

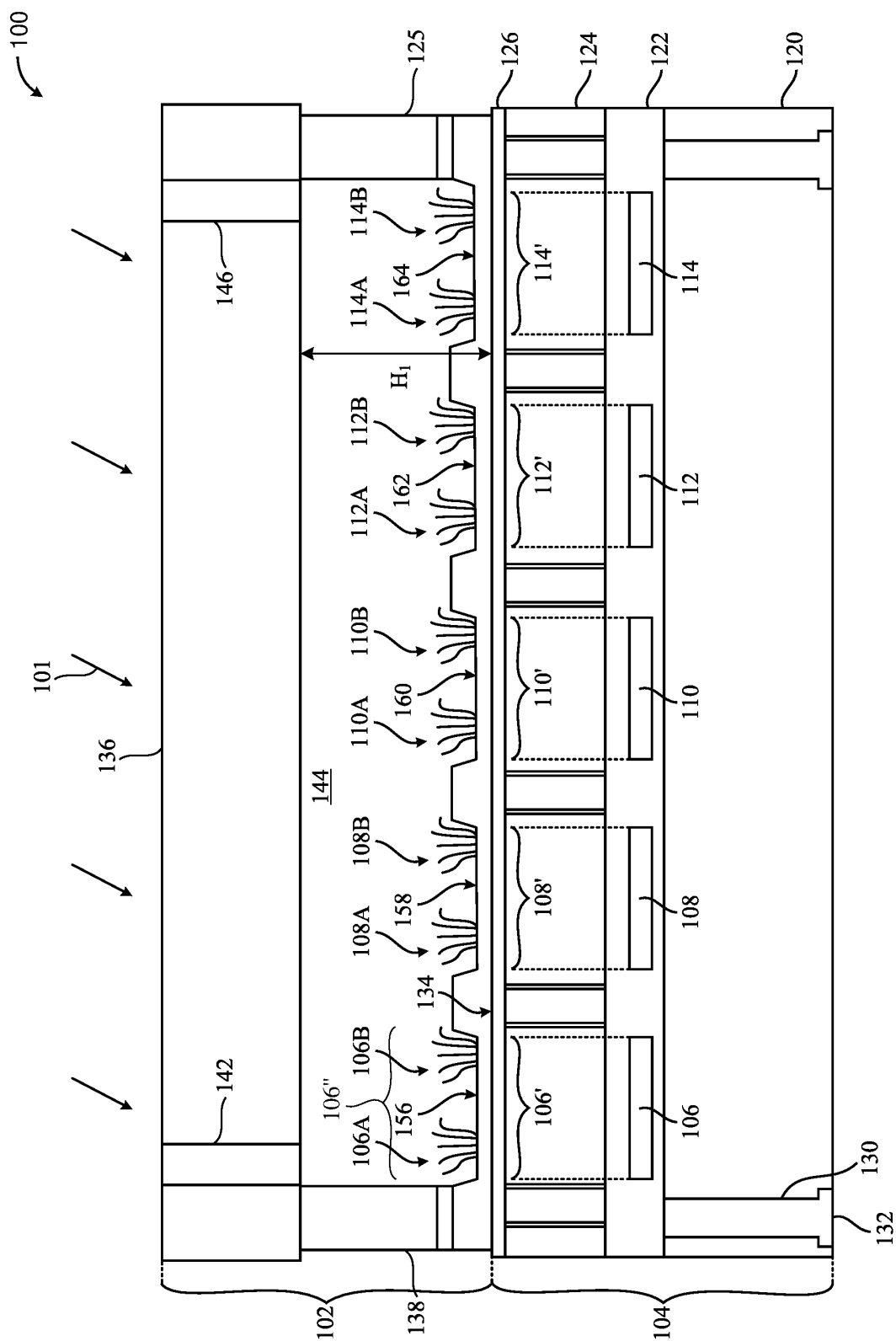


Fig. 1

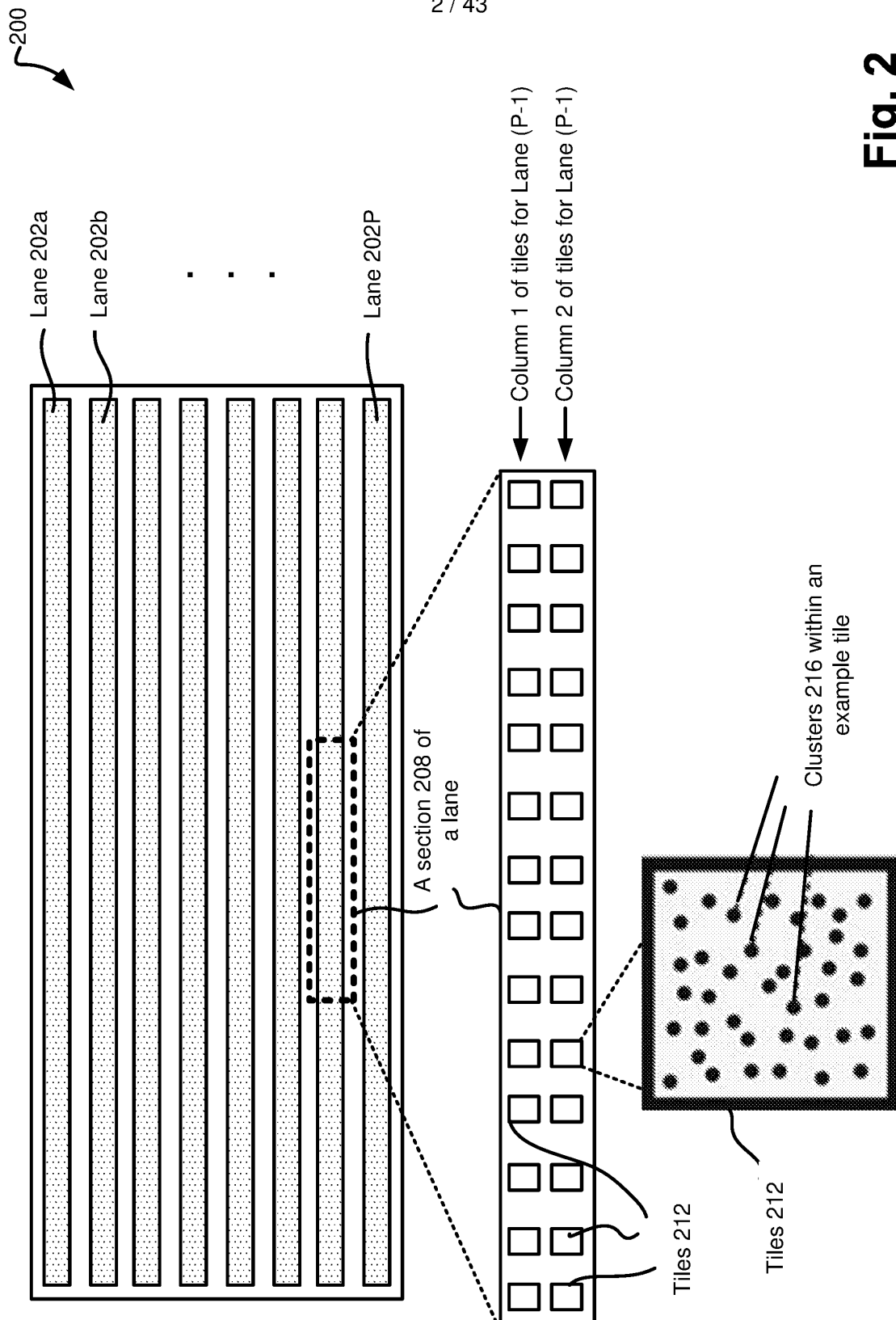


Fig. 2

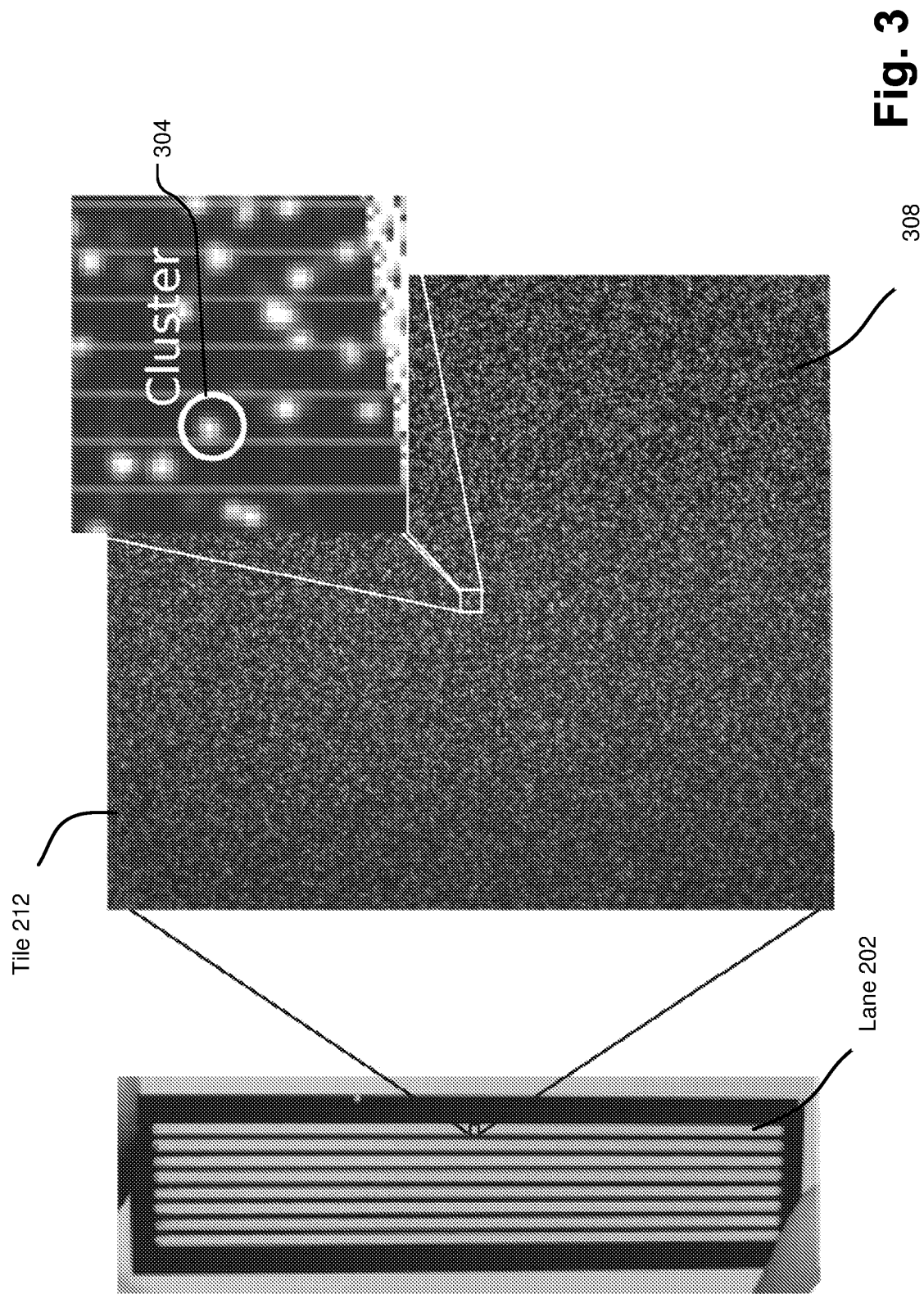


Fig. 3

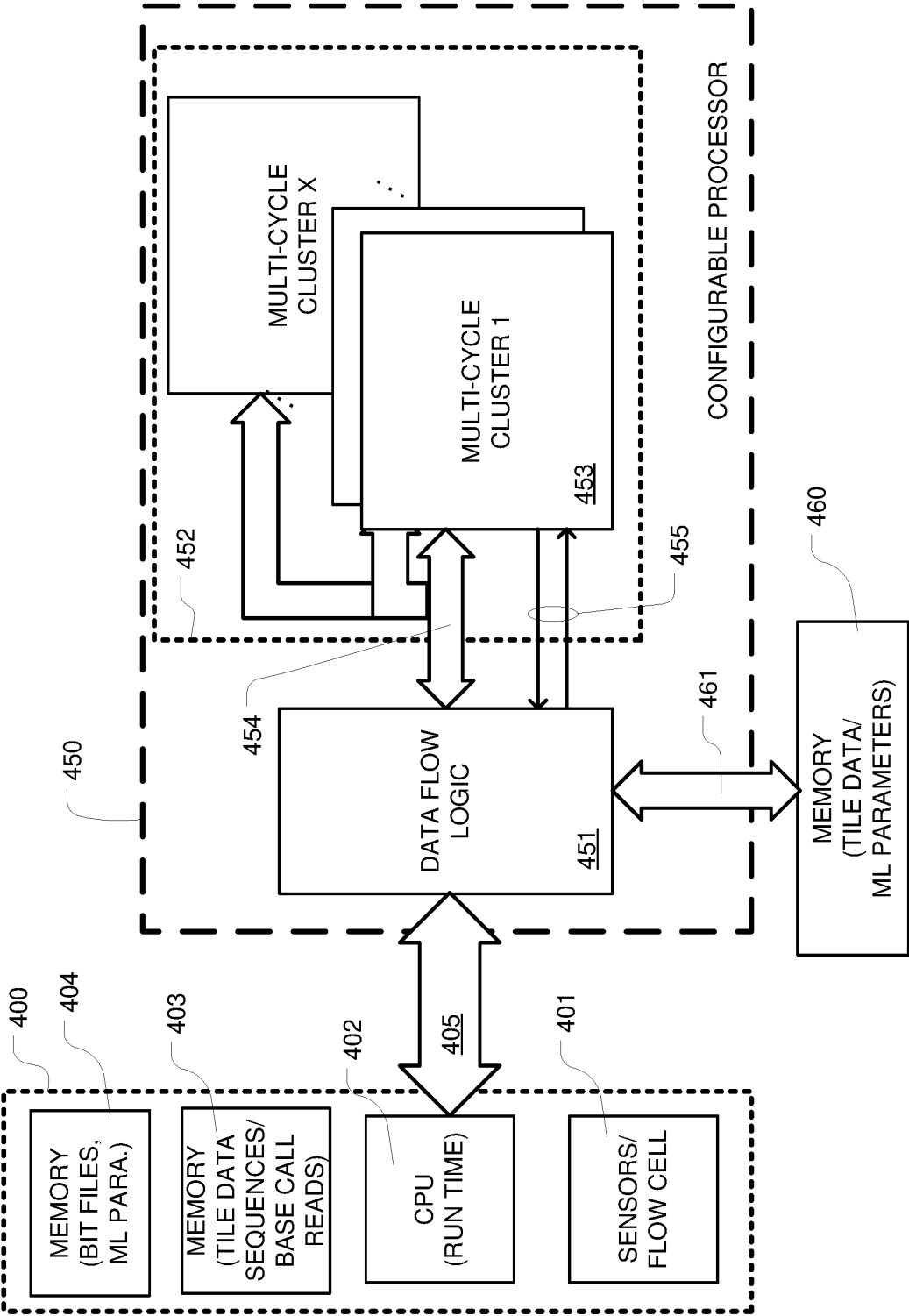


Fig. 4

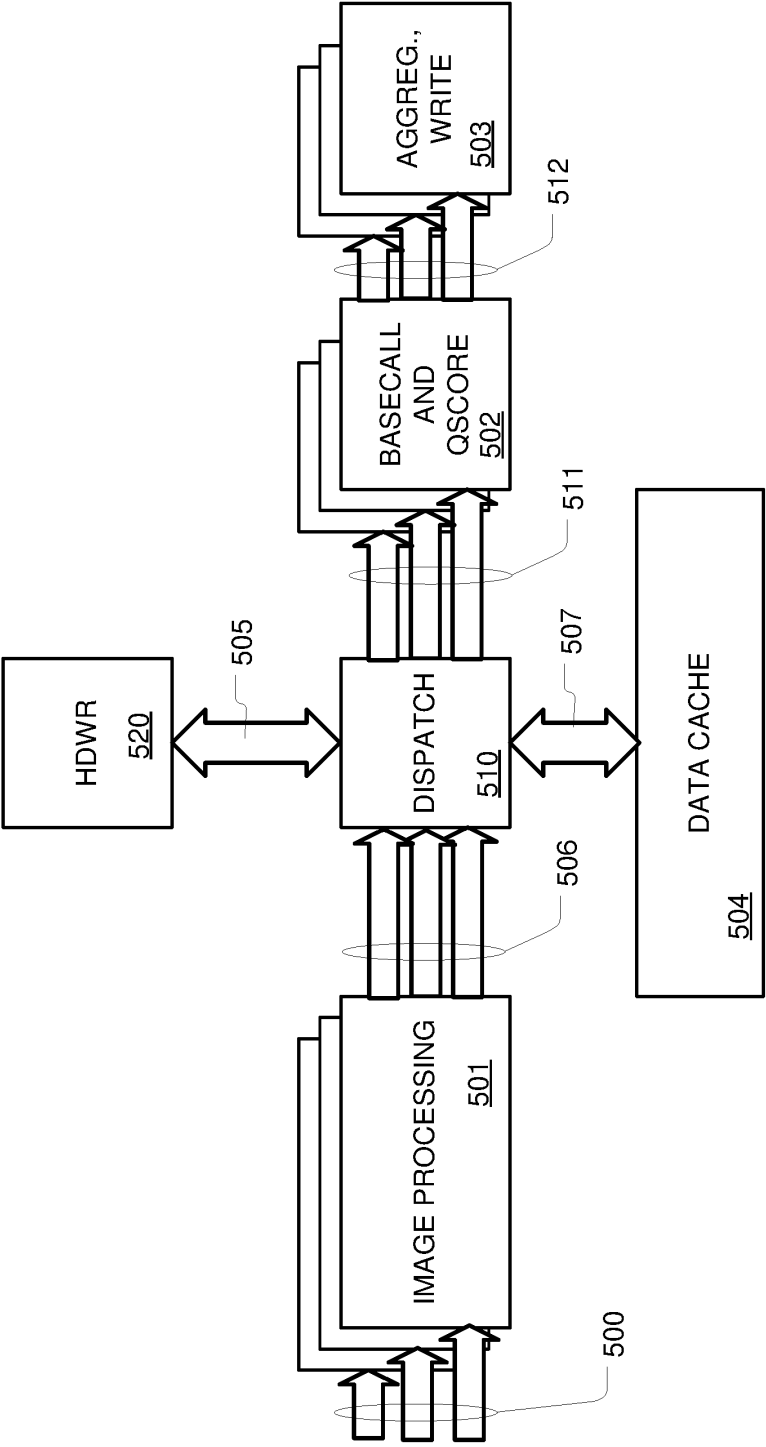


Fig. 5

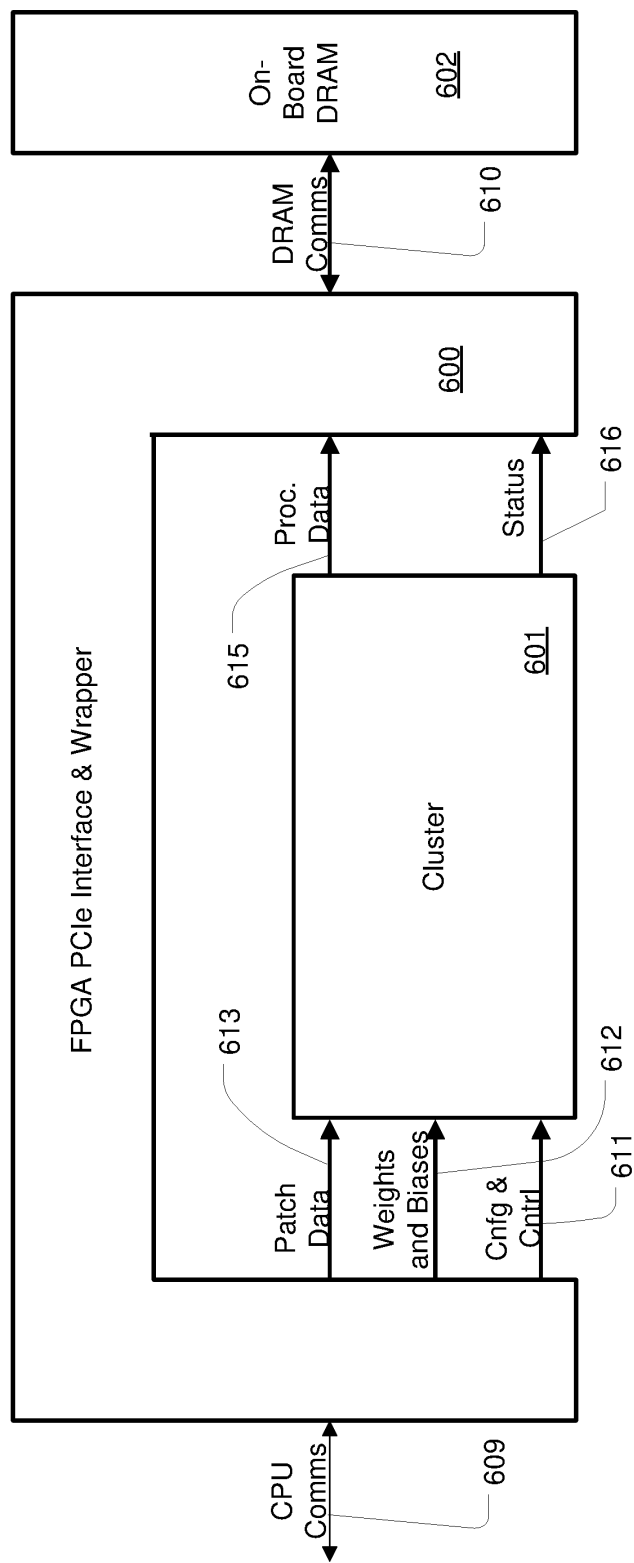
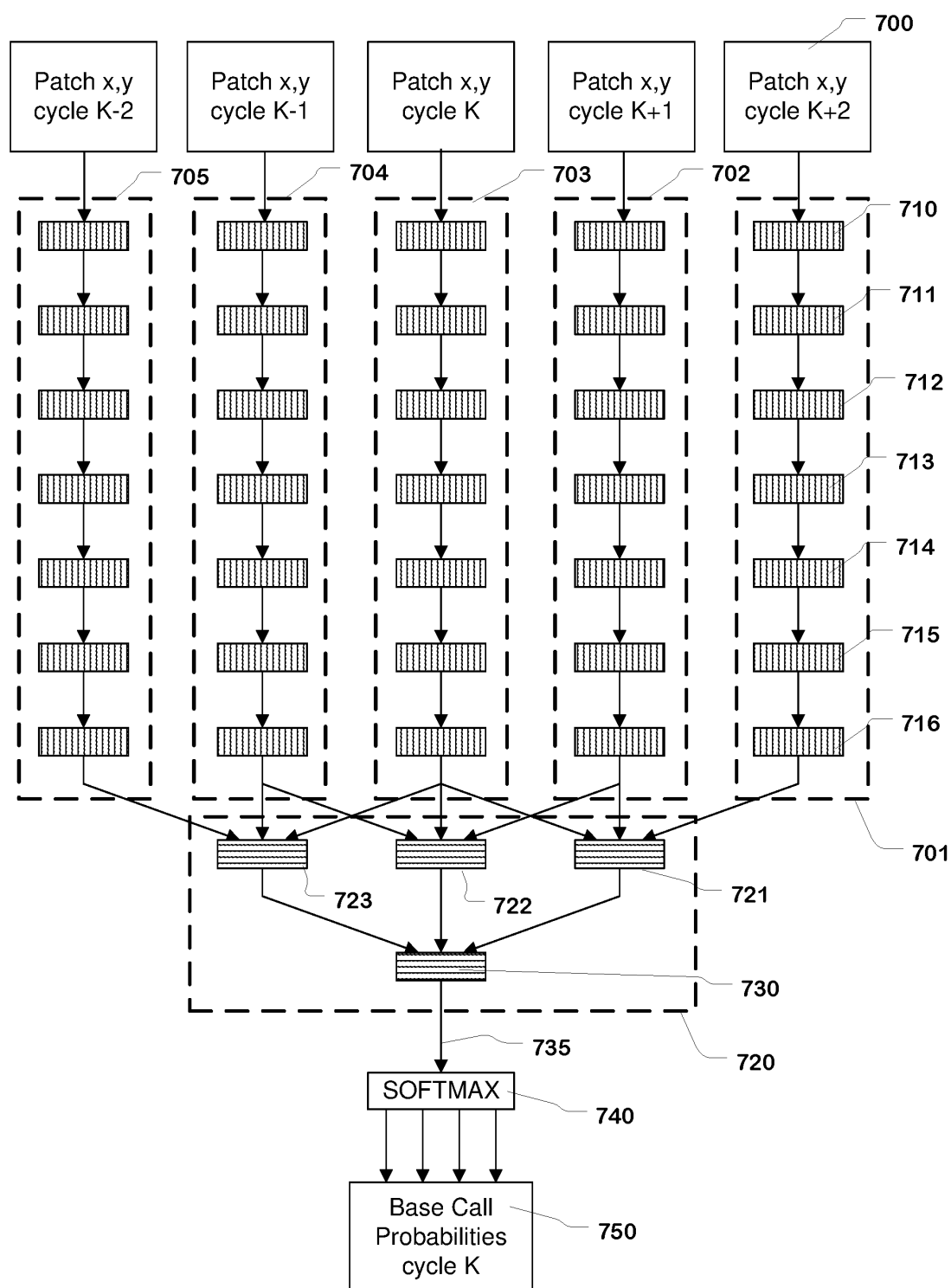


