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Corrigendum

Corrigendum to 'Single-nucleotide variants, tumour mutational burden and microsatellite instability in patients with metastatic colorectal cancer: Next-generation sequencing results of the FIRE-3 trial'. [European Journal of Cancer 137 (2020) 250–259]

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The authors regret there were mistakes in some graphics for the subpopulation with BRAF mutated tumors in above publication. These mistakes were found in Figure 2C (small BRAF graphic), Figure 2D (only

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BRAF) and Figure 4 (BRAF V600E MUT and BRAF non-V600E MUT subgraphic).

To support these corrections, the Authors also note that the following section of text require some updates:

In Section 3.8. *Association of KRAS, BRAF and SMAD4 SNVs, TMB-H and MSI-H with CMSs,* page 254 of the printed paper

> Combined NGS and CMS data were available for 349 of 373 patients (93.6%). *KRAS*- and *BRAF* V600E-MUT tumours were mainly classified as CMS2 and 4. CMS4 was detected in 6 of 11 (54.5%) *BRAF* non-V600E-MUT tumours. Eight, 10 and 9 *SMAD4*-MUT tumours were classified as CMS1, CMS2 and CMS4, respectively, and CMS3 was detected once. Eight of 10 *MSI-H* tumours (80.0%) were associated with CMS1, and one tumour was associated with CMS3 and CMS4. *TMB-H* tumours were enriched by CMS1, followed by CMS2, CMS4 and CMS3 (Fig. 4).

Should be corrected to

> Combined NGS and CMS data were available for 349 of 373 patients (93.6%). *KRAS*-MUT tumours were mainly classified as CMS2 and 4, and *BRAF* V600E-MUT CMS1 (75.0%), respectively. CMS2 was detected in 4 of 11 (36.3%) *BRAF* non- V600E-MUT tumours. Eight, 10 and 9 *SMAD4*-MUT tumours were classified as CMS1, CMS2 and CMS4, respectively, and CMS3 was detected once. Eight of 10 *MSI-H* tumours (80.0%) were associated with CMS1, and one tumour was associated with CMS3 and CMS4. *TMB-H* tumours were enriched by CMS1, followed by CMS2, CMS4 and CMS3 (Fig. 4).

Furthermore, in the Discussion section, page 256, the following text

> Eventually, we investigated the enrichment of relevant alterations in the previously reported mRNA expression-based CMSs (CMS1: immune, CMS2: canonical; CMS3: metabolic; CMS4: mesenchymal) [7]. While we confirmed enrichment of *MSI-H, TMB-H* and *BRAF* V600E-MUT tumours in CMS1 [7e9], *BRAF* non-V600E-MUT tumours were associated with CMS4, indicating again the possibility of a distinct subgroup.

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The outcome results and survival curves are not affected. The corrected figures are given here.

