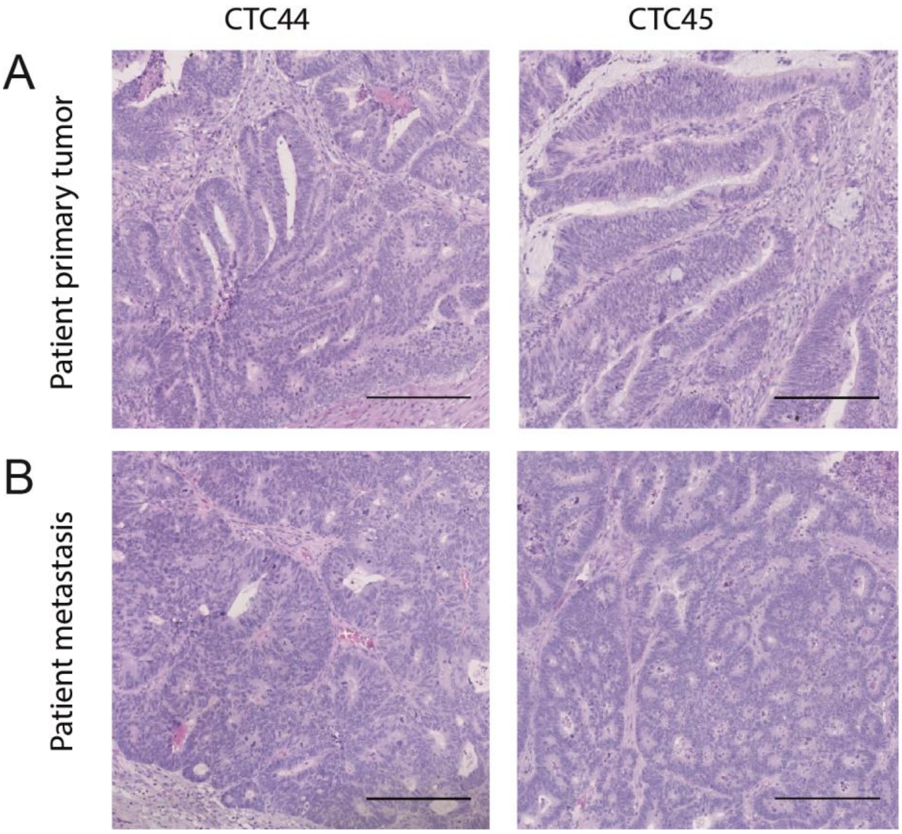
Supplementary Figure 1:

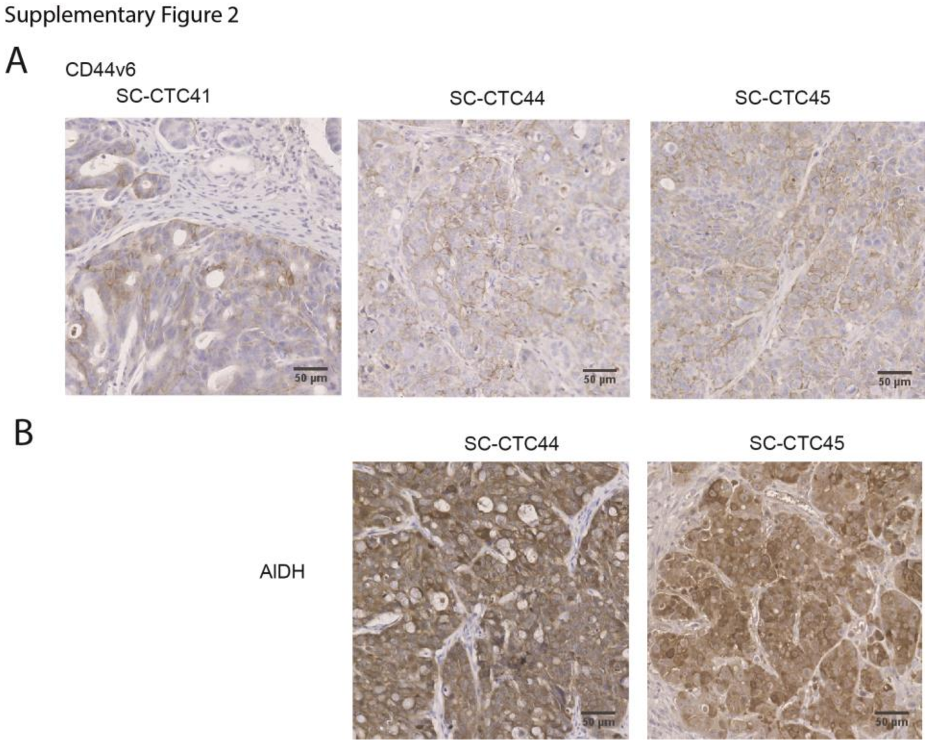
Hematoxylin and eosin staining on primary tumor and metastasis of patients 44 and 45 (scale bar 250 µm)

