Additional information (it will be freely available at <https://github.com/mariavica/VIGex> once the article is published). The files included are:

- **Clinical\_information.xlsx**: excel file with sample id’s and clinical annotations (used in figure 3A-D) .

- **metadata\_nanostring.xlsx**: excel file including information from all samples analysed in nanostring.

- **metadata\_rna.xlsx**: excel file with sequencing statistics of RNAseq samples.

- **Nanostring\_data.xlsx**: excel file including raw counts of the samples analysed (Raw\_counts), normalized counts (Housekeeping\_normalization), and finally the log2 and centered expression values (log2-centered) that are used for downstream analysis.

- **expression\_input\_vigex.xlsx**: example of input data for computing VIGex scores (the same data from Nanostring\_data.xlsx “log2-centered” sheet)

- **nanostring\_normalization.R & Vigex\_calculation.R**: minimal R script used to process nanostring data and compute VIGex scores.

- **raw\_counts\_RNA.txt**: file including the raw counts for the RNASeq data.

- **RNAseq\_normalization.R**: minimal R script used to process and normalize RNASeq counts.

- **Tils.xlsx**: excel file including a table with the percentage of TILS in each sample (used in Figure 2E).

- **VIGEX\_RNA\_PM\_annot.xlsx**: concordance between the samples used for external validation of VIGEX signature.

- **VIGEX\_rsem\_expression\_results\_genes\_counts.tsv**: gene counts of the samples used for the external validation of VIGEX signature.

- **raw\_counts\_additional\_datasets.xlsx**: nanostring counts of the colon and lung datasets.

- **additional\_datasets**: clinical information of the colon and lung datasets.