

Figure 1

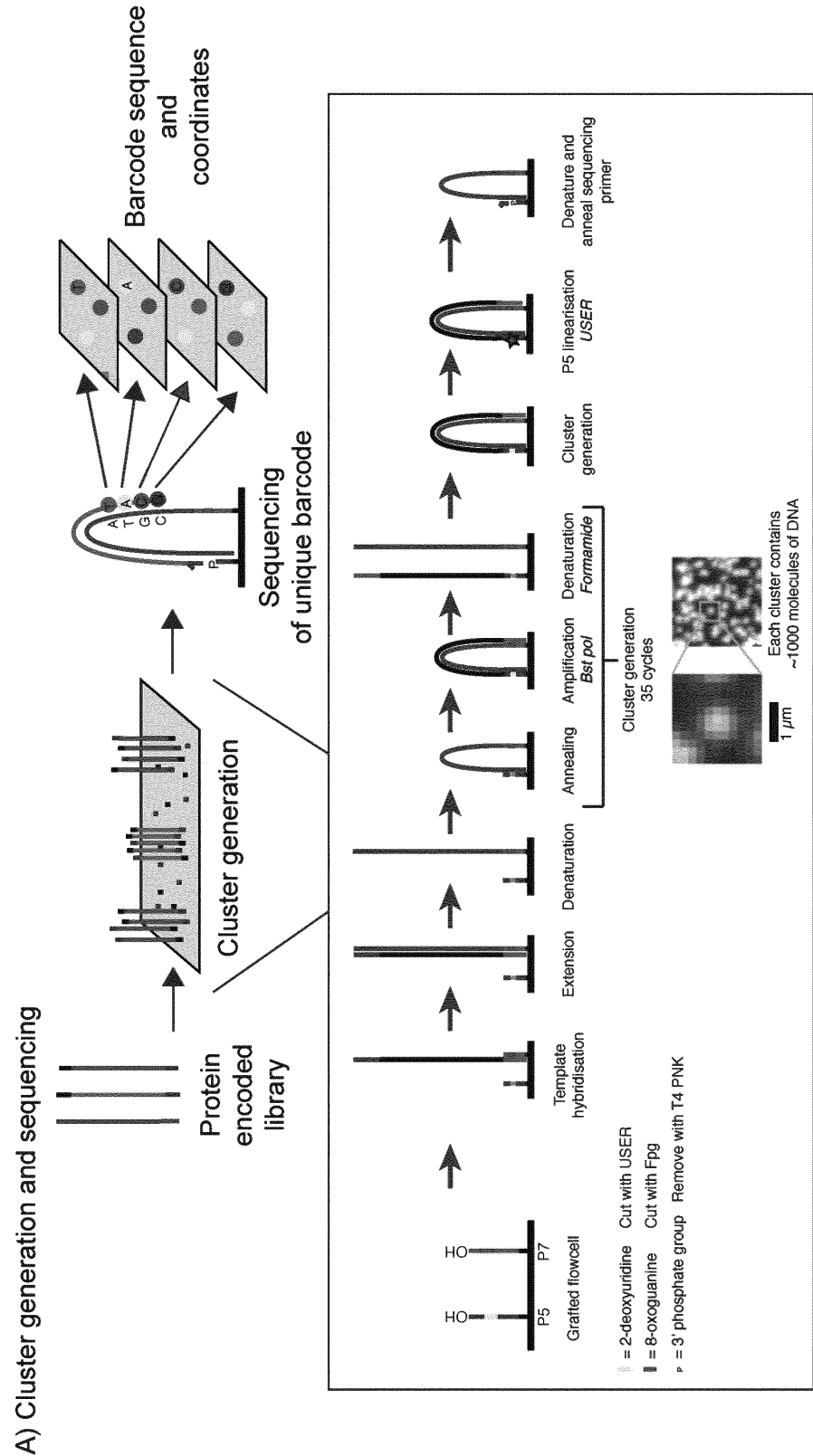


Figure 1 (cont)

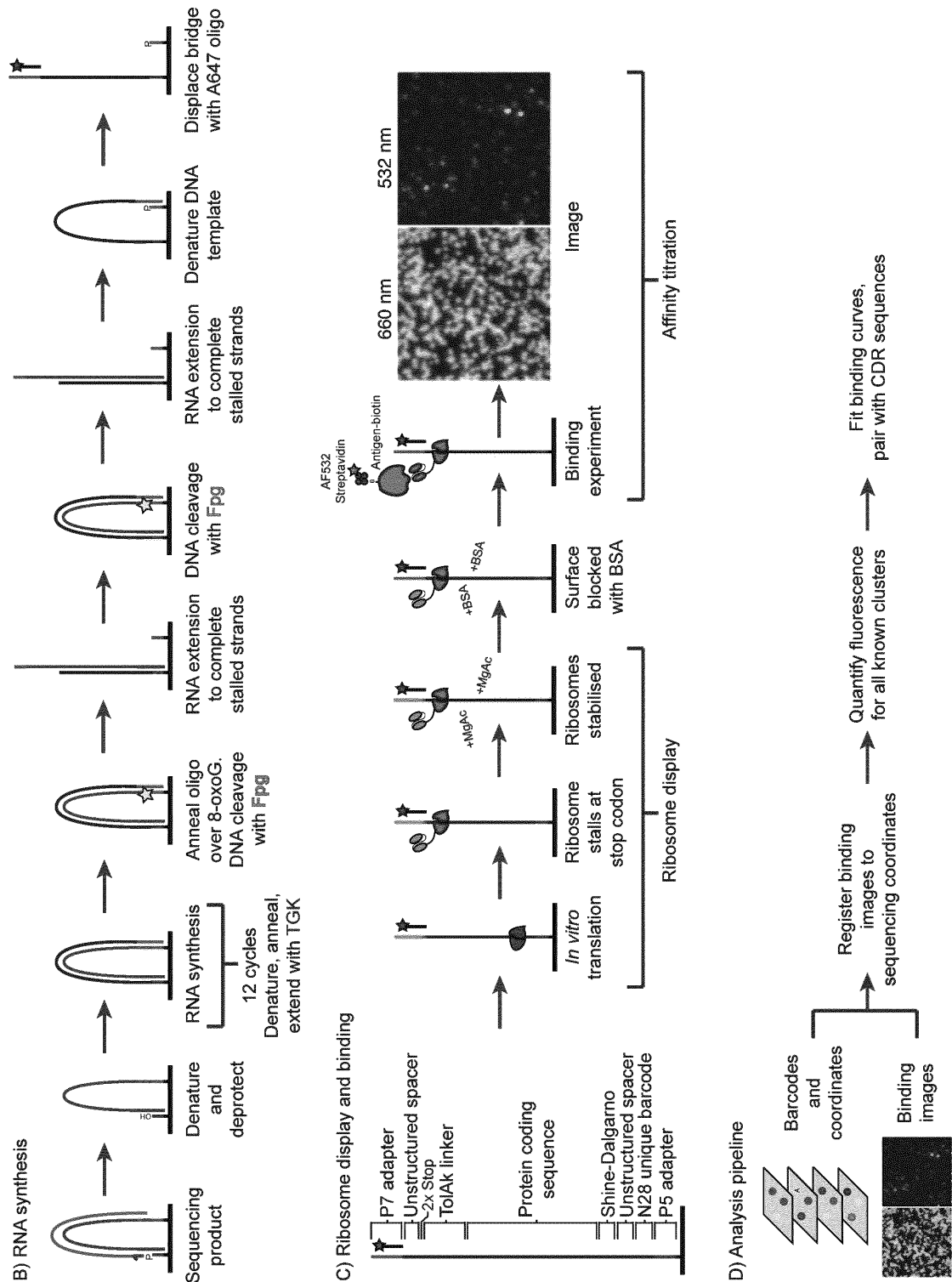
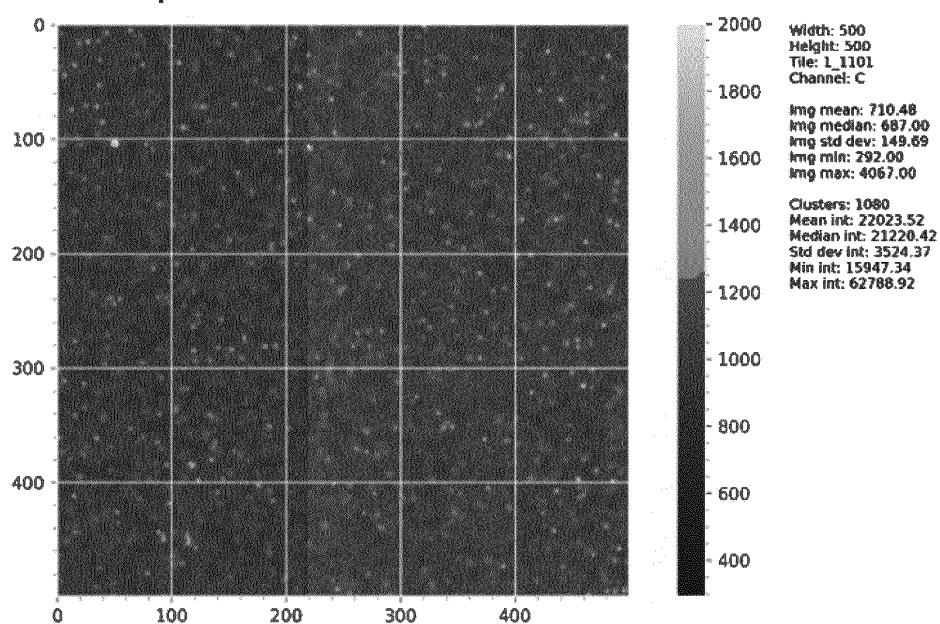
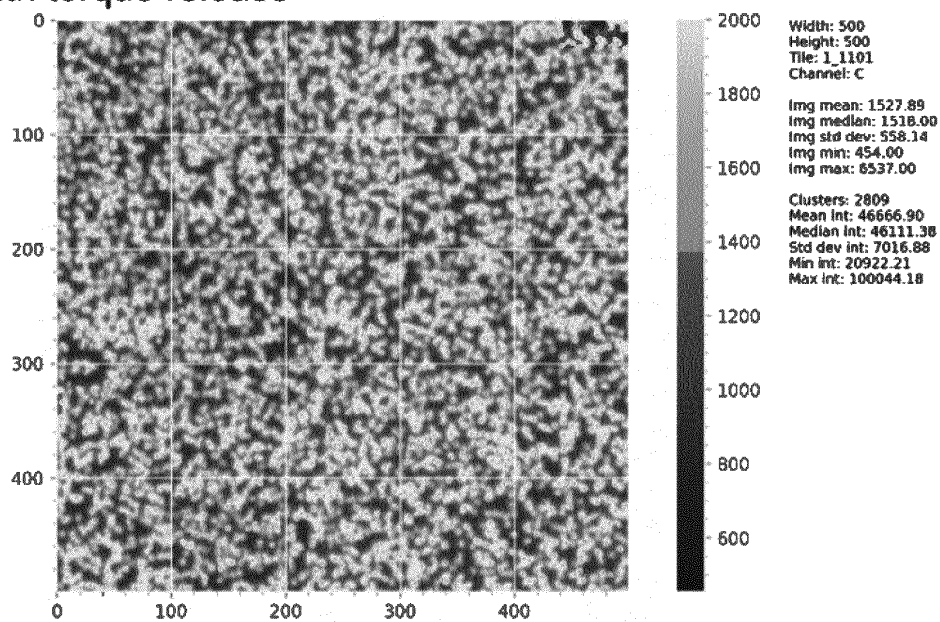


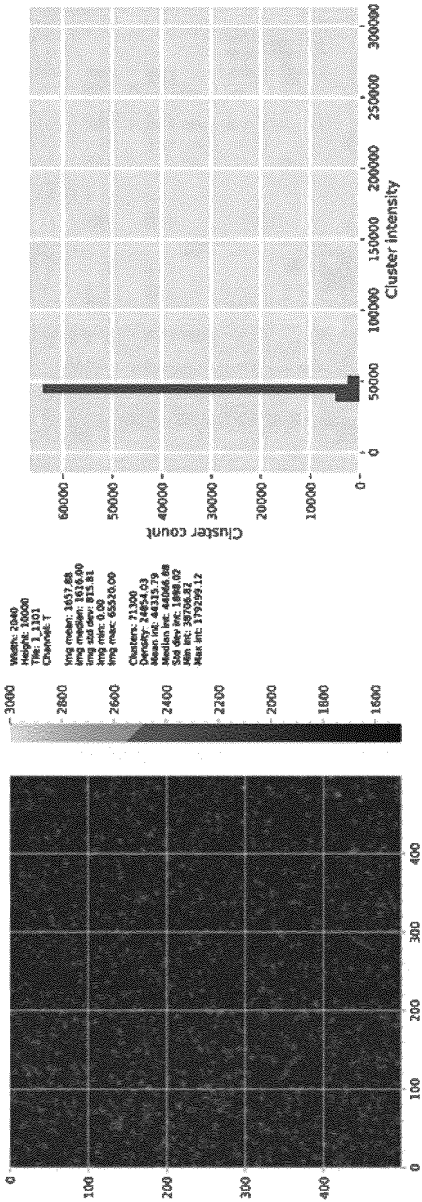
Figure 2**Without torque release****With torque release**

Signal: A647N oligo probe bound to 3' end of RNA clusters

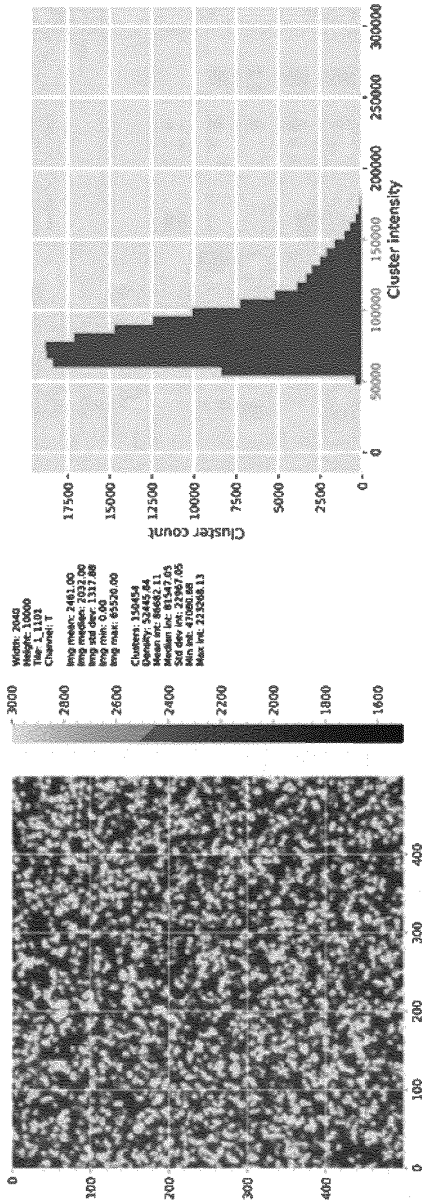
Figure 3

Protein display and binding is significantly improved by using a buffer containing 50 mM MgAc vs 7 mM MgCl₂

