




# NovaSeq X Plus Concordance Data Whole Transcriptome Sequencing

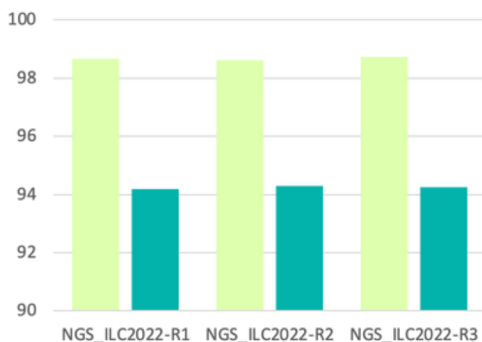
## Whole Transcriptome Raw Data Statistics

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.

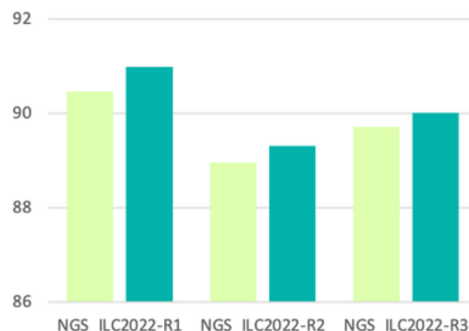
Platform	Q30	Q30
	TruSeq Stranded mRNA Kit	TruSeq Stranded Total RNA with Ribo-Zero H/M/R
NovaSeq X Plus	90.89	89.76
NovaSeq 6000	95.79	95.78

 NovaSeq X Plus       NovaSeq 6000

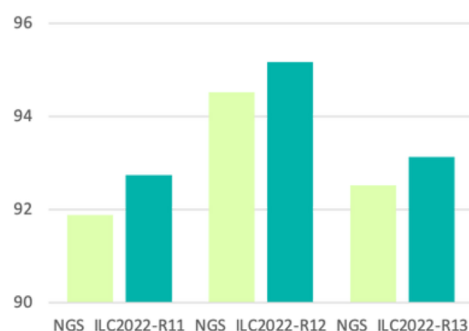
### Mapping Rate with mRNA Kit



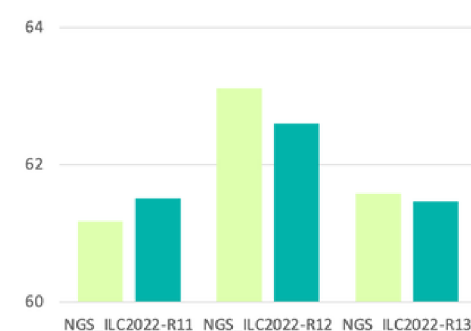
### Exonic Mapping Rate with mRNA Kit



### Mapping Rate with Ribo-Zero Kit



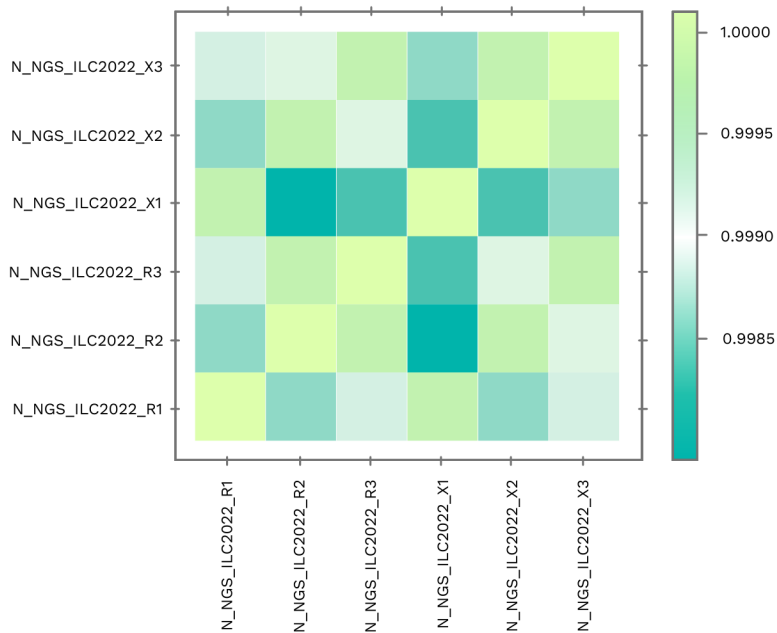
### Exonic Mapping Rate with Ribo-Zero Kit



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

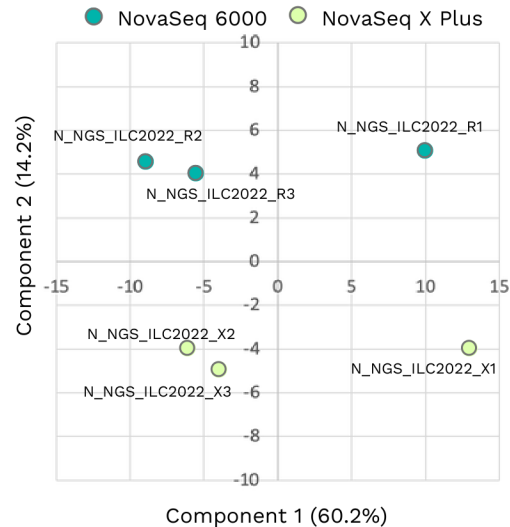
Human Kidney Samples (X1, X2, and X3 from the NovaSeq X Plus and R1, R2, and R3 from the NovaSeq 6000 are replicated samples)

