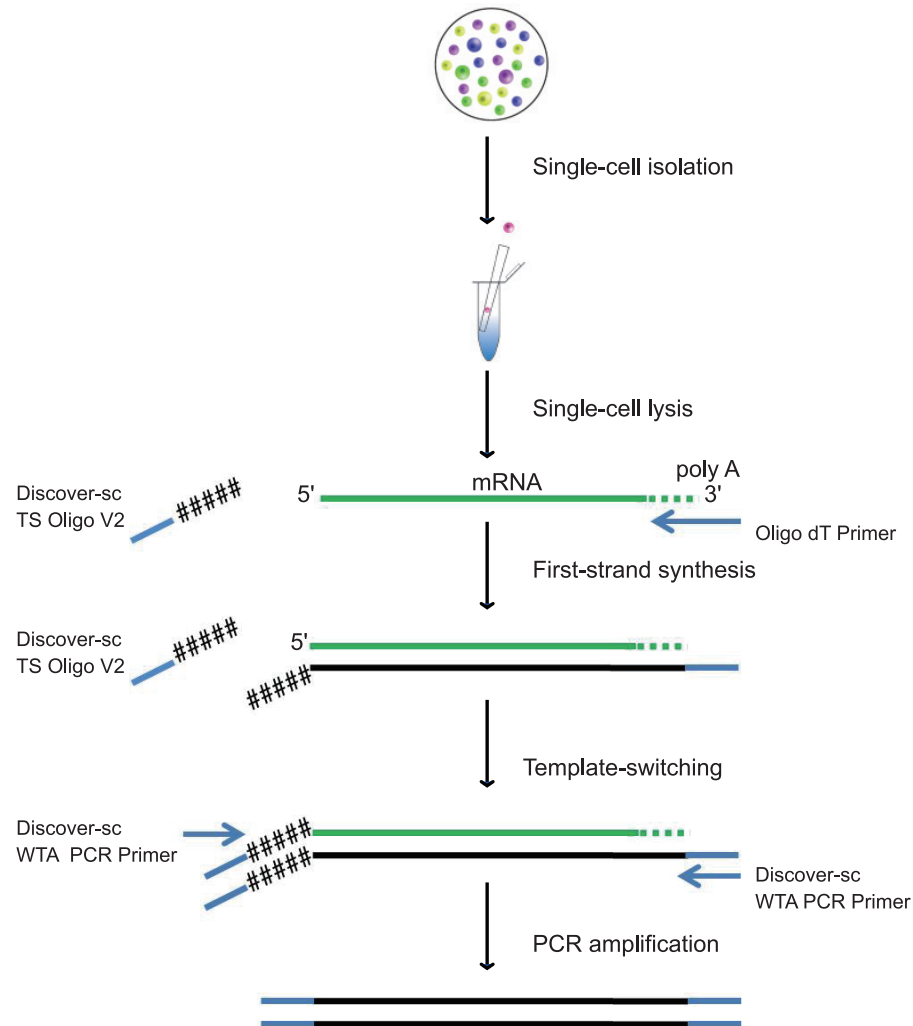


Discover-sc WTA Kit V2 (Vazyme #N711)

Discover-sc WTA Kit V2 is capable of obtaining sufficient samples for sequence analysis through first-strand cDNA synthesis and amplification using 1 - 1,000 cells or 10 pg - 10 ng of total RNA as templates, thus overcoming the technical difficulty that the conventional mRNA-seq method cannot be used for sequence analysis of trace samples such as single cells due to the low RNA content. The upgraded version features substantially improved detection sensitivity and volume compatibility, and is more suitable for the detection of low-abundance genes and low-concentration templates.



Workflow



Features

• High gene detection rate

Vazyme #N711 detects amplification products with high sensitivity and up to 15,000 genes were detected in a single 293T cell.

Table 1 Mapped rate from different companies

Samples	Expression Genes	Mapped to genome	Mapped to rRNA	Mapped to exon	Mapped to intron	Mapped to intergenic
Vazyme-1	14807	88.4%	1.24%	86.1%	10.5%	3.46%
Vazyme-2	15138	88.2%	3.06%	86.9%	9.4%	3.72%
Supplier C-1	14367	84.6%	1.76%	85.9%	10.3%	3.77%
Supplier C-2	15285	84.7%	2.27%	82.0%	13.5%	4.56%

• High uniformity and no bias

The result shows that Vazyme #N711 ensures good coverage of the 5' and 3' genes.

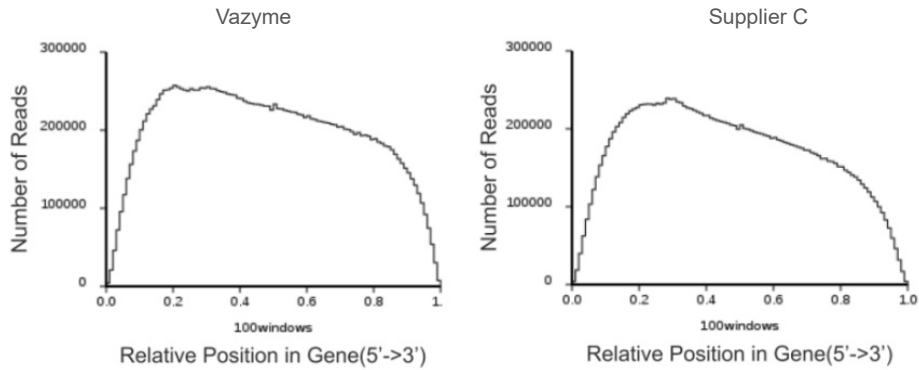


Figure 1 Relative position in gene and number of reads

• High expression replicate correlation

The results show that Vazyme #N711 has higher expression replicate correlation than Supplier C.

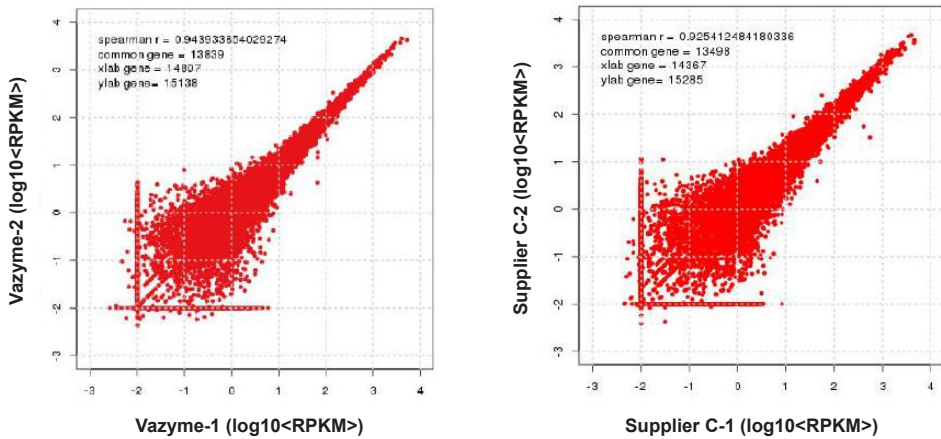


Figure 2 Expression replicate correlation