

Development of a high-throughput, miniaturized, semiautomated rapid transduction inhibition assay (TIA) for the characterization of anti-AAV antibodies in gene therapy

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Introduction

- Adeno-associated virus (AAV) is a commonly used vector for gene therapy because it is relatively simple to engineer and is non-pathogenic.¹
- However, most people will be exposed to at least one strain of AAV during their lives, resulting in development of anti-AAV antibodies that can reduce or eliminate the efficacy of AAV-based gene therapy.
- Transduction inhibition assays (TIAs) are functional cell-based assays that estimate the extent of AAV neutralization in patient plasma to determine patient eligibility for AAV gene therapy.²
- We previously described the development of a 6-hour (rapid) and 24-hour TIA method, which was subsequently validated.³
- This assay is suitable for determining titers of neutralizing antibodies (NAbs) in prospective gene therapy patients, but throughput limitations hinder use in population-based seroprevalence studies.

Objective

- To develop a high-throughput TIA via miniaturization and automation that will enable more widespread seroprevalence assessments and novel capsid screening.

Methods

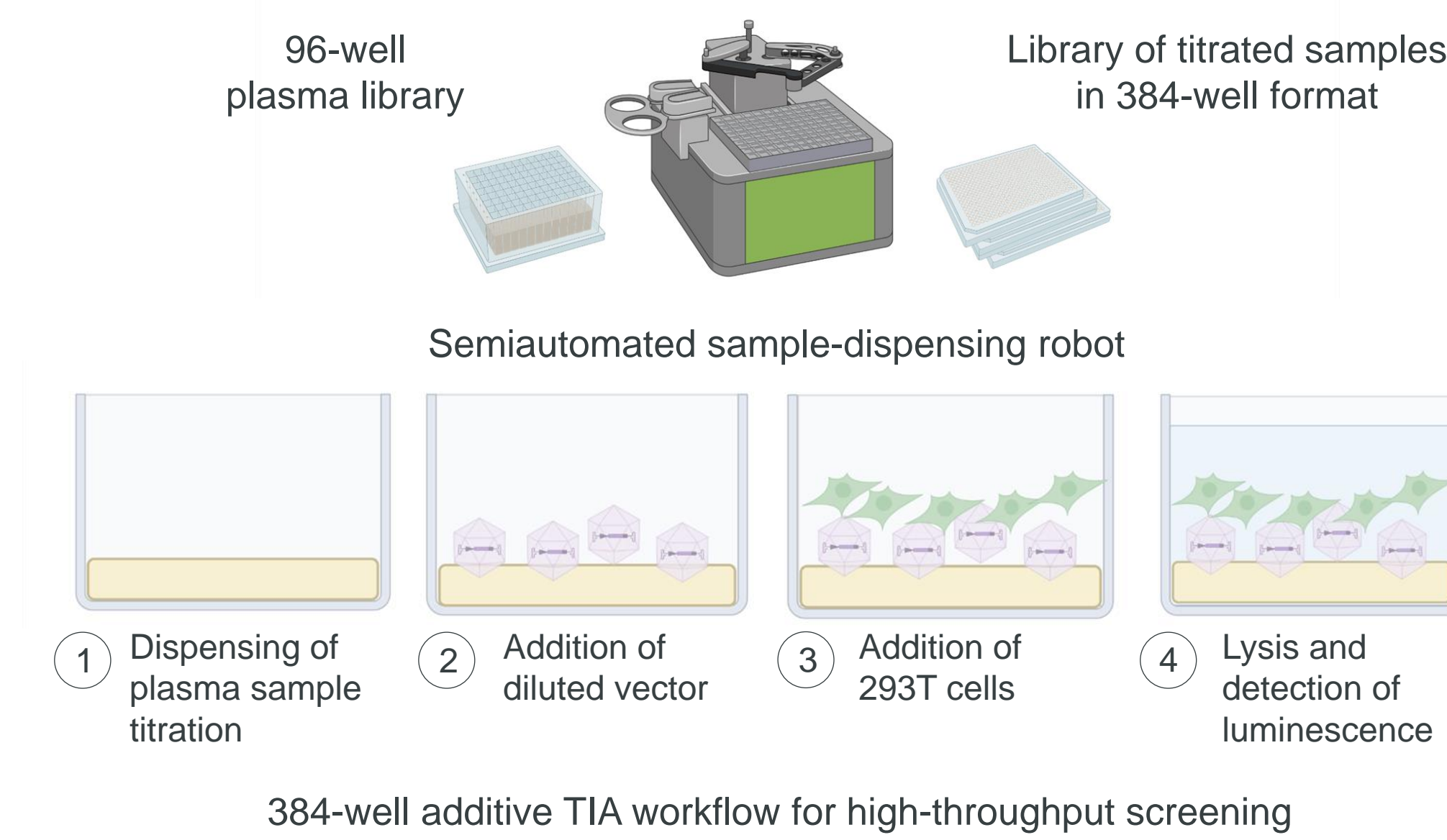
Development of a semiautomated, additive assay workflow

