

Goal: Study the effect of the **cooling process** and **Feed** on the tenderness of pork

Design: 72 pigs were fed either with High or Low feed (H vs L)

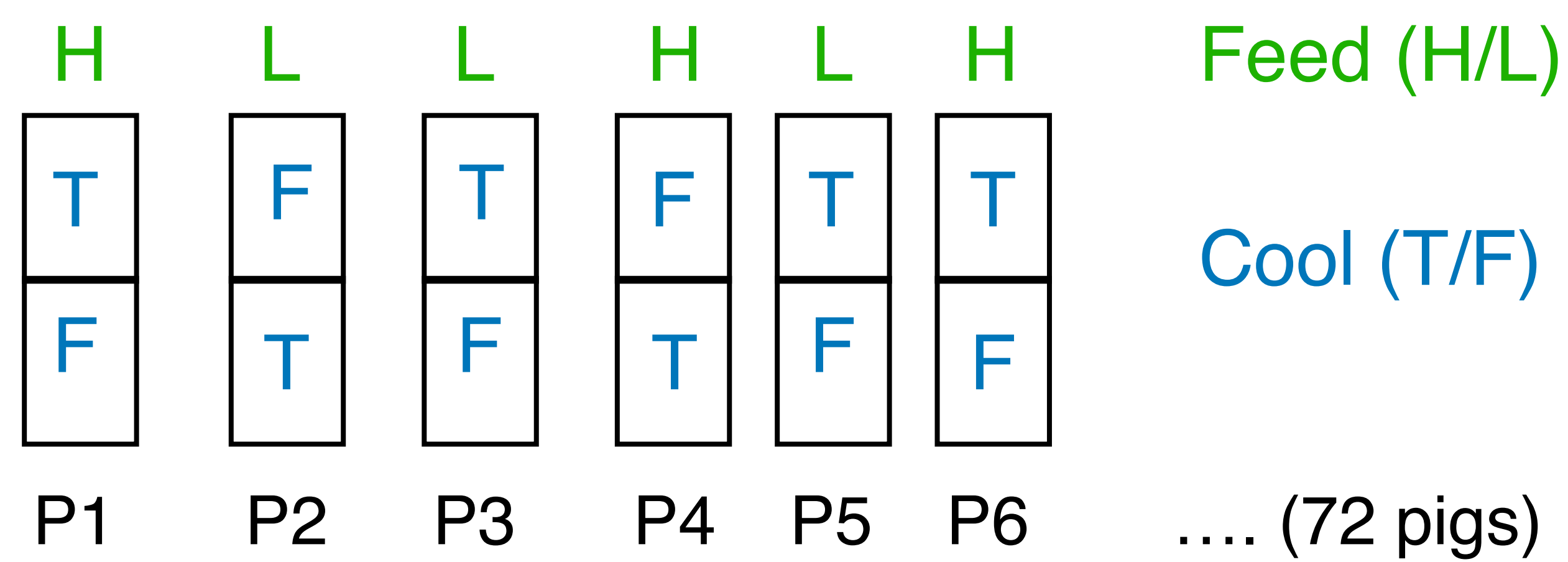
Two cuts were made on the right side of each carcass, and each cut was treated with either Tunnel cooling, or Fast (conventional) cooling.

After a storage period the tenderness of each piece was measured

Structure	Variable	#levels	Block	EU

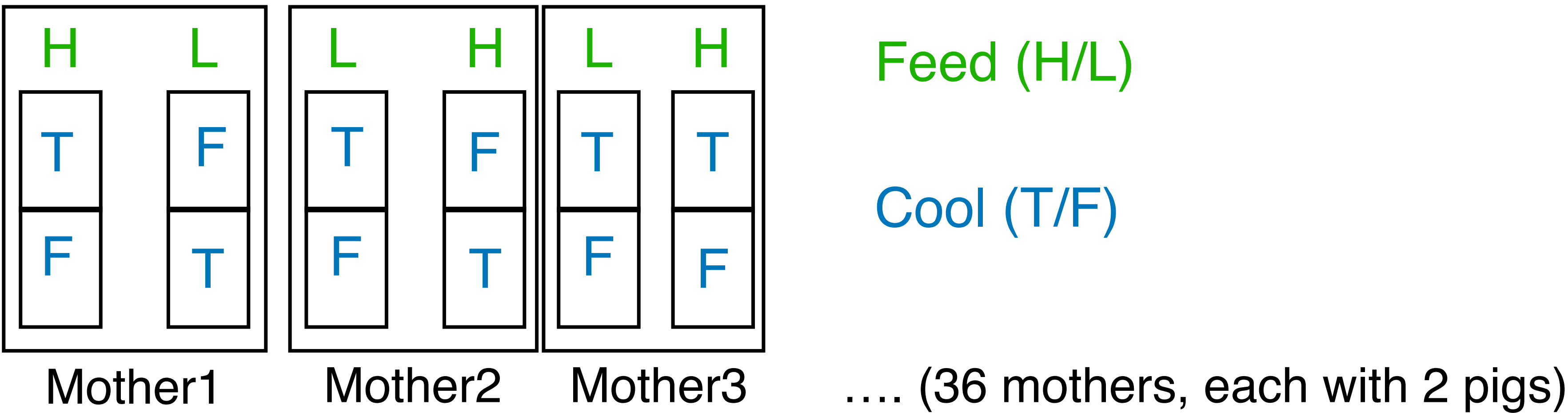
What **questions** should we ask?

