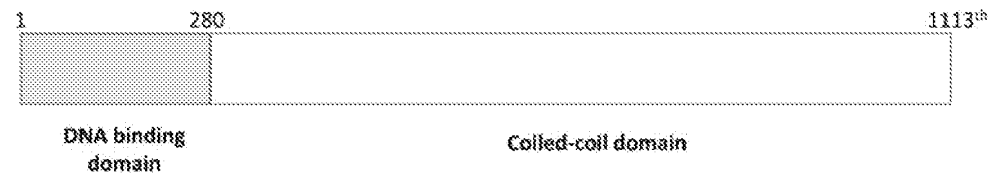


FIGURE 1

A

Ttpa36 protein (protein based temperature sensor)



B

Thermal-T7RNAP (an engineered fusion polymerase; between Split T7 protein units and coiled-coil domain)

Original system (wild-type)

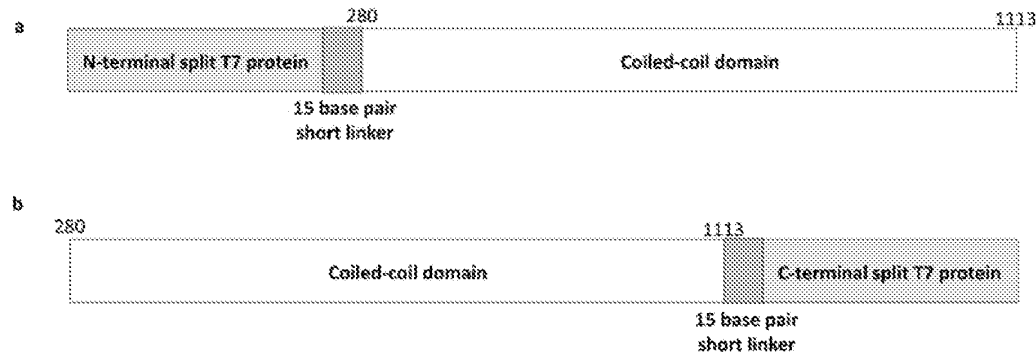


FIGURE 2

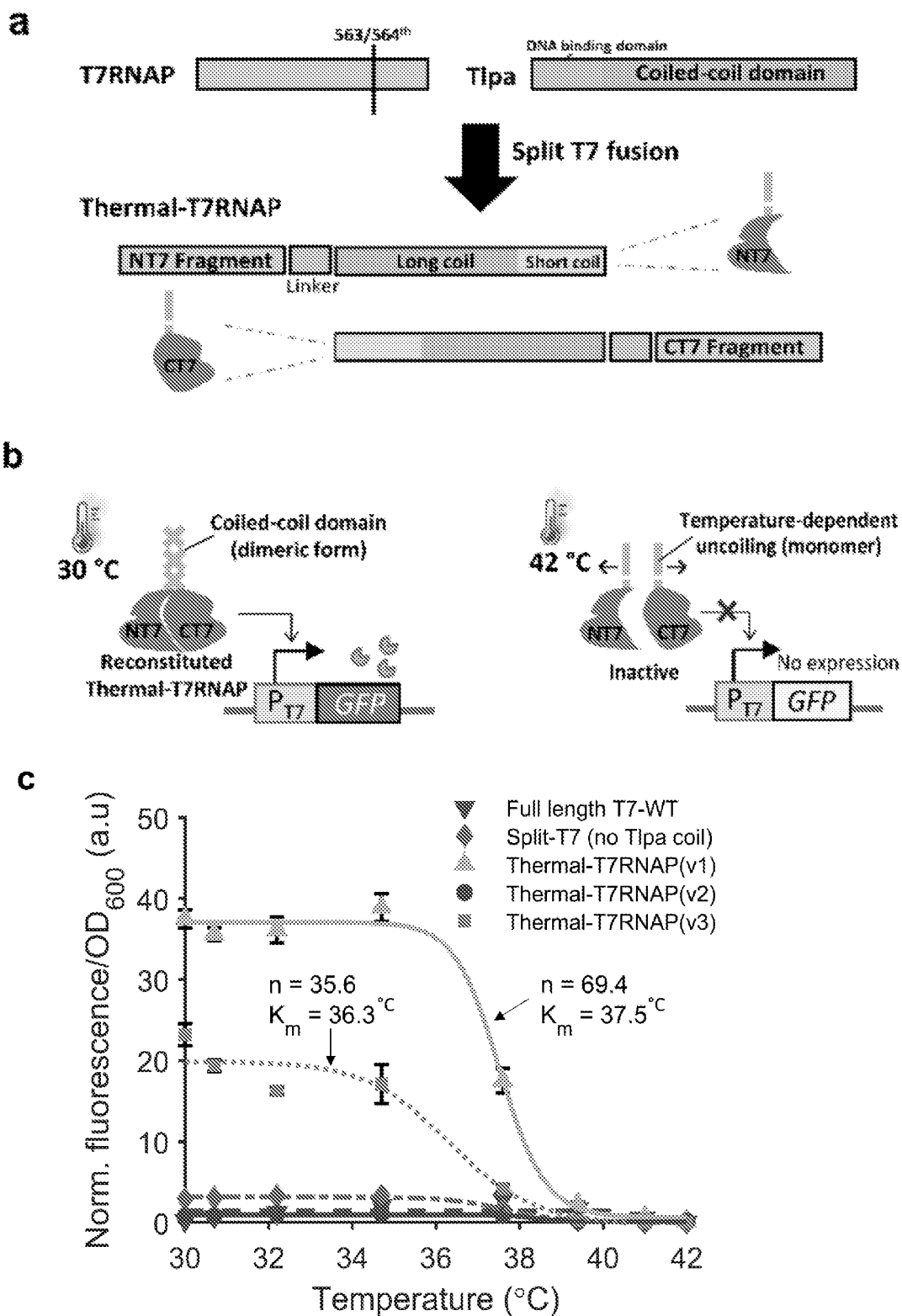


FIGURE 2 (continued)

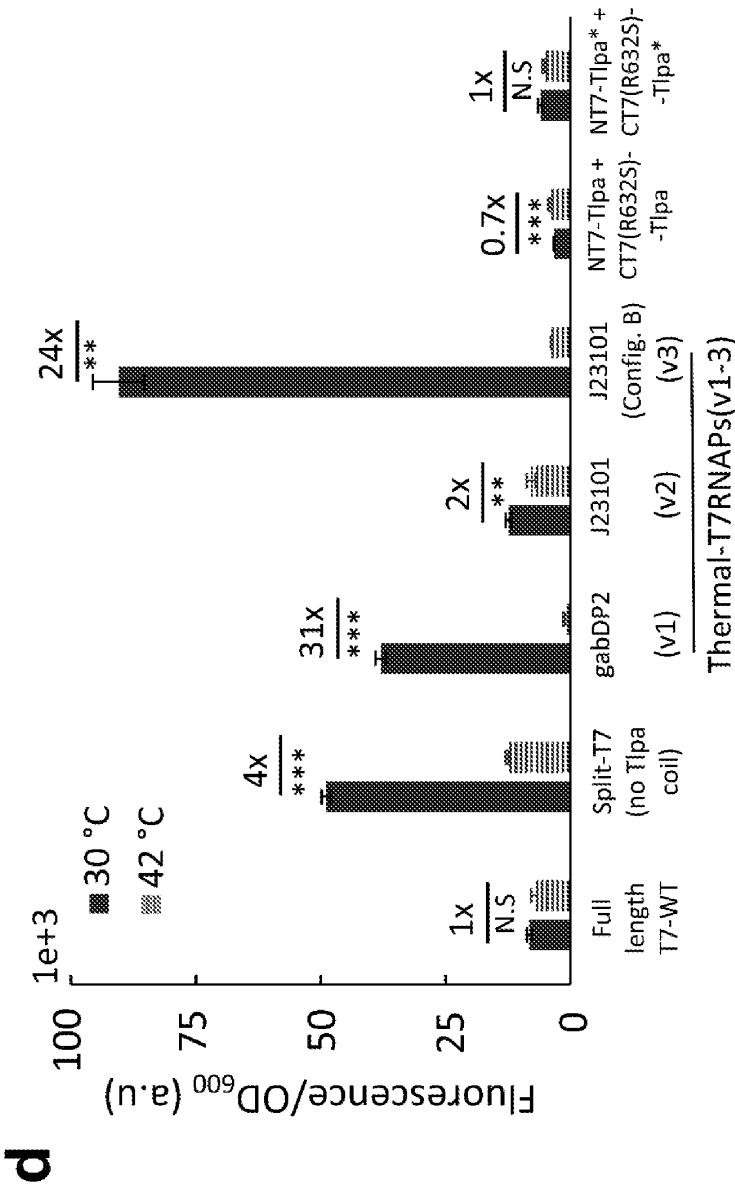


FIGURE 2 (continued)

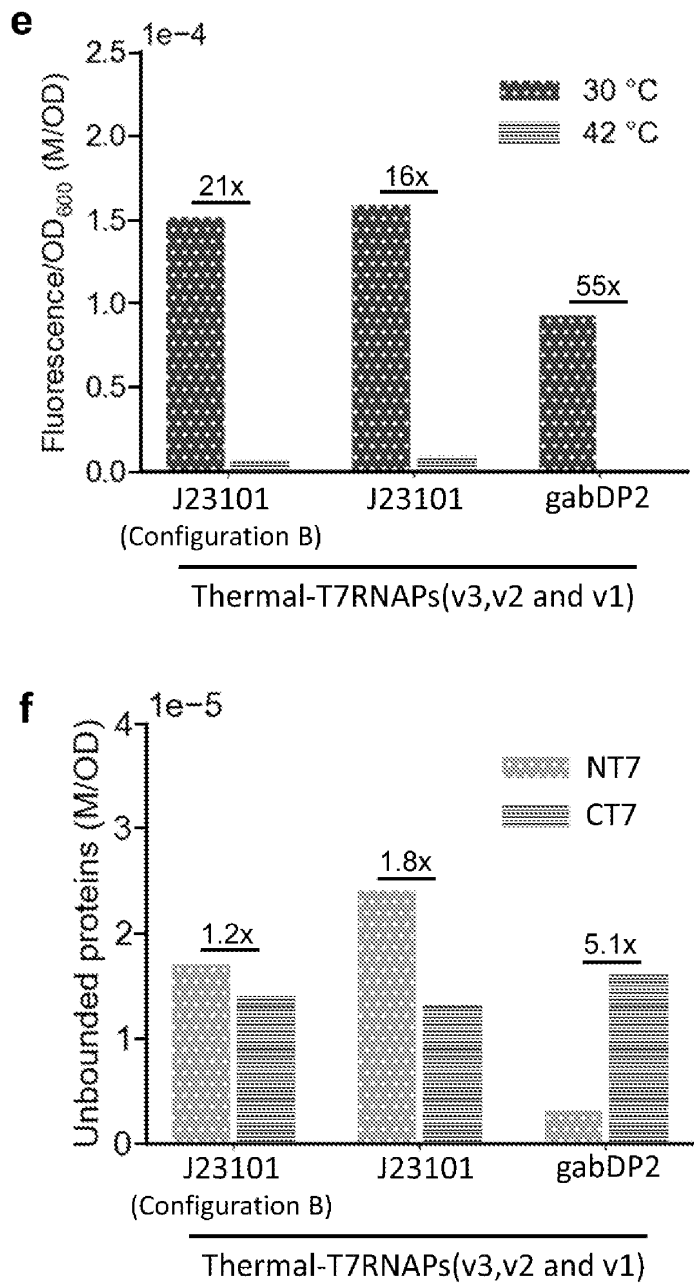


FIGURE 2 (continued)

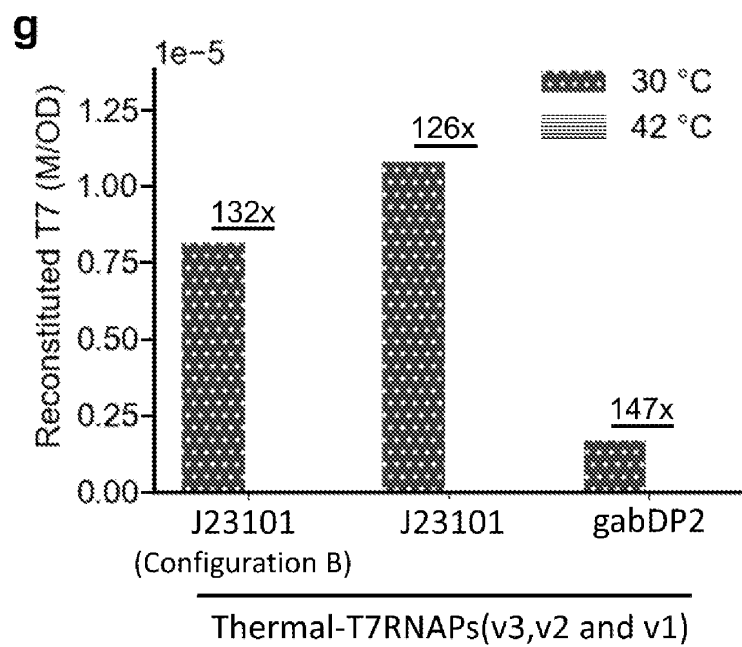
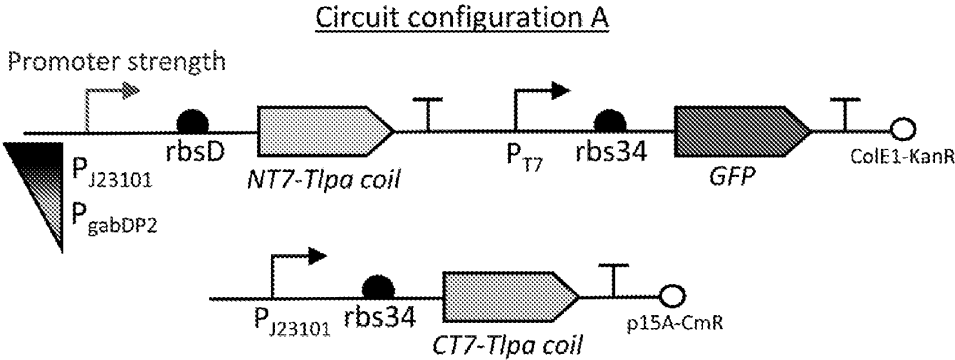