Buffer: PBST + 0.1% BSA + 7 mM MgCl₂

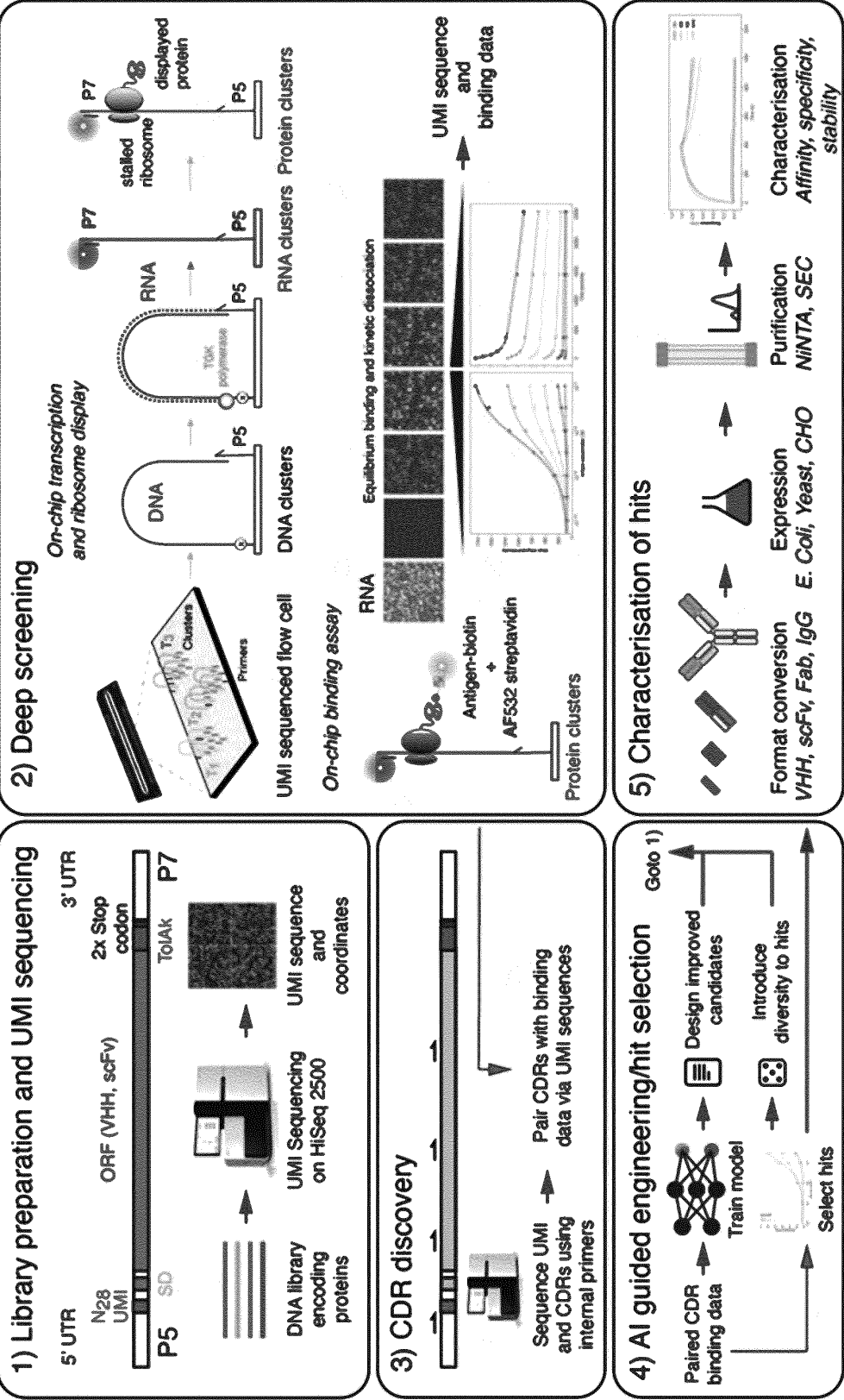


Buffer: 50 mM TrisAc, 150 mM NaCl, 0.1% Tween-20, 0.1% BSA, 50 mM MgAc



Signal: 100 nM Her2-biotin + 100 nM AF532 streptavidin

Figure 4



A) Naive yeast surface display library

Diagram illustrating the iterative selection process for the naive yeast surface display library:

- Round 1:** 500 nM Lysozyme, MACS: Streptavidin beads
- Round 2:** 300 nM Lysozyme, MACS: Streptavidin beads
- Round 3:** 200 nM Lysozyme, MACS: Streptavidin beads
- Deep screen:** R3 FACS, Lysozyme: AF532 streptavidin 1, 10, 100, 300 nM, Dissociation assay
- Round 3 FACS:** 200 nM Lysozyme, FACS: Neutravidin-PE
- Plate:** Pick 96 colonies

B) R3 FACS at 300nM

Flow cytometry plots showing R3 FACS at 300nM. The left plot shows R3 MACS at 300nM (p=0.361) and the right plot shows R3 FACS at 300nM (p=0.462). Both plots show Abundance vs. Intensity (0 to 1000).

C) R3 FACS at 300nM

Flow cytometry plots showing R3 FACS at 300nM. The left plot shows R3 MACS at 300nM (p=0.361) and the right plot shows R3 FACS at 300nM (p=0.462). Both plots show Abundance vs. Intensity (0 to 1000).

D) ORF VHH

Diagram illustrating the ORF VHH structure, showing the 5' UTR, N28, P5, SD, CDR1, CDR2, CDR3, 2x Stop codon, 3' UTR, and P7.

E) Equilibrium binding

Graph showing Equilibrium binding (log scale) vs. Antigen concentration (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

F) Kinetic observation

Graph showing Kinetic observation (log scale) vs. Time (s). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 0 to 1000. Data points are shown for 100, 200, and 300 nM Lysozyme.

G) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

H) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

I) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

J) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

K) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

L) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

M) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

N) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

O) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

P) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

Q) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

R) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

S) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

T) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

U) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

V) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

W) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

X) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

Y) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

Z) CDR3 length distribution

Graph showing CDR3 length distribution (log scale) vs. CDR3 length (log scale). The y-axis ranges from 10⁰ to 10⁴, and the x-axis ranges from 10⁰ to 10⁴. Data points are shown for 100, 200, and 300 nM Lysozyme.

