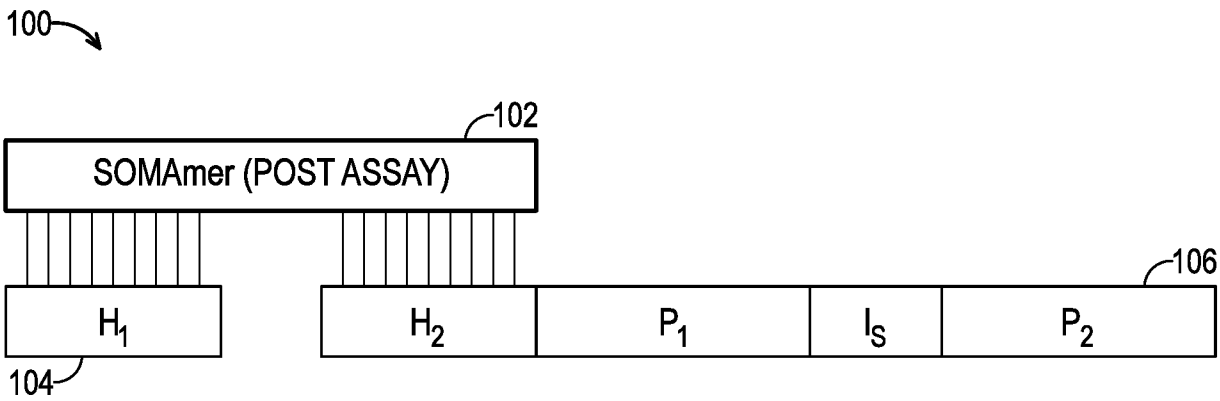


FIG. 1

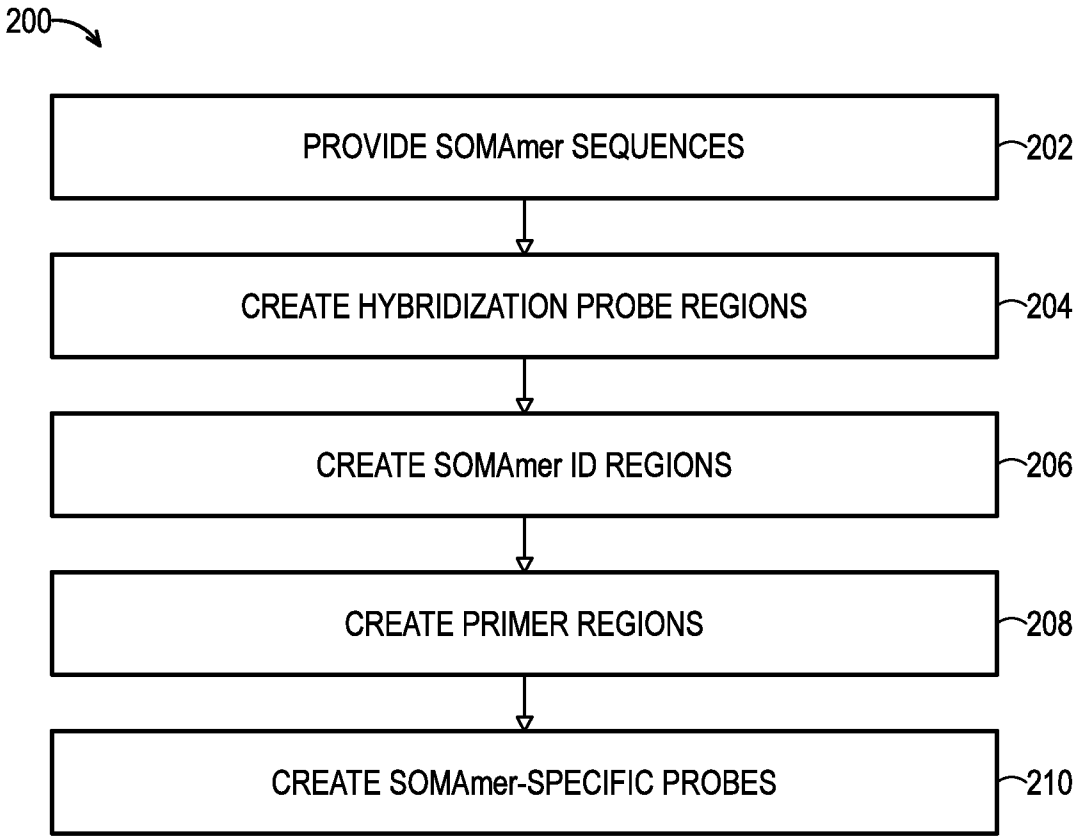

200
PROVIDE SOMAmer SEQUENCES
202
CREATE HYBRIDIZATION PROBE REGIONS
204
CREATE SOMAmer ID REGIONS
206
CREATE PRIMER REGIONS
208
CREATE SOMAmer-SPECIFIC PROBES
210

FIG. 2A

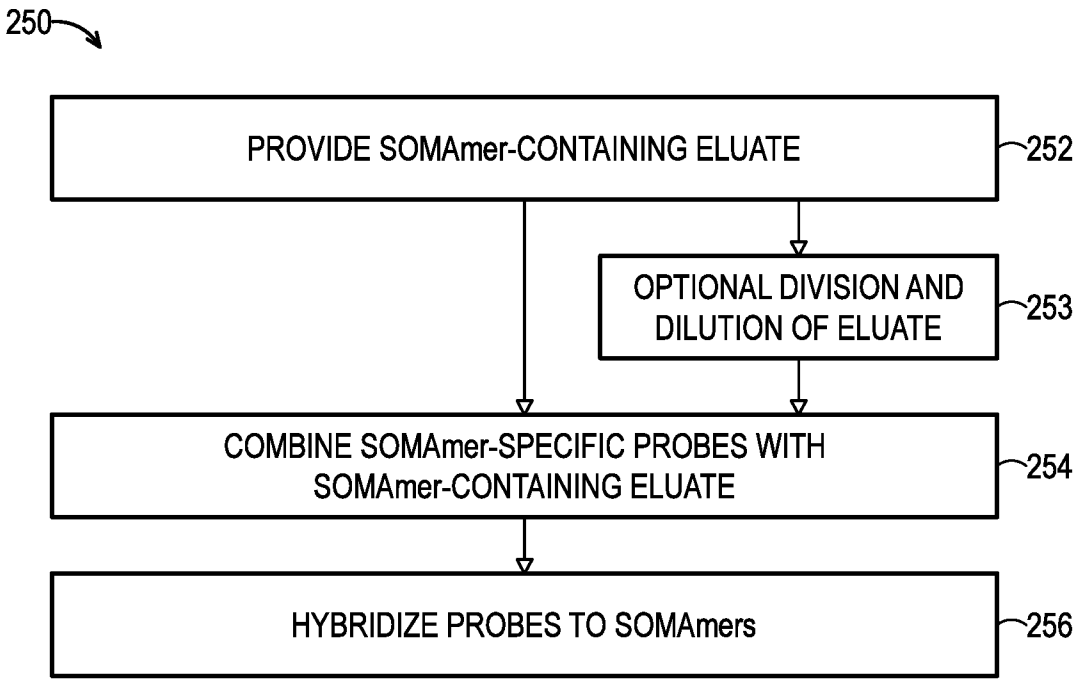

250
PROVIDE SOMAmer-CONTAINING ELUATE
252
OPTIONAL DIVISION AND DILUTION OF ELUATE
253
COMBINE SOMAmer-SPECIFIC PROBES WITH SOMAmer-CONTAINING ELUATE
254
HYBRIDIZE PROBES TO SOMAmers
256