Fig. 6

**Fig. 7**

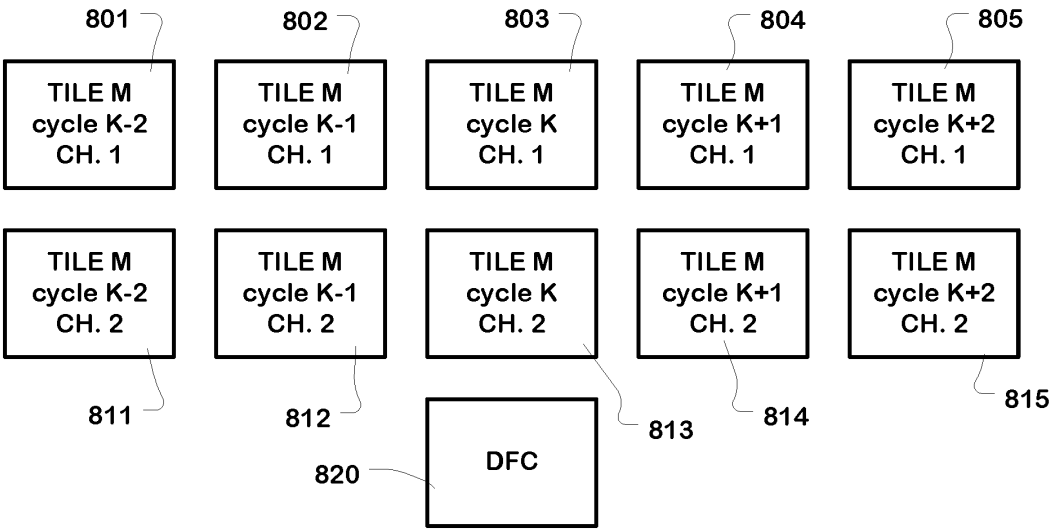


Fig. 8A

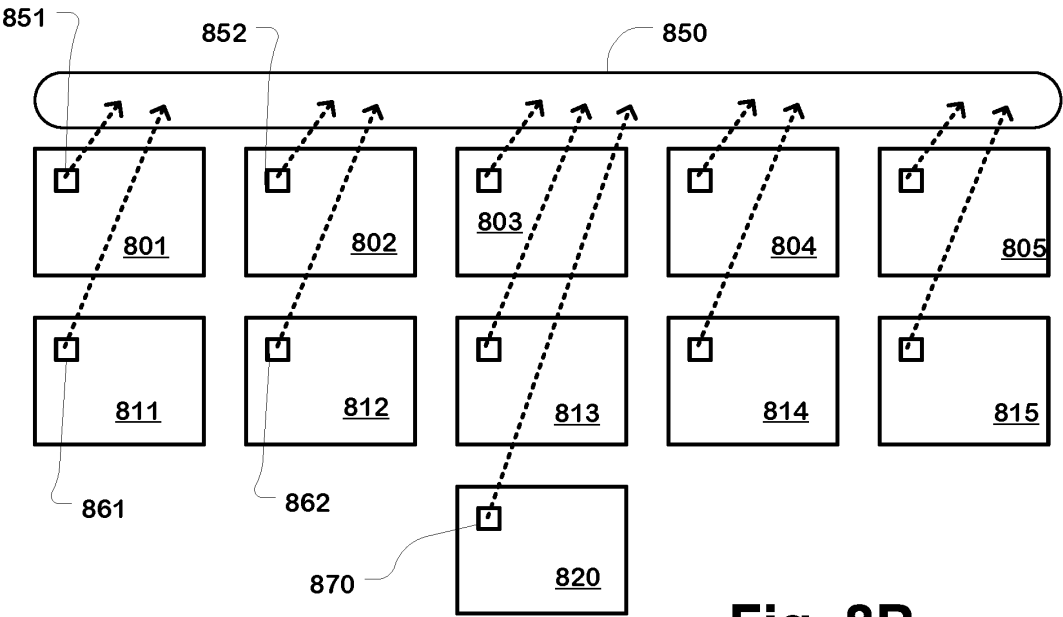


Fig. 8B

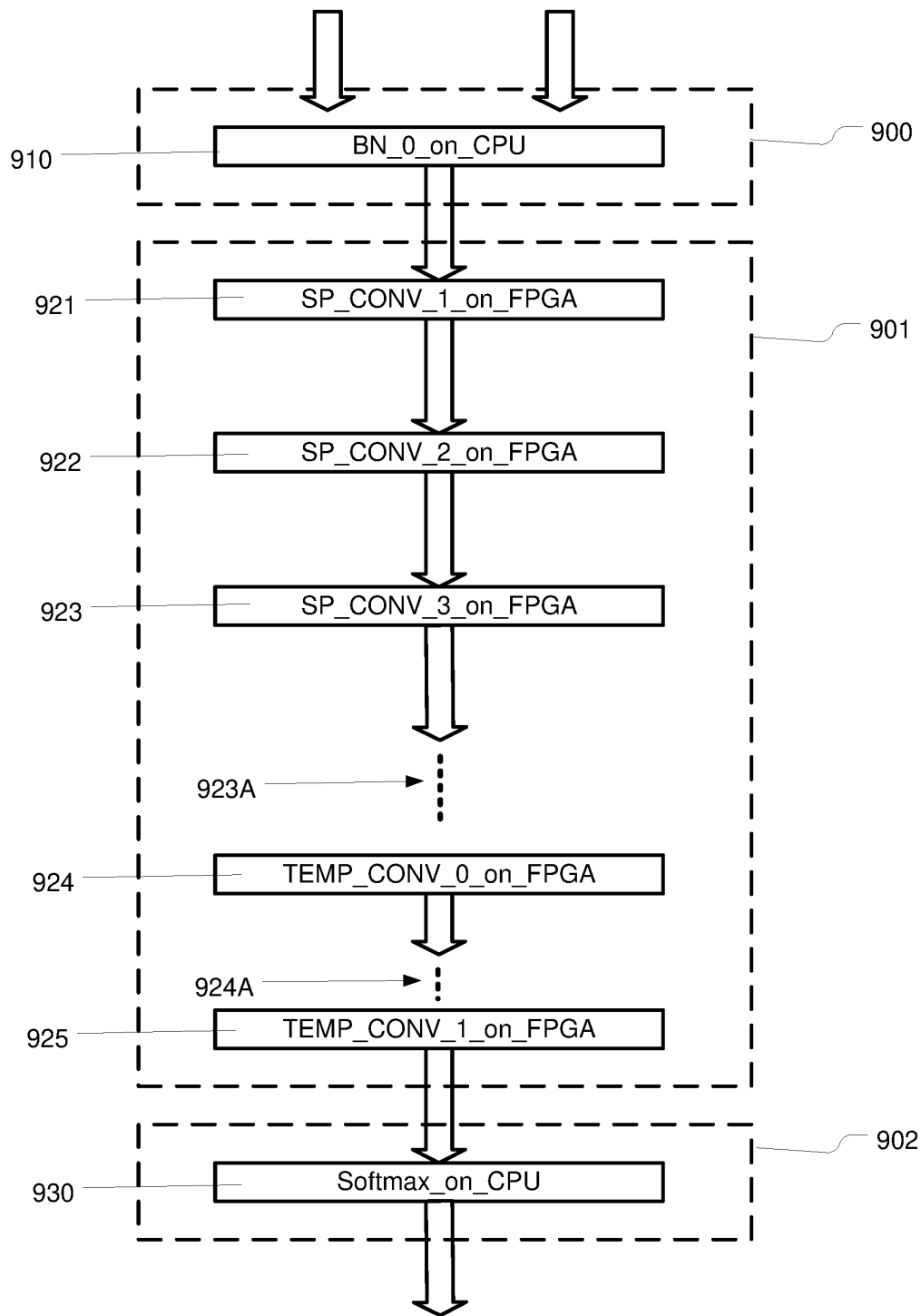


FIG. 9

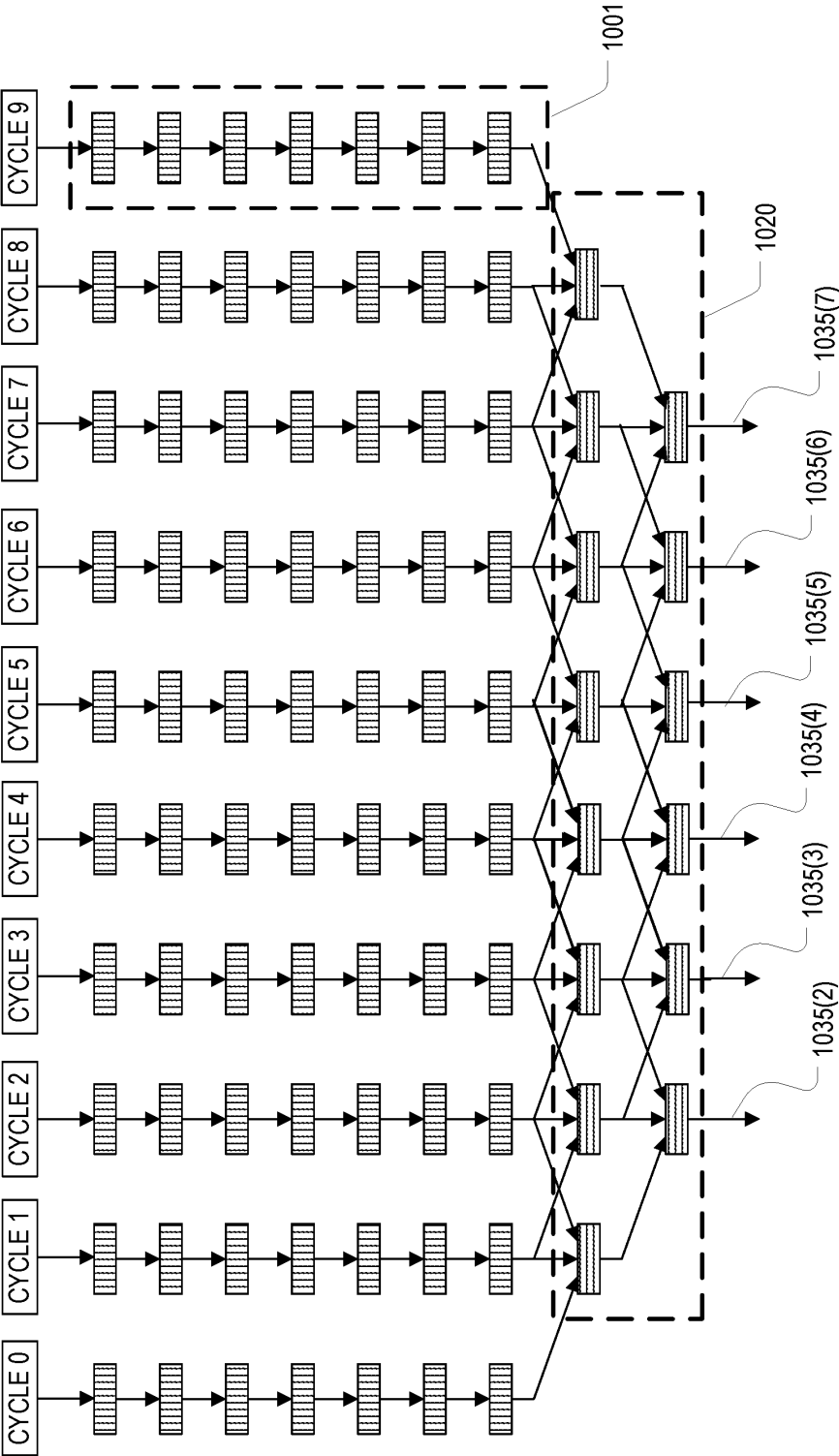


FIG. 10

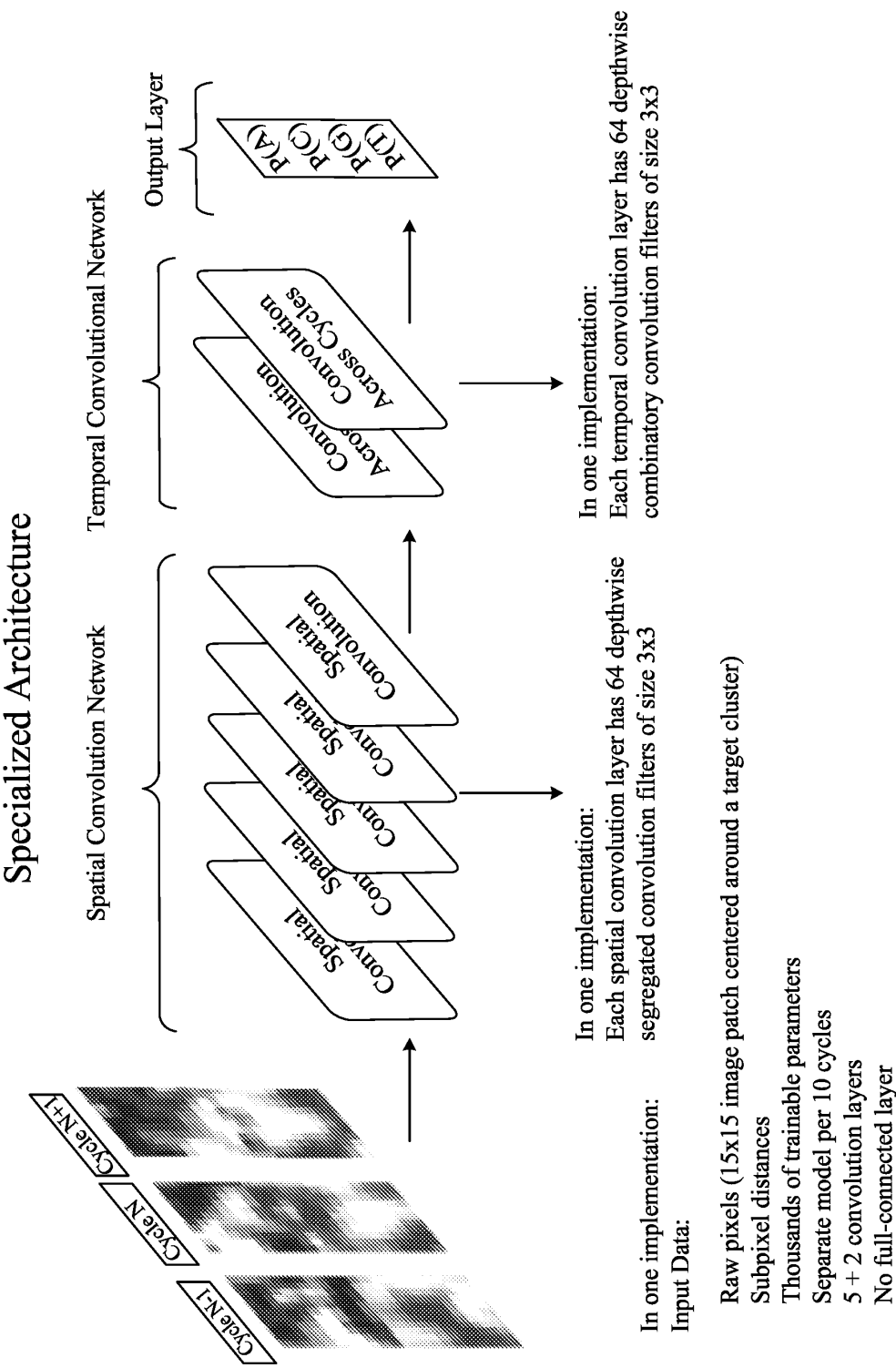
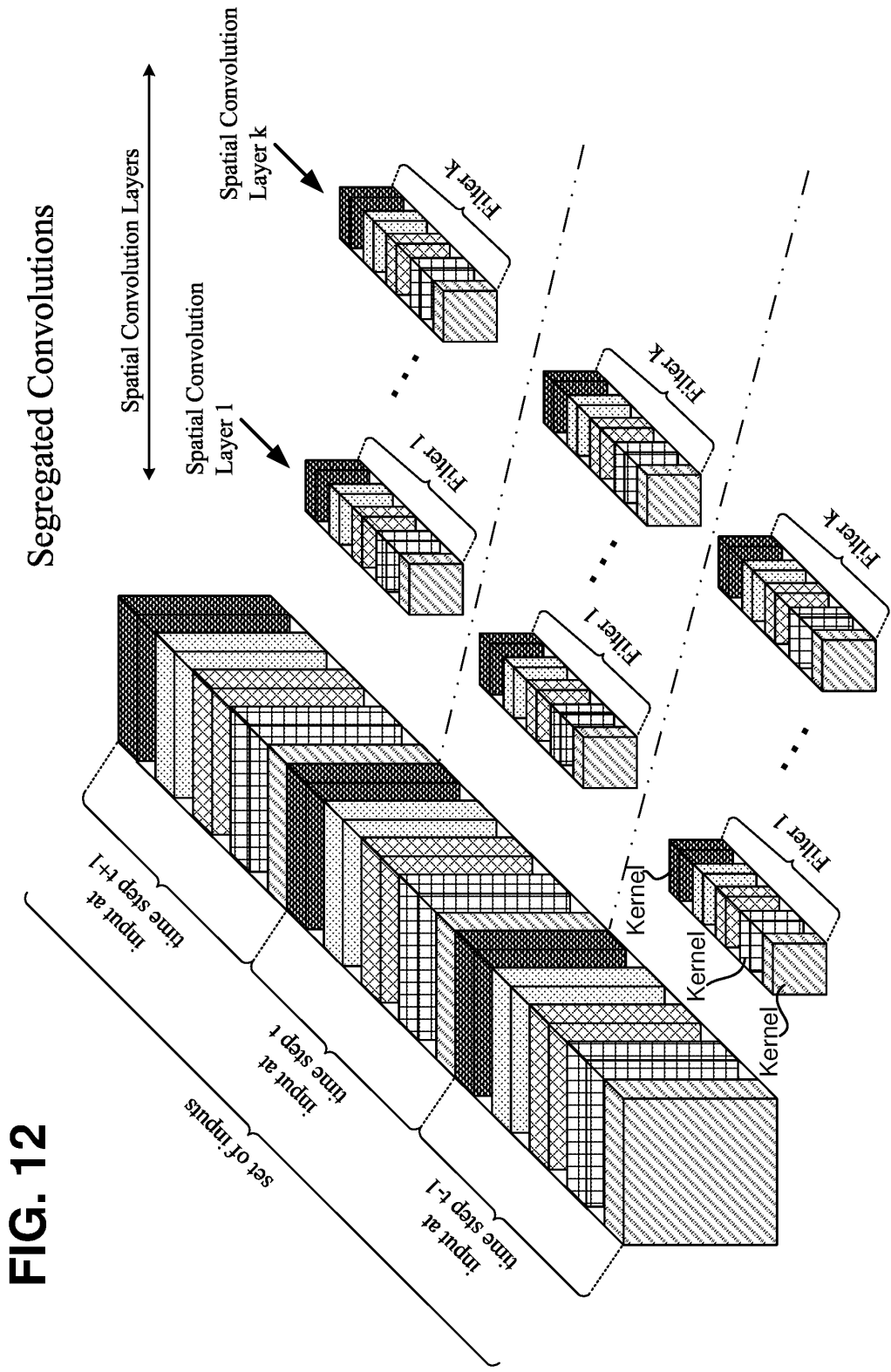
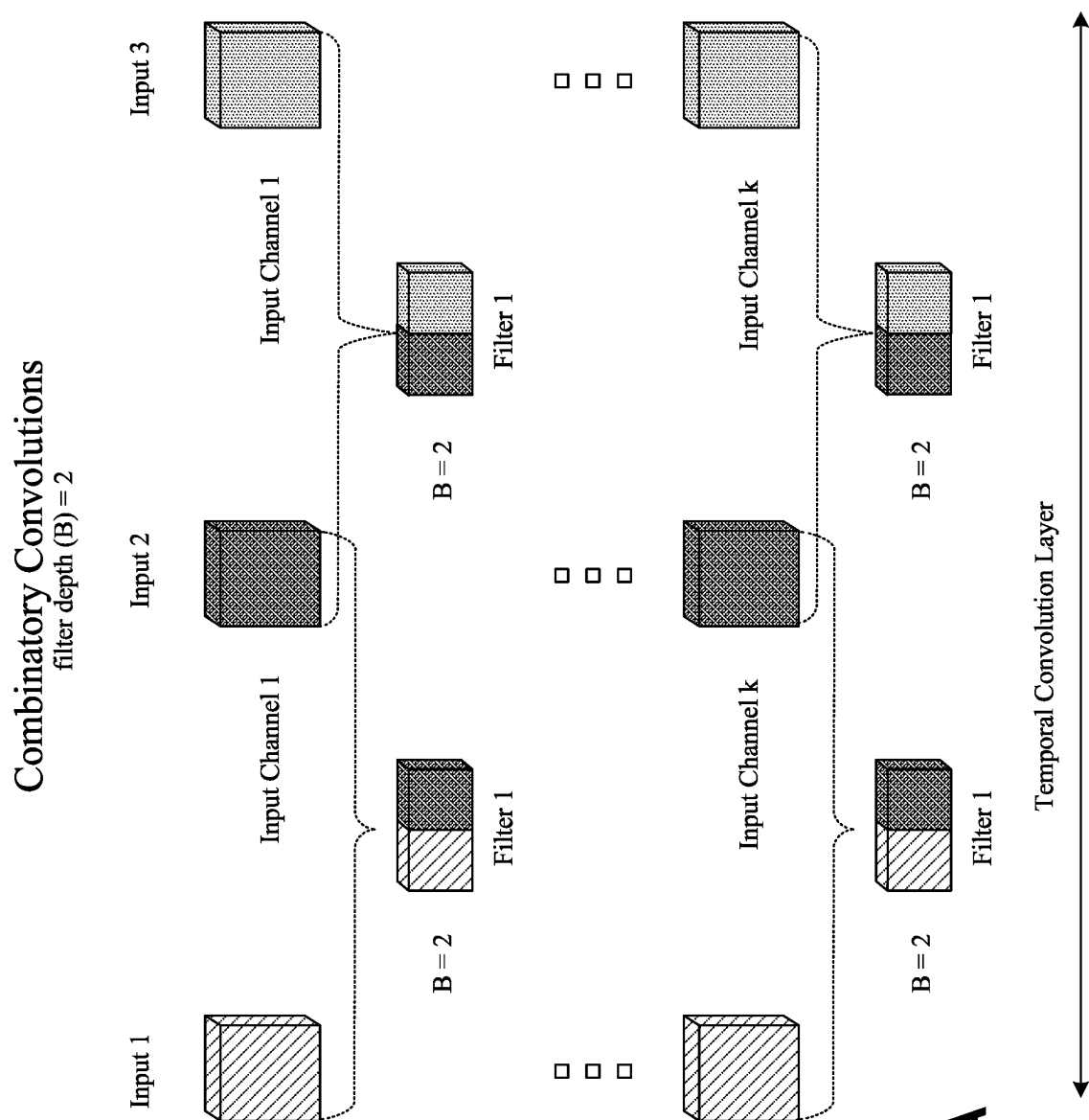