FIGURE 3

a



b

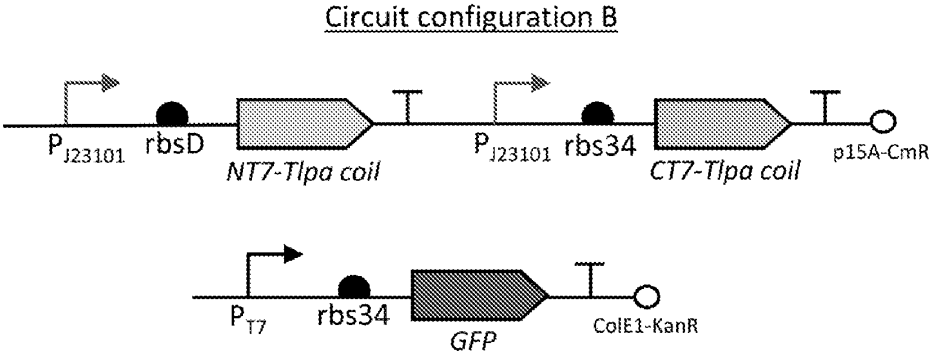
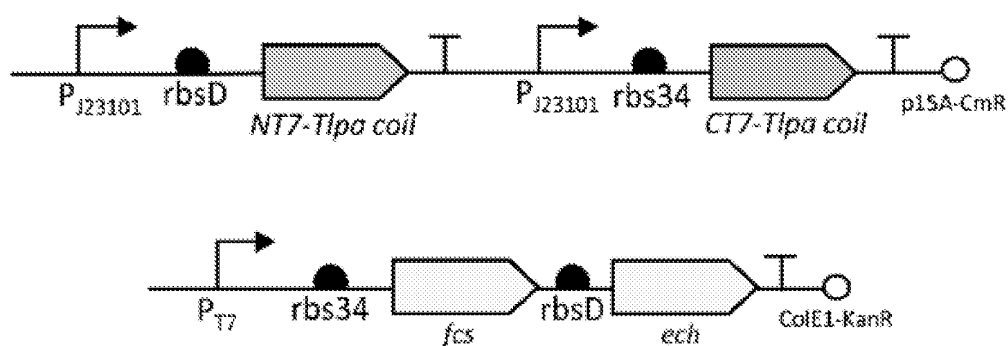


FIGURE 4

a



b

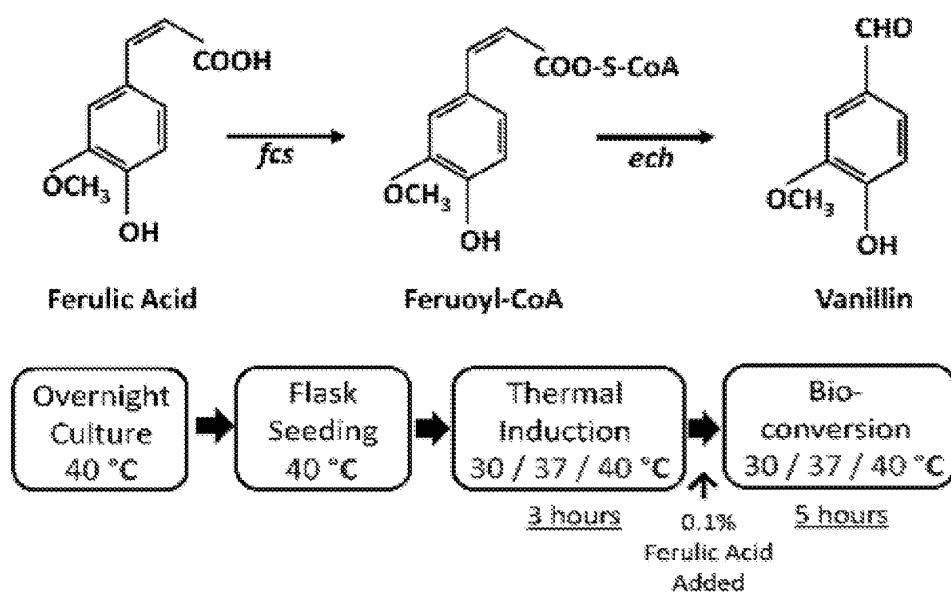


FIGURE 4 (continued)

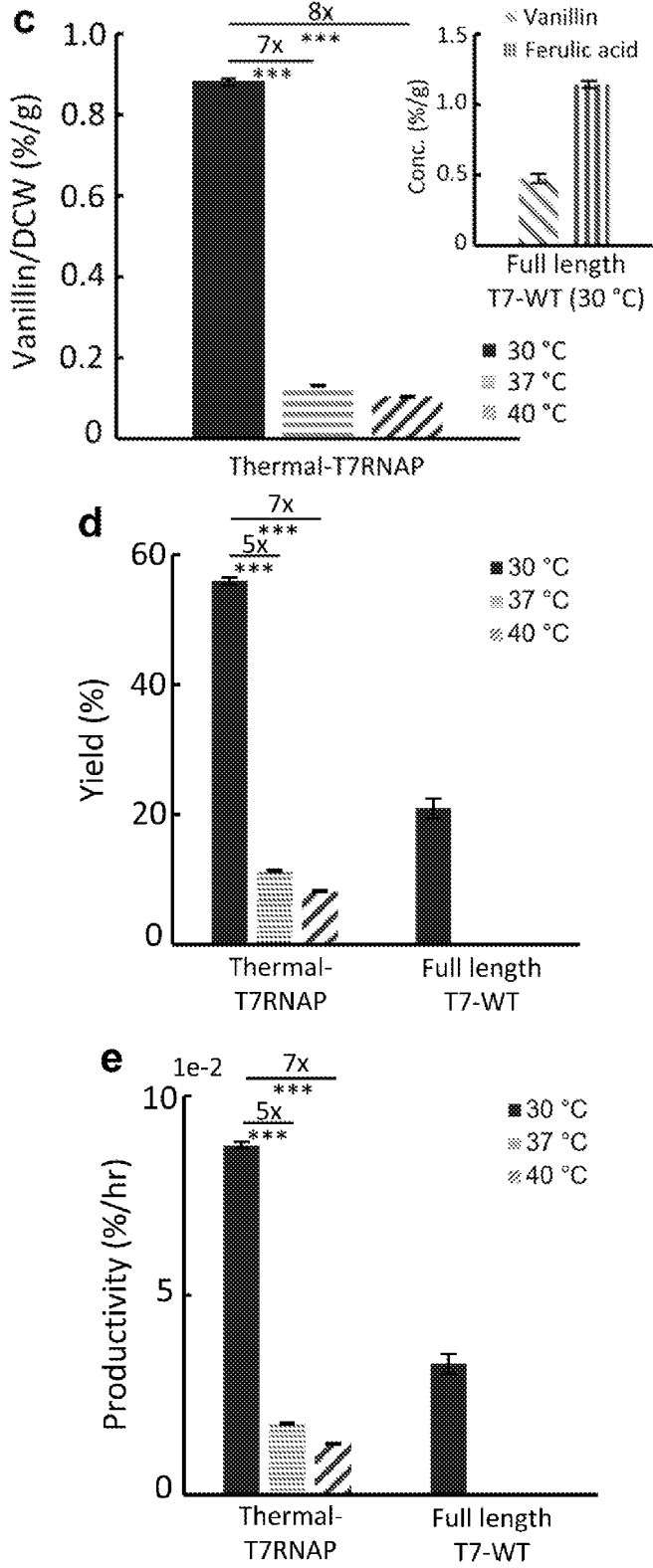


FIGURE 5

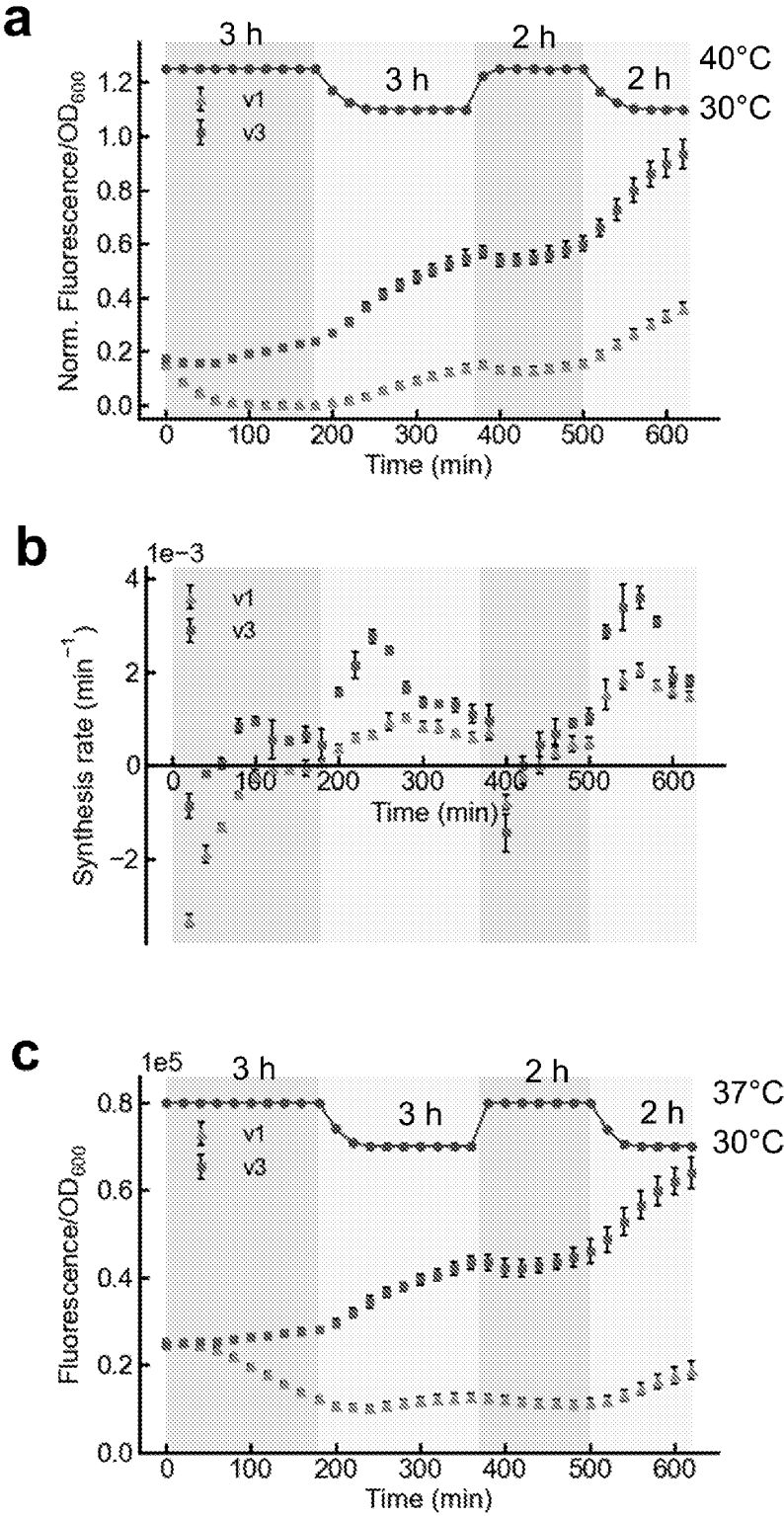


FIGURE 5 (continued)