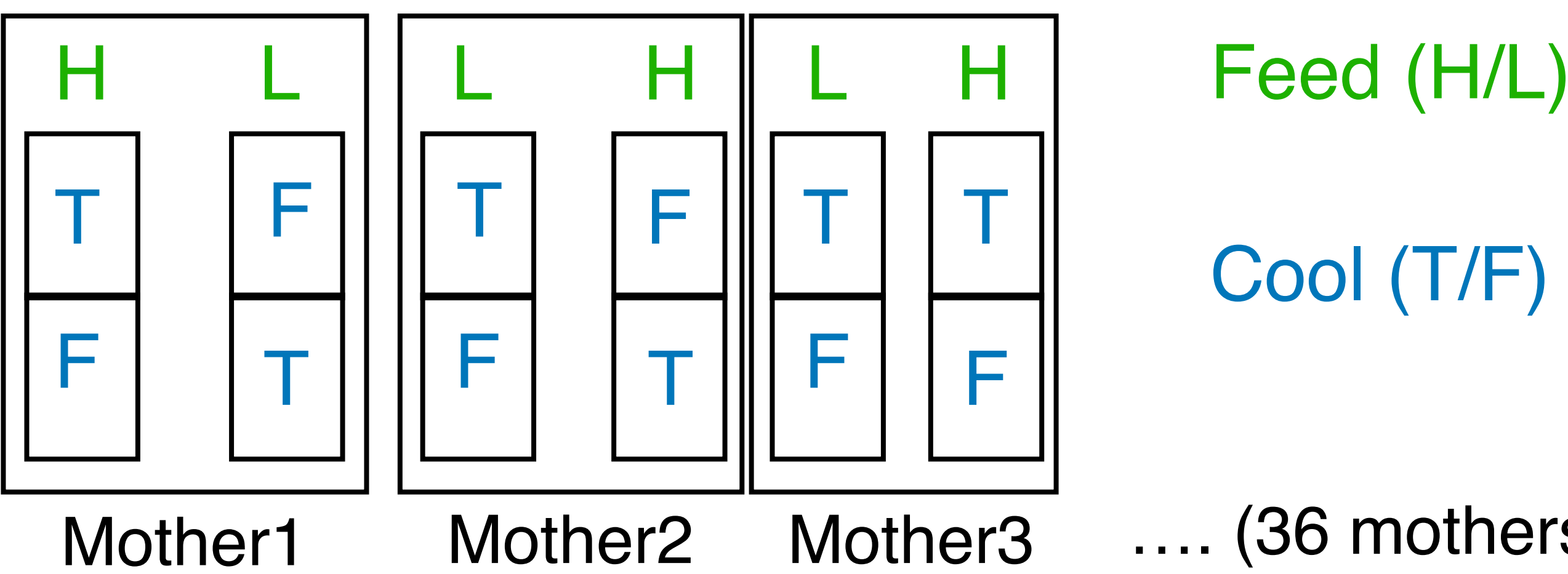
What **contrasts** should we estimate?



Structure	Variable	#levels	Block	EU
Focal	Feed	2	Cool	Pig
Moderator	Cool	2	Pig	Cut
Combo	Feed:Cool	4	Pig	Cut
Design	Pig	72		
	Cut	144		
	Cool:Pig	144		
	Feed:Cool:Pig	144		
Response	Tenderness	144		

lmer(Tenderness~Feed+Cool+Feed:Cool+(1|Pig))





Structure	Variable	#levels	Block	EU
Focal	Feed	2	Cool, Mother	Pig
Moderator	Cool	2	Mother, Pig	Cut
Combo	Feed:Cool	4	Mother, Pig	Cut
			Cool:Mother	
Design	Mother	36		
	Pig	72		
	Feed:Mother	72		
	Cool:Mother	72		
	Feed:Cool:Mother	144		
	Cut	144		
	Cool:Pig	144		
Response	Tenderness	144		