**Correlation Matrix for All Samples**



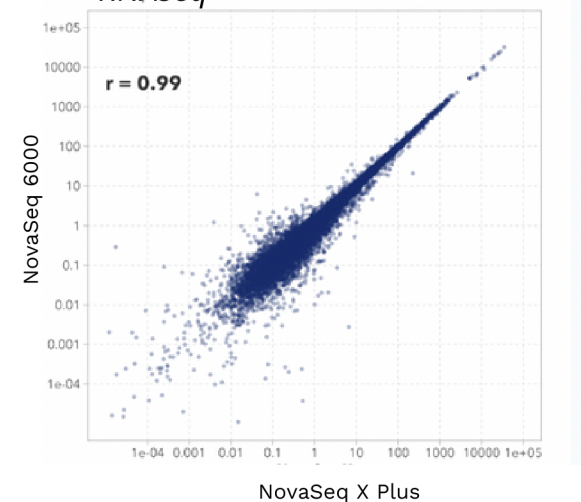
The similarity between samples is obtained through Pearson's coefficient of sample's log transformation RLE normalized values. The closer the value is to 1, the more similar the samples are.

**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\_ILC2022-R1  
RNAseq**

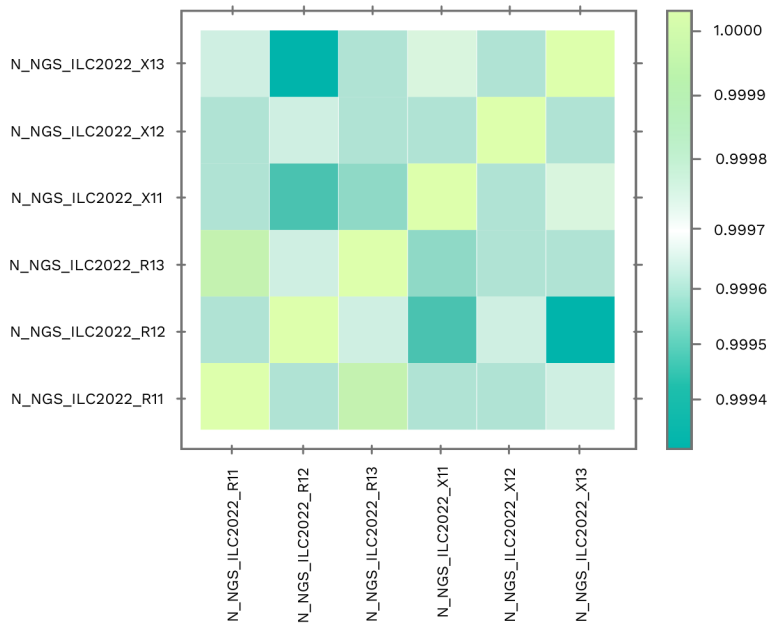


Correlation analysis between NovaSeq X Plus and NovaSeq 6000 data using expression profiling data. Data points were log transformed. Based on the correlation value, all samples show a good concordance result.

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

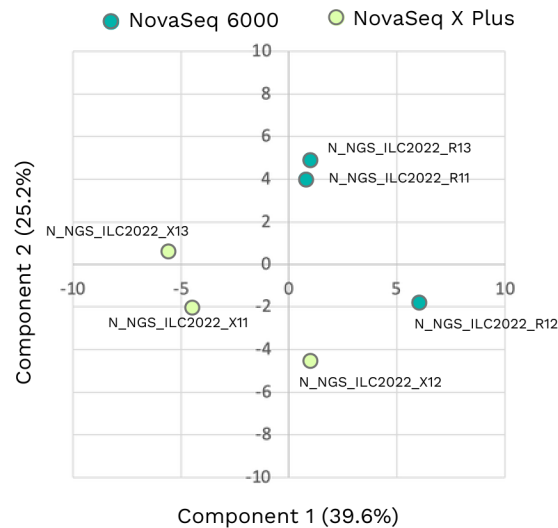
Human Kidney Samples (X1, X2, and X3 from the NovaSeq X Plus and R1, R2, and R3 from the NovaSeq 6000 are replicated samples)

## Correlation Matrix for All Samples



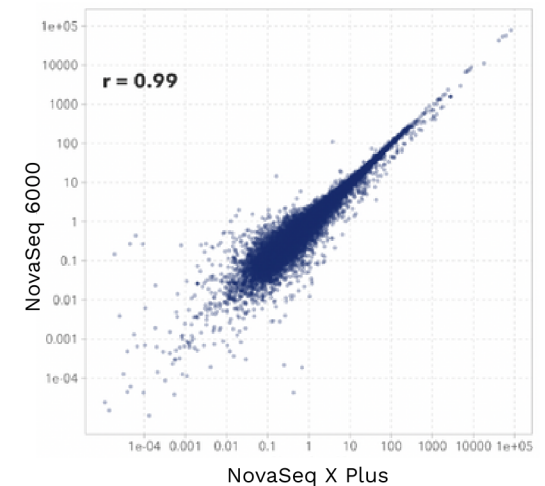
The similarity between samples is obtained through Pearson's coefficient of sample's log transformation RLE normalized values. The closer the value is to 1, the more similar the samples are.

## 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.