Supplementary Figure 1

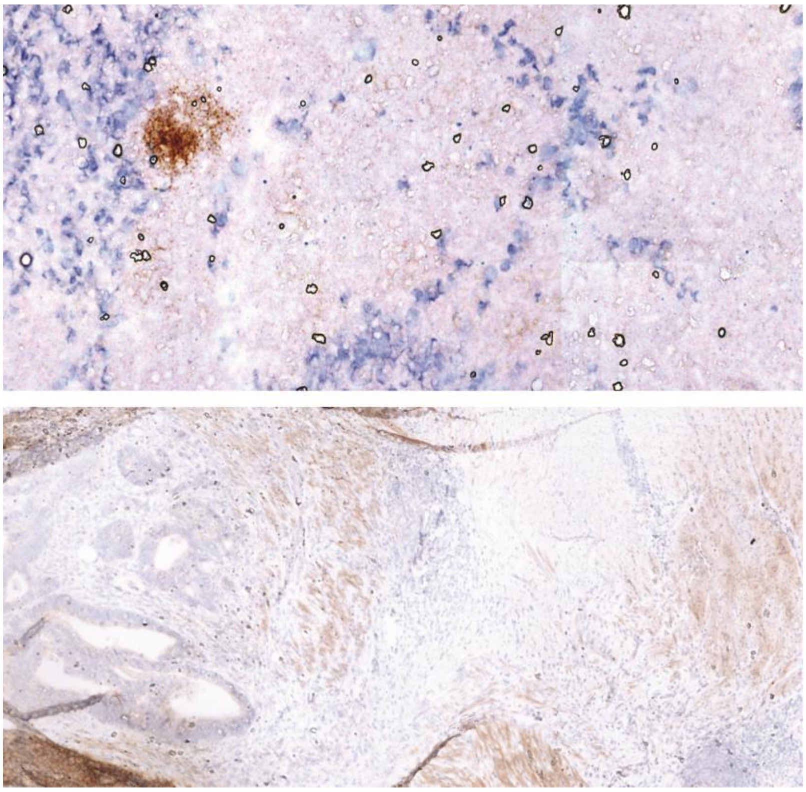


Supplementary Figure 2:

(A) CD44V6 staining on tumors following subcutaneous injections of CTC lines (scale bar 250µm**)** (scale bar 50µm**)**. (B) ALDH staining on tumors following subcutaneous injections of CTC lines (scale bar 50µm**)**.



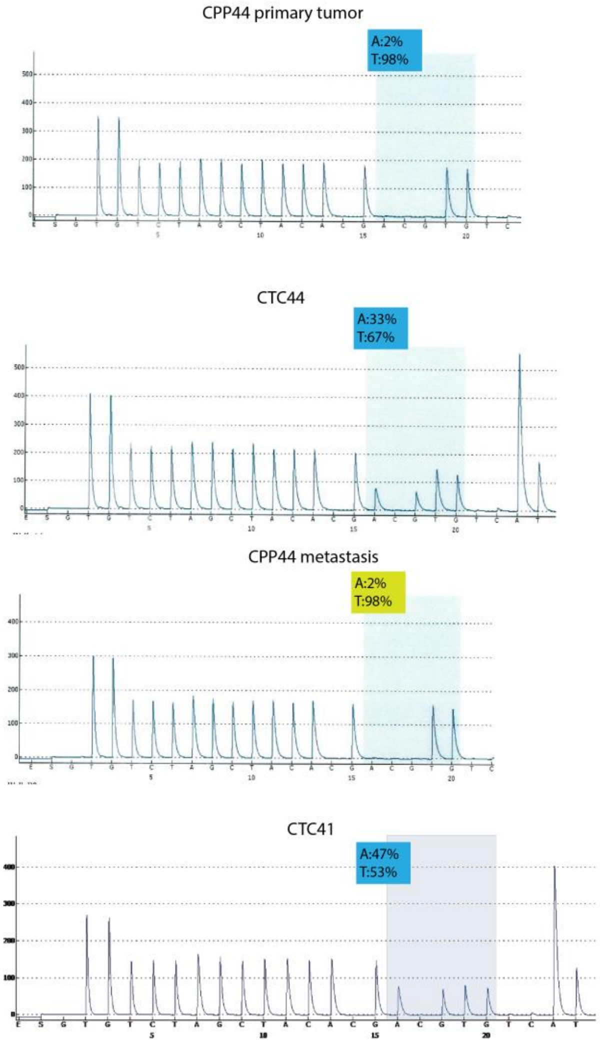
Supplementary figure 3:



Supplementary figure 4:

Detection of BRAF V600E mutation in CTC lines using pyrosequencing. In the mutated samples, “T” is replaced by “A”.

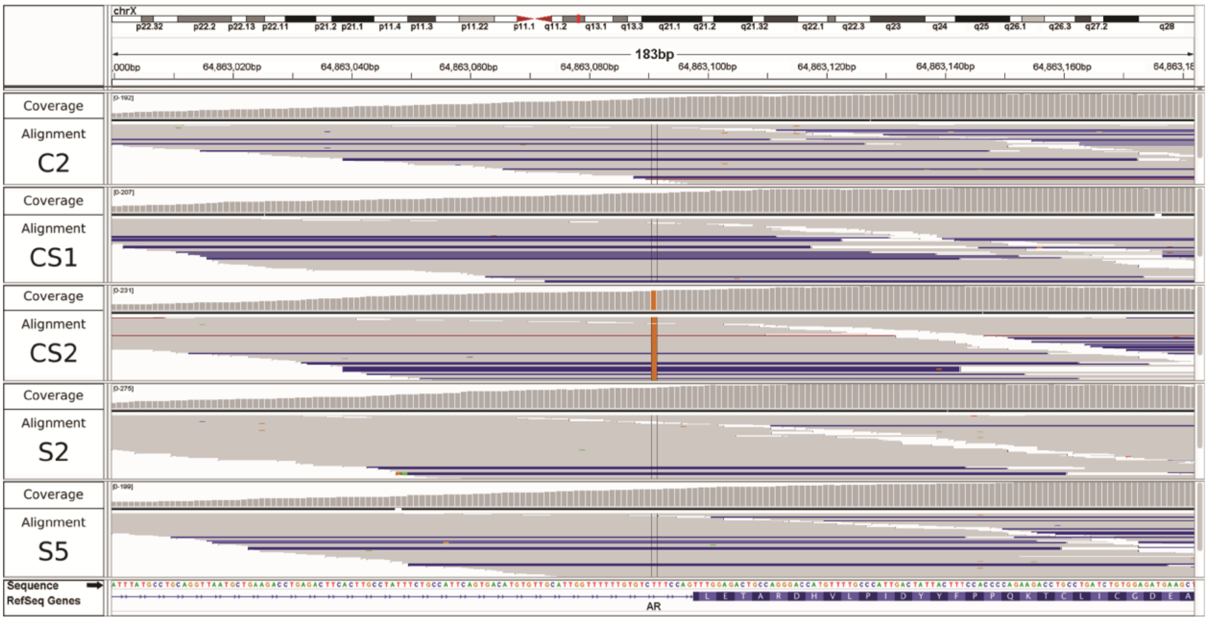
Supplementary Figure 4



Supplementary figure 5:

IGV snapshot depicting the heterogeneous Androgen Receptor gene variant (red bars) that was detected in subclone cs2 only. To aid legibility, only five of the ten subclones are depicted.