`lmer(Tenderness ~ Feed + Cool + Feed:Cool + Mother + (1:Cool:Mother) + (1|Pig))`

Mother is a **complete block** for all treatments

It doesn't matter if it is declared random

Feed:Mother is **aliased** with Pig. Since Pig is an EU, it must be random

You can choose either term

Cool:Mother and Pig are incomplete blocks for Feed:Cool **crossed** blocks

Without Mother as a big block, we'd have a normal split-plot with Pig as a main plot

Pig is a block for **specific effects** of cool

Cool:Mother is a block for **specific effects** of Feed (though less effective)

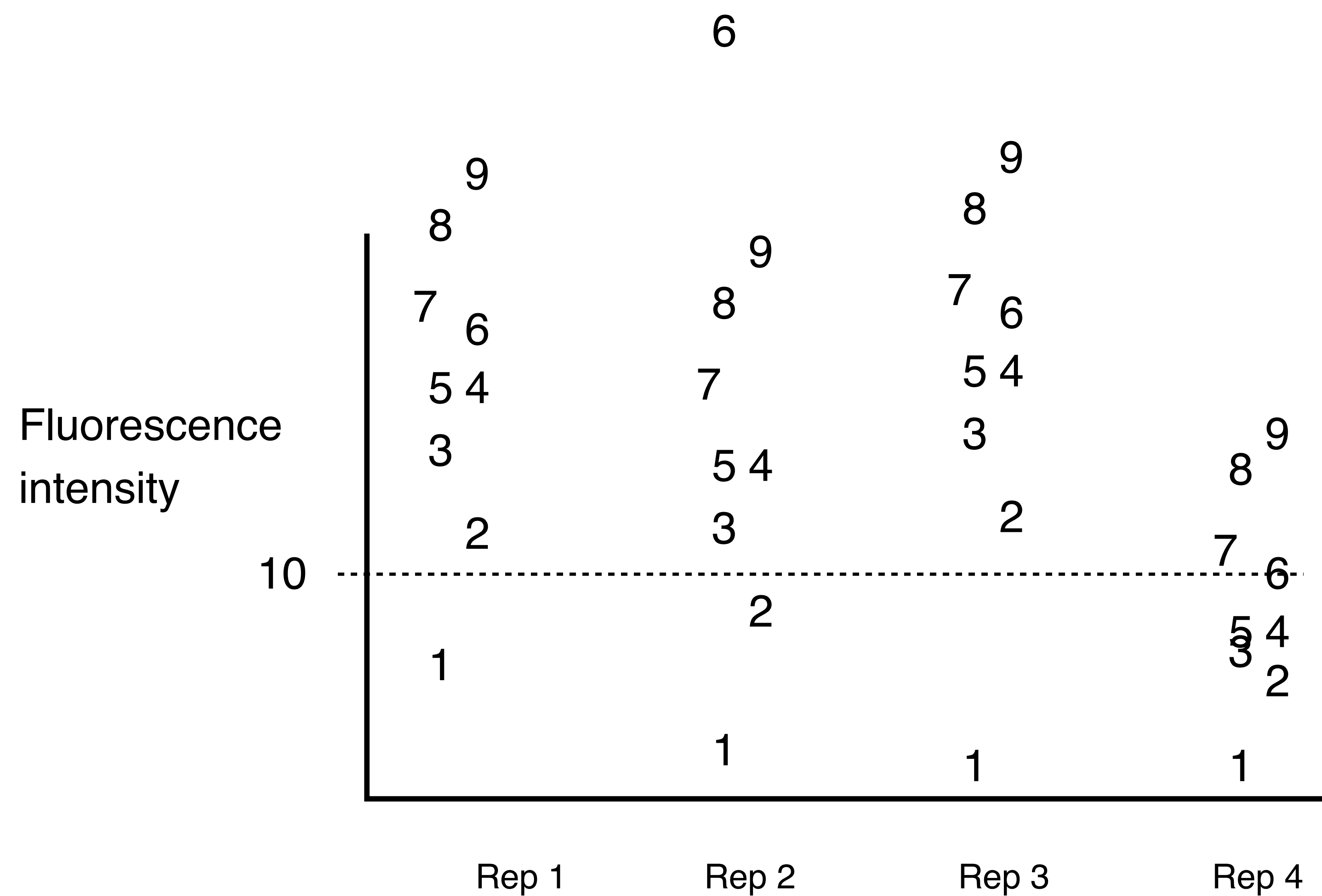
Rep 1	Rep 2	Rep 3	Rep 4
1 3 2	8 5 2	3 8 4	2 4 9
6 4 5	1 7 4	7 6 2	8 6 1
7 8 9	6 9 3	5 9 1	7 5 3

