AB039. P010. Use GeCKO lentiviral pooled libraries screen to identify genes which contribute to chemoresistance of pancreatic cancer

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Abstract: Pancreatic cancer is one of the most lethal malignancies and 5-year survival rate is below 7%. It is known that pancreatic cancer is highly resistant to systemic therapy. The Genome-scale CRISPR Knock-Out (GeCKO) pooled libraries consist of specific single guide RNA (sgRNA) sequences for gene knock-out in either the human or mouse genome. In this study, we generate Cas9 positive mouse pancreatic cancer cell line TB32047 and human pancreatic cancer cell line PANC1. Then transduce the libraries into the cells by lentivirus with multiplicity of infection (MOI) =0.3 and select the positive cells by puromycin. After puromycin selection, we use gemcitabine and oxaliplatin to screen the chemoresistant cells and extract genomic DNA for deep sequencing to identify which gene deletion contribute chemoresistance of pancreatic cancer. This study can help us to identify the critical genes that determine treatment response.