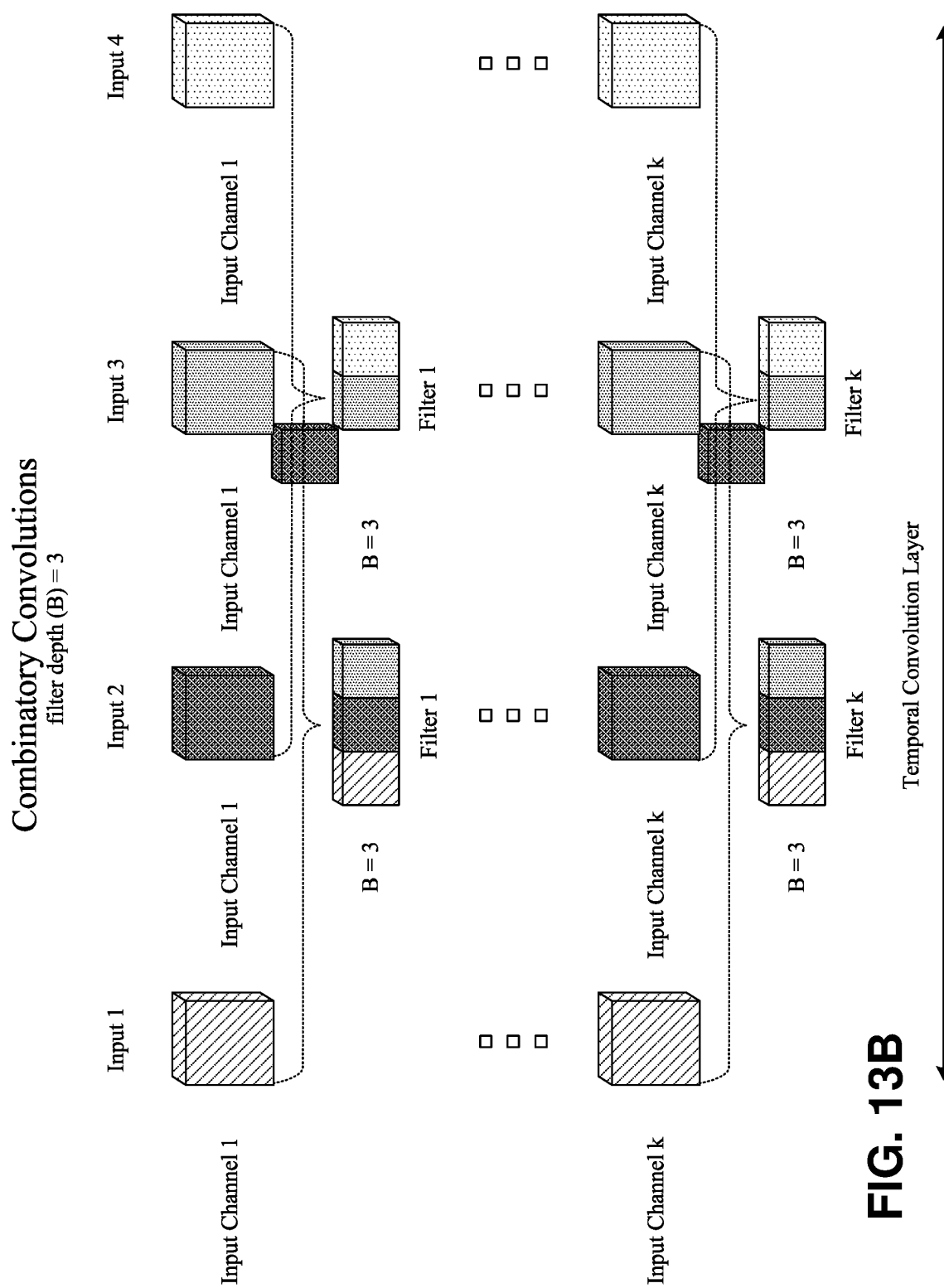
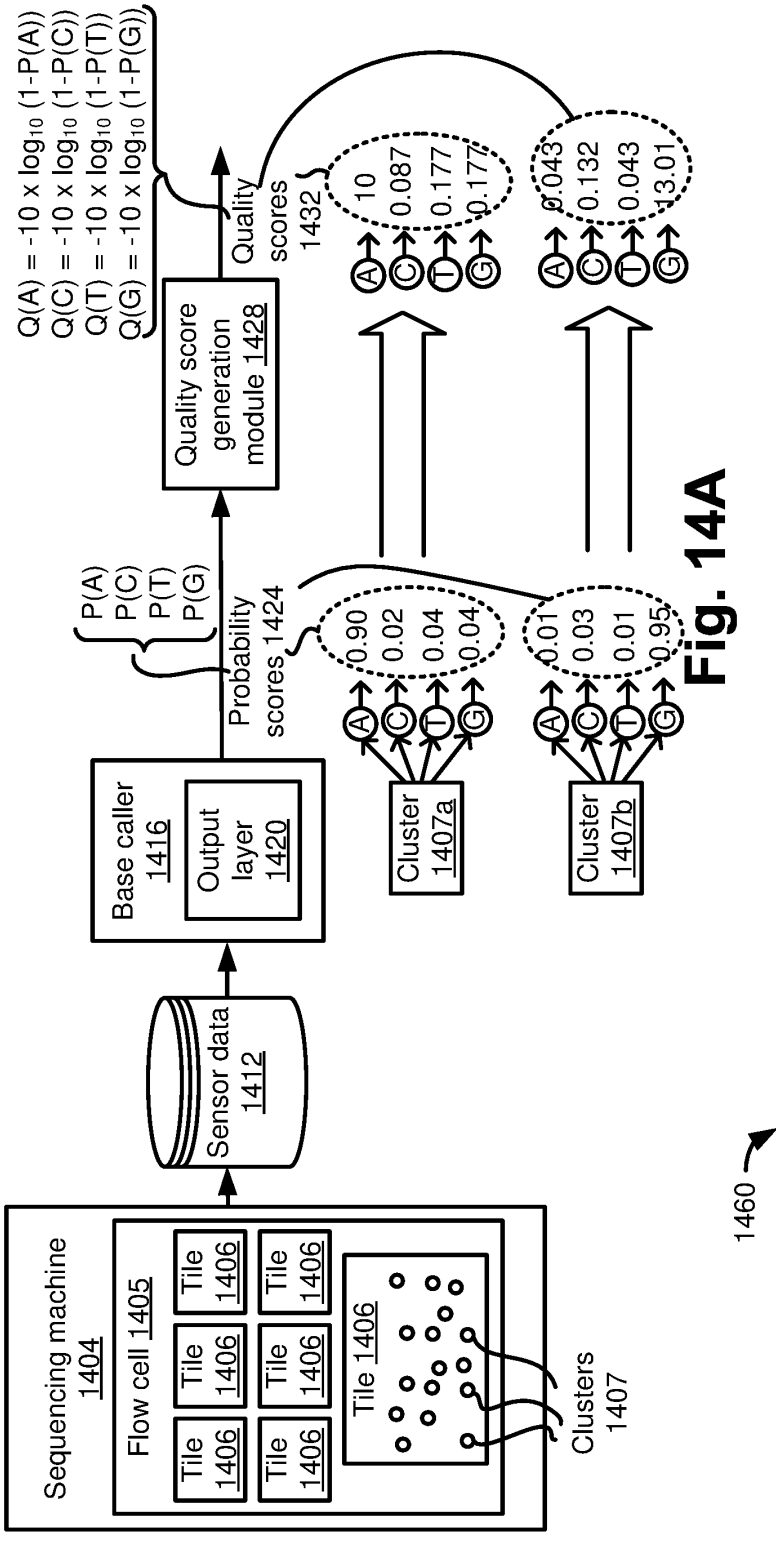


FIG. 11









1460

Example probability score	Corresponding quality score	Corresponding error probability	Corresponding error rate
0.9	10	1 in 10	10%
0.99	20	1 in 100	1%
0.999	30	1 in 1,000	0.1%
0.9999	40	1 in 10,000	0.01%
0.99999	50	1 in 100,000	0.001%
0.999999	60	1 in 1,000,000	0.0001%

