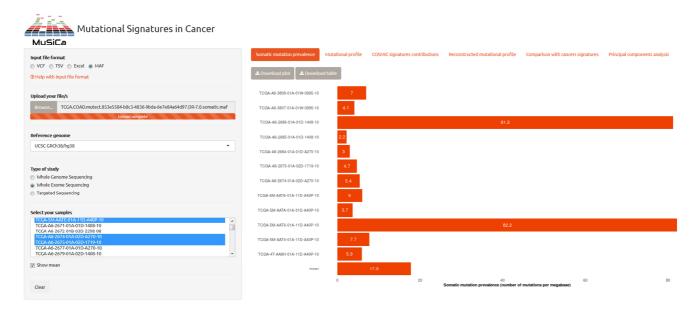
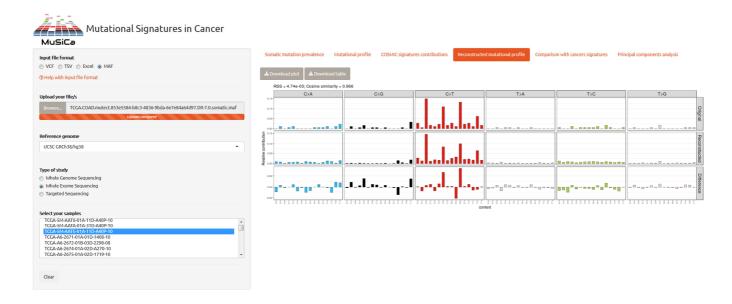
Supplementary Material



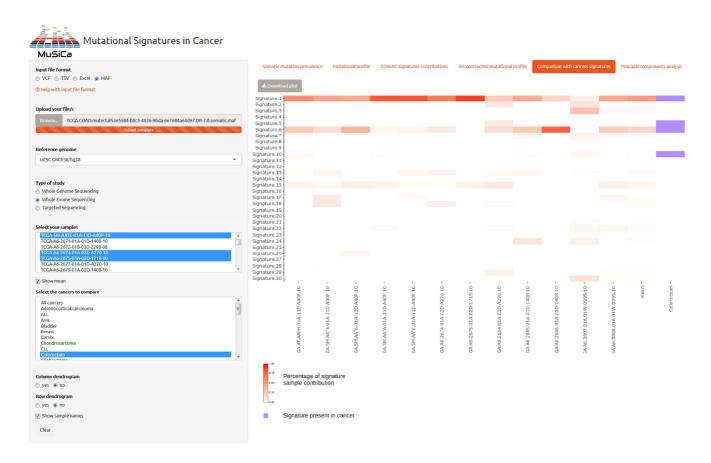
Supplementary Fig. 1. Somatic mutational prevalence in MuSiCa web app. Mutational burden output tab showing a subset of the TCGA-COAD project samples and its mean value.



Supplementary Fig. 2. Mutational profile representation in MuSiCa web app. Mutational profile output tab showing a subset of the TCGA-COAD samples.



Supplementary Fig. 3. Reconstruction of mutational profile in MuSiCa web app. Reconstructed mutational profile output tab showing a specific sample of the TCGA-COAD project.



Supplementary Fig. 4. Comparison with cancer signatures in MuSiCa web app. Output tab presenting a comparison of known signatures contributions with mutational signatures reported in different human cancer types in a subset of the TCGA-COAD samples and its mean value.



Supplementary Fig. 5. Principal component analysis in MuSiCa web app. Principal component analysis output tab presenting a classification of a specific subset of the TCGA-COAD samples according to the quantification of known signatures contributions.