FIG. 2B

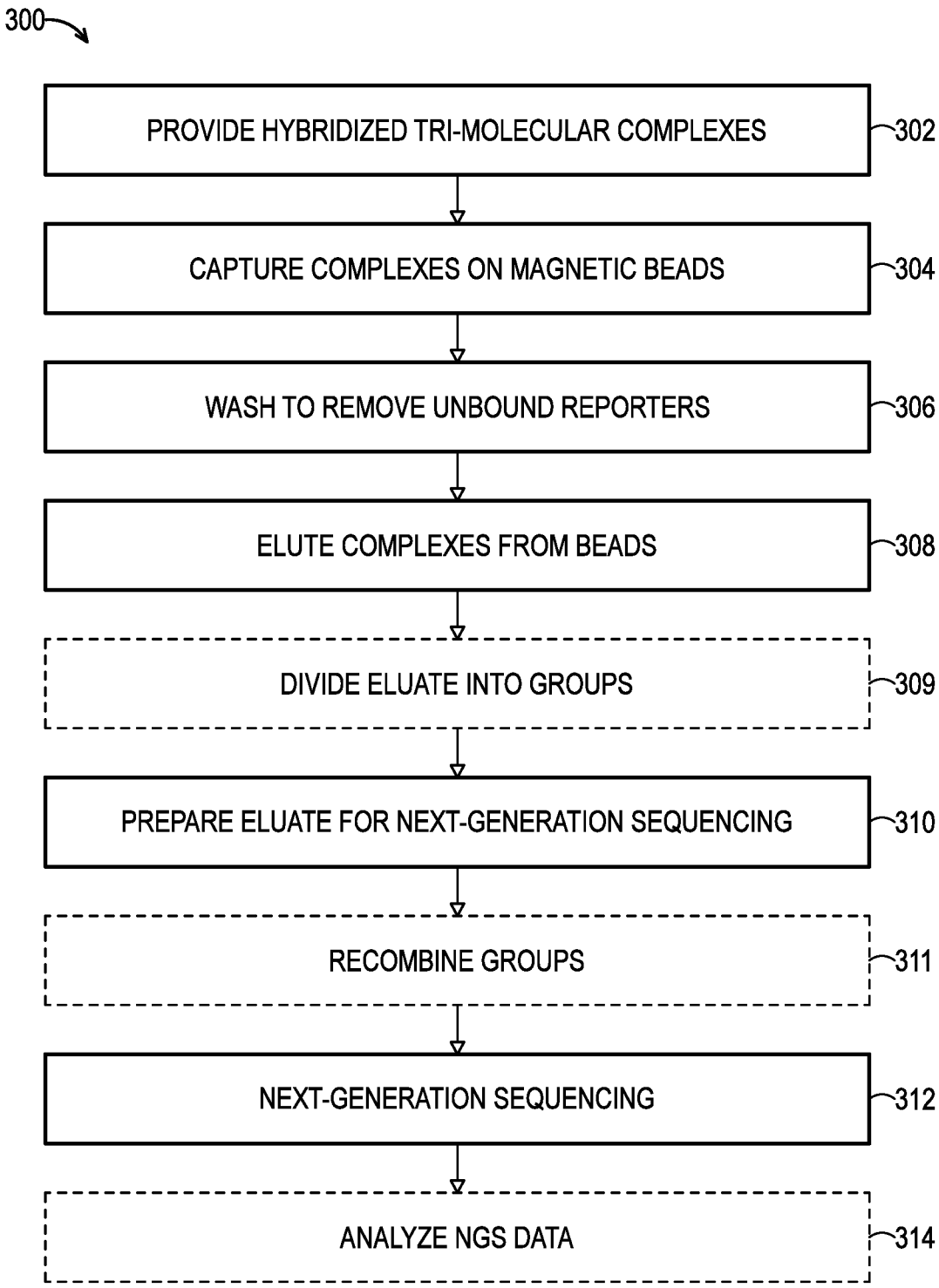

300
PROVIDE HYBRIDIZED TRI-MOLECULAR COMPLEXES
302
CAPTURE COMPLEXES ON MAGNETIC BEADS
304
WASH TO REMOVE UNBOUND REPORTERS
306
ELUTE COMPLEXES FROM BEADS
308
DIVIDE ELUATE INTO GROUPS
309
PREPARE ELUATE FOR NEXT-GENERATION SEQUENCING
310
RECOMBINE GROUPS
311
NEXT-GENERATION SEQUENCING
312
ANALYZE NGS DATA
314

