

# Build Better mAbs with Machine Learning and Synbio

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# ATUM

Quantitative Biology

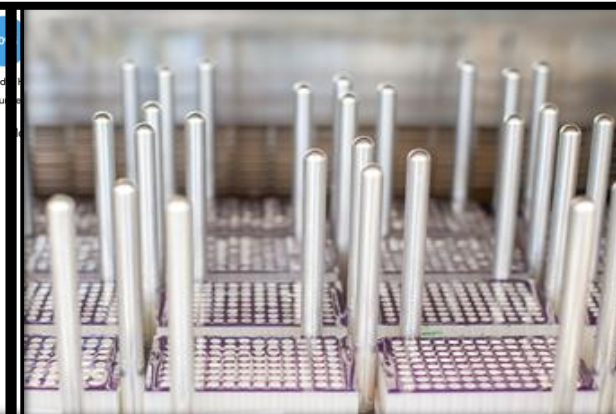
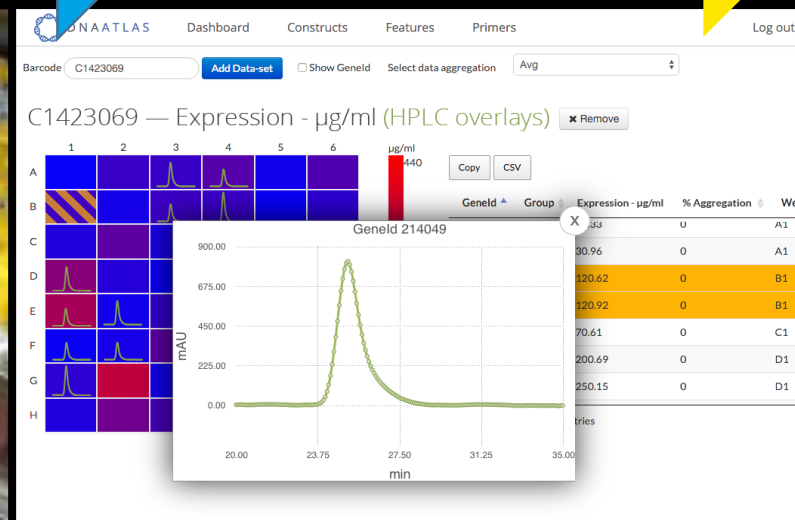
- Founded in 2003
- Based in SF Bay Area
- ~100 Employees
- Genes/Proteins/Cell lines
- Acquired **Migs** 2016
- Rebranded to **ATUM** 2016

# High Throughput Biologics Production

Genes

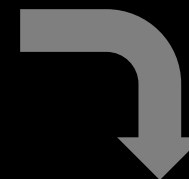
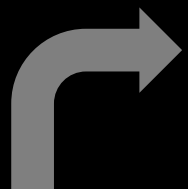
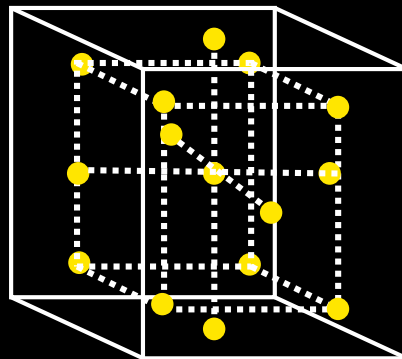
Proteins

Cell lines

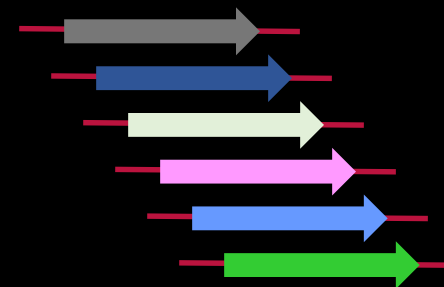
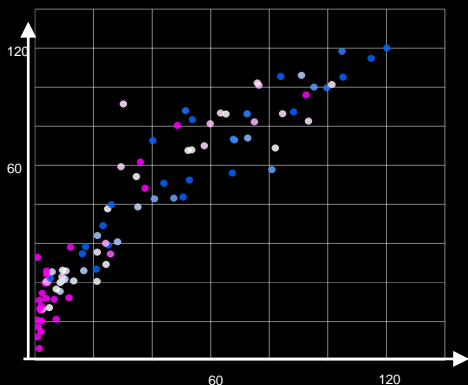


# Design of Experiment

Genomic Data



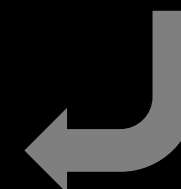
Machine Learning



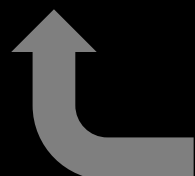
Synthetic Biology



Biology



Drug Candidate

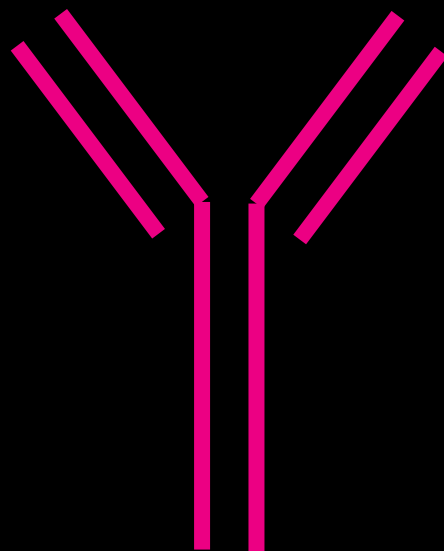


# Testing 184 Variants To Capture the Space of $10^{23}$ Variants

Total available space:

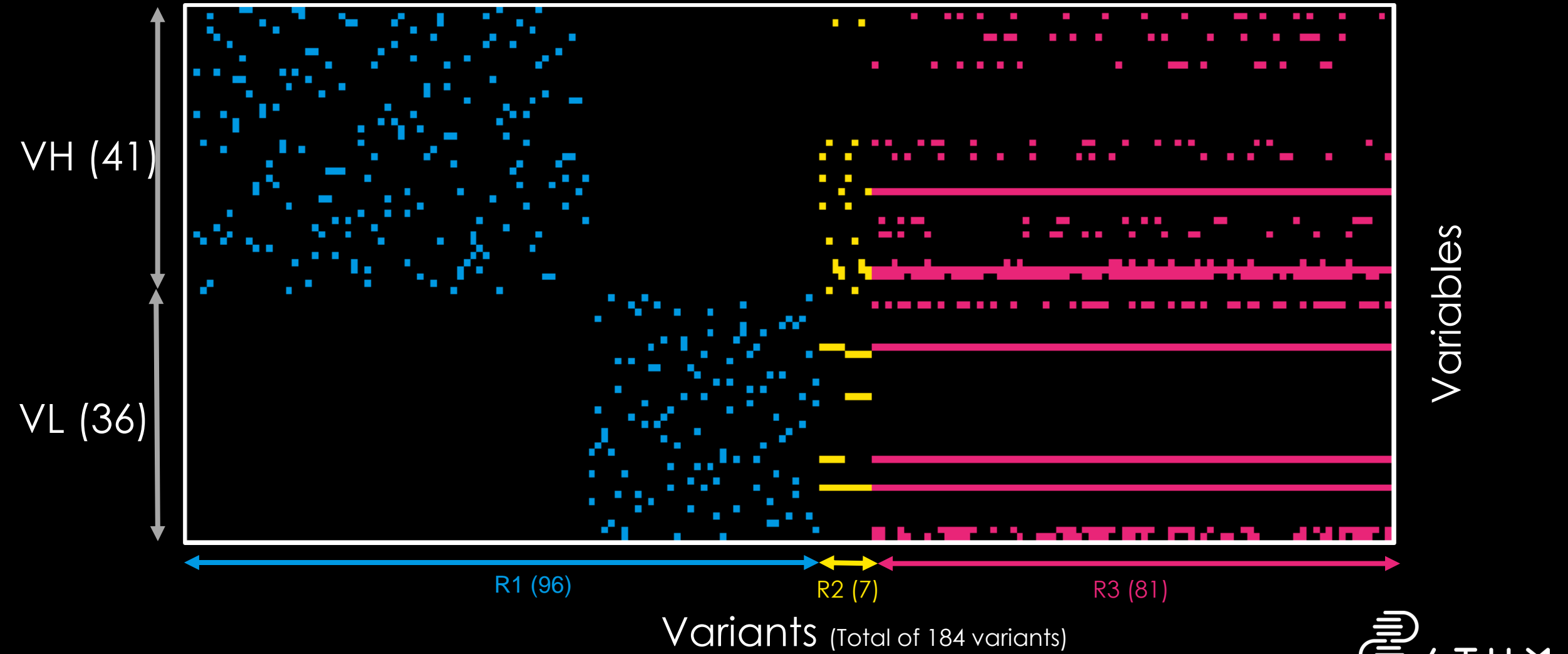
$$V_H = 2^{41} (\sim 10^{12})$$

$$V_L = 2^{36} (\sim 10^{10})$$

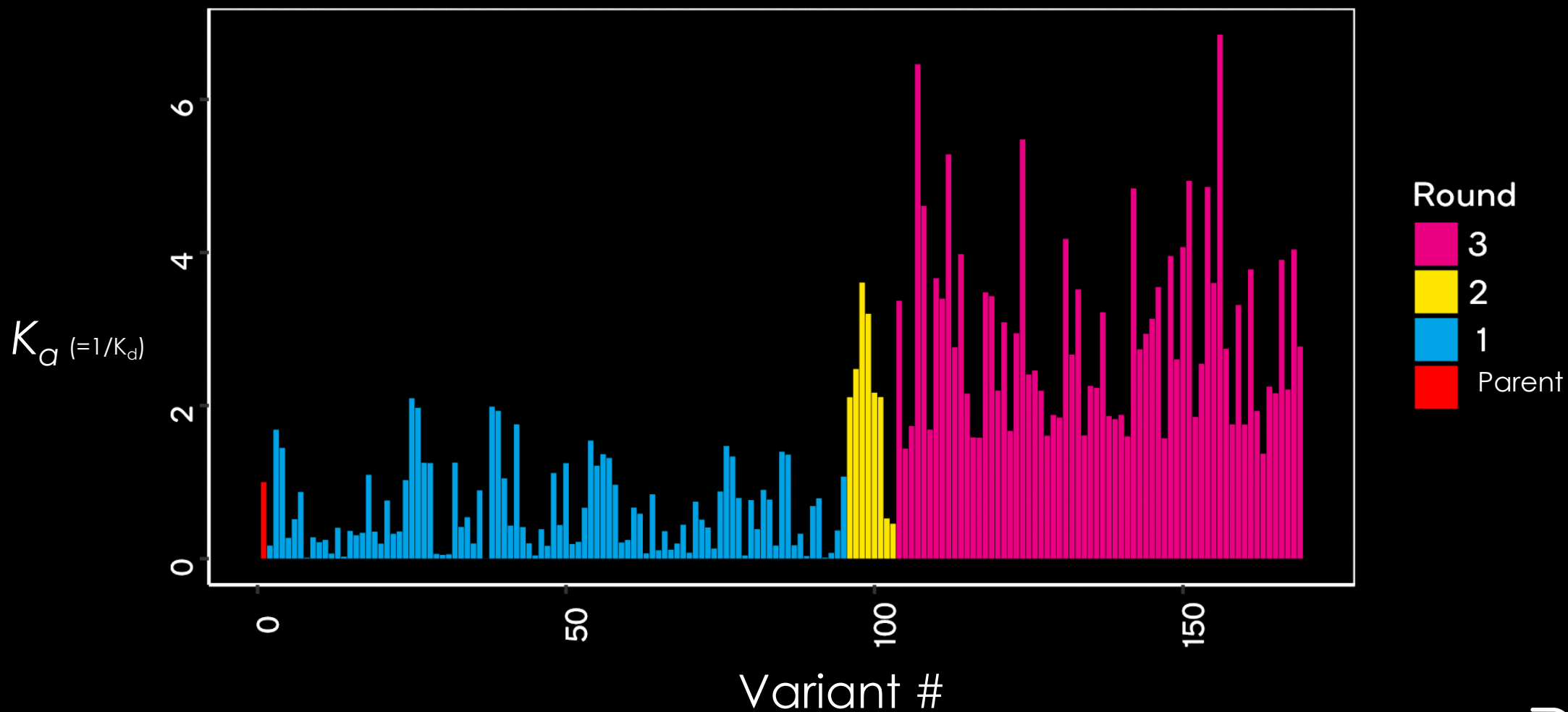


Starting from commercial molecule

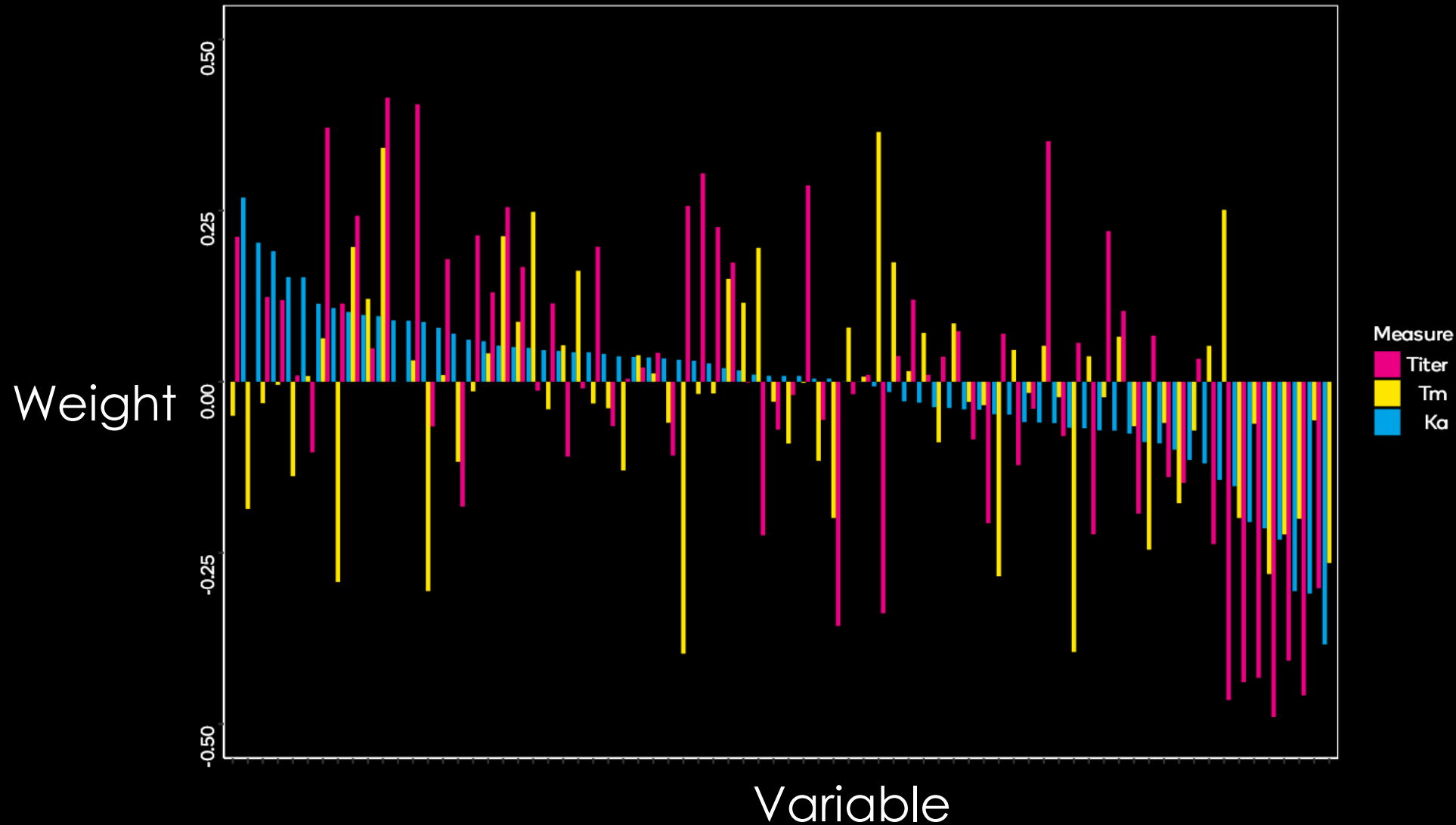
# Variable Matrix



# $K_d$ Improvement by Round