- 96 plasma samples (76 male and 20 female) were purchased from a commercial supplier of normal donor plasma and aliquoted into a screening-ready library in a 96-well format (**Figure 1**).
- A precision liquid handler (Mantis®, Formulatrix) was used to develop a protocol for serial titration and dispensing of samples and controls into a 384-well plate, allowing simultaneous assay of 8 samples per plate.
- Previously validated 96-well TIA parameters, such as plasma dilution, multiplicity of infection (MOI), and cell number, were retained and developed into an additive format with automated dispensing of samples, viral vector, cells, and detection reagent.

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Figure 1: Outline of assay workflow for HTS-TIA



Optimization of MOI and assay workflow

- To enable testing of combinations of AAV serotypes and cell lines with reduced transduction efficiency, MOIs of 5 and 50 were investigated.
- To facilitate screening, a continuous and an 'interrupted' workflow, in which plates with pre-dispensed plasma sample dilutions were stored at -20° C for a prolonged period prior to running the TIA, were tested.

Screening of the plasma library

- The 96-sample plasma library was screened using the assay workflow for AAVS3 vector in human embryonic kidney 293T (HEK293T) cells.
- Half-maximal inhibitory concentration (IC50) and goodness-of-fit data were extracted from four-parameter fitting software, and signal to background (S/B) ratios and Z' values were calculated.

Results

Effect of MOI on assay performance

- Five plasma samples of increasing neutralizing capacity with an MOI of 5 (validated) and 50 (10-fold increase) were tested.
- No significant differences in IC50s were observed (**Figure 2**).

Effect of 'interrupted' workflow on assay performance

- Eight plasma samples of increasing neutralizing capacity with the continuous and 'interrupted' workflows were tested.
- No significant differences in IC50s were observed (**Figure 3**).