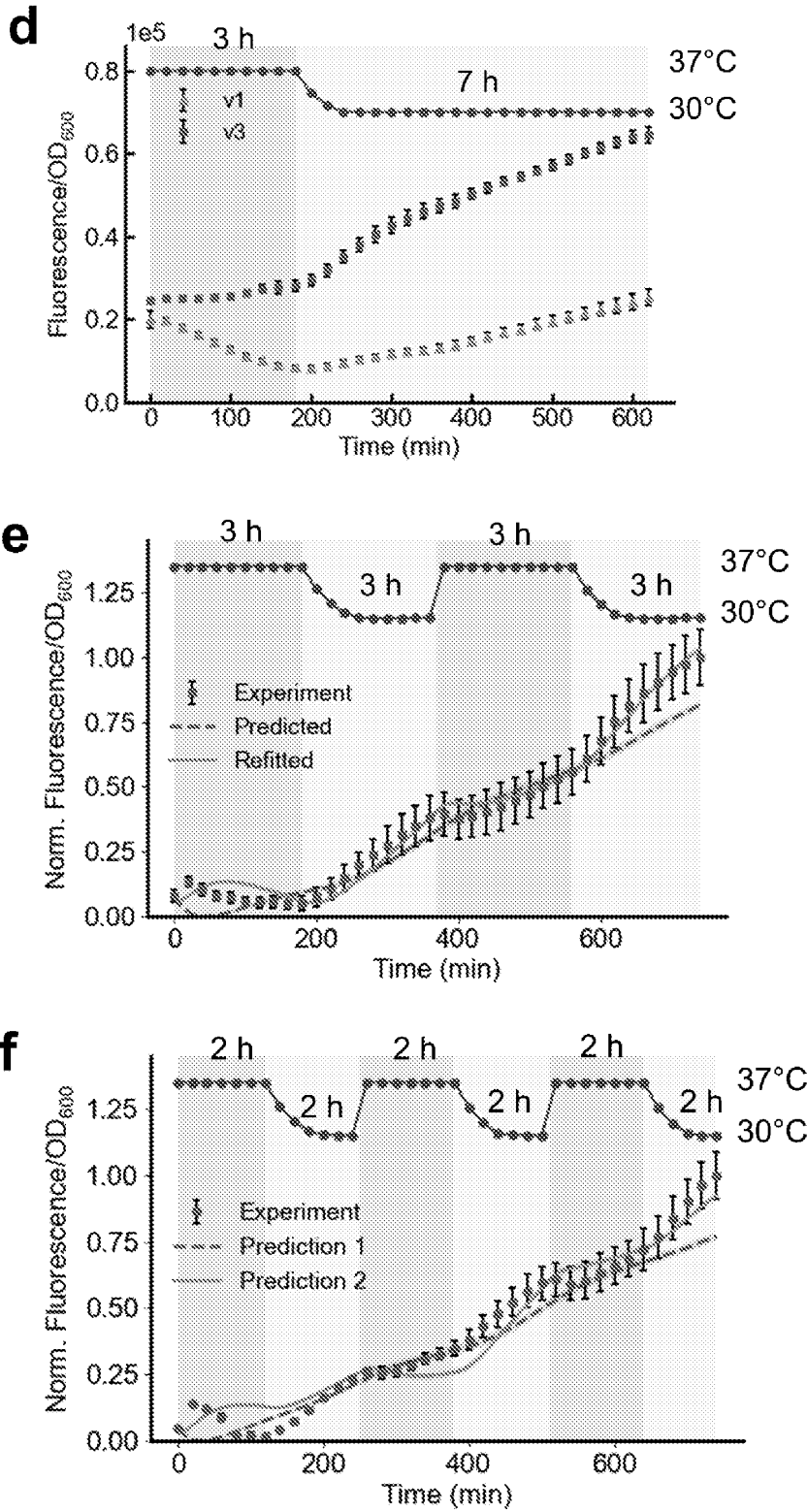


FIGURE 5 (continued)

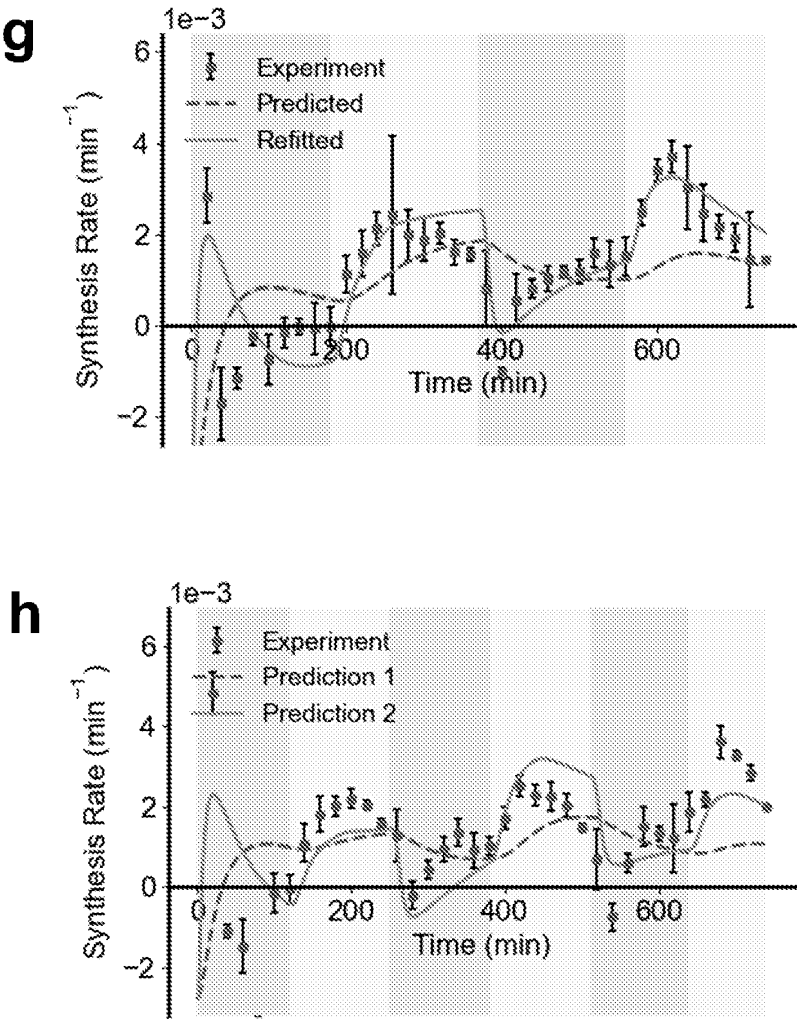
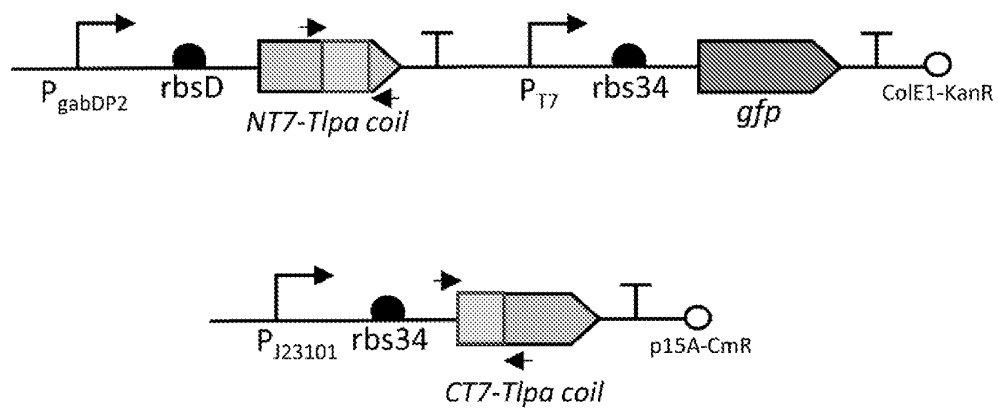


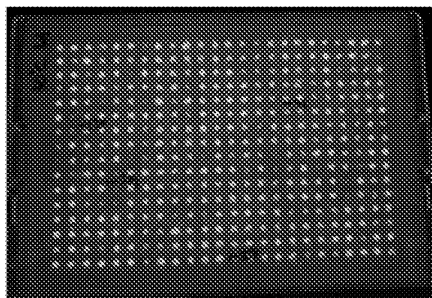
FIGURE 6

a

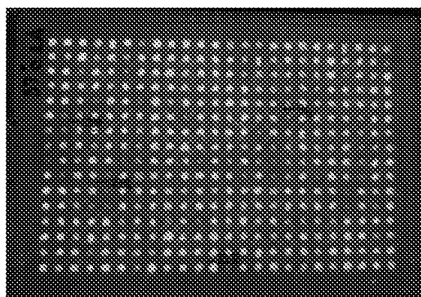


b

30 °C



37 °C



40 °C

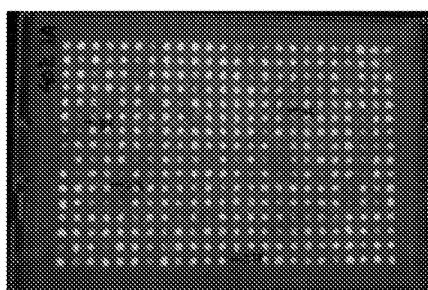


FIGURE 7

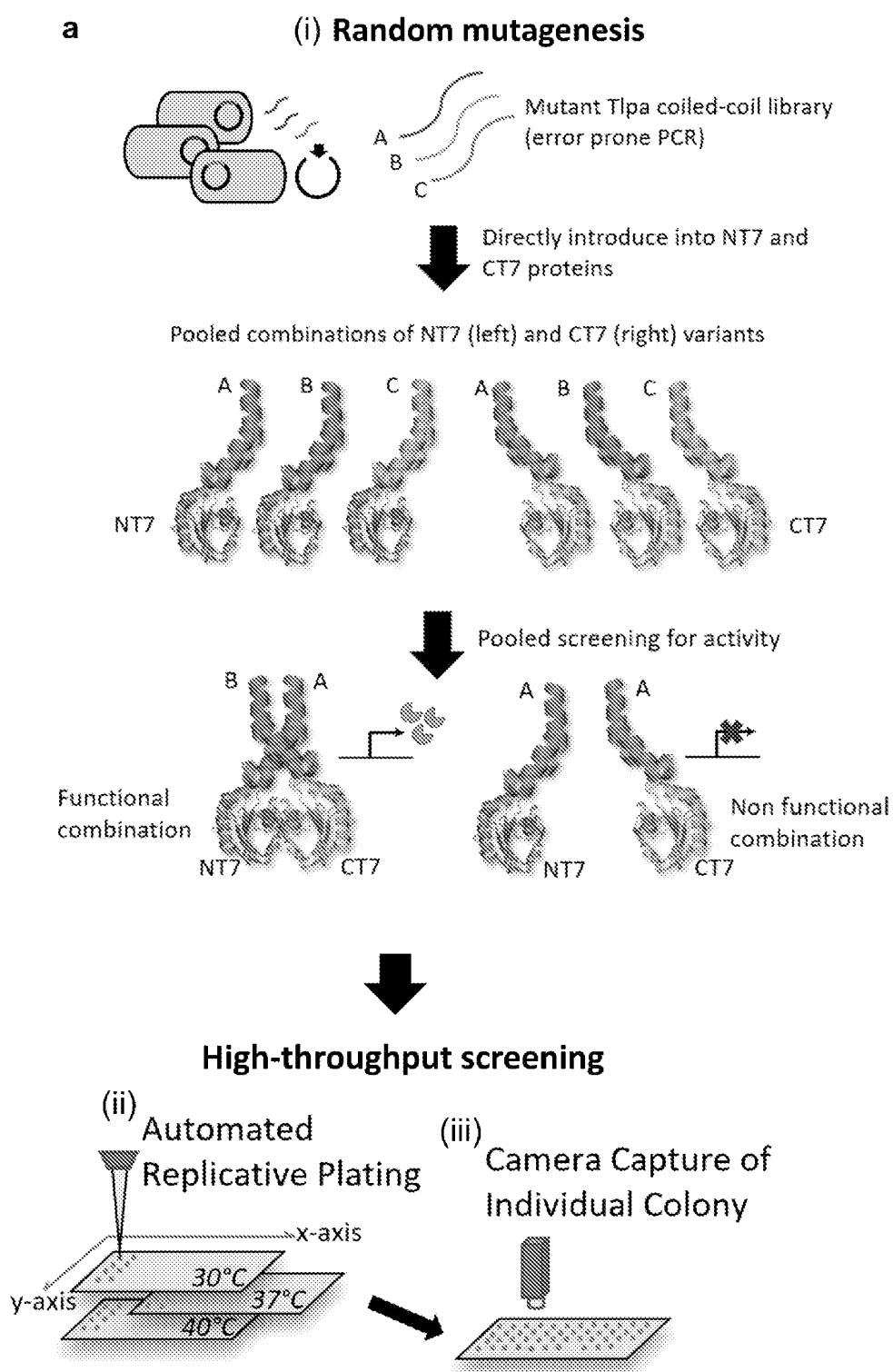


FIGURE 7 (continued)

