Technical note

DNBSEQ-T7 & Olink® Explore Platform - Overview of Compatibility Test

Background

Olink Explore products empower genomics studies by enabling targeted discovery of novel and biologically relevant protein biomarkers. The Explore series offers advanced multi-target proteomics assays with high specificity and throughput capabilities via sequencing platforms. This cutting-edge approach utilizes two uniquely labeled oligonucleotide antibodies for targeted protein binding, driving high specificity and sensitivity in the measurement of protein abundance with minimal sample requirements. Olink® Explore HT model further extends its prowess, with the ability to simultaneously quantify the concentrations of in excess of 5400 proteins on 172 samples. Remarkably, the detection range of proteins spans 84% of established signaling pathways, providing an extensive and insightful survey of the proteomic terrain.

DNBSEQ-T7, a high-throughput sequencing platform engineered by MGI, has garnered widespread application across genomics and multi-omics research domains. This platform is underpinned by MGI's exclusive DNBSEQ™ technology and boasts a suite of thoroughly refined biochemical, fluidic, and optical systems. Capable of delivering up to 7 Tb of premium data within a mere 24-hour window. Additionally, DNBSEQ-T7 also offers a constellation of distinctive benefits, including its ultra-high throughput, elevated accuracy, minimized duplication rates, and reduced index hopping, setting a new benchmark for sequencing performance.

To empower DNBSEQ-T7 users to harness Olink's exceptional high-throughput and precision detection capabilities for avant-garde proteomics investigations, we have meticulously crafted an experimental protocol has been tailored to adapt Olink Explore HT with the DNBSEQ-T7 system. Furthermore, We have conducted a comparative analysis of the test outcomes against those obtained from previously validated workflows. This Technical Note is dedicated to delineating the insights gleaned from these experimental endeavors.

Methods

Effectiveness and repeatability

In this investigation, two proximity extension assay (PEA™) libraries were synthesized utilizing select standard plasma specimens, following the Olink Explore HT library preparation protocol.

These libraries underwent sequencing on one Illumina NovaSeq 6000 S4 flow cell each. Subsequently, the identical libraries were subjected to sequencing on the DNBSEQ-T7 platform, with each library distributed in two flow cells and sequenced concurrently in a singular run.

Real sample pilot

In this experiment, in a preliminary assessment, plasma samples from a cohort of 66 male and 66 female healthy individuals were utilized. These samples were processed into Olink Explore HT libraries by SEQUANTA, a preeminent entity in multi-omics research and clinical service provision. The resulting library was concurrently sequenced using both the NovaSeq 6000 and DNBSEQ-T7 platforms.

Experiment protocol

All PEA libraries were produced in accordance with the Olink Explore HT protocol and underwent circularization with the MGIEasy® Olink Library Circularization Set. This procedure facilitated the circularization of the library without the necessity for PCR amplification, followed by enzymatic digestion and bead-based purification steps. The libraries were quantified using the Qubit® DNA assay, and calibrated quantities of the libraries were employed in the sequencing process on the DNBSEQ-T7 platform.

The output data folder generated by the sequencer was subjected to preprocessing using software developed by Olink, known as ngs2counts. Quality control and analysis of the results were conducted using Olink's NPX™ Explore software. The comparative analysis of the data was also executed by Olink.

Results

Effectiveness and repeatability

The results were highly correlated between the two platform. Figure 1 compares the matched counts (left) and NPX values (right) from the same library sequenced on the Illumina NovaSeq 6000 and the MGI T7 system, showing high correlation both before and after normalization. Other evaluated parameters, including signal-to-noise ratio and detectability, also showed comparable performance between the platforms (data not shown).