Figure 6

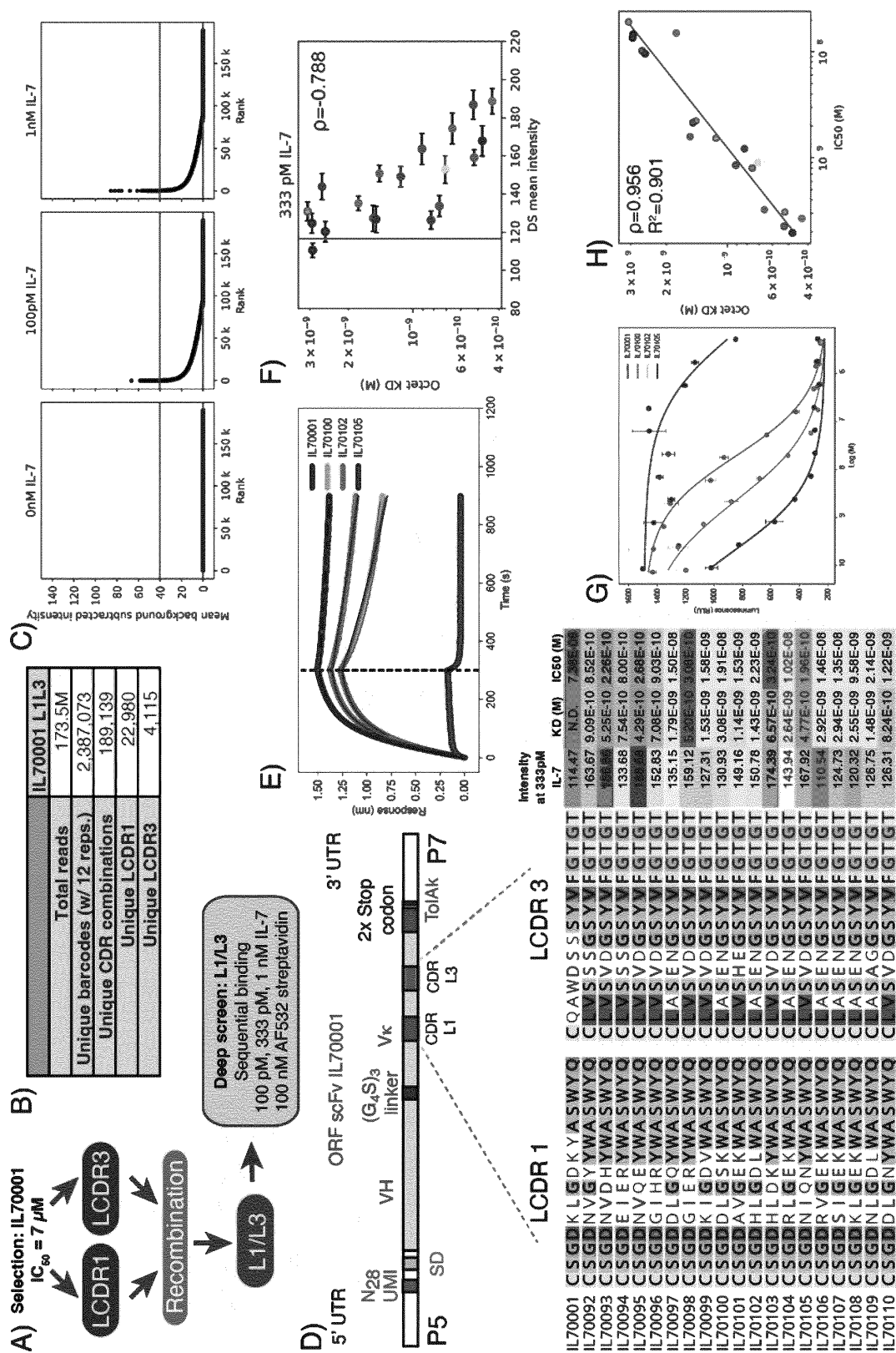


Figure 7

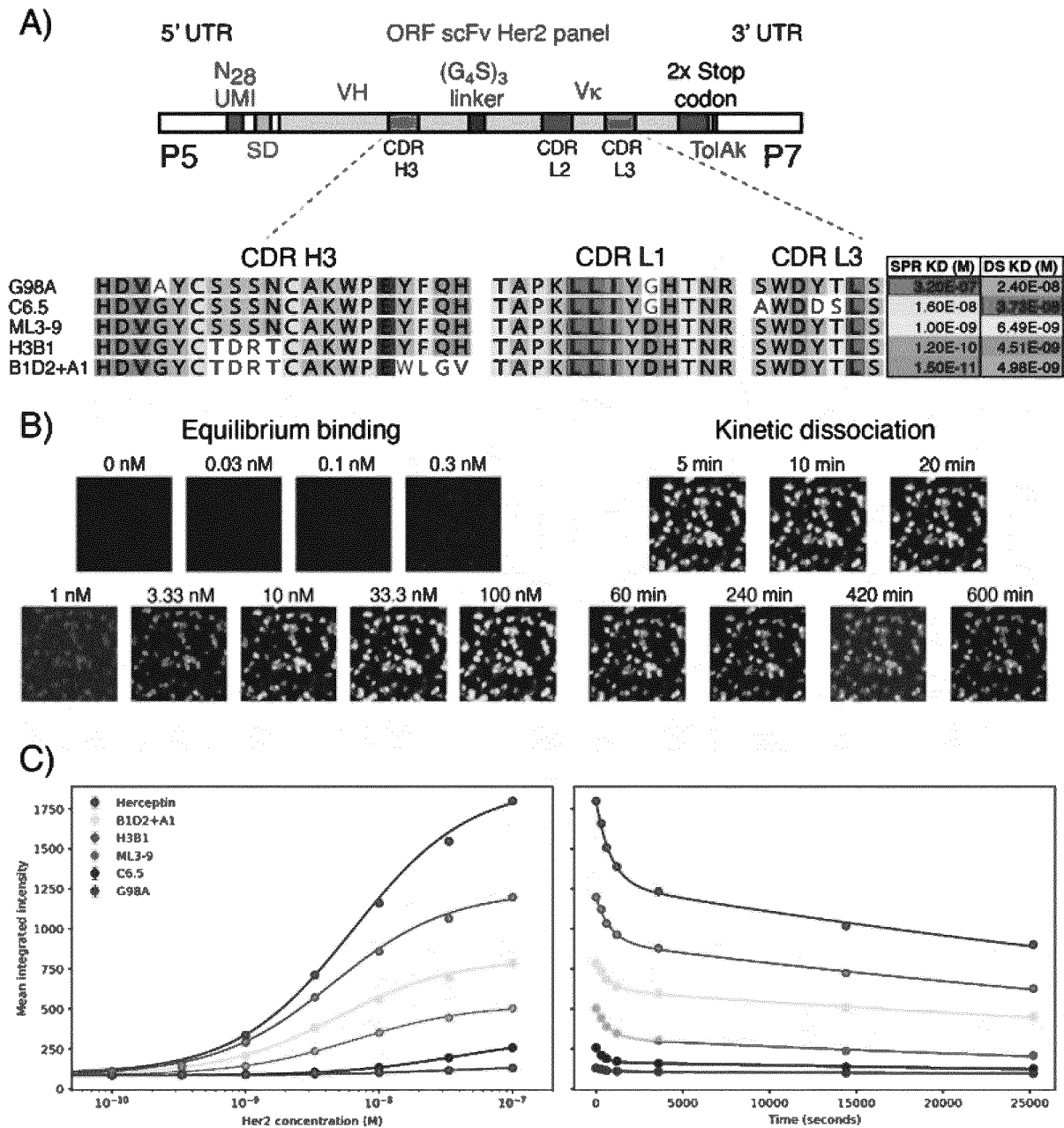


Figure 8

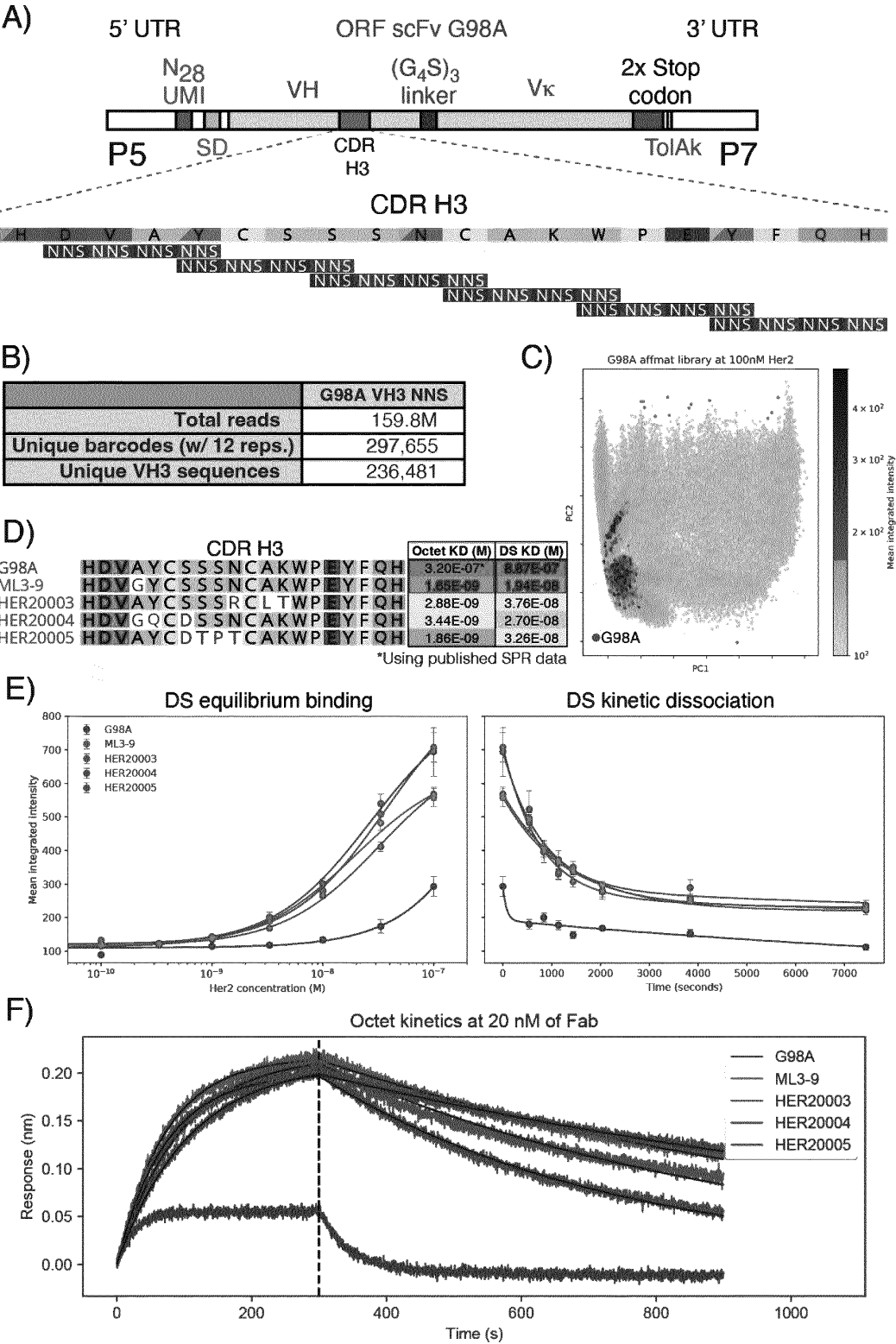


Figure 9

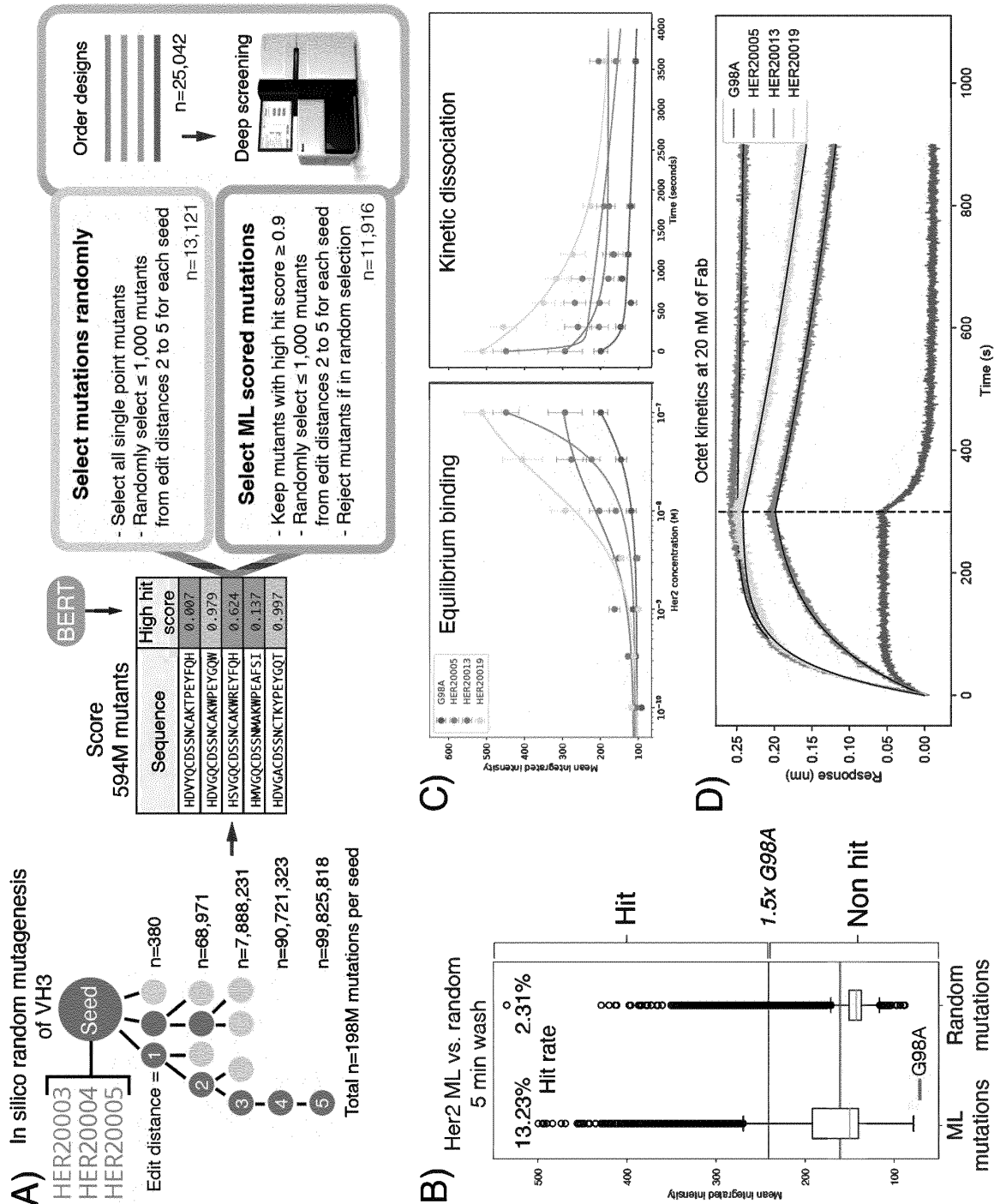


Figure 10

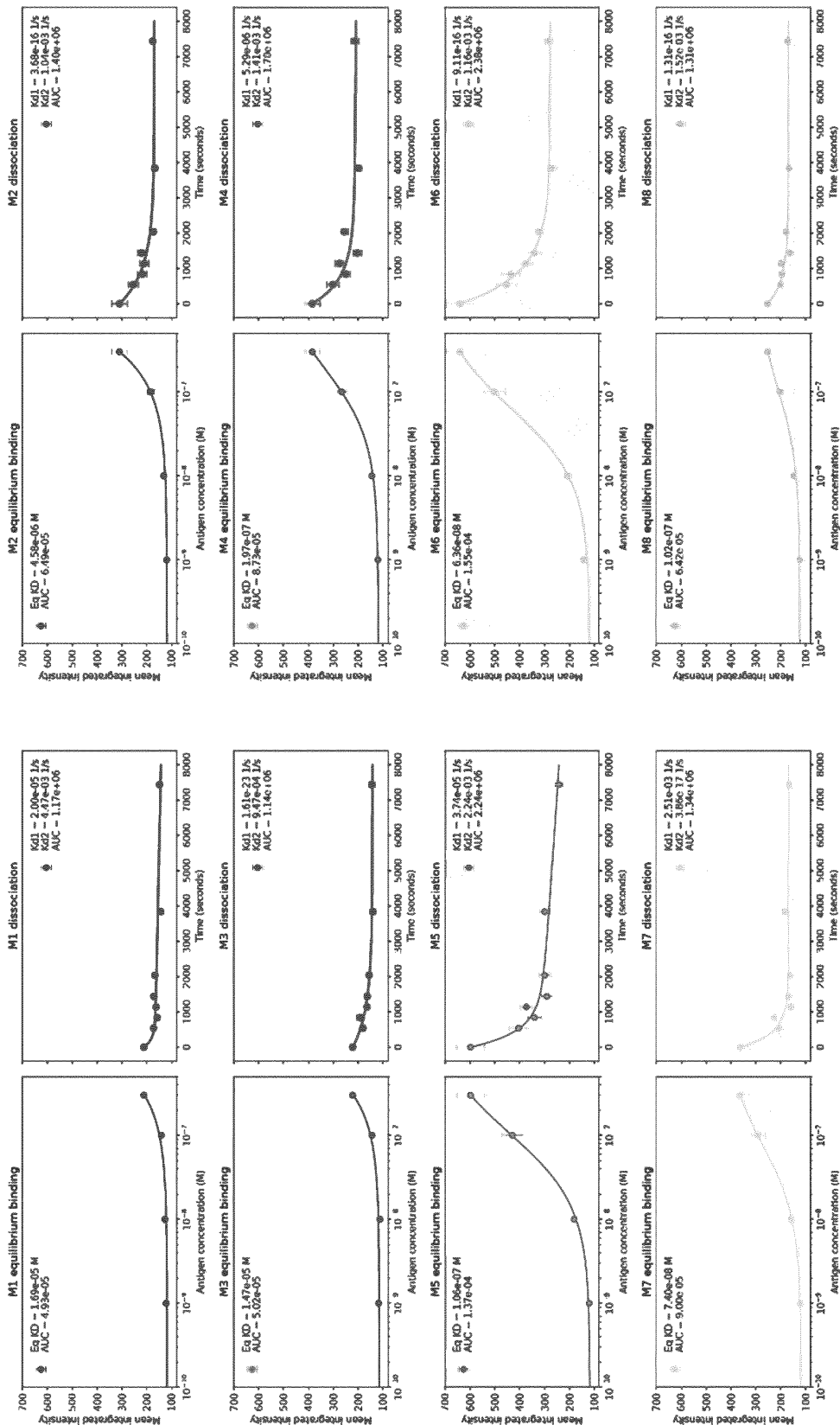


Figure 10 (cont)

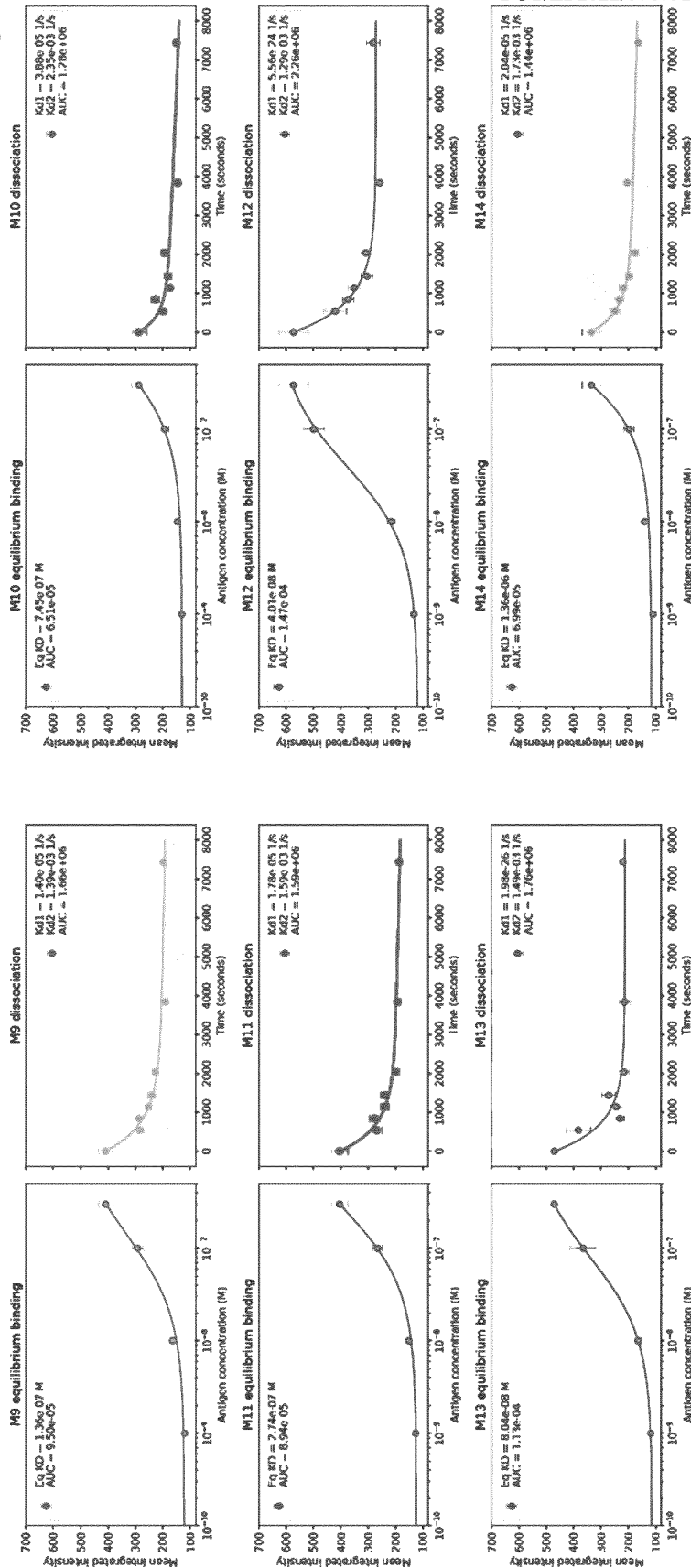


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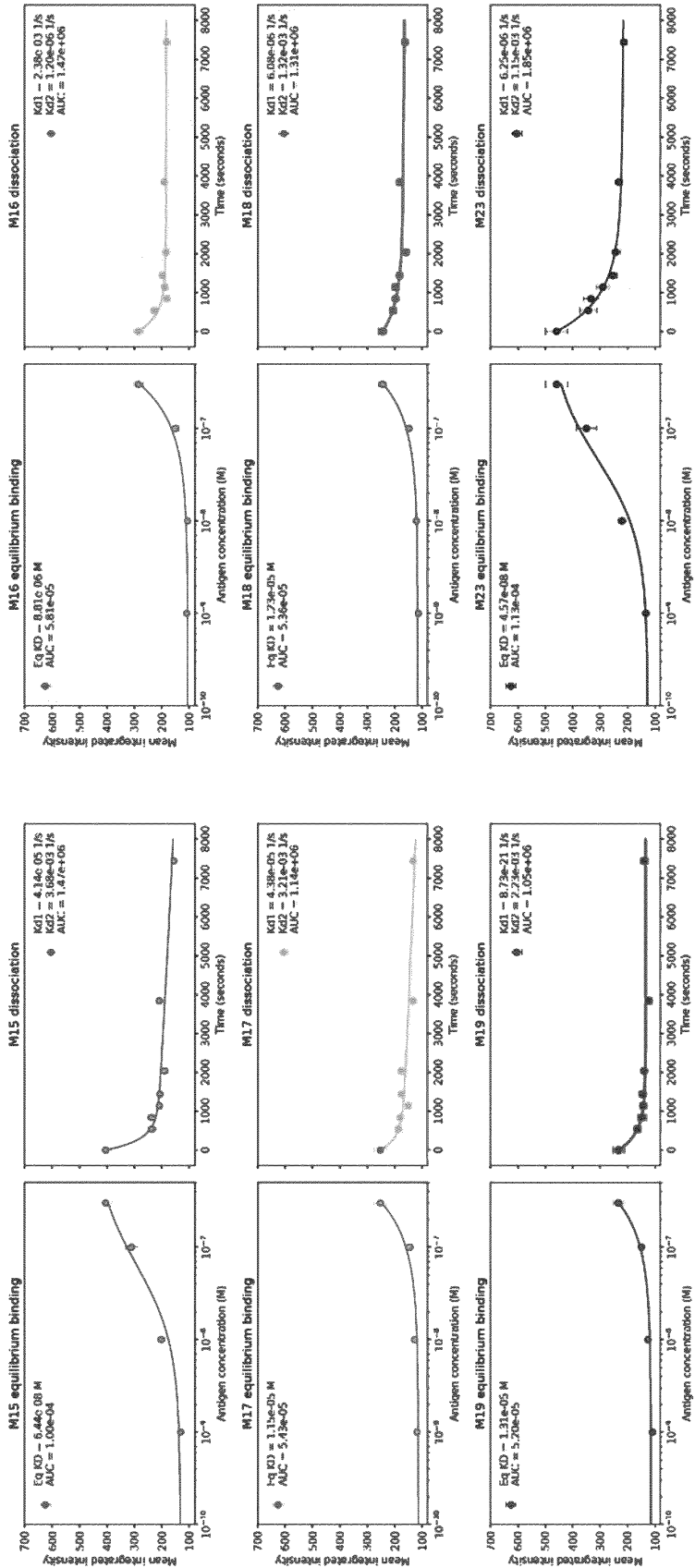