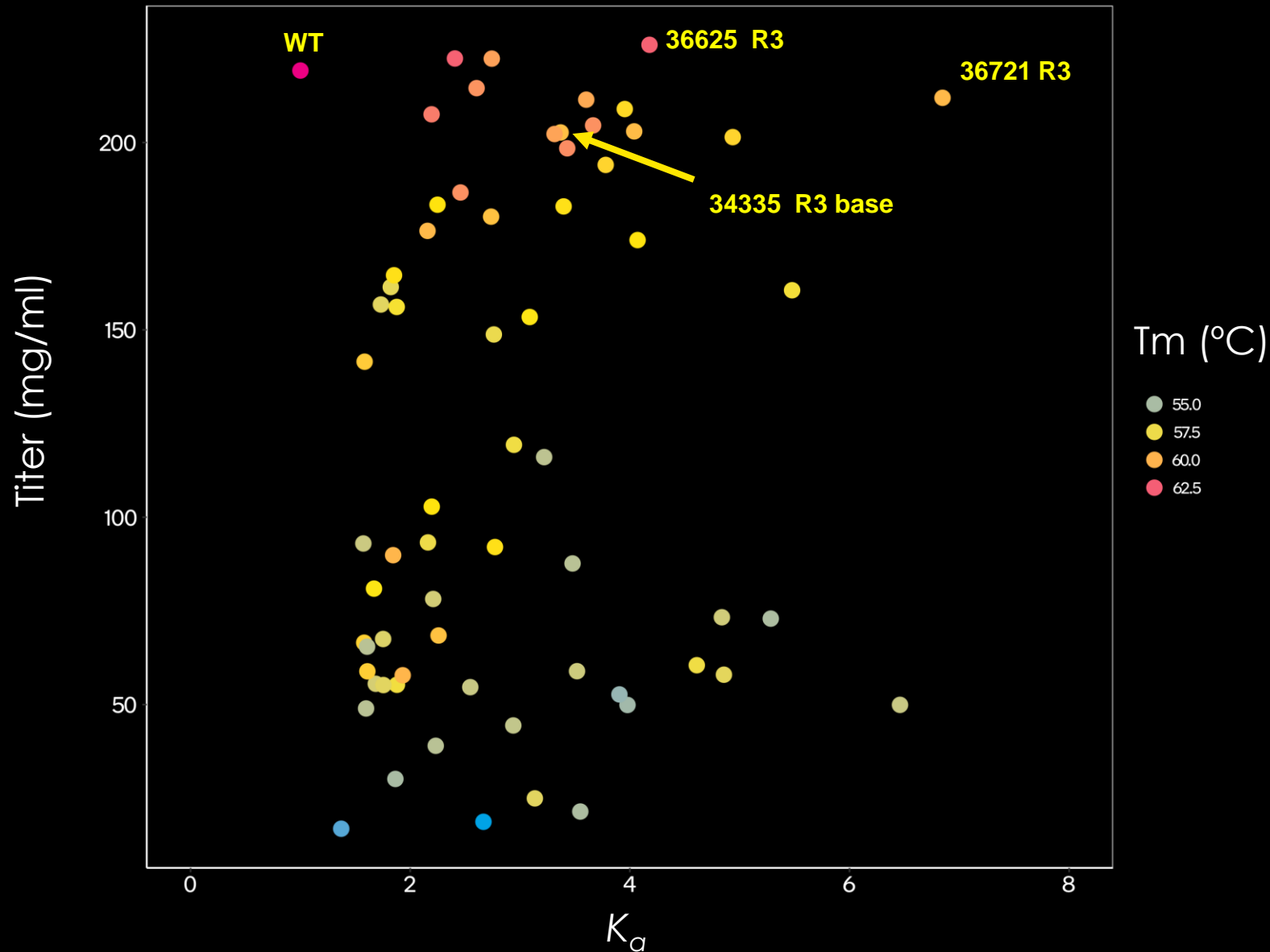


# Multidimensional Variable Weight Plot



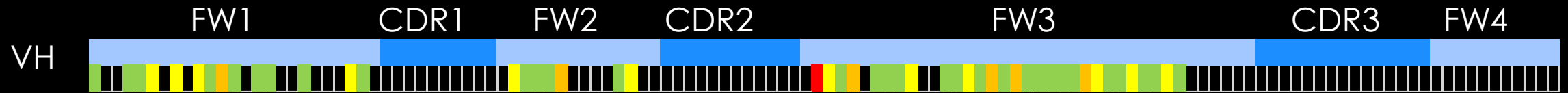


# Multi-Dimensional Improvements(R3)



Clone	Titer (mg/L)	$T_m$ (°C)	$K_d$ (nM)
36721	212	59.8	0.16
36625	226	62.4	0.25
Parent	219	63.8	0.98