FIG. 3A

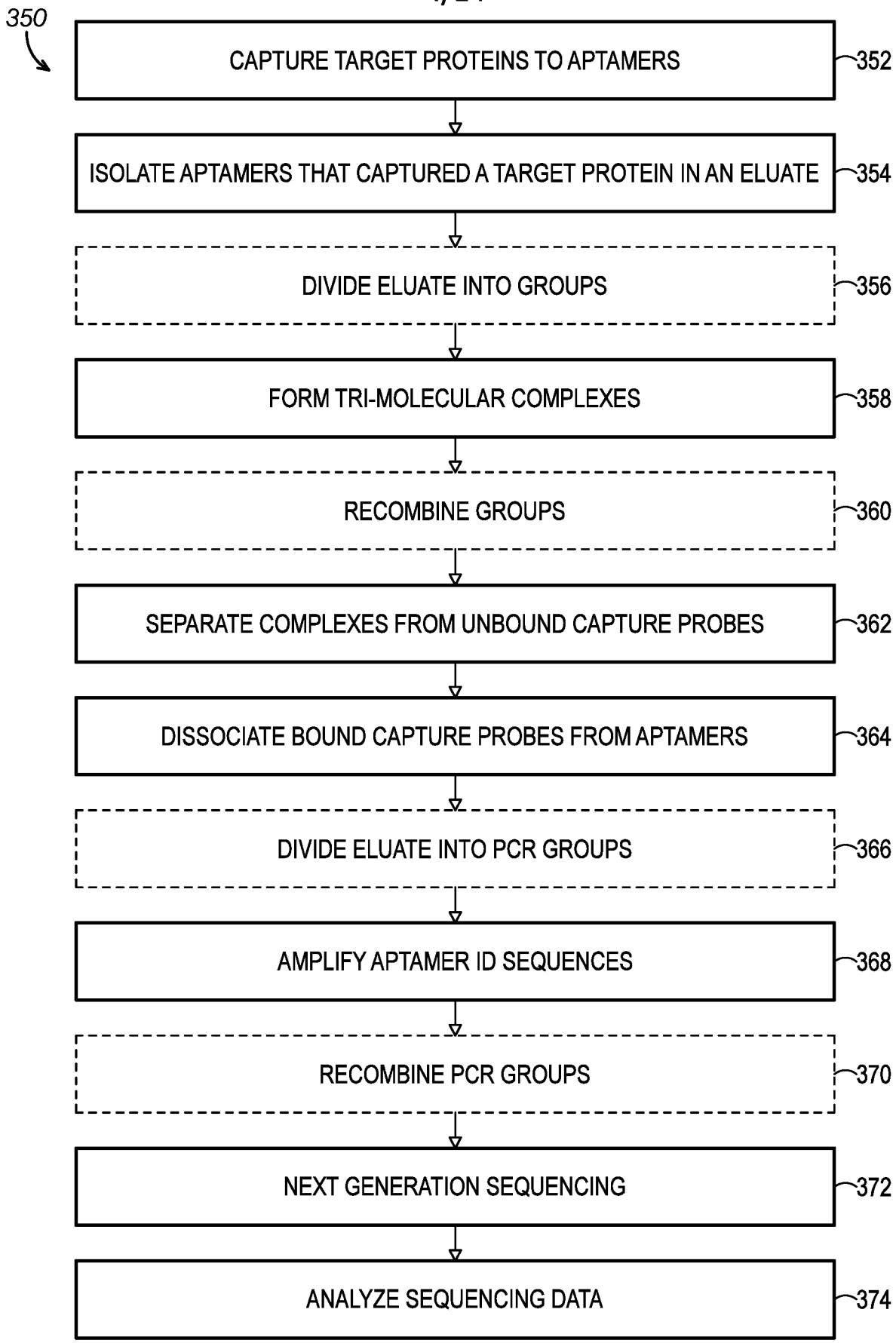

350
CAPTURE TARGET PROTEINS TO APTAMERS
352
ISOLATE APTAMERS THAT CAPTURED A TARGET PROTEIN IN AN ELUATE
354
DIVIDE ELUATE INTO GROUPS
356
FORM TRI-MOLECULAR COMPLEXES
358
RECOMBINE GROUPS
360
SEPARATE COMPLEXES FROM UNBOUND CAPTURE PROBES
362
DISSOCIATE BOUND CAPTURE PROBES FROM APTAMERS
364
DIVIDE ELUATE INTO PCR GROUPS
366
AMPLIFY APTAMER ID SEQUENCES
368
RECOMBINE PCR GROUPS
370
NEXT GENERATION SEQUENCING
372
ANALYZE SEQUENCING DATA
374

FIG. 3B

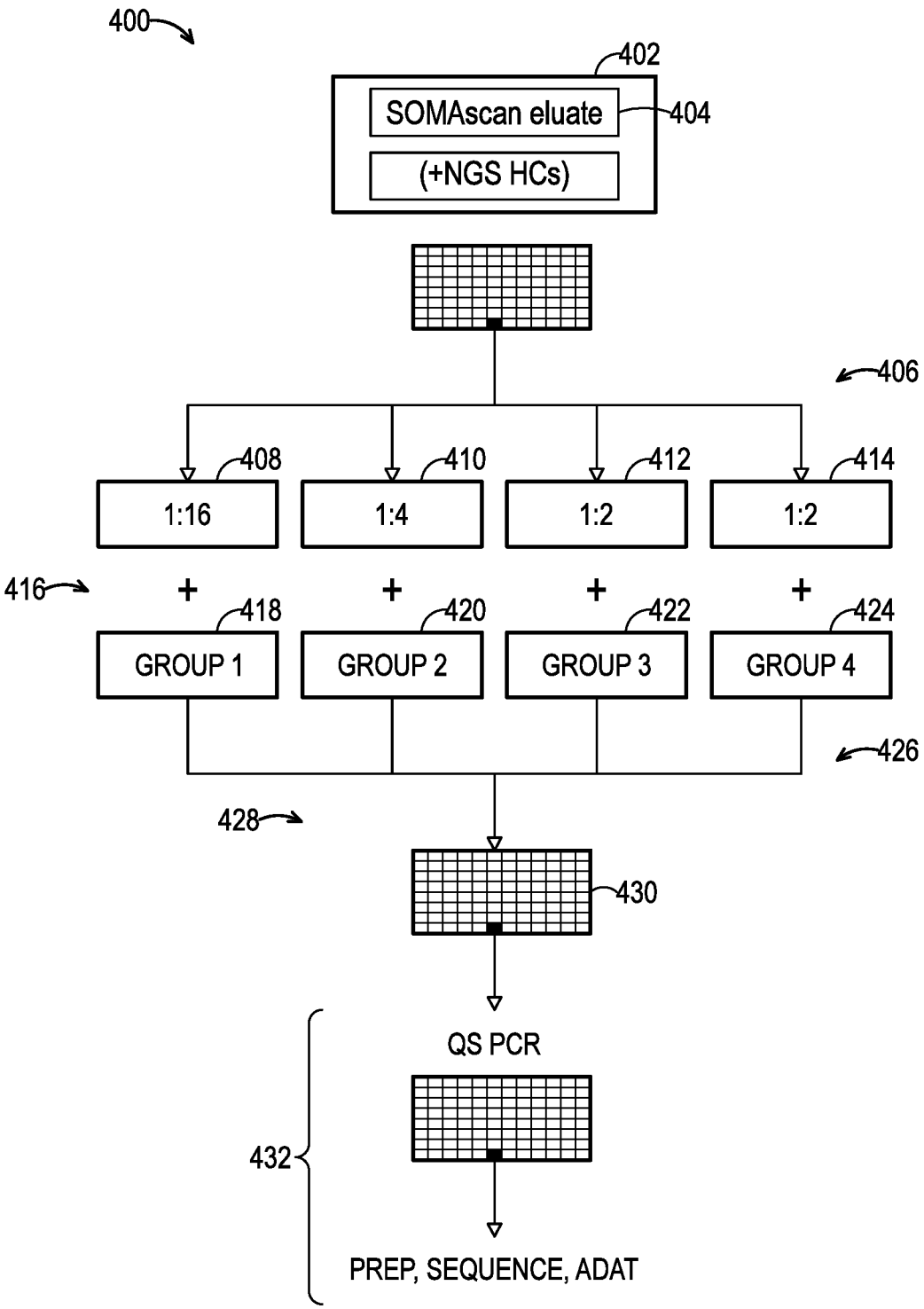

400
402
SOMAscan eluate
(+NGS HCs)
404
406
408
410
412
414
1:16
1:4
1:2
1:2
416
+
+
+
+
418
420
422
424
GROUP 1
GROUP 2
GROUP 3
GROUP 4
426
428
430
QS PCR
432
PREP, SEQUENCE, ADAT