Figure 11

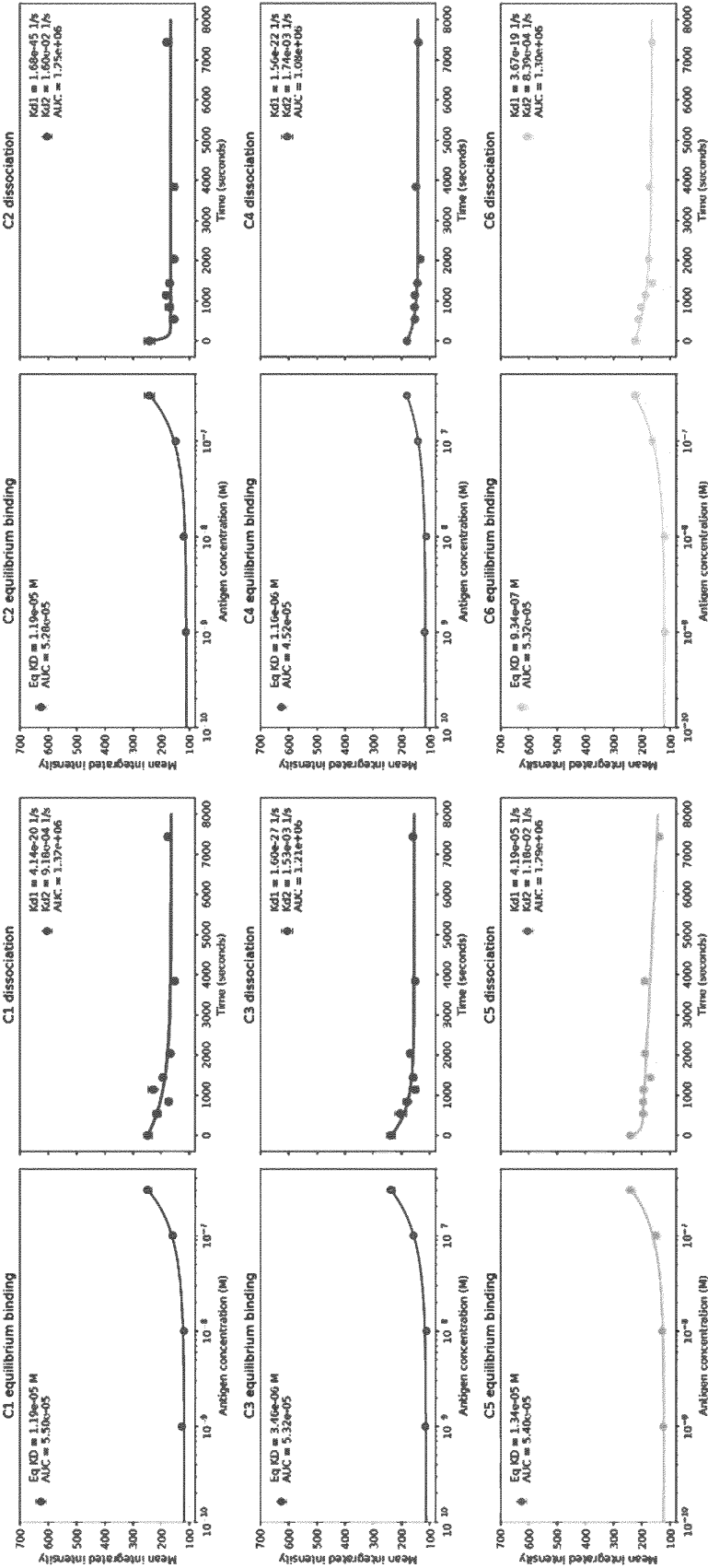


Figure 11
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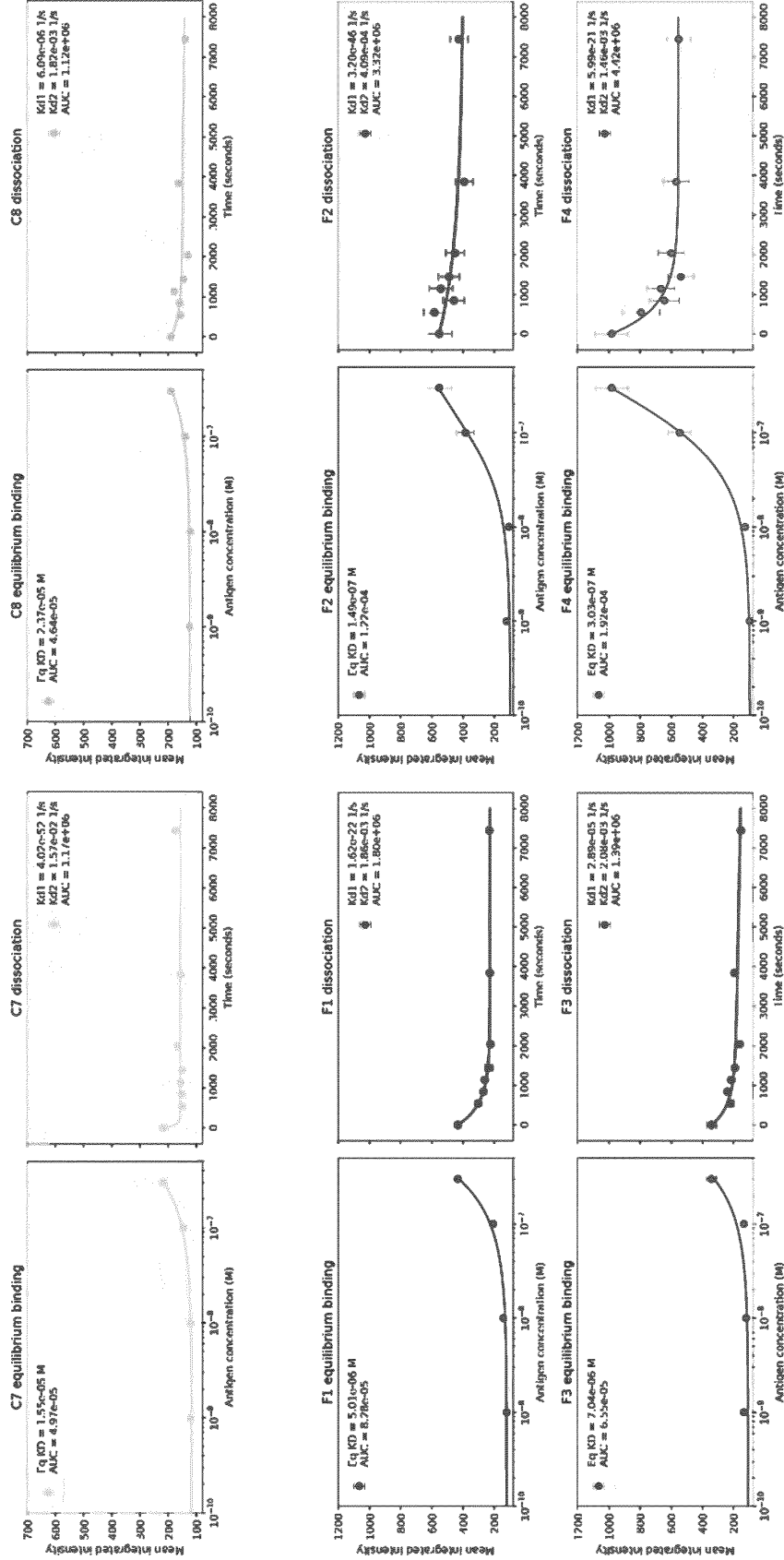


Figure 11
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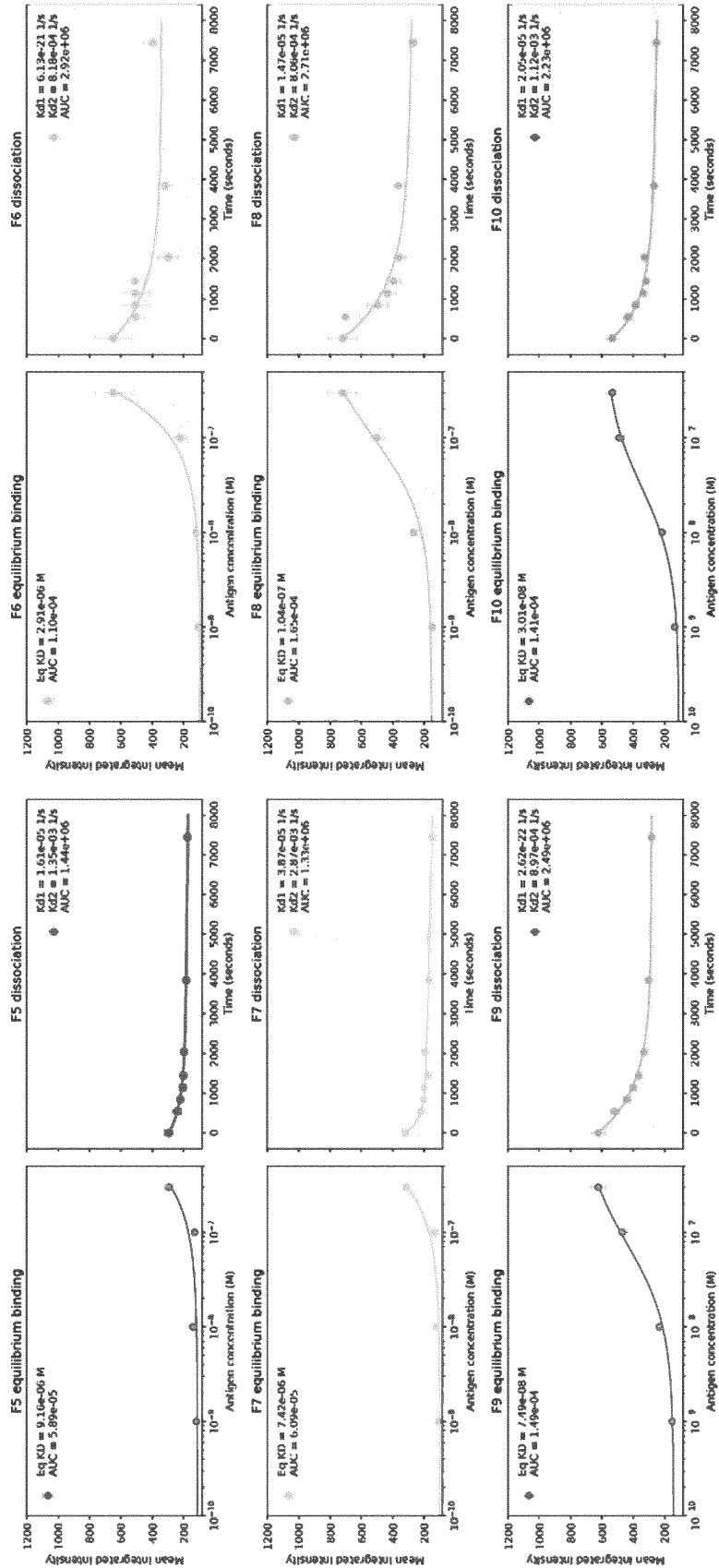


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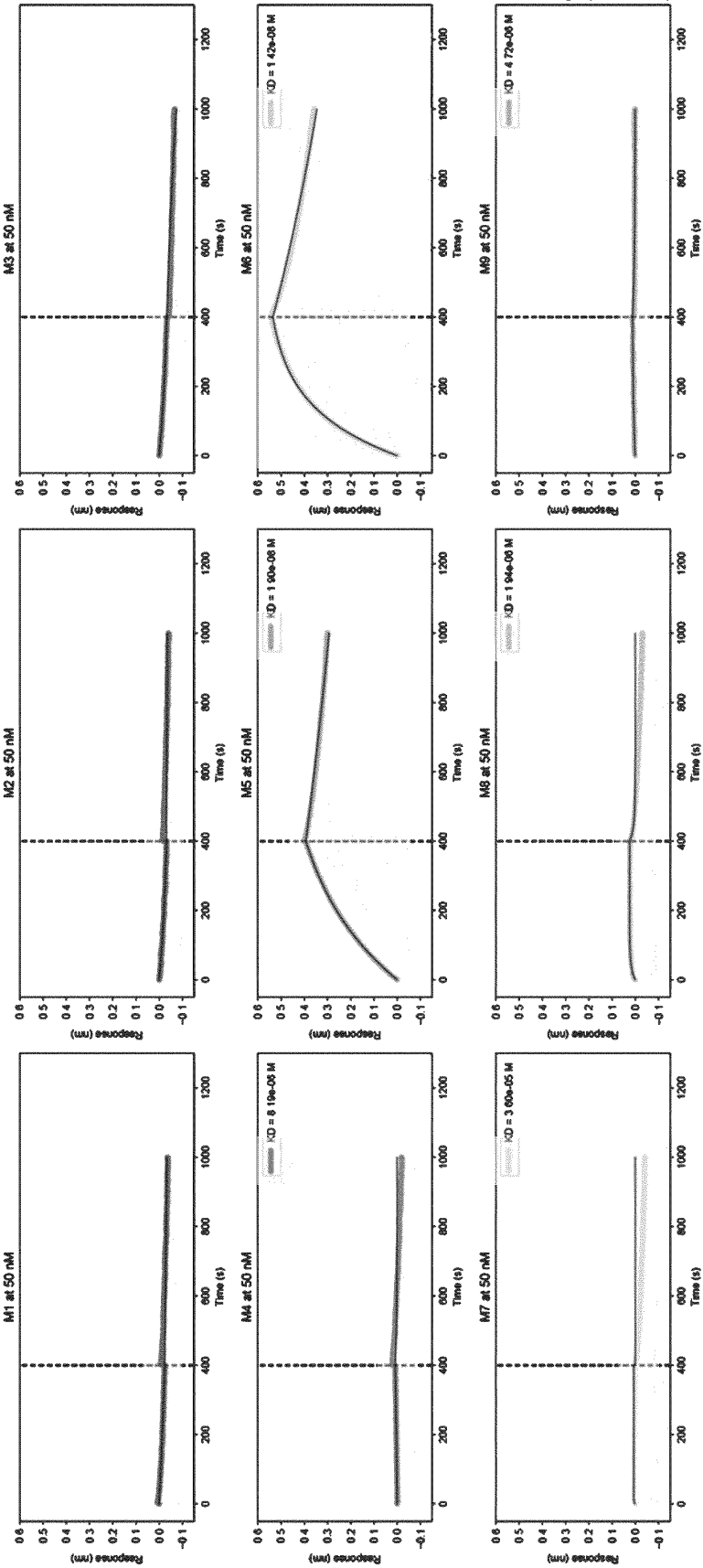


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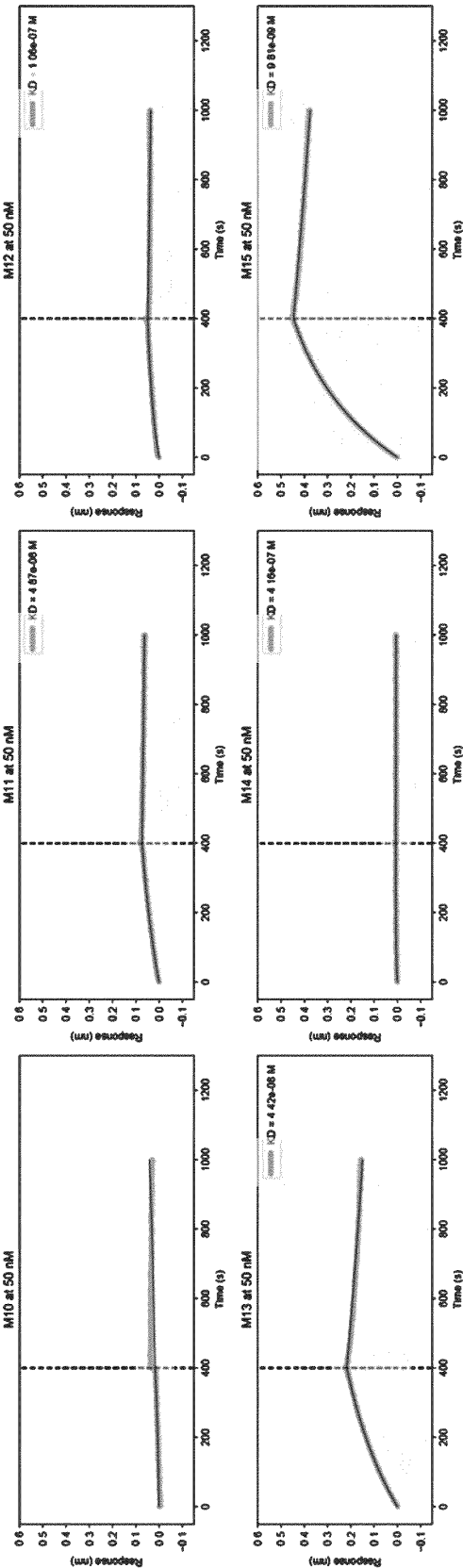


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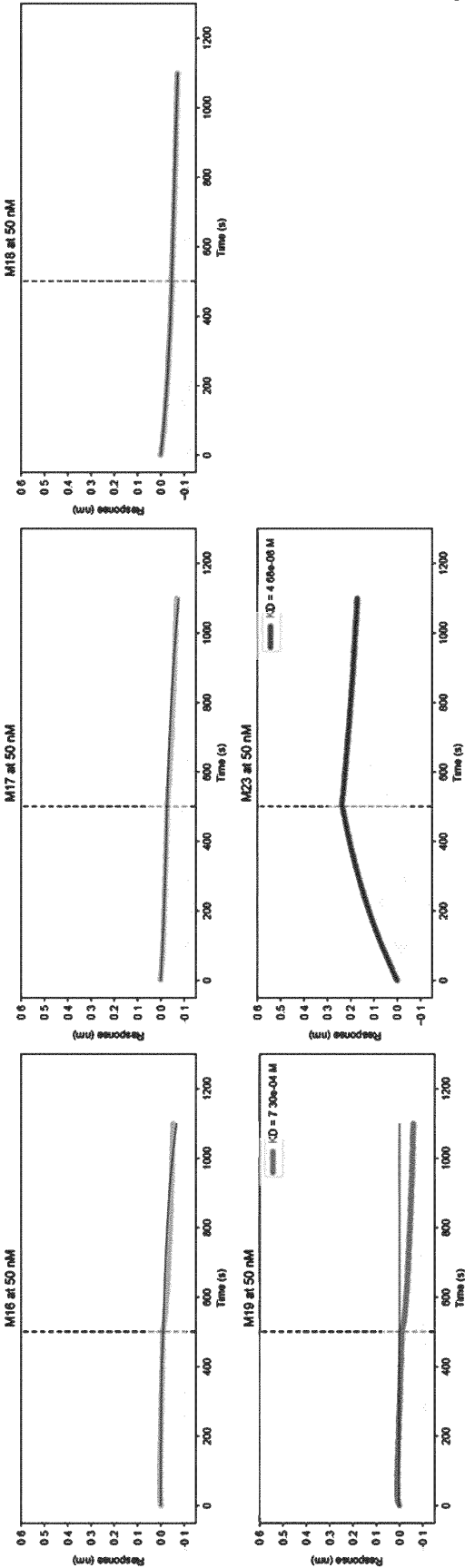