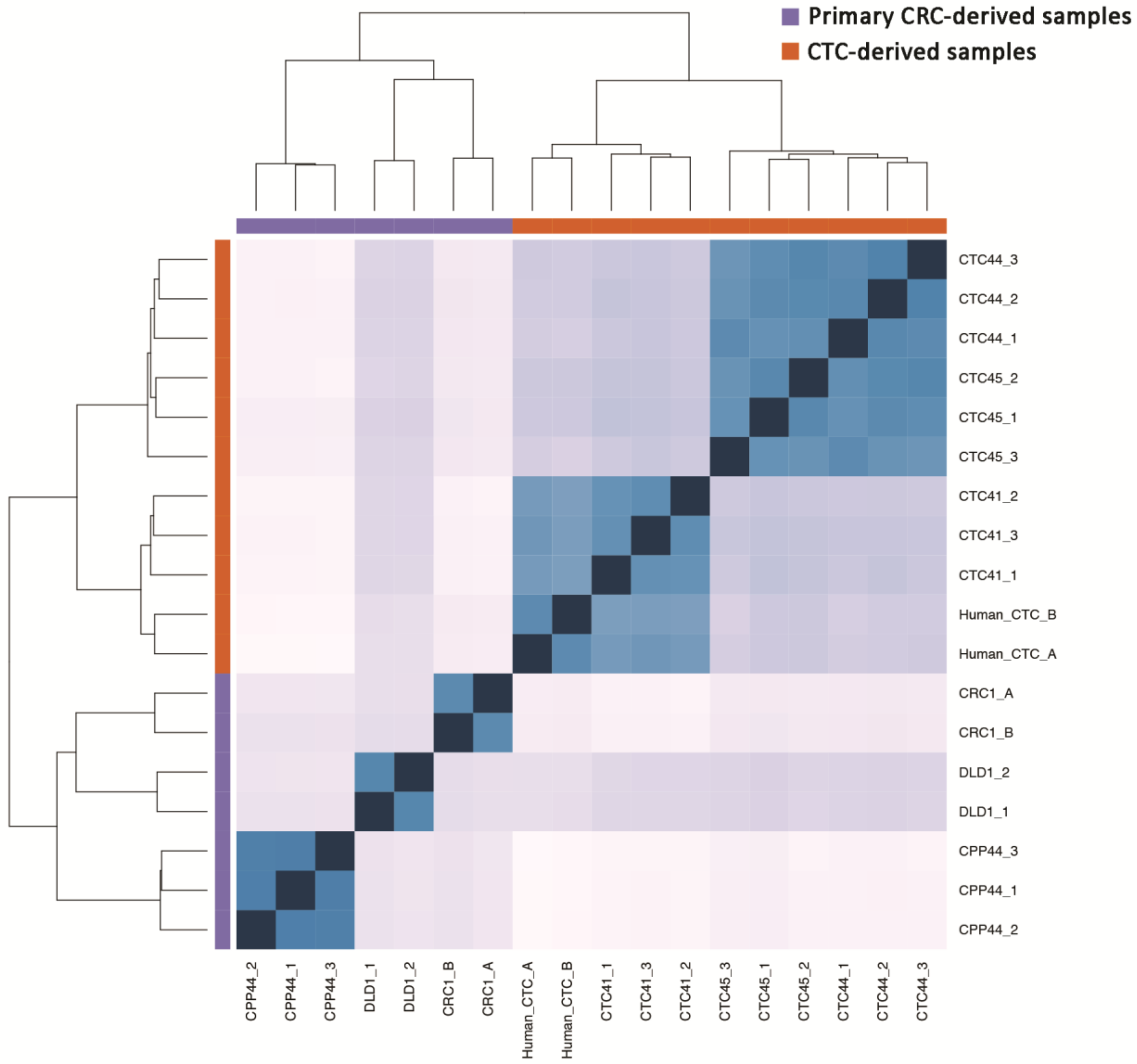
Supplementary Figure 5



Supplementary figure 6:

Heatmap and dendogram depicting the unsupervised clustering analysis of RNAseq results for the three CTC lines, two lines established by ourselves from primary CRC samples (CRC1 and CPP44) and for DLD1 CRC cell line, all grown under the same conditions. CTC41 was sequenced a second time (Human-CTC_A and CTC_B) as an internal control. Colored squares indicate the similarity between samples, with darker colors being more similar and lighter colors more different.

Supplementary Figure 6



Heatmap and dendrogram depicting the unsupervised clustering analysis of RNAseq results for the three CTC lines, two lines established by ourselves from primary CRC samples (CRC1 and CPP44) and for the DLD1 CRC cell line, all grown under the same culture conditions. CTC41 was sequenced a second time (Human-CTC_A and CTC_B) as an internal control. Coloured squres indicate the similarity between samples, with darker colours being more similar and lighter colours more different..

Supplementary figure 7:

Metabolism of xenobiotics by cytochrome P450. Colored boxes highlights genes that are differentially expressed between CTC lines and primary tumor samples.

Supplementary Figure 7