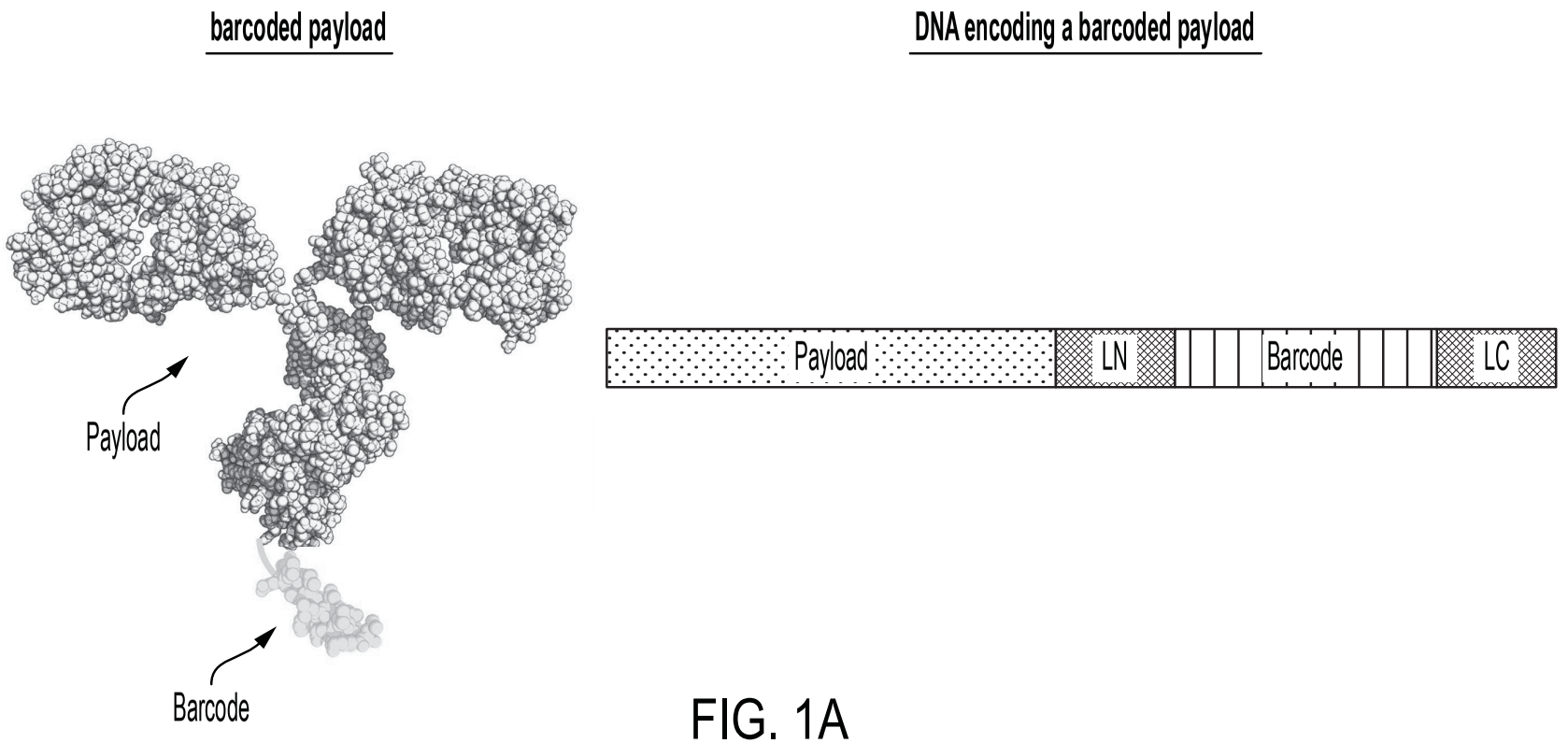

barcoded payload
DNA encoding a barcoded payload
Payload
Barcode
Payload
LN
Barcode
LC

FIG. 1A

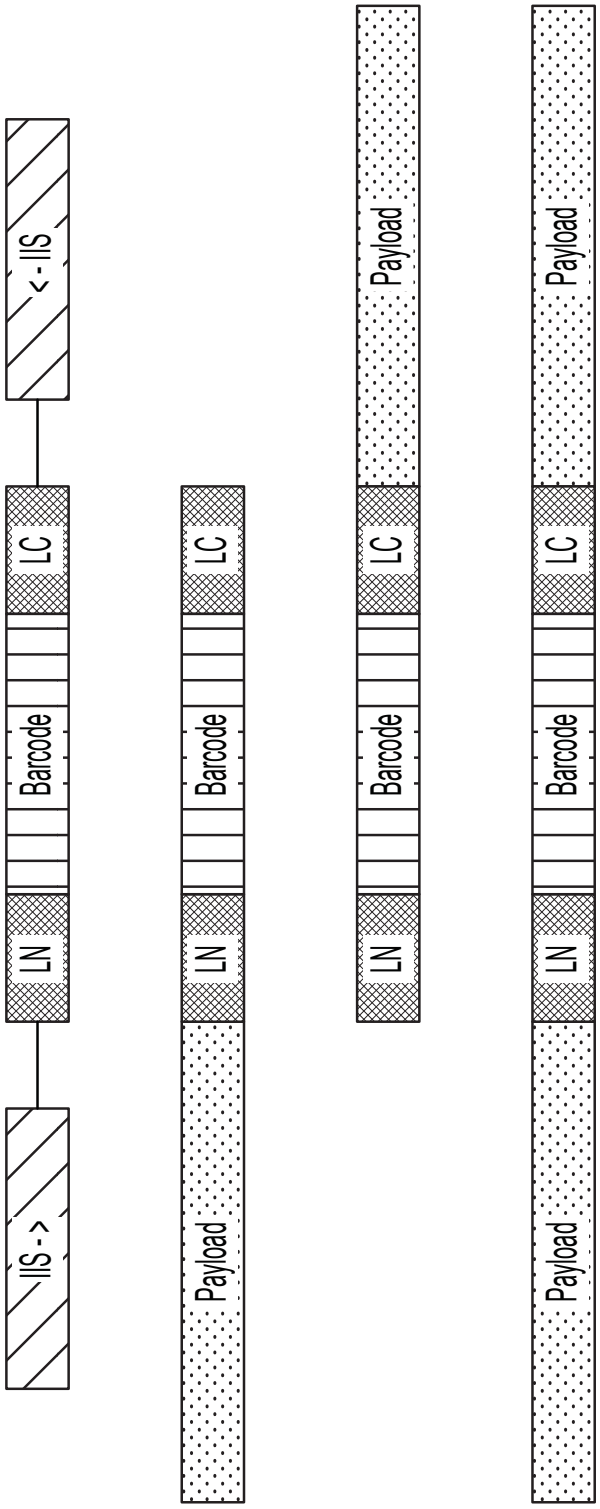

IIS - >
LN
Barcode
LC
< - IIS
Payload
LN
Barcode
LC
Payload
LN
Barcode
LC
Payload

FIG. 1B

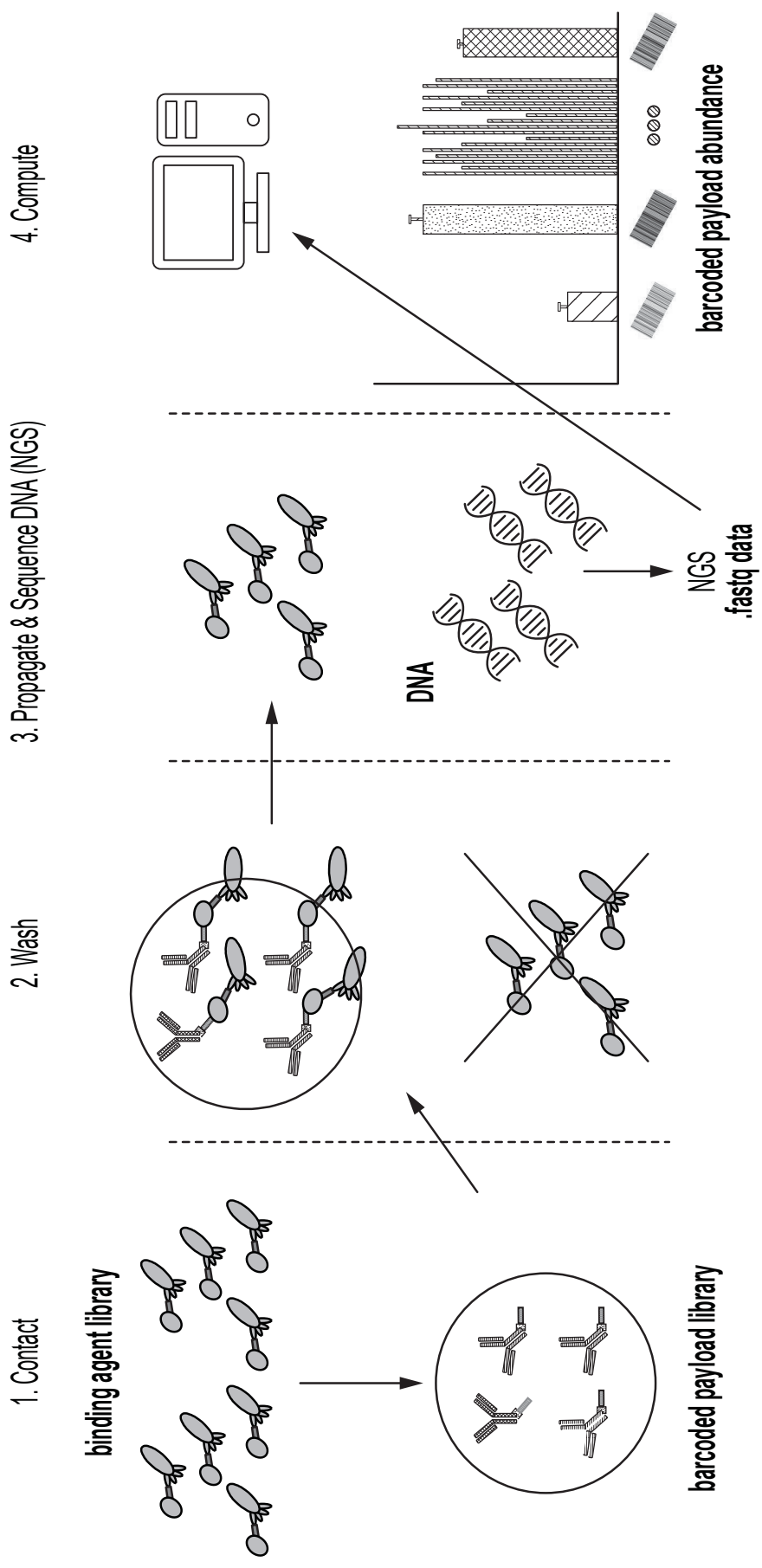

1. Contact
binding agent library
barcoded payload library
2. Wash
3. Propagate & Sequence DNA (NGS)
DNA
NGS
.fastq data
4. Compute
barcoded payload abundance

FIG. 2

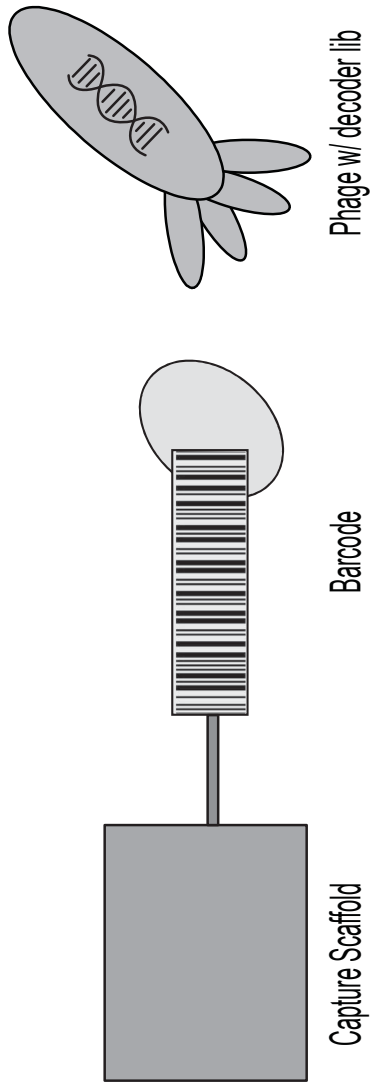


FIG. 3A

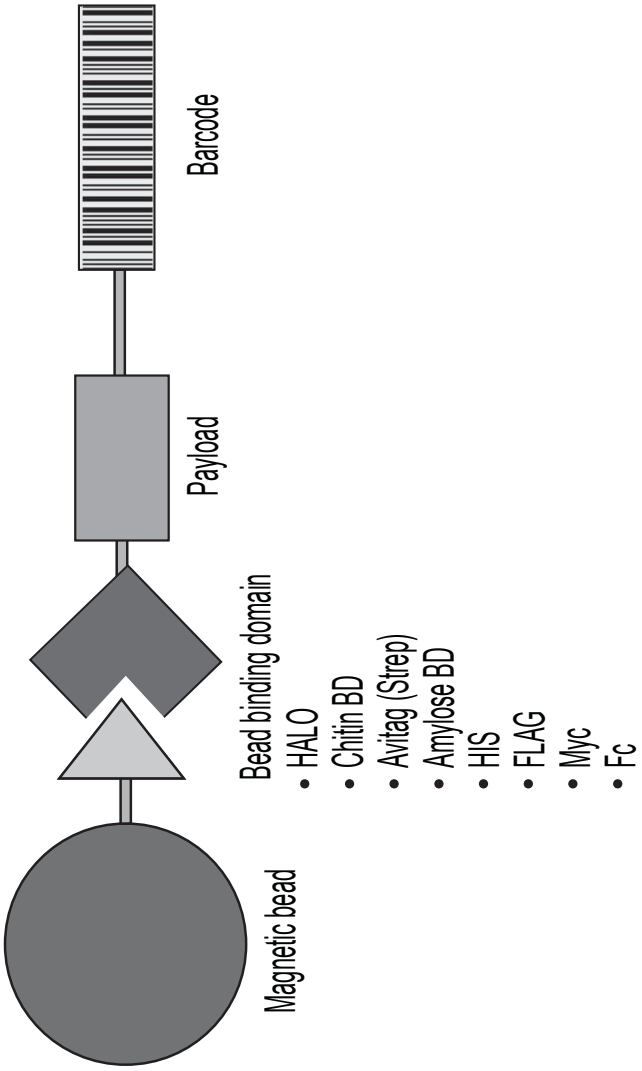

Barcode
Payload
Bead binding domain
• HALO
• Chitin BD
• Avitag (Strep)
• Amylose BD
• HIS
• FLAG
• Myc
• Fc
Magnetic bead

