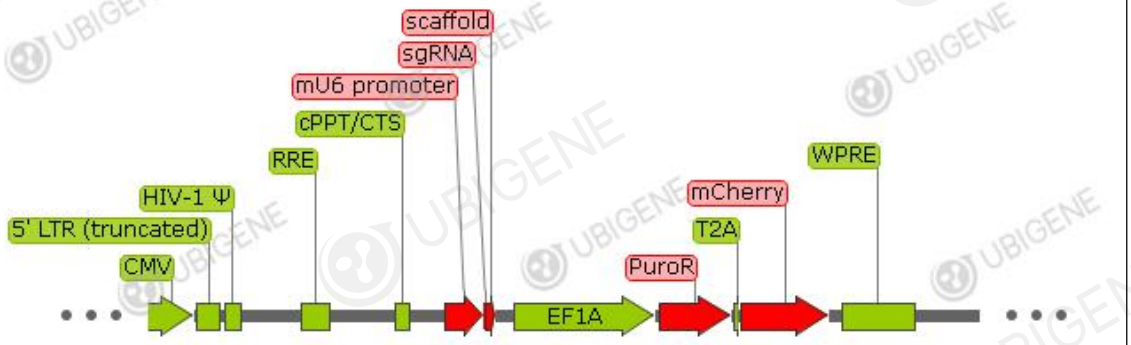
Use Instruction - Human CRISPR Deletion Library - Drug targets, kinases, phosphatases†

Product Info

The CRISPR knockout library targets 2,333 human genes related to drug targets, kinases, phosphatases, with a total of 24,569 knockout plasmid vectors, of which 10 different gRNA vectors are designed for each gene, in addition to 1,500 control vectors targeting intergenic sequences. The library uses pMCB320 as the backbone, which is a two-plasmid system that expresses only gRNA, while the Cas9 gene is on a separate vector that needs to be used in conjunction.

Library Details

Product Name	Human CRISPR Deletion Library - Drug targets, kinases, phosphatases†
Product Catalog	LIBR-H010-P
Product Details	24569gRNAs (gRNA sequences see attachment); Dual-plasmid system; The vector contains mCherry marker, which can be used to sort library cells using flow cytometry. Plasmids paired with 3rd lentivirus packaging system can be directly used for virus packaging. * It is recommended to use Ubigene's Lentiviral Packaging Kit(Cat# YK-LVP-05) Targeting 2333 genes,10gRNAs per gene; 1500non-target control sgRNAs（750 targeting non-genic sequences, 750 targeting safe harbor sequences）.

Backbone Map	
Verification Primers	pMCB320-F: CAGCACAAAAGGAAACTCACC pMCB320-R: GCCTAATGGATCCTAGTACTCGAG PCR Fragment: 226 bp he above primers can be used for PCR fragment amplification before library NGS sequencing. The amplified fragments can be purified and used for NGS sequencing.
Product Specifications	Ready-to-use, endotoxin-free, maxiprep plasmids, verified by Next Generation Sequencing, with coverage>95% and uniformity<10.

Product Use Instruction

Part 1. Lentivirus Packaging

Mix library plasmid constructs with 3rd generation lentiviral packaging constructs to be co-transfected into 293T cells (Recommend: Ubigene's 293T cell line specialized for virus packaging, cat#YC-A006). 48 or 72 hours upon transfection, collect lentiviral supernatant and the virus can be used upon concentration. The virus should be stored at -80℃.

Part 2. Library Plasmid Amplification

1.Library plasmid electroporation

Add50 ng library plasmid to 25 μL electrocompetent cells with transformation efficiency≥10^9 cfu/ug, electroporate cells as per electroporation parameters.Upon electroporation, add 975 μL recovery medium, mix well and transfer to a tube, then add 1 ml recovery medium to the tube and mix well again.Repeat above steps for 三 times and get 4 electroporation end products, share the tubes at 37℃, 250 rpm for 1 hour.

2.Culture of amplified library and calculation of transformation efficiency

1) Mix the 4 tubes of electroporation end products and take 10 μL and dilute with 990 μL recovery medium.Plate 20 μL dilution onto a 10 cm Petri dish and incubate plates at 32℃ for 14 hours.Count the colonies in the dish.If the number of colonies is 40000X greater than 7.37 x 10^6, move on to the next step.If it is less than 7.37 x 10^6, redo this step.

* Note: It is recommended that the number of colonies should be 40000X greater than1.23 x 10^7 to ensure the uniformity of Library gRNA.

2)Inoculate the remaining electrotransformation products into 4 bottles of 500ml LB+Amp liquid medium, and incubate at 37 ℃, 225rpm for 16h.

3.Collect transformation products

1) Collect the bacteria to a 50 mL centrifuge tube.

2) Centrifuge tubes to pellet bacteria, decant LB and weigh pellet (bacteria).

4.Maxiprep

Maxiprep the plasmid DNA according to the instruction for maxiprep kit, it is recommended to use endofree maxiprep kit from well-known, commercial brands such as QIAGEN and MACHEREY-NAGEL. (E.g. EndoFree Plasmid Mega Kit from QIAGEN)

Part 3. Library Screen

1.Determine infect MOI

Dilute the library virus into different gradients, such as MOI=0.3, 0.5, 1, 5, 10, 30, 100 to infect the target cells (the cell confluency is 30-50%). Each gradient needs to be set with 2 wells. After 48 hours of infection, add puromycin according to the settings in the table below for screening, and stop antibiotic screening when all cells in the blank group (cells not infected with virus) die. The MOI with a survival rate of 30% after antibiotic screening is the virus infection condition for the library screening experiment, that is, infect MOI.

Group#	MOI	Antibiotic screening	Cell amount upon antibiotic screening	Survival rate upon antibiotic screening
Experimental group 1	0.3	Yes	N1	N1/M1
Experimental group 1	0.5	Yes	N2	N2/M2

Experimental group 3	1	Yes	N3	N3/M3
Experimental group 4	5	Yes	N4	N4/M4
Experimental group 5	10	Yes	N5	N5/M5
Experimental group 6	30	Yes	N6	N6/M6
Experimental group 7	100	Yes	N7	N7/M7
Infection blank group 1	0.3	No	M1	--
Infection blank group 2	0.5	No	M2	--
Infection blank group 3	1	No	M3	--
Infection blank group 4	5	No	M4	--
Infection blank group 5	10	No	M5	--
Infection blank group 6	30	No	M6	--
Infection blank group 7	100	No	M7	--
Blank group	0	Yes	--	--

2.Transduction with library virus

①Determine the amount of cells and virus

Cell amount = gRNA# × gRNA coverage / 30% * gRNA coverage>500 fold

Virus amount = cell amount × infect MOI

②Expand the cells according to the cell amount calculated in step ①, and prepare sufficient virus.

③Use library virus to infect the target cells, upon Puro screening, divide the screened cells into experimental group and control group.Add target drugs to the experimental group for screening, upon screening, collect cells respectively from experimental group and control group (It is recommended to get at least 1.23 x 10^7 cells from control group; get all the cells from experimental group and the cell amount before cryopreservation should be greater than 2*10^6). Perform genome extraction for Next Generation Sequencing, and then compare and analyze the gRNAs of the experimental group and the control group.

Relevant products and service

Ubigene provides off-shelf libraries including Human/Mouse genome-wide plasmid library and some sub-libraries, and one-stop customized screening services for CRISPR-KO, CRISPRa, and CRISPRi including high-throughput sgRNA library construction, virus packaging, cell infection, drug screening, NGS sequencing, and data analysis, etc. Multiple deliverables fulfill different research needs!