FIG. 4

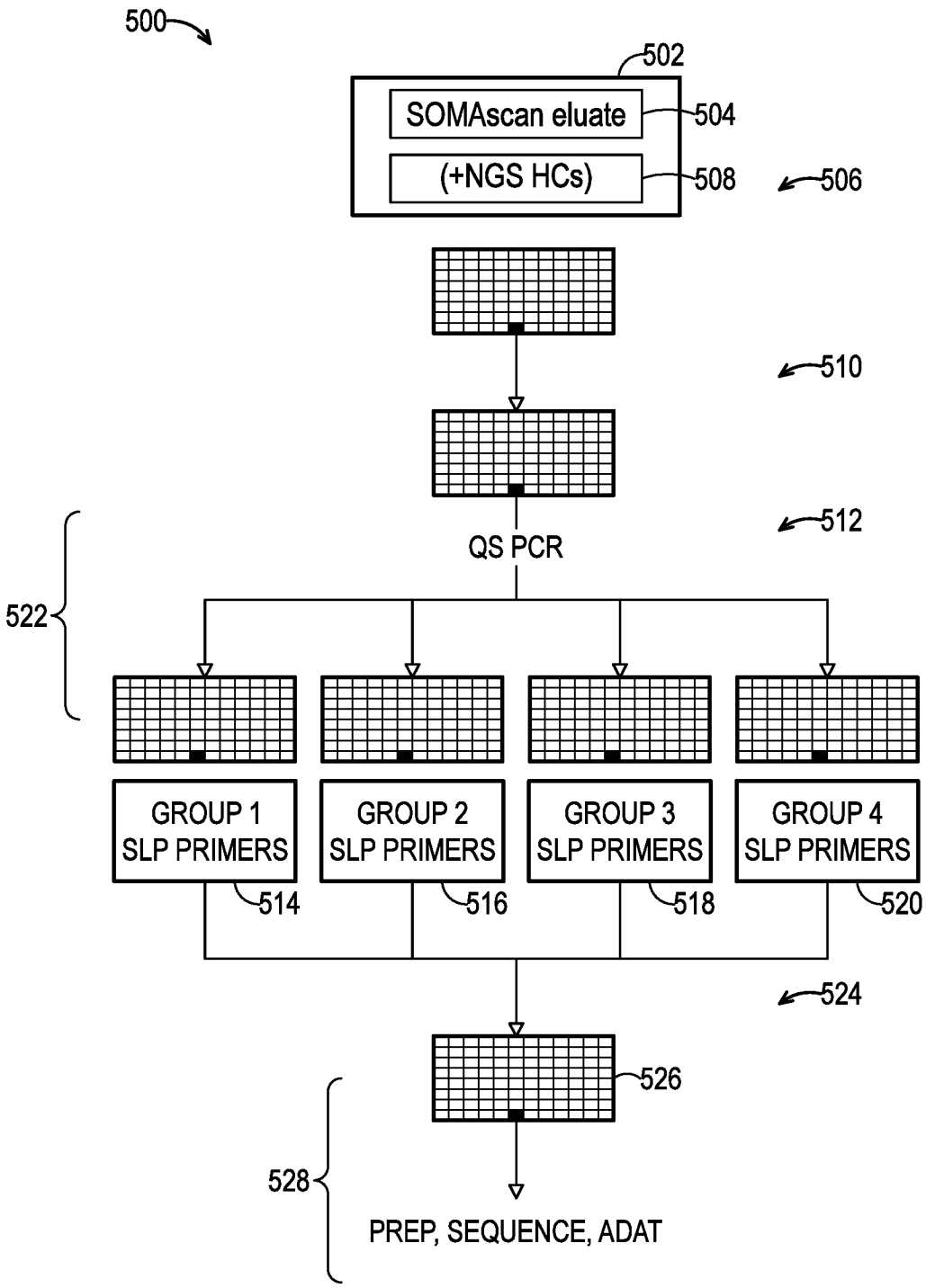

500
502
SOMAscan eluate
504
(+NGS HCs)
508
506
510
512
QS PCR
522
GROUP 1 SLP PRIMERS
GROUP 2 SLP PRIMERS
GROUP 3 SLP PRIMERS
GROUP 4 SLP PRIMERS
514
516
518
520
524
526
528
PREP, SEQUENCE, ADAT

FIG. 5

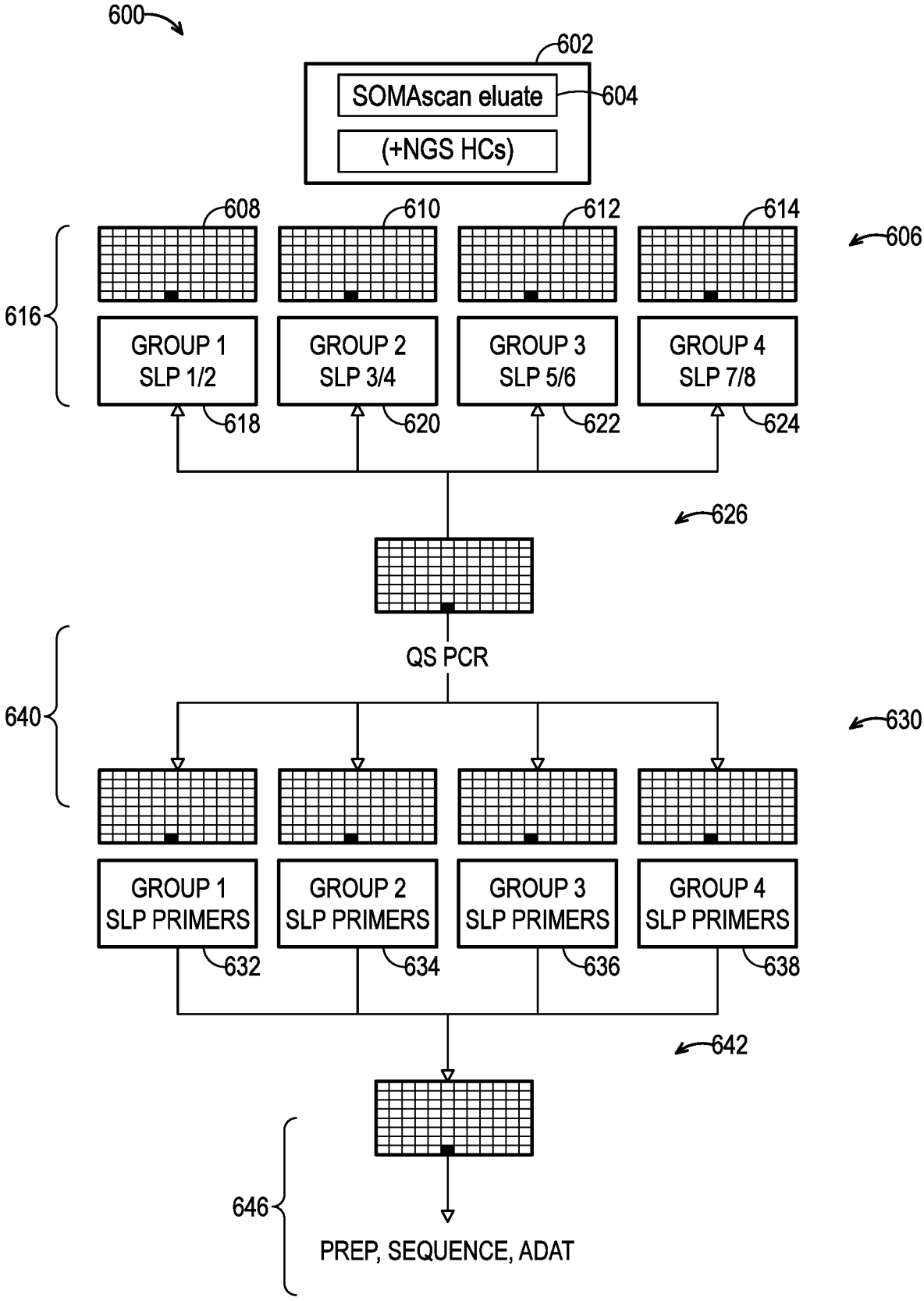

600
602
SOMAscan eluate
(+NGS HCs)
604
608
610
612
614
606
616
GROUP 1
SLP 1/2
GROUP 2
SLP 3/4
GROUP 3
SLP 5/6
GROUP 4
SLP 7/8
618
620
622
624
626
QS PCR
640
630
GROUP 1
SLP PRIMERS
GROUP 2
SLP PRIMERS
GROUP 3
SLP PRIMERS
GROUP 4
SLP PRIMERS
632
634
636
638
642
646
PREP, SEQUENCE, ADAT