FIG. 3B

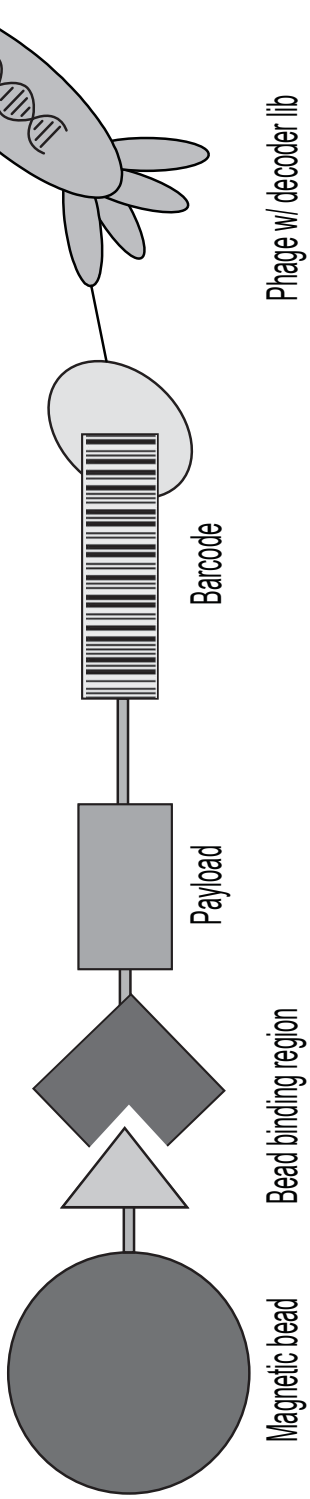

Phage w/ decoder lib
Barcode
Payload
Bead binding region
Magnetic bead

FIG. 3C

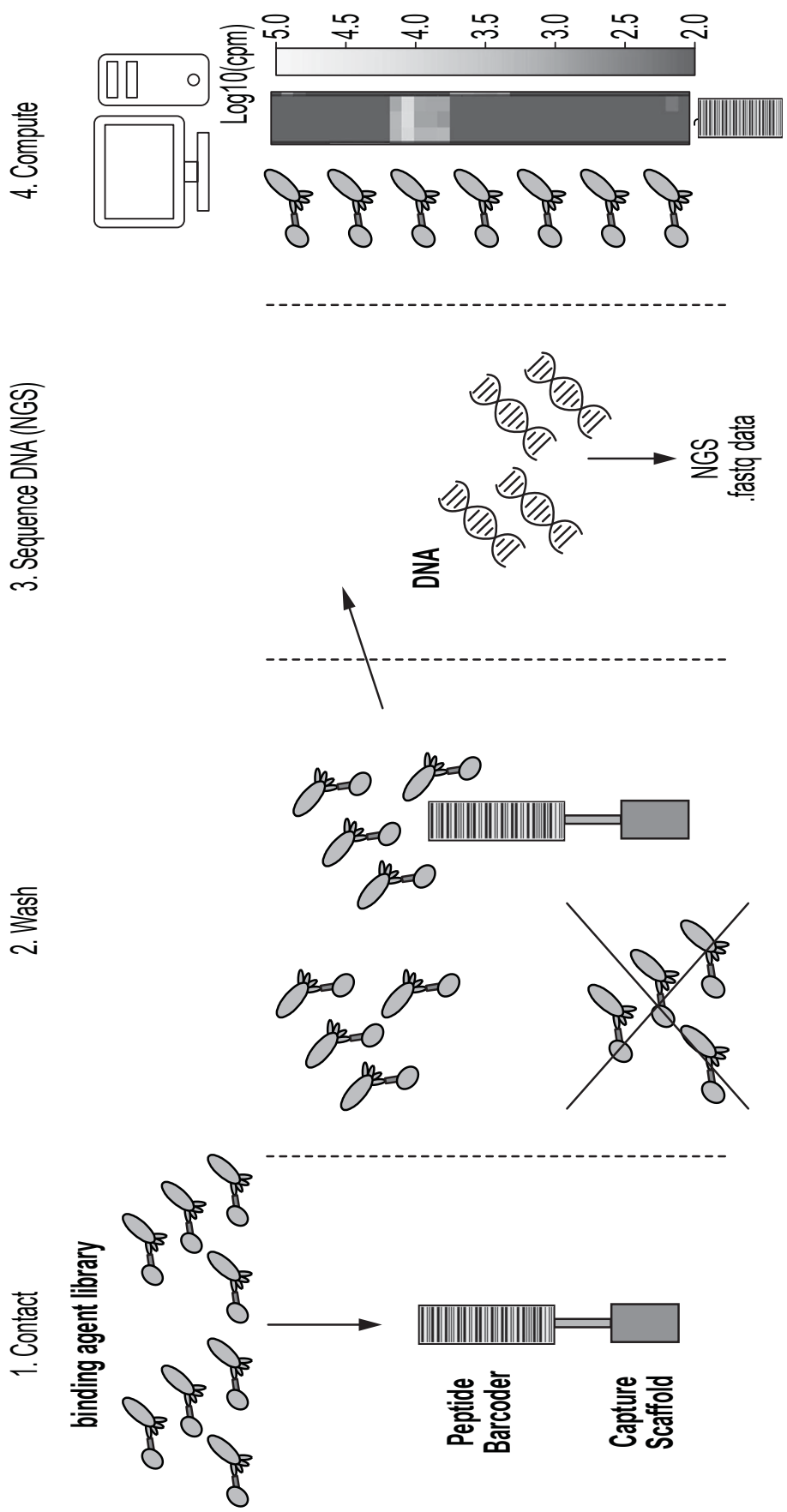

1. Contact
binding agent library
Peptide Barcoder
Capture Scaffold
2. Wash
3. Sequence DNA (NGS)
DNA
NGS .fastq data
4. Compute
Log10(cpm)
5.0
4.5
4.0
3.5
3.0
2.5
2.0

FIG. 4

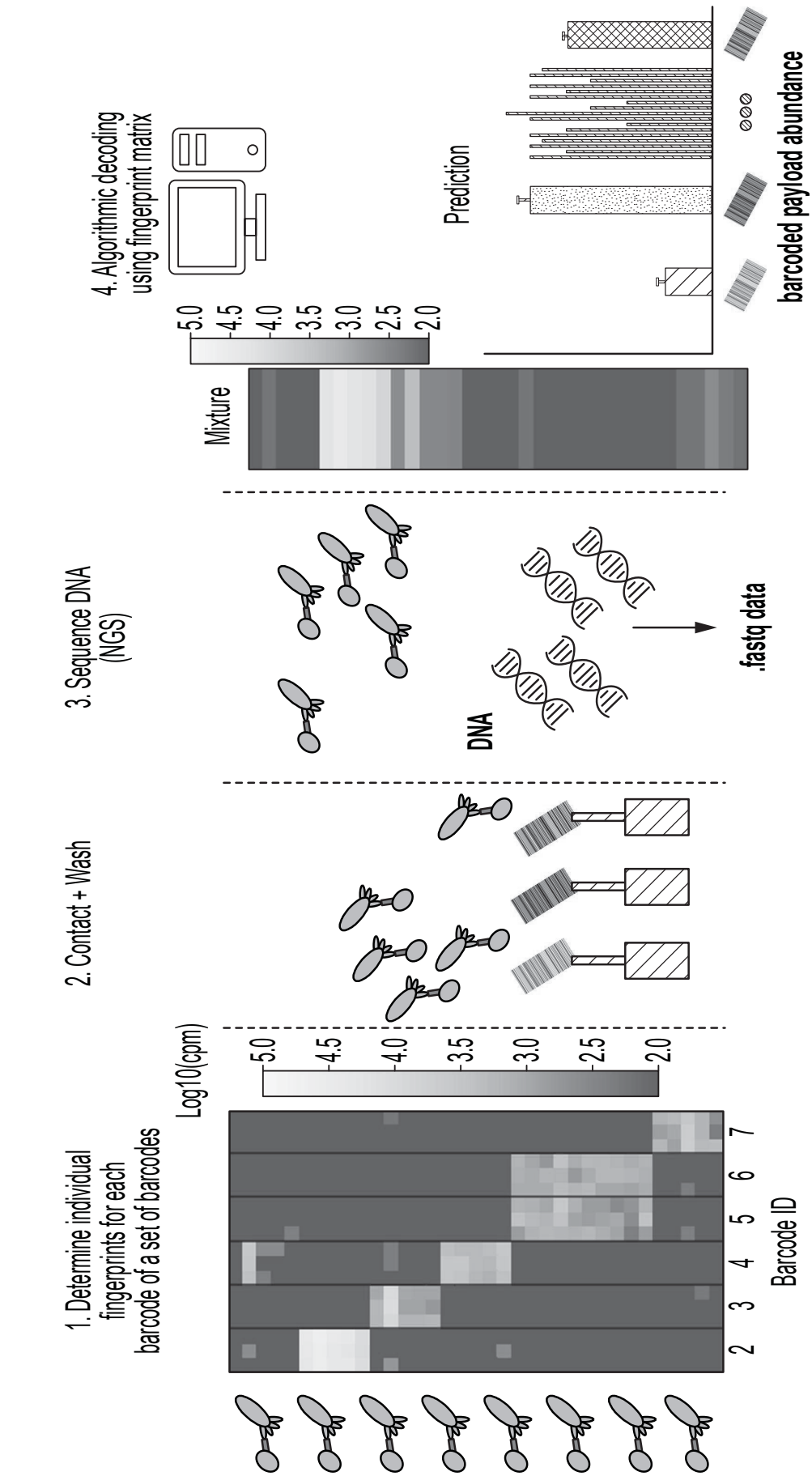

1. Determine individual fingerprints for each barcode of a set of barcodes
Log10(cpm)
5.0
4.5
4.0
3.5
3.0
2.5
2.0
2
3
4
5
6
7
Barcode ID
2. Contact + Wash
3. Sequence DNA (NGS)
DNA
.fastq data
Mixture
4. Algorithmic decoding using fingerprint matrix
Prediction
barcoded payload abundance

FIG. 5

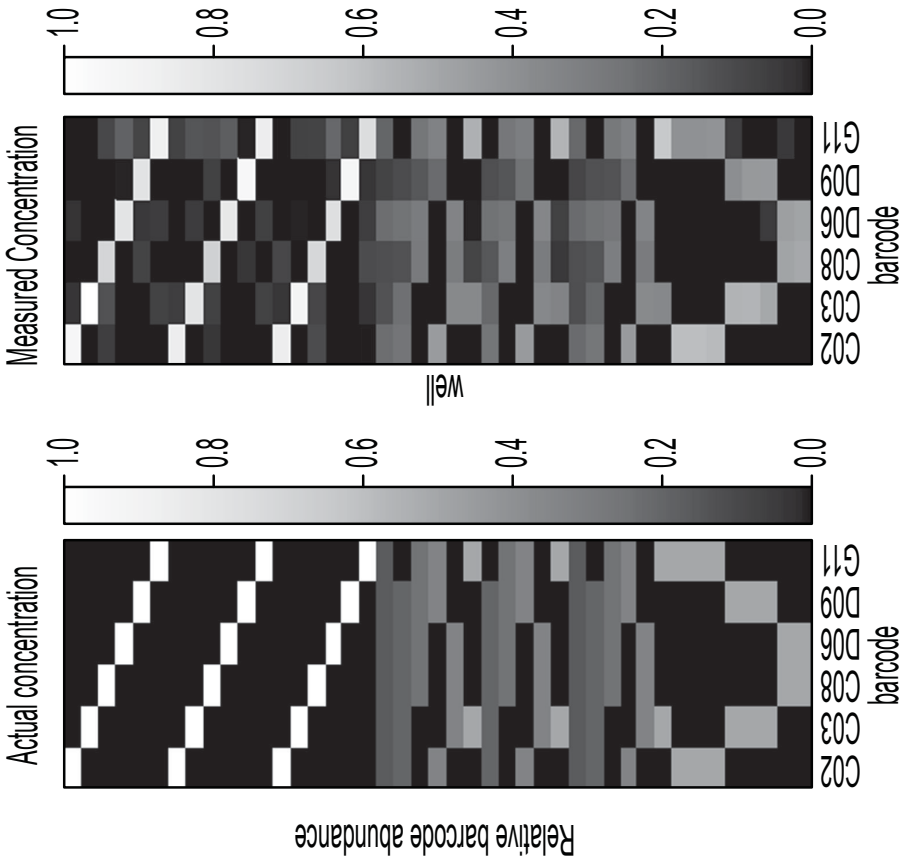

Actual concentration
Measured Concentration
barcode
C02
C03
C08
D06
D09
G11
well
Relative barcode abundance
1.0
0.8
0.6
0.4
0.2
0.0

FIG. 6A

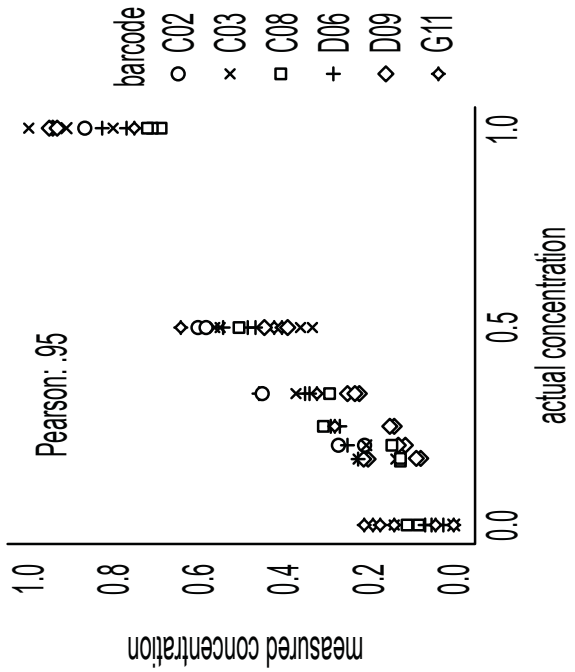
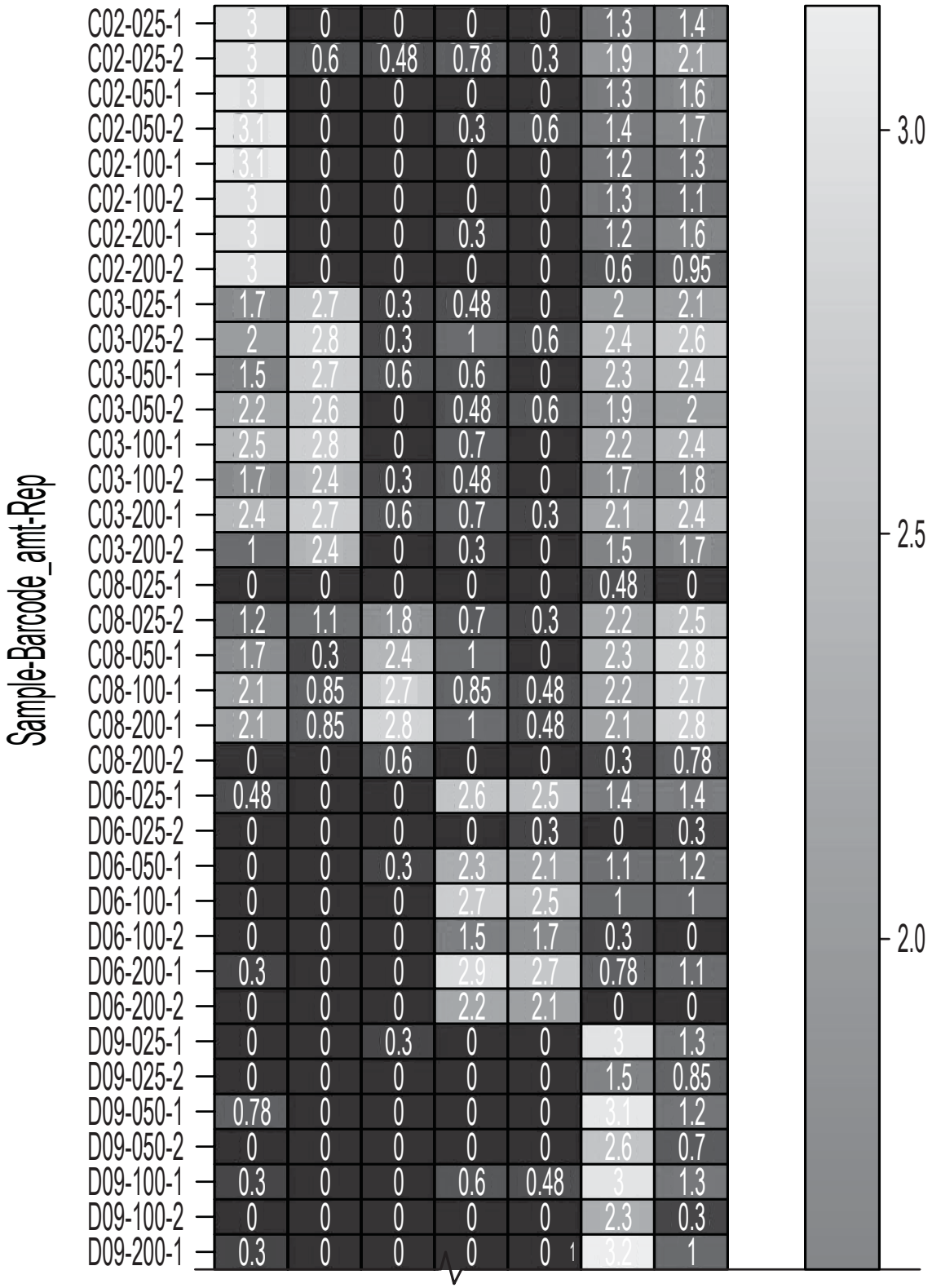

barcode
C02
C03
C08
D06
D09
G11
Pearson: .95
actual concentration
measured concentration
0.0
0.5
1.0
0.2
0.4
0.6
0.8