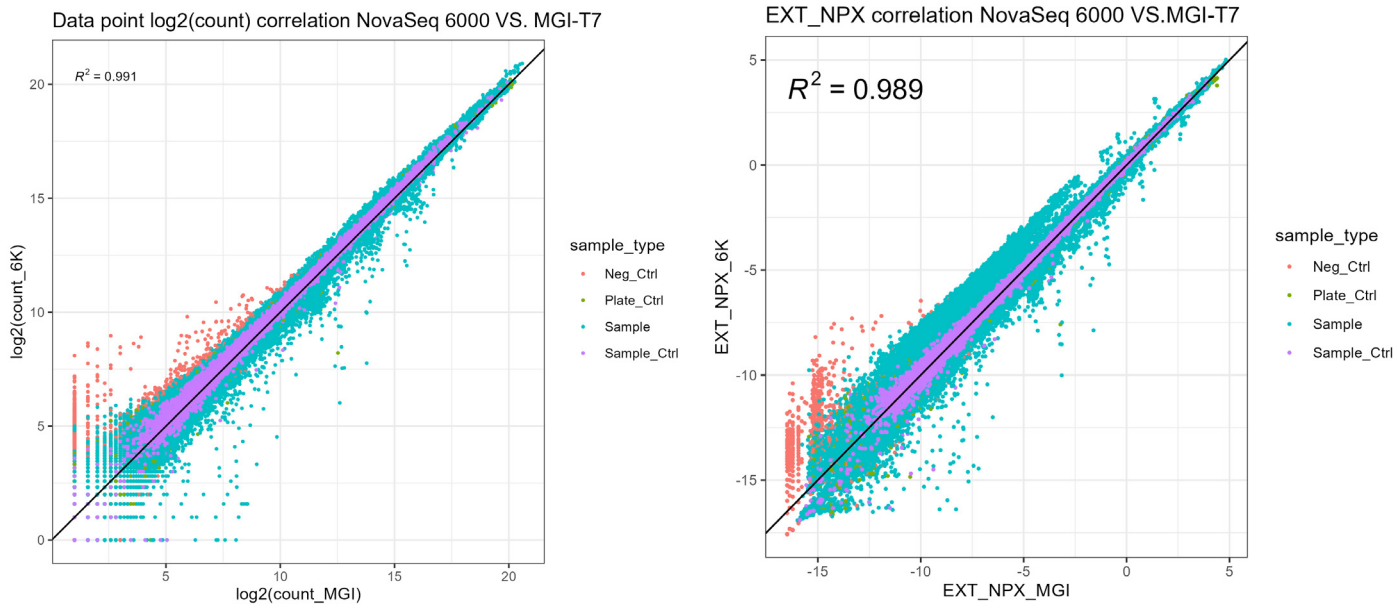

Fig 1. Analysis of Olink Explore HT libraries that were sequenced on either Illumina's NovaSeq 6000 or MGI's DNBSEQ-T7, either based on matched counts (left) or NPX values (right). The results show high correlation between the platforms.

Real sample pilot

Analysis of the Pilot study shows that biological differences in protein abundance between male and female can be detected using the combined Olink Explore HT and MGI T7 solution, as seen in Figure 2. The analysis further shows that the differences in NPX values between male and female when sequenced on NovaSeq 6000 and T7, seen in figure 3, are highly correlated, showing that the biology is recreated across the platforms.