Lattice design

nested blocks

The smaller blocks form a **balanced incomplete** block design

all pairwise treatment effects have the same CI

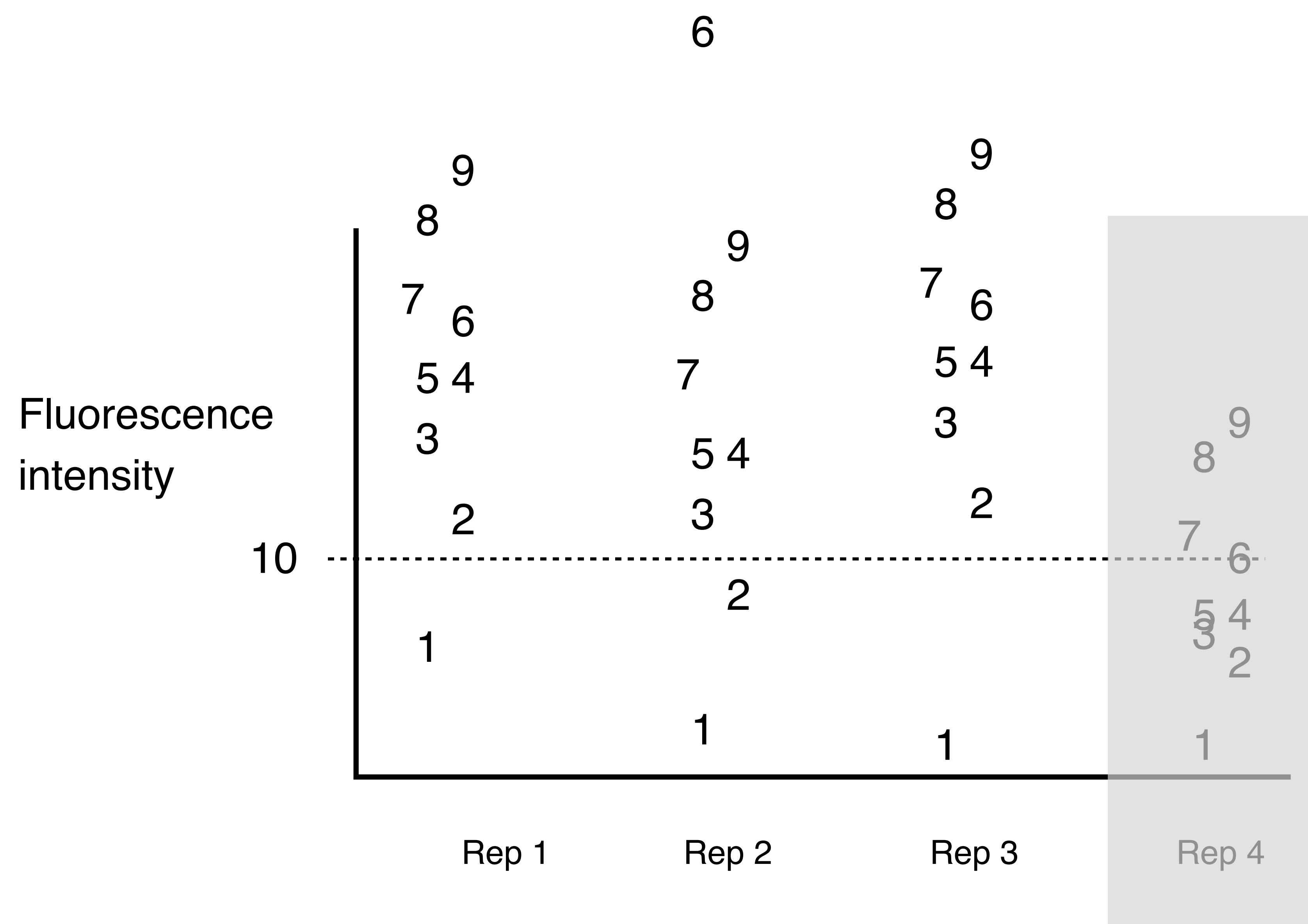


Should we conclude there are **treatment effects != 0**?

What happens if:

- 1) We lose Rep 4
- 2) We decide to drop treatment 1 (we suspect it didn't work right)
- 3) We exclude the observation of trt-6 from Rep-2 because it looks like an outlier?
- 4) We lose all values below 10 because of the detection threshold of our instrument?

These all generate **missing data** (N/A values) in our data.



