



NOVASEQ X PLUS CONCORDANCE DATA WHOLE TRANSCRIPTOME SEQUENCING

Psomagen labs conducted concordance analysis on our NovaSeq X Plus, and got results that are highly accurate, specific, and sensitive — at levels comparable to the NovaSeq 6000.

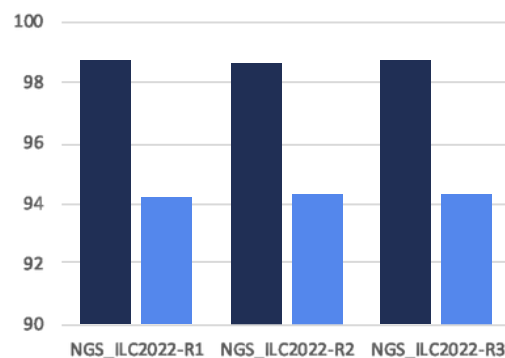
We're thrilled to gather positive results on the NovaSeq X Plus — our lab is continuing to improve our processes and get to know one of the newest members of our fleet. Please [visit our website](#) for additional concordance data, a white paper with further performance details, and much more. Here's to many successful runs to come!

Whole Transcriptome Raw Data Statistics

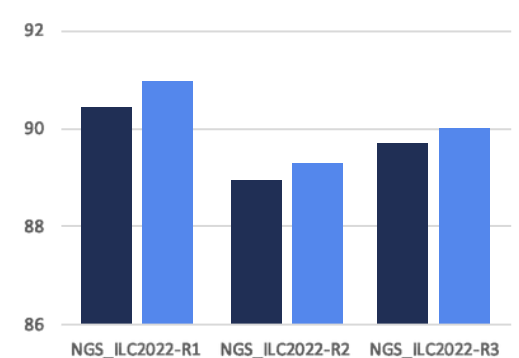
There is a high correlation between NovaSeq X Plus and NovaSeq 6000 with whole transcriptome sequencing. Illumina guarantees $\geq 85\%$ of bases higher than Q30.

Platform	Q30 TruSeq Stranded mRNA Kit	Q30 TruSeq Stranded Total RNA with Ribo-Zero H/M/R
NovaSeq X Plus	90.89	89.76
NovaSeq 6000	95.79	95.78

