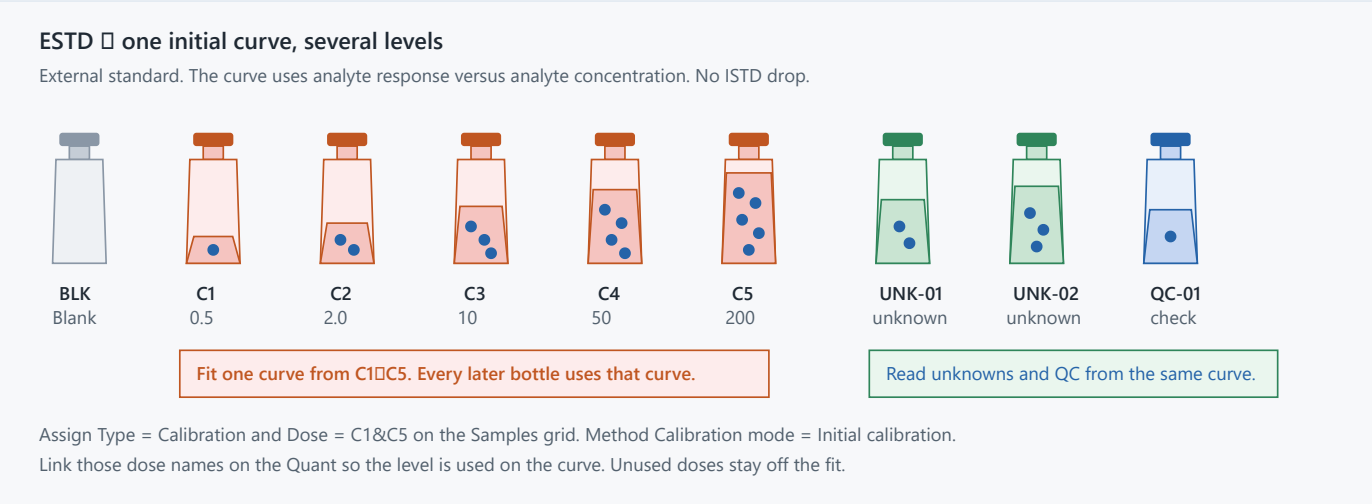
QUANTO USER GUIDE

ESTD initial calibration

External standard, multi-level, one curve.

External standard. The target is in the calibration bottles at known levels. Samples have an unknown amount. There is **no ISTD drop**. One curve serves the whole batch.



Blank, C1–C5, unknowns, and QC

When to use it

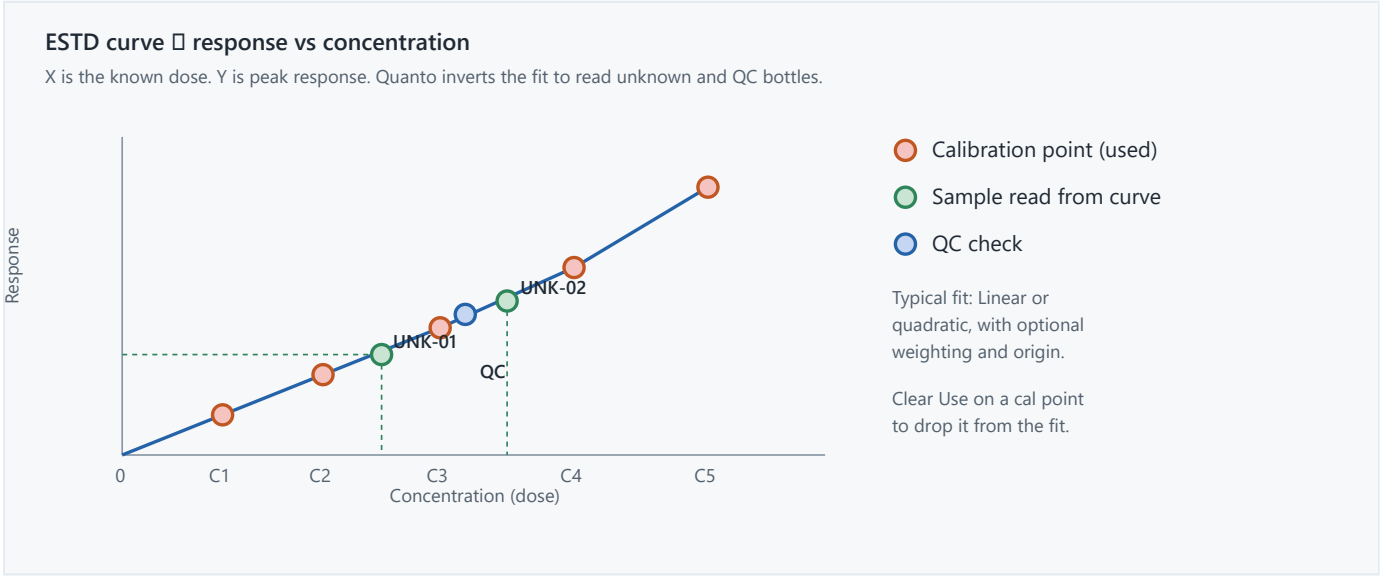
- One instrument, one acquisition method.
- You trust injection volume and recovery enough not to spike an ISTD.
- You ran a full multi-level set once (or you will reuse a saved method curve — see multi-batch).

Method **Calibration mode** = **Initial calibration**. Quant **ISTD** column empty.

Set it up

1. Import or build the method. Create dose names **C1**, **C2**, **C3**, … and type the concentrations on each analyte.
2. On the Quant, assign those doses (Quant doses). Only assigned doses go on the curve.
3. Add the sequence. Mark bottles: - Blank → Type **Blank** - Standards → Type **Calibration**, Dose **C1** … **C5** - Checks → Type **QC**, Dose of the check level - Unknowns → Type **Sample**
4. **Analyze**.

How the curve is read



Response versus concentration with unknowns read from the line

Axis	Value
X	Known dose concentration (÷ sample dilution)
Y	Peak response

Quanto fits the Quant's **Curve fit** (linear, quadratic, average response factors, power, first- or second-order ln), with the Quant's weighting and origin. It then inverts the fit for every Sample and QC.

A blank is not a curve point. Use it to confirm the target is gone, not to pin the origin, unless you chose a through-origin fit.

Multi-level rules

- Two or more distinct levels: the chosen fit is used.
- A single level: Quanto forces **average of response factors** through the origin so the one point can still be inverted.
- Clear **Use** on a point to drop it. The rest of the batch keeps the same curve (initial calibration is global).

After Analyze

- Residuals and back-calculated concentrations appear on the calibration rows.
- QC is read like a sample and flagged if it misses the method limits.
- Sample **FinalConcentration** = curve concentration × **Dilution**.

Next: add an ISTD (ISTD), split the sequence into brackets (bracketing), or keep this curve and update only some levels later (multi-batch).