FIG. 6B



To FIG. 6C Continued

FIG. 6C

From FIG. 6C

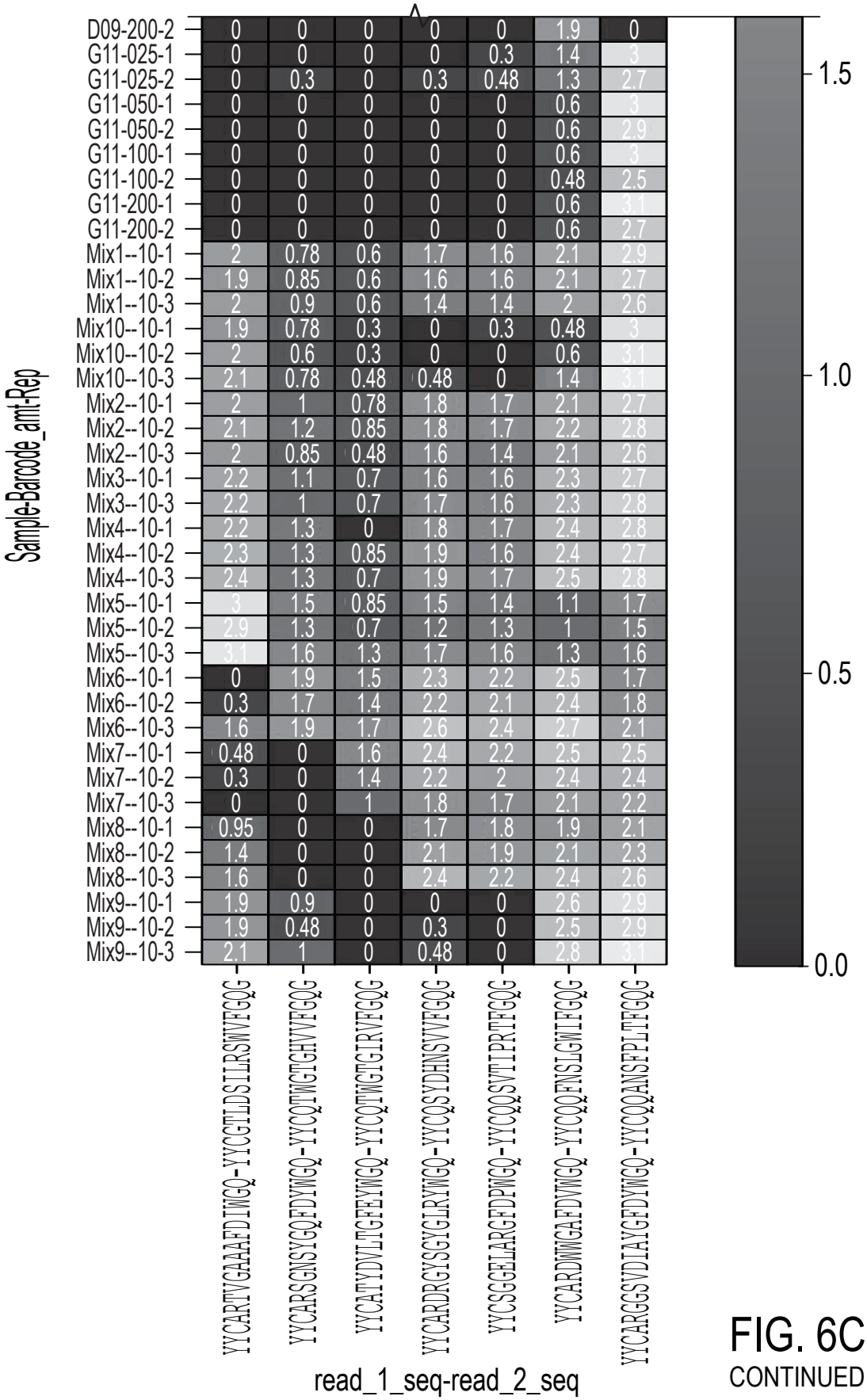


FIG. 6C
CONTINUED

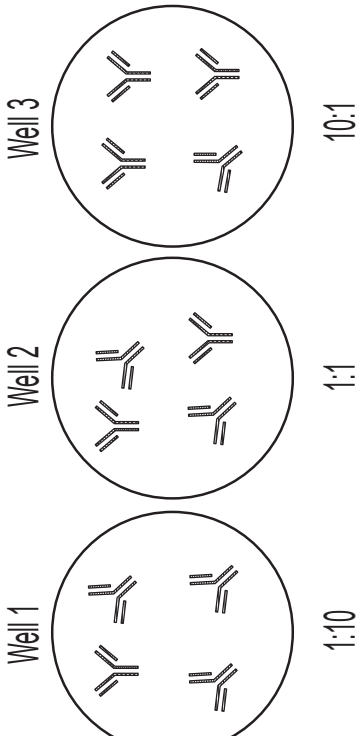

1. Pool
BC1 : BC2
Well 1
1:10
Well 2
1:1
Well 3
10:1
2. Quantify
{Protocol for Contact by Binding Agent + Computational Algorithm}
3. Report Quantification

FIG. 7A

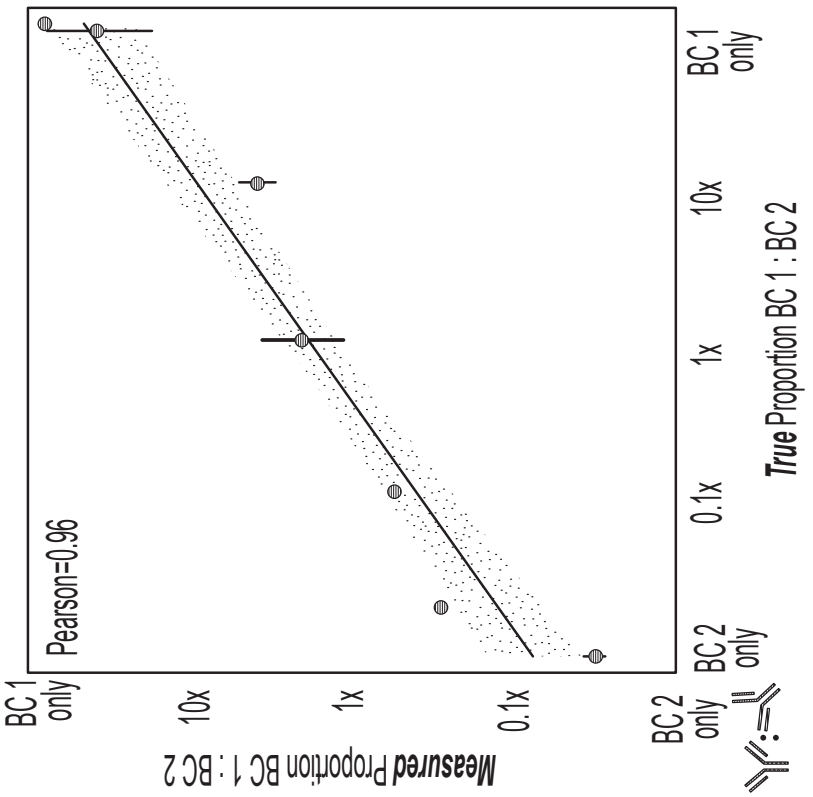

Measured Proportion BC 1 : BC 2
BC 1 only
10x
1x
0.1x
BC 2 only
Pearson=0.96
BC 2 only
0.1x
1x
10x
BC 1 only
True Proportion BC 1 : BC 2

FIG. 7B

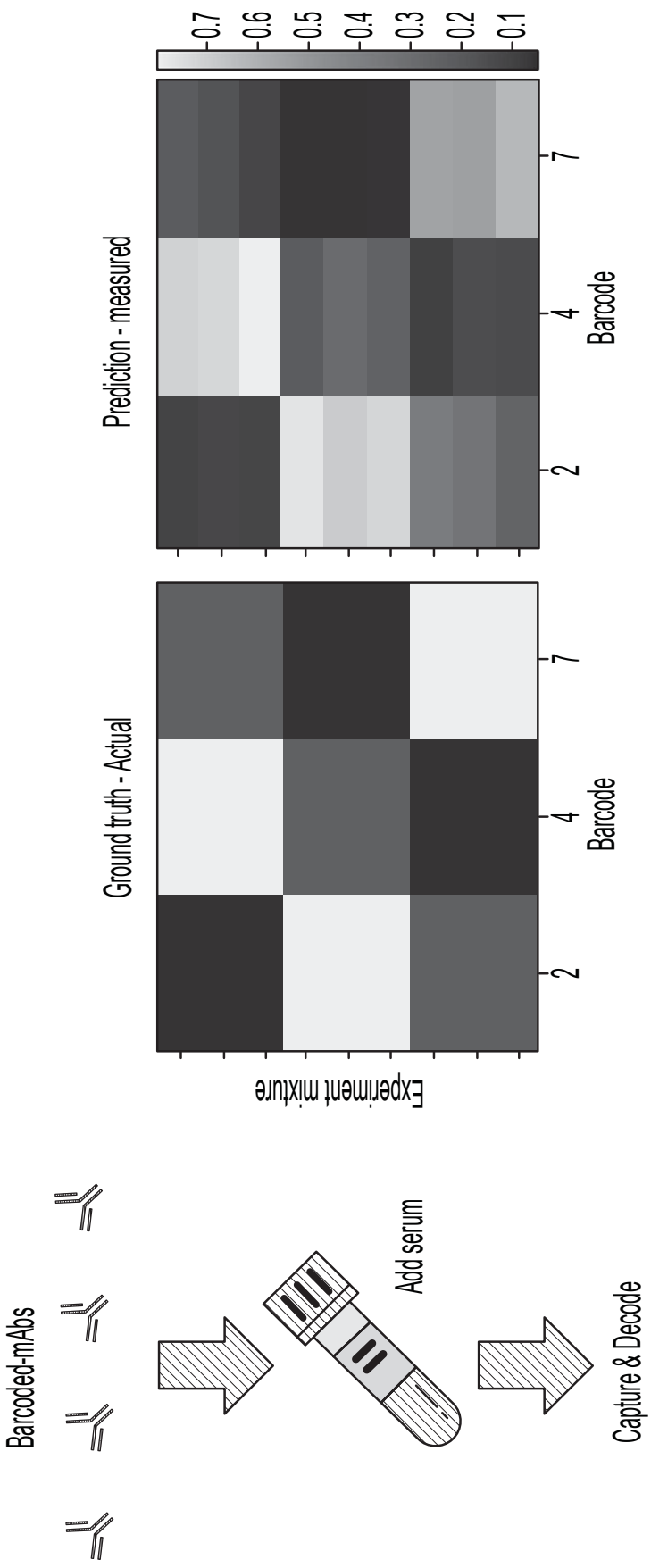

Barcoded-mAbs
Add serum
Capture & Decode
Experiment mixture
Ground truth - Actual
Prediction - measured
Barcode
Barcode
2
4
7
2
4
7
0.7
0.6
0.5
0.4
0.3
0.2
0.1