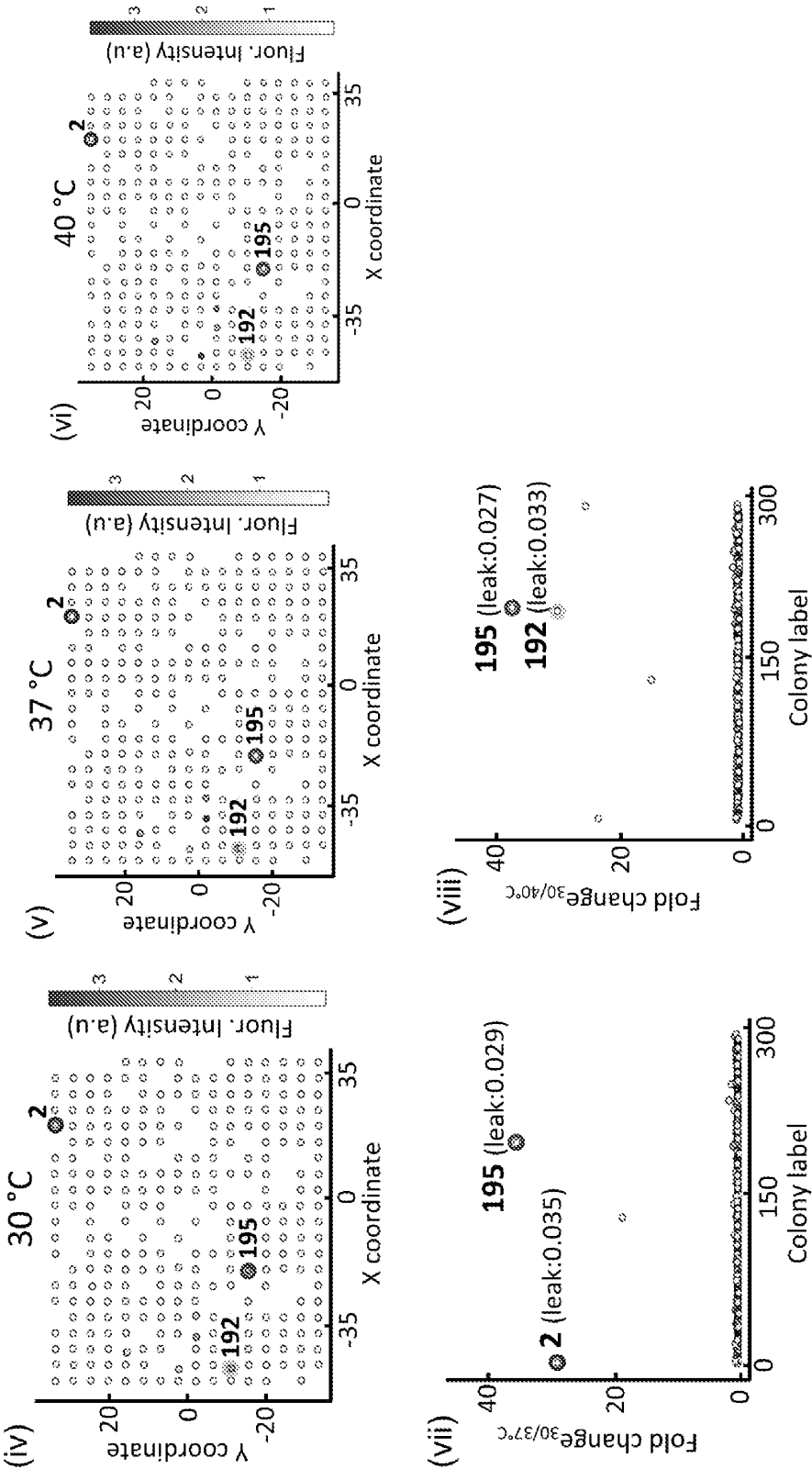


FIGURE 7 (continued)



High precision screening

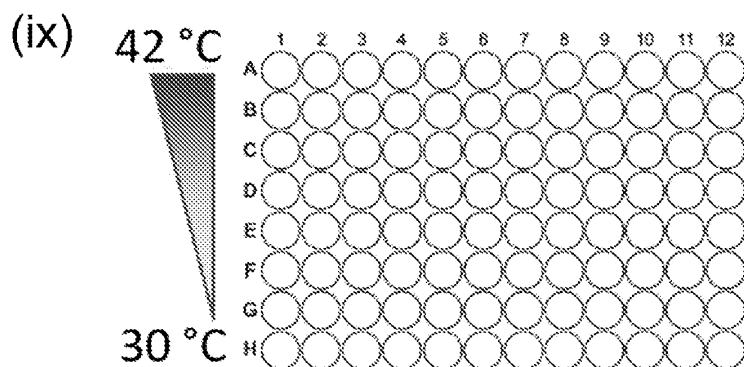
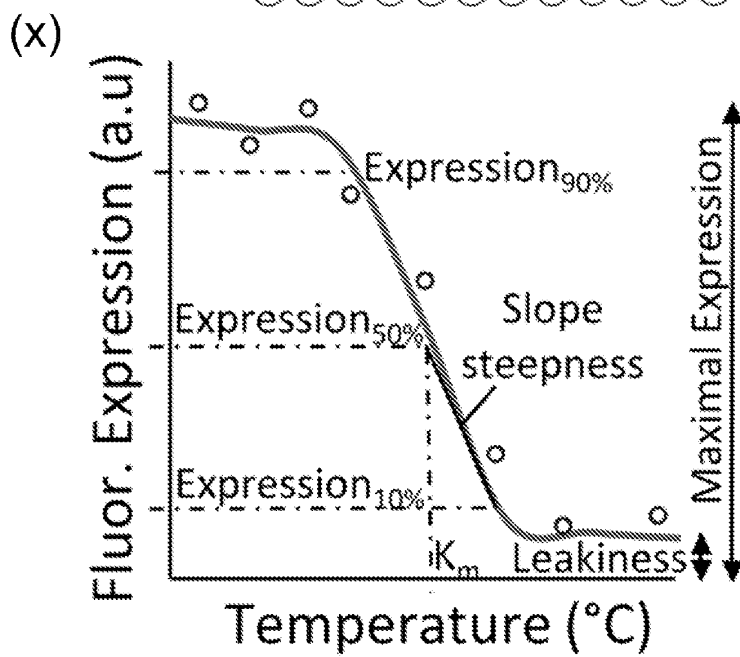


FIGURE 7 (continued)

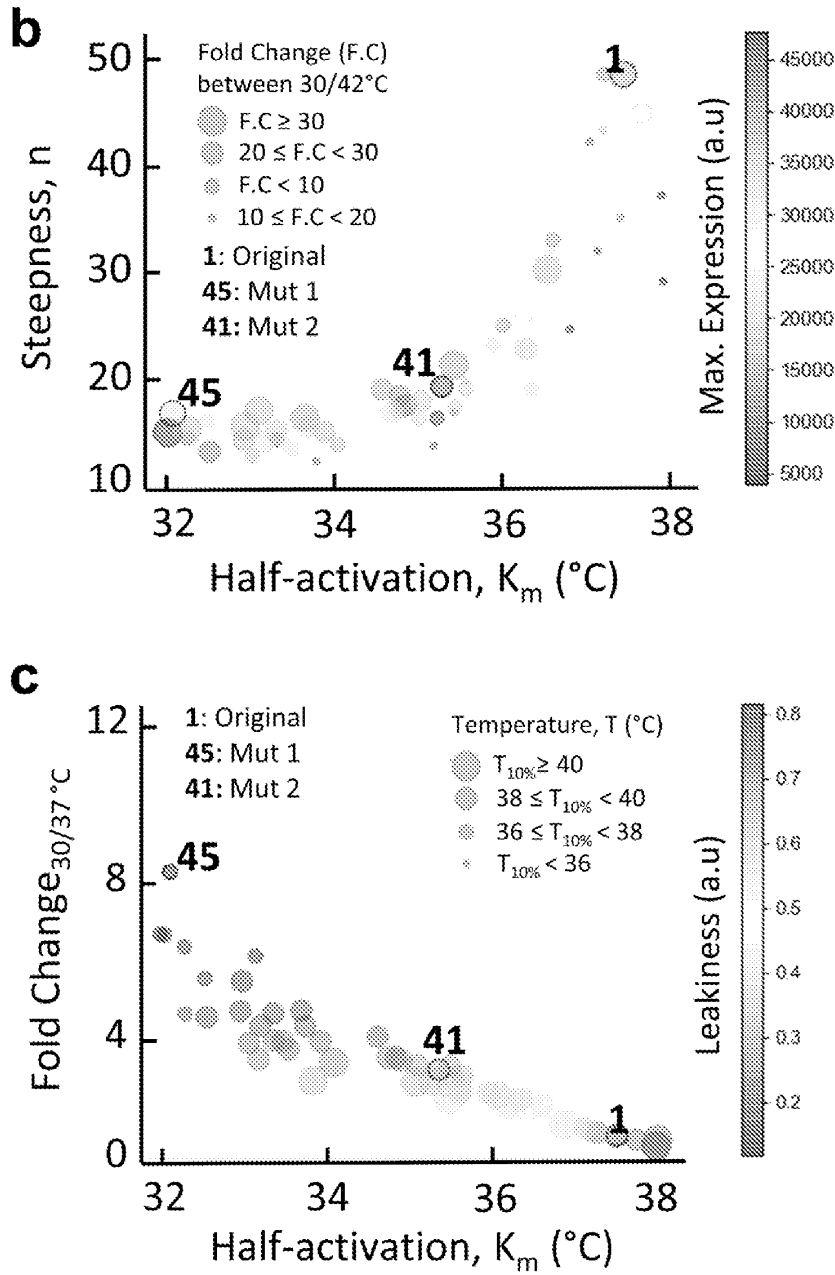


FIGURE 7 (continued)

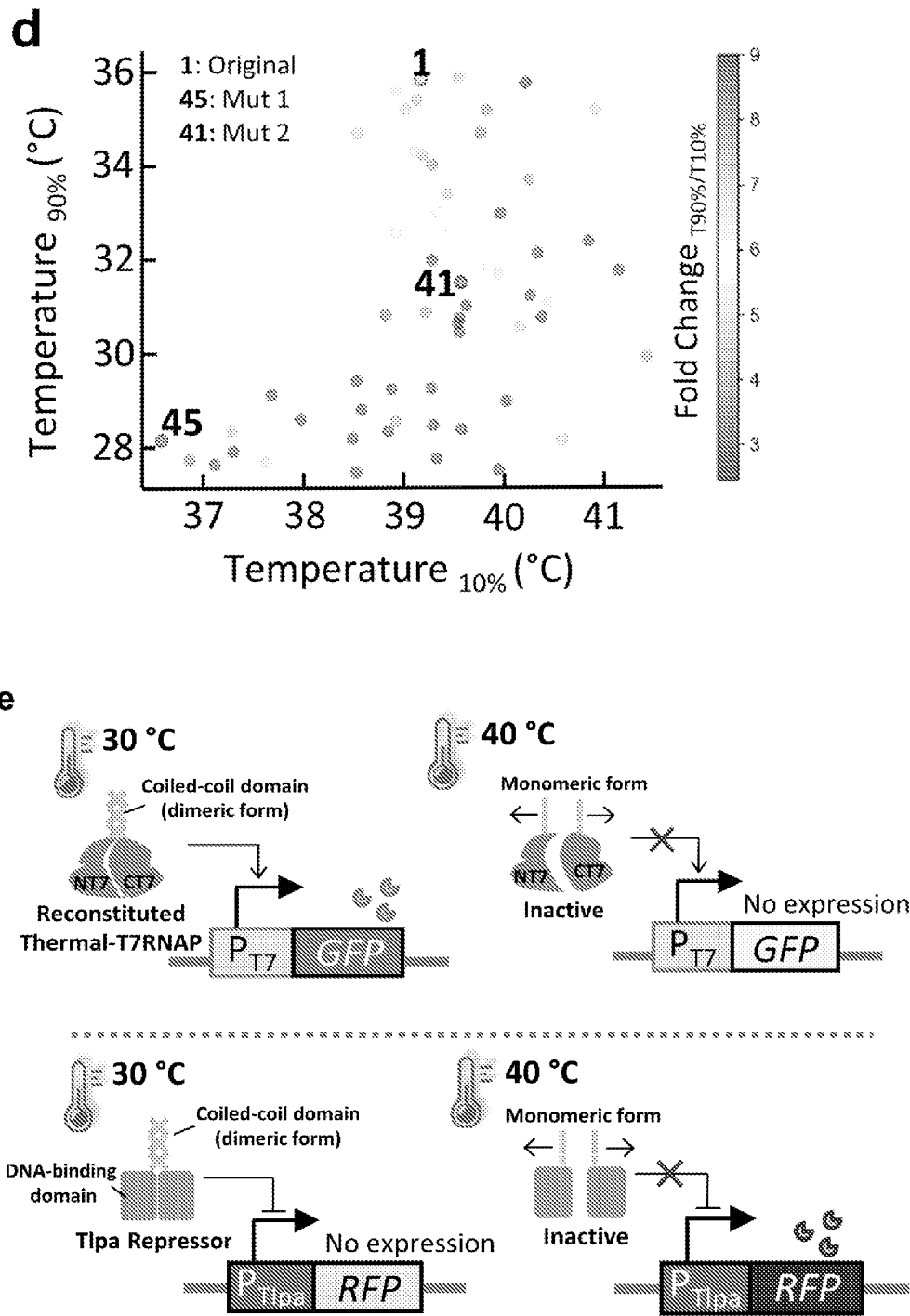


FIGURE 7 (continued)

