**SUPPLEMENTARY MATERIAL**

**Supplementary Table 1.** Frameshift mutations within target genes in microsatellite unstable colorectal cancers. Frequency of mutations and proportion of tumors with mutations in all malignant cells are given for two independent series and for all patients (n=87, n=35 and n=122).

**Supplementary Table 2.** Number of frameshift mutations according to several clinical characteristics.

 Number of frameshift mutations are given for two independent series and for all patients (n=87, n=35 and n=122). *P* values are given in bold; n, number of patients; ns, not significant; \*, for the smaller second series, no significant association between number of frameshift mutations and clinical characteristics could be found.

**Supplementary Figure 1.** Correlation between CD3+ tumor-infiltrating lymphocyte densities calculated from whole slides and from TMA samples.

For the 52 tumors included in our previous study (16), X axis gives the percentage of anti-CD3 antibody-stained areas calculated from six representative fields from whole slides, for each tumor. For the same tumors, Y axis gives the percentage of anti-CD3 antibody-stained areas calculated from tissue micro array (TMA) samples (Spearman test).

**Supplementary Figure 2.** Associations between frameshift mutations and CD8+ TIL densities for the second series.

 (A) Associations between frameshift mutation percentage and CD8+ TIL density. For 35 patients, X axis gives the percentage of mutations found within the 22 studied coding repeat sequences and Y axis gives the density of CD8+ immunostained cells (Spearman test).

(B)CD8+ TIL density in the invasion front of tumors harboring no frameshift mutation or at least one frameshift mutation in the *HNF1A* or *TCF7L2* gene. Mean values are shown with SEM. Mann-Withney test was performed. (C) CD8+ TIL density in the invasion front of the tumors harboring no mutation, at least one mutation in some tumor cells only and at least one mutation within all tumor cells, in the *HNF1A* or *TCF7L2* gene. Bars indicate the mean values ± SEM. Pairwise comparisons were performed with a Kruskal-Wallis post-hoc test. (B and C) \*, *P* < .05.

**Supplementary Figure 3.** *In vitro* cytotoxic activity of peripheral TLs from donors harboring or not mutations in *TGFBR2*, *TAF1B* and *ASTE1* genes.

(A) Peripheral TLs from an HLA-A\*02+ MSI Lynch patient, with a tumor harboring the (-1) *TGFBR2* and (-1) *TAF1B* mutations, were stimulated with AAPCA2.1/FSP02, AAPCA2.1/FSP27 orAAPCA2.1/FSP30. Specific cytotoxic activityof these TLs was assessed in standard 51Cr release assays at different effector to target (E:T) ratios. Upper panel: assays performed on HLA-A\*0201+ T2 cells pulsed with an irrelevant or a relevant (FSP02, FSP27 or FSP30) peptide. Lower panel: assays performed on HLA-A\*0201+ HCT116 (MSI) and Colo205 (MSS) colorectal cancer cell lines.

 (B) Specific cytotoxic activity of peripheral TLs stimulated with AAPCA2.1/FSP02, AAPCA2.1/FSP27, AAPCA2.1/FSP30 orAAPCA2.1/M1m was assessed in standard 51Cr release assays at different effector to target (E:T) ratios. Assays were performed with peripheral TLs from two HLA-A\*02+ patients with tumors in which no mutation in *TGFBR2*, *TAF1B* or *ASTE1* gene was detected (an MSI Lynch patient, upper panel, and an MSS patient, middle panel) and with peripheral TLs from two HLA-A\*02+ healthy donors (representative results are shown in the lower panel).