Fig. 14B

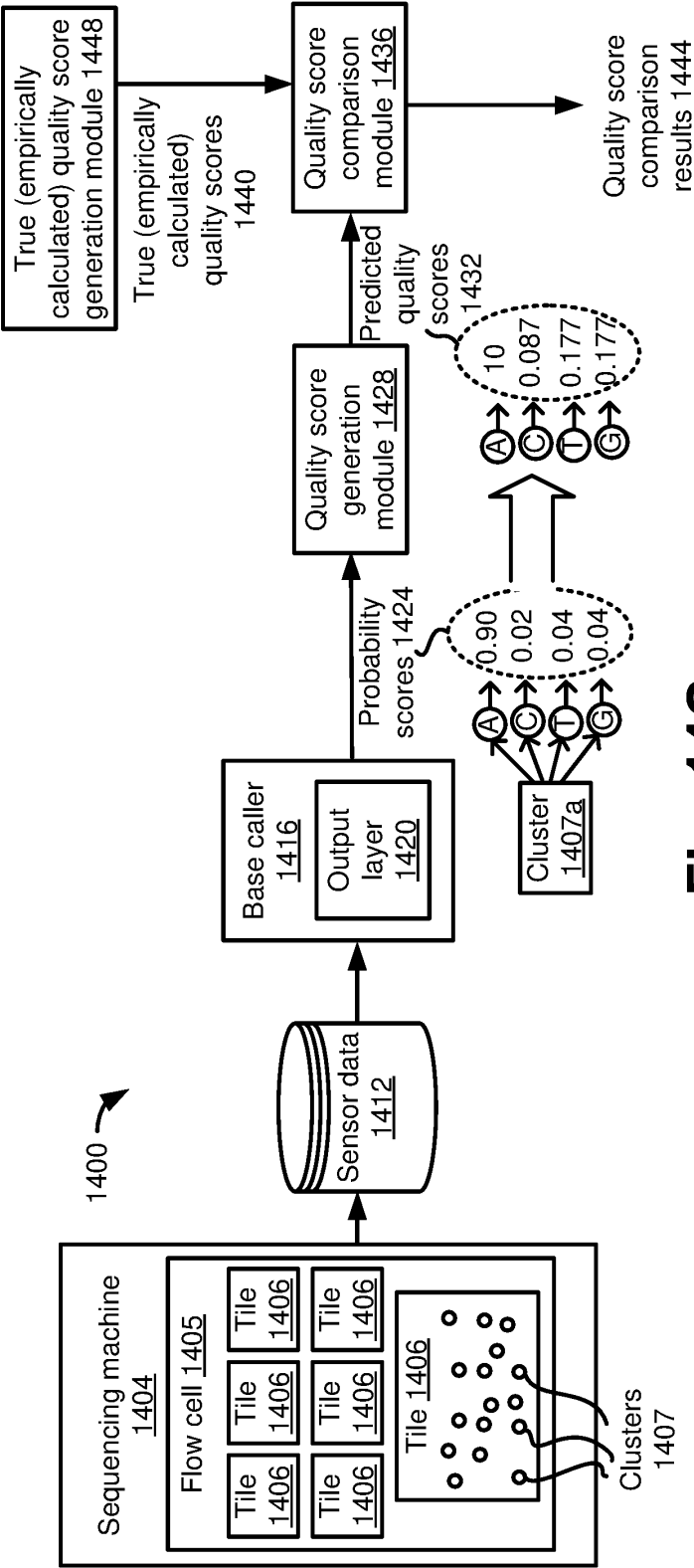


Fig. 14C

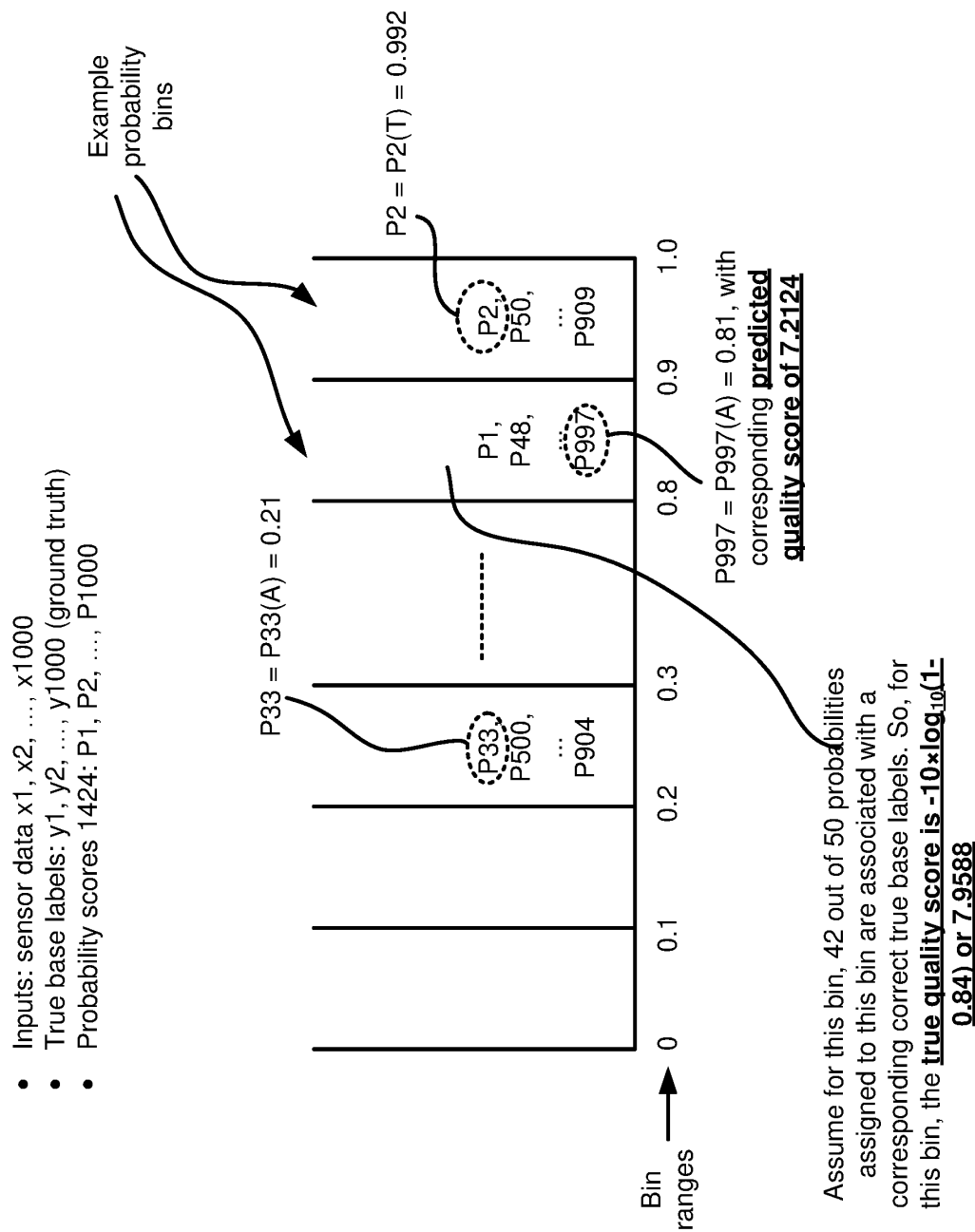


Fig. 14D

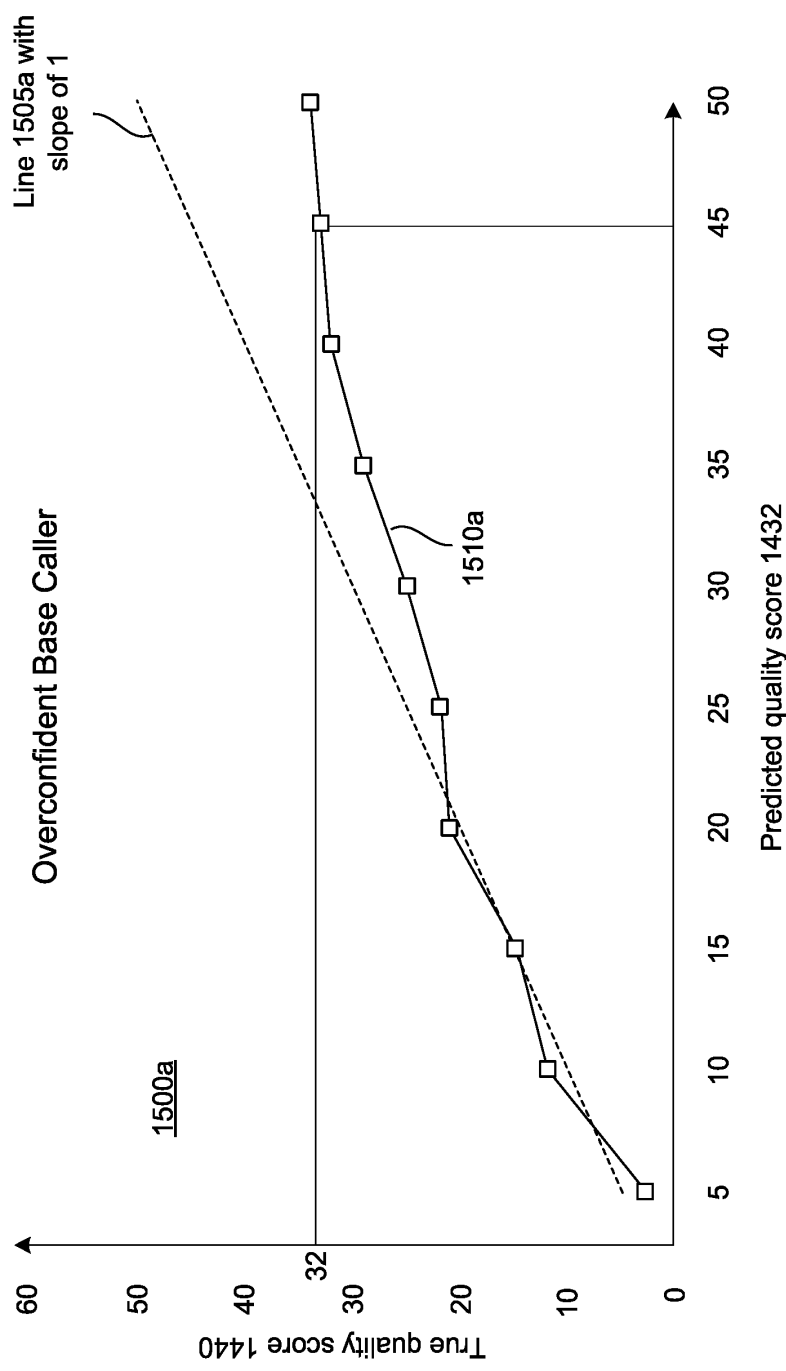


Fig. 15A

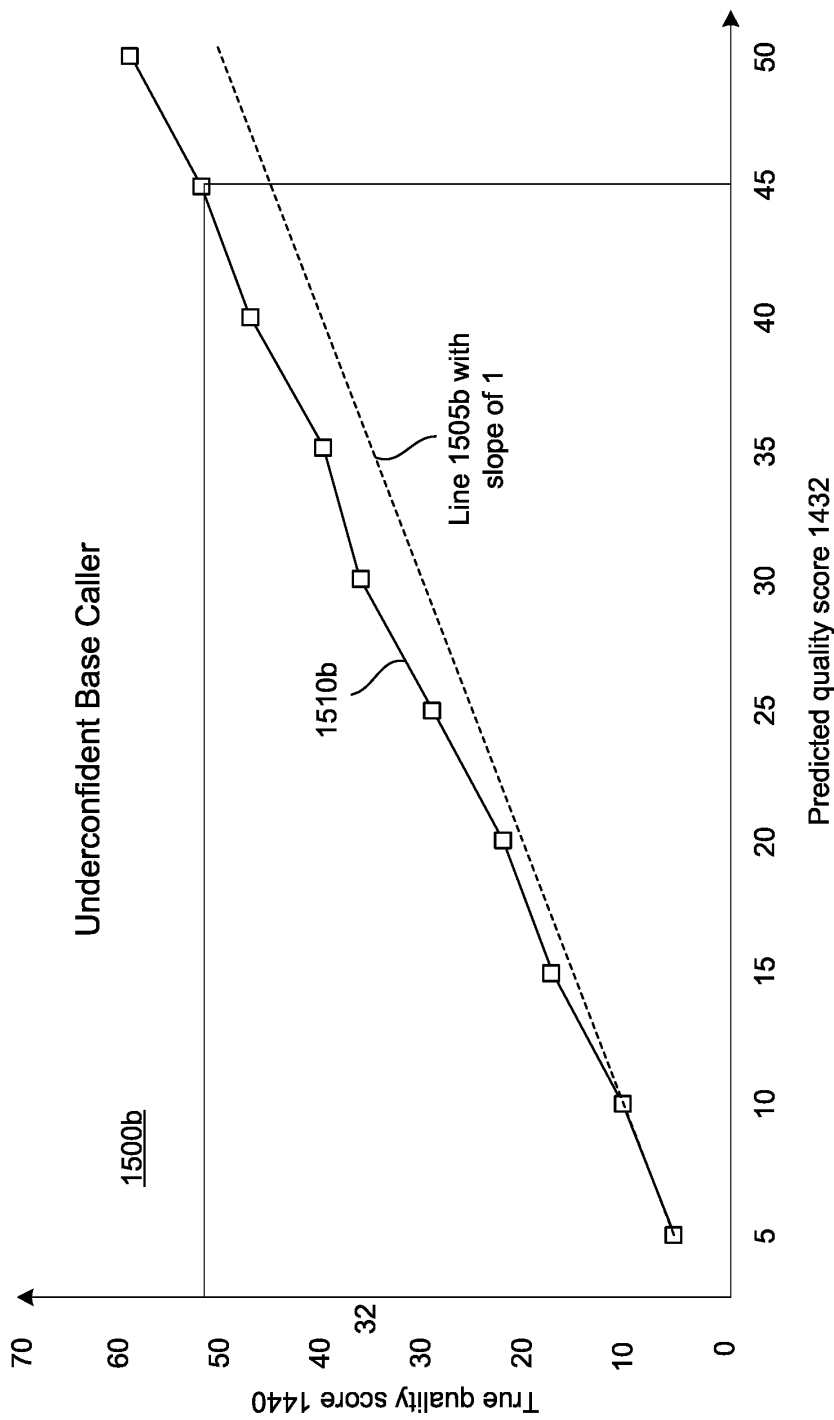


Fig. 15B

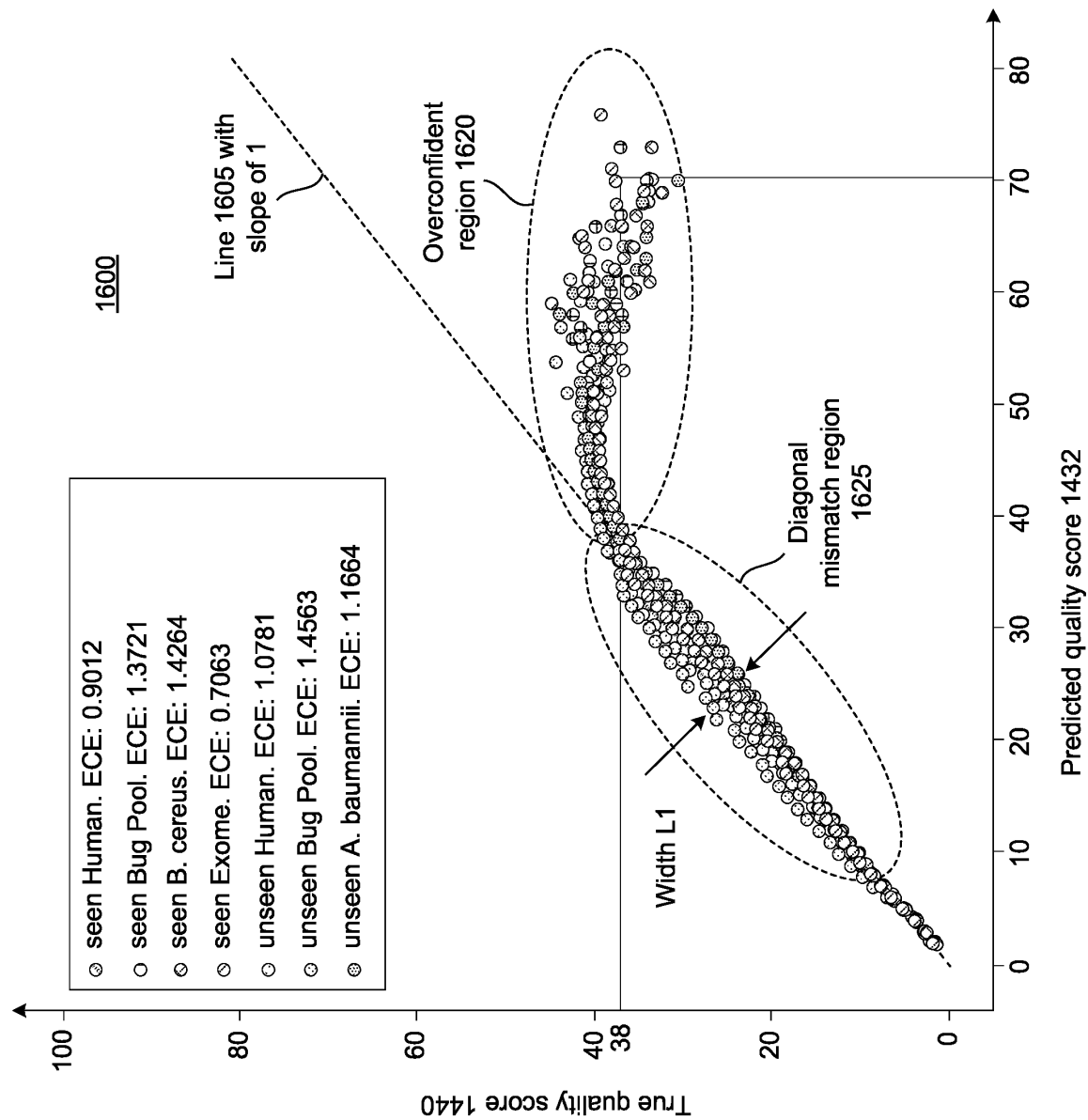