FIG. 8A

FIG. 8B

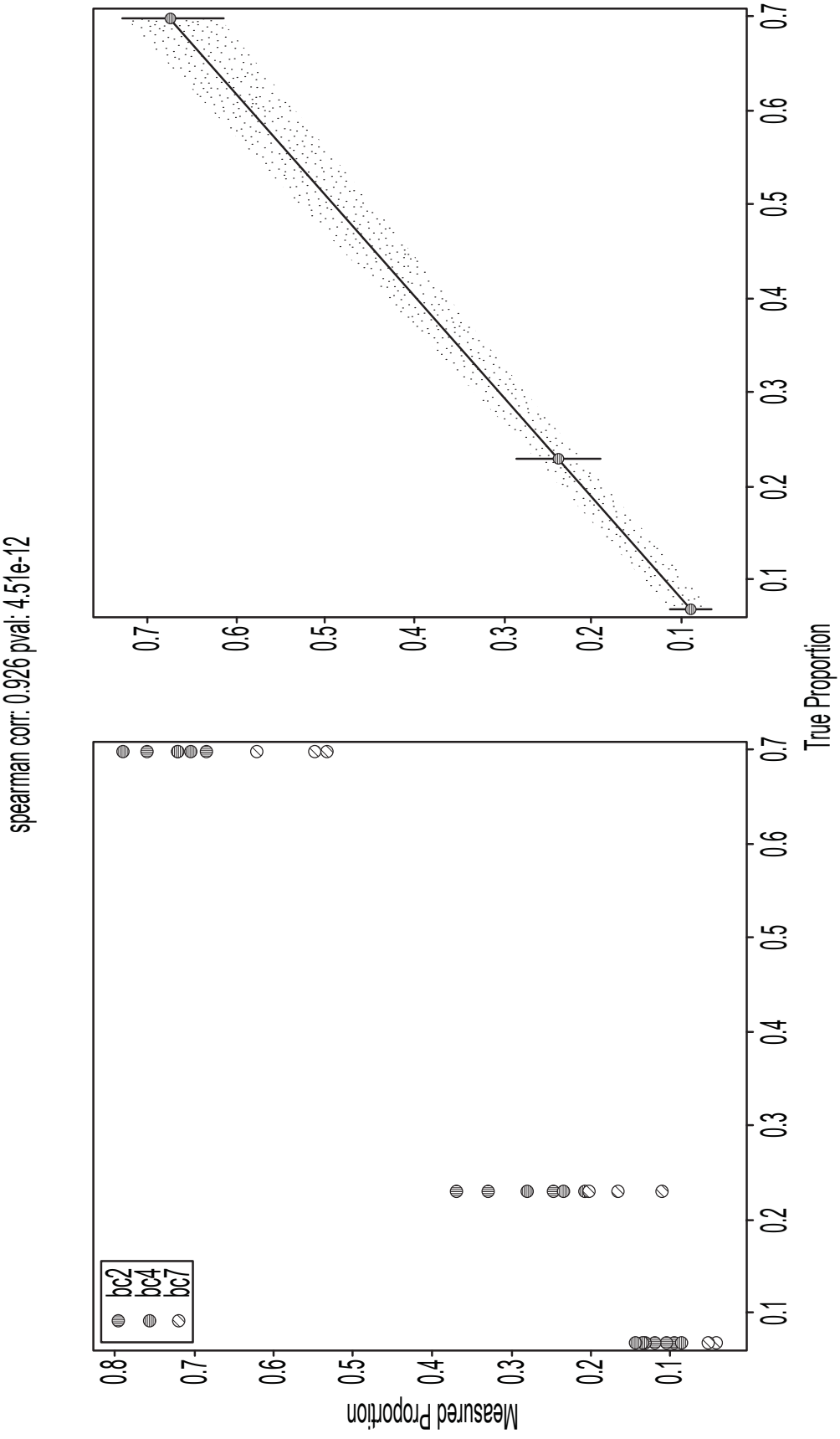

spearman corr: 0.926 pval: 4.51e-12
Measured Proportion
True Proportion
bc2
bc4
bc7
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8

FIG. 8C

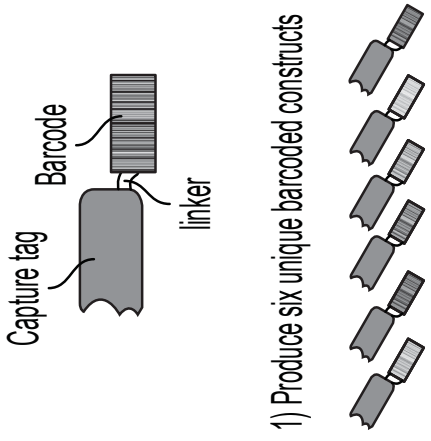

Capture tag
Barcode
linker
1) Produce six unique barcoded constructs
2) Mix at known proportions
3) Decode

FIG. 9A

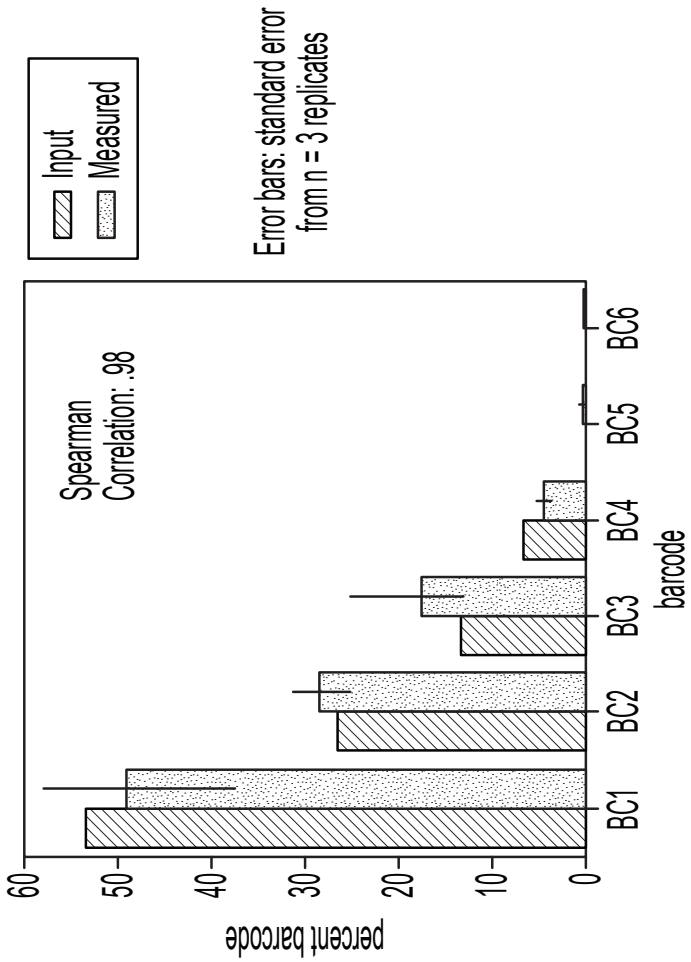

Input
Measured
Error bars: standard error
from n = 3 replicates
Spearman
Correlation: .98
percent barcode
60
50
40
30
20
10
0
BC1
BC2
BC3
BC4
BC5
BC6
barcode

FIG. 9B

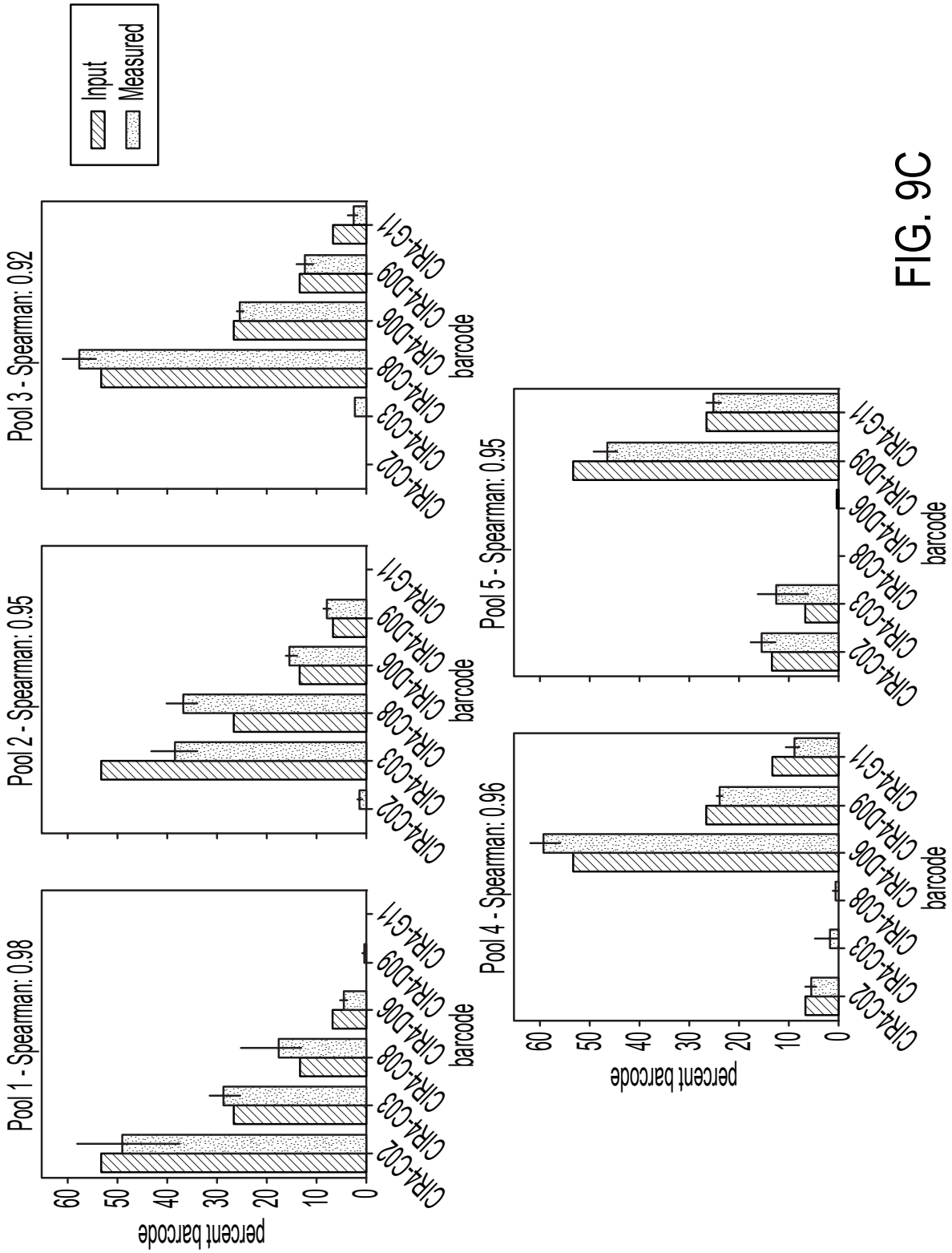

Input
Measured
Pool 1 - Spearman: 0.98
Pool 2 - Spearman: 0.95
Pool 3 - Spearman: 0.92
Pool 4 - Spearman: 0.96
Pool 5 - Spearman: 0.95
percent barcode
0
10
20
30
40
50
60
barcode
CR4-C02
CR4-C03
CR4-C08
CR4-D06
CR4-D09
CR4-G11

FIG. 9C

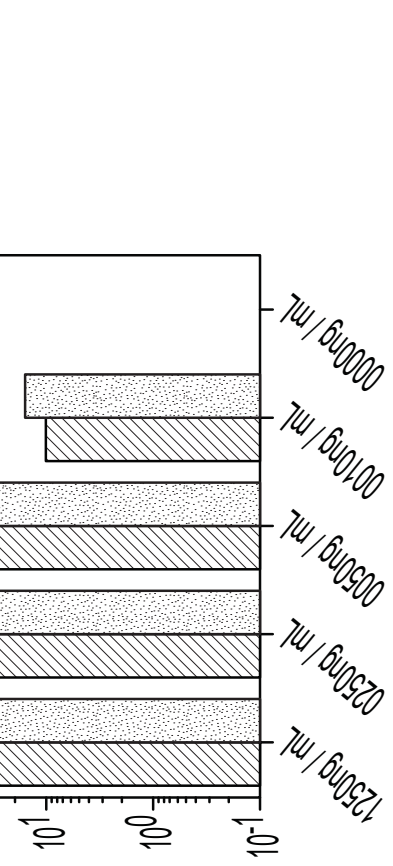


FIG. 10B

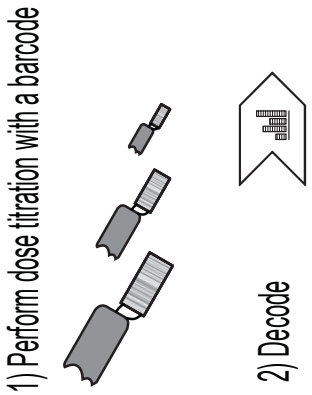


FIG. 10A

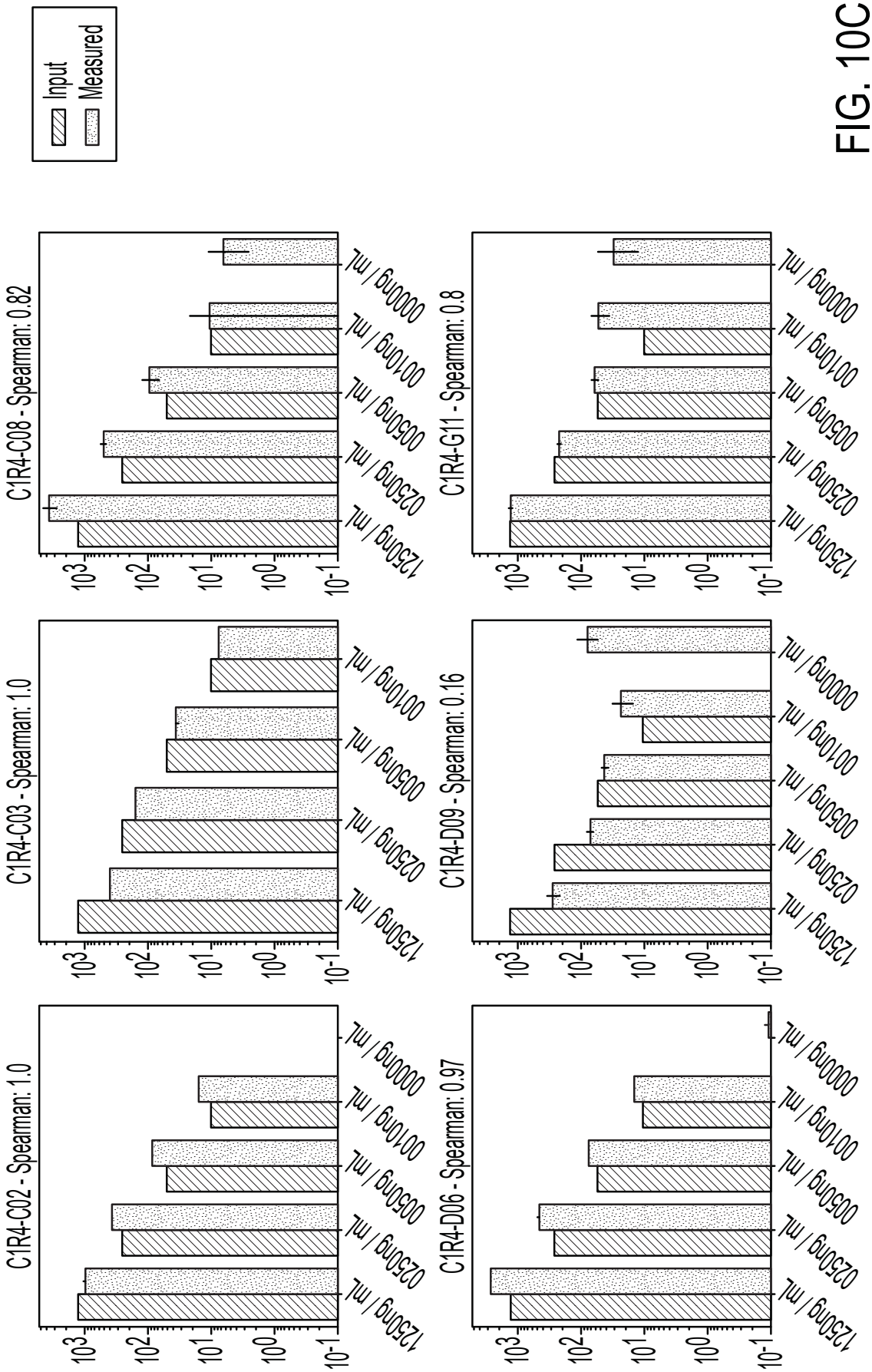

Input
Measured
C1R4-C02 - Spearman: 1.0
C1R4-C03 - Spearman: 1.0
C1R4-C08 - Spearman: 0.82
C1R4-D06 - Spearman: 0.97
C1R4-D09 - Spearman: 0.16
C1R4-G11 - Spearman: 0.8
10^3
10^2
10^1
10^0
10^-1
1250ng / mL
0250ng / mL
0050ng / mL
0010ng / mL
0000ng / mL