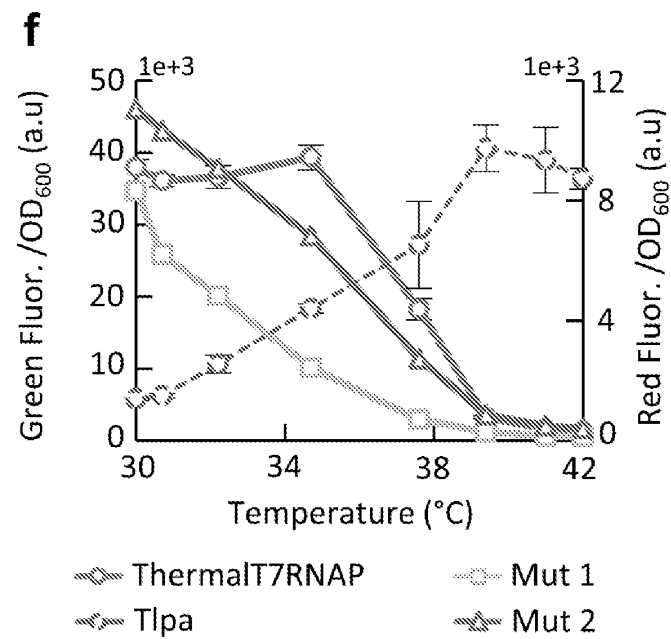
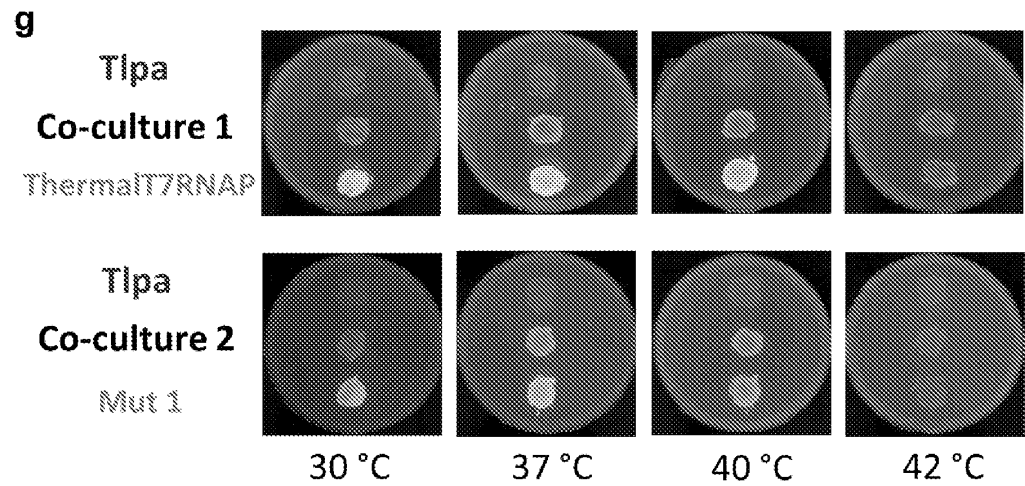


FIGURE 8

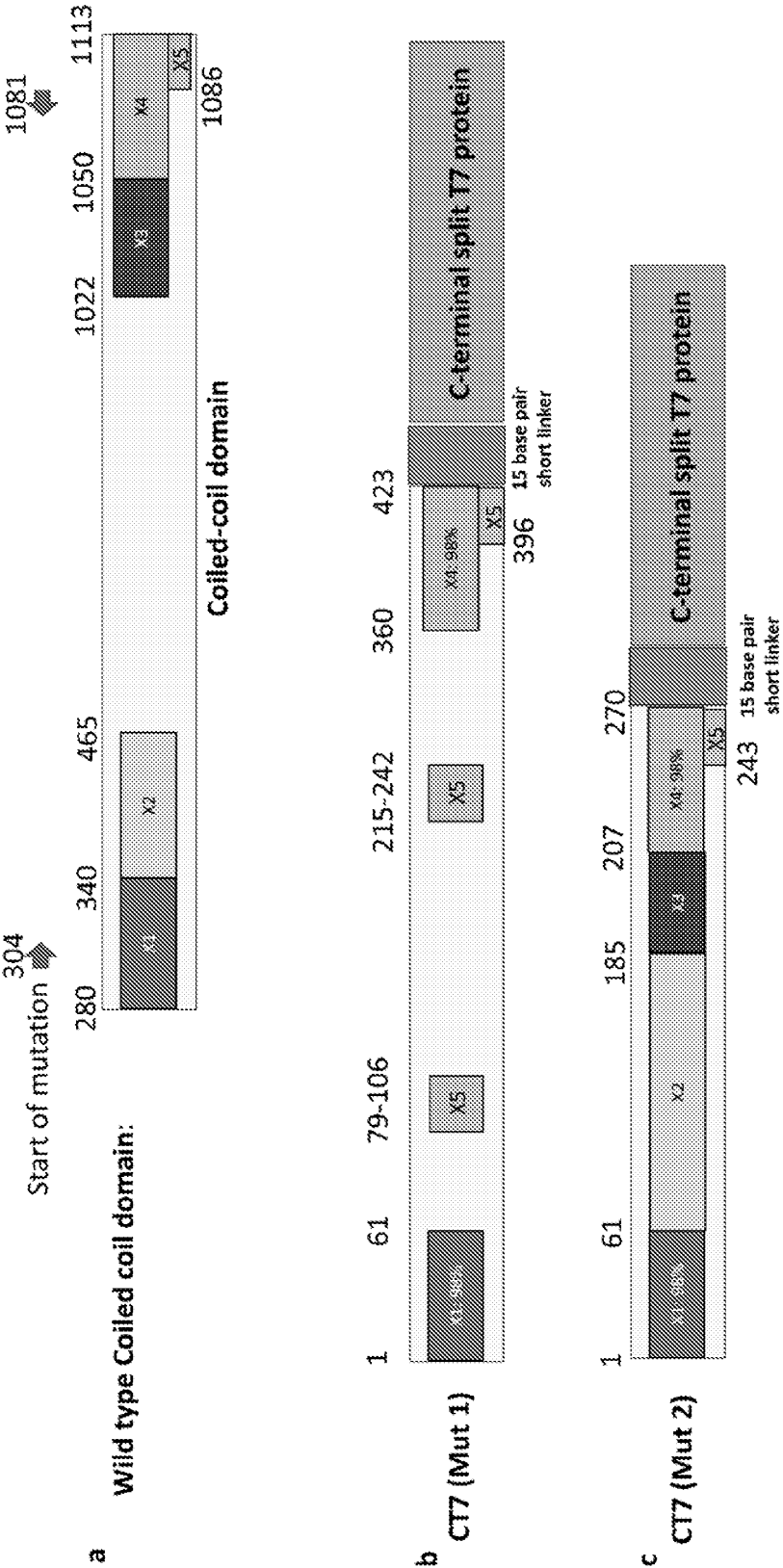


FIGURE 9

A

Region	Protein	Nucleotide Position	Sequences producing significant alignments	Sequence Homology (%)	SEQ ID NO:
1	Tlpa	1050-1113	GCGTCAGAACCACTGCTGATGGC GGCGCTTTCAGGCAATAAACAGAC CGGTGGCCAGAATGCG	98	19
	Mut1	360- 423	GCGACAGAACCACTGCTGATGG CGGCGCTTTCAGGCAATAAACAGA CCGGTGGCCAGAATGCG		20
2	Tlpa	280-340	GCGGTCCGGGCTGCAGAACGCCG GGTTGCGGAAGTCACGCGTGCTG CCGGTGAACAGACCG	98	21
	Mut1	1-61	GCGGTCCGGGCTGCAGAACGCCG GGTTGCGGAAGTCACGCGTGCTG CCGGTGAACAGACCG		22
3	Tlpa	1086-1113	CAATAAACAGACCGGTGGCCAGAA TGCG	100	23
	Mut1	79-106	Conserved		-
4	Tlpa	1086-1113	CAATAAACAGACCGGTGGCCAGAA TGCG	100	23
	Mut1	215-242	Conserved		-

B

Region	Protein	Nucleotide Position	Sequences producing significant alignments	Sequence Homology (%)	SEQ ID NO:
1	Tlpa	280-465	GCGGTCCGGGCTGCAGAACGCCG GGTTGCGGAAGTCACGCGTGCTG CCGGTGAACAGACC GCACAGGCAGAGCGGGAGCTGGC CGACGCCGCGCAGACAGTCGACG ACCTGGAAGAAAAA CTGGTTGAACTGCAGGACAGATAT GACAGTTTGACGCTGGCGCTGGA GTCAGAACGTTCA CTGCGT	100	24
	Mut2	1-186	Conserved		-
2	Tlpa	1022-1113	CACTGCGTGGTGAGGCTGAAGCC CTGAAGCGTCAGAACCACTGCTG ATGGCGGCGCTTT CAGGCAATAAACAGACCGGTGGC CAGAATGCG	100	25
	Mut2	179-270	Conserved		-

FIGURE 9 (continued)**C**

Region	Protein	Nucleotide Position	Sequences producing significant alignments	Sequence Homology (%)	SEQ ID NO:
1	Mut1	341-465	CACAGGCAGAGCGGGAGCTGGC CGACGCCGCGCAGACAGTCGAC GACCTGGAAGAAAAAC TGGTTGAACTGCAGGACAGATAT GACAGTTTGACGCTGGCGCTGG AGTCAGAACGTTTAC TGCCT	100	26
	Mut2	1-125	Conserved		-
2	Mut1	1022-1049	CACTGCGTGGTGAGGCTGAAGC CCTGAA	100	27
	Mut2	118-145	Conserved		-

FIGURE 10

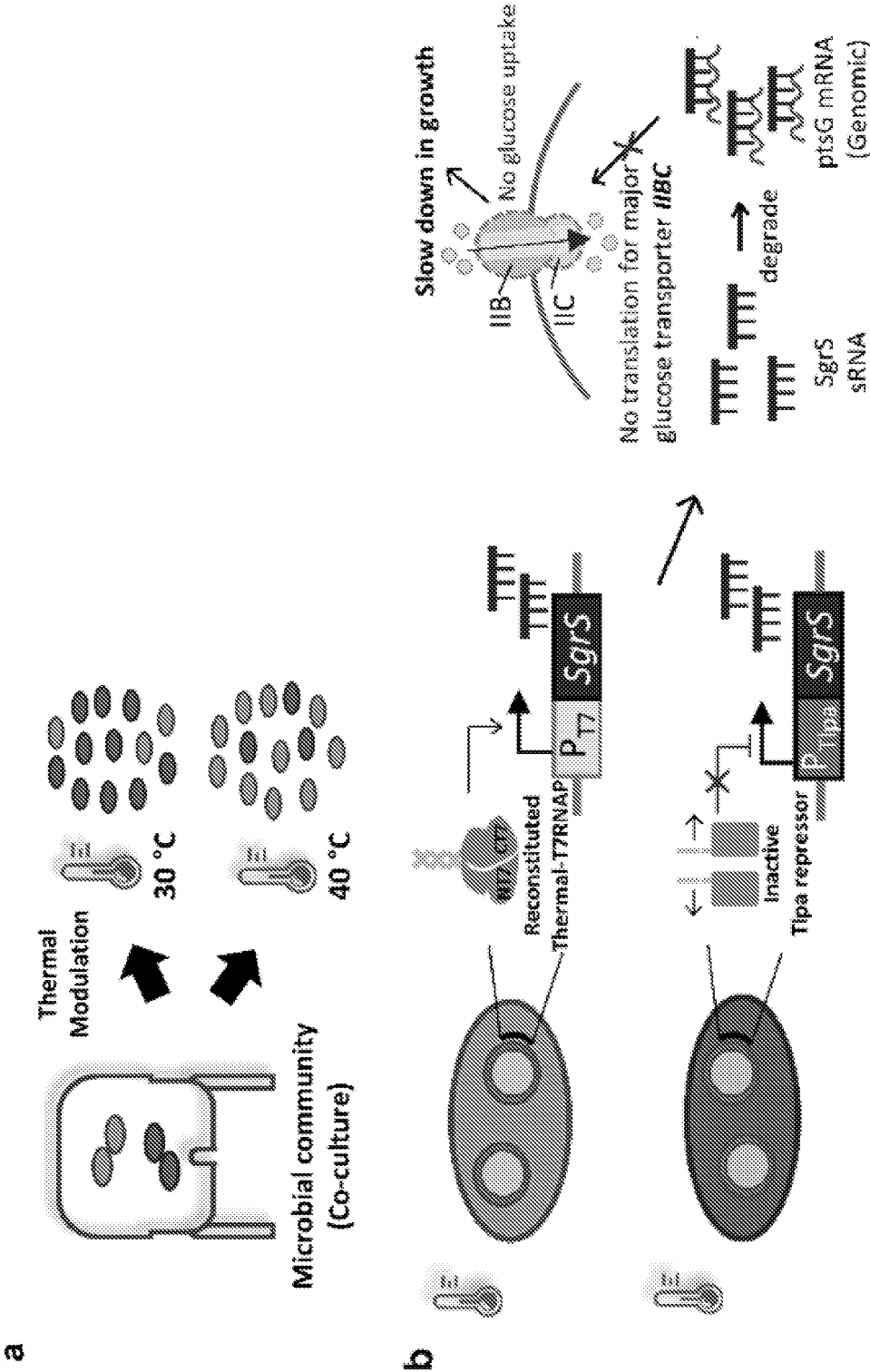


FIGURE 10 (continued)