# mAb Framework Protein Engineering



2 options, 3 options, 4 options, 5 options on 2 leads: FW1, FW2

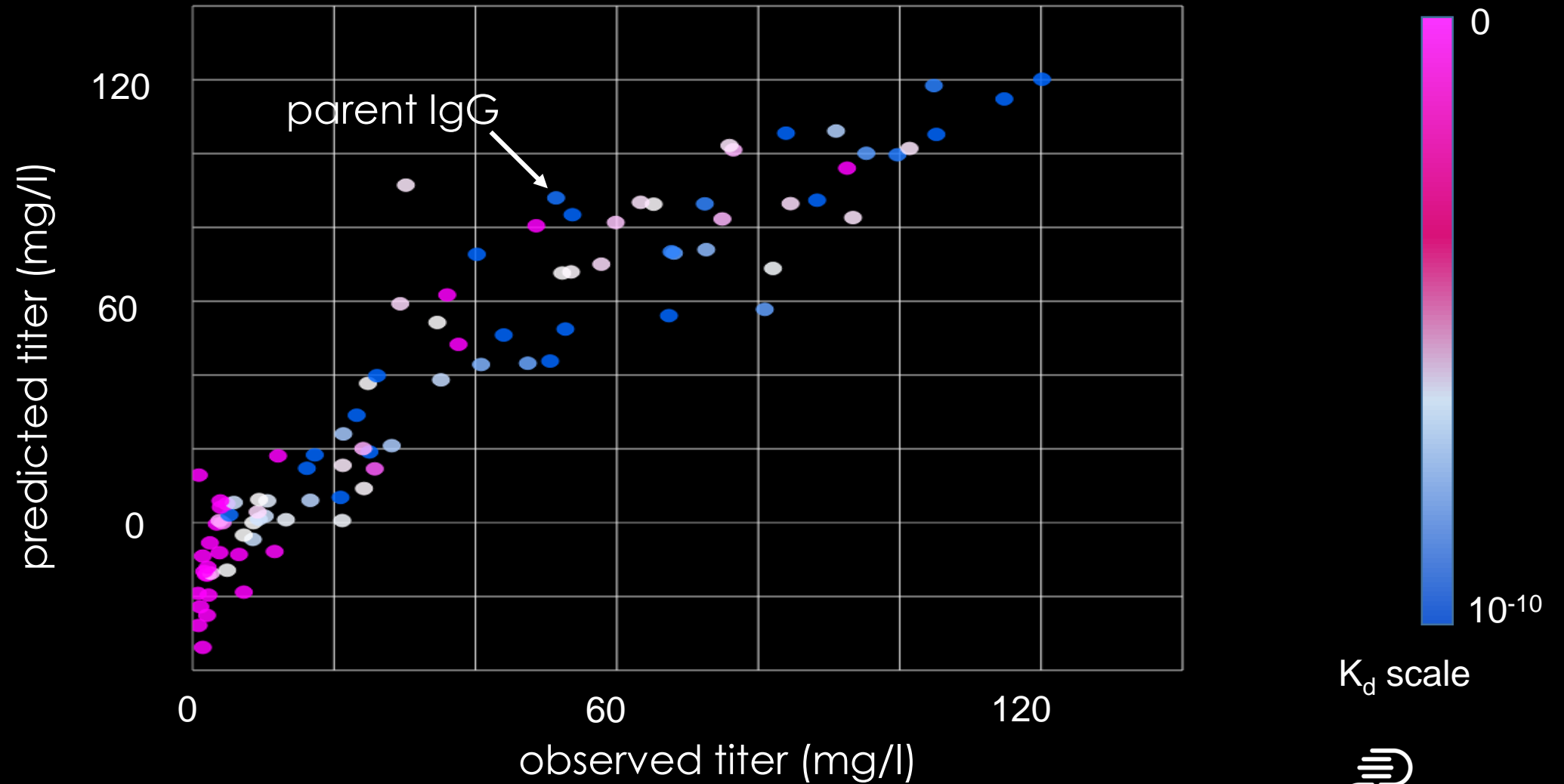
Total explored diversity:  $\sim 2 \times 10^{19}$ .

Total number of genes made: 96 – The Power of DoE

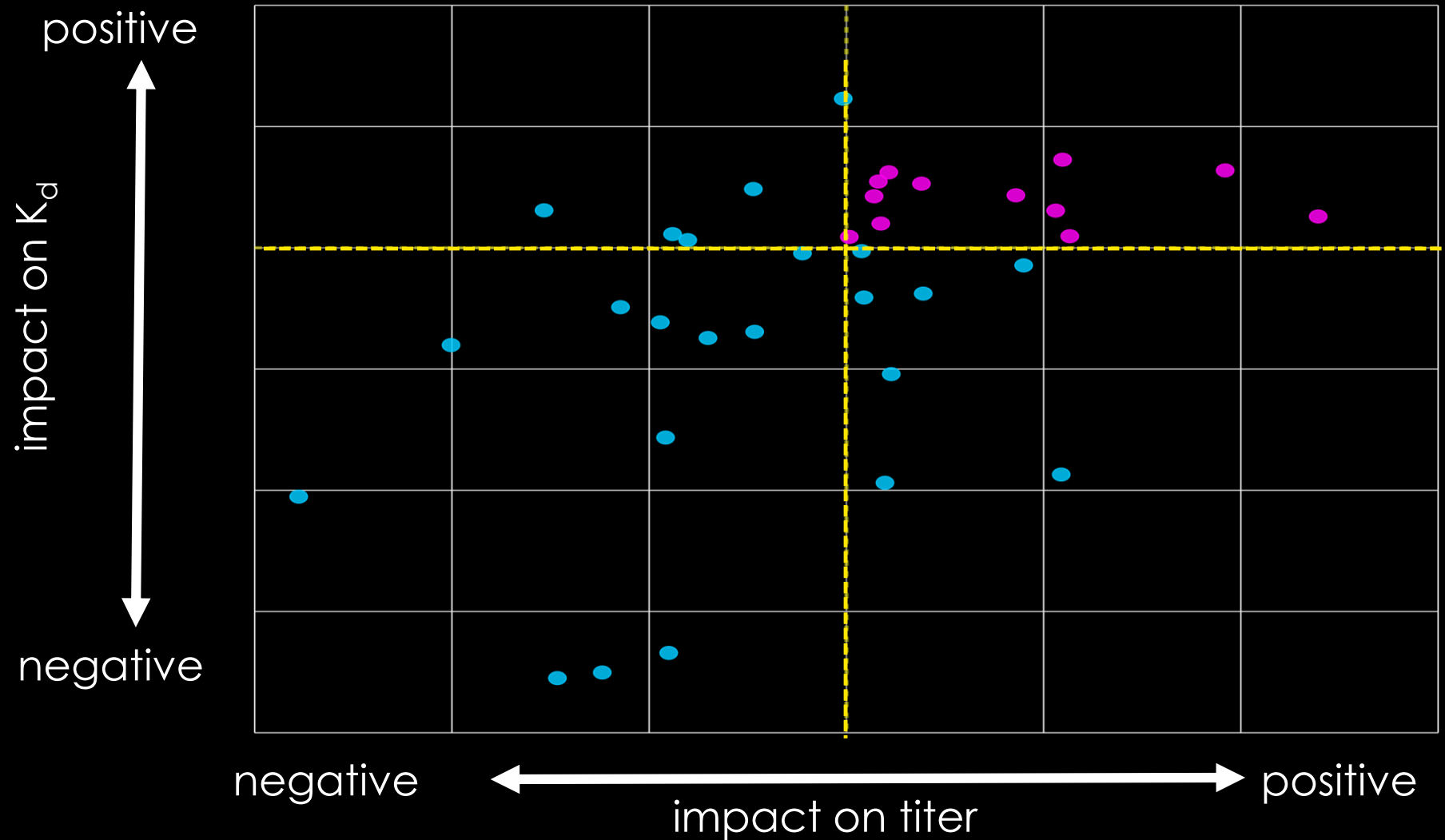
Measured output:

- Titer post purification
- $T_m$
- Kinetic off-rate

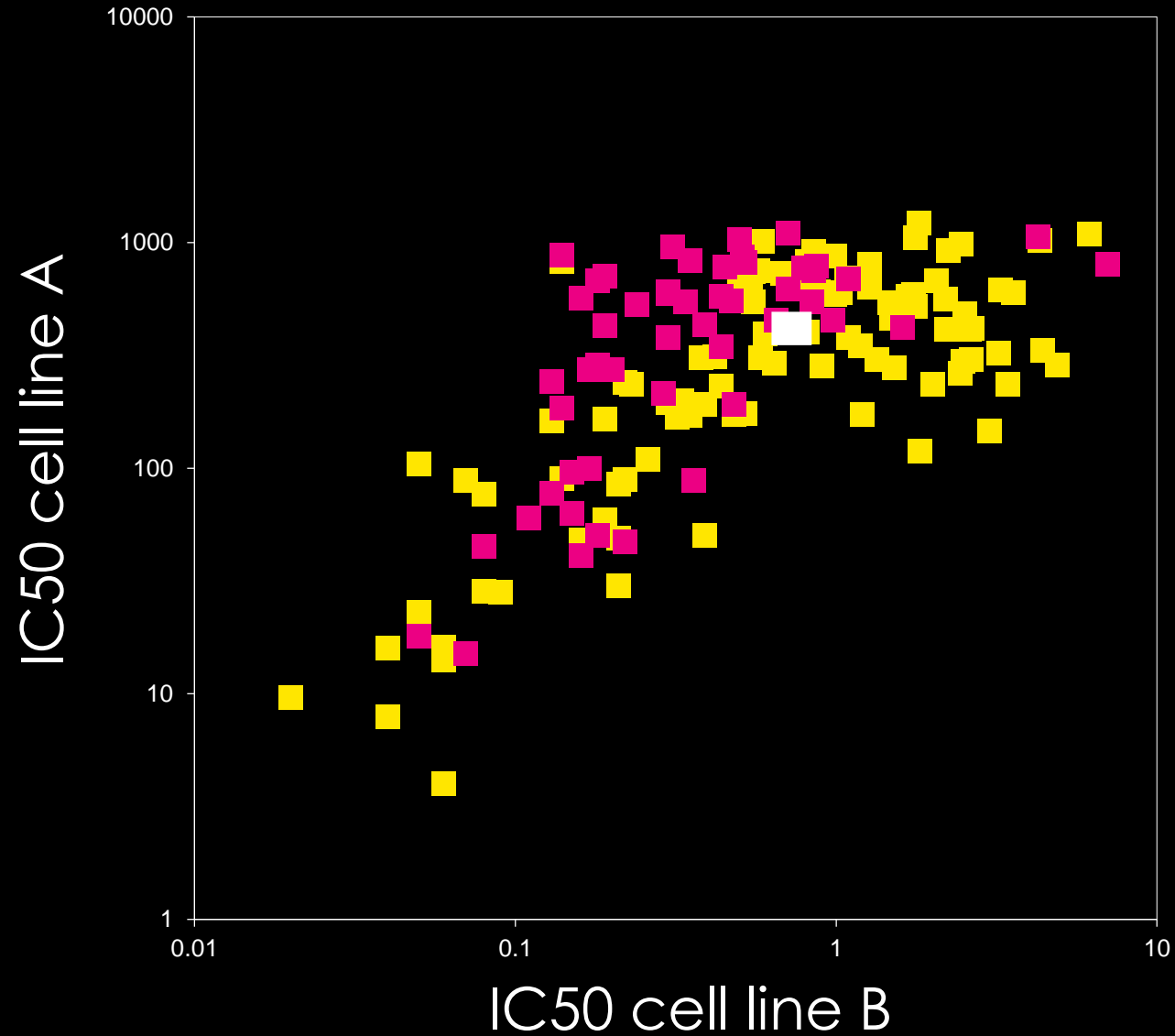
# Modeling of Titer



# Impact of Sequence Variables

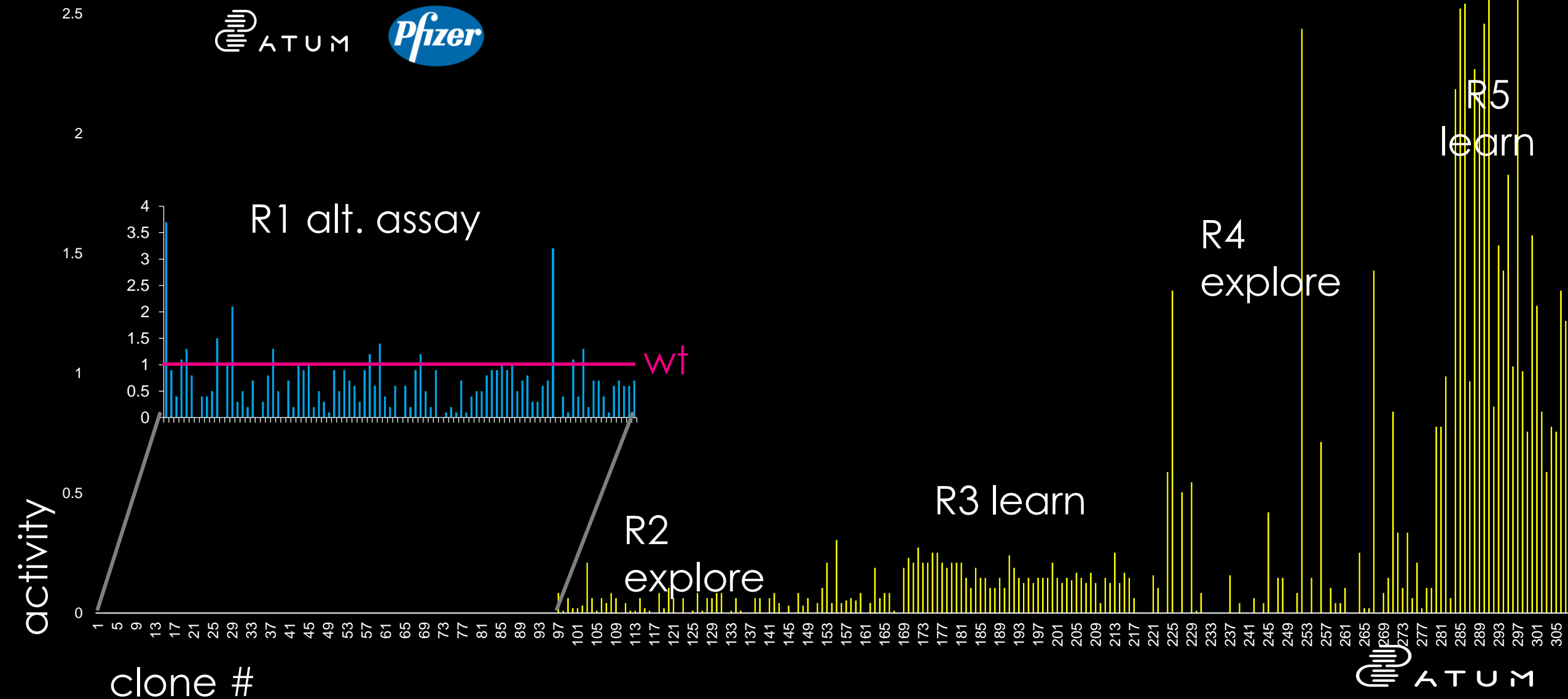


# Cell Based Assay (log log)

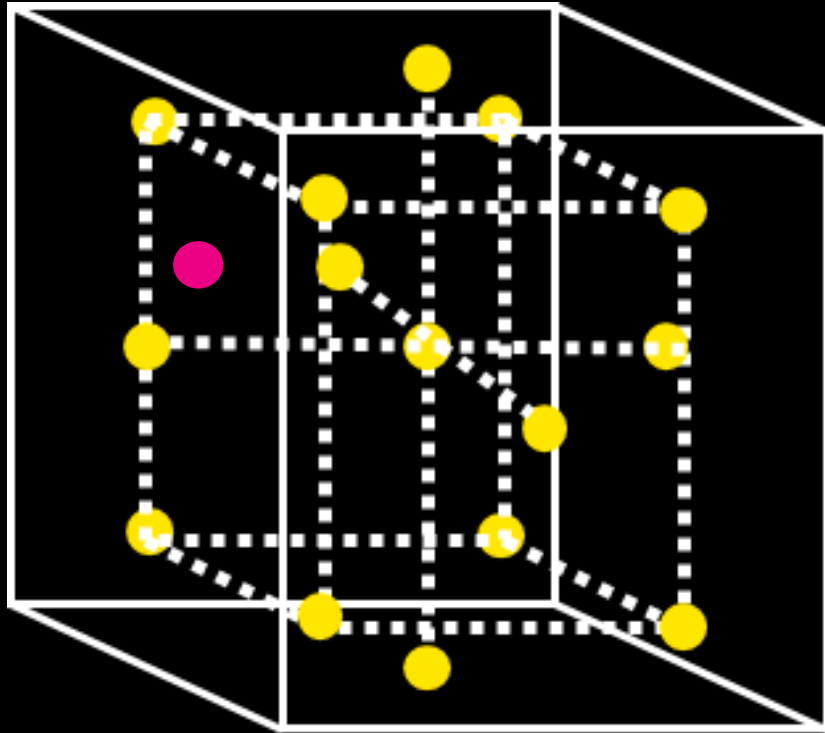


Parent  
Round 1  
Round 2

# Case Study - Biocatalysis



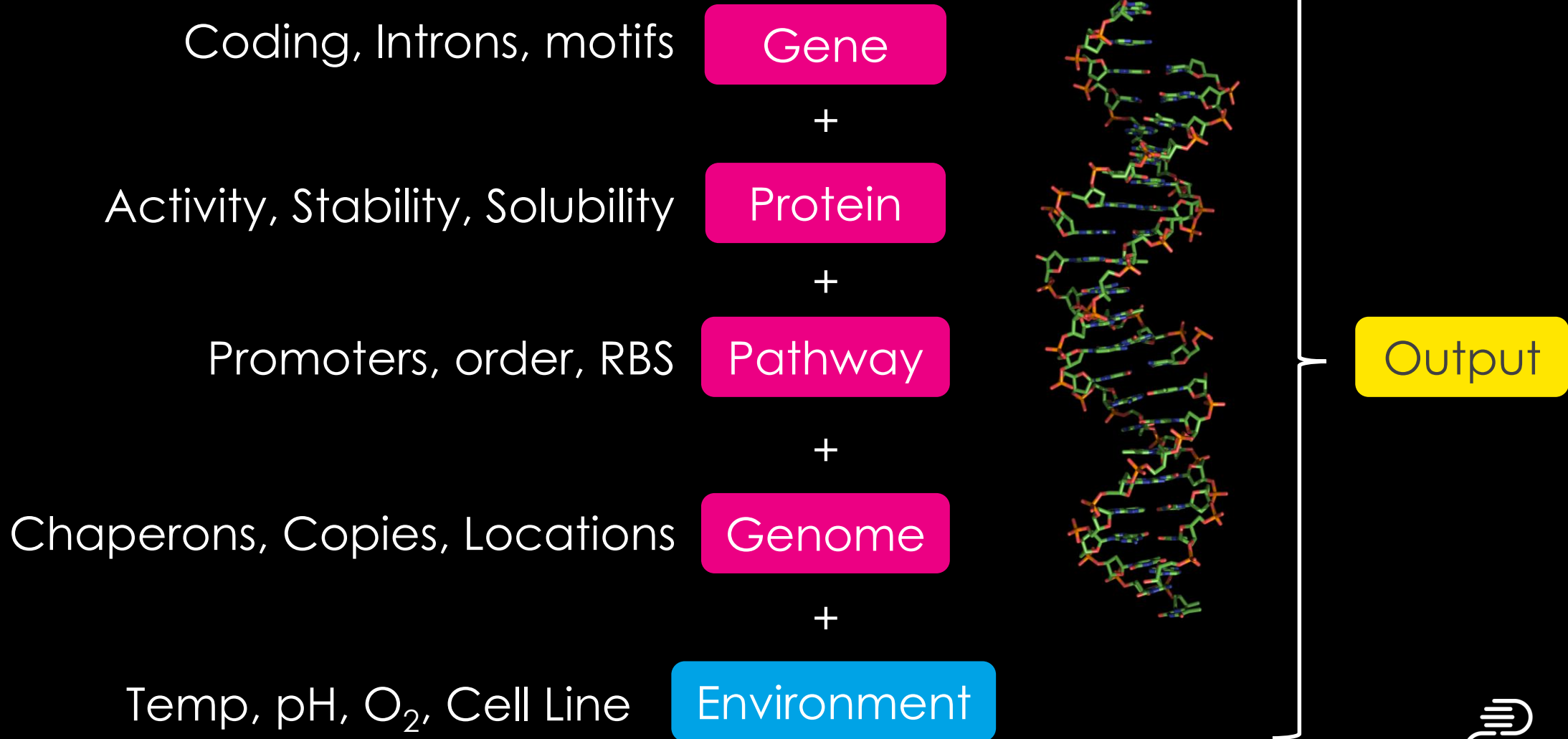