What happens if: **We lose Rep 4**

As long as this is not due to the low fluorescence intensity of Rep 4, we are OK

Design is no-longer a BIBD (with small blocks)

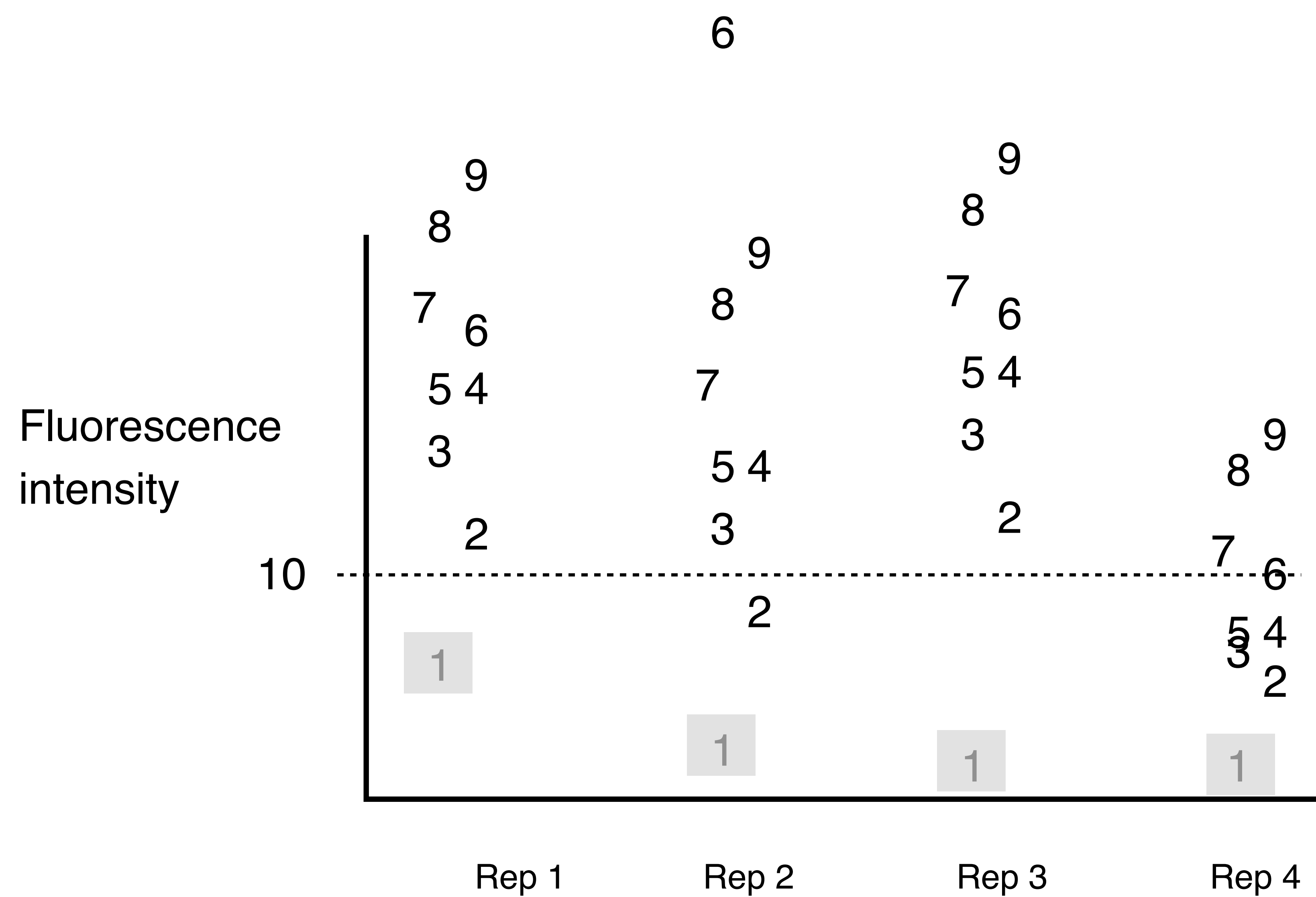
Design is still connected

Missing At Random (MAR)

Missing values are caused only by design variables in your experiment

Solution: Just delete these rows of your data.frame and continue with the analysis

As long as design is still connected, the results are valid (just a little lower power)



What happens if: **We decide to drop treatment 1 (we suspect it didn't work right)**

Missing values are caused only by design variables in your experiment

Missing At Random (MAR) Rubin (1976)