FIG. 10C

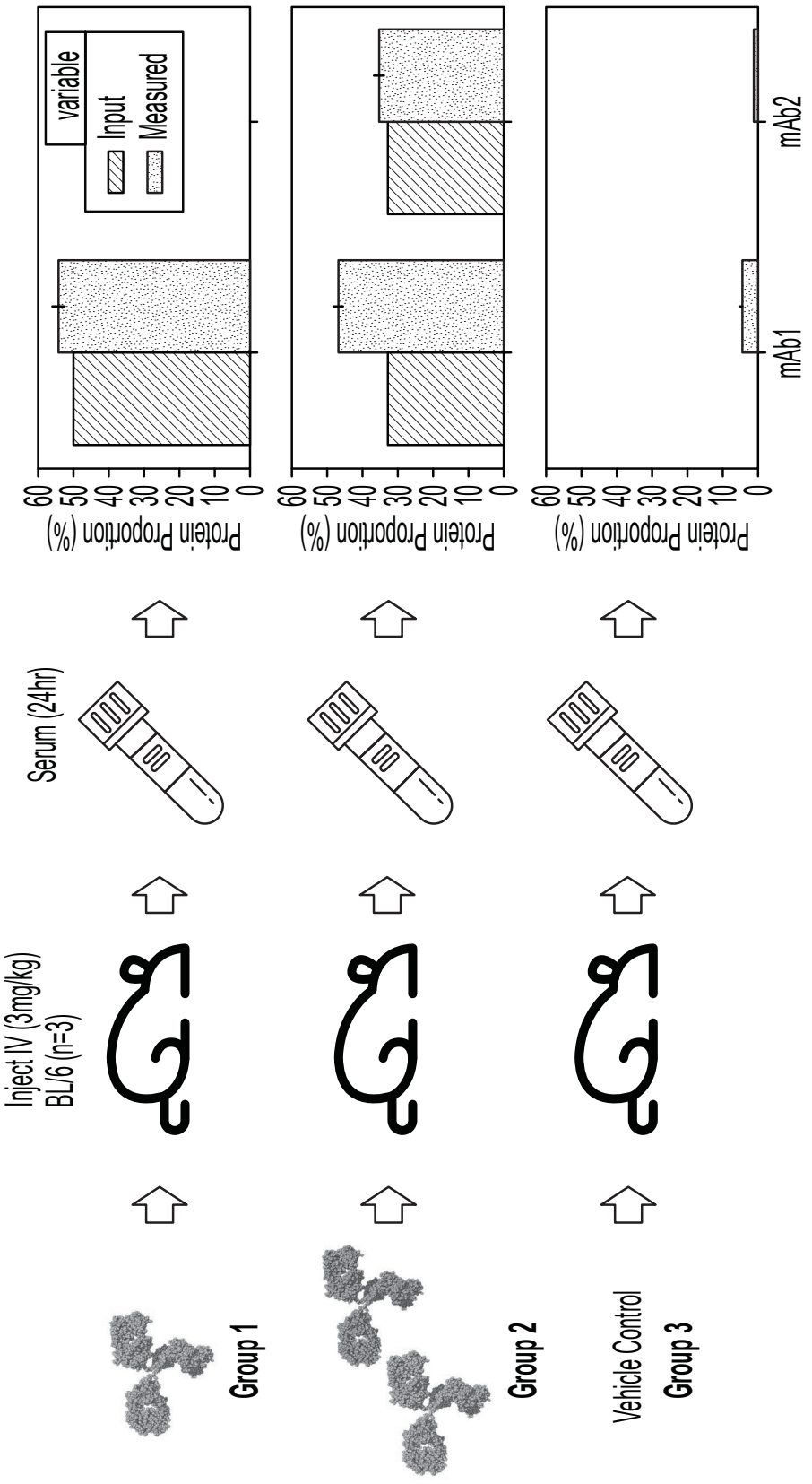

Group 1
Group 2
Vehicle Control
Group 3
Inject IV (3mg/kg)
BL/6 (n=3)
Serum (24hr)
Protein Proportion (%)
60
50
40
30
20
10
0
variable
Input
Measured
mAb1
mAb2

FIG. 11

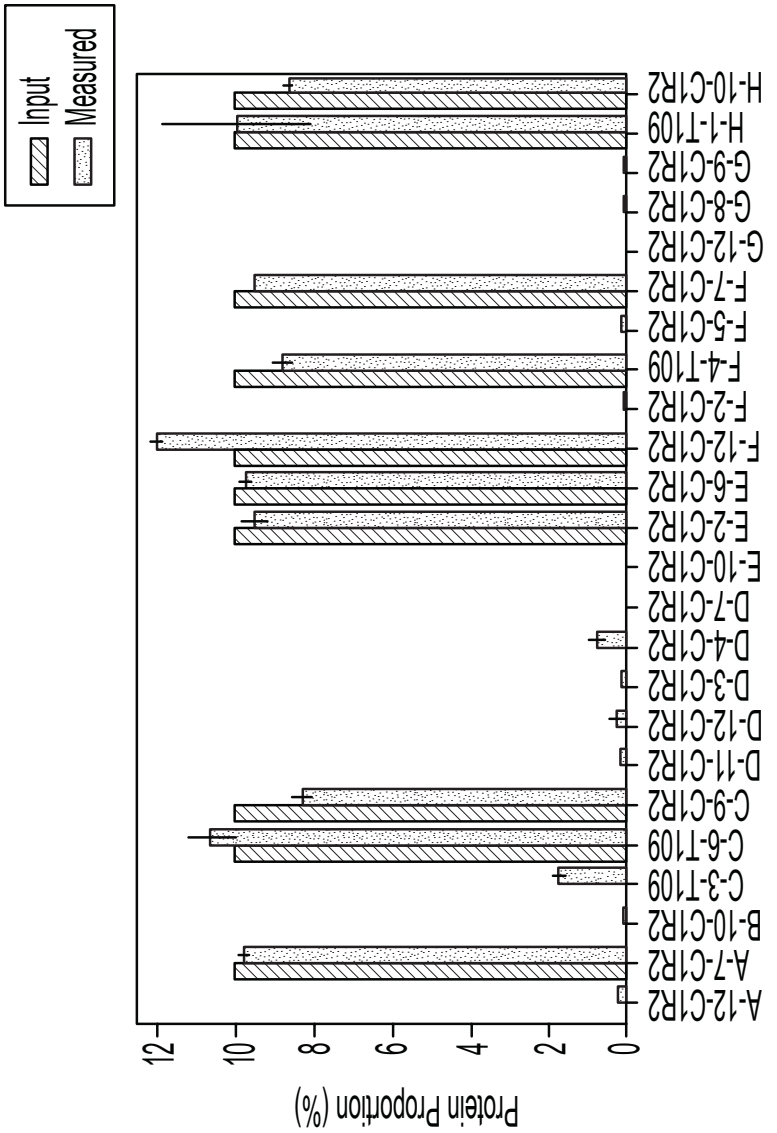


FIG. 12B

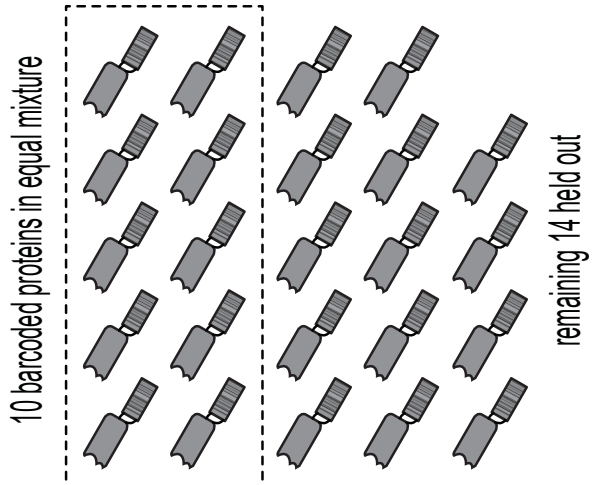


FIG. 12A

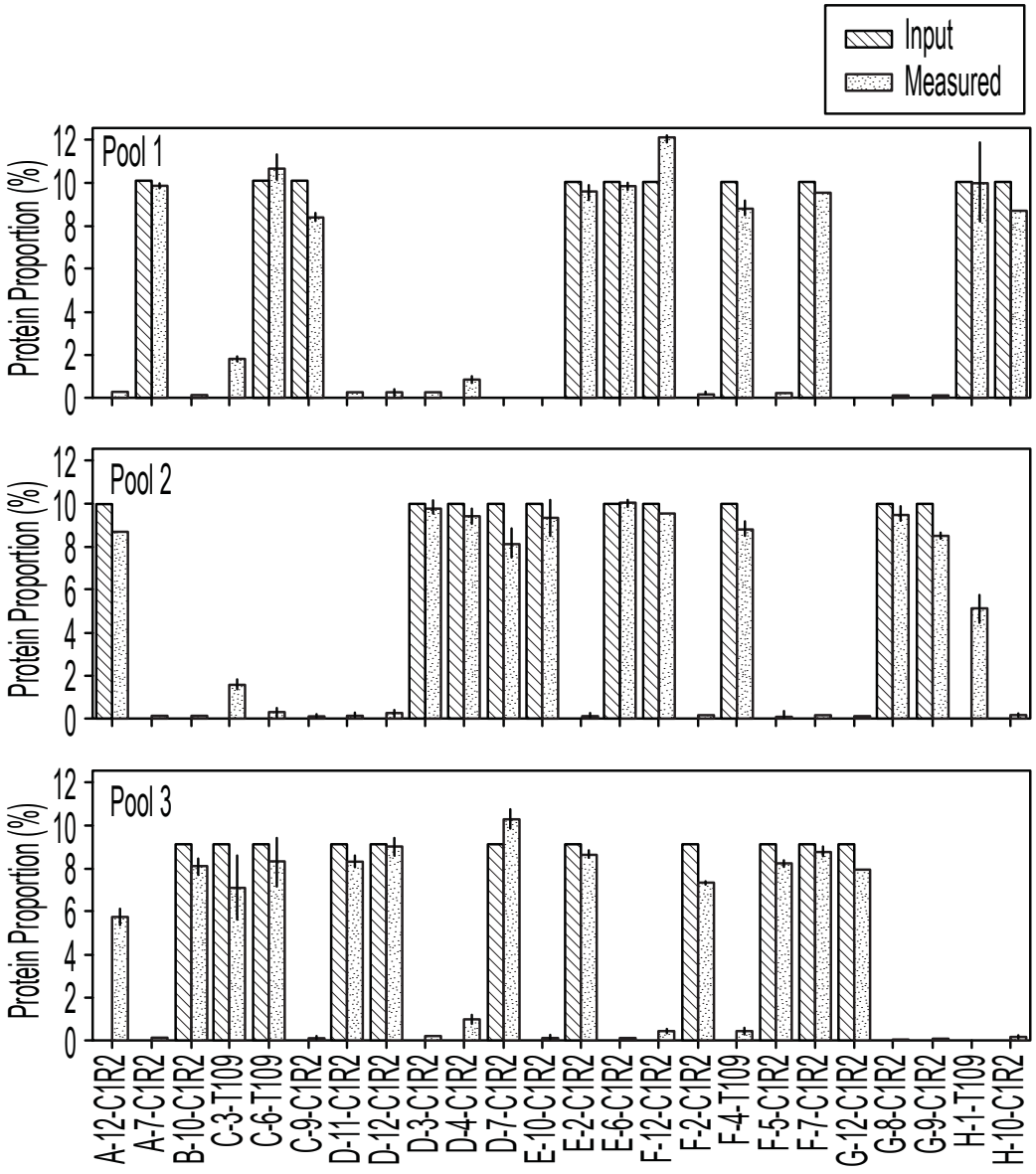

Input
Measured
Pool 1
Pool 2
Pool 3
Protein Proportion (%)
0
2
4
6
8
10
12
A-12-C1R2
A-7-C1R2
B-10-C1R2
C-3-T109
C-6-T109
C-9-C1R2
D-11-C1R2
D-12-C1R2
D-3-C1R2
D-4-C1R2
D-7-C1R2
E-10-C1R2
E-2-C1R2
E-6-C1R2
F-12-C1R2
F-2-C1R2
F-4-T109
F-5-C1R2
F-7-C1R2
G-12-C1R2
G-8-C1R2
G-9-C1R2
H-1-T109
H-10-C1R2

