

High-throughput screening of a CRISPR/Cas9 library for functional genomics in human cells

With the support of the National Natural Science Foundation of China and the National Basic Research Program of China, Prof. Wei Wensheng’s laboratory at the School of Life Sciences, Peking University, published a research article “High-throughput screening of a CRISPR/Cas9 library for functional genomics in human cells” in *Nature* (**2014**, 509(7501): 487—491).

Targeted genome editing technologies are powerful tools for studying biology and disease and have a broad range of research applications. In contrast to the rapid development of toolkits to manipulate individual genes, large-scale screening methods based on the complete loss of gene expression are only now beginning to be developed. Here we report the development of a focused CRISPR/Cas-based lentiviral library in human cells and a method of gene identification based on functional screening and high-throughput sequencing analysis. Using knockout library screens, we successfully identified the host genes essential for the intoxication of anthrax and diphtheria toxins, which were confirmed by functional validation. The broad application of this powerful genetic screening strategy will not only facilitate the rapid identification of genes important for bacterial toxicity but will also enable the discovery of genes that participate in other biological processes.

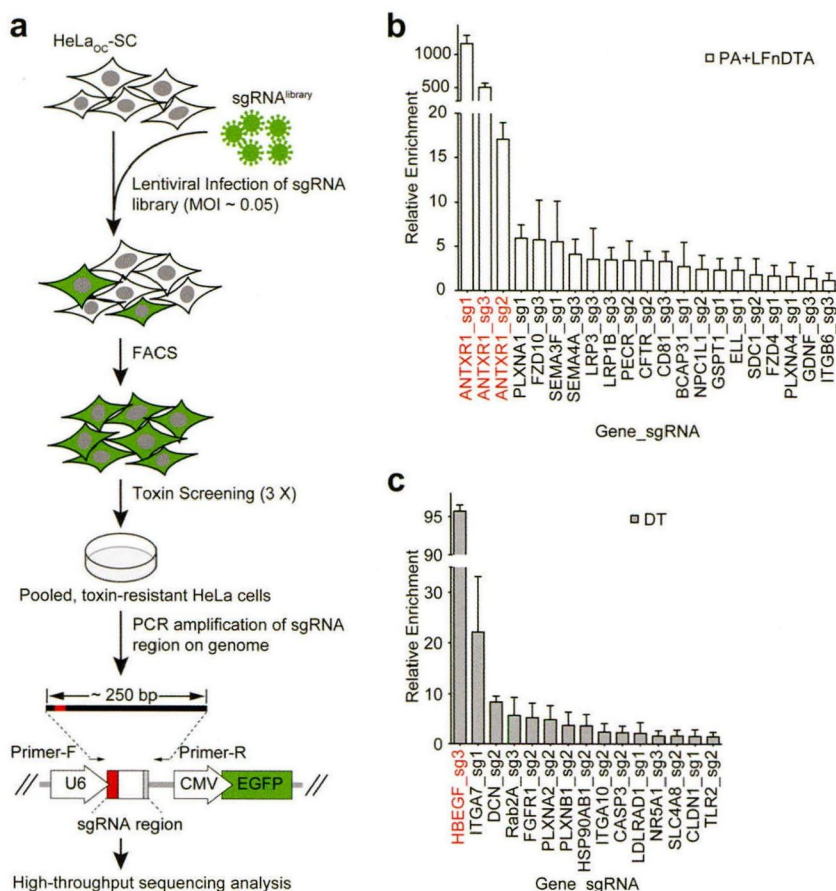


Figure Schematic of sgRNA library construction (a), and functional screening for essential genes for PA/LFnDTA (b) and DT toxicity (c).