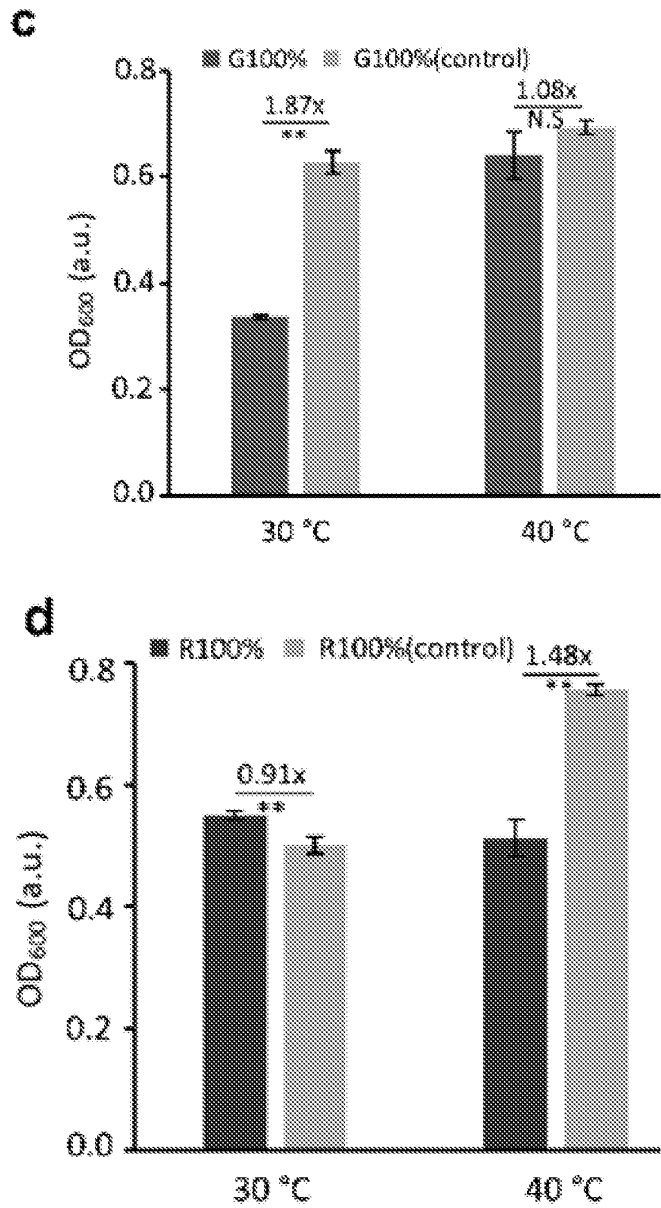


FIGURE 10 (continued)

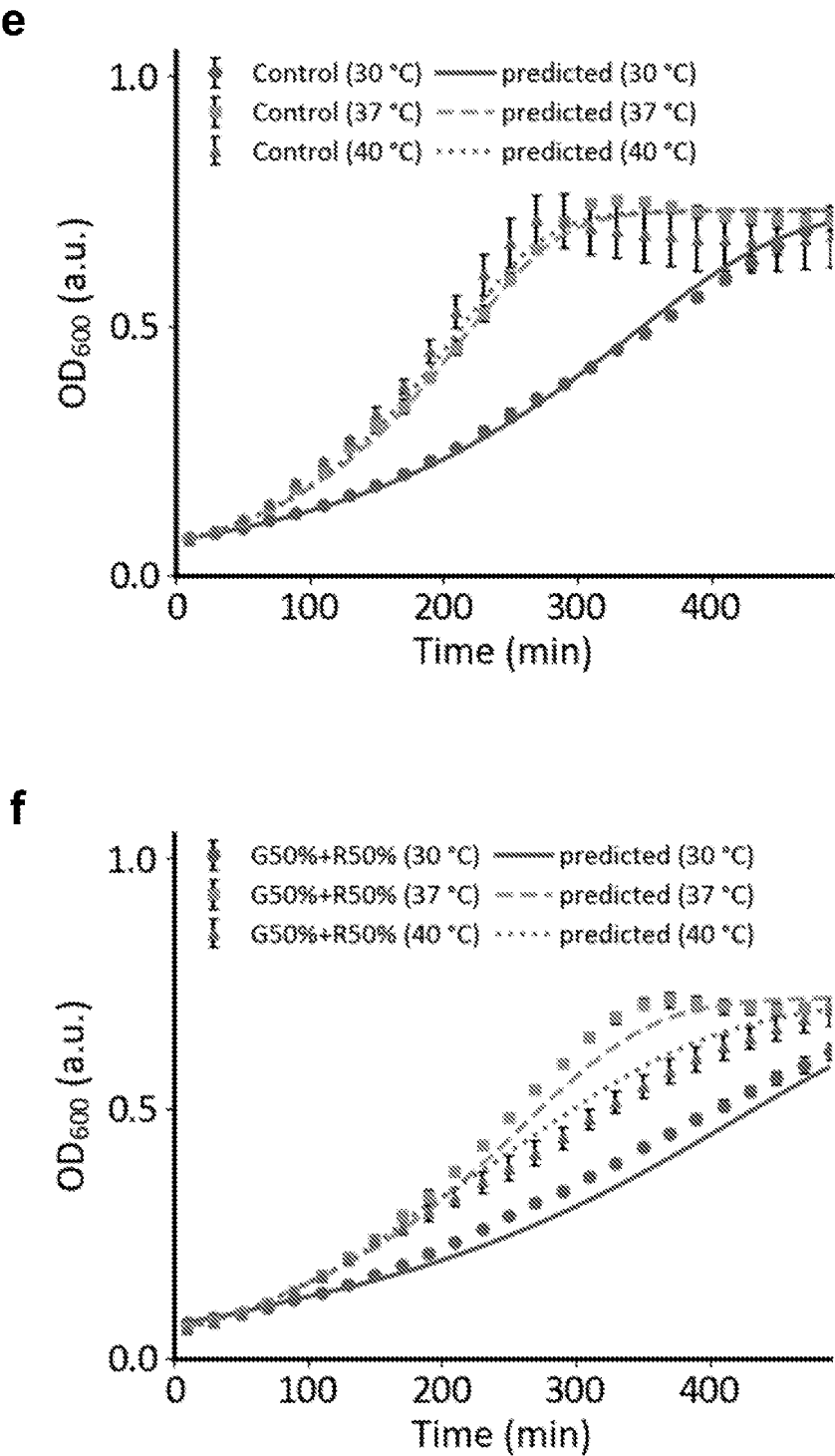


FIGURE 10 (continued)

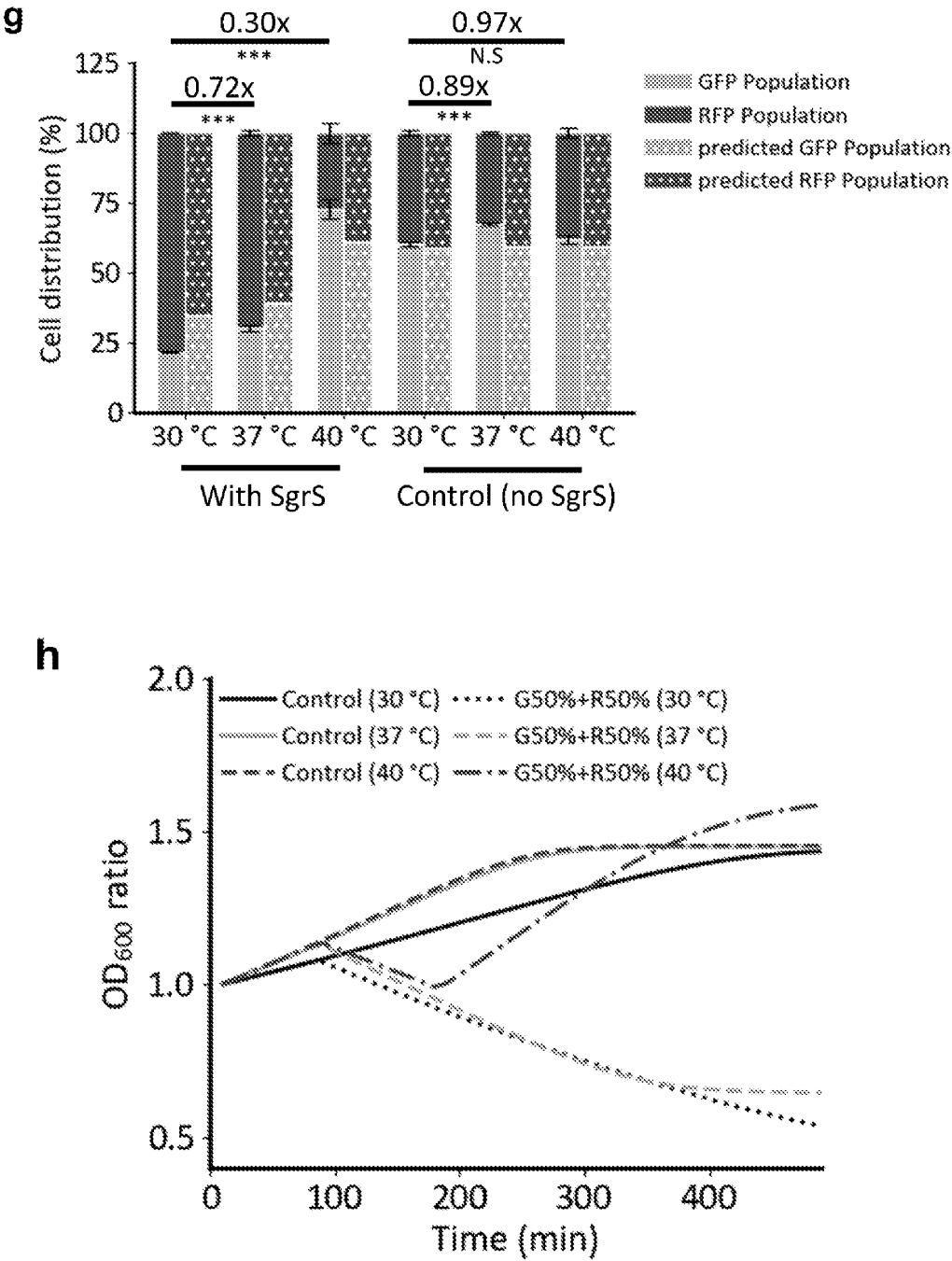


FIGURE 10 (continued)

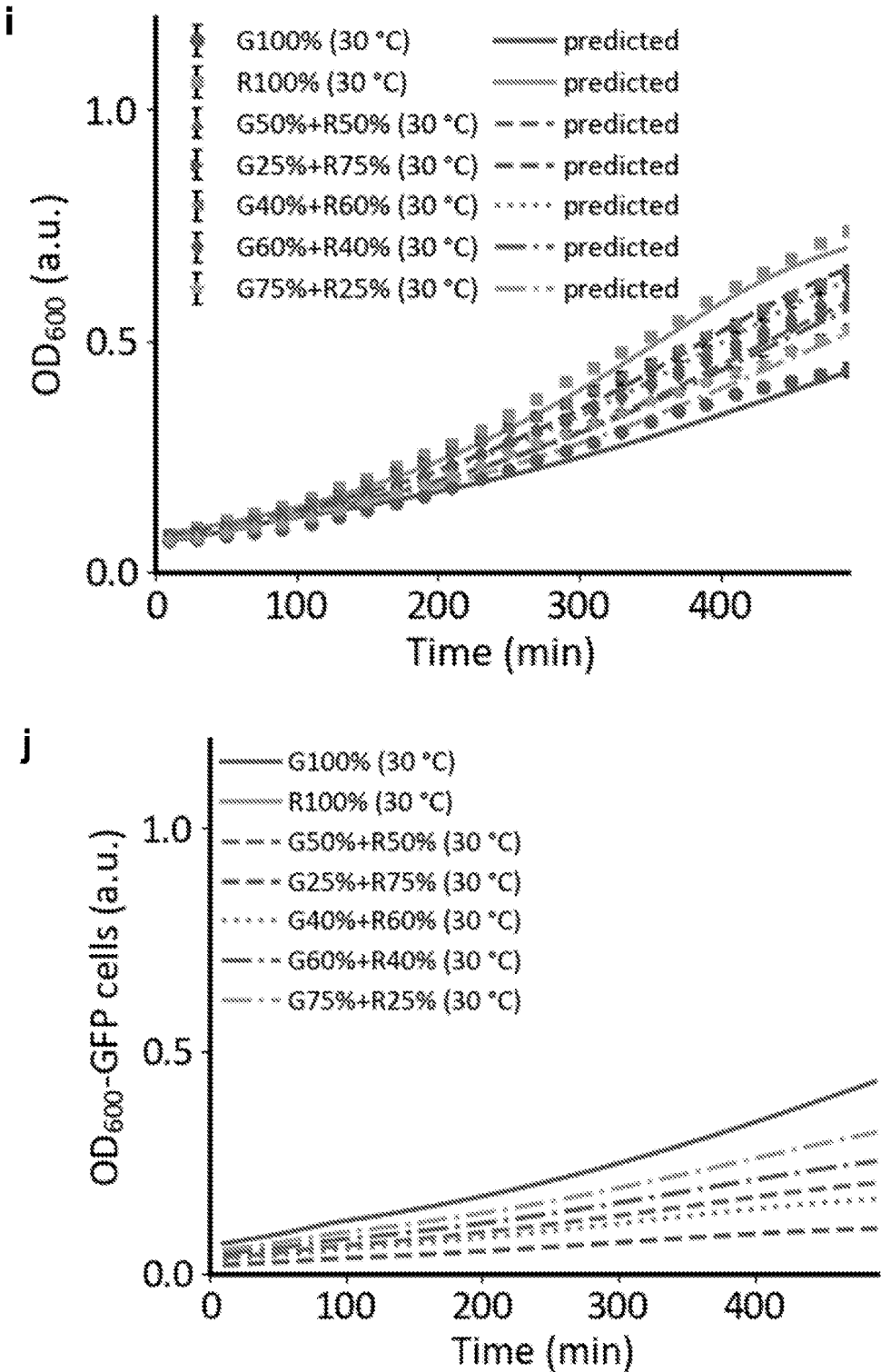


FIGURE 10 (continued)