Fig. 2

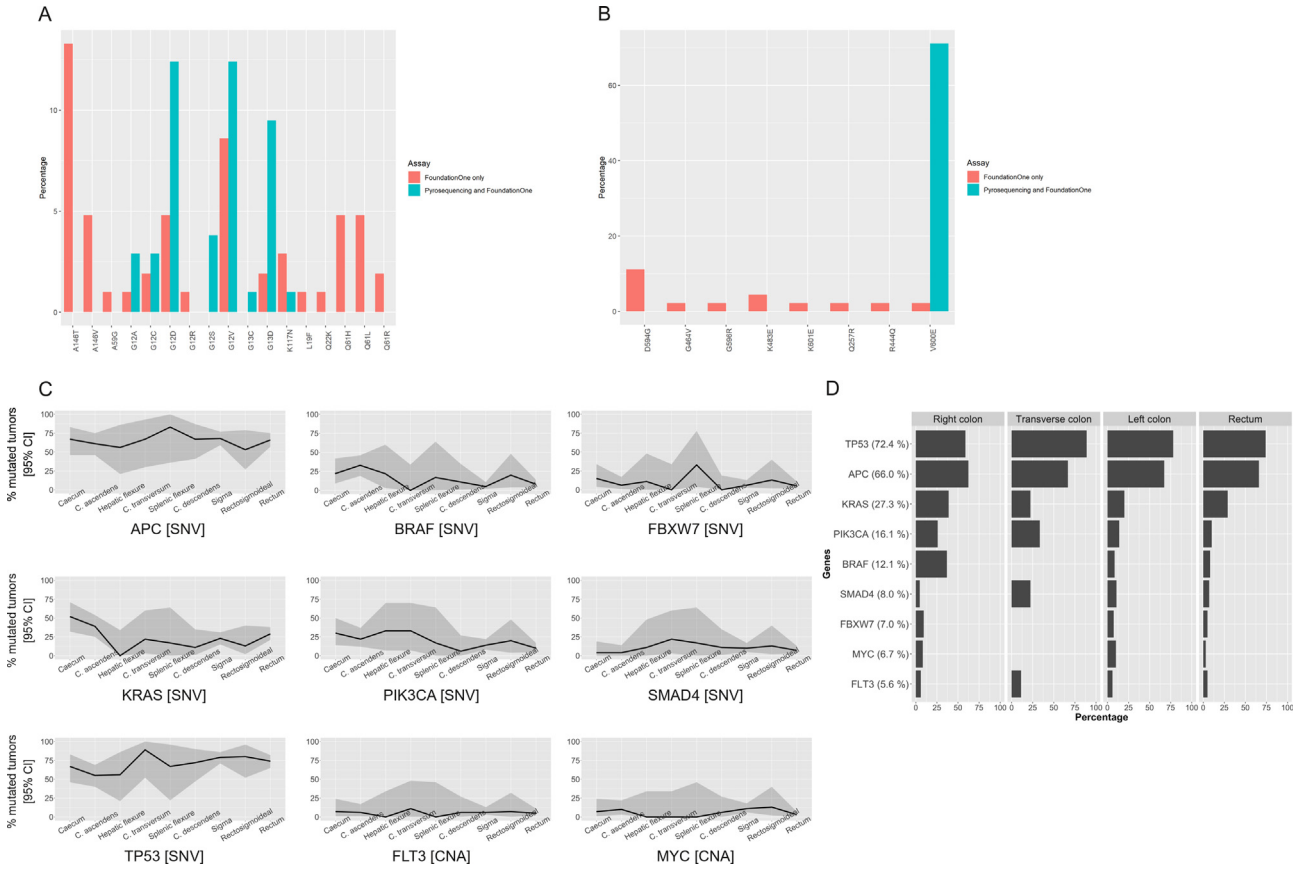
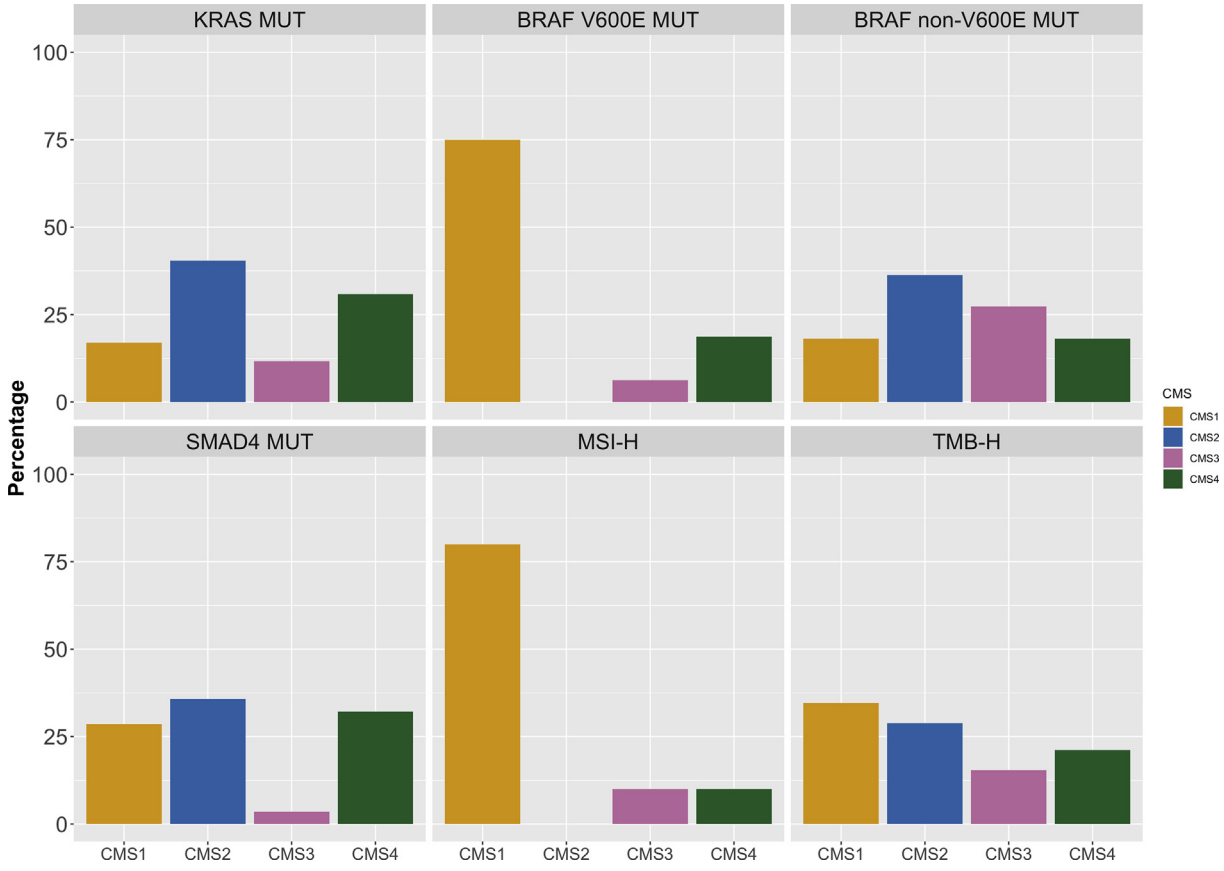


Fig. 4



The authors would like to apologise for any inconvenience caused.