Fig. 16

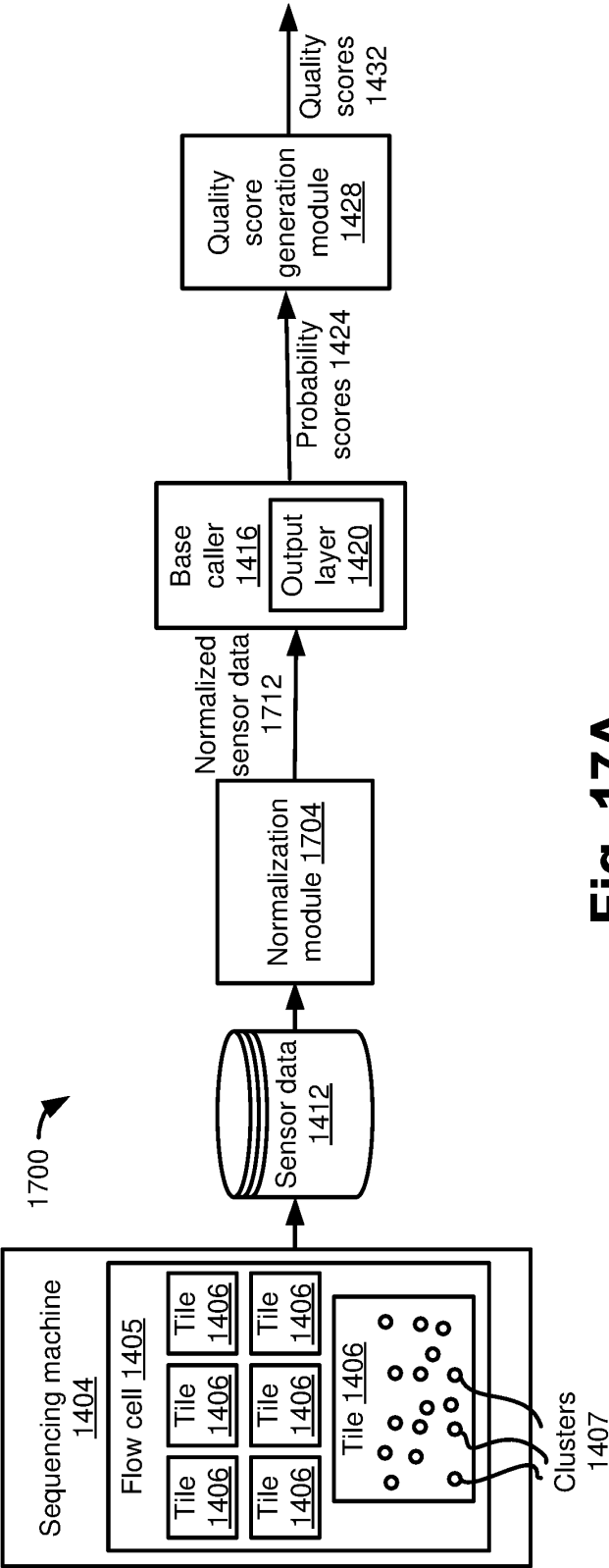


Fig. 17A

Fig. 17B

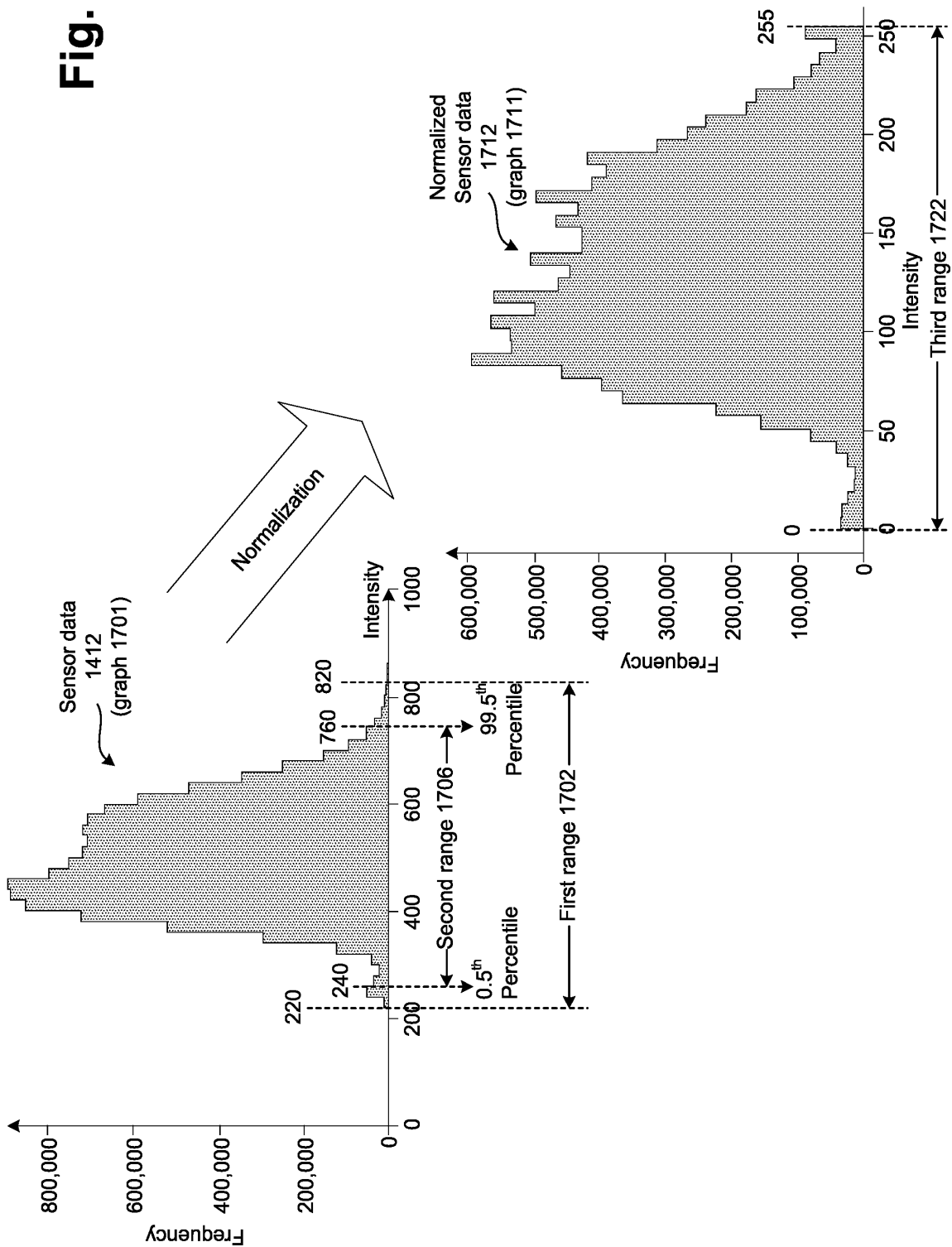
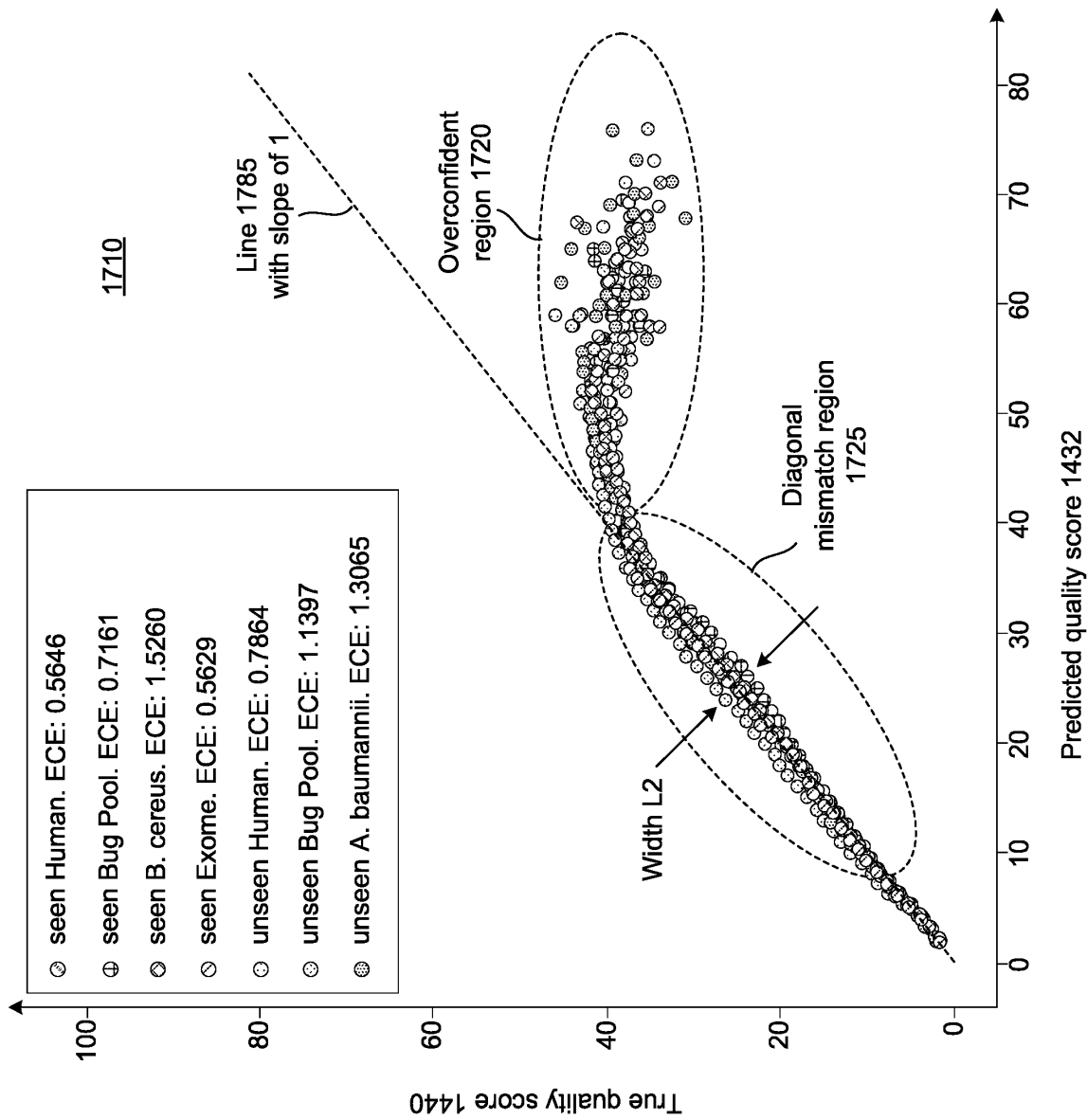


Fig. 17C



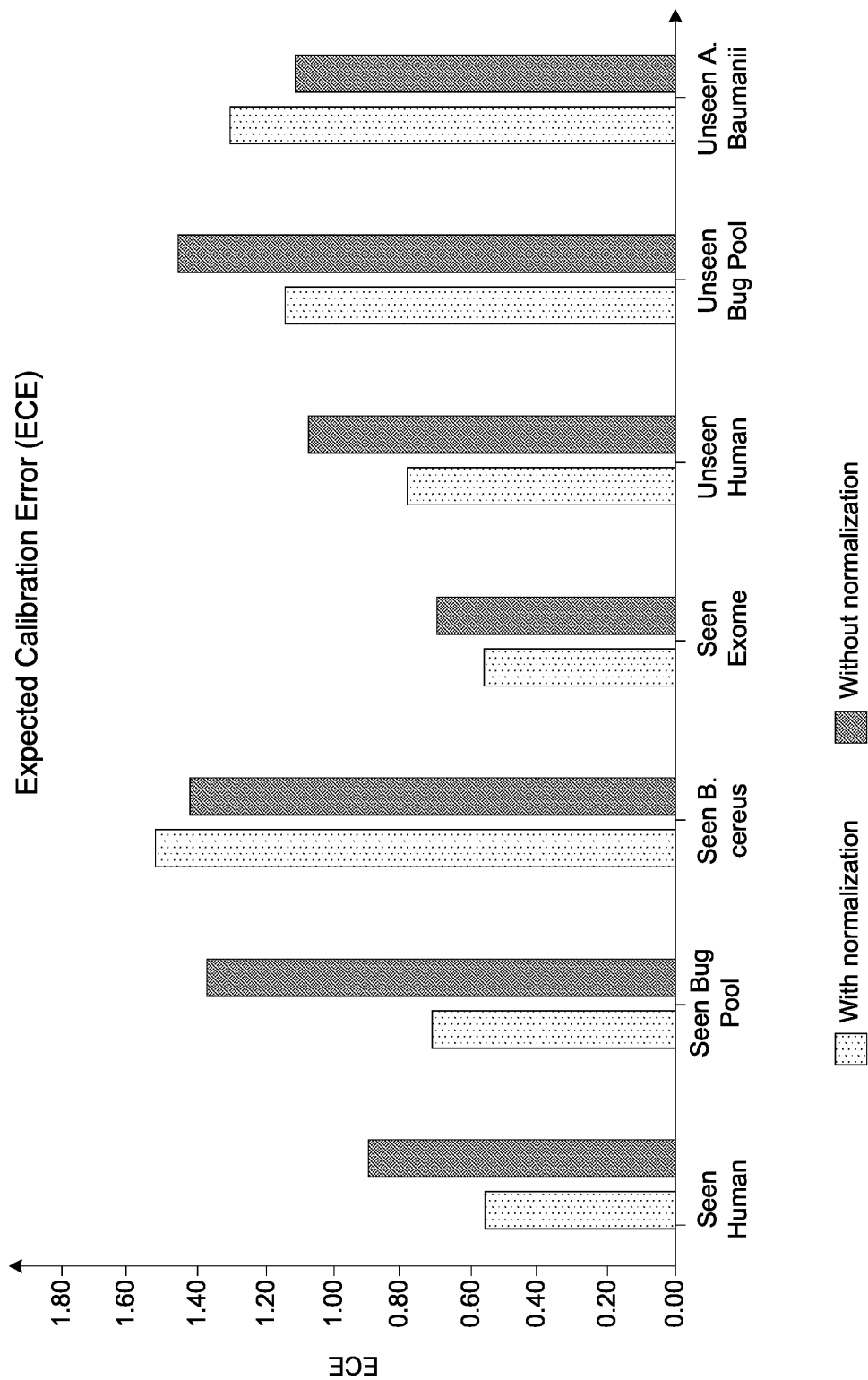
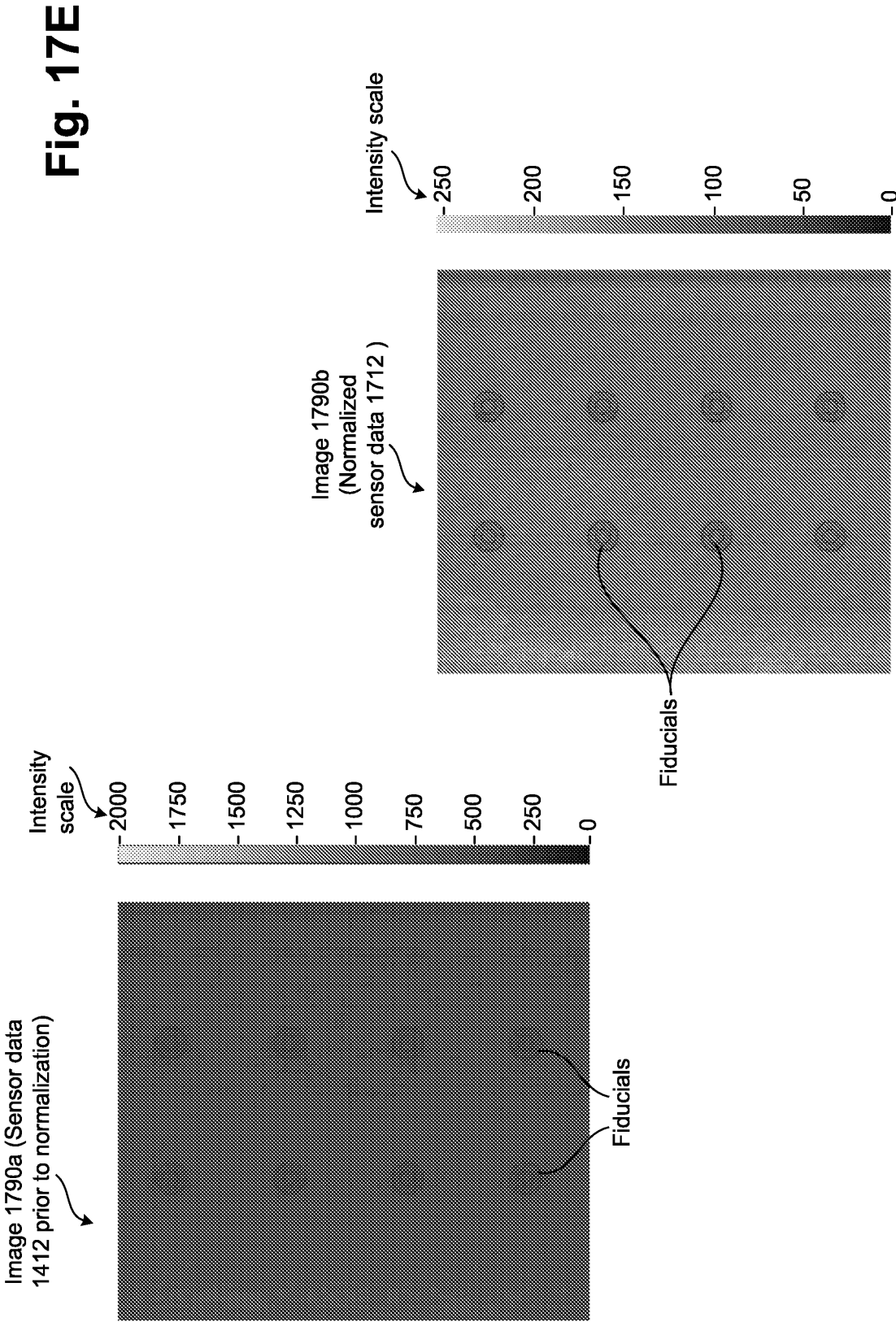


