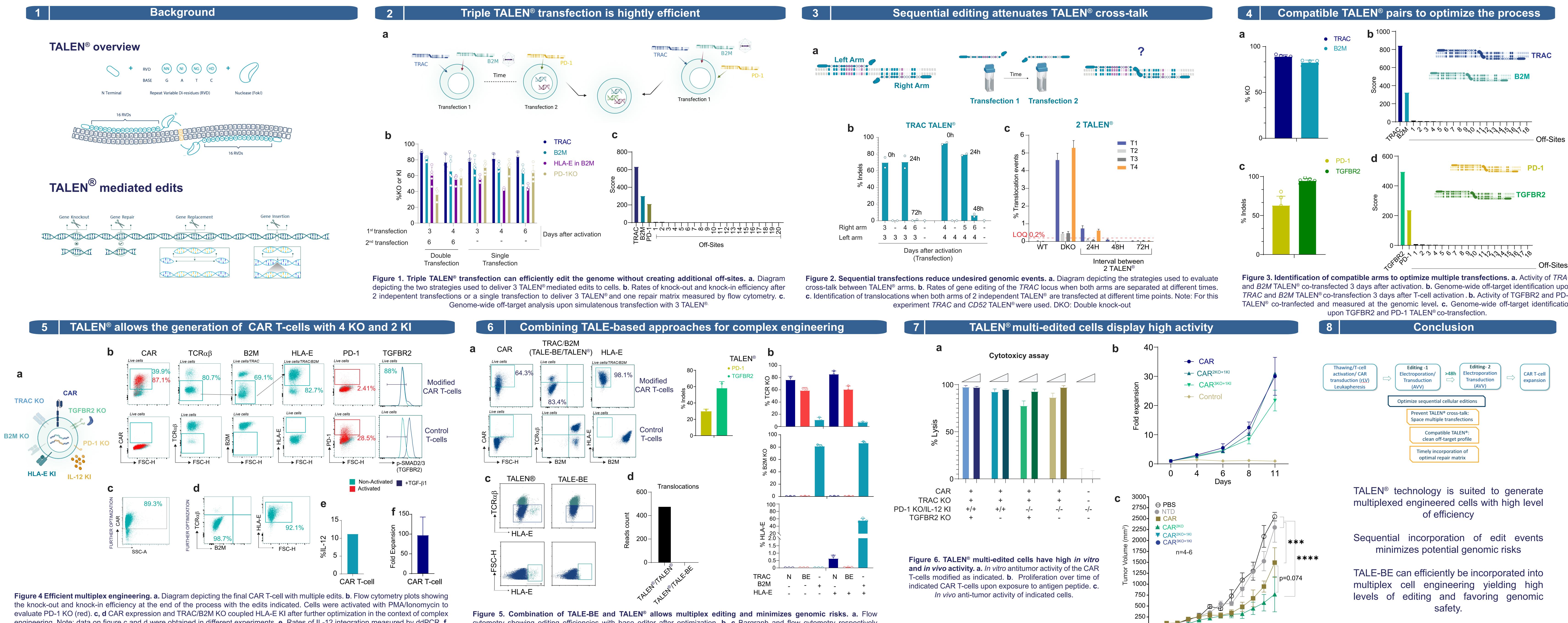
## Jordan Skinner<sup>1</sup>, Emilie Dessez<sup>2</sup>, Sandra Rozlan<sup>2</sup>, Maria Feola<sup>1</sup>, Diane Le Clerre<sup>2</sup>, Alexandre Juillerat<sup>1</sup>, David Sourdive<sup>2</sup>, Phillipe Duchateau<sup>2</sup>, Laurent Poirot<sup>2</sup>, Beatriz Aranda-Orgilles<sup>1</sup>.

