Poster: P18 **Présenté par : CATONE christelle**

Characterization of SilenciX® cell lines as stable, syngenic and loss-of-function model

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Silencing is today the most adopted method to study gene function. The most classic approaches are based on siRNA expressed in the cell through different channels like transient transfection of RNA duplexes, of plasmids or of virus expressing RNA constructs. While efficient, these strategies suffer from the lack of stability that renders the study of some proteins challenging. To overcome this issue, short hairpin RNAs (shRNA) can be used to increase stability but they disrupt genomic integrity.

Our solution to this technical challenge is SilenciX®. Derived from our in-house technical knowledge and scientific collaboration, SilenciX® combines RNAi technology, DSIR Program and pEBV (Epstein Barr Virus) derived vector to generate knock-down clones in numerous cell lines, covering various fields of research.

To demonstrate the advantages of a stable and functional model to study loss-of-function, we have chosen here the example of Xeroderma Pigmentosum, complementation group C (XPC). XPC is a major protein of the nucleotide excision repair (NER) pathway involved in damage recognition, open complex formation, and repair protein complex formation. Mutations in this gene or some other NER components result in Xeroderma pigmentosum, a rare autosomal recessive disorder characterized by increased sensitivity to sunlight with the development of carcinomas at an early age.