Fig. 17D



1750

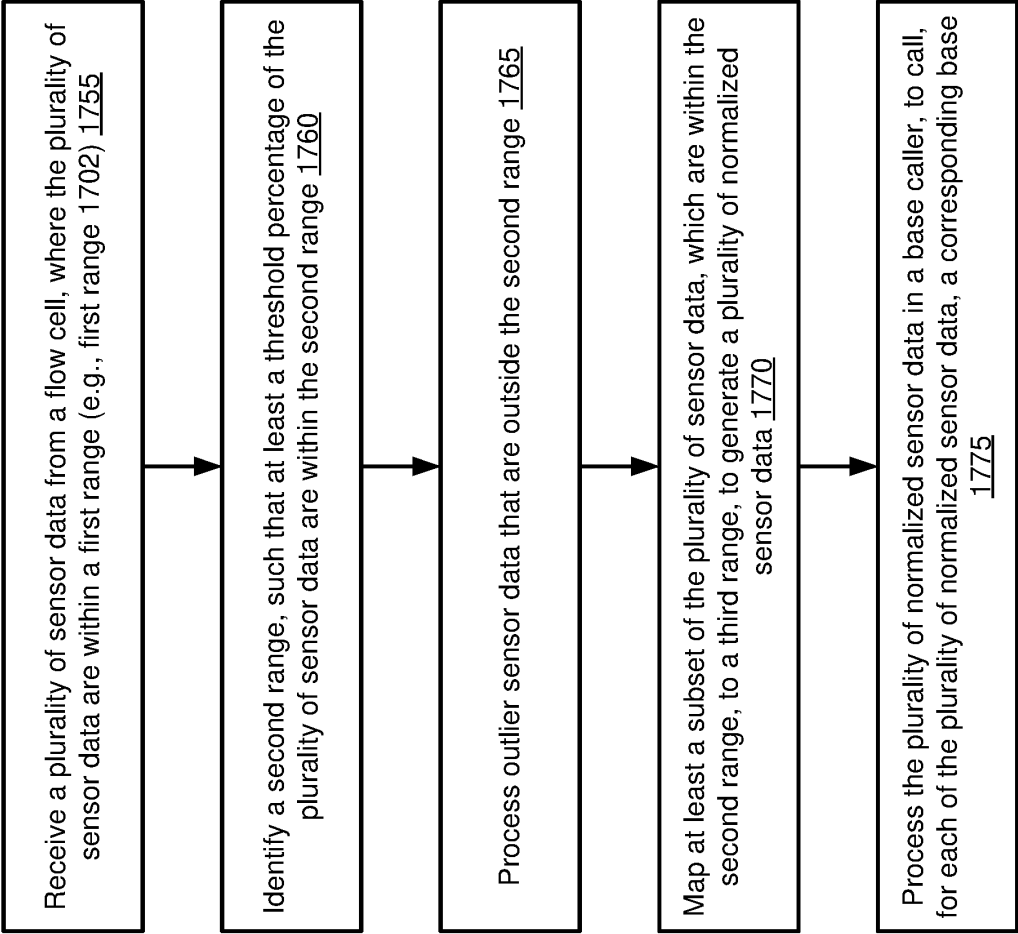


Fig. 17F

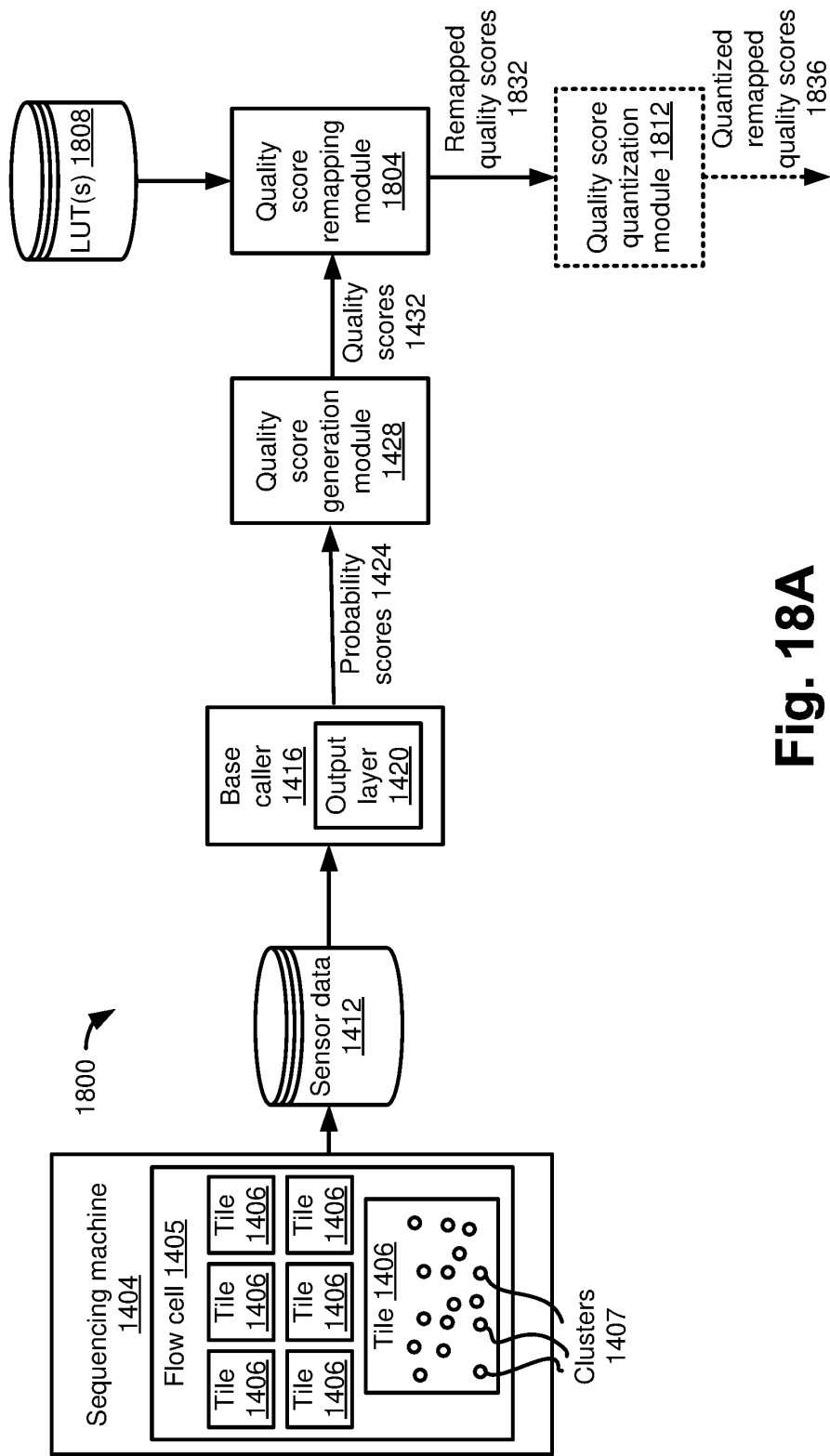
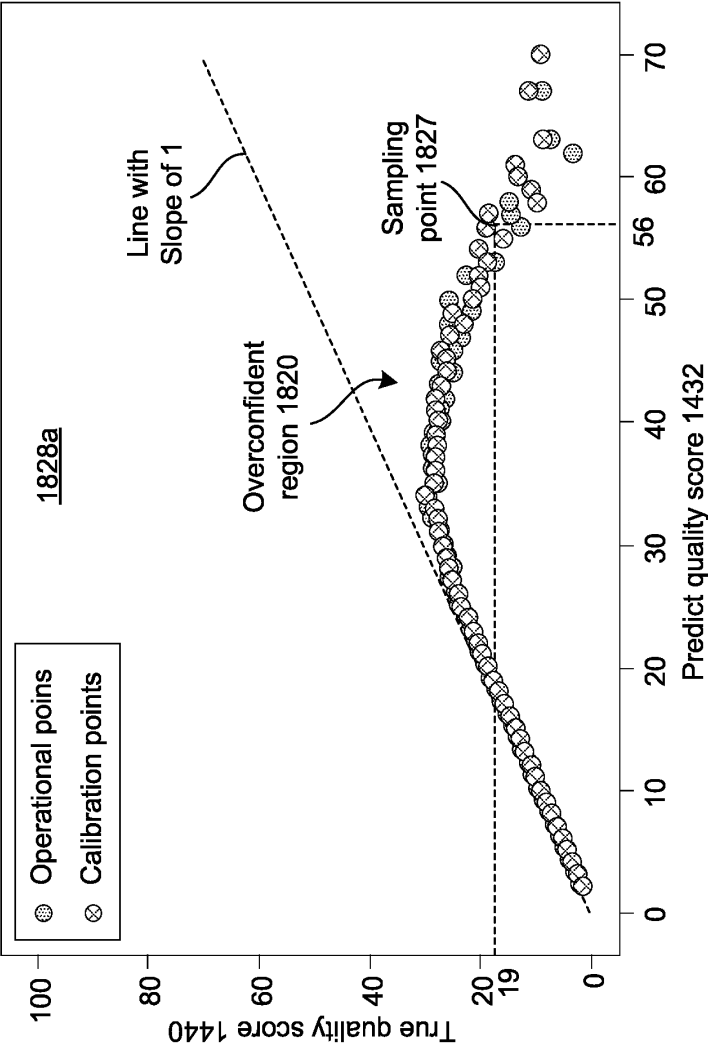


Fig. 18A



1808a

Predicted quality score 1432	True quality score 1440
56	19
60	18.5
40	30

Fig. 18B1

Fig. 18B2

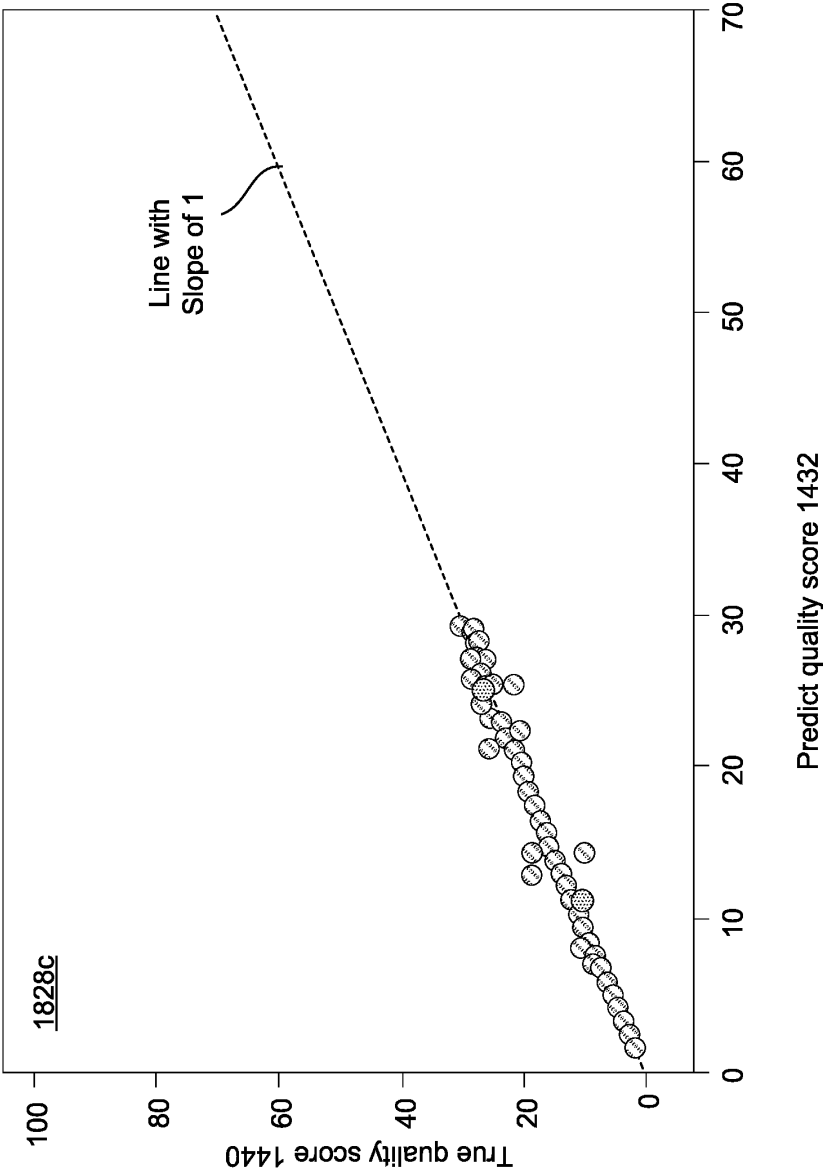


Fig. 18B3

1808b

Bins for remapped quality score 1832	Quantized remapped quality score 1836	Average of not-remapped quality scores
[0,18)	9.550	9.347
[18,30)	22.840	23.726
[30,inf)	37.382	37.668

Fig. 18B4

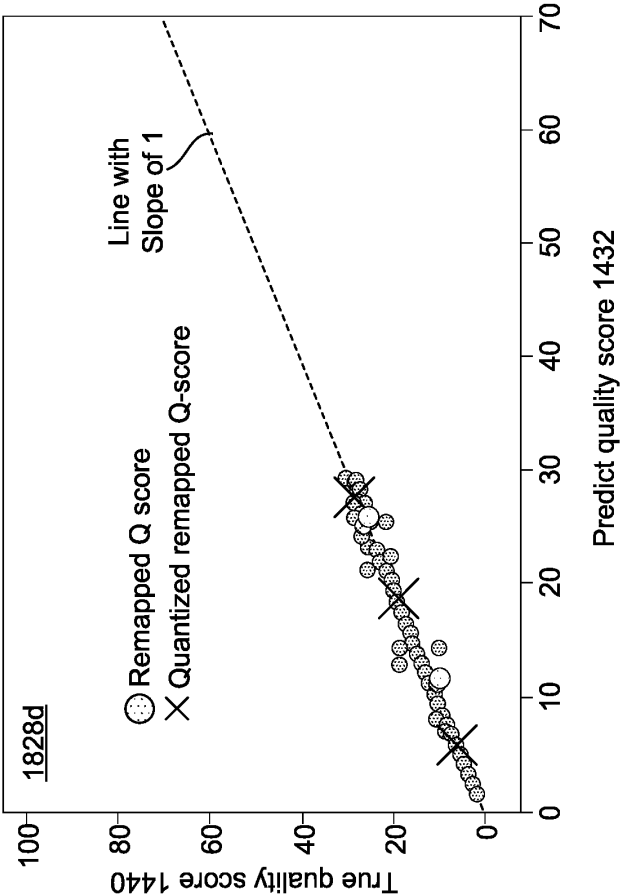


Fig. 18B5

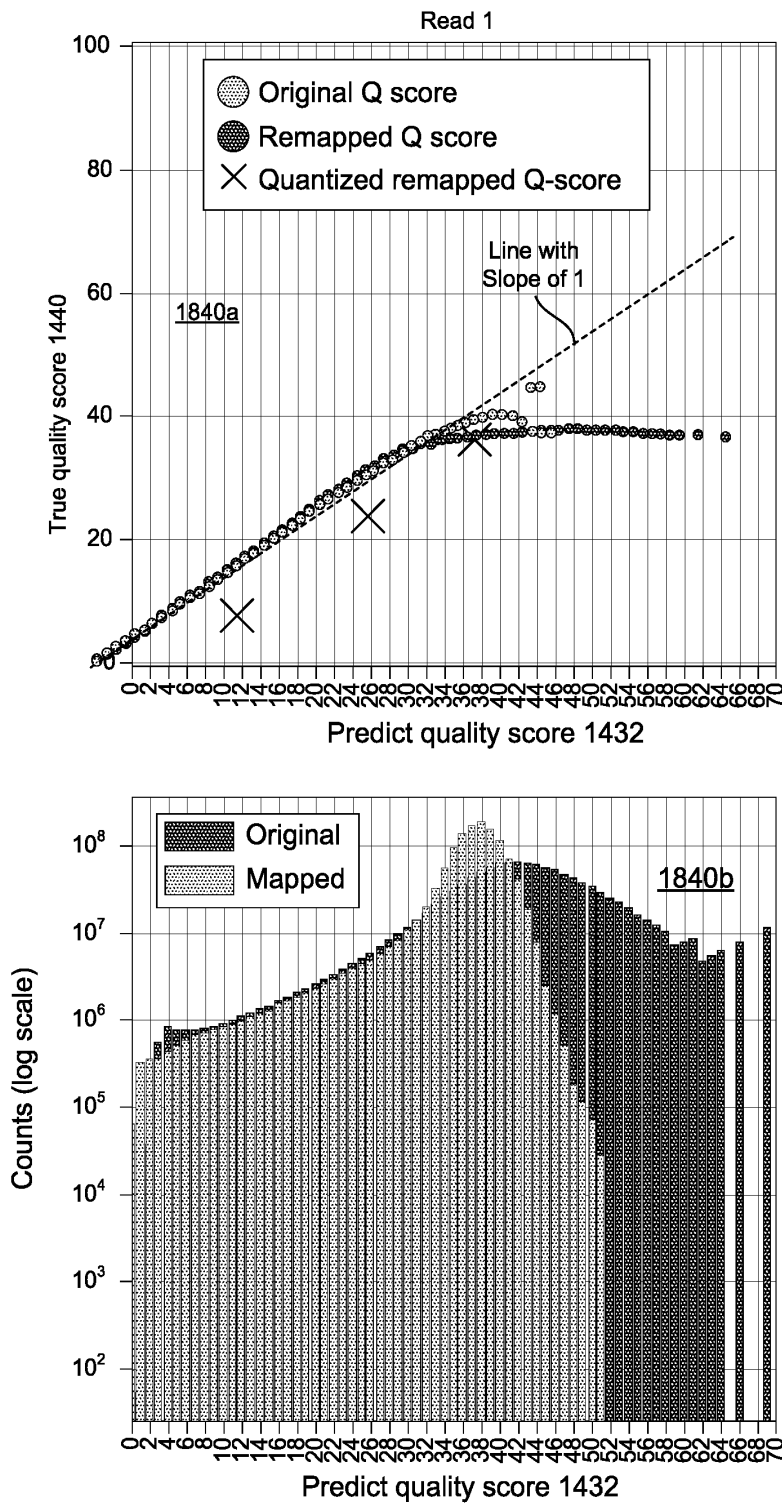


Fig. 18C1

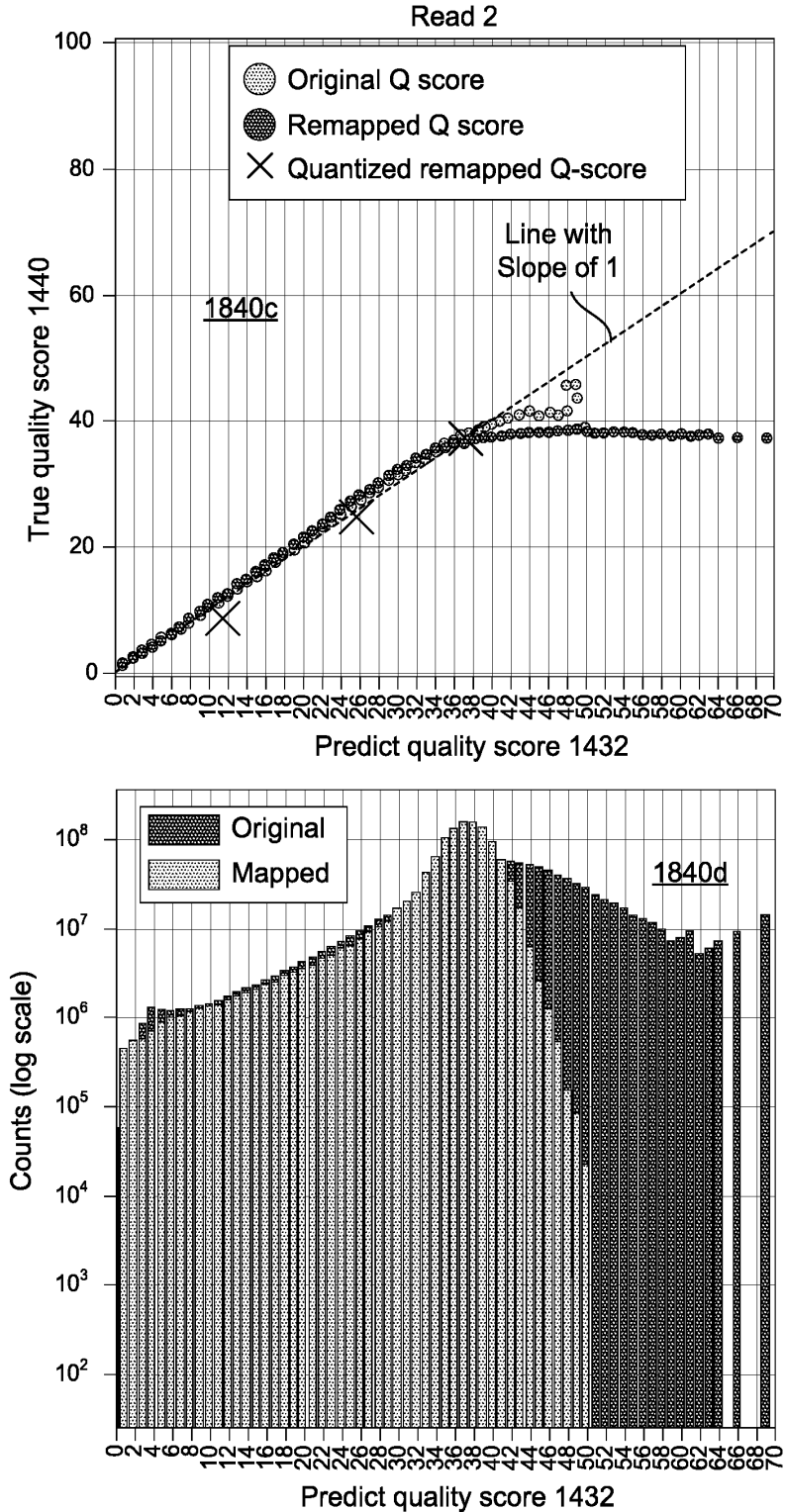


Fig. 18C2

Specific base sequences

33 / 43

1901a

read	kmer	A.baum deviation	A.baum counts	human0160 deviation	human0160 counts	human0161 deviation	human0161 counts
1	ACGGC	3.89	3059226.0	3.37	143641.0	3.54	286670.0
2	TCGAG	3.92	1928088.0	3.74	203424.0	3.76	405932.0
1	TCGAC	3.28	2372022.0	3.63	87579.0	3.27	175801.0
1	CGCCA	3.93	3912331.0	3.05	261794.0	4.76	517920.0
1	TCGAG	3.79	1959371.0	3.74	210796.0	4.30	420332.0
1	GTCAA	3.43	4295356.0	3.07	937442.0	4.64	1870719.0
1	AGCTA	3.57	3585455.0	3.03	1219158.0	4.16	2437487.0
1	TACGC	4.43	3044333.0	4.09	90791.0	5.37	180986.0
2	GGTCG	3.67	2130085.0	3.75	102718.0	4.98	205265.0
1	GGTCG	3.13	2172691.0	4.95	108146.0	5.65	213835.0
1	GGGGG	3.32	539053.0	5.97	796436.0	5.72	1582140.0
1	GGTGG	4.60	3864959.0	6.98	1574784.0	6.13	3127824.0
2	GGTGG	5.94	3776067.0	6.95	1509038.0	6.75	2999842.0
2	GGGGG	6.69	528663.0	8.37	771719.0	9.04	1551607.0