the microenvironment has limited the ability to target solid tumors. In recent years, advances in genomic-based cellular engineering are bringing us a step closer to conquer solid tumors. In recent years, advances in genomic-based cellular engineering are bringing us a step closer to conquer solid tumors. This glimpse of success also demonstrated that we need to be a step closer to conquer solid tumors. In recent years, advances in genomic-based cellular engineering are bringing us a step closer to conquer solid tumors. In recent years, advances in genomic-based cellular engineering are bringing us a step closer to conquer solid tumors. able to creatively modify and equip CAR T-cells to target these tumors. A caveat to this is that increasing the number of genetic modifications at the cellular level of editional payloads to increase the efficacy as well as lead to genomic toxicities. Here, we show that we can use our state-of-the-art TALEN® technology to precisely edit up to four loci simultaneously while delivering several additional payloads to increase the efficacy as well as lead to genomic toxicities. Here, we show that we can use our state-of-the-art TALEN® technology to precisely edit up to four loci simultaneously while delivering several additional payloads to increase the efficacy as well as lead to genomic toxicities. Here, we show that we can use our state-of-the-art TALEN® technology to precisely edit up to four loci simultaneously while delivering several additional payloads to increase the efficacy as well as lead to genomic toxicities. arange of gene and cell engineering approaches, we can develop CAR T-cells focused on unmet medical needs with a high level of efficiency for gene editing and cell engineering technologies including TALE base editors to increase the efficiency for gene editing and cell engineering technologies including TALE base editors to increase the efficiency of multiplexed gene editing while protecting genomic integrity. By carefully choosing a range of gene and cell engineering technologies including TALE base editors to increase the efficiency for gene editing and cell engineering technologies including TALE base editors to increase the efficiency for gene editing and cell engineering technologies including TALE base editors to increase the efficiency for gene editing and cell engineering technologies including technologies show that multiplexed engineering does not compromise CAR T-cell function, which in turn can be enhanced and display improved anti-tumor activity. Thus, multiplexed engineering does not compromise CAR T-cell function, which in turn can be enhanced and display improved anti-tumor activity. Thus, multiplexed engineering at superior efficiency rates while preserving genomic integrity has the potential to increased gene endineering at superior efficiency in TALEN®-mediated gene endineering at superior efficiency rates while preserving genomic integrity has the potential to increased gene endineering at superior efficiency rates while preserving genomic integrations at undesired loci. generate highly functional CAR T-cells to advance in the fight against solid tumors



engineering. Note: data on figure c and d were obtained in different experiments. e. Rates of IL-12 integration measured by ddPCR. f. Fold cell expansion calculated by dividing the number of cells obtained at the end of the production by the number of cells seeded in culture vessels after the last electroporation.

## Expanding the Scope of Multiplex Engineering for Superior Generation of Efficient CAR T-cells

## <sup>1</sup>Cellectis Inc, New York, NY; <sup>2</sup>Cellectis SA, Paris, France

Figure 3. Identification of compatible arms to optimize multiple transfections. a. Activity of TRAC and B2M TALEN<sup>®</sup> co-transfected 3 days after activation. **b.** Genome-wide off-target identification upon TRAC and B2M TALEN<sup>®</sup> co-transfection 3 days after T-cell activation. b. Activity of TGFBR2 and PD-1 TALEN<sup>®</sup> co-tranfected and measured at the genomic level. c. Genome-wide off-target identification

cytometry showing editing efficiencies with base editor after optimization. b, c Bargraph and flow cytometry respectively showing potential non-homology arm mediated trappping of HLA-E repair matrix into the TRAC locus and integration in B2M as control (N: nuclease; BE: base editor). d. Translocation analysis between 2 TALEN<sup>®</sup> and 1 TALEN<sup>®</sup> and 1 TALE-BE.

This communication expressly or implicitly contains certain forward-looking statements concerning Cellectis and its business. Cellectis is providing this communication. TALEN® and Cellectis is providing this communication, future events or otherwise. This communication contains Cellectis and its business. Cel



Days