Suppl. Fig. 1. Visualization of viral integration of human endogenous retrovirus K113 (HERV-K113). Example of HERV-K113 mapping to the viral genome observed in two patients (CRC001 and CRC-002), each with a trio of normal colon, primary colorectal tumour, and liver metastases tissues. The upper part of the figure shows the artificial viral chromosome (ChrV) obtained by concatenating the genomes of 10,384 viruses, with the vertical red bar indicating the relative position within ChrV of the window of 143 nucleotides represented in the lower part of the figure. The lower part shows the alignment of the sequences (horizontal red bars) obtained by whole-genome sequencing analysis. The number of overlapping sequences represents the coverage of a given position. If a virus is integrated into the human chromosomes, it will be present at the same rate as the human genomes (average coverage here: 28.33), which is the case for HERV-K113, suggesting the integration of this virus. The coloured vertical bars in the lower part of the figure represent point mutations.
Suppl. Tab. 1. Read counts stratified by tissue (normal colon, primary colorectal tumour, and metastases, all except one case* liver metastases), coverage, map on the combined human and viral genome (including the properly paired fraction), map on the viral genomes only (raw), and filtered by blast alignment.

| ID   | Tissue | Coverage | Mapped       | Paired       | Raw   | Filtered |
|------|--------|----------|--------------|--------------|-------|----------|
| CRC-001 | Normal | 21.01    | 779,397,638  | 778,605,033  | 300,798 | 41       |
|       | Tumour | 23.72    | 896,697,974  | 876,094,251  | 253,369 | 54       |
|       | Metastasis | 21.68 | 805,144,453  | 804,468,293  | 277,357 | 105      |
|       | Normal | 26.01    | 936,079,958  | 935,287,433  | 351,351 | 135      |
|       | Tumour | 29.94    | 1,079,271,673| 1,078,764,616| 369,370 | 109      |
|       | Metastasis | 27.98 | 1,008,685,786| 1,008,251,678| 273,478 | 66       |
| CRC-002 | Normal | 26.13    | 982,716,164  | 981,971,563  | 341,459 | 133      |
|       | Tumour | 29.94    | 1,079,271,673| 1,078,764,616| 369,370 | 109      |
|       | Metastasis | 27.98 | 1,008,685,786| 1,008,251,678| 273,478 | 66       |
| CRC-003 | Normal | 28.03    | 1,018,199,477| 1,017,726,620| 366,773 | 118      |
|       | Tumour | 28.66    | 1,040,473,204| 1,039,983,717| 316,752 | 93       |
|       | Metastasis | 28.69 | 1,045,172,871| 1,044,705,882| 317,503 | 84       |
| CRC-004 | Normal | 110.30   | 3,911,696,560| 3,885,312,466| 933,138 | 579      |
|       | Tumour | 0.06     | 2,088,708    | 2,079,005    | 3,244   | 0        |
|       | Metastasis | 54.8   | 1,938,146,693| 1,931,803,009| 794,909 | 243      |
| CRC-005 | Normal | 30.07    | 1,475,461,382| 1,473,293,013| 3,608   | 43       |
|       | Tumour | 6.8      | 258,767,127  | 258,225,606  | 2,458   | 19       |
|       | Metastasis | 40.94 | 1,650,547,553| 1,648,181,520| 2,449   | 40       |
| CRC-006 | Normal | 27.13    | 969,377,475  | 968,812,774  | 453,638 | 96       |
|       | Tumour | 26.39    | 1,033,819,939| 1,033,354,717| 293,122 | 45       |
|       | Metastasis | 24.46 | 924,277,632  | 923,852,284  | 283,739 | 41       |
| CRC-007 | Normal | 28.60    | 1,035,732,054| 1,035,261,070| 385,441 | 126      |
|       | Tumour | 28.4     | 1,025,719,304| 1,025,271,172| 379,141 | 82       |
|       | Metastasis | 25.7   | 940,518,663  | 940,132,382  | 302,218 | 51       |
| CRC-008 | Normal | 29.92    | 1,089,082,375| 1,087,181,322| 316,749 | 133      |
|       | Tumour | 28.17    | 1,019,788,712| 1,019,192,980| 337,252 | 80       |
|       | Metastasis | 26.20 | 945,330,703  | 944,159,934  | 339,072 | 77       |
| CRC-009 | Normal | 25.69    | 935,507,282  | 934,969,254  | 321,960 | 64       |
|       | Tumour | 26.30    | 953,170,594  | 952,164,051  | 337,122 | 91       |
|       | Metastasis | 26.04 | 943,092,032  | 942,638,079  | 354,361 | 78       |

| 28.33 ± 16.21 | 37,681,568,357 | 37,585,317,033 | 11,518,759 | 3,485 |

* Lung tissue.