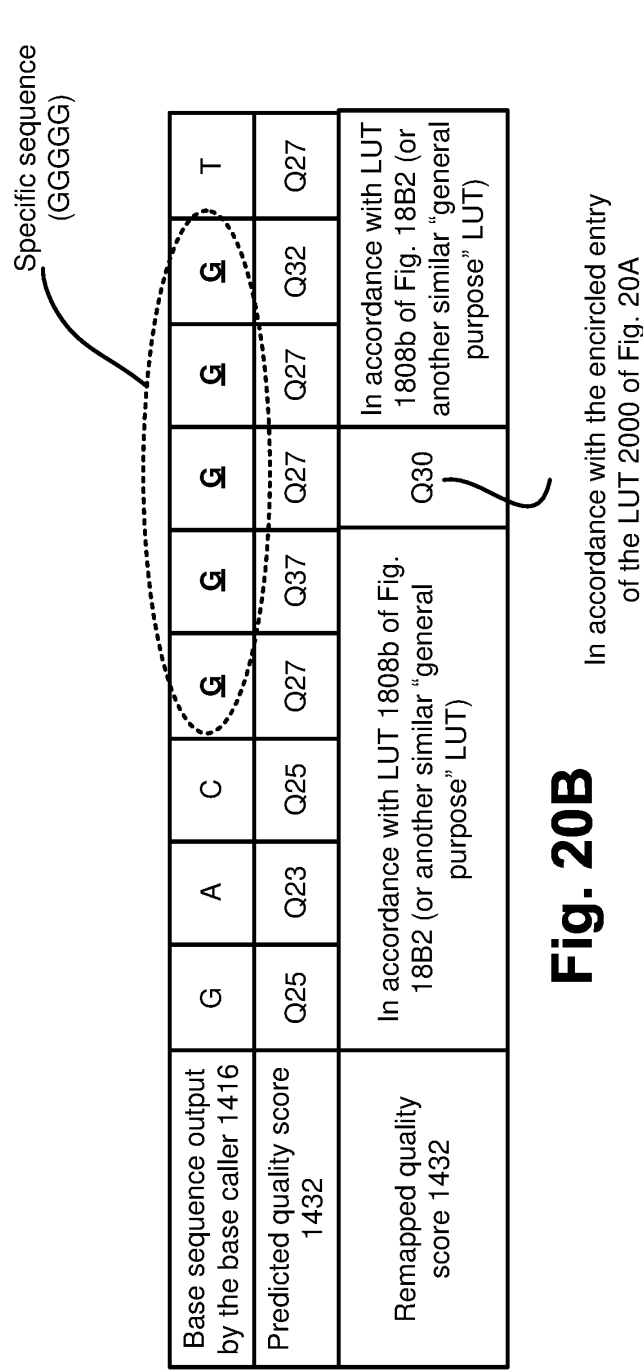
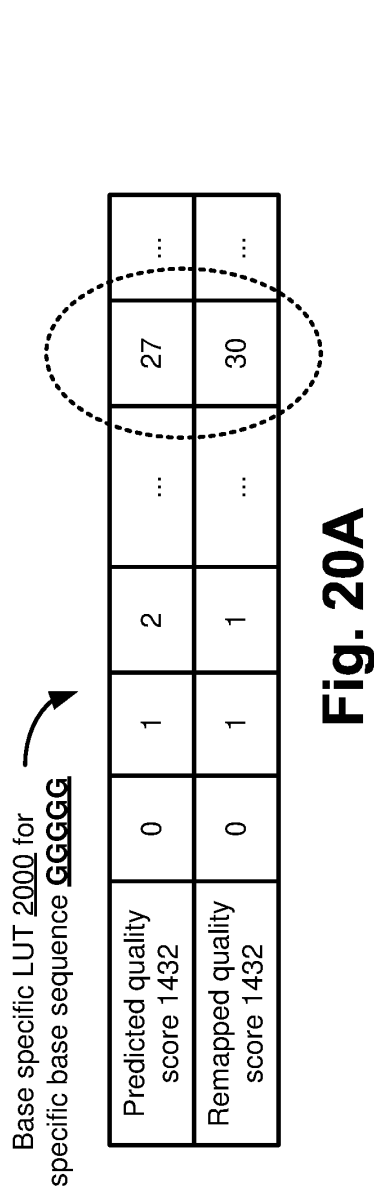
Specific base sequences

1901b

read	kmer	B.Cereus deviation	B.Cereus counts	Rhodo deviation	Rhodo counts	avg deviation
1	ACGGC	3.01	995049.0	3.07	4778765.0	3.37
2	TCGAG	3.25	749681.0	3.18	7824628.0	3.57
1	TCGAC	4.14	732174.0	3.77	5716158.0	3.62
1	CGCCA	3.50	1544514.0	3.37	5988869.0	3.72
1	TCGAG	4.09	761012.0	3.57	8119856.0	3.90
1	GTCAA	4.26	1591019.0	4.15	774331.0	3.91
1	AGCTA	4.83	2457010.0	4.38	289860.0	3.99
1	TACGC	3.09	1733872.0	3.34	439357.0	4.06
2	GGTCG	6.27	560330.0	3.52	6075083.0	4.44
1	GGTCG	5.26	570454.0	3.55	6352600.0	4.51
1	GGGGG	3.80	649880.0	8.04	2091261.0	5.37
1	GGTGG	3.32	1691289.0	6.62	4513456.0	5.53
2	GGTGG	3.59	1664091.0	6.75	4551446.0	6.00
2	GGGGG	4.22	636420.0	9.25	2092470.0	7.51

Fig. 19

SUBSTITUTE SHEET (RULE 26)



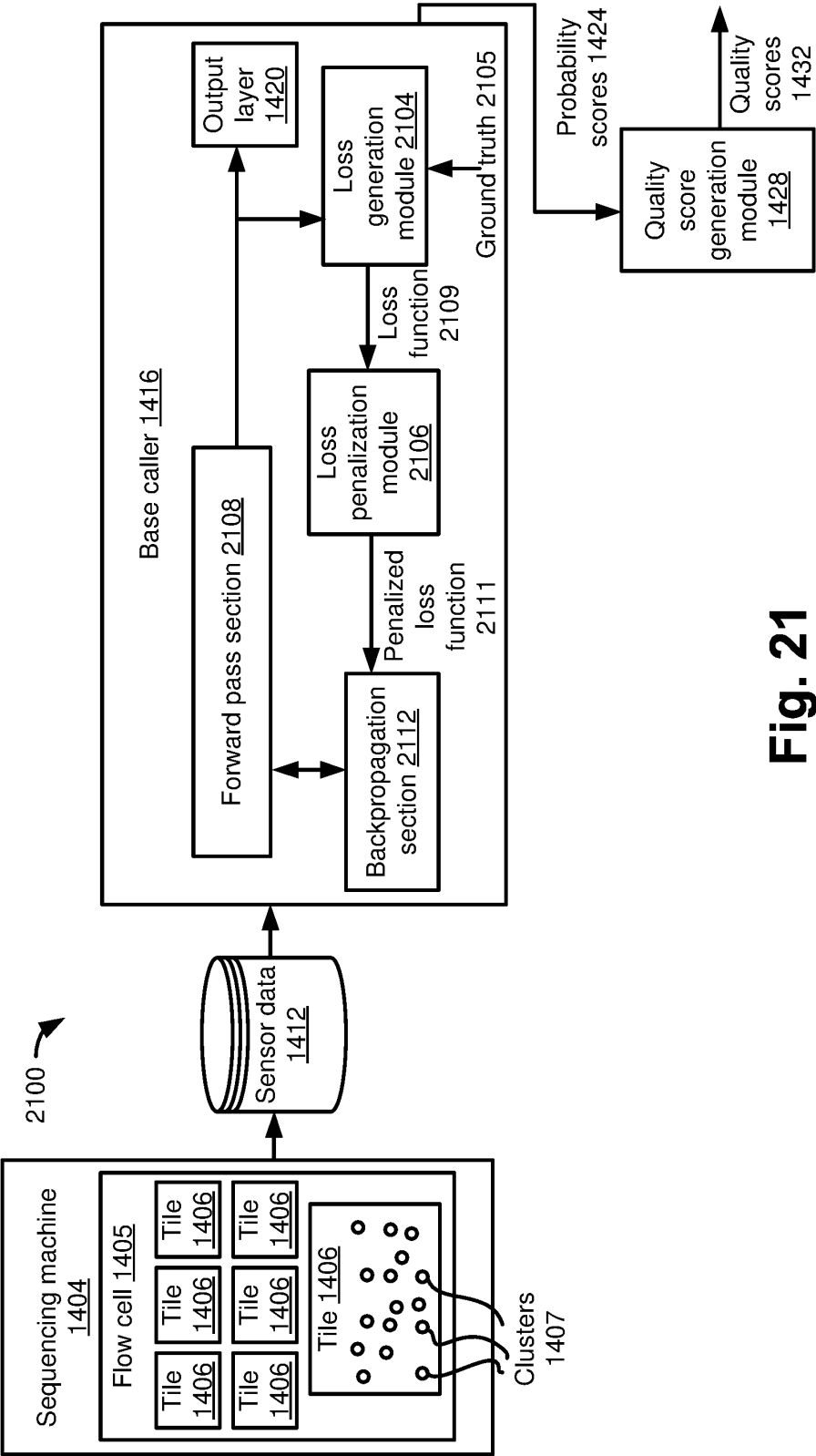


Fig. 21

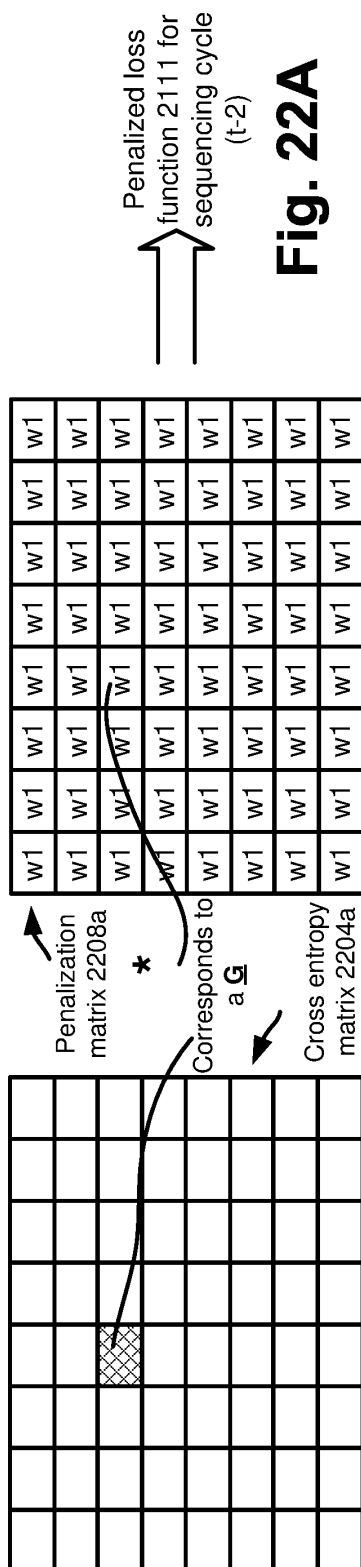


Fig. 22A

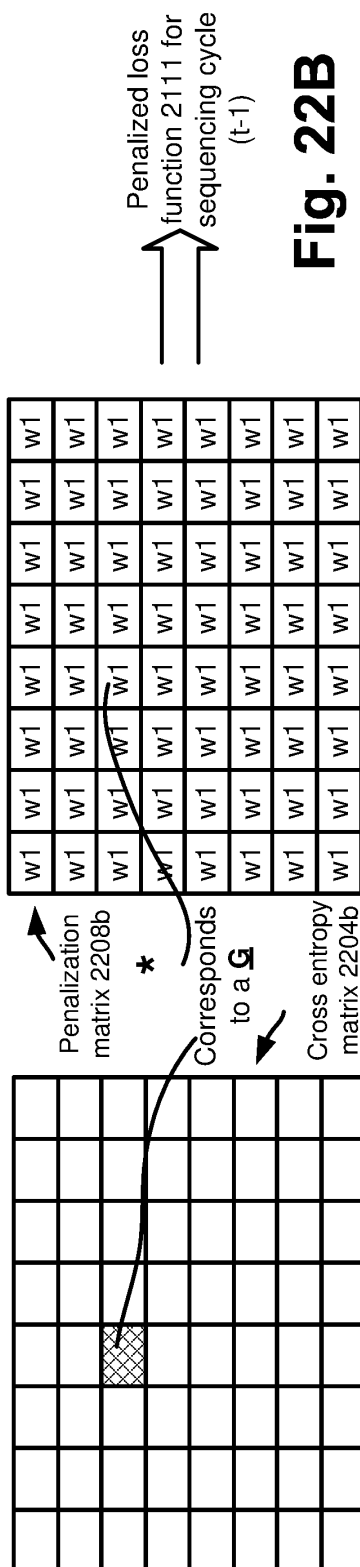


Fig. 22B

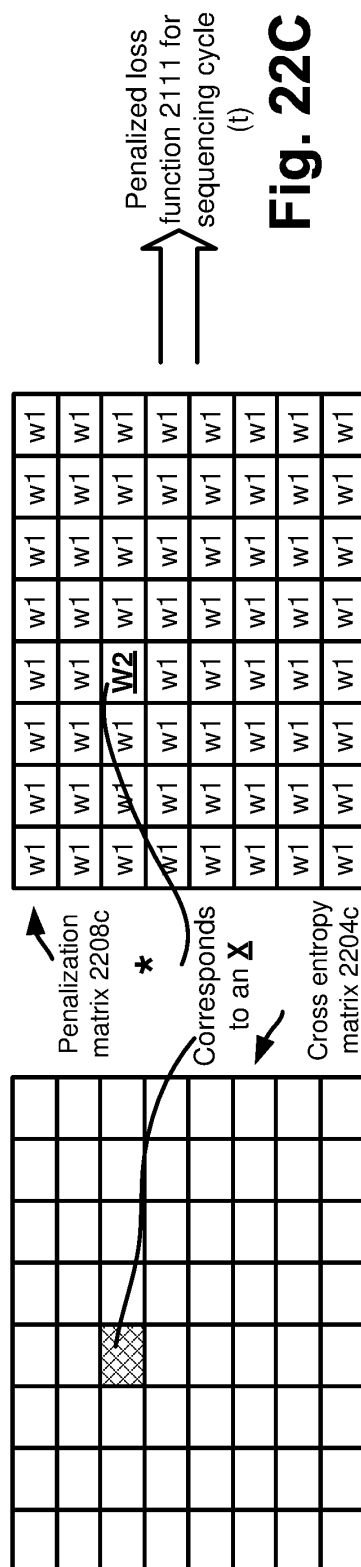
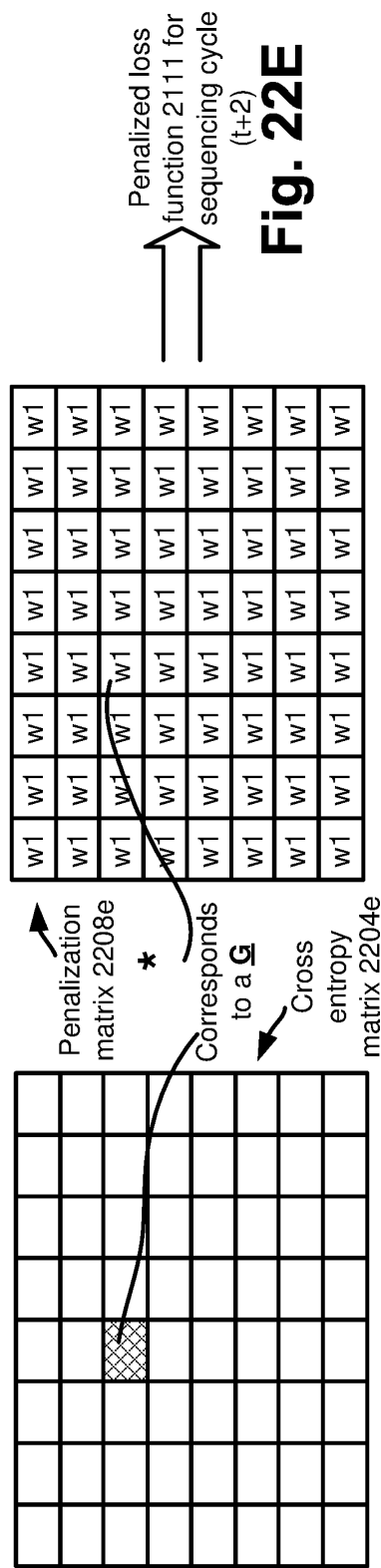
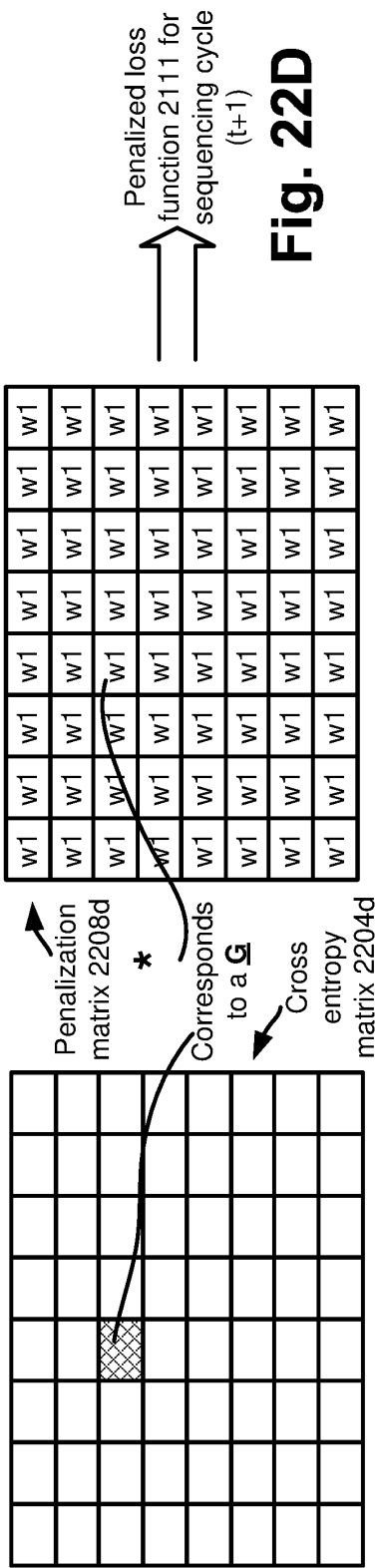


