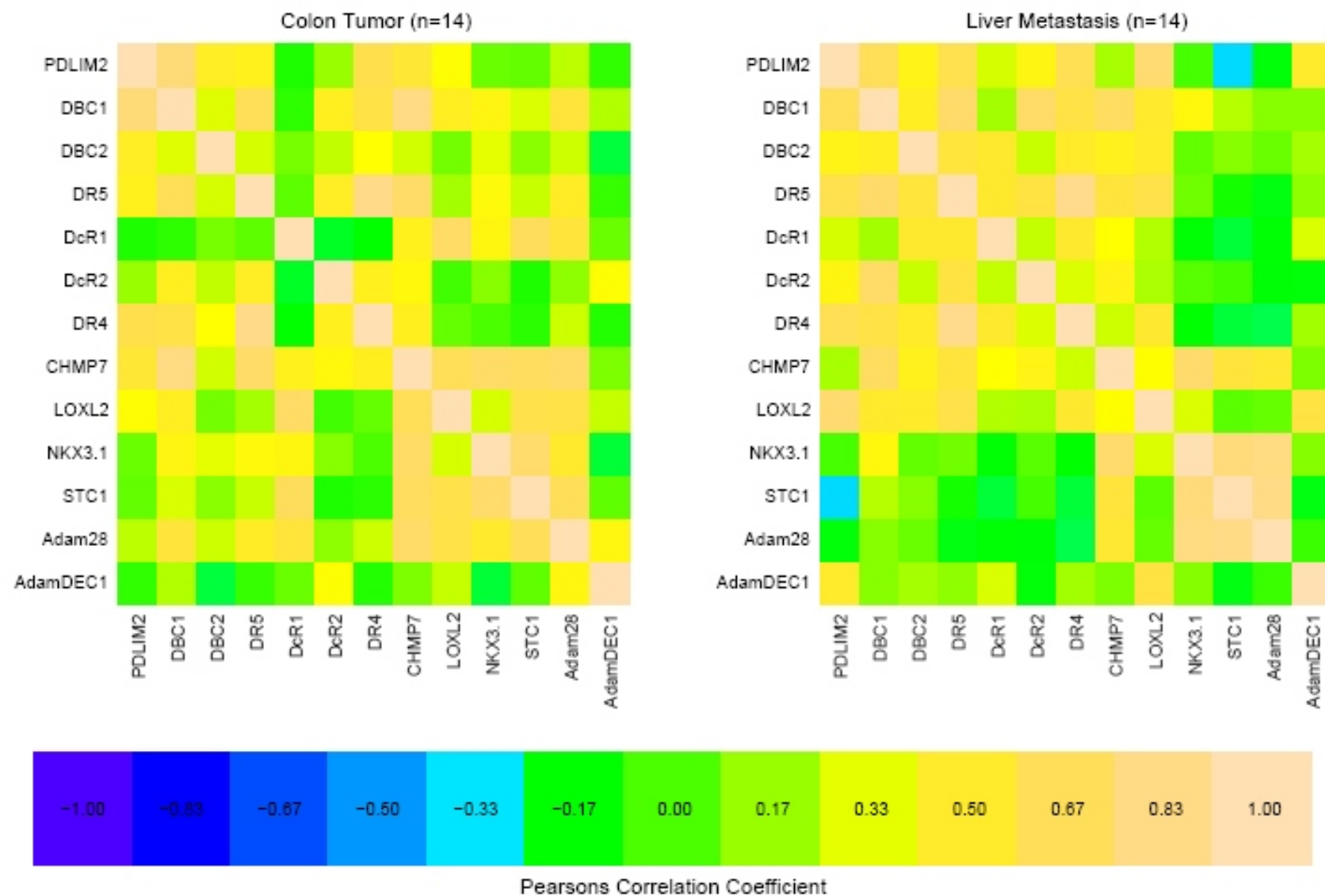




Gene-by-gene mRNA expression correlations in colon tumour and matched liver metastasis samples (n=14).

To investigate the possibility of transcriptional relationships between the 13 candidate genes and to see whether any such relationship might differ between the two tumour tissues we used Pearson's correlation analysis. Expression data (Mean dCt) for each gene in 14 matched CT and LM was interrogated. The analysis revealed potential transcriptional relationships between a number of genes in the two tissues.