

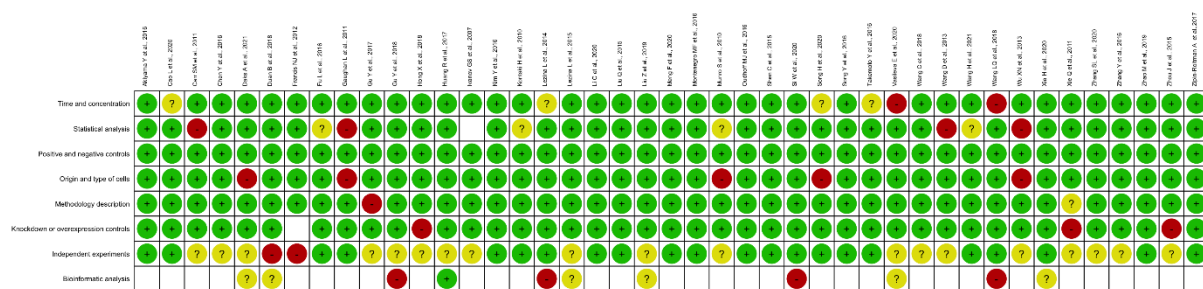
# A Systematic Review to Define the Multi-Faceted Role of the Lysine Methyltransferase SETD7 in Cancer

Fátima Liliana Monteiro <sup>1</sup>, Cecilia Williams <sup>2</sup> and Luisa A. Helguero <sup>1,\*</sup>

<sup>1</sup> Institute of Biomedicine – iBiMED, Department of Medical Sciences, University of Aveiro, Portugal;

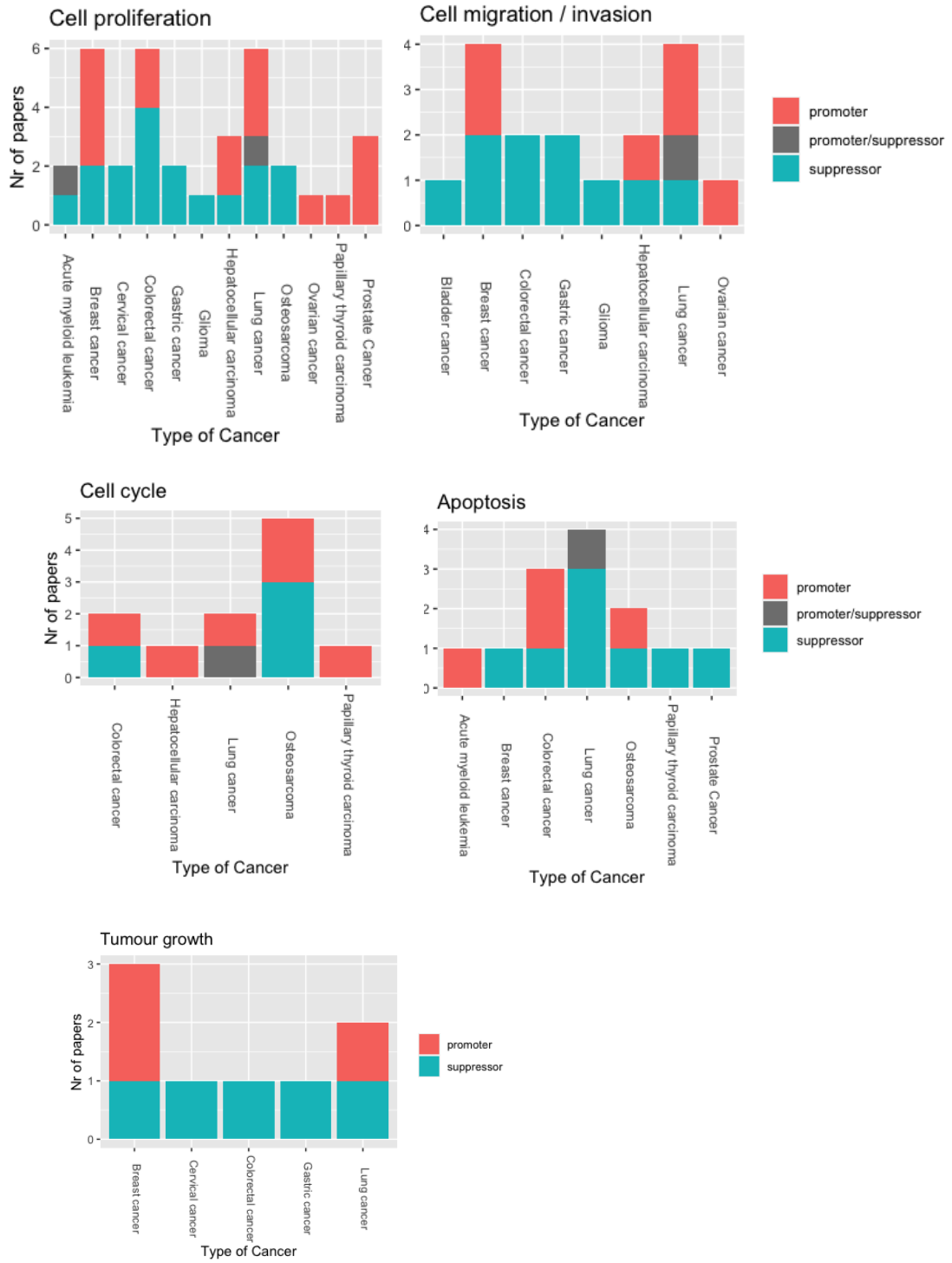
<sup>2</sup> SciLifeLab, Department of Protein Science, KTH Royal Institute of Technology, Sweden;