Figure 2: Effect of MOI on assay performance

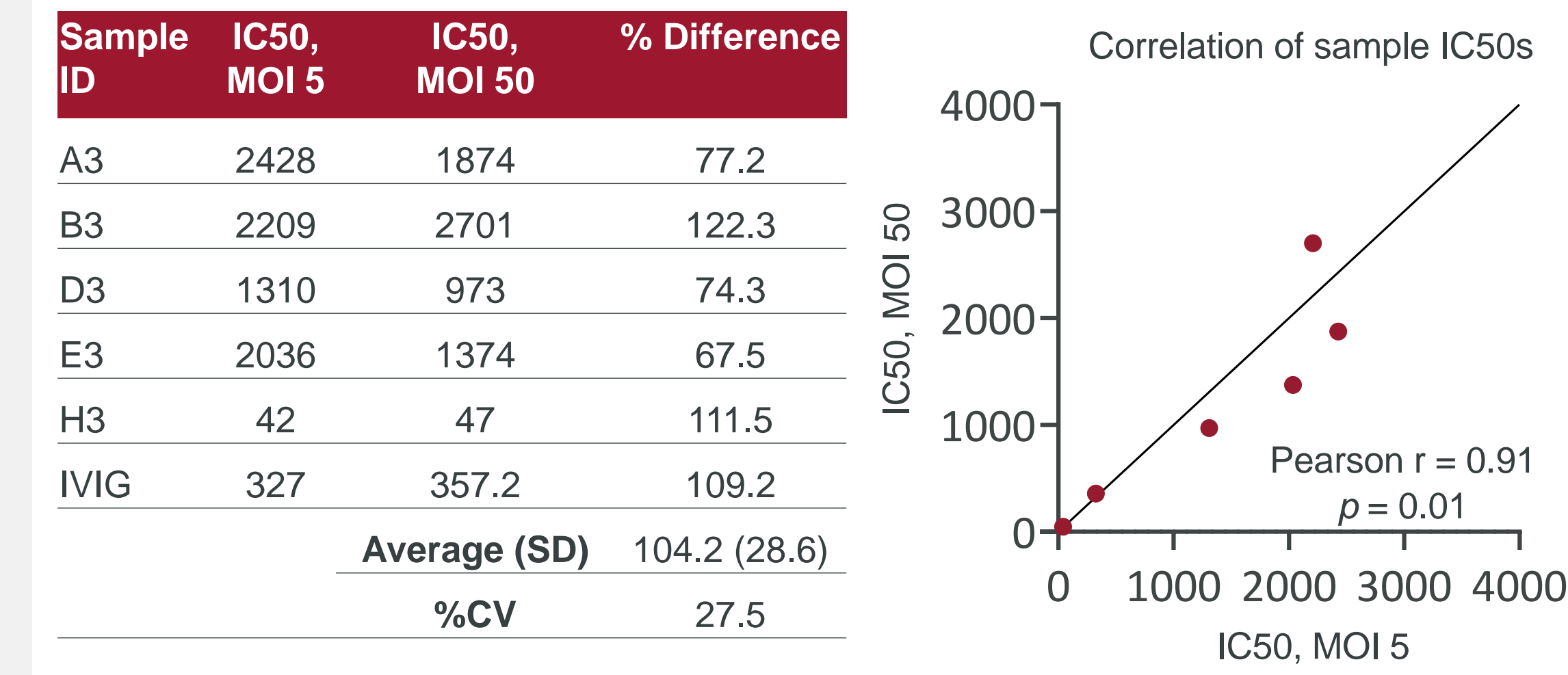
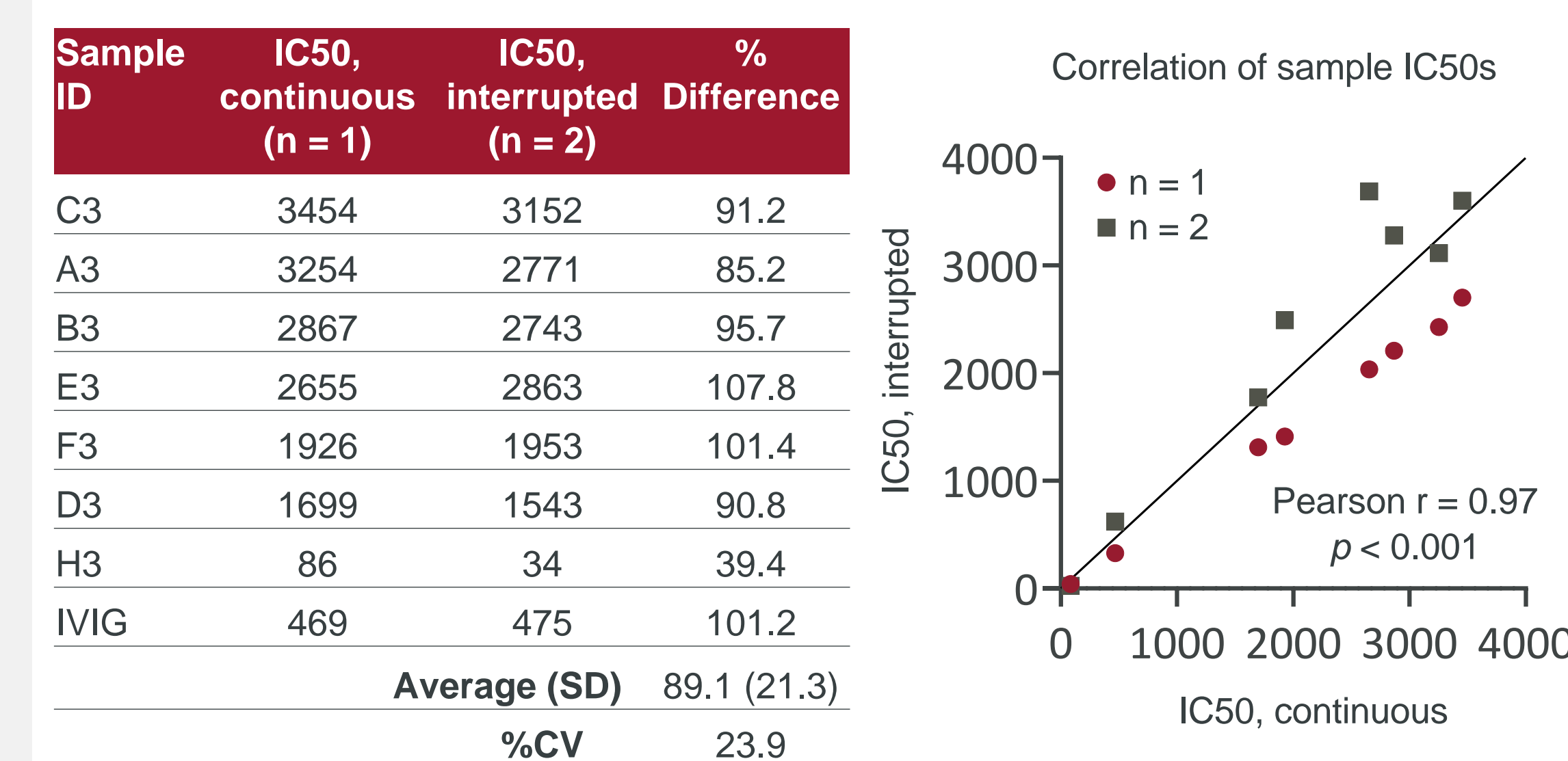


