illumina®

Make room for more **discoveries**

Higher-quality, lower-cost multiomics on the NovaSeq™ X Series and 25B flow cell[1]

Here is what 16 billion MORE reads means for your research:

Single-cell RNA sequencing (scRNA-Seq)	Whole-transcriptome sequencing (WTS)	Whole-genome sequencing (WGS) + WTS
600K more cells[1]	**320** more samples[1]	**40** more samples[1]

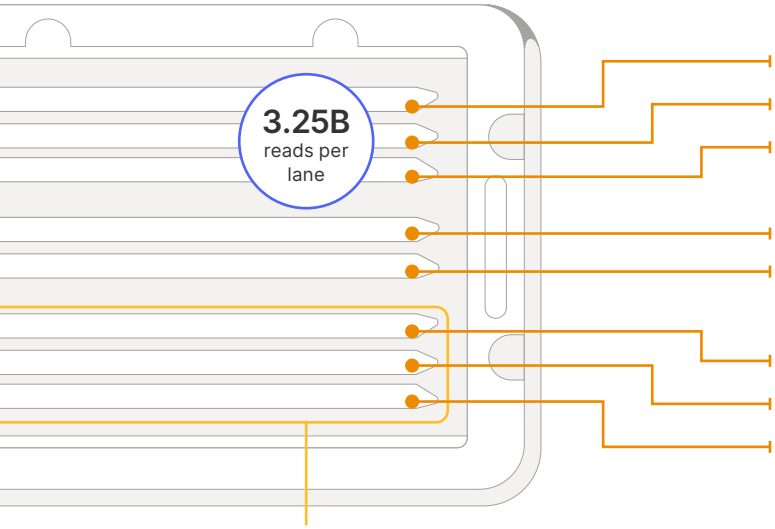
~2.5× more samples for the same budget[1] compared to the S4 flow cell on NovaSeq 6000

Multiomics at a lower cost than one “ome” alone: sequencing both whole exomes and whole transcriptomes on the NovaSeq X Series 25B flow cell is **more cost effective** than running whole-exome sequencing alone on previous platforms.

Be confident in your results with:

- Fewer batch effects
- Better variant calling
- Higher statistical significance

Enable many diverse projects using 8 individually addressable lanes



Three lanes of the new 25B flow cell equal one entire NovaSeq 6000 S4 flow cell

Here is an example of diverse libraries that can be run **simultaneously** on a NovaSeq X 25B flow cell:

- 8 whole genomes
- 5–6 samples whole-genome bisulfite sequencing (WGBS)[2]
- 65 whole transcriptomes[3]
- 130 coding transcriptomes[4]
- 65 samples assay for transposase-accessible chromatin using sequencing (ATAC-Seq)[5]
- 9 samples scRNA-Seq + protein[6]
- 4 samples scRNA-Seq + scATAC-Seq[7]
- 65 samples chromatin immunoprecipitation using sequencing (ChIP-Seq)[8]

With automated independent lane loading and 384 unique dual indexes available, researchers can multiplex over **3000 samples** on a single flow cell.[9]

Multiomics made more accessible on the NovaSeq X Series

3× higher accuracy with XLEAP-SBS™ chemistry[1]

~2× faster[1]

2.5× more flow cells stored in the same refrigerator space[1]

Onboard DRAGEN™ bioinformatics at **no additional cost**[1]

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Learn more about the methods made easier, faster, and more affordable on the NovaSeq X Series

Click here to download the new NovaSeq X eBook

1. Compared to S4 flow cell on NovaSeq 6000 System. WGTS on NovaSeq X Series assumes 7 lanes loaded with WGS libraries, 1 lane loaded with matched WTS libraries, for NovaSeq 6000 System assumes 3 lanes loaded with WGS libraries, 1 lane loaded with matched WTS libraries. 2. Whole-genome bisulfite sequencing assumes 500M reads per sample. 3. Assumes 50M reads per sample. 4. Assumes 25M reads per sample. 5. Assay for transposase-accessible chromatin assumes 50M reads per sample. 6. Assumes 10K cells per sample, 10K reads per cell, 100 reads per antibody derived tag. 7. Assumes 10K cells per sample, 25K reads per cell for scATAC-Seq, 20K reads per cell for scRNA-Seq. 8. Assumes 50M reads per sample. 9. Not guaranteed, actual sample number and read depth requirement may vary.

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