Figure 13

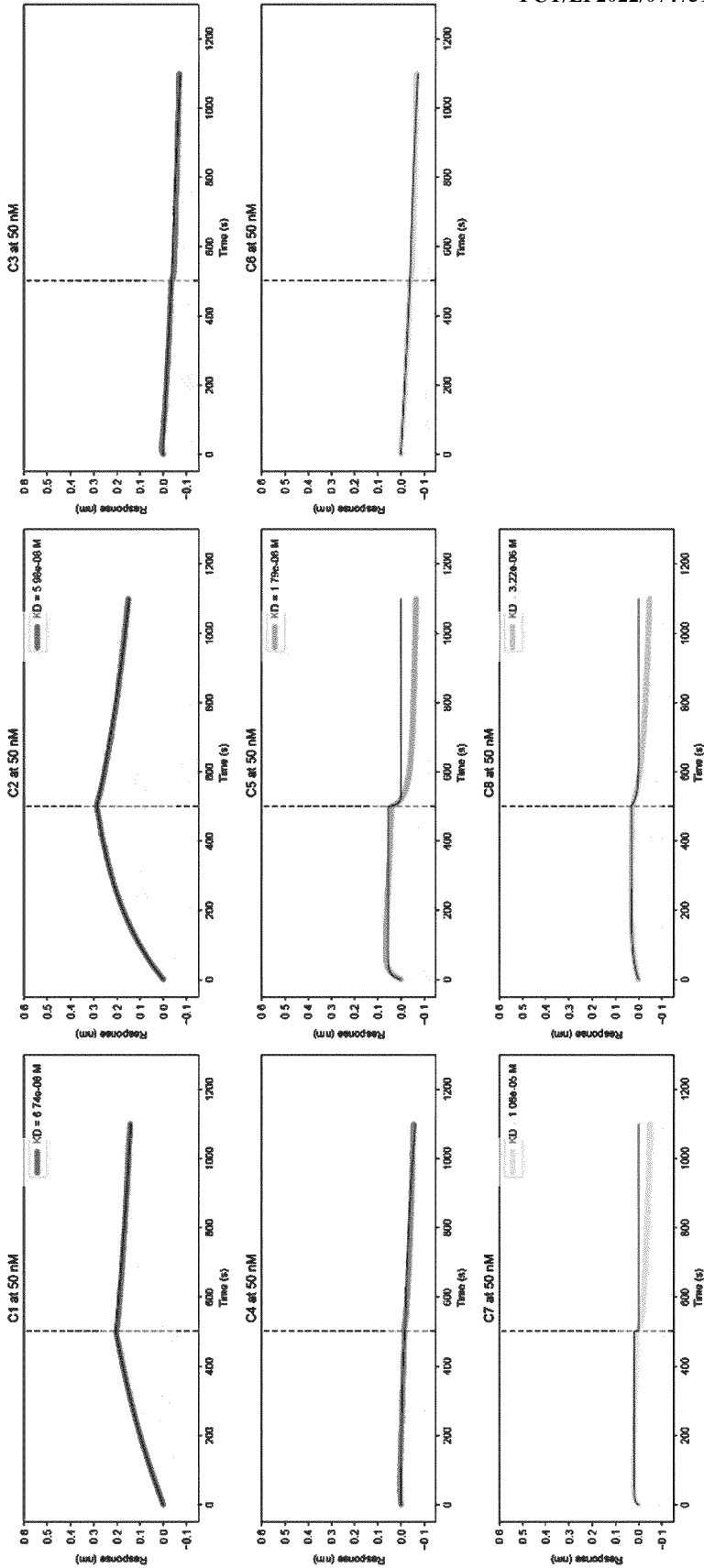


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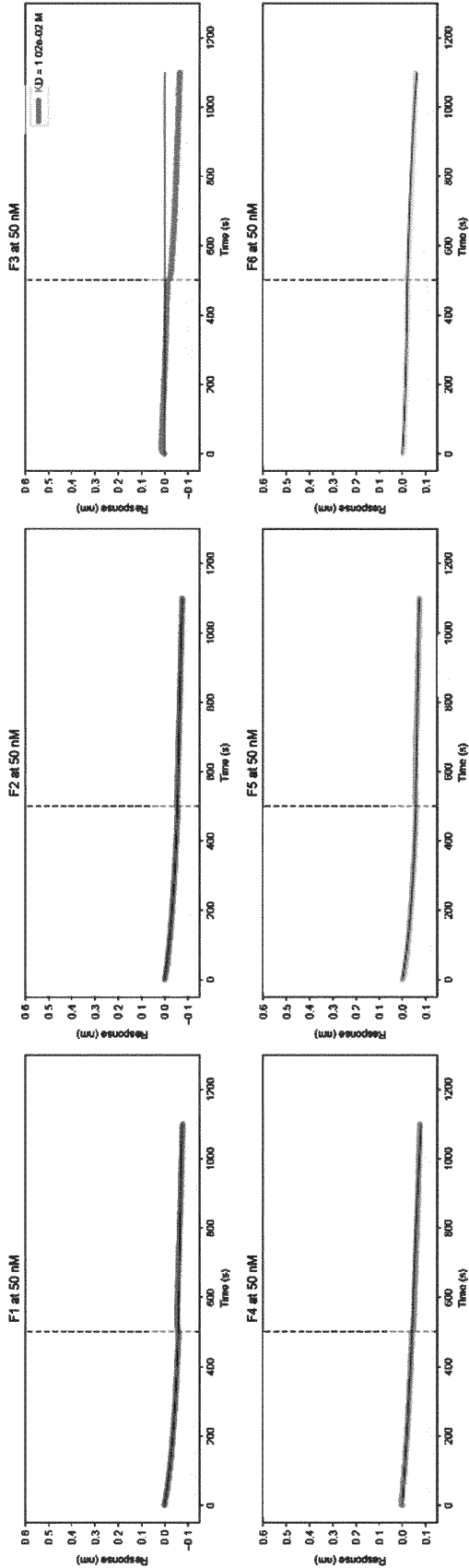


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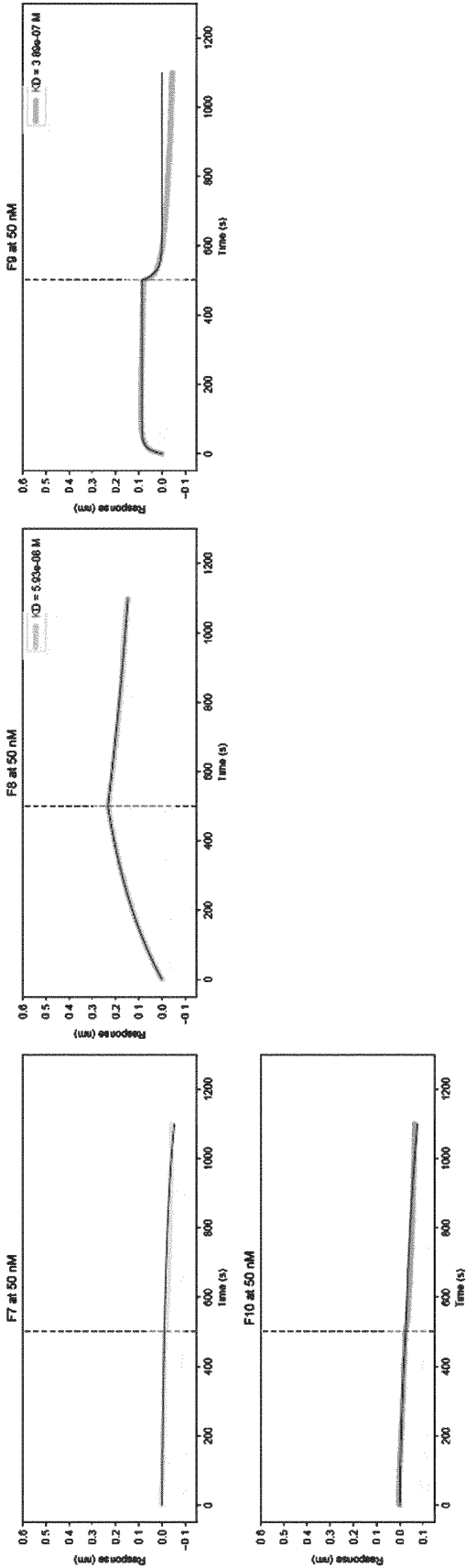


Figure 14

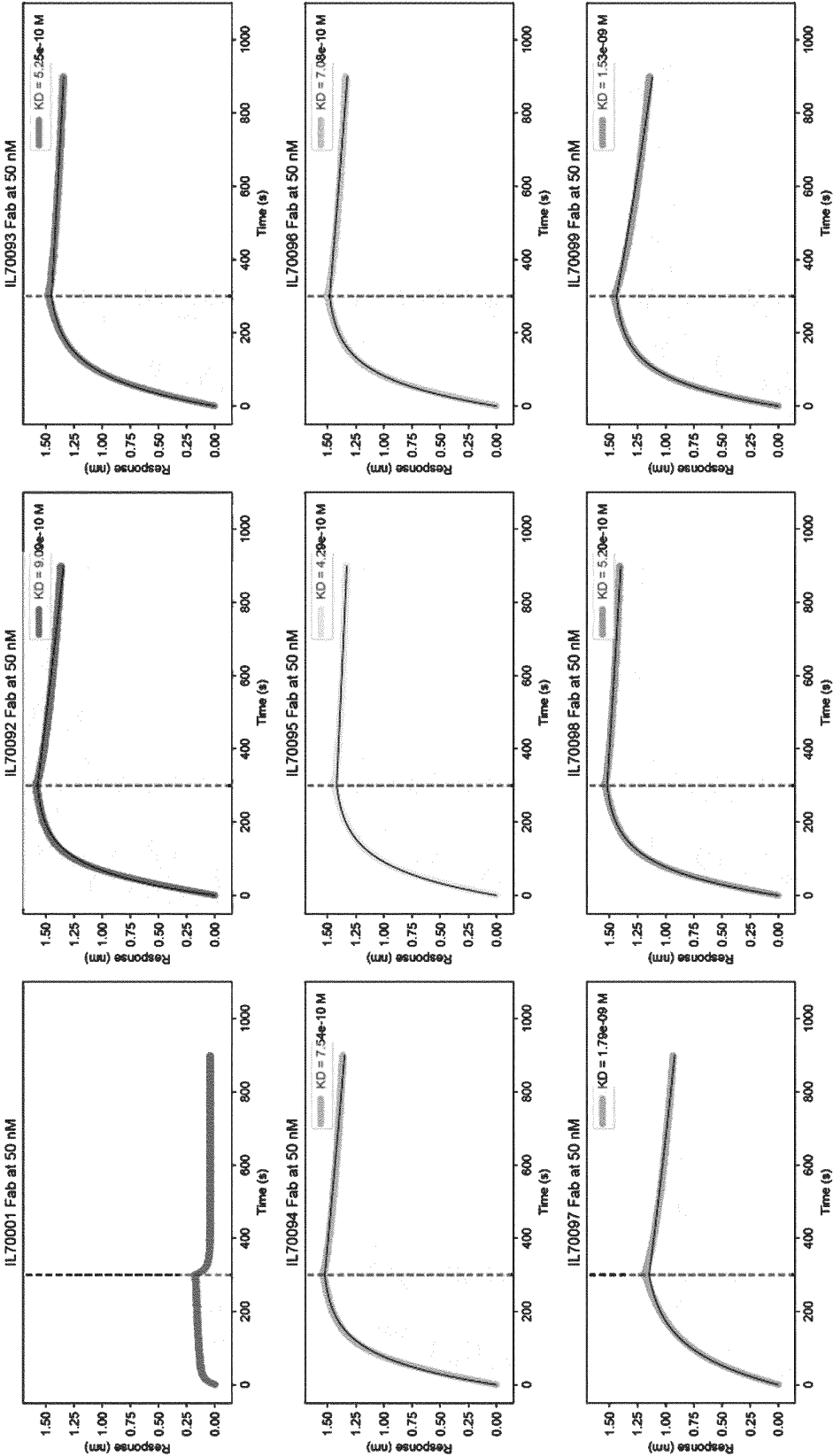


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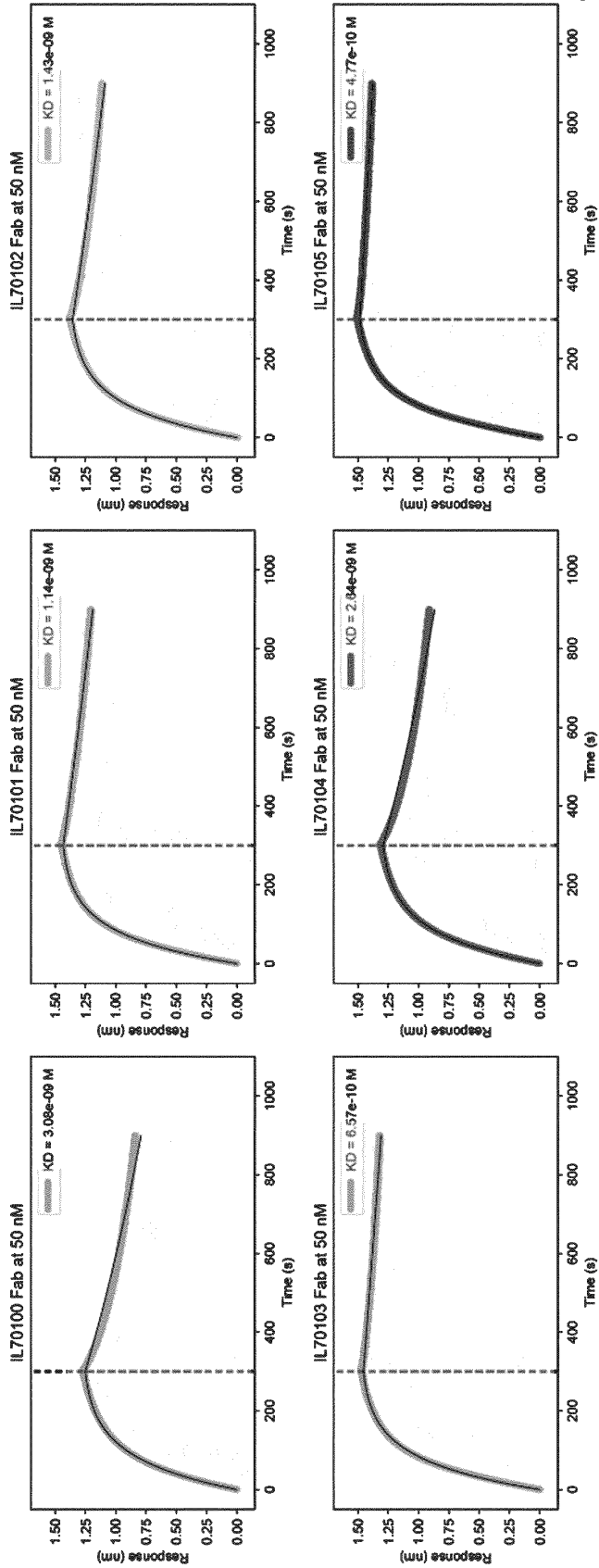


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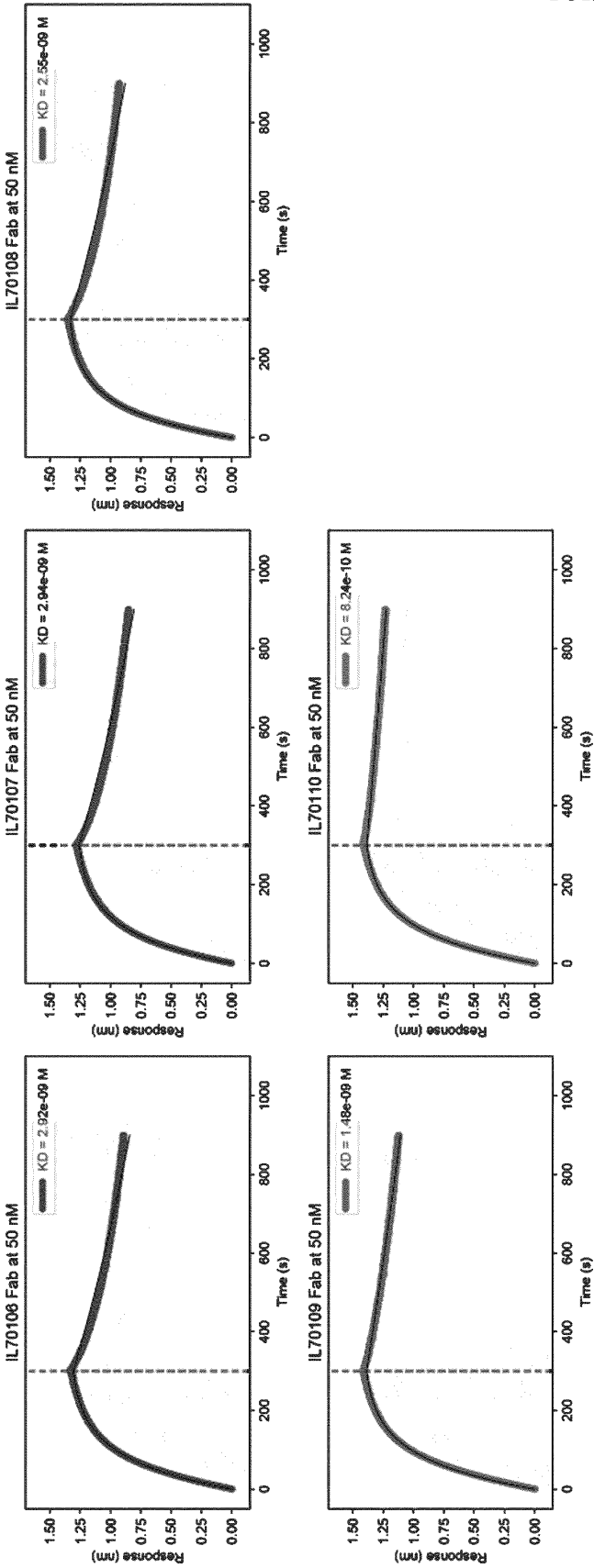