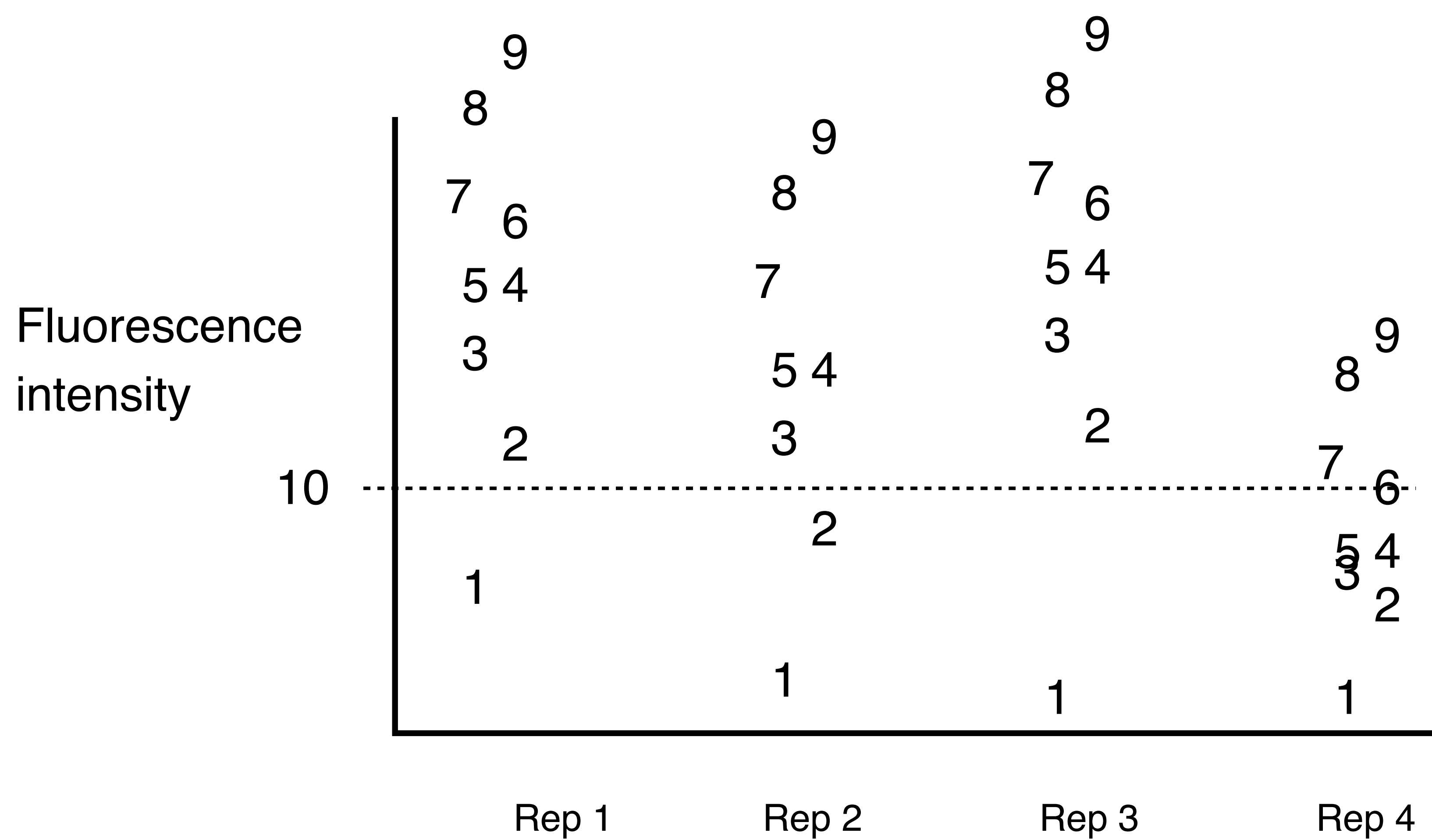
As long as design is still connected, the results are valid (just a little lower power)

What happens if: **We lose 5 random values**

Missing Completely At Random (MCAR)

Solution: Just delete these rows of your data.frame and continue with the analysis

As long as design is still connected, the results are valid (just a little lower power)



What happens if:

We exclude the observation of trt-6 from Rep-2 because it looks like an outlier?

Why was it an outlier?

