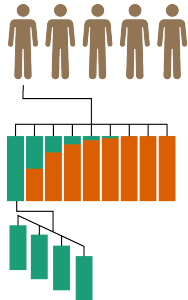


# A Assessment Dataset



Bioinformatic Pipeline

	Count Table															
	PreA	PreB	PreC	PreD	T1A	T1B	T1C	T1D	T2A	T2B	T2C	T2D	T3A	T3B	T3C	T3D
A																
B																
C																
D																
E																
F																
G																
	PostA	PostB	PostC	PostD												

# B Feature Types

Unmixed-Specific

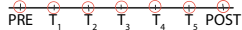


Qual AFP Spar Rel Diff

Qual	AFP	Spar	Rel	Diff
Unmixed-Specific	Yes	Yes	No	No
Titration-Specific	Yes	Yes	No	No
Pre-Specific	No	Yes	Yes	No
Pre-Dominant	No	Yes	Yes	No
Post-Specific	No	Yes	No	Yes
Post-Dominant	No	Yes	No	Yes
Informative	Yes	Yes	Yes	Yes

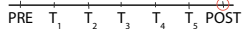
Features only observed in unmixed samples (PRE or POST)

Titration-Specific



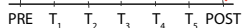
Features only observed in titrations.

Pre-Specific



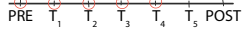
Features observed in all PRE PCR replicates and no POST PCR replicates.

Pre-Dominant



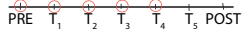
Features observed in all PRE PCR replicates and one or more POST PCR replicates with a log FC > 5 between PRE and POST.

Post-Specific



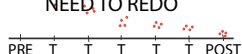
Features observed in all POST PCR replicates and no PRE PCR replicates.

Post-Dominant



Features observed in all POST PCR replicates and one or more PRE PCR replicates with a log FC < -5 between PRE and POST.

Informative



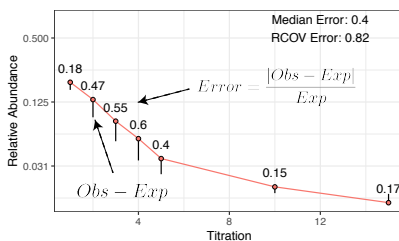
Features present in all or none of the PRE and POST PCR replicates, observed in any 14 of 28 titration PCR replicates, and a 2-fold different between PRE and POST.

# C Assessment Metrics

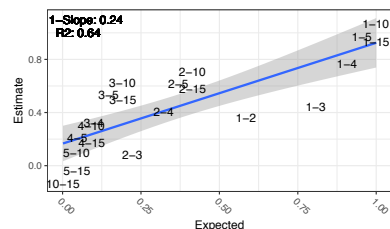
Sparsity

$$\frac{\#0s}{\text{Total Cells}} = 0.##$$

Relative Abundance



Differential Abundance



$$RCOV = \frac{IQR(Error)}{Median(Error)}$$