Figure 15

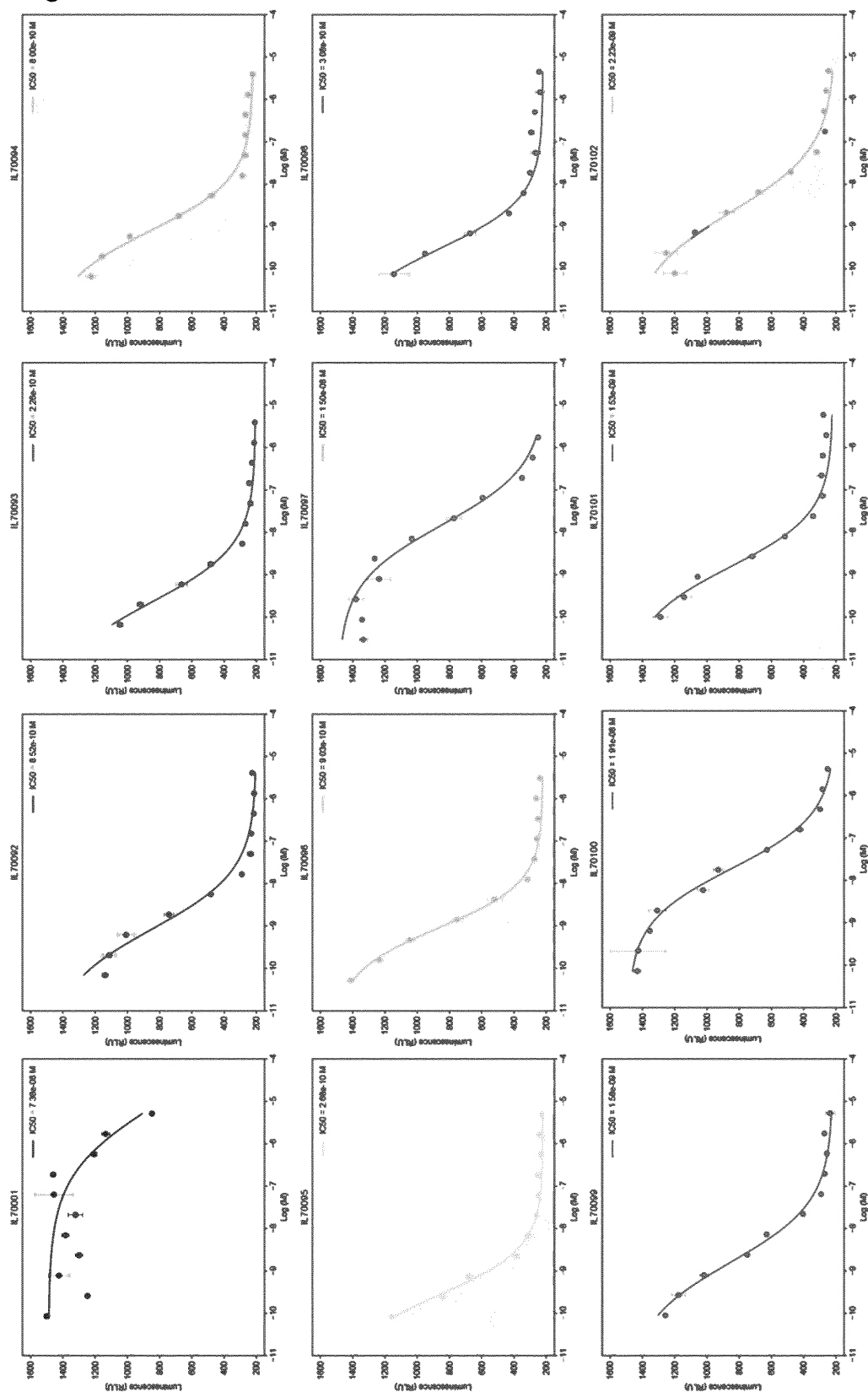


Figure 15
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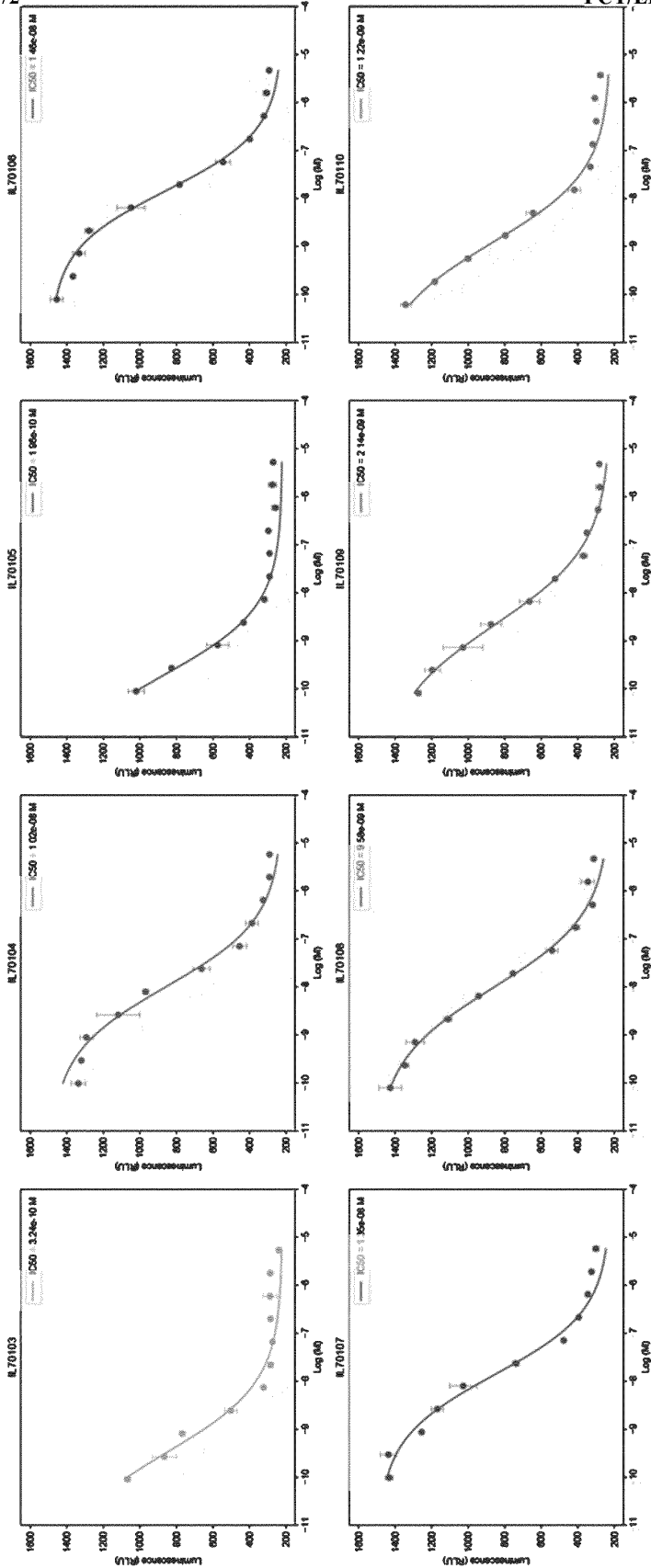


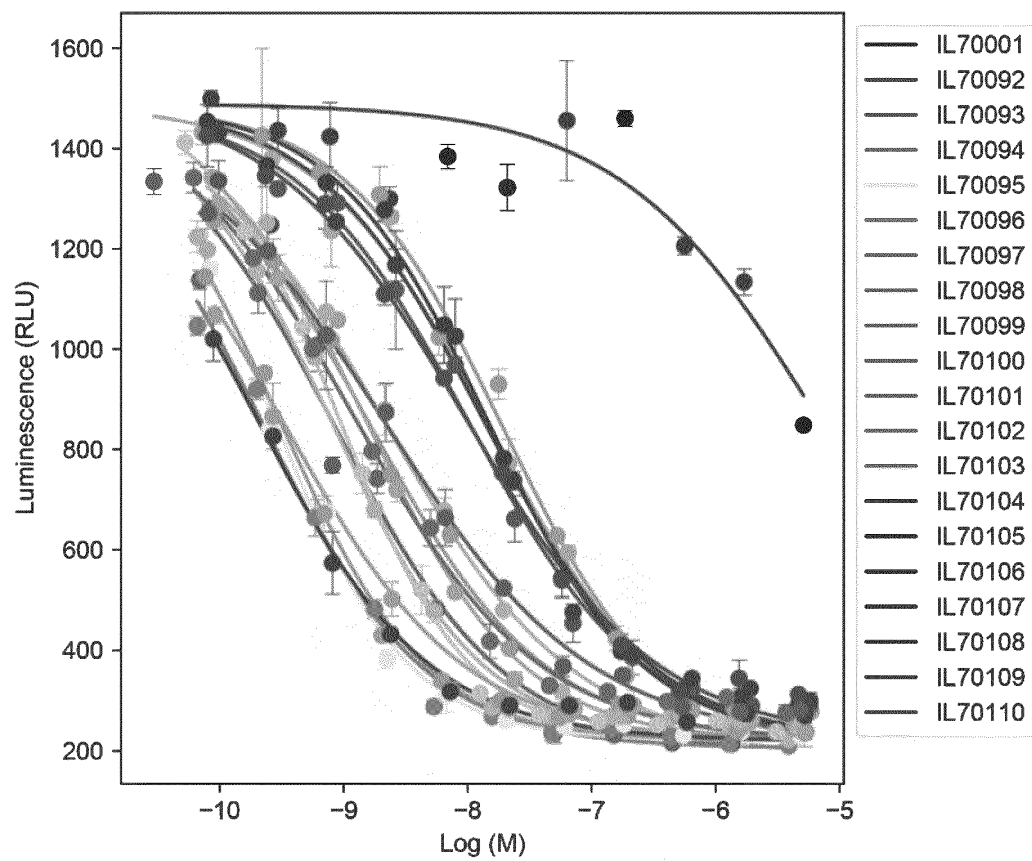
Figure 16

Figure 17

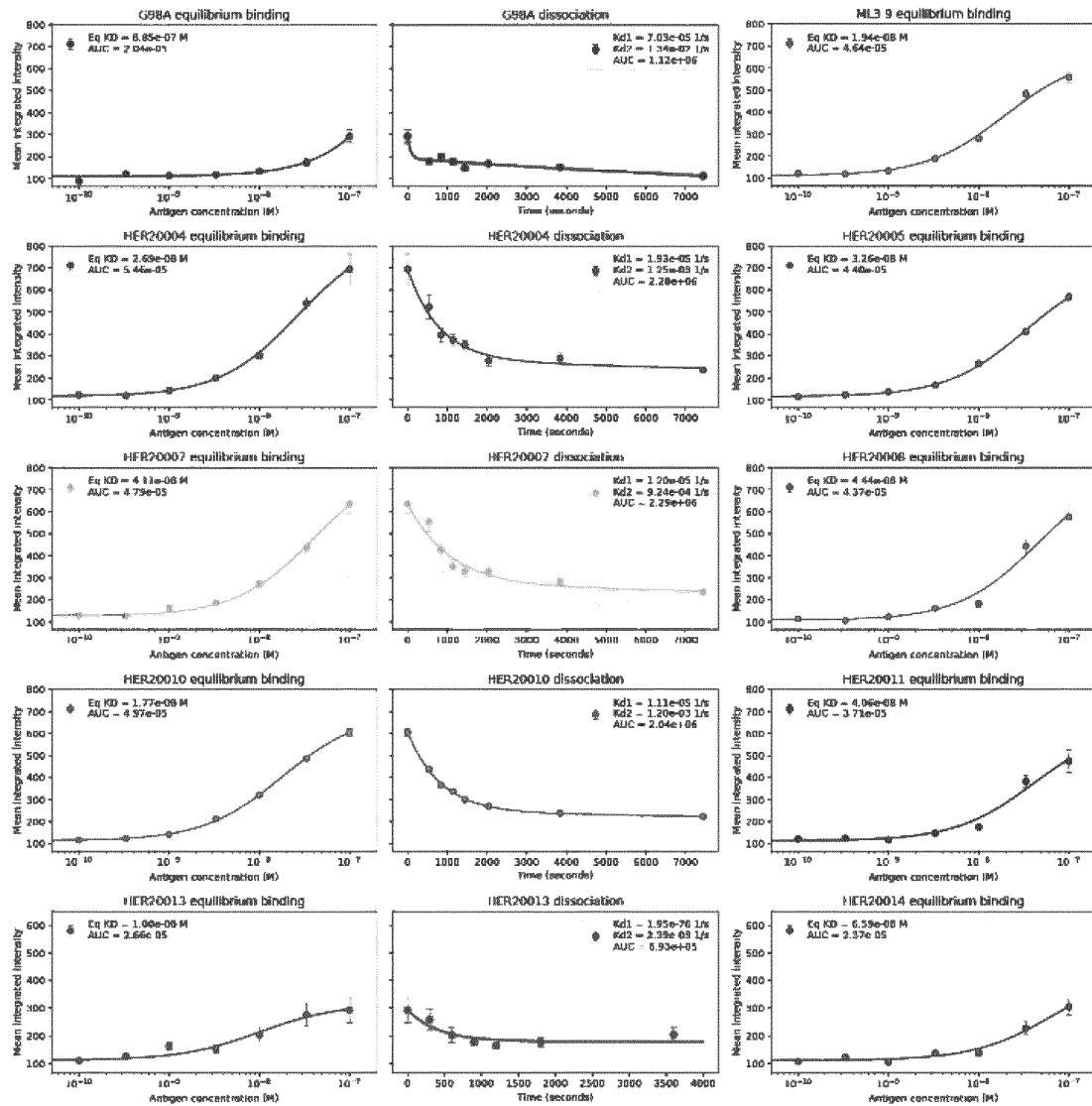


Figure 17 (cont)