FIG. 6

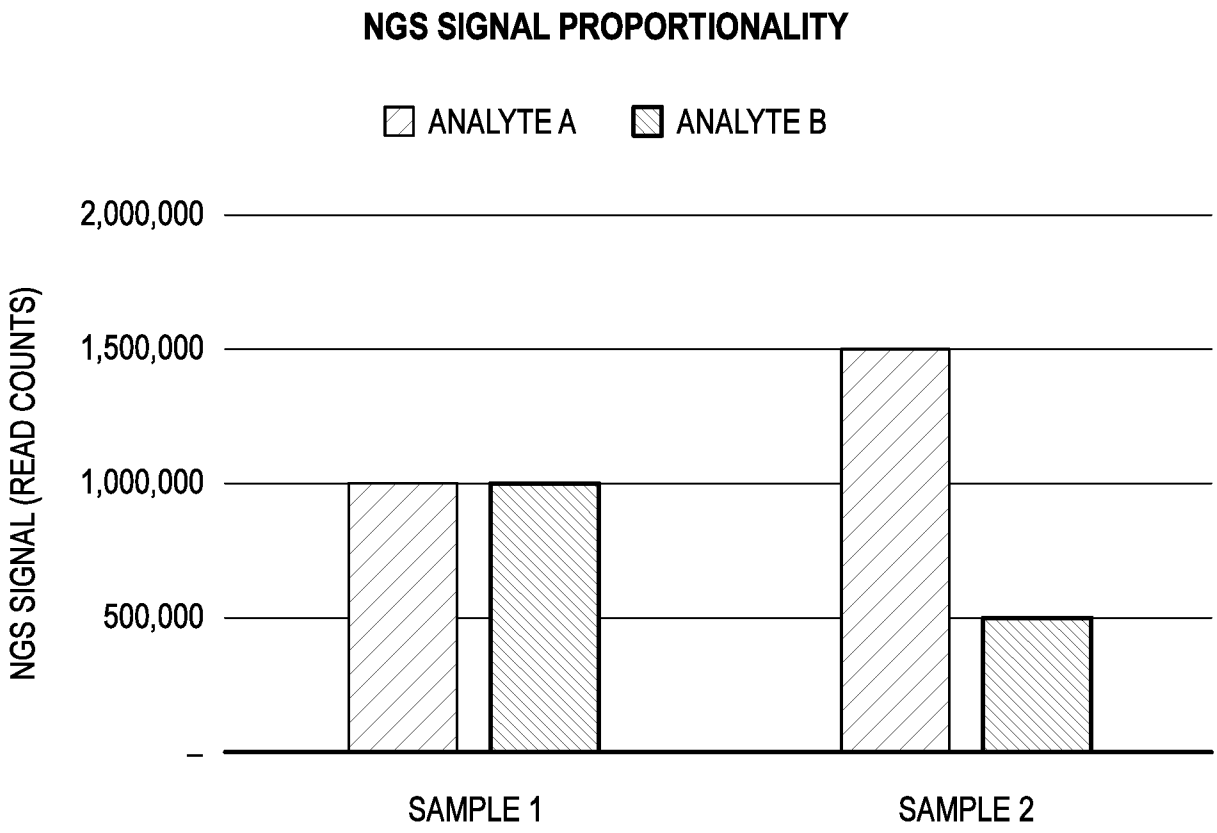

NGS SIGNAL PROPORTIONALITY
ANALYTE A
ANALYTE B
NGS SIGNAL (READ COUNTS)
2,000,000
1,500,000
1,000,000
500,000
–
SAMPLE 1
SAMPLE 2

FIG. 7

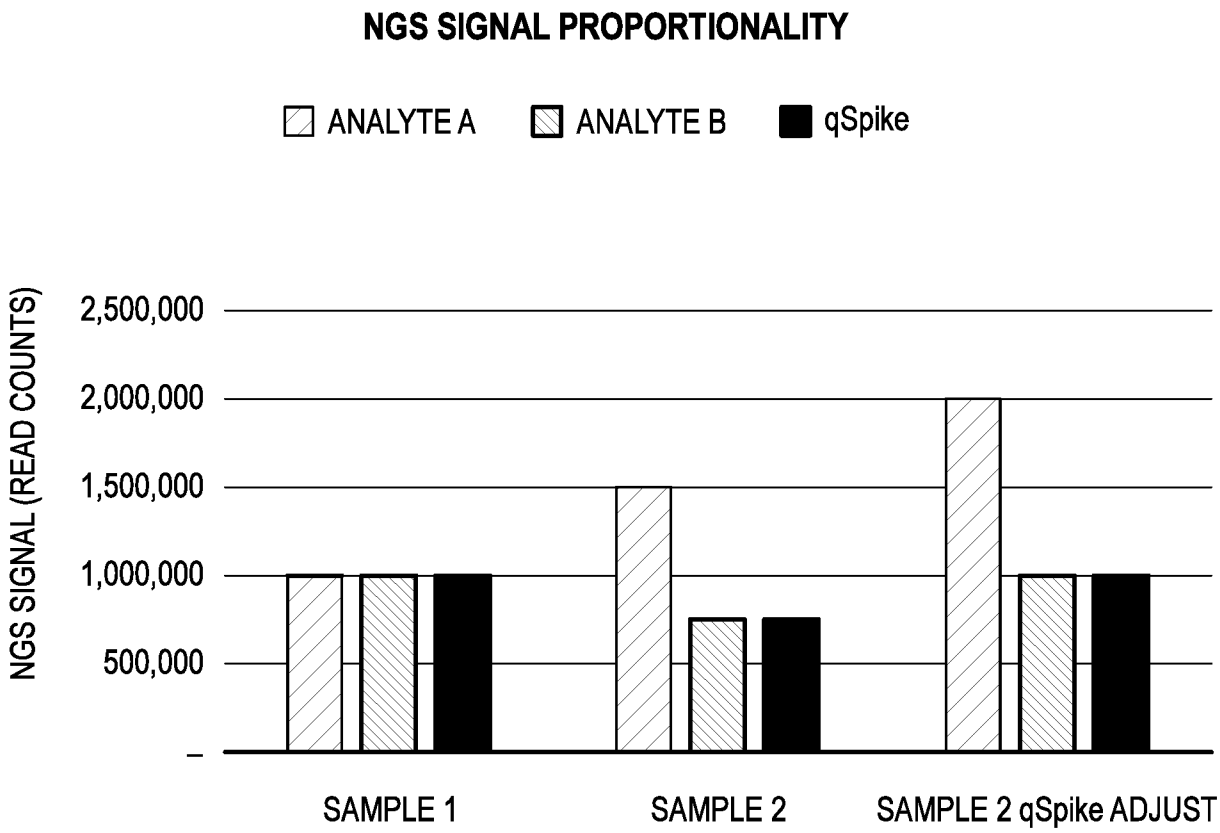

NGS SIGNAL PROPORTIONALITY
ANALYTE A
ANALYTE B
qSpike
NGS SIGNAL (READ COUNTS)
2,500,000
2,000,000
1,500,000
1,000,000
500,000
–
SAMPLE 1
SAMPLE 2
SAMPLE 2 qSpike ADJUST