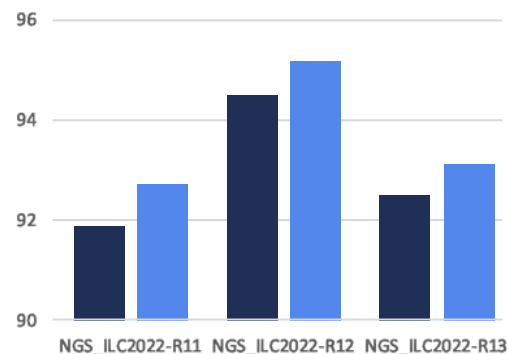
Mapping Rate with mRNA Kit



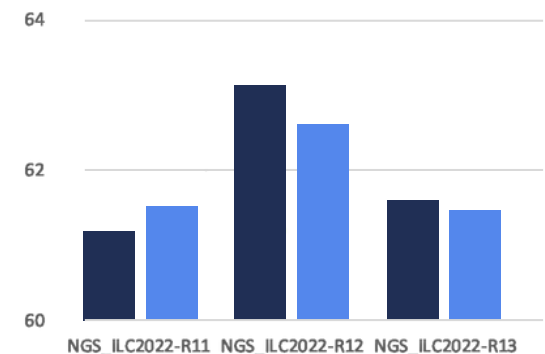
Exonic Mapping Rate with mRNA Kit





Mapping Rate with Ribo-Zero Kit



Exonic Mapping Rate with Ribo-Zero Kit

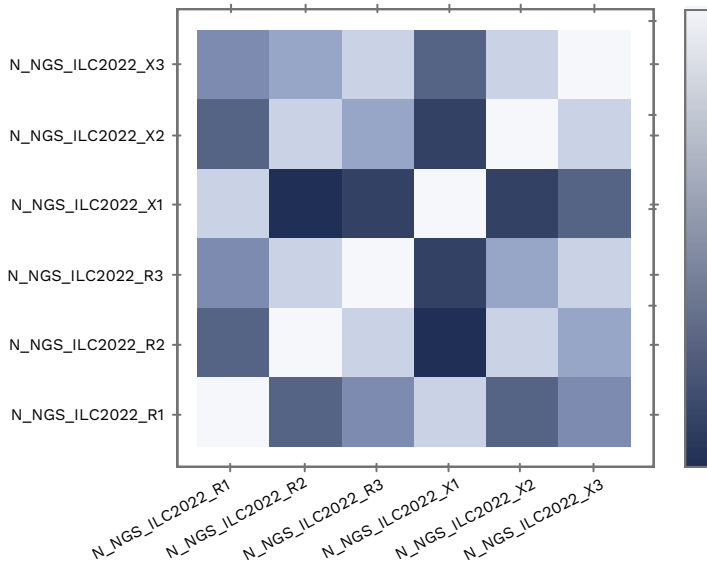


 NovaSeq X Plus
 NovaSeq 6000

High Correlation between NovaSeq X Plus and NovaSeq 6000 Using Whole Transcriptome with TruSeq Stranded mRNA Selection Kit

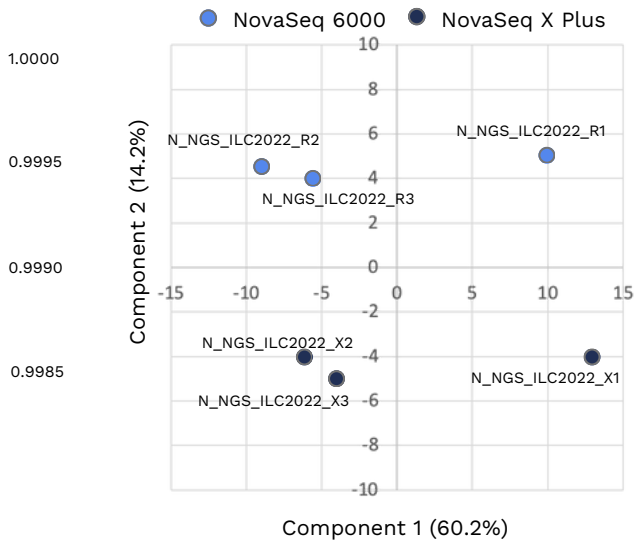
Human Kidney Samples (X1, X2, and X3 from the NovaSeq X Plus and R1, R2, and R3 from the NovaSeq 6000 are replicated samples)

Correlation Matrix for All Samples



The similarity between samples is obtained through Pearson's coefficient of sample's log transformation RLE normalized values. The closer the value is to 1, the more similar the samples are.

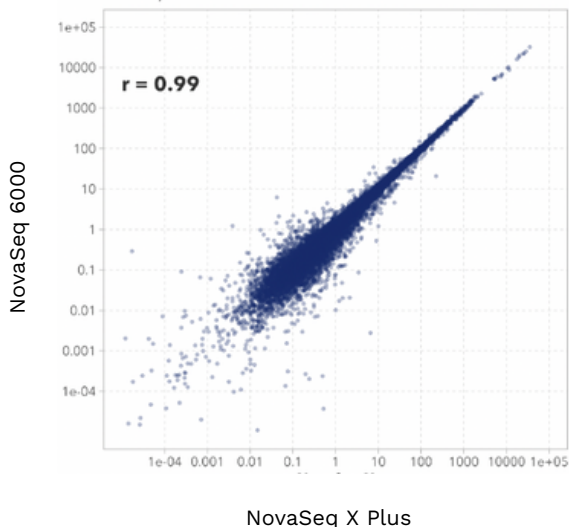
MDS (Multidimensional Scaling)



The similarity between samples is graphically shown in a 2D plot to show the variability of the total data. This graph allows identification of any outlier samples or similar expression patterns among samples.