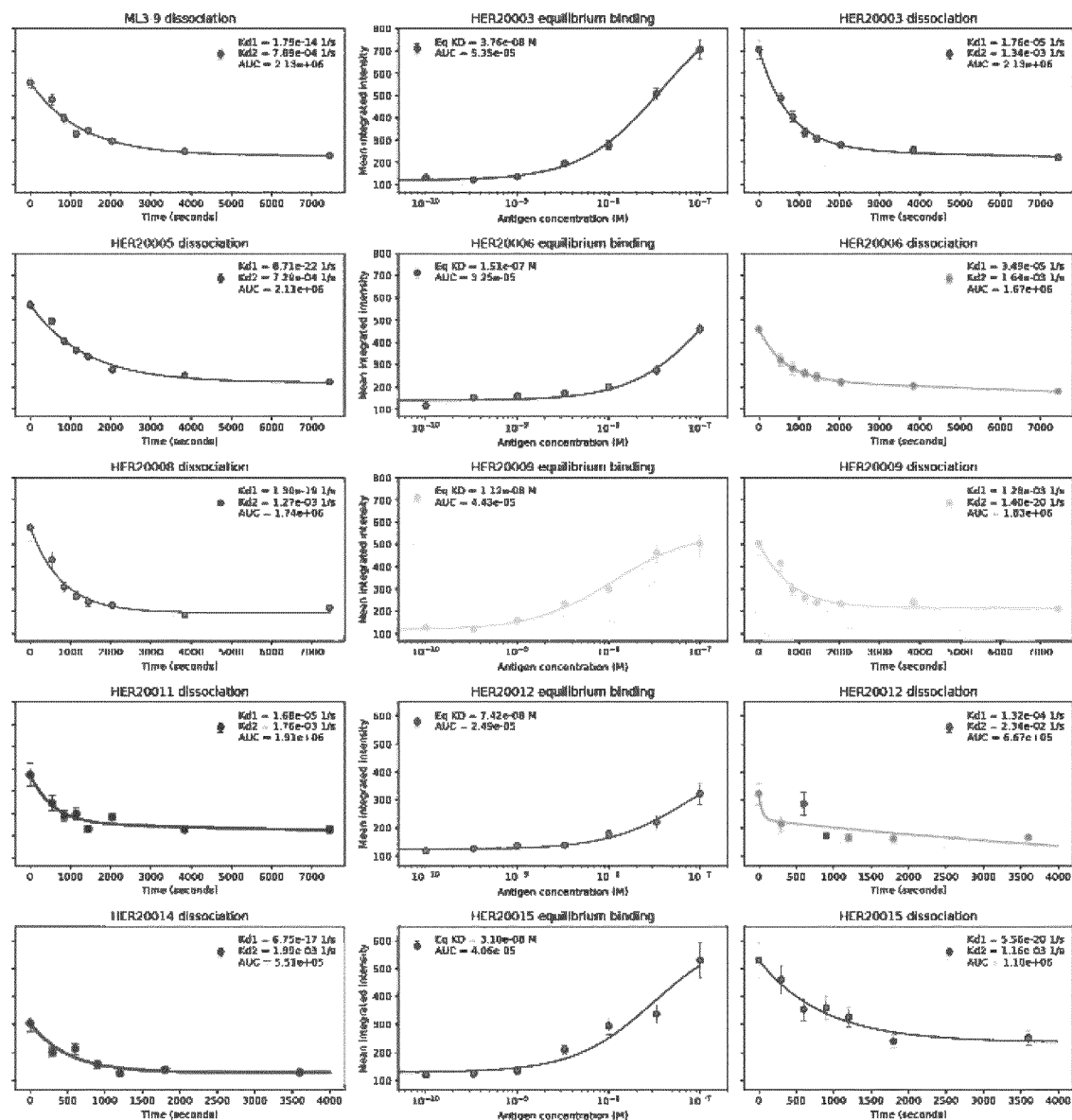


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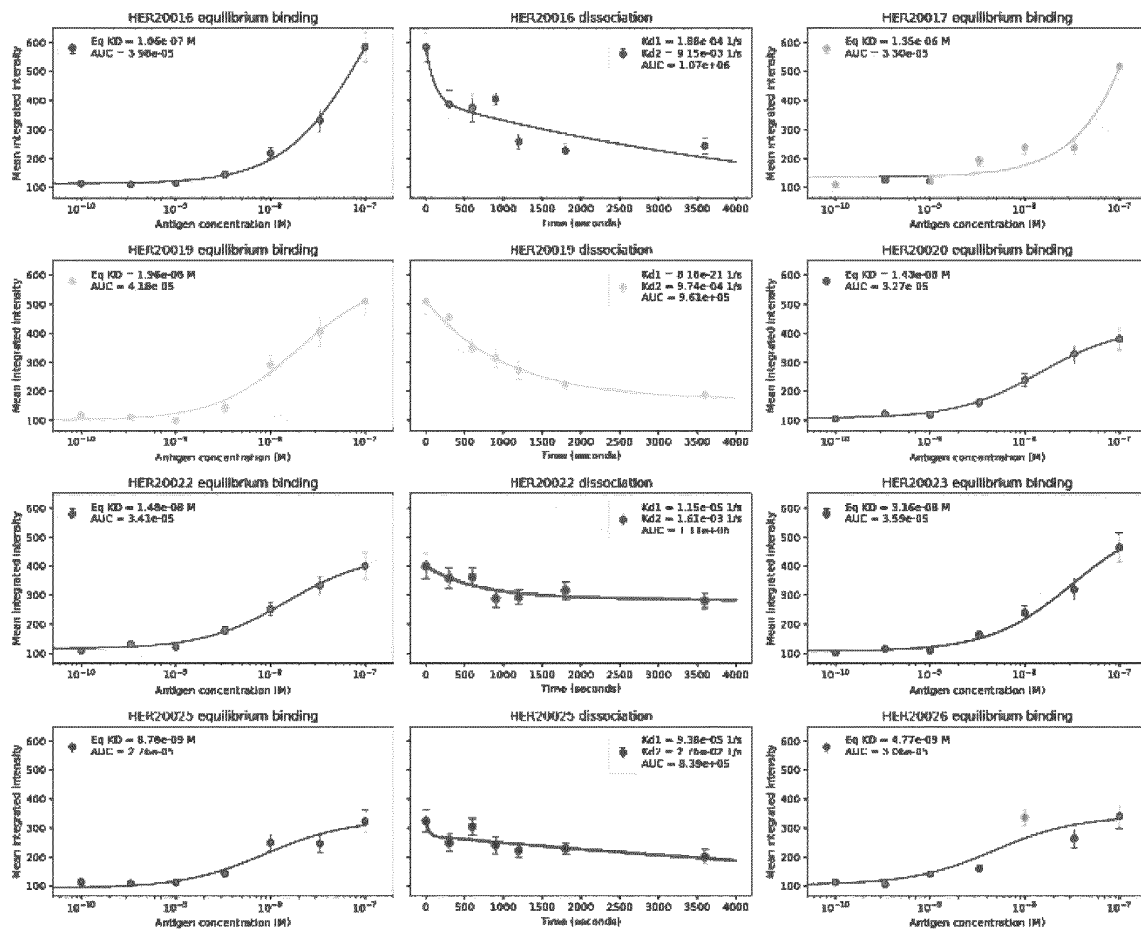


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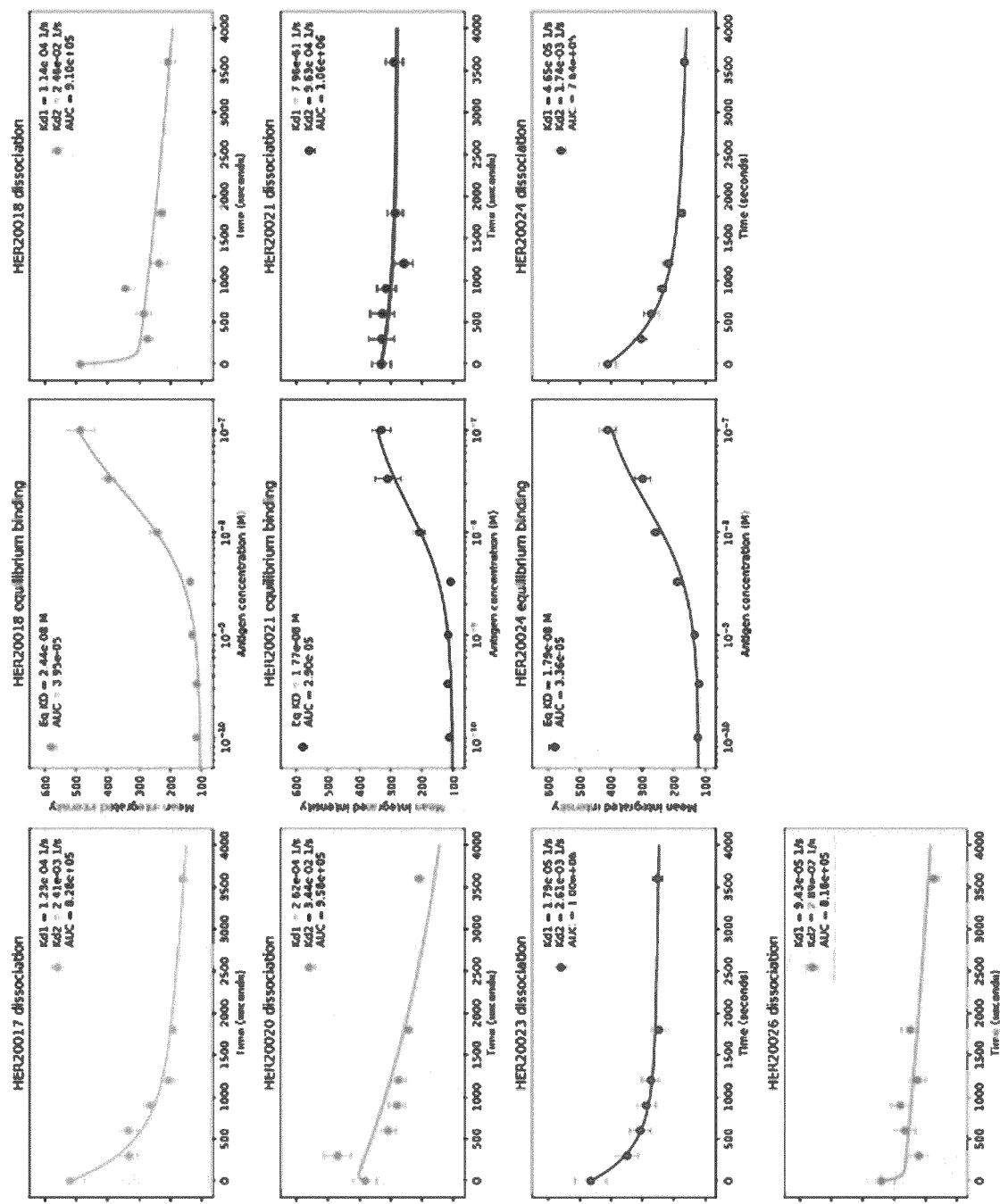


Figure 18

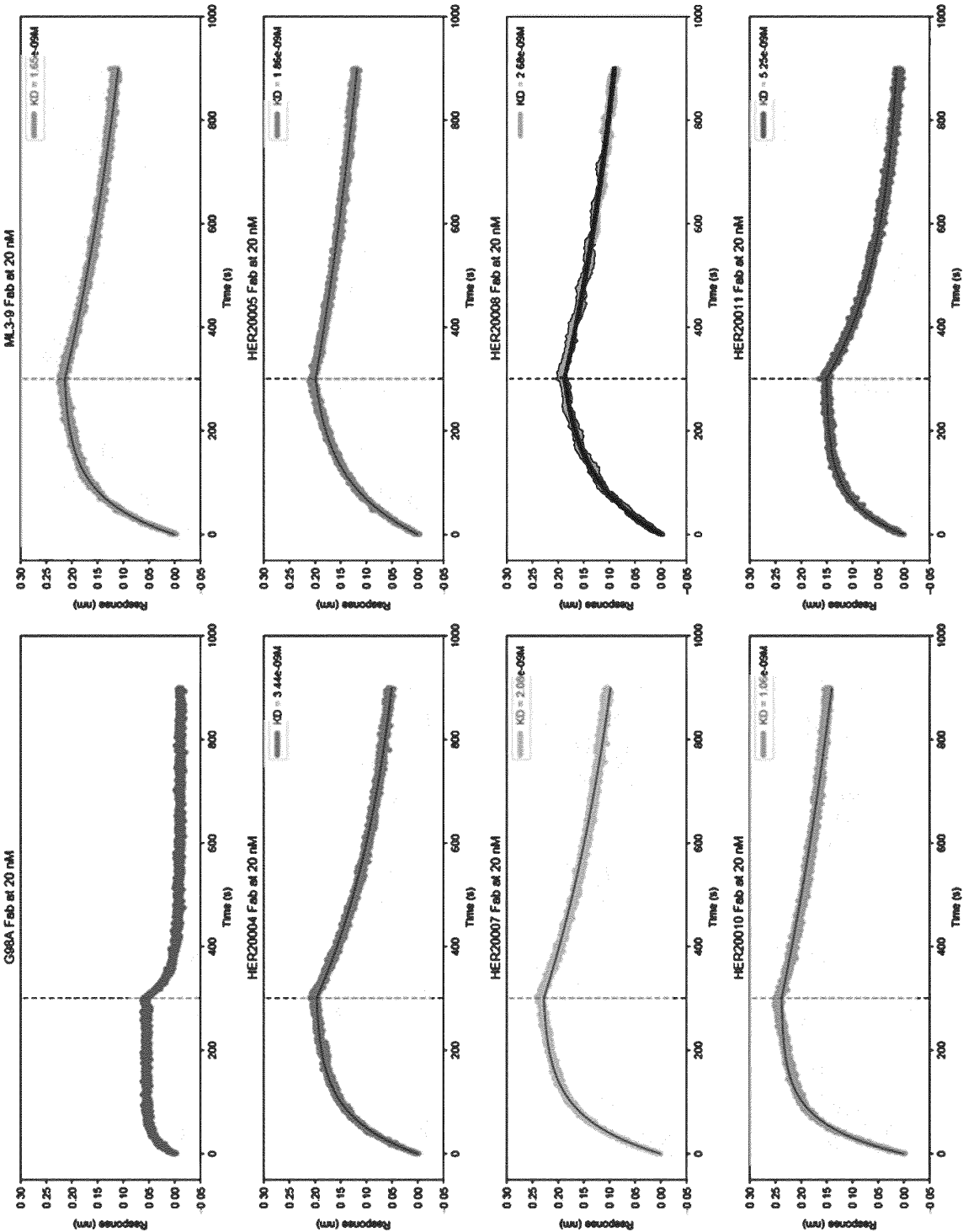


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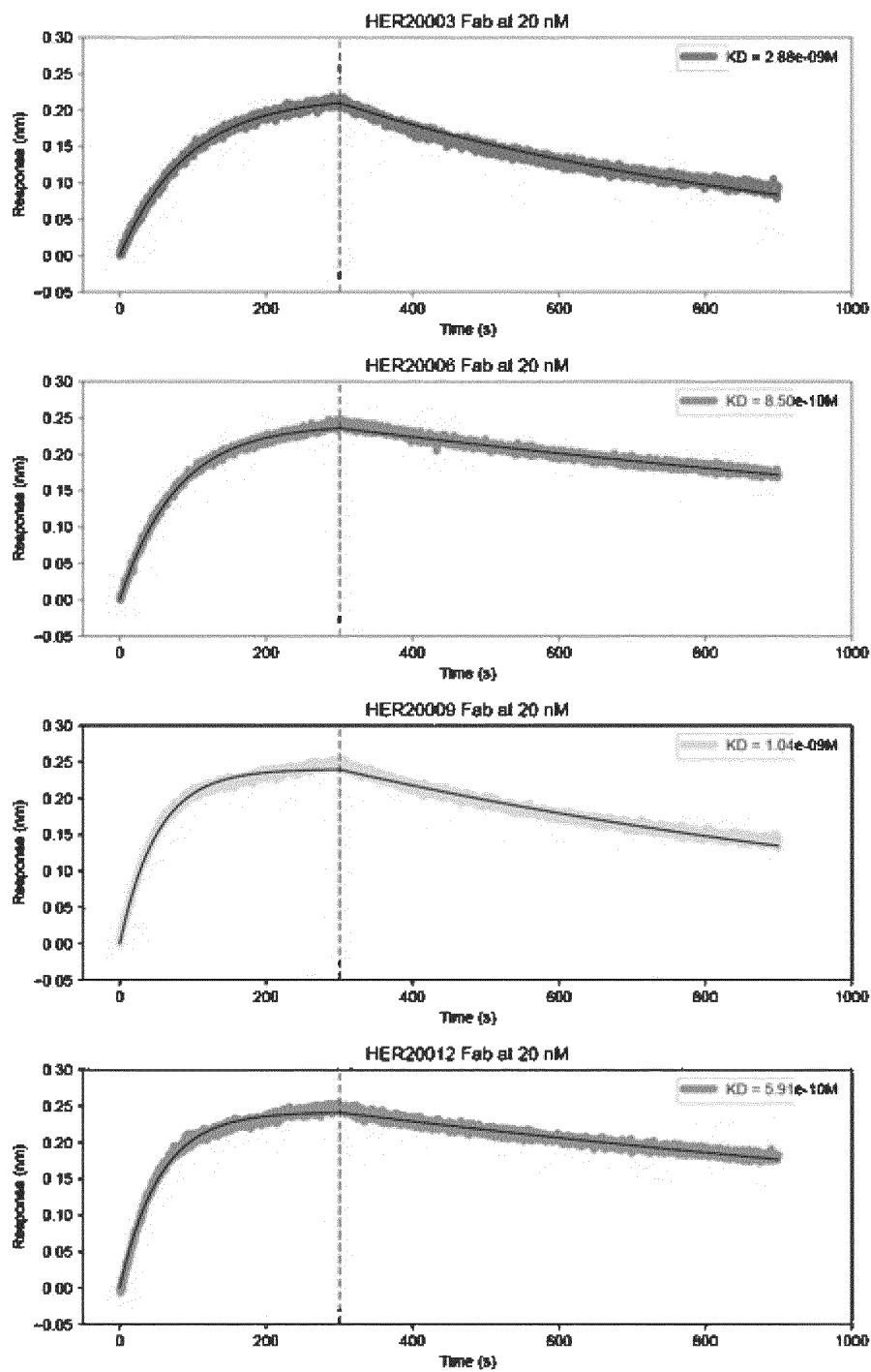


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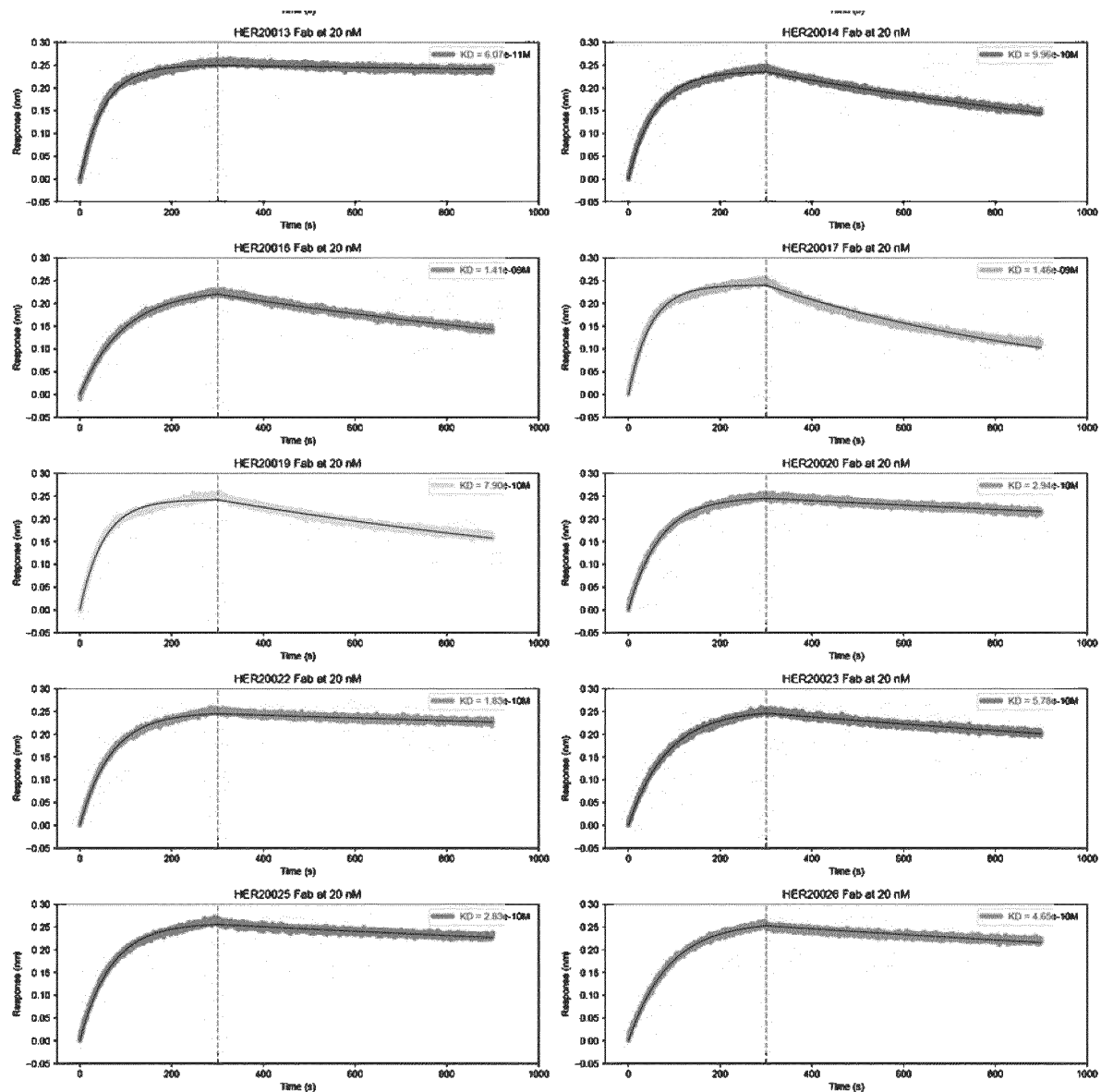