FIG. 8

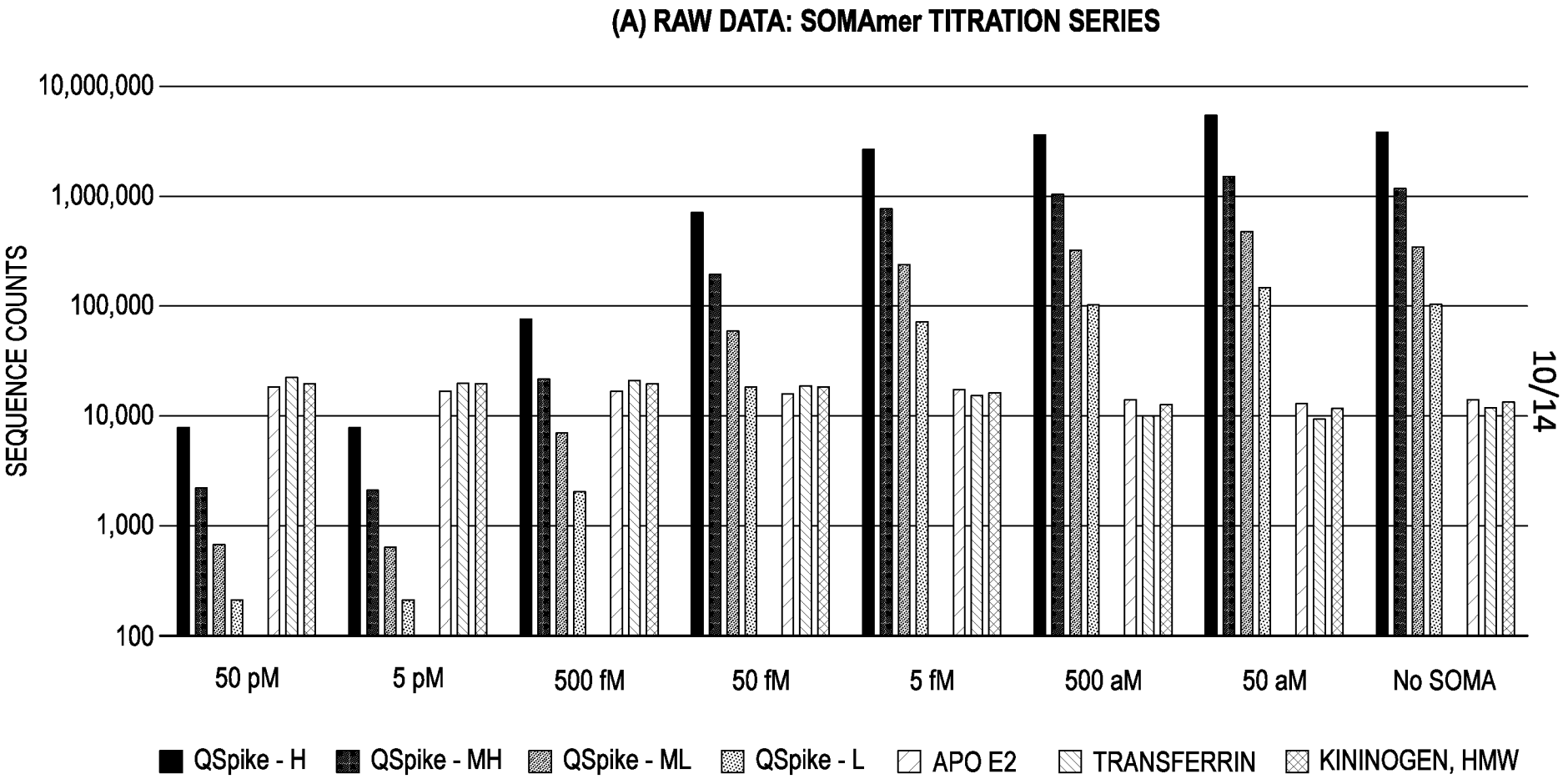

(A) RAW DATA: SOMAmer TITRATION SERIES
SEQUENCE COUNTS
10,000,000
1,000,000
100,000
10,000
1,000
100
50 pM
5 pM
500 fM
50 fM
5 fM
500 aM
50 aM
No SOMA
QSpike - H
QSpike - MH
QSpike - ML
QSpike - L
APO E2
TRANSFERRIN
KININOGEN, HMW