FIG. 12C

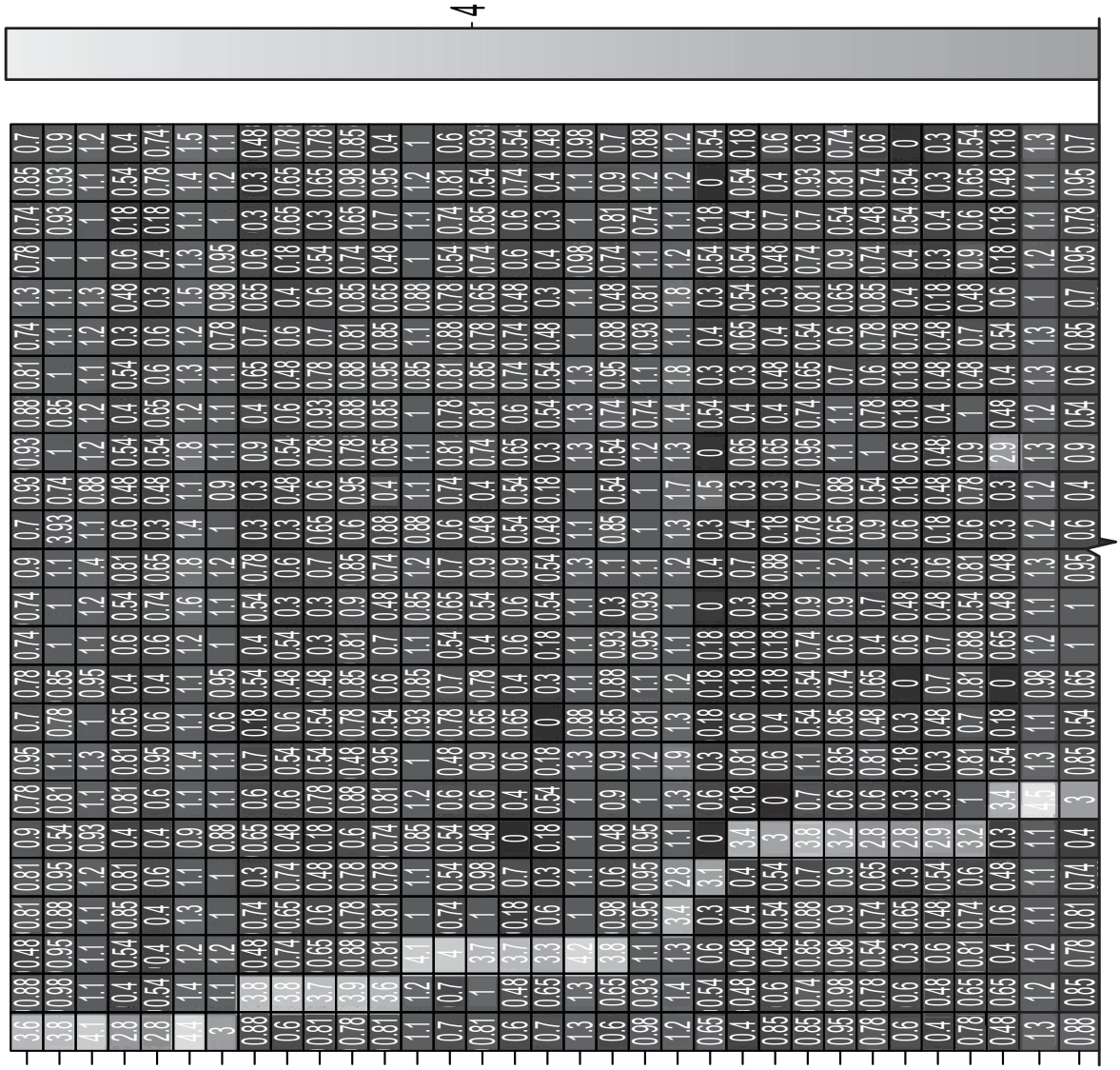


FIG. 12D

From FIG. 12D

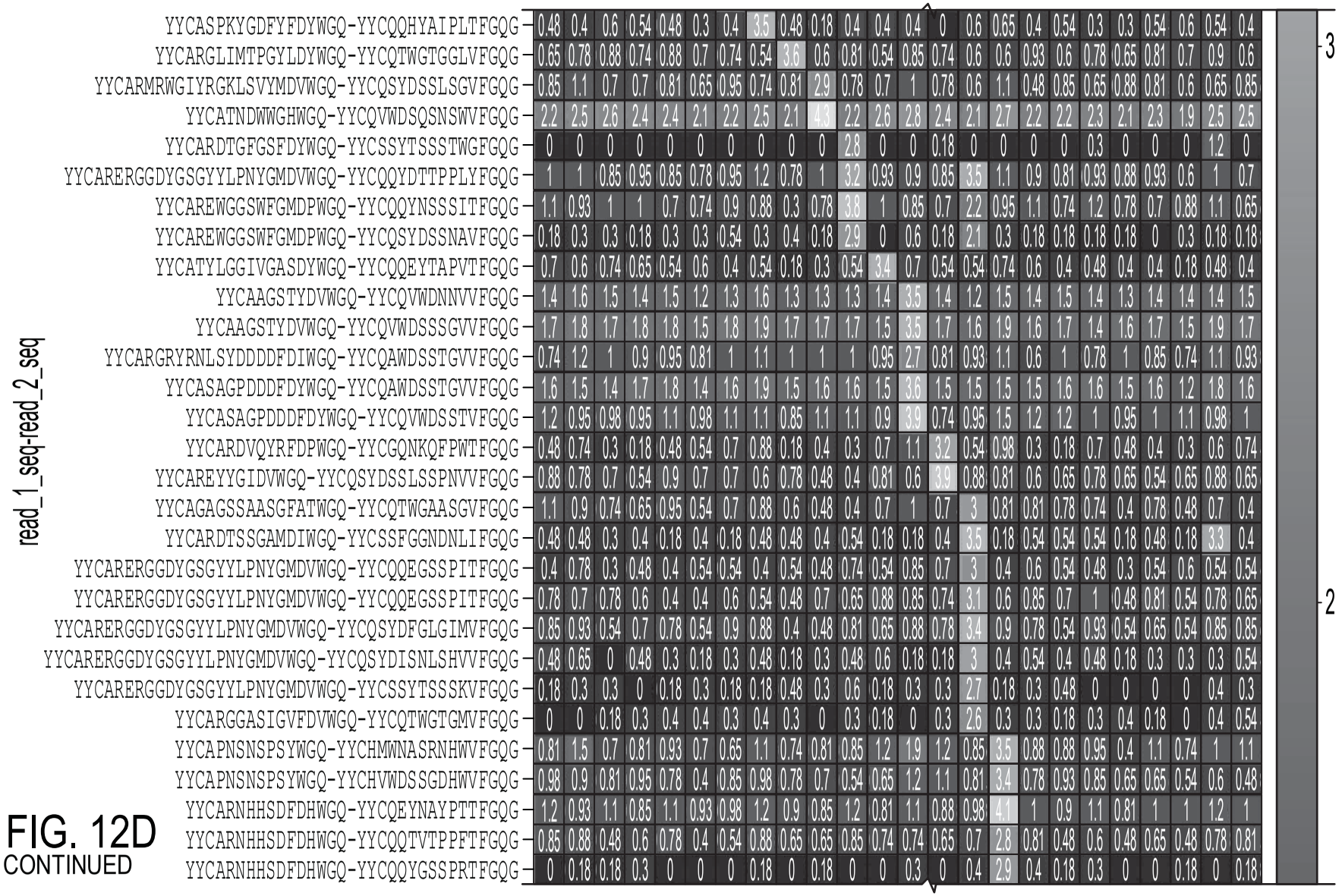


FIG. 12D
CONTINUED

To FIG. 12D Continued

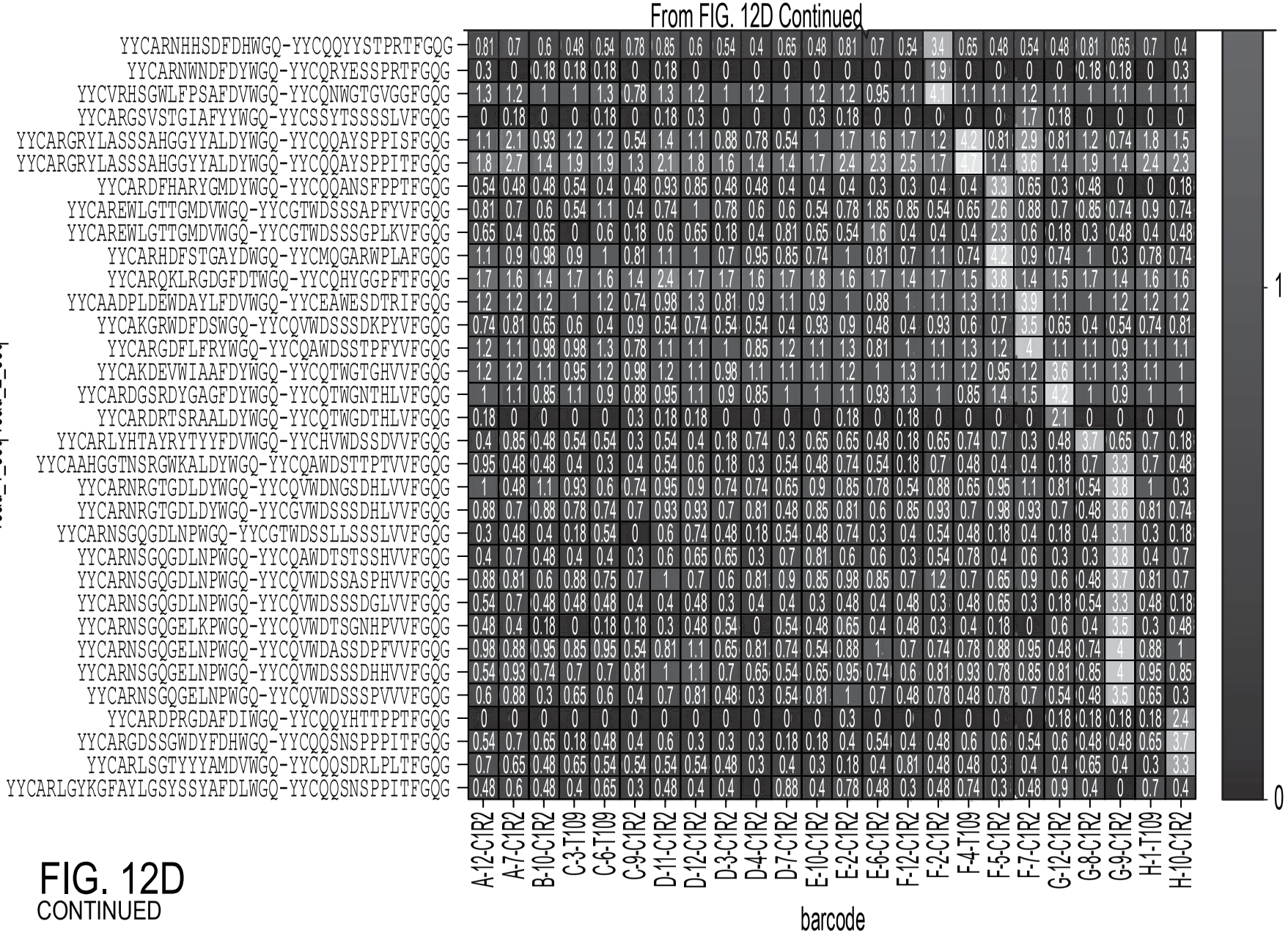
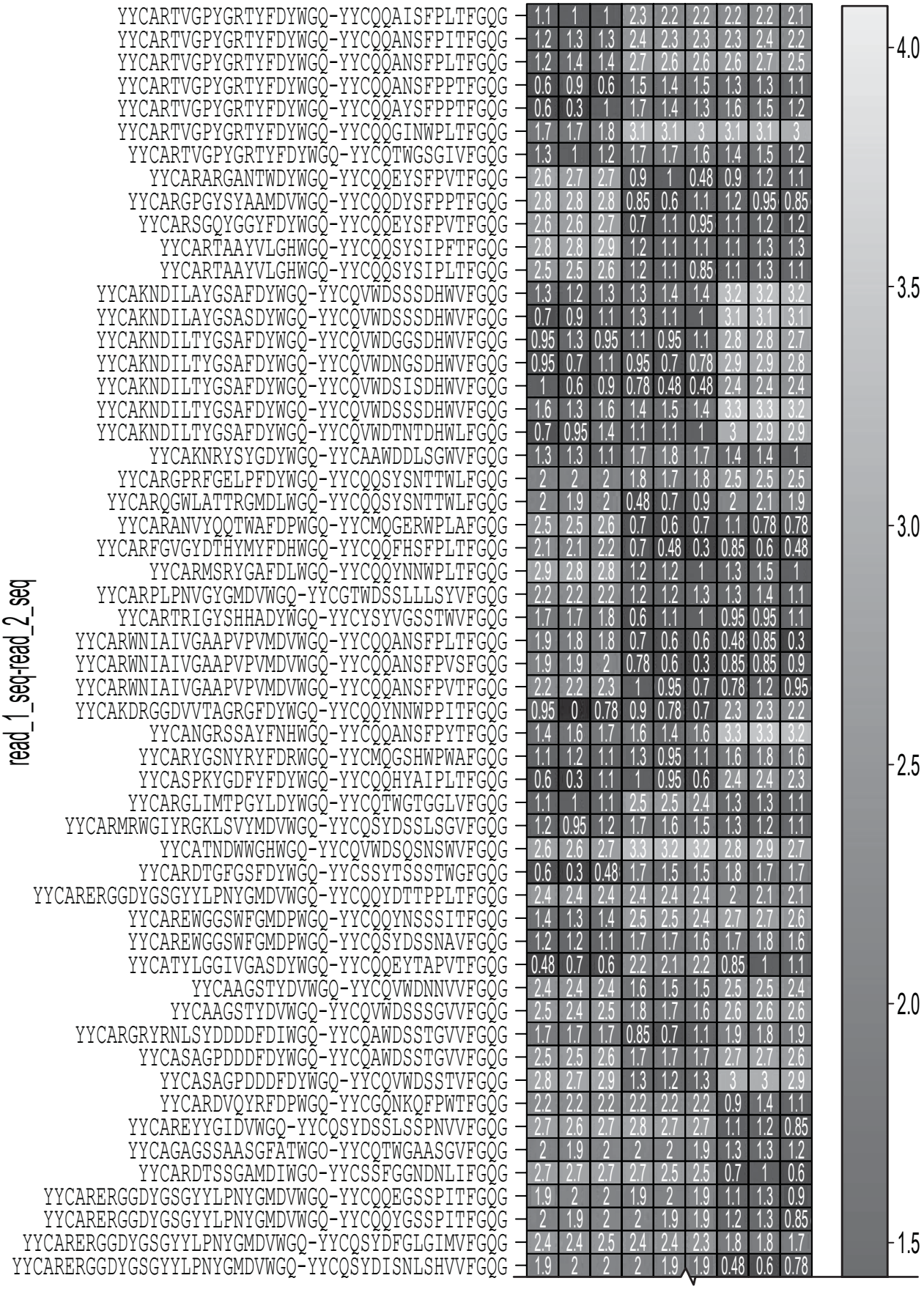