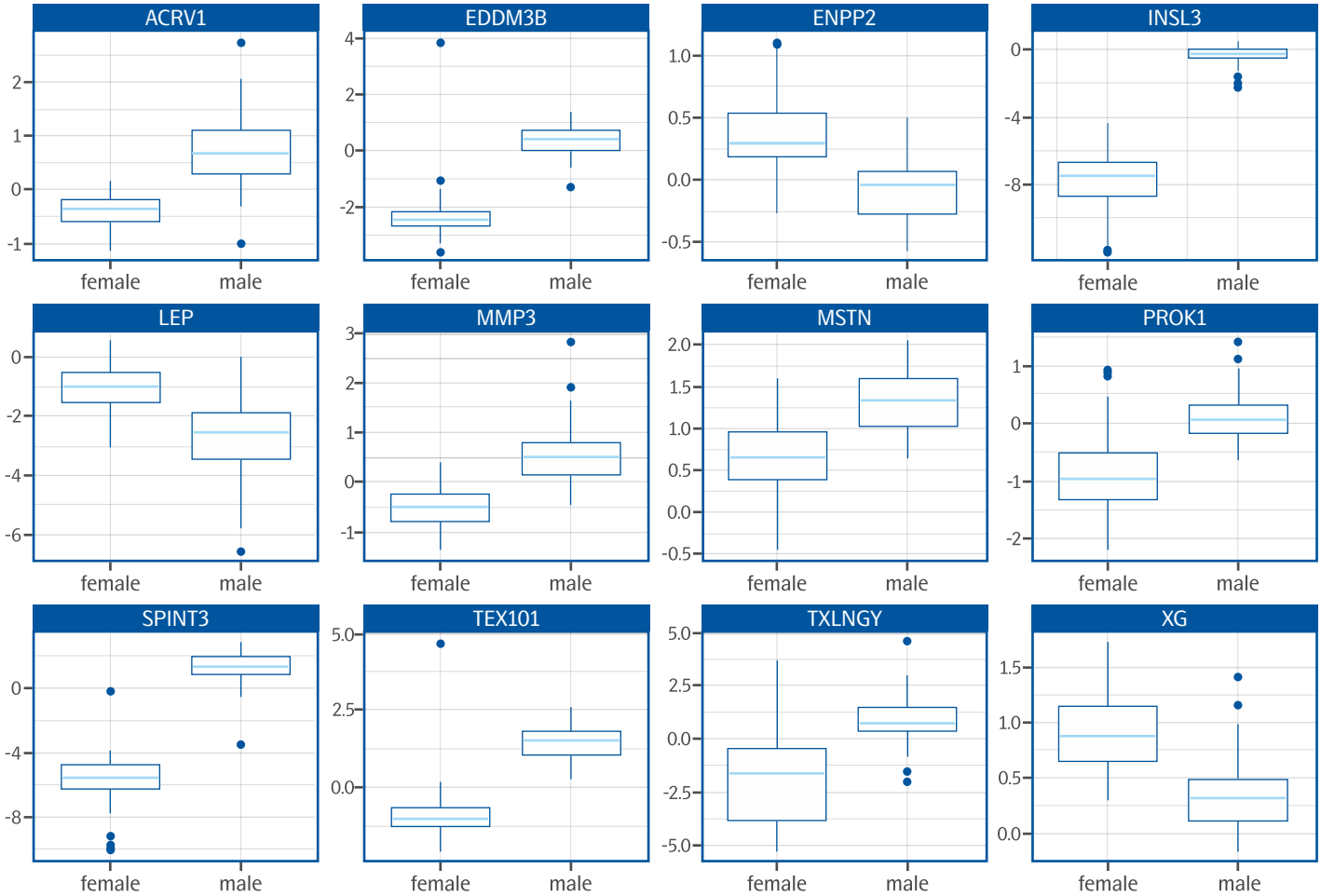

Fig 2. Distribution of NPX values for the twelve proteins in the pilot study that were most differentiated between females and males, including proteins which are believed to play a role in testicular function (INSL3)[1], sperm maturation (EDDM3B)[2] and fertilization (TEX101)[3].

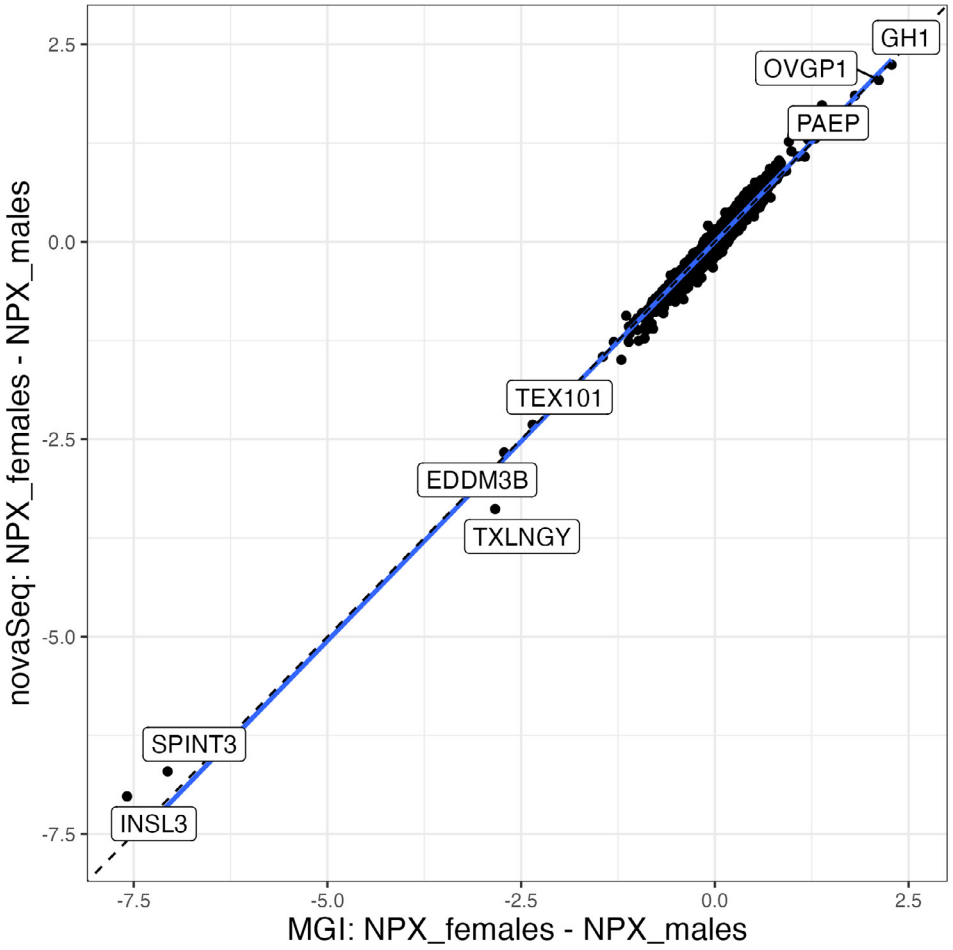

Fig 3. Difference in NPX values between males and females when sequenced on MGI T7 and Illumina NovaSeq 6000. The high correlation shows that the biology is recreated across the platforms.

Conclusion

The findings demonstrate exceptional data quality and strong compatibility between Olink® Explore HT and the MGI DNBSEQ-T7. This indicates that the MGI NGS system could serve as a viable detection alternative for Olink® Explore, expanding accessibility to this high-plex proteomics solution throughout the NGS ecosystem.

References

1. https://www.uniprot.org/uniprotkb/P51460/entry
2. https://www.uniprot.org/uniprotkb/P56851/entry
3. https://www.uniprot.org/uniprotkb/Q9BY14/entry

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