Fig. 22C



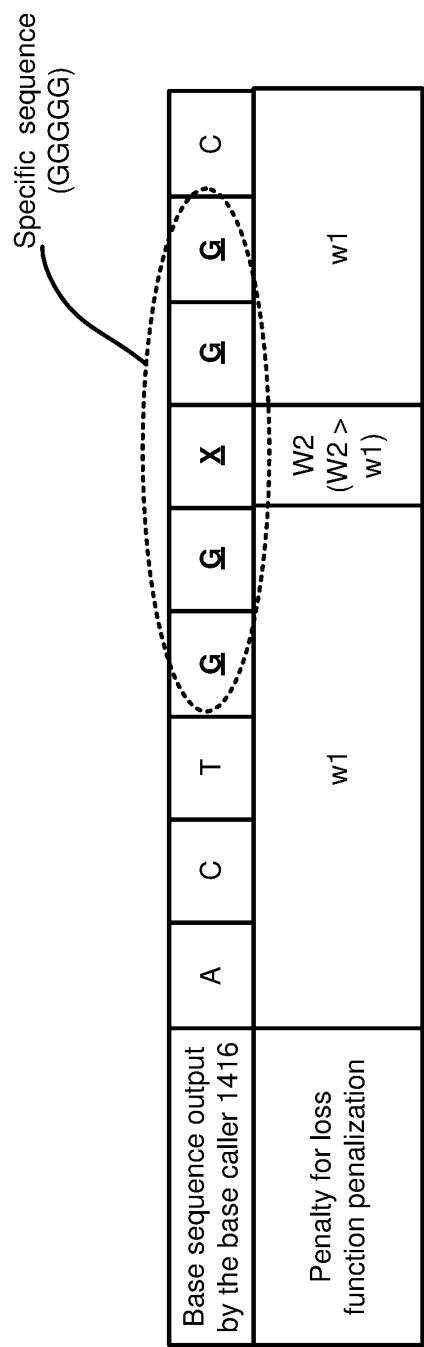


Fig. 22F

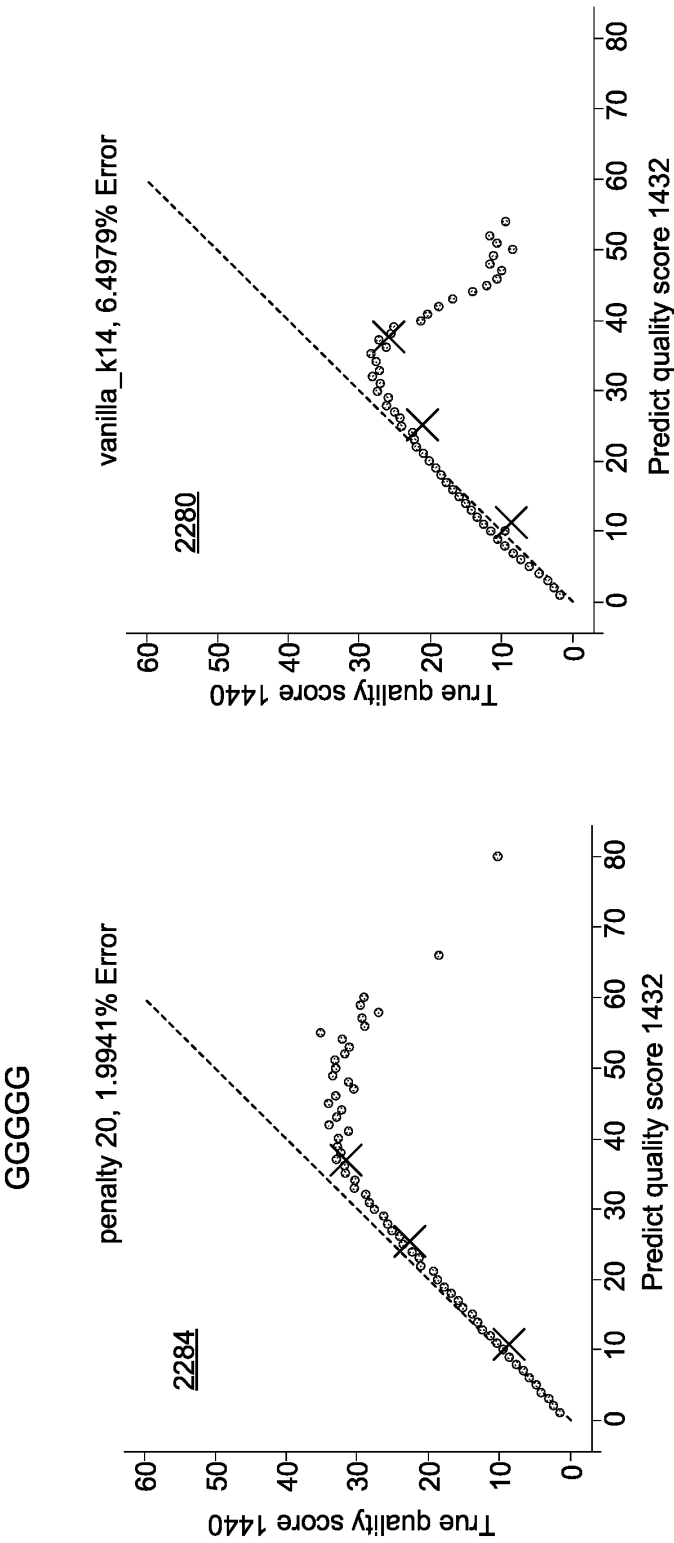


Fig. 22G

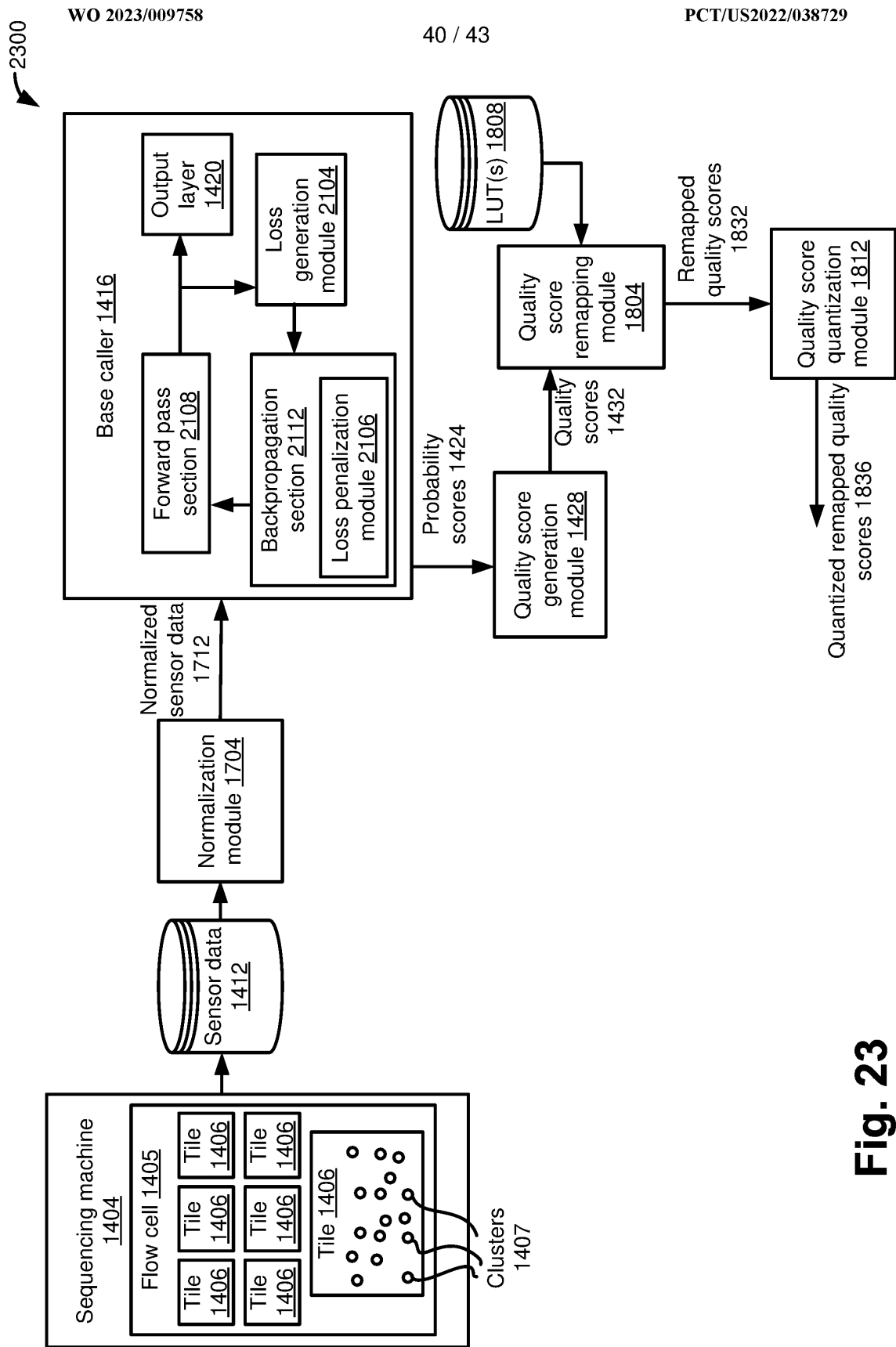


Fig. 23

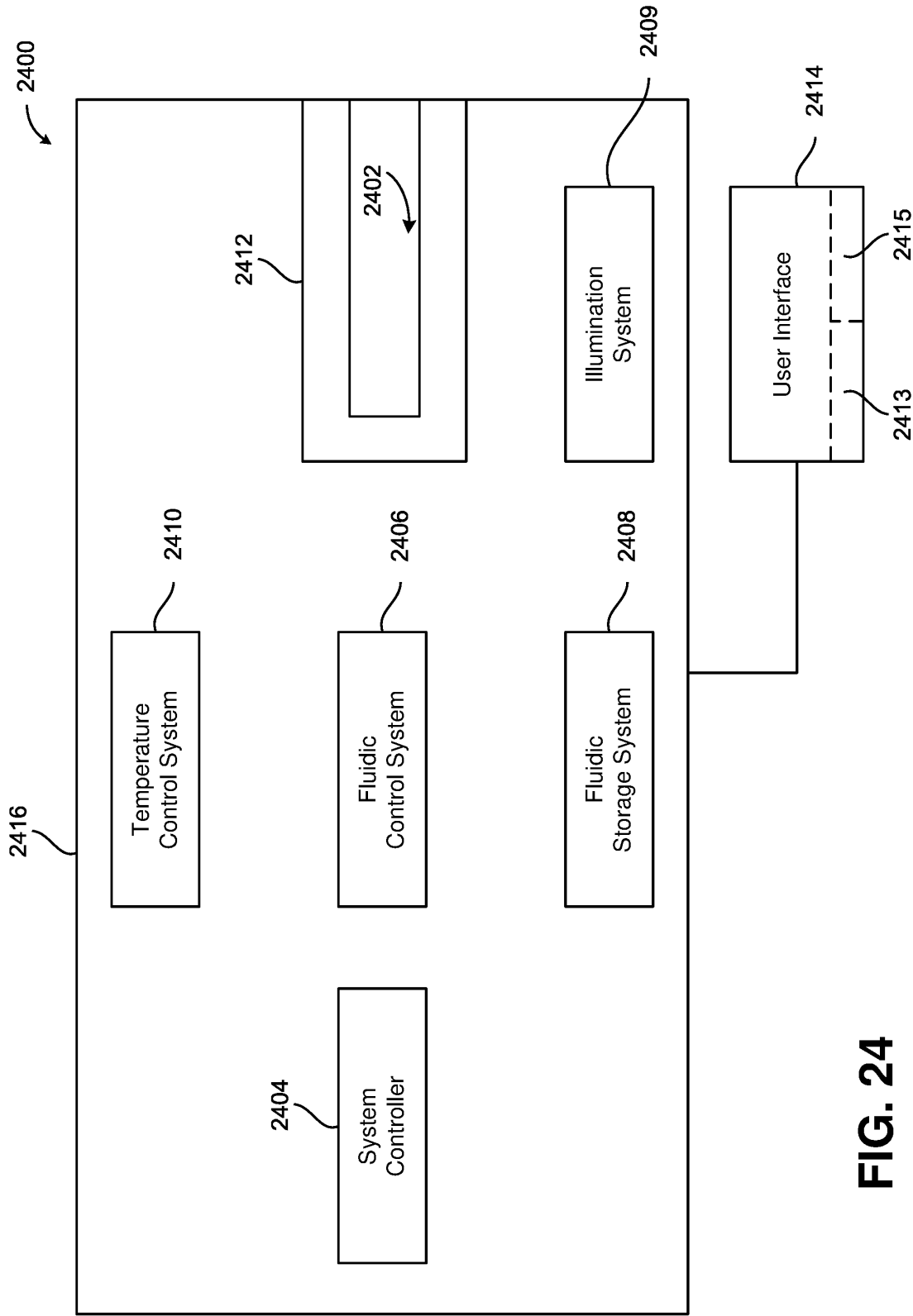


FIG. 24

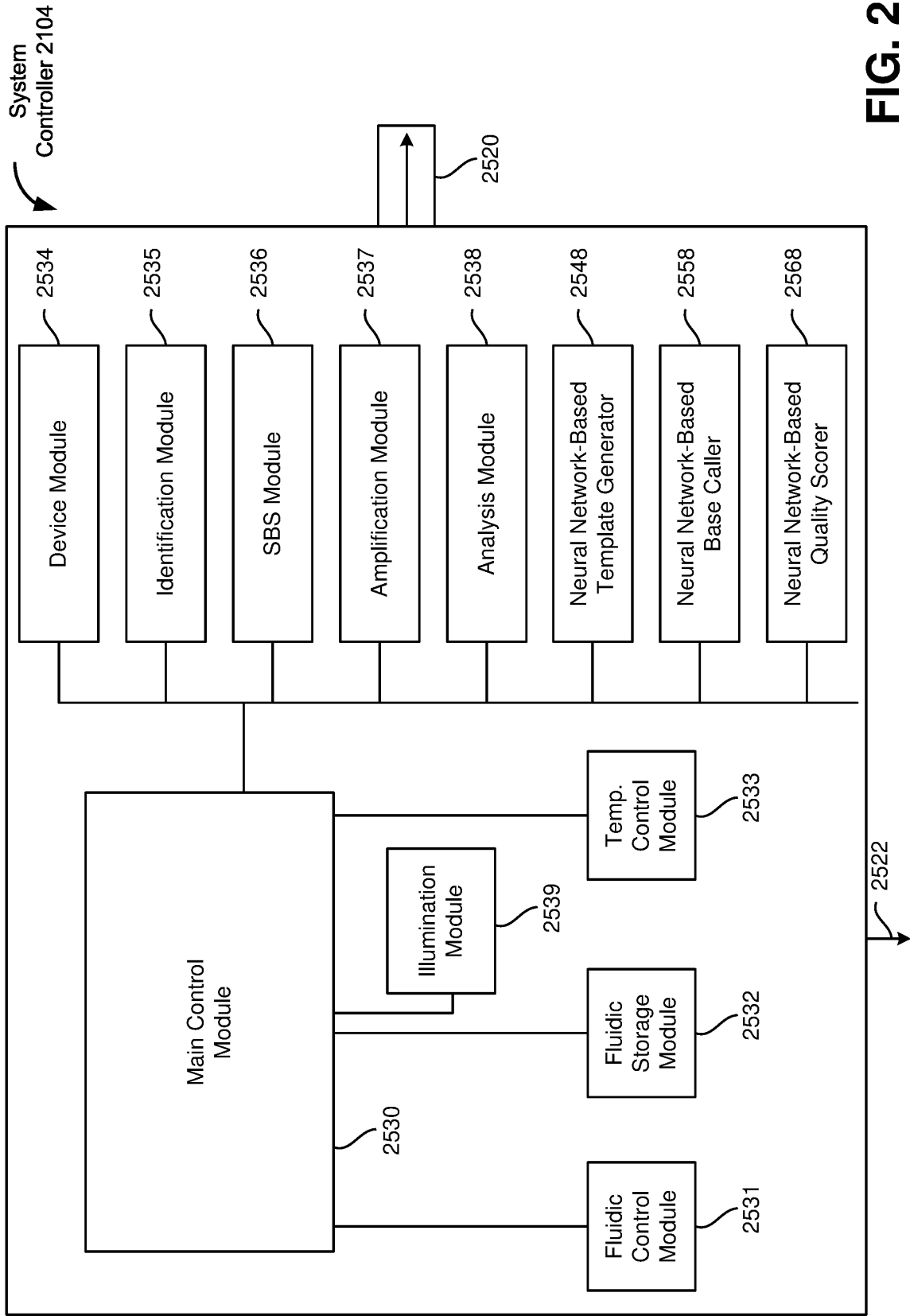


FIG. 25

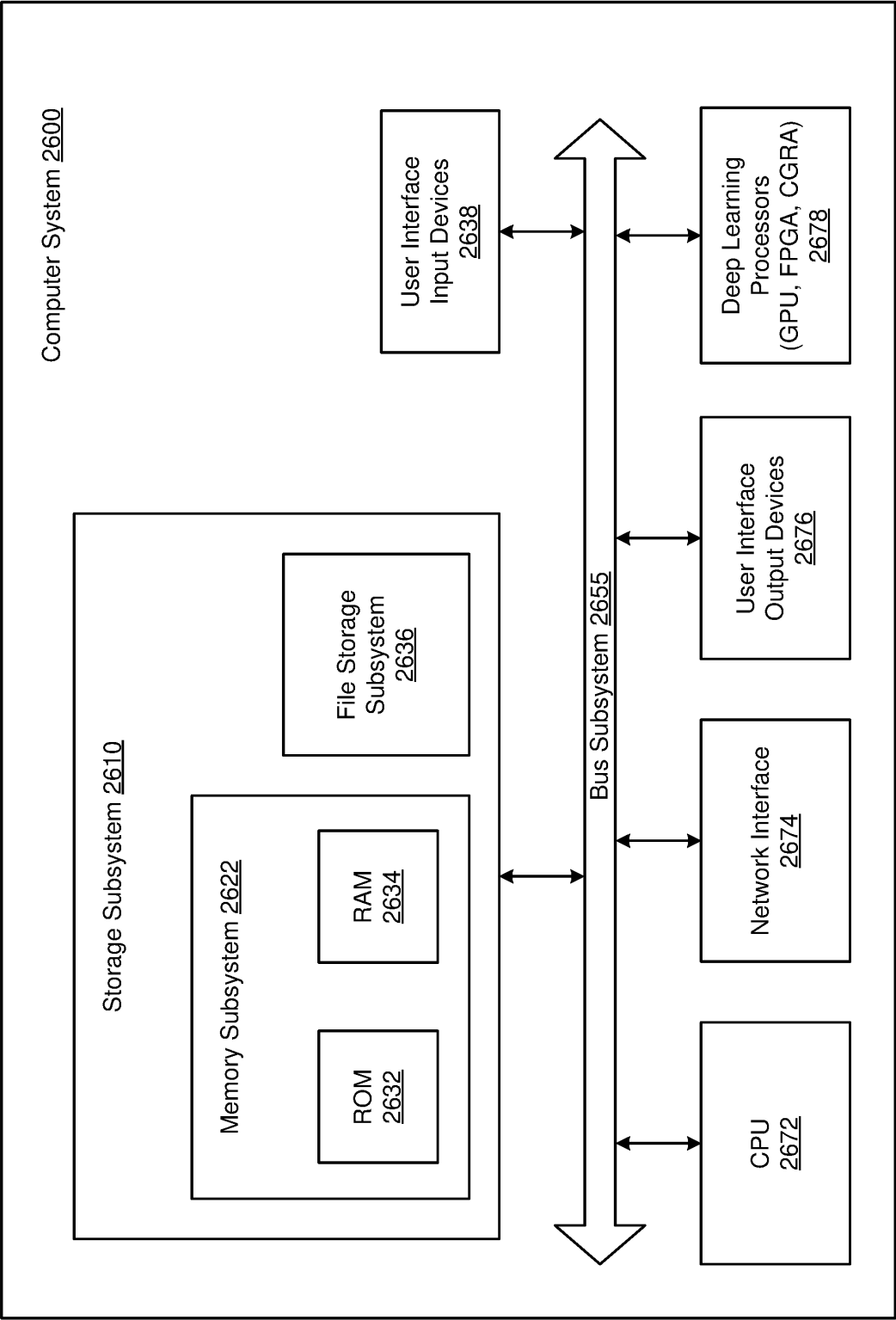


FIG. 26