FIG. 9

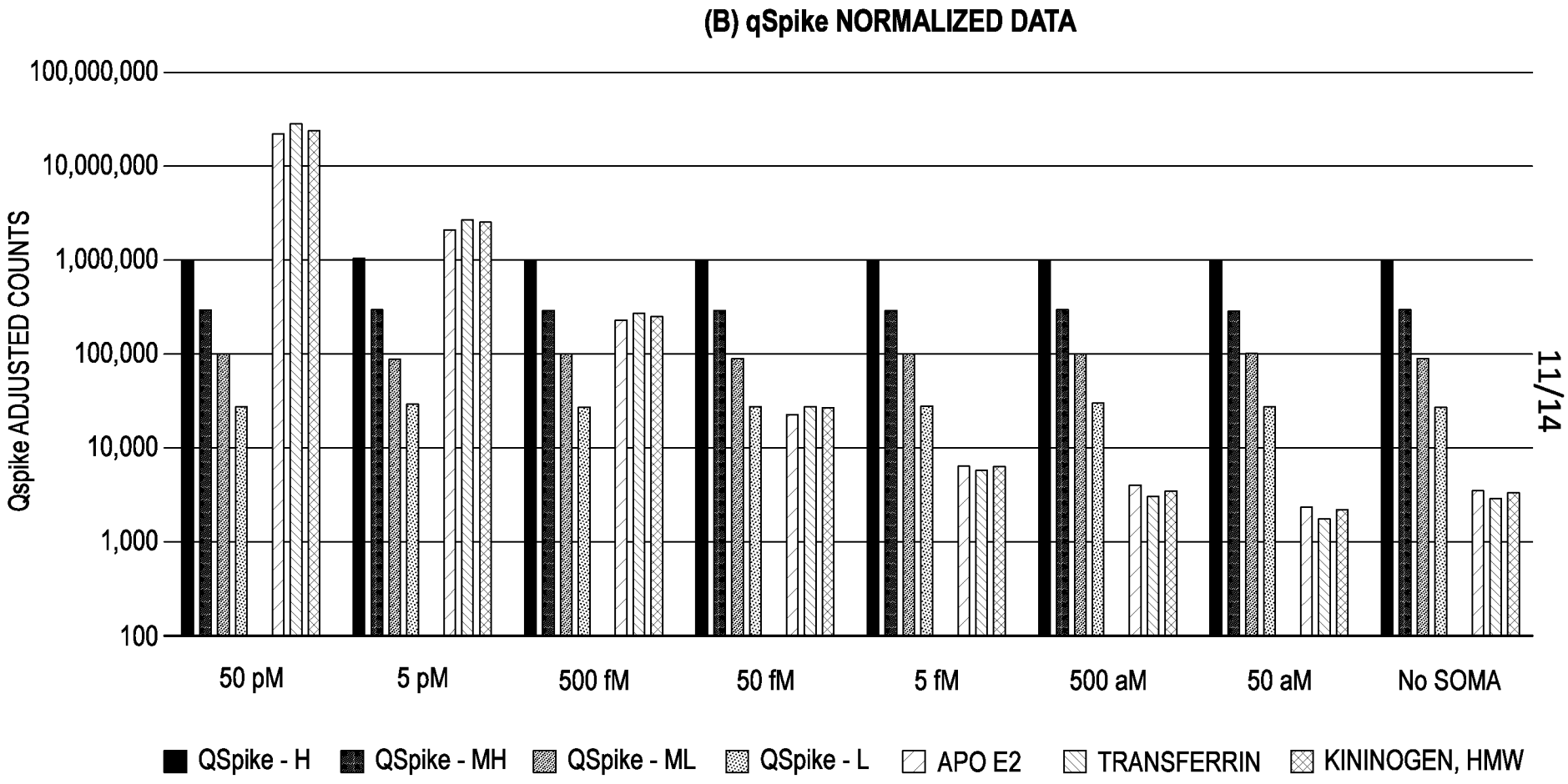

(B) qSpike NORMALIZED DATA
Qspike ADJUSTED COUNTS
100,000,000
10,000,000
1,000,000
100,000
10,000
1,000
100
50 pM
5 pM
500 fM
50 fM
5 fM
500 aM
50 aM
No SOMA
QSpike - H
QSpike - MH
QSpike - ML
QSpike - L
APO E2
TRANSFERRIN
KININOGEN, HMW

FIG. 10

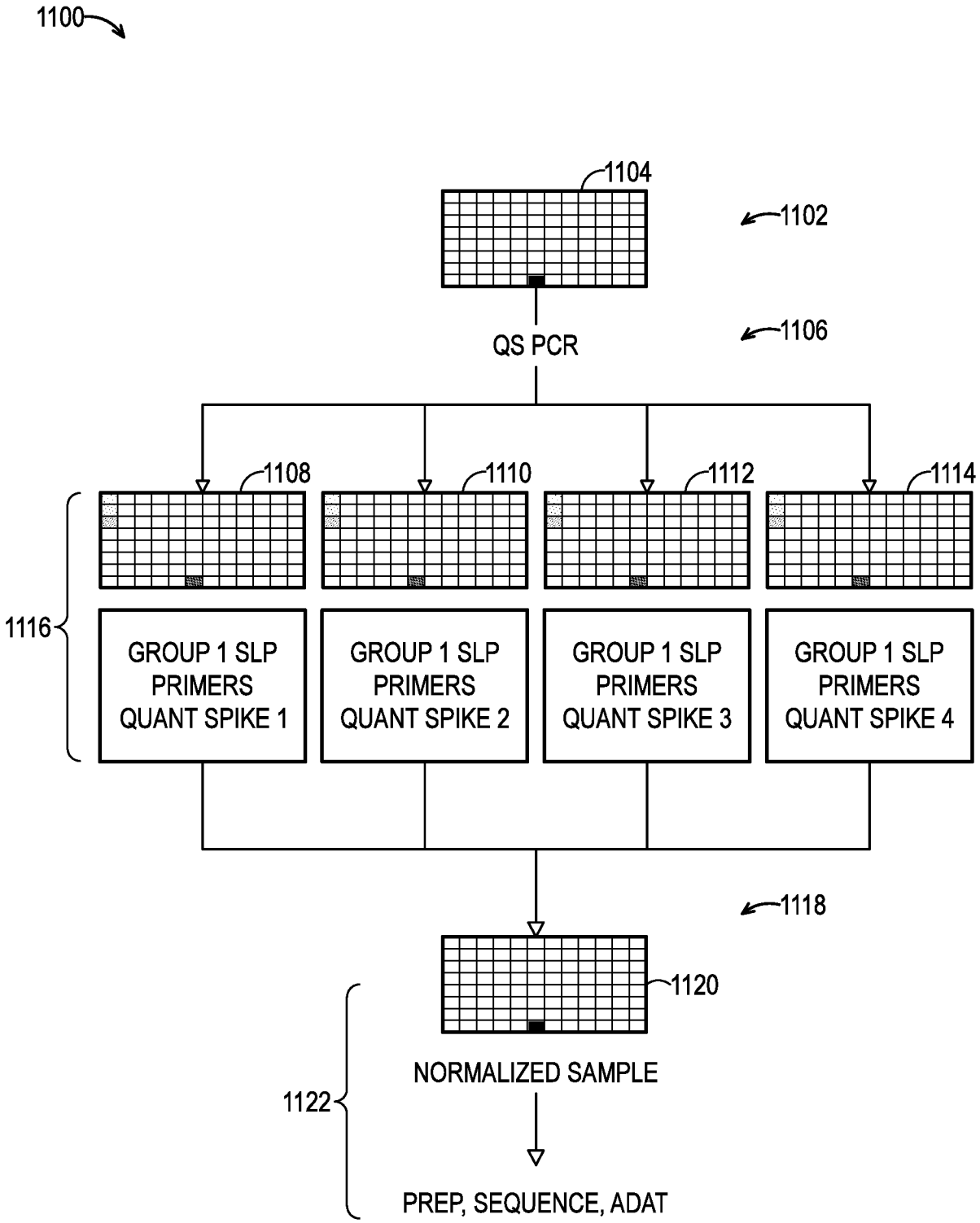

1100
1104
1102
QS PCR
1106
1108
1110
1112
1114
1116
GROUP 1 SLP PRIMERS QUANT SPIKE 1
GROUP 1 SLP PRIMERS QUANT SPIKE 2
GROUP 1 SLP PRIMERS QUANT SPIKE 3
GROUP 1 SLP PRIMERS QUANT SPIKE 4
1118
1120
NORMALIZED SAMPLE
1122
PREP, SEQUENCE, ADAT