FIG. 12D
CONTINUED



To FIG. 12E Continued

FIG. 12E

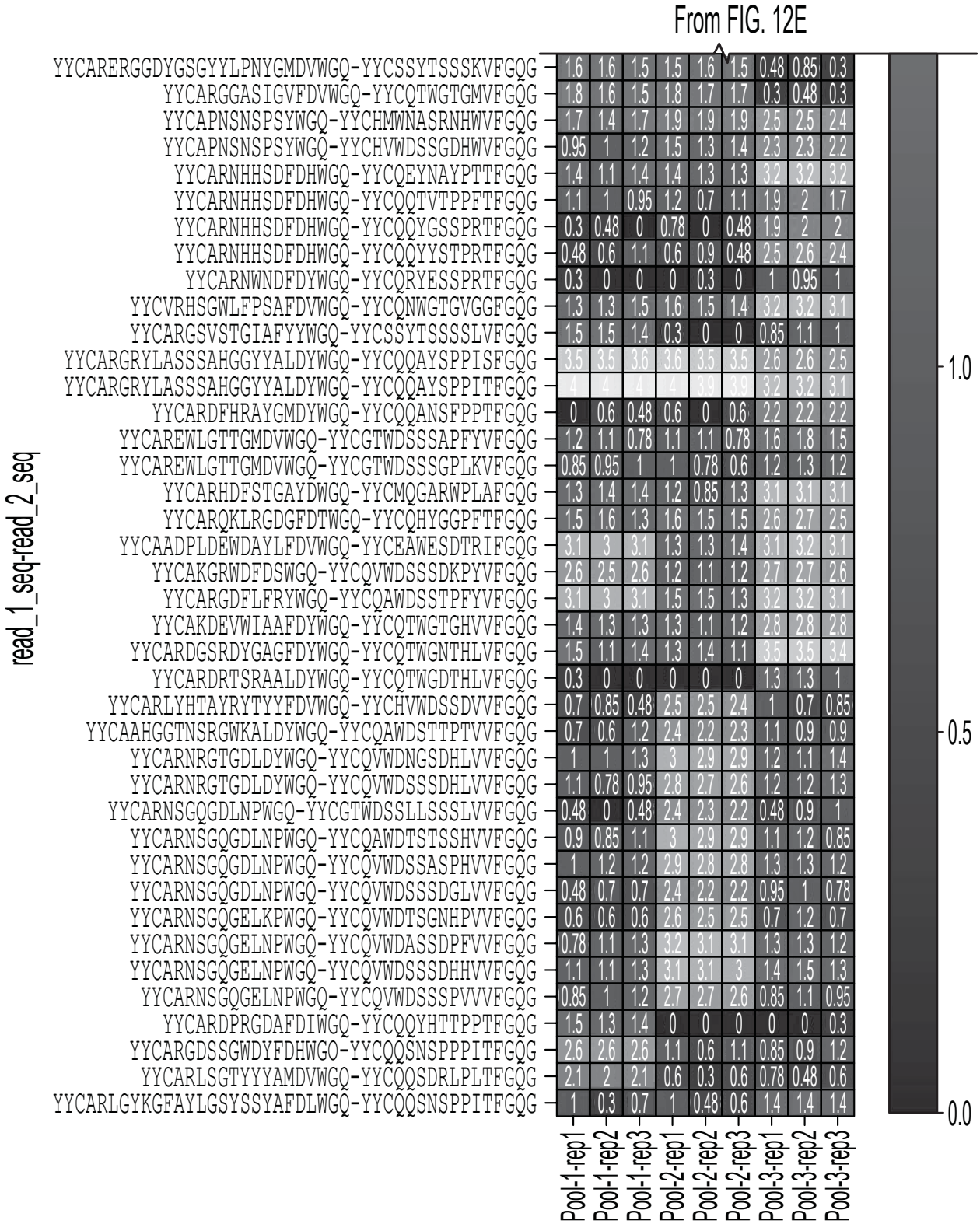


FIG. 12E
CONTINUED

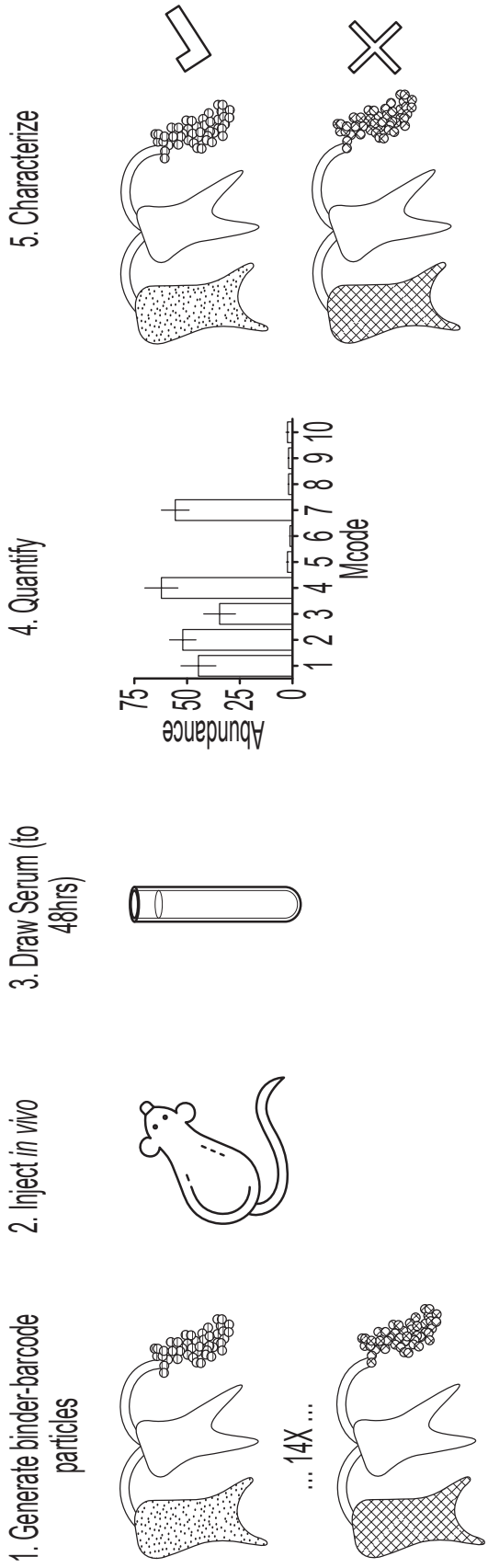

1. Generate binder-barcode particles
2. Inject *in vivo*
3. Draw Serum (to 48hrs)
4. Quantify
5. Characterize
...14X...
Abundance
75
50
25
0
1 2 3 4 5 6 7 8 9 10
Mcode

FIG. 13A

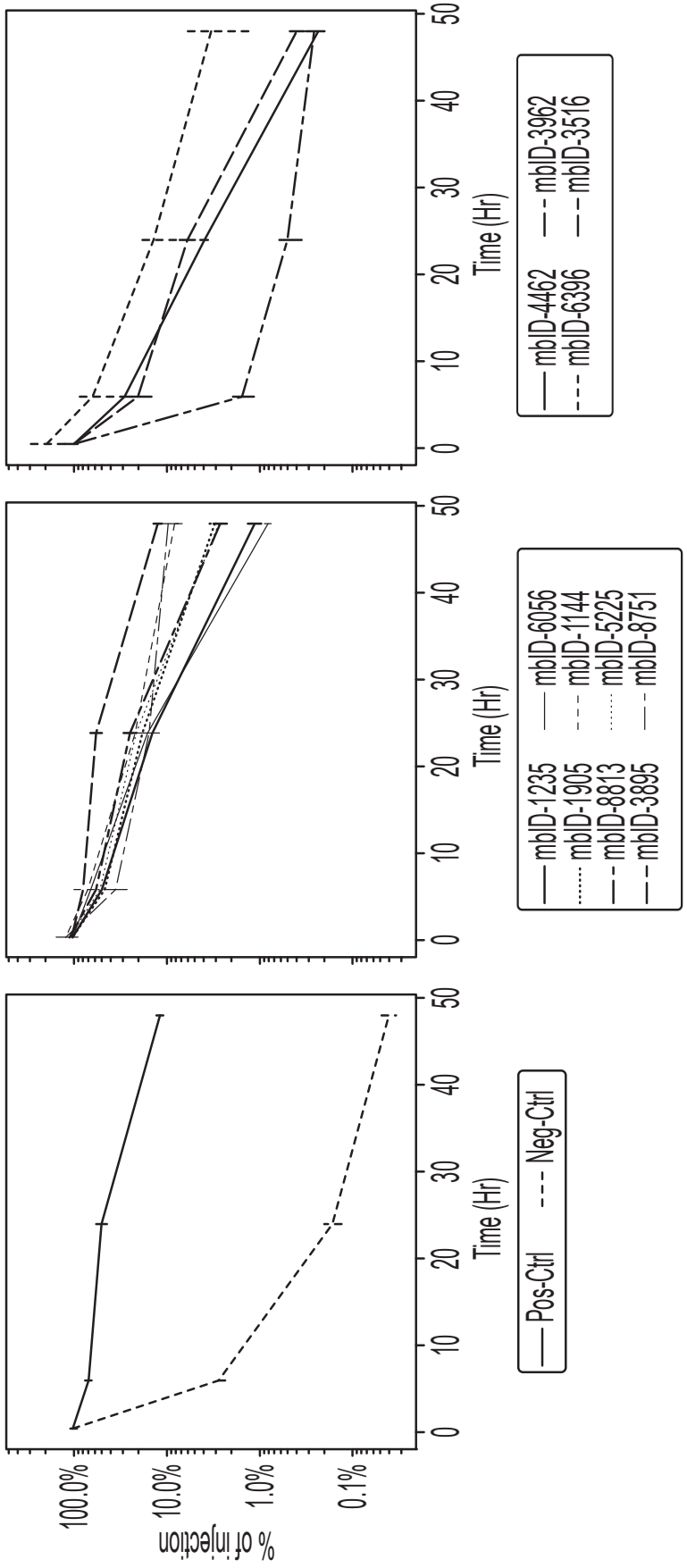

% of injection
100.0%
10.0%
1.0%
0.1%
0
10
20
30
40
50
Time (Hr)
Pos-Ctrl
Neg-Ctrl
mbID-1235
mbID-1905
mbID-8813
mbID-3895
mbID-6056
mbID-1144
mbID-5225
mbID-8751
mbID-4462
mbID-6396
mbID-3962
mbID-3516

FIG. 13B

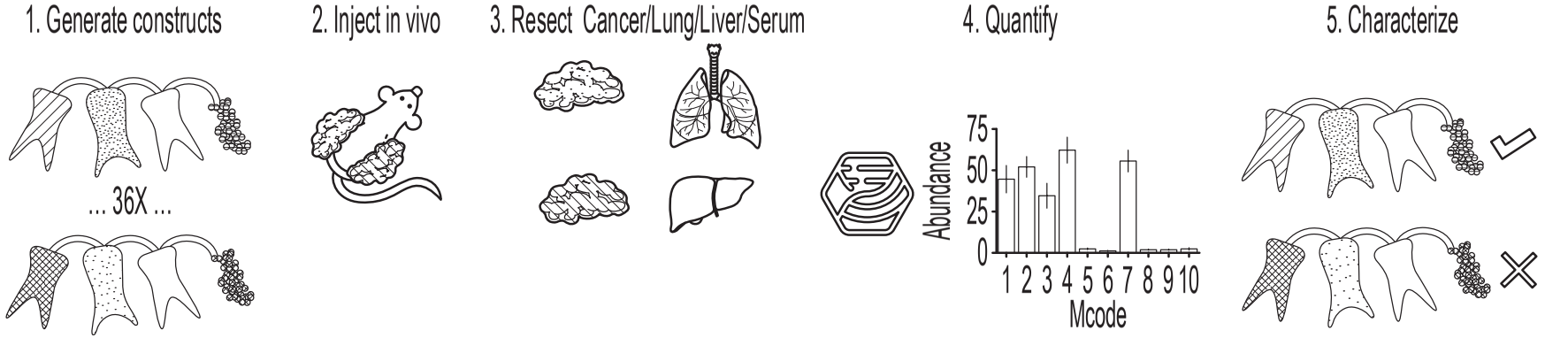

1. Generate constructs
... 36X ...
2. Inject in vivo
3. Resect Cancer/Lung/Liver/Serum
4. Quantify
Abundance
75
50
25
0
1 2 3 4 5 6 7 8 9 10
Mcode
5. Characterize

FIG. 14A

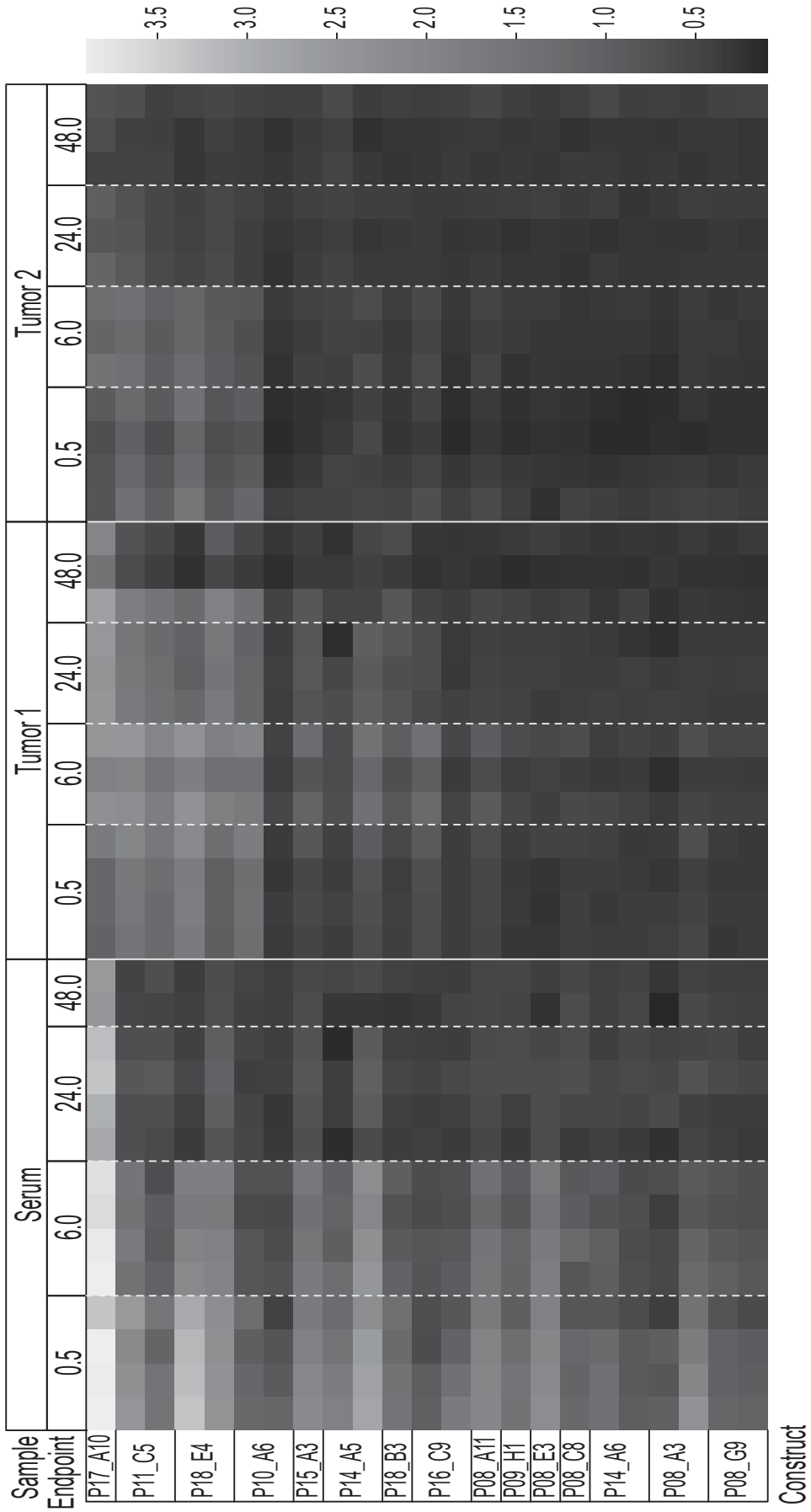

Sample
Endpoint
Serum
Tumor 1
Tumor 2
0.5
6.0
24.0
48.0
0.5
6.0
24.0
48.0
0.5
6.0
24.0
48.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
P17_A10
P11_C5
P18_E4
P10_A6
P15_A3
P14_A5
P18_B3
P16_C9
P08_A11
P09_H1
P08_E3
P08_C8
P14_A6
P08_A3
P08_G9
Construct

