## **Supplementary information**

## Droplet-based microfluidic platform for high-throughput screening

## of Streptomyces

Ran Tu<sup>1,2,#</sup>, Yue Zhang<sup>1,2,#</sup>, Erbing Hua<sup>3</sup>, Likuan Bai<sup>2,3</sup>, Huamei Huang<sup>2,3</sup>, Kaiyue

Yun<sup>2,3</sup>, Meng Wang<sup>1,2,\*</sup>

## \*Corresponding author:

Dr. Meng Wang, E-mail: wangmeng@tib.cas.cn



Supplementary Figure 1. Relative strength of promoters from e-lib (a) and g-lib (b) in 24-well plate. Wild-type  $ermE^*p$  and gapdh(EL)p were normalized to 100% for e-lib and g-lib variants, respectively. For each experiment, three replicate samples were analyzed (n=3). Error bars represented the standard deviation.  $*p\leq0.05$  and  $***p\leq0.001$  (Student's two-tailed *t*-test). Source data were provided in Supplementary Data 1.



**Supplementary Figure 2. Schematics of the droplet making device (a) and the droplet sorting device (b).** Channels are 50 μm deep. The specific size of the junction was marked in microns (μm).



**Supplementary Figure 3. Schematic of the optical setup of microfluidic system.** The orange line indicated the 850-nm light used for observation by the camera. Microfluidic chip was exposed under 488-nm laser (blue line). The 520-nm fluorescent light (green line) emitted by droplets was detected by the photomultiplier tube (PMT). The data was acquired by the FPGA data acquisition card (blue box) to record the fluorescence intensity of droplets and analyzed by the computer (PC). High voltage amplifier (red box) was used to apply a voltage to the droplets for deflection and sorting.

Promoter	Sequence (5'-3')	Fold-change	Relative
			strength
ermE*p	TTGACGGCTGGCGAGAGGTGCGGGGAGGAT	100%	3.4
е_С6р	TTGACGCATTTGCAGCGCTTTGGGGAGGAT	133.5%	4.5
<i>e_A3p</i>	TTGACGTACTGTCTGTCGATGGGAGAGGAT	343.2%	11.6
e_D1p	TTGACGAAAGAGTGGGATGTGGGGGGAGGAT	347.9%	11.8
g_C1p	TTGCAGCACACACTCGGAACGTCATATGAT	10.1%	10.1
<i>g_C4p</i>	TTGCAGAAAGAGGAAGCAAGAAAATATGAT	24.7%	24.7
g_D1p	TTGCAGCTACATTGGATTATCTGGTATGAT	94.6%	94.6
gapdh(EL)p	TTGCAGCATCTGGGCGGCTACCGCTATGAT	100%	100

**Supplementary Table 1. The sequences of promoter variants sorted from e-lib and g-lib.** -35 regions were indicated by solid lines, and -10 regions were indicated by dot lines.