\* Correspondence: luisa.helguero@ua.pt

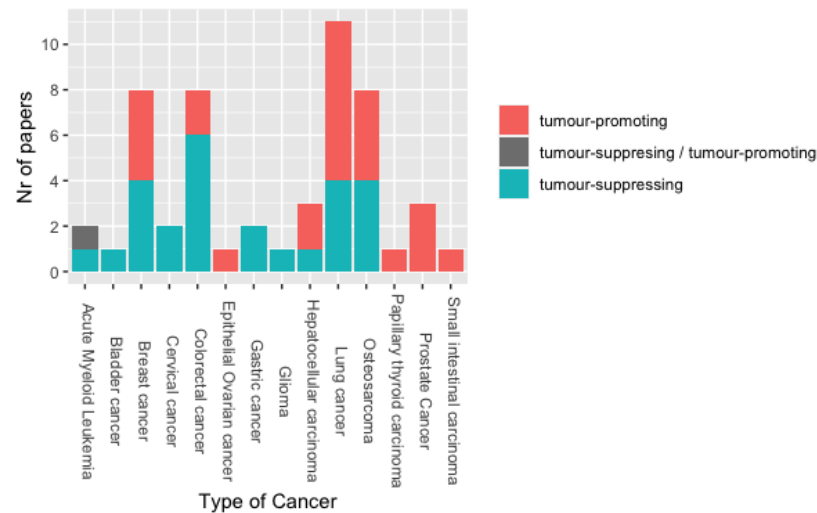


**Supplementary Figure S1** Risk of bias in individual studies. The following criteria were considered for functional studies: information on time and concentration when a treatment (like chemicals, knockdown, etc.), description and complete report of statistical analysis, usage of positive and negative controls, description of the origin and type of cells used, methodology detail, assessment of gene/protein expression after loss and/or gain of function experiments and usage of independent experiments, and description of bioinformatics methodology used for analysis of public datasets or own cohorts. Green: low risk of bias; yellow: risk of bias is unclear in at least one domain, but no domains with high risk; red: high risk of bias; white: not applicable to the study in question.

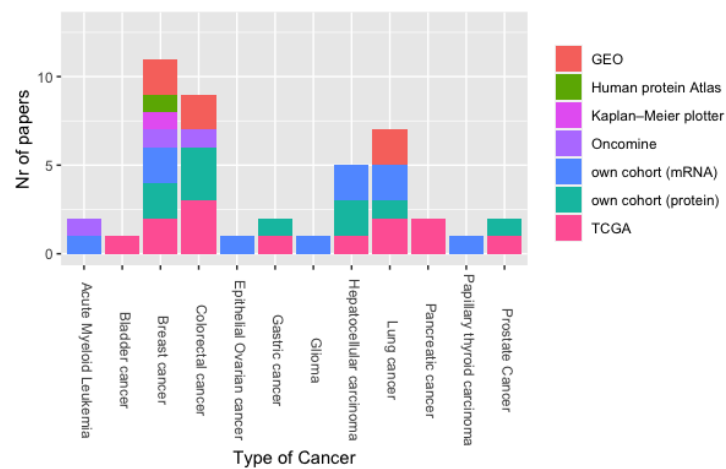
(a)



(b)



(c)



**Supplementary Figure S2** Analysis of the literature. (a) Literature categorization according to SETD7 function over the most studied cancer-related processes by cancer type. For the most studied cancer-related cellular processes (cell proliferation and cell migration / invasion), studies were grouped by cancer type and SETD7 was categorized as having a promoter (red) or suppressor (green) function or both (depending of the cell signalling context – grey); (b) SETD7 function according to cancer type. Cellular processes modulated by SETD7 in each cancer type were grouped into tumour-promoting (red) or tumour-suppressing (green) or both (depending of the context – grey). The y axis shows the number of published papers describing SETD7 function included in this review; (c) Type of dataset used to study SETD7 mRNA and protein expression in human cancer samples. Studies were divided according to the source of mRNA and protein data used. The number of published papers in relation to the type of cancer is shown. Note that in some cases the same paper was considered more than once if it analysed SETD7 expression by more than one approach.