Figure 3: Effect of 'interrupted' workflow on assay performance



Screening of the plasma library and assay performance characteristics

- The 96-sample plasma library was screened using 15 assay plates over three occasions, the last of which retested out-of-range samples.
- The mean S/B ratio was 474, and the mean Z' value was >0.5 (**Figure 4**).
- Intravenous immunoglobulin (IVIG), the positive control included on each plate, had an IC50 of 0.63 µg/mL and R² of 0.97 (**Figure 4**).
- Median (range) IC50 across samples was 3040 (50, 32000).
 - Ten samples exceeded 32000, and 11 samples were under the detection limit of 50 (**Figure 5**).
- Median IC50 values were 2825 and 4166 across 76 male and 20 female donors, respectively.

LLOQ, lower limit of quantification; MOI, multiplicity of infection; S/B, signal to background; SD, standard deviation; TIA, transduction inhibition assay; ULOQ, upper limit of quantification

Figure 4: Summary of assay performance

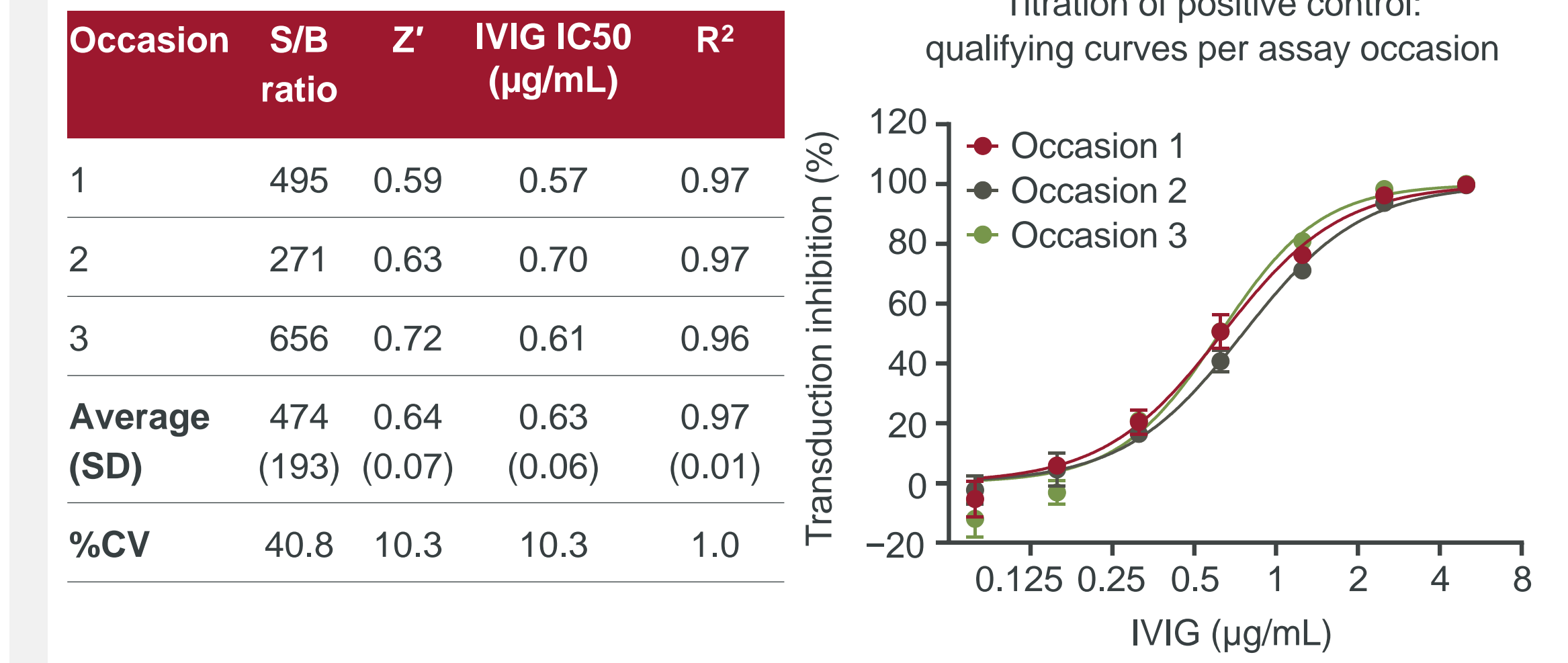
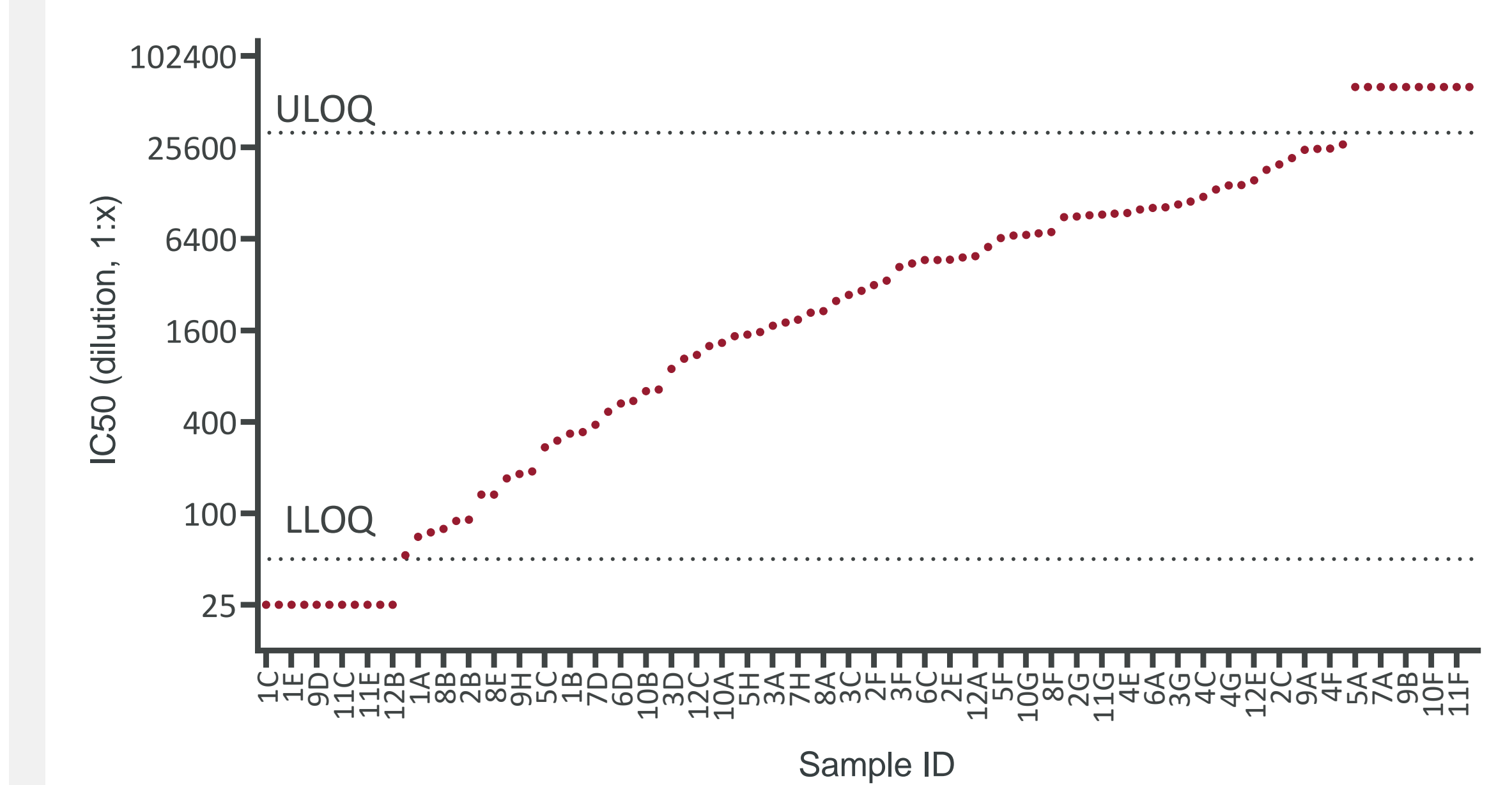


Figure 5: IC50 of 96 plasma samples by AAVS3 HTS-TIA



Conclusions

- A high-throughput 384-well TIA was developed, which showed a 6-fold increase in productivity compared to a prior validated TIA.
- There were no significant differences in IC50s at MOIs of 5 and 50, which enables testing of different serotype and cell line combinations.
- This work shows that once cumbersome functional cell-based assays, such as TIA, can be scaled up and standardized, thereby facilitating pre-clinical and clinical development of gene therapies.

References: 1. Naso MF *et al. BioDrugs* 2017;31(4):317–34. 2. Calcedo R and Wilson *J Front Immunol* 2013;4:341. 3. Shehu E *et al. Haemophilia* 2020;26(Suppl 2):P011.