# Life is Multidimensional



## Winner

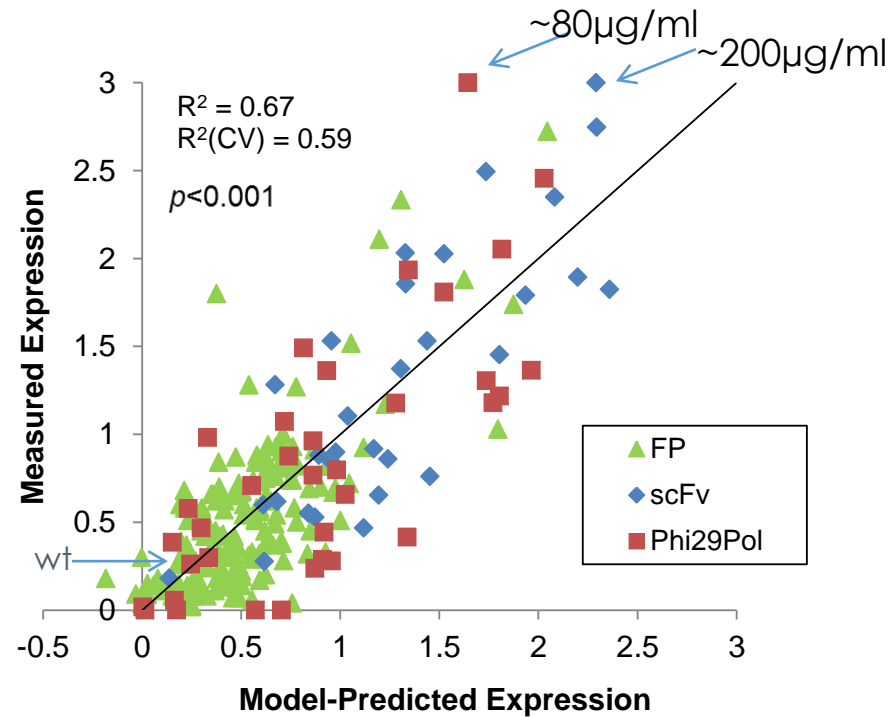
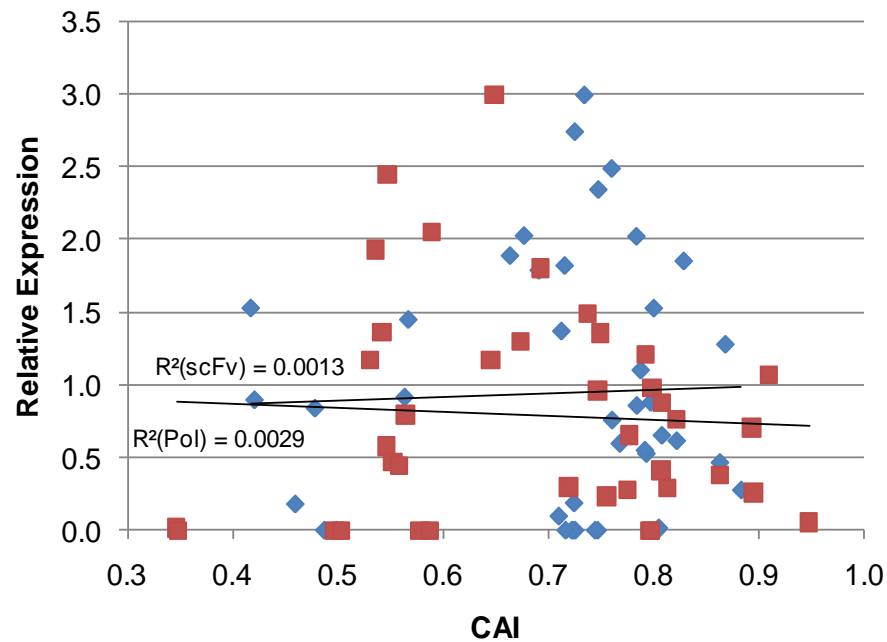
- ✓ Cell binding
- ✓ Antigen binding
- ✓ SEC HPLC
- ✓ T<sub>m</sub> stable
- ✓ Humanized
- ✓ ...And more

# Biology – Just a String of ACGT





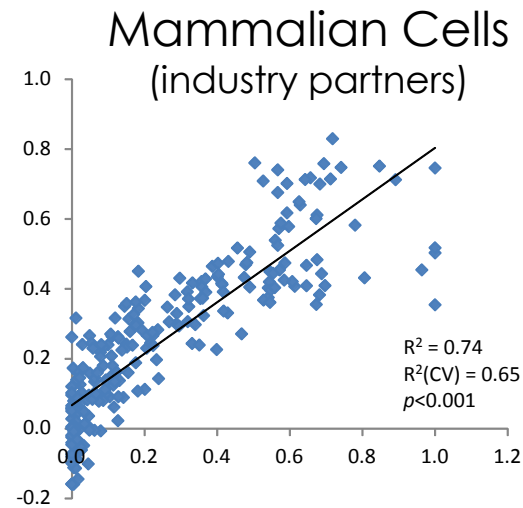