FIG. 11

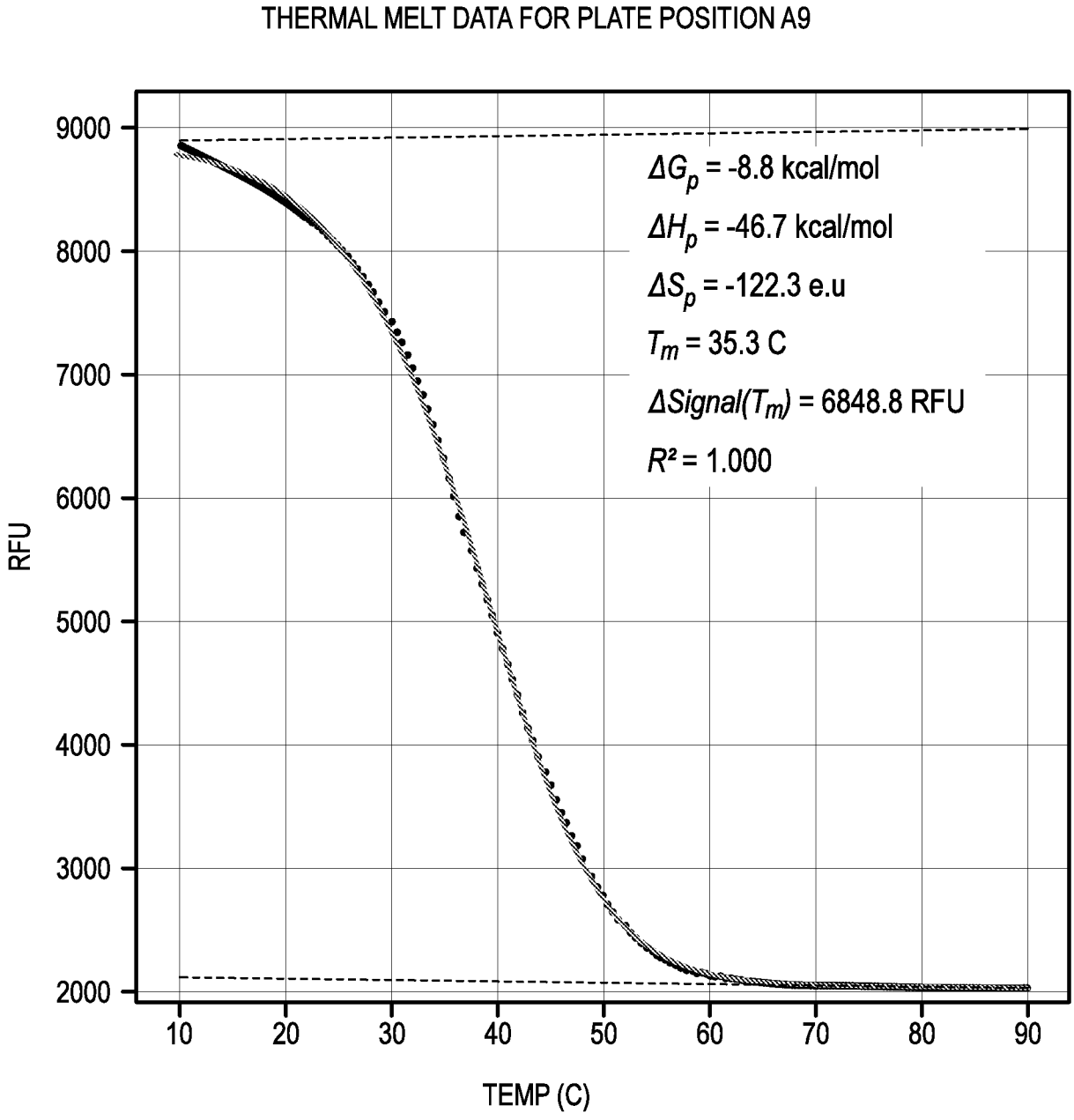

THERMAL MELT DATA FOR PLATE POSITION A9
ΔG_p = -8.8 kcal/mol
ΔH_p = -46.7 kcal/mol
ΔS_p = -122.3 e.u
T_m = 35.3 C
ΔSignal(T_m) = 6848.8 RFU
R² = 1.000
RFU
9000
8000
7000
6000
5000
4000
3000
2000
10
20
30
40
50
60
70
80
90
TEMP (C)

FIG. 12

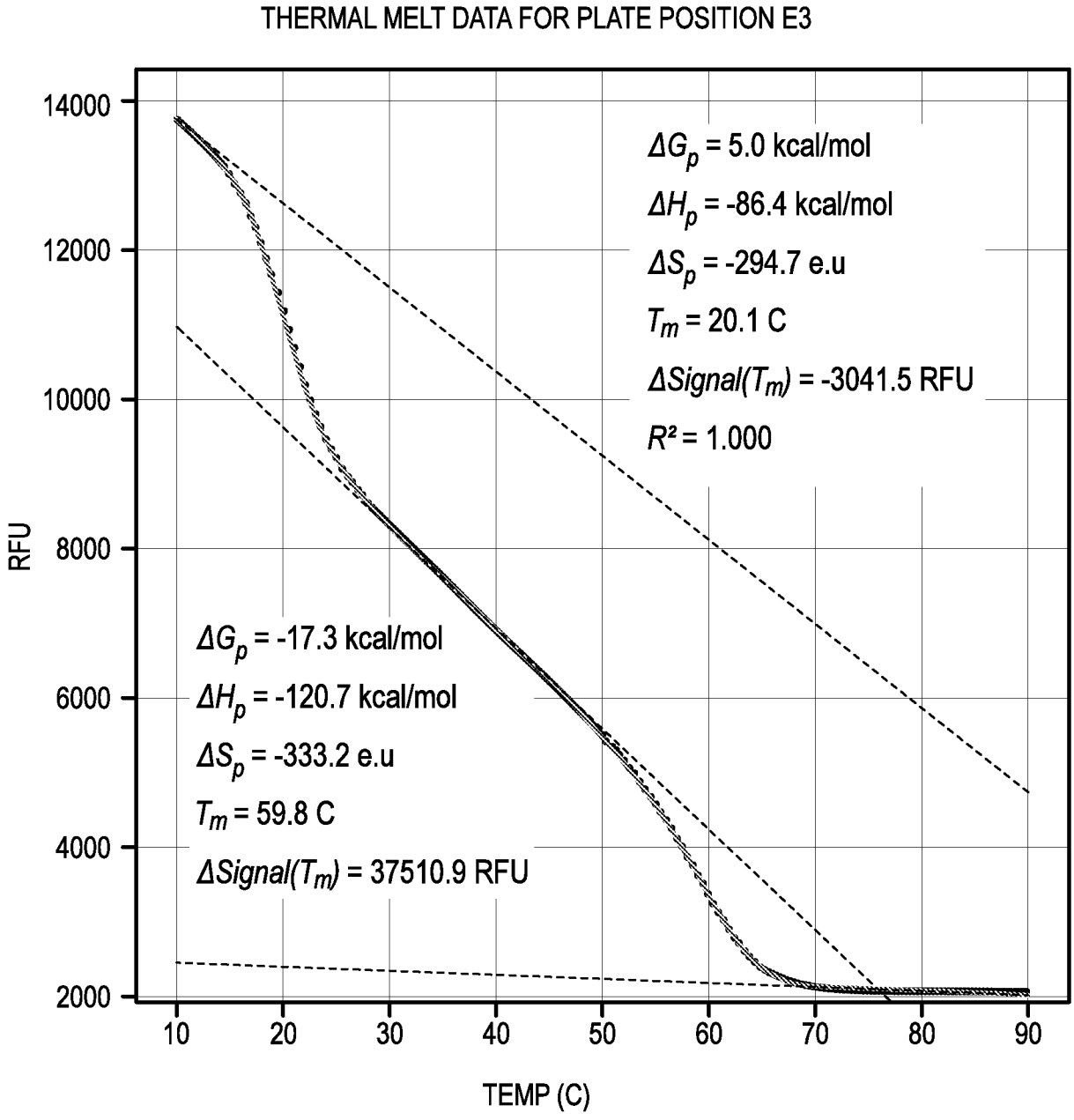

THERMAL MELT DATA FOR PLATE POSITION E3
ΔGp = 5.0 kcal/mol
ΔHp = -86.4 kcal/mol
ΔSp = -294.7 e.u
Tm = 20.1 C
ΔSignal(Tm) = -3041.5 RFU
R² = 1.000
ΔGp = -17.3 kcal/mol
ΔHp = -120.7 kcal/mol
ΔSp = -333.2 e.u
Tm = 59.8 C
ΔSignal(Tm) = 37510.9 RFU
RFU
14000
12000
10000
8000
6000
4000
2000
10
20
30
40
50
60
70
80
90
TEMP (C)

FIG. 13