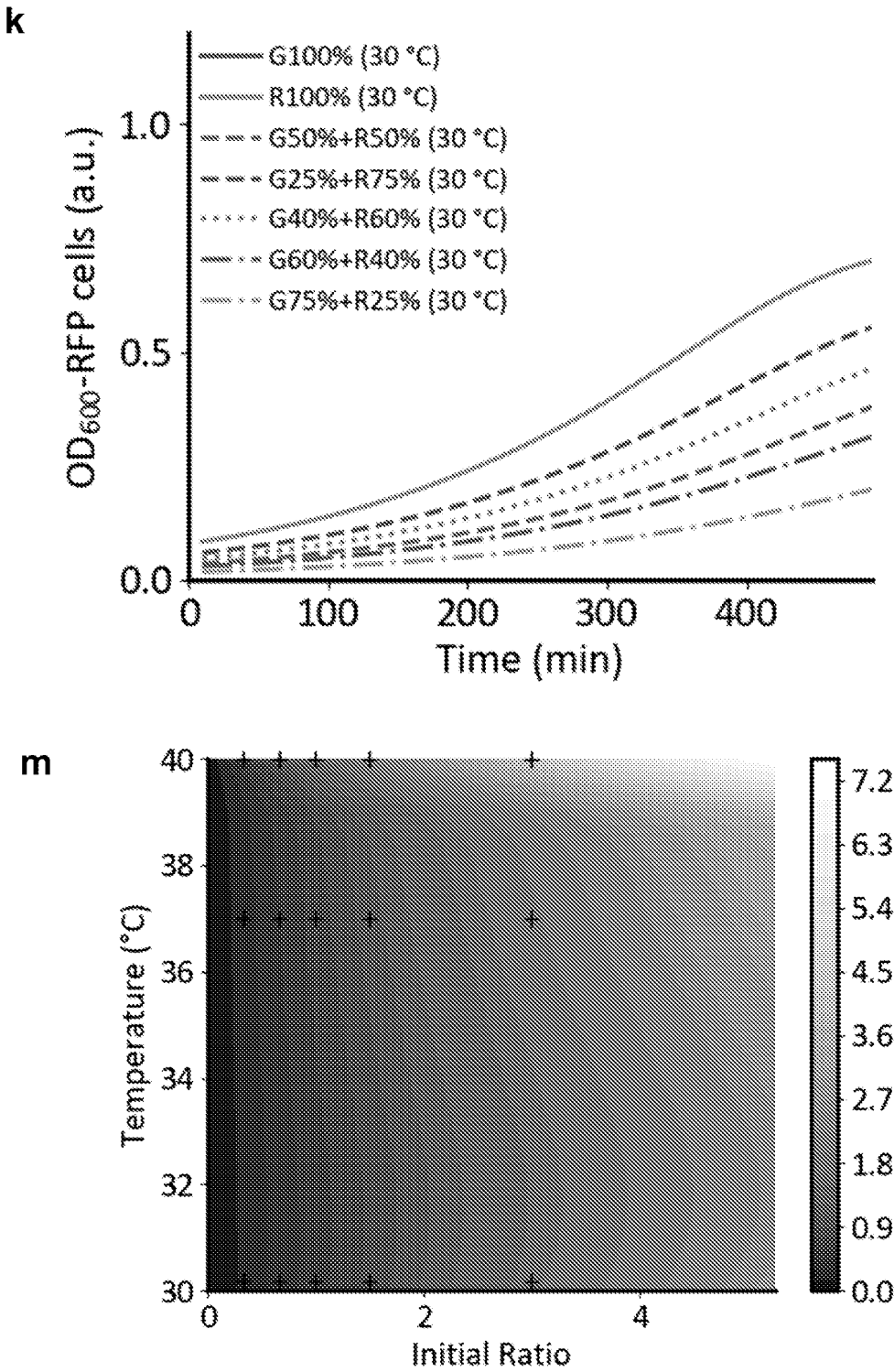


FIGURE 10 (continued)

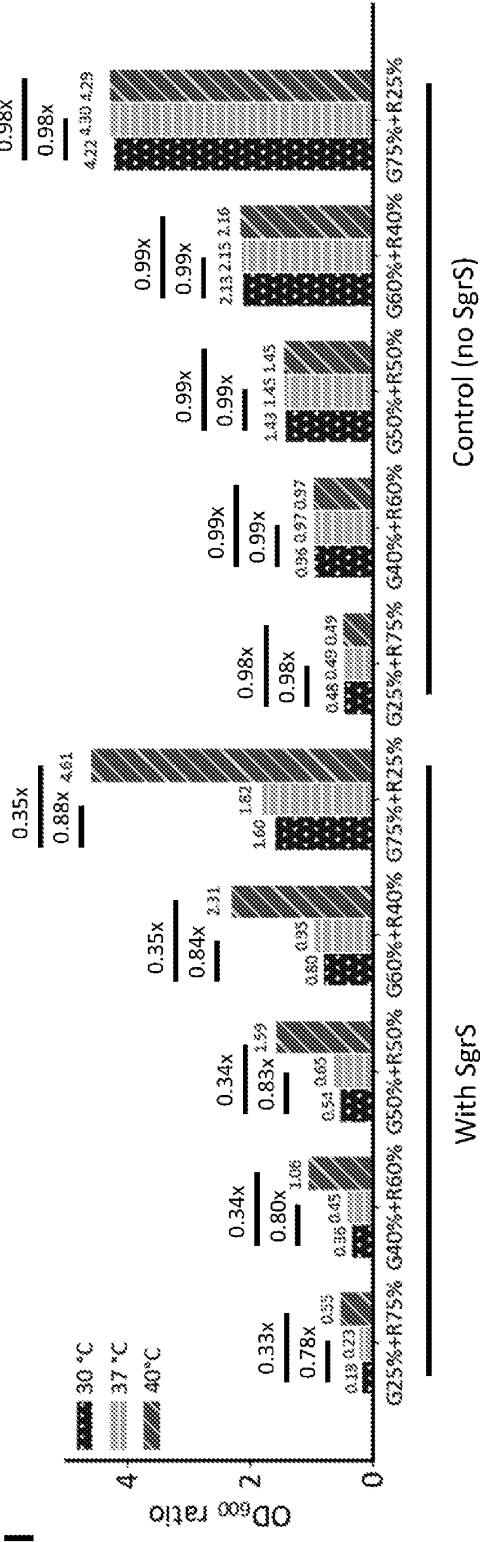


FIGURE 11

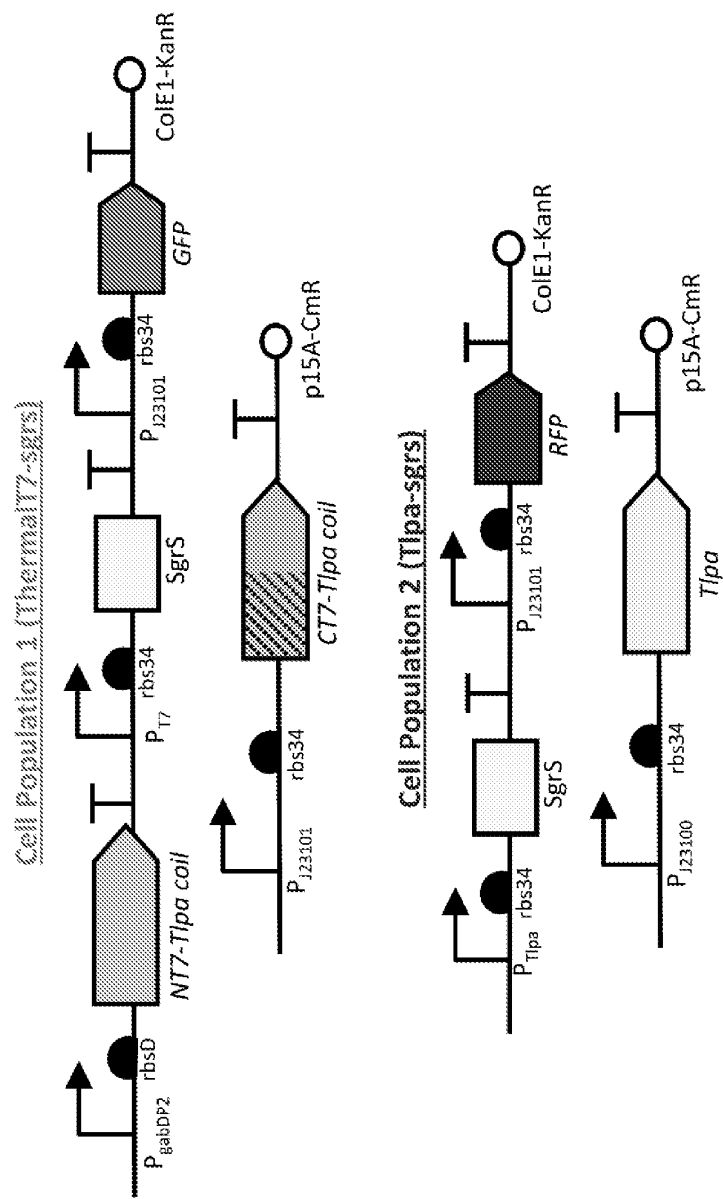


FIGURE 12

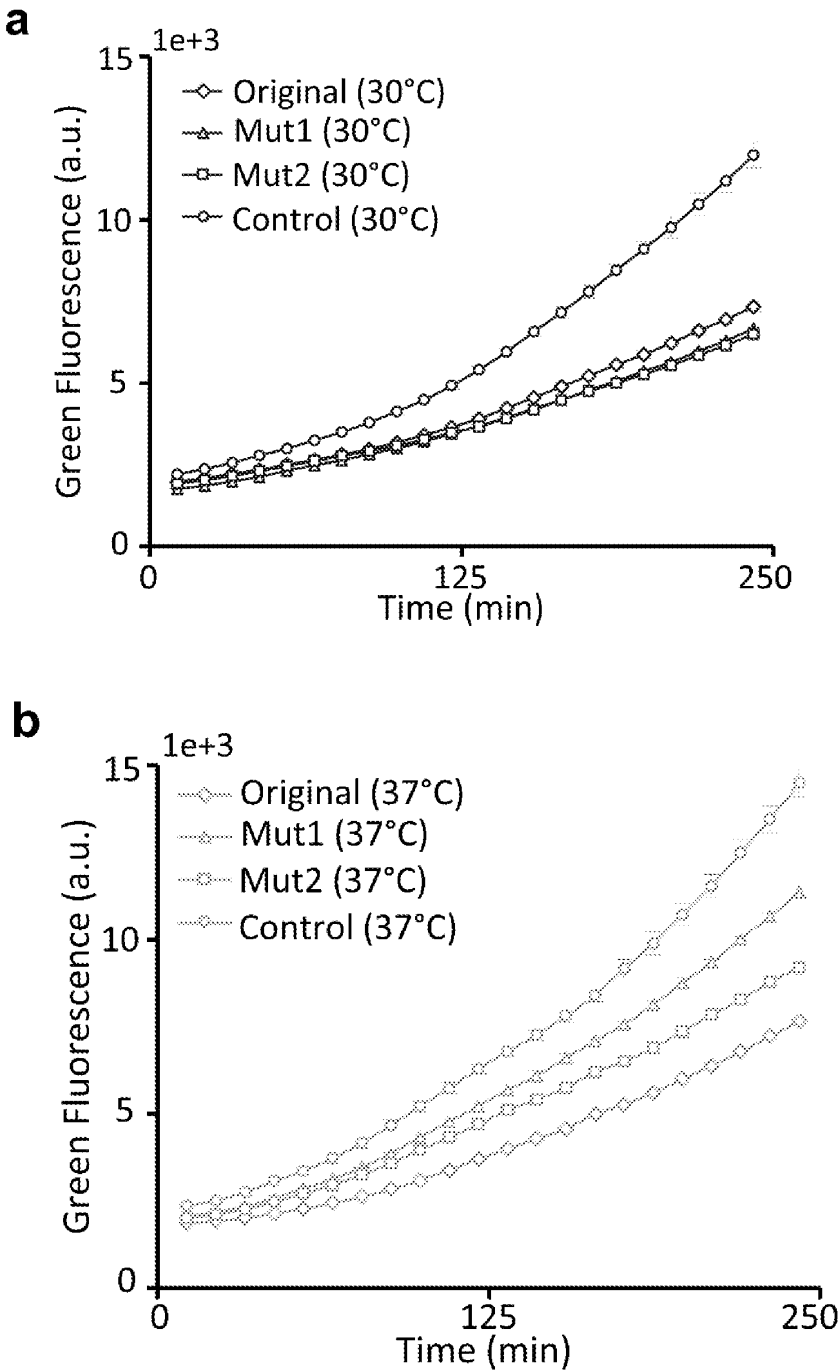


FIGURE 12 (continued)