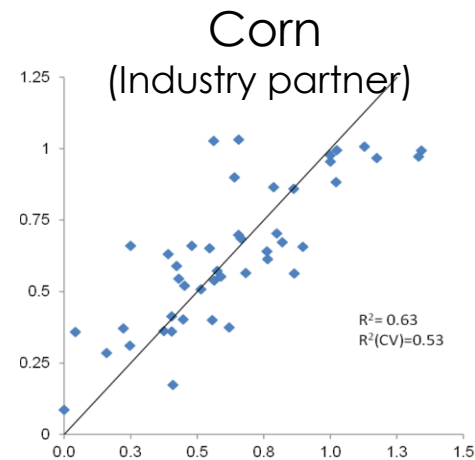
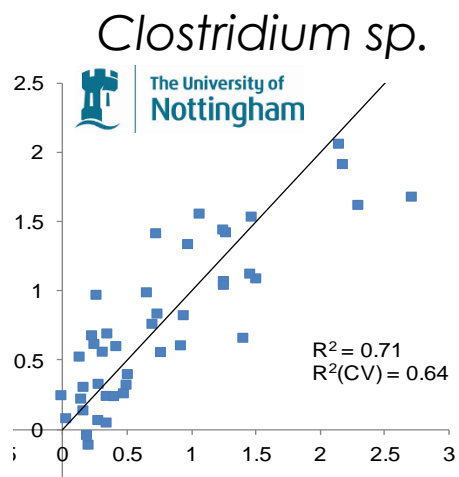
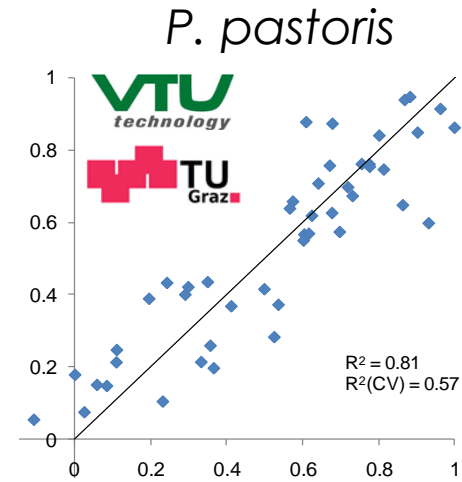
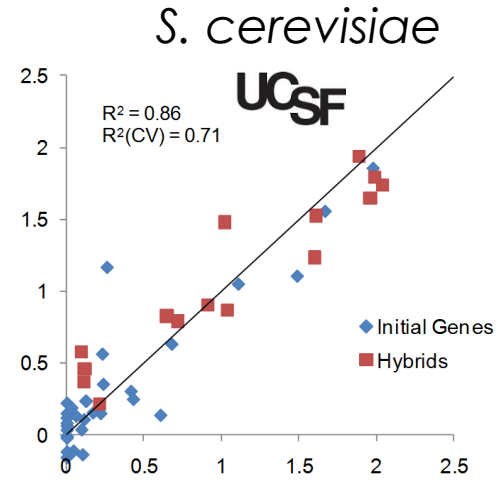
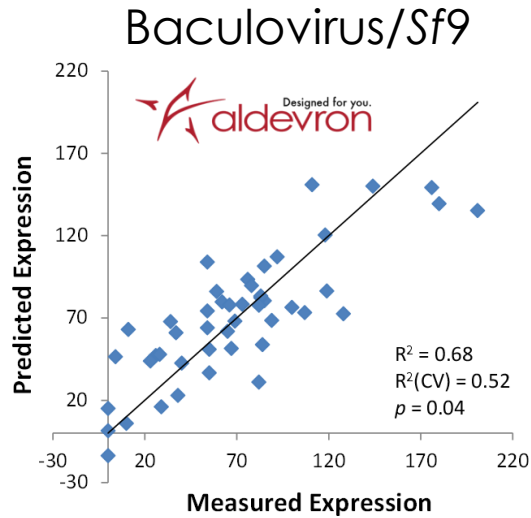
# Case Study - Codon Optimization



- Prot Exp Purif 2012 83(1):37-46. Gustafsson, et al.
- PLoS ONE 2009 4(9):e7002. Welch, et al.