NGS_IL2022-R1

RNAseq

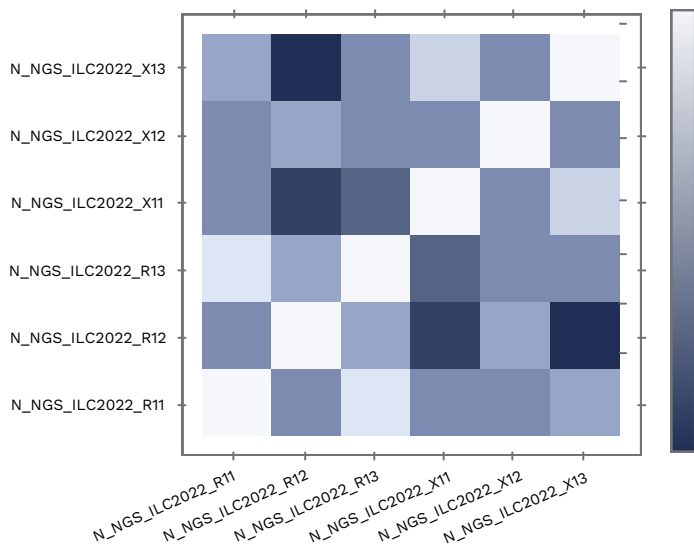


Correlation analysis between NovaSeq X Plus and NovaSeq 6000 data using expression profiling data. Data points were log transformed. Based on the correlation value, all samples show a good concordance result.

High Correlation between NovaSeq X Plus and NovaSeq 6000 Using TruSeq Stranded Total RNA with Ribo-Zero H/M/R Kit

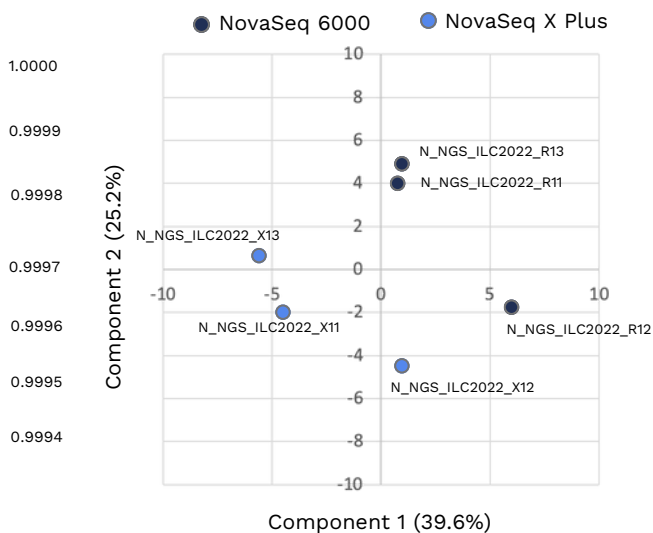
Human Kidney Samples (X1, X2, and X3 from the NovaSeq X Plus and R1, R2, and R3 from the NovaSeq 6000 are replicated samples)

Correlation Matrix for All Samples



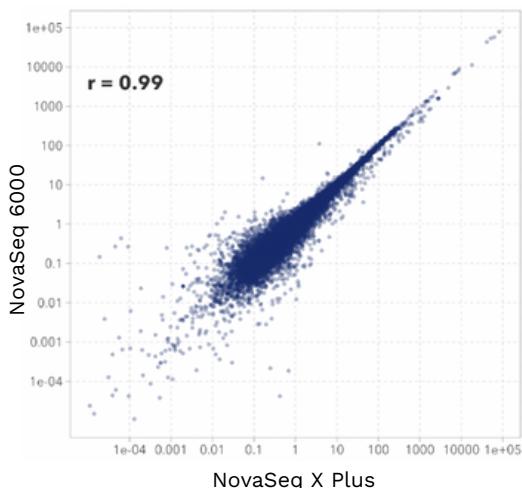
The similarity between samples is obtained through Pearson's coefficient of sample's log transformation RLE normalized values. The closer the value is to 1, the more similar the samples are.

MDS (Multidimensional Scaling)



The similarity between samples is graphically shown in a 2D plot to show the variability of the total data. This graph allows identification of any outlier samples or similar expression patterns among samples.

NGS_IL2022-R11 RNAseq



Correlation analysis between NovaSeq X Plus and NovaSeq 6000 data using expression profiling data. Data points were log transformed. Based on the correlation value, all samples show a good concordance result.