FIG. 14B

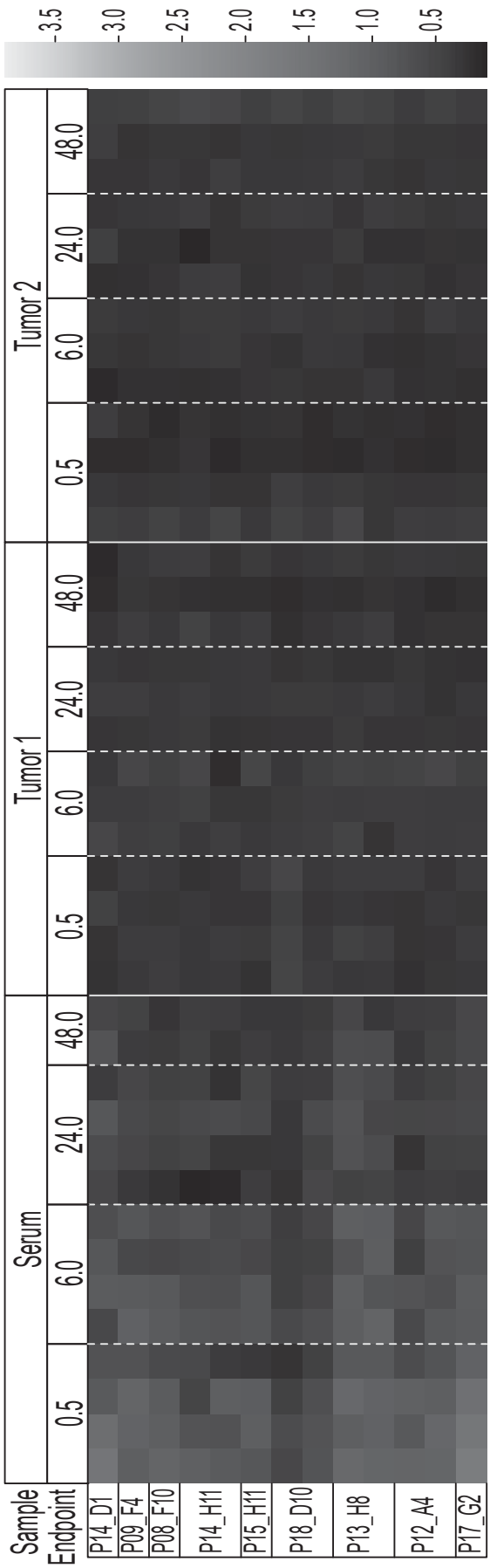


FIG. 14B
CONTINUED

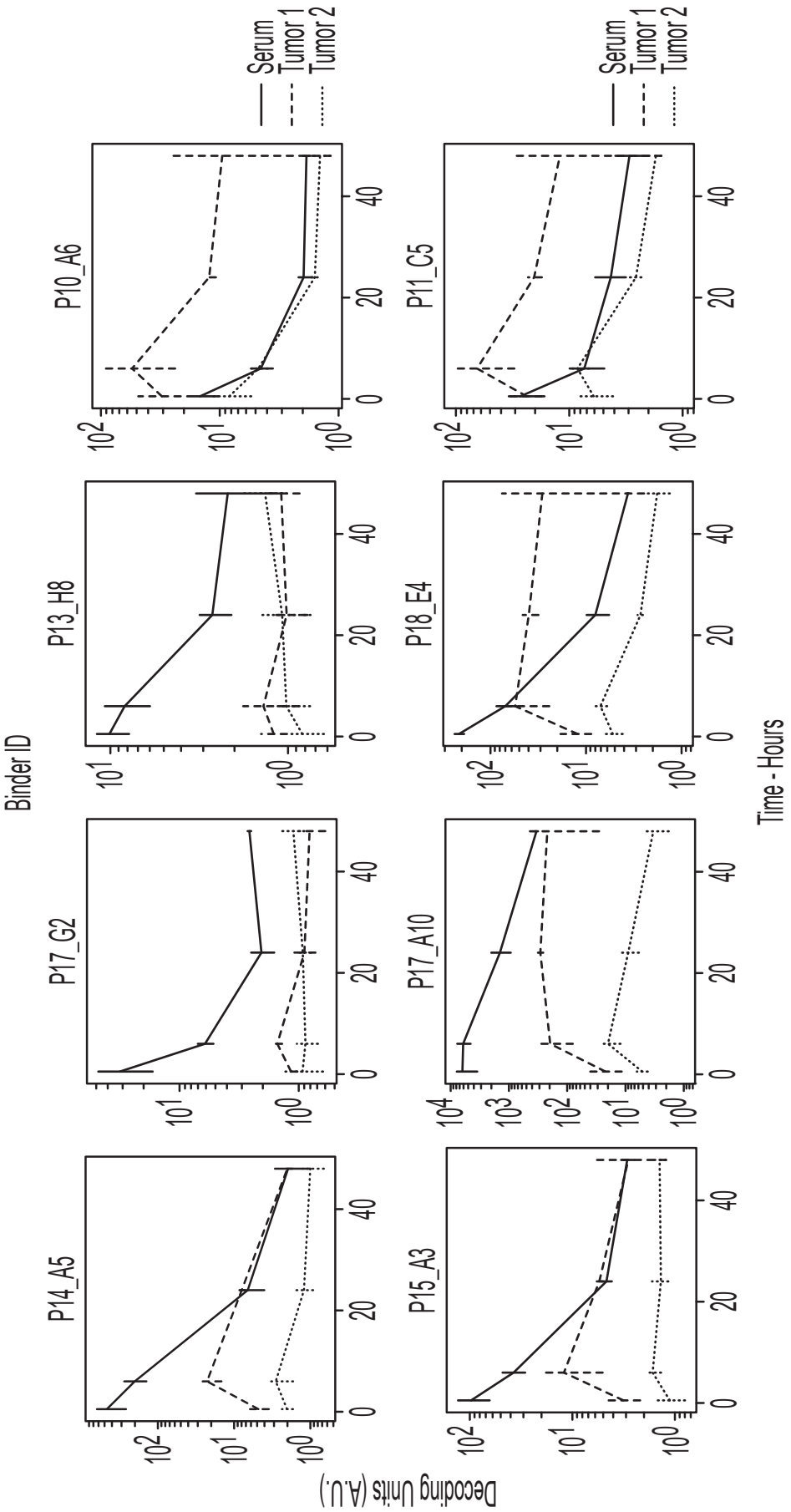

Decoding Units (A.U.)
Binder ID
Time - Hours
P14_A5
P17_G2
P13_H8
P10_A6
P15_A3
P17_A10
P18_E4
P11_C5
Serum
Tumor 1
Tumor 2

FIG. 14C

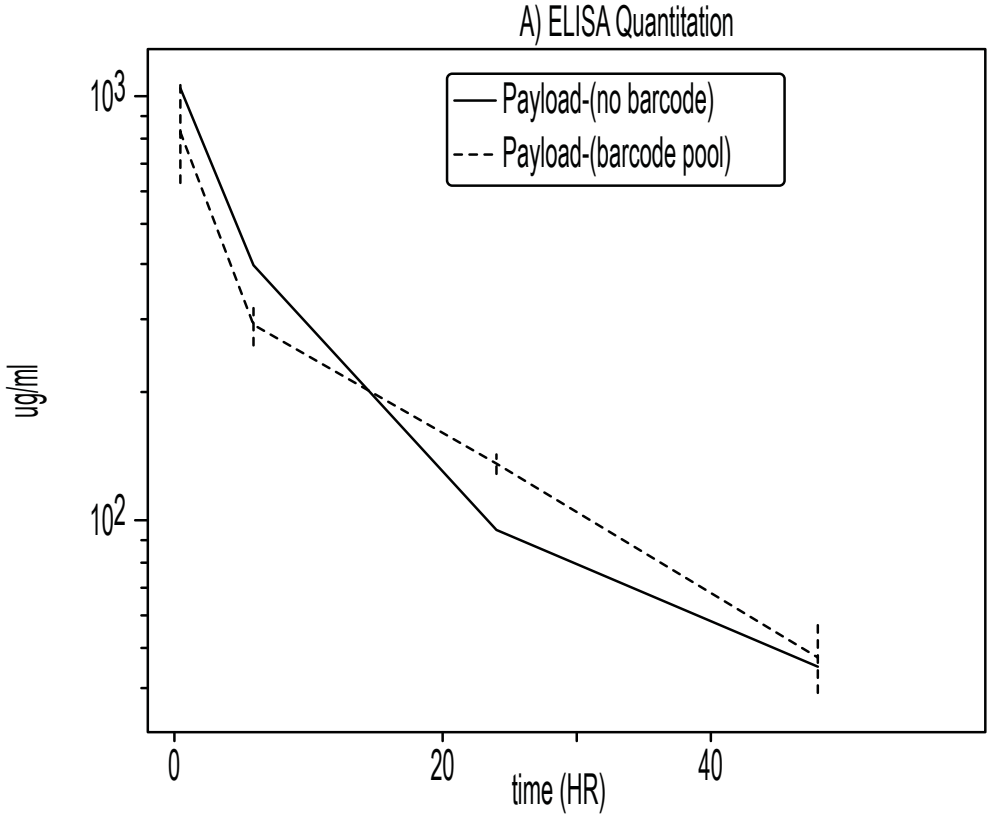


FIG. 15A

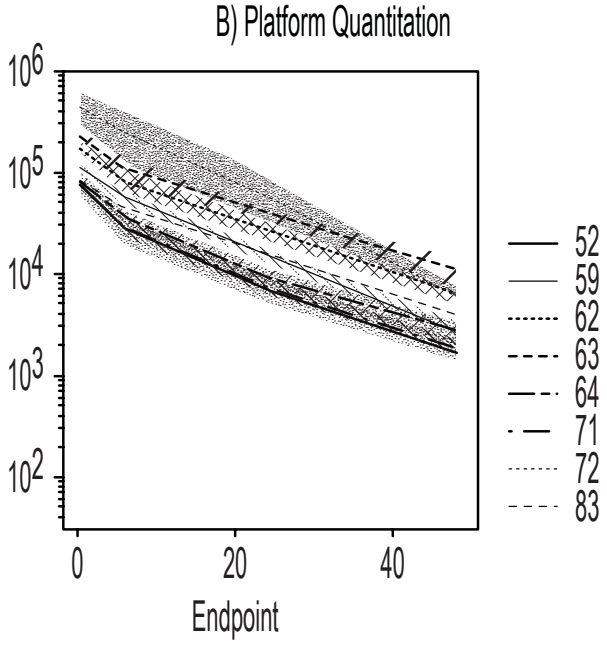


FIG. 15B

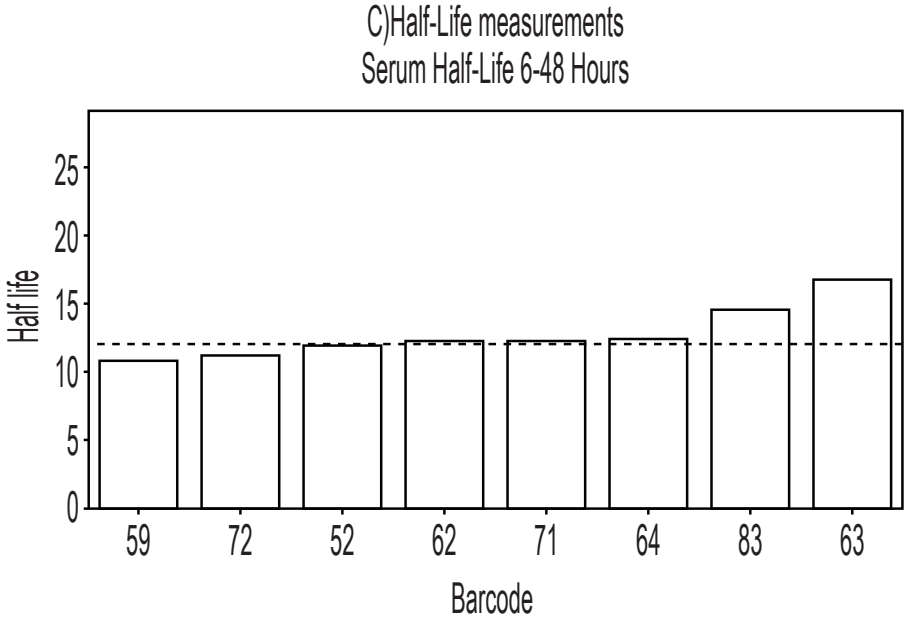

C)Half-Life measurements
Serum Half-Life 6-48 Hours
Half life
25
20
15
10
5
0
59
72
52
62
71
64
83
63
Barcode

FIG. 15C

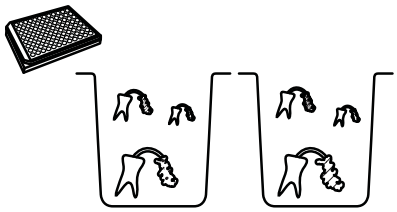
1. Produce {constant scaffold}-barcode



35X (highest sensitivity)



2. Array *in mixtures*



3. Quantify



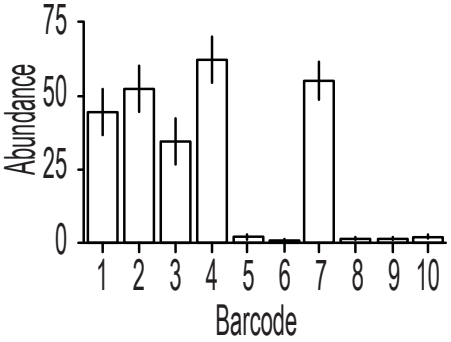


FIG. 16A

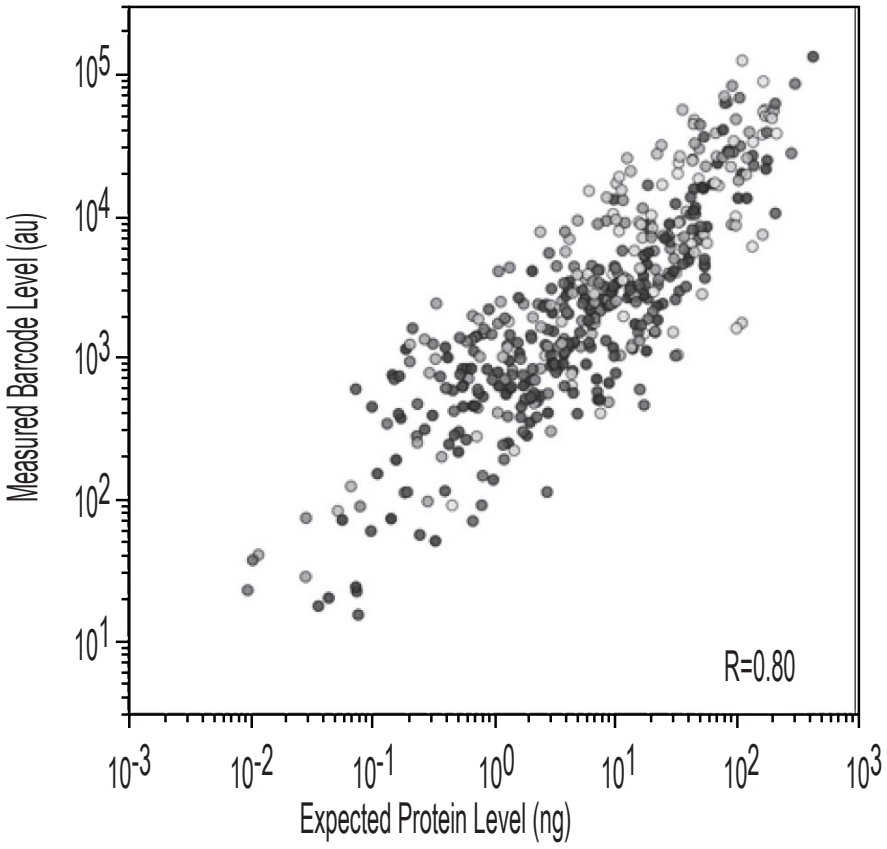

Measured Barcode Level (au)
10^5
10^4
10^3
10^2
10^1
R=0.80
10^{-3}
10^{-2}
10^{-1}
10^0
10^1
10^2
10^3
Expected Protein Level (ng)

FIG. 16B