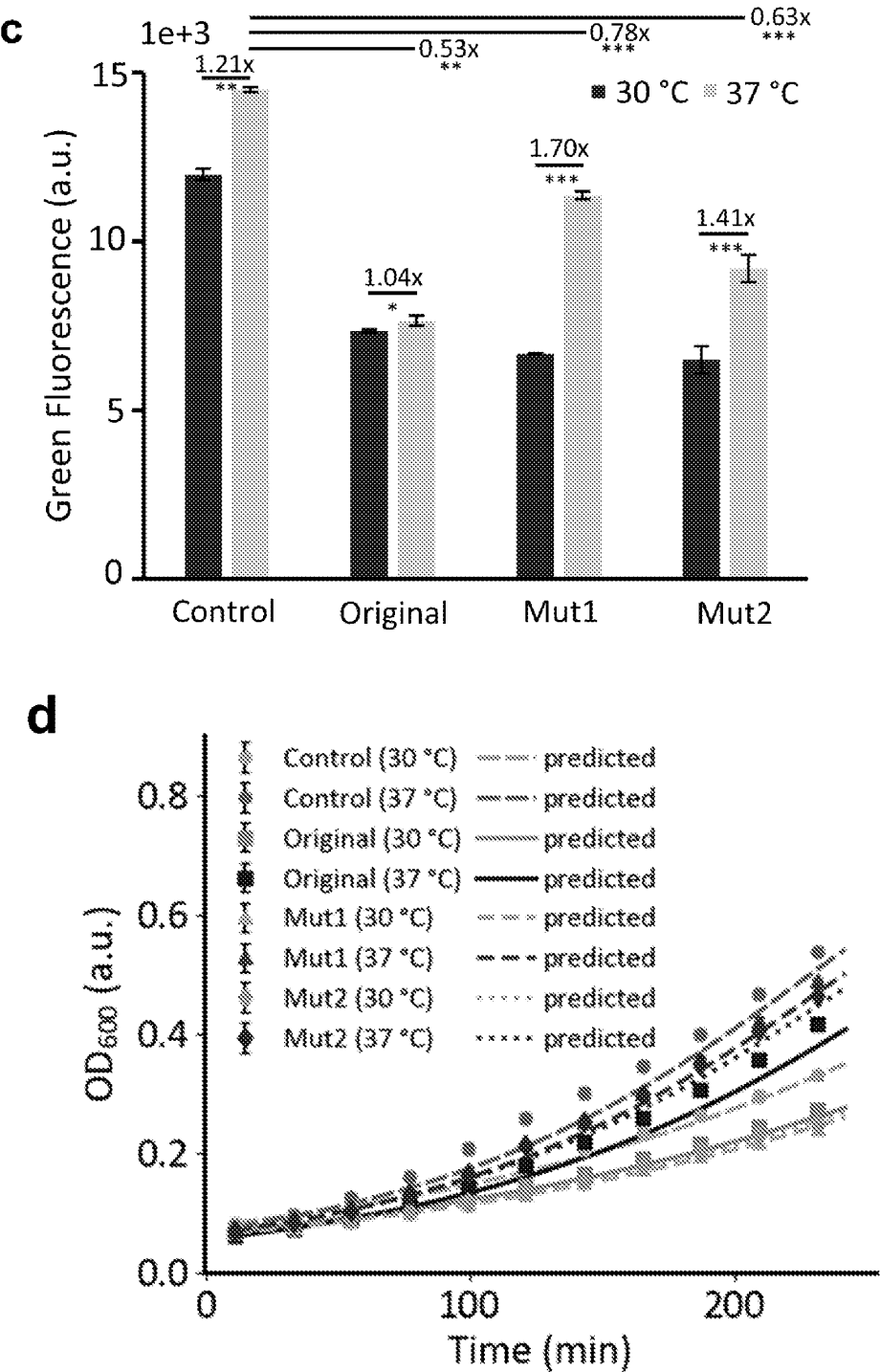


FIGURE 12 (continued)

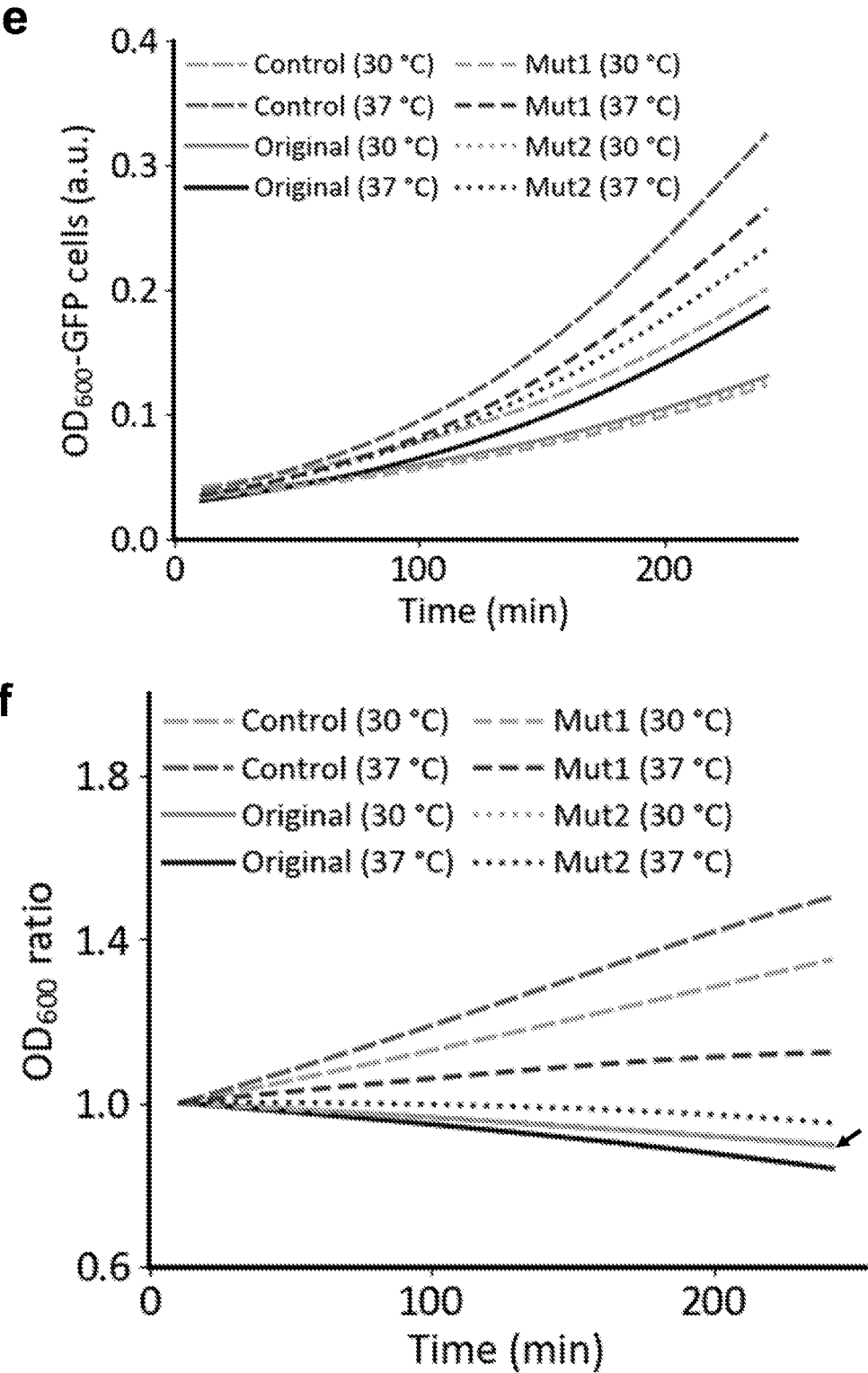


FIGURE 12 (continued)

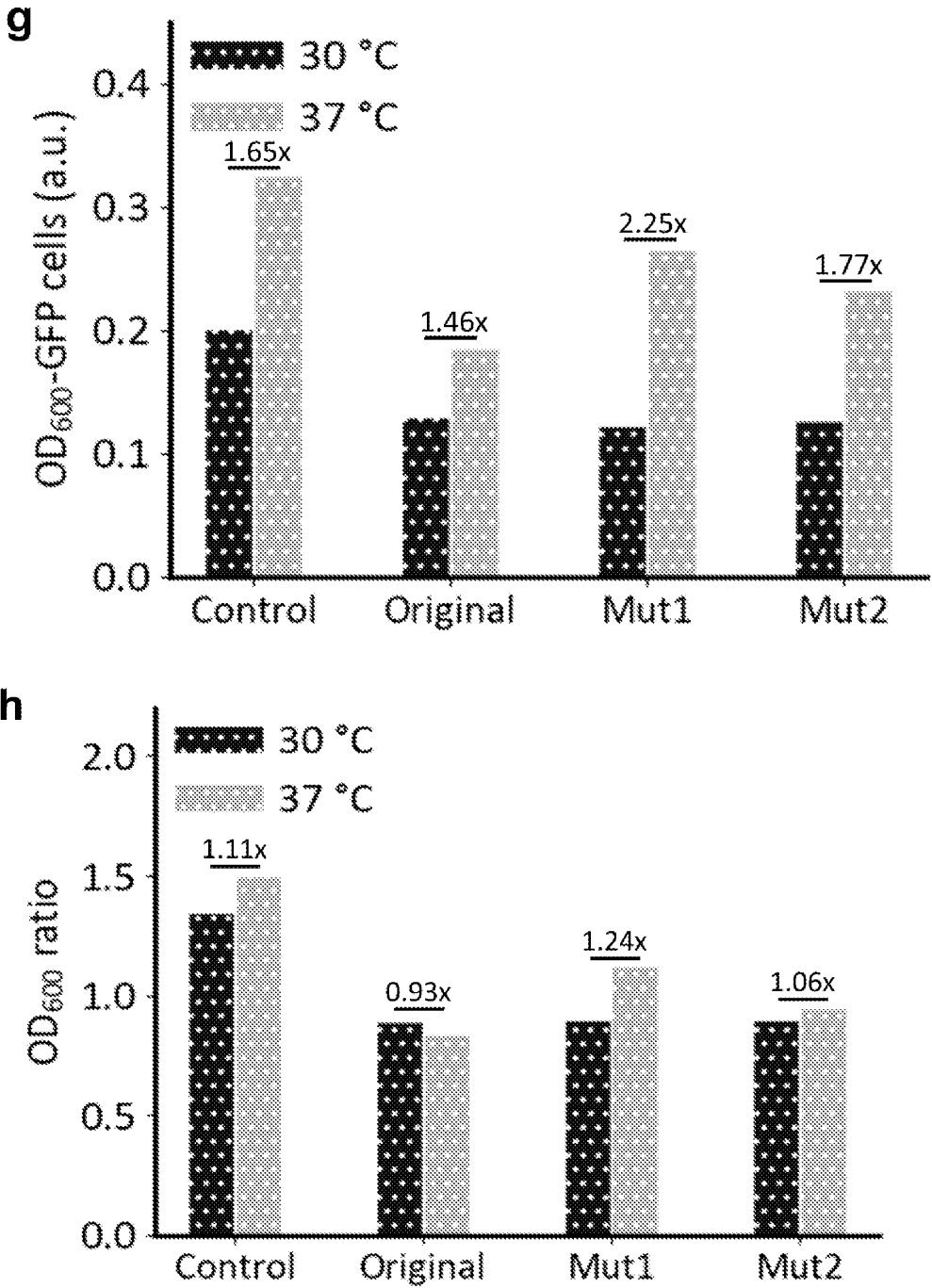


FIGURE 12 (continued)