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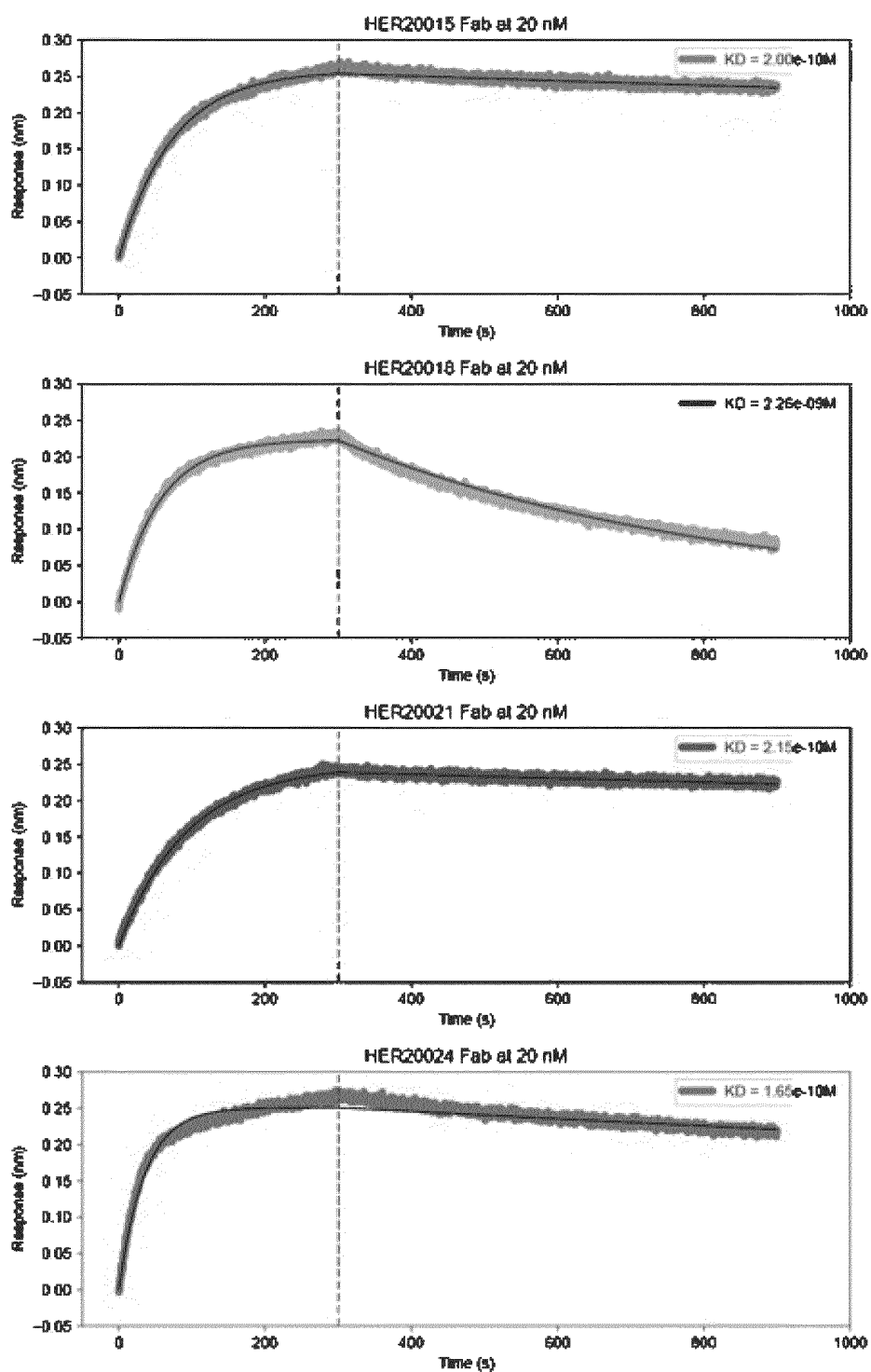


Figure 19

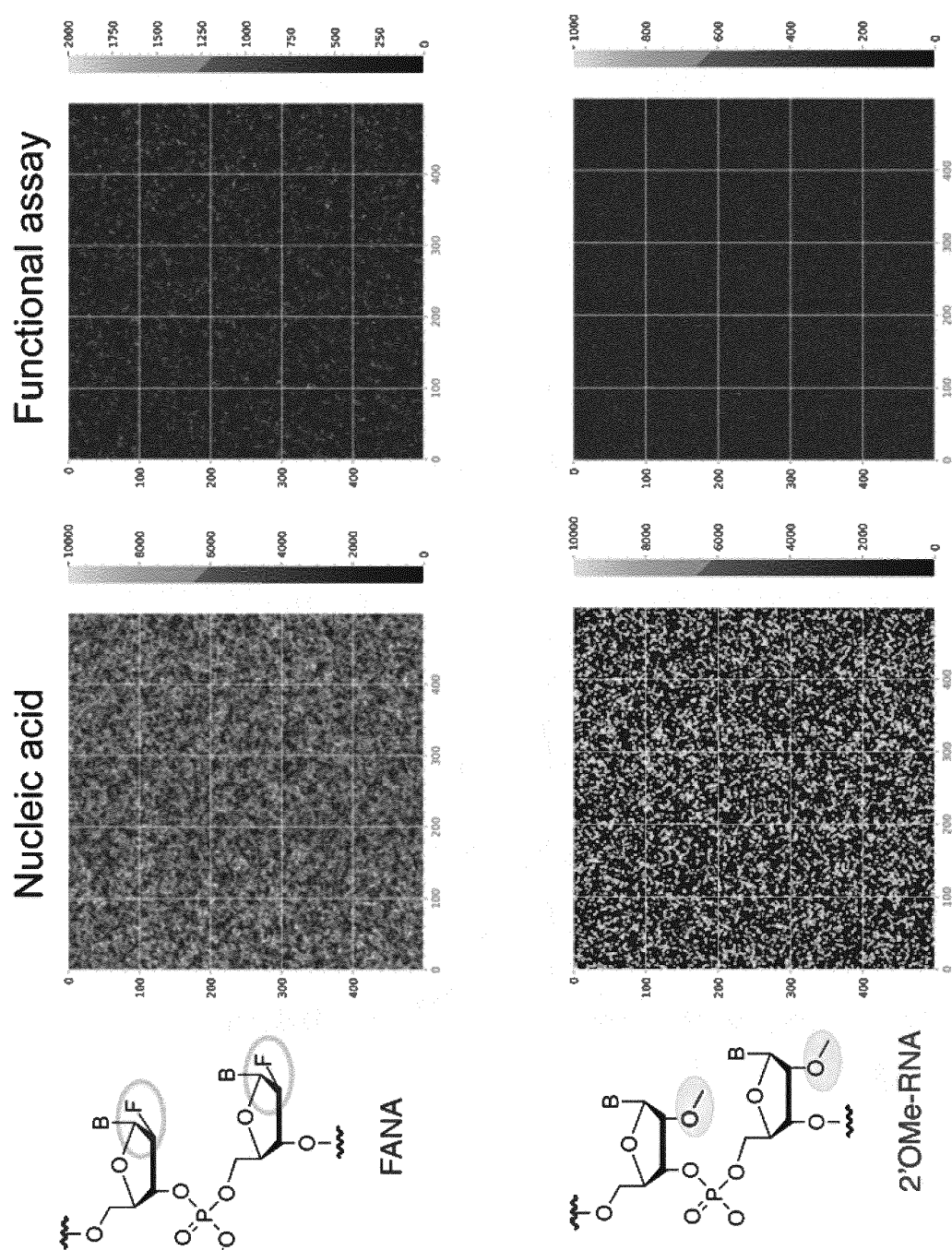


Figure 20

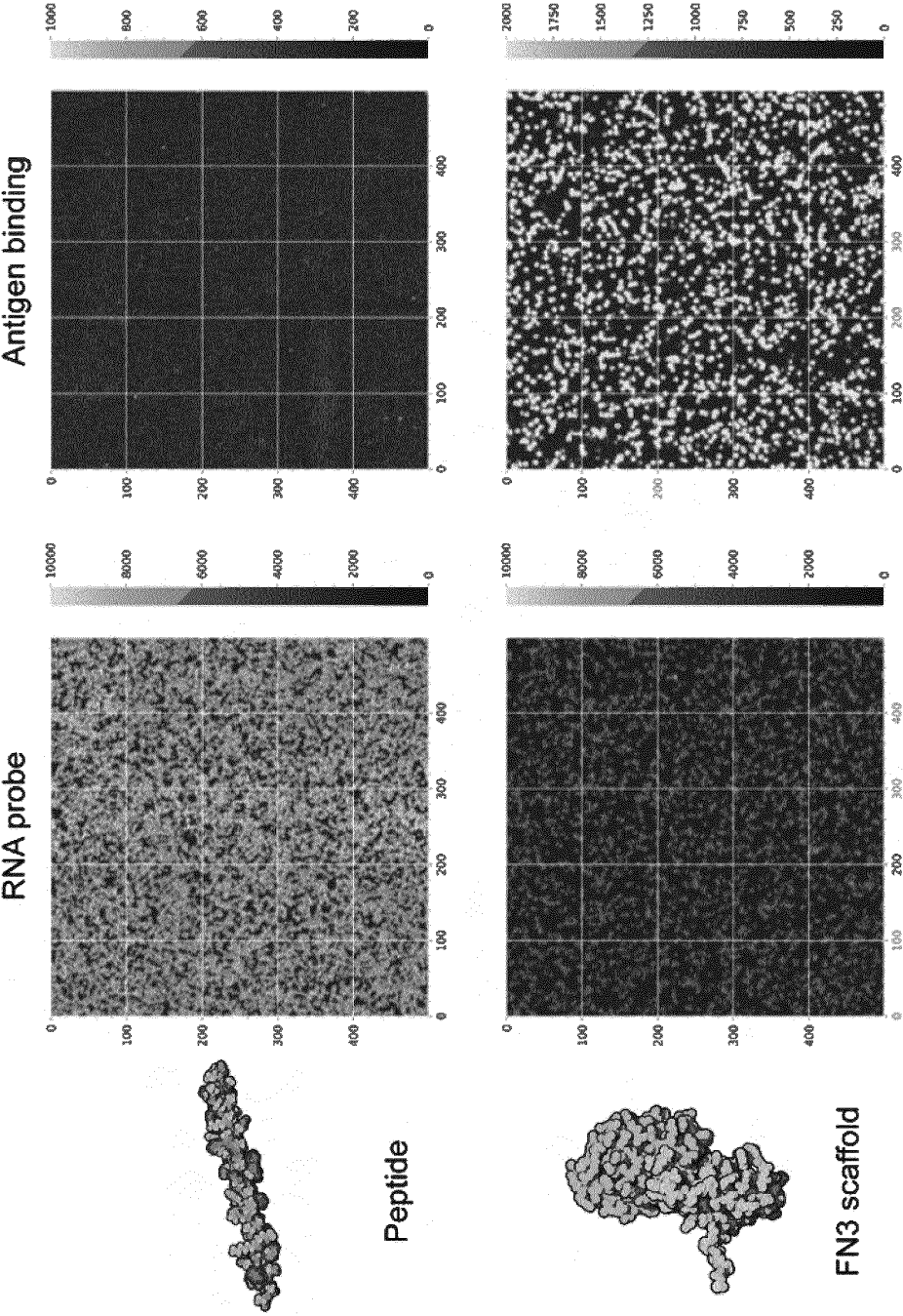
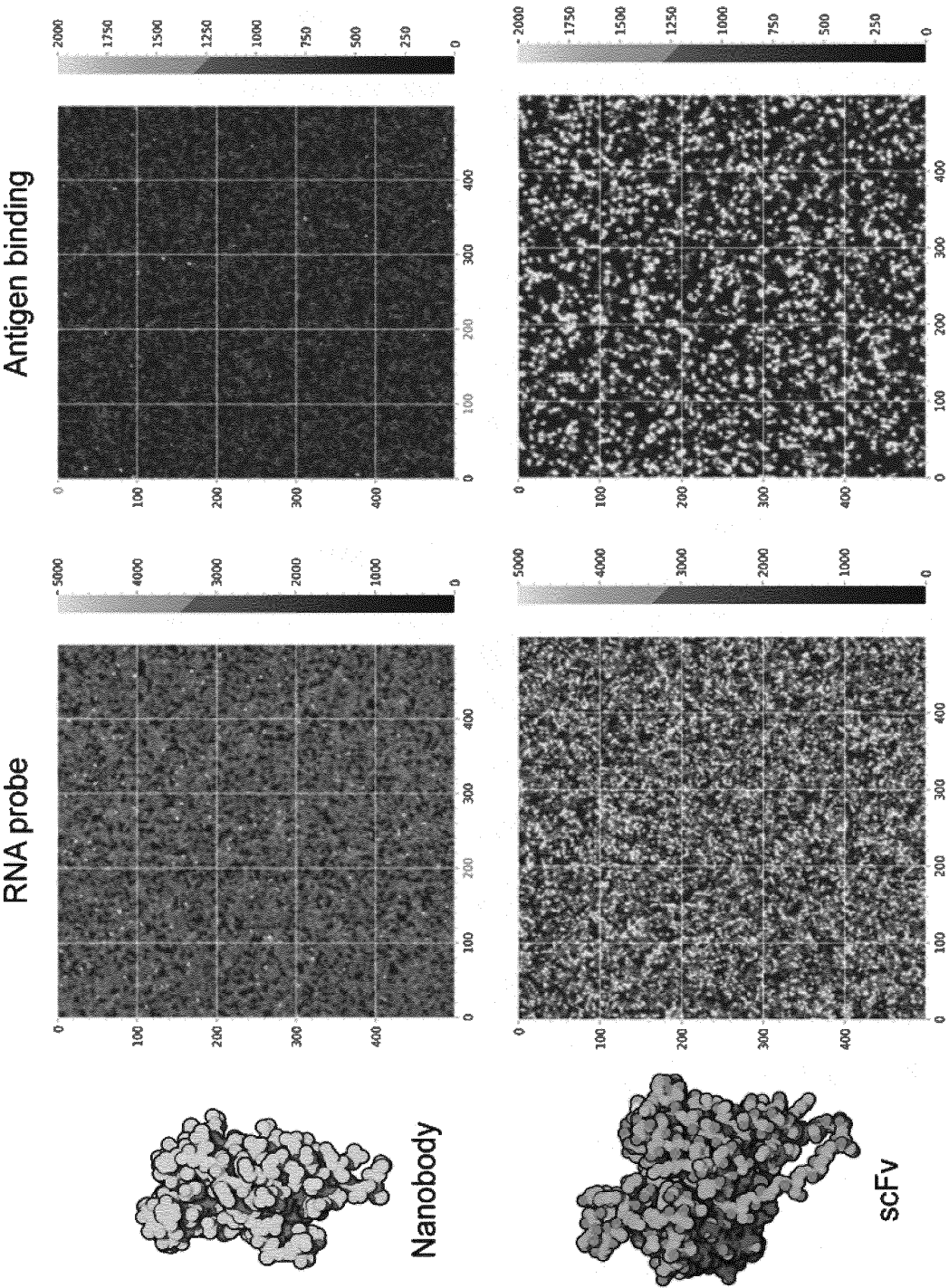


Figure 20 (cont)



$$R = -CH_3, CH_2CH_3, -CH(CH_3)_2$$