Some plausible technical error (e.g. loaded too much sample)?: **MCAR**

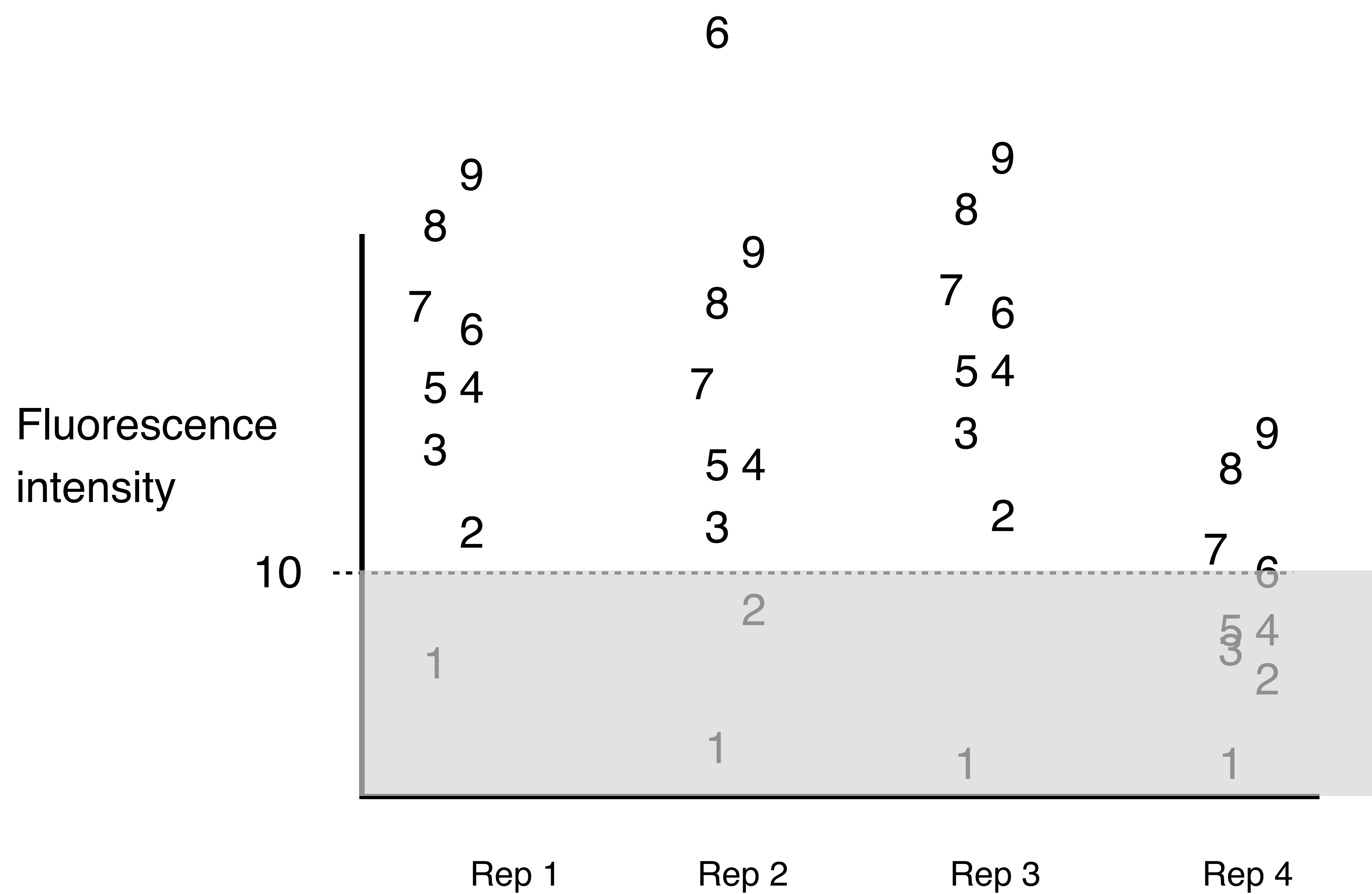
It actually was this large (just a-typical)?

Dropping it **is not valid** - leads to biased estimates:

s^2 will be too small (we'll under-estimate CIs)

Trt-6's mean will be underestimated

Missing Not At Random (MNAR)



What happens if:

We lose all values below 10 because of the detection threshold of our instrument?

When values are missing **because of their TRUE value**

We **cannot** just drop the rows of the table!

s^2 will be too small (we'll under-estimate CIs)

Any treatment level with dropped observations will be over-estimated

Missing Not At Random (MNAR)

Solution:

1) Best: **Model the missing values** (e.g. Survival model, censored model)

2) OK(ish): Impute the missing values based on the threshold (e.g. insert the threshold as the value or threshold/2)

s^2 will be too small (we'll under-estimate CIs)

Any treatment level with dropped observations will be over-estimated

But not as severely as if you had dropped the values

Study: Precision with ancient archery

Question: How does the weight and/or size of the arrowhead affect shooting precision?

Design: 10 archers were recruited.

Each shot 12 arrows, 3 with each combination of two factors: Weight (light or heavy) and Size (small or large).

Response: Precision was defined as the distance from the place of impact to the center of the target

Structure	Variable	#levels	Blocks	EU

Treatments: What questions?

Design:
What type of design?
Blocks?
EU?

What if the same 12 arrows were re-used by each archer?

What if a different 12 arrows were used by each archer?

Archer1		Archer2		Archer3	
W1S1	W1S2	W2S2	W2S1	W1S2	W1S1
123	456	789	abc	456	123
W2S2	W2S1	W1S2	W1S1	W2S1	W2S2
789	abc	456	123	abc	789

12 arrows
Does it matter if arrows are randomized within each archer?

