(A)

| ID | metastasis | meta site | sample | age | sex | location | TNM | Stage | Differentiation | |
|---------|------------|-----------|------------|-----|-----|----------|-----------|-------|-----------------|--|
| CRC-9 | - | - | primary | 57 | М | Rectum | T3N0M0 | IIA | Mod | |
| CRC-17 | - | - | primary | 76 | М | Sigmoid | T3N2M0 | IIIC | Well to mod | |
| CRC-19 | - | - | primary | 48 | F | Rectum | T2N0M0 | I | Well | |
| CRC-20 | - | - | primary | 60 | М | Left | T3N0M0 | IIA | Mod | |
| CRC-6 | + | liver | primary | 41 | F | Right | T4N2M1 | IV | Mod | |
| CRC-29 | + | liver | primary | 56 | F | Sigmoid | T3N0M1a | IVA | Well | |
| CRC-32 | + | liver | primary | 53 | F | Rectum | T4aN2bM1a | IVA | Mod to well | |
| CRC-29M | + | liver | liver meta | 56 | F | - | - | - | - | |
| CRC-31M | + | liver | liver meta | 80 | F | - | - | - | - | |
| CRC-24M | + | liver | liver meta | 56 | м | - | - | - | - | |
| CRC-26M | + | liver | liver meta | 79 | М | - | - | - | - | |

Ligands



Kynurenine derivatives

Pearson r=0.96

CRC-29M

CRC-26M

0.4

0.6

Relative TDO2 expression

0.2

•

CRC-29

0.8

1

1.2

0.1

0

0

(E)



| | | | | | | _ | | | | | | |
|-------------------|--------|-----------------------------|--------|--------|----------------------------|--------------|--------|--------------|---------|---------|---------|---------|
| | Gene | primary (w/o liver meta) | | | primary (w. liver meta) | | | liver meta | | | | |
| pathway | | CRC-9 | CRC-17 | CRC-19 | CRC-20 | CRC-6 | CRC-29 | CRC-32 | CRC-29M | CRC-31M | CRC-24M | CRC-26M |
| | APC | 48.3 48.6 | 100.0 | | 99.2 | 63.9 29.3 | 92.6 | 65.5 33.9 | 92.5 | 49.3 | | 100.0 |
| WNT | FBXW7 | 100.0 | | | | | | | | 49.9 | | |
| | CTNNB1 | | | | 41.1 | | | | | | | |
| | ARID1A | | | | | | | | | | 33.1 | |
| | KRAS | 29.5 | | 64.6 | | 67.5 | | | | | | |
| RTK/RAS/PI3-K/AKT | TSC1 | | | | 48.6 | | | | | | | |
| | BRAF | | | | | | | 50.5 | | | | |
| n53 | TP53 | | | 99.9 | | 99.8 | 100.0 | 99.6 | 99.9 | 99.6 | | 99.9 |
| P 33 | ATM | 47.2 | 99.9 | | | | | | | | | |
| TGF-β | SMAD4 | | | | | | | | | | | |
| | FGFR1 | | | | | | | | | | | |
| | NOTCH3 | | | | | | 23.3 | | 20.0 | | | 32.0 |
| others | NT5C2 | | | | | | | | | | | 67.0 |
| | NTRK2 | | | | | | | | | 30.0 | | |
| | NTRK3 | | | | | | | 59.1 | | | | |

(F)

CRC-24M



Figure S1

FIGURE S1 Systematic Screening of Charged Metabolites that are Upregulated in Metastatic Spheroids. A, Clinical data of colorectal cancer from which spheroids shown in this paper were derived. Note that only CRC-29 and CRC-29M are derived from the same patients. B, Volcano plot of the relative ratio and *p*-value of quantified value of anionic metabolites from non-metastatic spheroids vs. metastatic spheroids. Amounts of the metabolites were measured by CE-TOF-MS in biological triplicate. The position of Octanoate is shown by the arrow. C, Explanation for the TDO2/IDO1-Kynurenine pathway. D, Correlation between Kynurenine production and *TDO2* expression. Association of L-kynurenine in supernatants and *TDO2* shown Figures 1C and 1D are presented. Pearson correlation coefficient was shown. E, Genomic alterations detected in the spheroids shown in (A). Percentages of allele frequency of the mutation are also shown. F, Clustering analyses of cancer spheroids and cell lines based on RNA-seq data. Prediction of CMS for the CRC spheroid cells by hierarchical clustering. The spheroid cells used in this study are stratified by hierarchical clustering together with the reference cells with pre-determined CMS subtypes ¹. Hierarchical clustering is performed using Ward's method. CMS subtypes of each cell line are shown by the indicated colors.

Linnekamp JF, Hooff SRV, Prasetyanti PR, et al. Consensus molecular subtypes of colorectal cancer are recapitulated in in vitro and in vivo models. *Cell Death Differ*. 2018; 25: 616-633.