# Custom Gene Design Algorithms

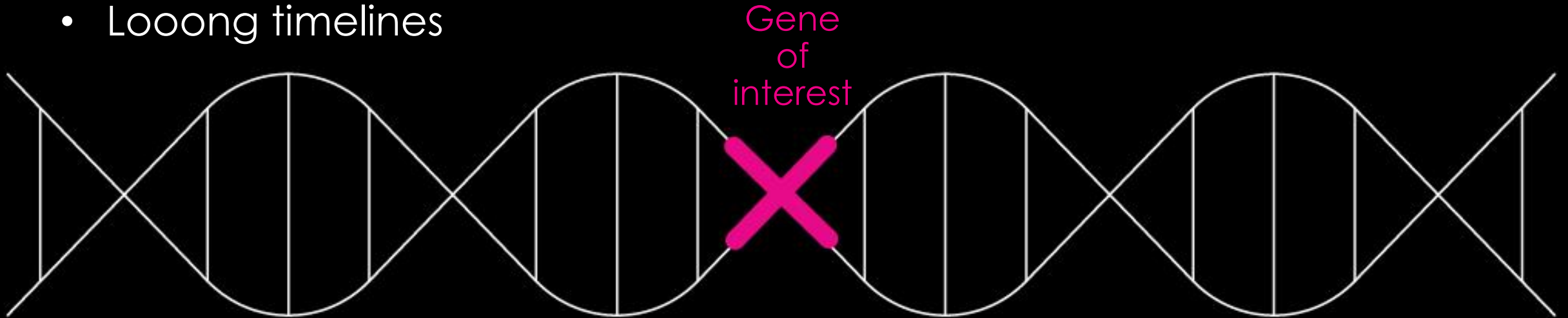
>50 host organisms interrogated to date



# Making Stable Cell Line is Hard

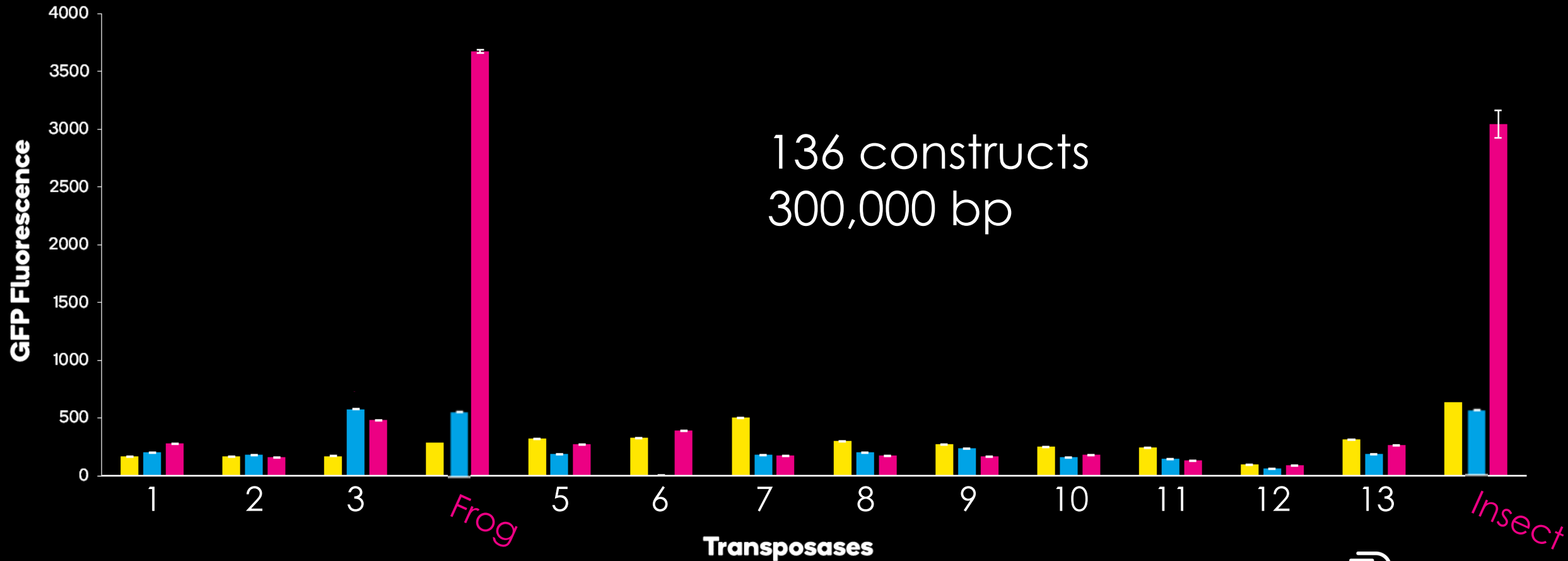
## Traditional technology

- Integration rate:  $\ll 1\%$
- Amplification often required
- Concatemer formation
- Transgene rearrangement
- Screening many clones
- Long timelines



# Two New Transposases - Leap In™

Activity tested in CHO K1 and yeast



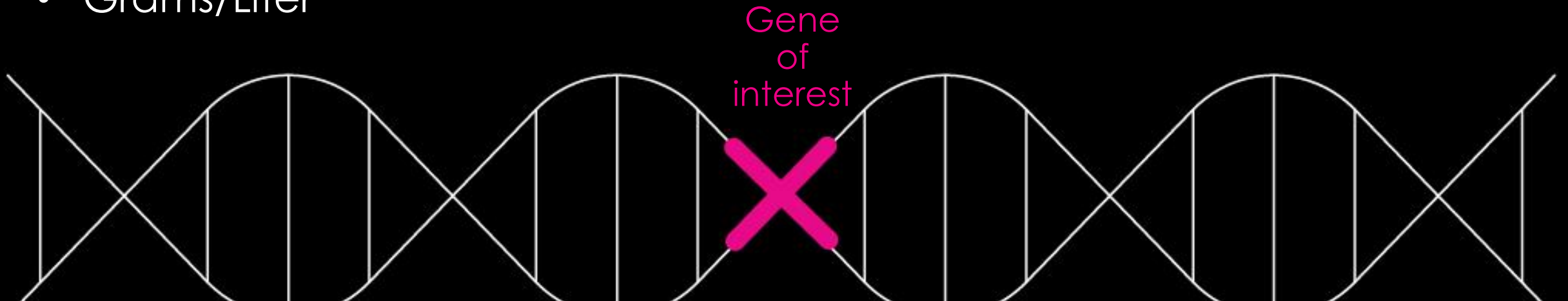
# Transposase Advantages

## Transposase technology

- Integration rate: >90%
- 2-40 copy integrations / genome
- Structural integrity
- Unlimited payload
- Unique locations
- Footprint-free excision
- 14 days from transfection to stable pool
- Grams/Liter

## Traditional technology

- Integration rate: <<1%
- Amplification required?
- Concatamer formation
- Transgene rearrangement
- Long timelines



# Cell Line Development

		<i>mg quantities</i>		<i>gram quantities</i>		
		Pool Generation		RCB Generation		
Time	2-3 weeks	3-4 weeks	3 weeks	8 weeks	10 weeks	4 weeks
	Codon opt	Transfection	Fed batch	Cloning	Stability testing	RCB generation
	Signal seq selection	Recovery	Pool ranking			Release
	Genesyn					Report
	DNA cloning					

- HD-BIOP3 GS null CHOK1 (Horizon Discovery)
- DG44 (Columbia University)

# Thank You



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Technology presented is protected by issued US patents 9771402, 9580697, 9574209, 9534234, 9493521, 9428767, 9290552, 9206433, 9102944, 8975042, 8825411, 8635029, 8412461, 8401798, 8323930, 8158391, 8126653, 8005620, 7805252, 7561973, 7561972 and pending applications