Archer1		Archer2		Archer3	
W1S1	W1S2	W2S2	W2S1	W1S2	W1S1
XXX	XXX	XXX	XXX	XXX	XXX
W2S2	W2S1	W1S2	W1S1	W2S1	W2S2
XXX	XXX	XXX	XXX	XXX	XXX

120 arrows

Archer1		Archer2		Archer3		120 arrows
W1S1	W1S2	W2S2	W2S1	W1S2	W1S1	
XXX	XXX	XXX	XXX	XXX	XXX	
W2S2	W2S1	W1S2	W1S1	W2S1	W2S2	
XXX	XXX	XXX	XXX	XXX	XXX	

Structure	Variable	#levels	Blocks	EU
focal	Weight	2	Size, Archer	Arrow
moderator	Size	2	Archer	Arrow
combo Design	Weight:Size	4	Archer	Arrow
	Archer	10		
	Weight:Archer	20		
	Size:Archer	20		
	W:S:Archer	40		
	Arrow	120		
	Precision	120		

Analysis #1: Average specific effects of Weight (over Archers)

Specific-effect model (drop “Weight”)

“Main effect” from RCBD (Treatment:Block is random) Treatment = Weight:Size

lmer(Precision ~ Size + Weight:Size + Archer + Weight:Archer
+ Size:Archer + (1|Weight:Size:Archer))

Weight:Archer and Size:Archer are **incomplete blocks** so **can be random** (but not required)

Analysis #2: Specific effects of Weight for each Archer

Specific-effect model (drop “Weight”)

Weight:Size:Archer is **not random** (Weight:Archer and Size:Archer cannot be random)

lm(Precision ~ Size + Weight:Size + Archer + Weight:Archer
+ Size:Archer + Weight:Size:Archer)

Archer1		Archer2		Archer3		120 arrows
W1S1	W1S2	W2S2	W2S1	W1S2	W1S1	
XXX	XXX	XXX	XXX	XXX	XXX	
W2S2	W2S1	W1S2	W1S1	W2S1	W2S2	
XXX	XXX	XXX	XXX	XXX	XXX	

Structure	Variable	#levels	Blocks	EU	EU
focal	Weight	2	Size, Archer	Arrow	Weight:Size:Archer
moderator	Size	2	Archer	Arrow	Weight:Size:Archer
combo	Weight:Size	4	Archer	Arrow	Weight:Size:Archer
Design	Archer	10			
	Weight:Archer	20			
	Size:Archer	20			
	W:S:Archer	40			
	Arrow	120			
Response	Precision	120			

What if individual arrows were not randomized within each archer?

arrows are **subsamples**

Analysis #1: Average specific effects of Weight (over Archers)

```
lmer( Precision ~ Size + Weight:Size + Archer + Weight:Archer
      + Size:Archer + (1|Weight:Size:Archer) )
```

no change!

Analysis #2: Specific effects of Weight for each Archer

```
lm( Precision ~ Size + Weight:Size + Archer + Weight:Archer
     + Size:Archer + Weight:Size:Archer )
```

Weight:Size:Archer **must be random because it is an EU**

We cannot do this analysis!

Archer1		Archer2		Archer3		12 arrows
W1S1 123	W1S2 456	W2S2 789	W2S1 abc	W1S2 456	W1S1 123	
W2S2 789	W2S1 abc	W1S2 456	W1S1 123	W2S1 abc	W2S2 789	Does it matter if arrows are randomized within each archer?

Structure	Variable	#levels	Blocks	EU
focal	Weight	2	Size, Archer	Arrow
moderator	Size	2	Archer	Arrow
combo	Weight:Size	4	Archer	Arrow
Design	Archer	10		
	Weight:Archer	20		
	Size:Archer	20		
	W:S:Archer	40		
	Arrow	12		
	Archer:Arrow	120		
Response	Precision	120		

Analysis #1: Average specific effects of Weight (over Archers)

```
lmer( Precision ~ Size + Weight:Size + Archer + Weight:Archer
      + Size:Archer + (1|Weight:Size:Archer) + (1|Arrow) )
```

Arrow is EU so it must be random

Weight:Size:Arrow is **nested in Arrow** so it must be random

It is OK if Arrows are always shot 1,2,3 (as long as the order of the W:S combos is different for each archer)

Analysis #2: Specific effects of Weight for each Archer

Weight:Size:Archer cannot be random for this analysis, but must be because it is nested in Arrow

So we cannot do this analysis again!

We can’t separate specific effects of the arrow for each Archer from specific effects of Weight for each Archer