated by unaligned (left) and CCA aligned (right) methods, respectively. **e** Phylogenetic analysis of myeloid subclusters using the BuildClusterTree function Seurat. By relating the 'average' cell from each identity class, this analysis confirms the separation between monocyte and macrophage subclusters. **f** Violin plot showing marker gene expressions for unaligned myeloid clusters. **g** Heatmap of some differentially expressed genes in unaligned clusters. The expression of *FCGR3A*(CD16) and *CX3CR1* are higher in both C2_CD16s and C7_CX3CR1s. **h** Fraction of cells derived from normal (red) or tumour tissue (green) for each myeloid cell subcluster in each cancer type. **i** Heatmap of differentially expressed genes between two subclusters of C5_CCL18 macrophages. **j** Differences in cancer hallmark pathway activities scored per cell by AUCell for myeloid cell subclusters. **k** Density plots for CRC, LC and OvC for monocyte-macrophage differentiation along the CCL18 and MMP9 lineages. **l-m** Activation dynamics of transcription factors for terminal differentiation of C5_CCL18 (**l**) and C6_MMP9 (**m**) macrophages. **n** EPAS1 activation dynamics in terminal differentiation of C5_CCL18 (left) or C6_MMP9 (right) macrophages.