**Accuracy Results – User-Flagged Standards (Test 5)**

Using your manually flagged standard concentrations:

* **Mean Accuracy:** 100.28%
* **Minimum Accuracy:** 91.96%
* **Maximum Accuracy:** 109.58%
* **Number of Standards:** 7

🔍 Excellent performance: all standard backfits are within ±10% of expected values.

**Precision Summary – Test 5**

Based on replicate wells with the same sample label:

* **Mean %CV:** 22.97%
* **Best (Min) %CV:** 1.13%
* **Worst (Max) %CV:** 82.08%
* **Number of Replicate Groups:** 21

⚠️ While some groups show excellent reproducibility, the overall average is **higher than the ideal <15% threshold**. This suggests issues with pipetting, plate handling, or well inconsistencies.

**Recovery Summary – Test 5**

One valid spiked vs. unspiked pair was detected (based on shared Categ):

* **Mean Recovery:** 66.12%
* **Min / Max Recovery:** 66.12%
* **Number of Recovery Pairs:** 1

⚠️ While this recovery is below the acceptable range (typically 80–120%), one data point isn't sufficient for meaningful evaluation. This could be due to:

* Incomplete mixing or pipetting loss
* Matrix effects suppressing signal
* Misalignment of spiked/unspiked pairings

It looks like only the **PC group** has valid OD and calculated concentration data across both spiked (PC2, PC4) and unspiked (PC1, PC3) replicates. The **TE group** currently lacks sufficient valid data — likely due to:

* Missing OD values
* Failed concentration back-calculation for one or more TE samples
* **Current Valid Recovery Pair**

| **Group** | **Unspiked Mean (pg/mL)** | **Spiked Mean (pg/mL)** | **Recovery (%)** |
| --- | --- | --- | --- |
| PC | 887.29 | 1473.97 | **66.12%** |