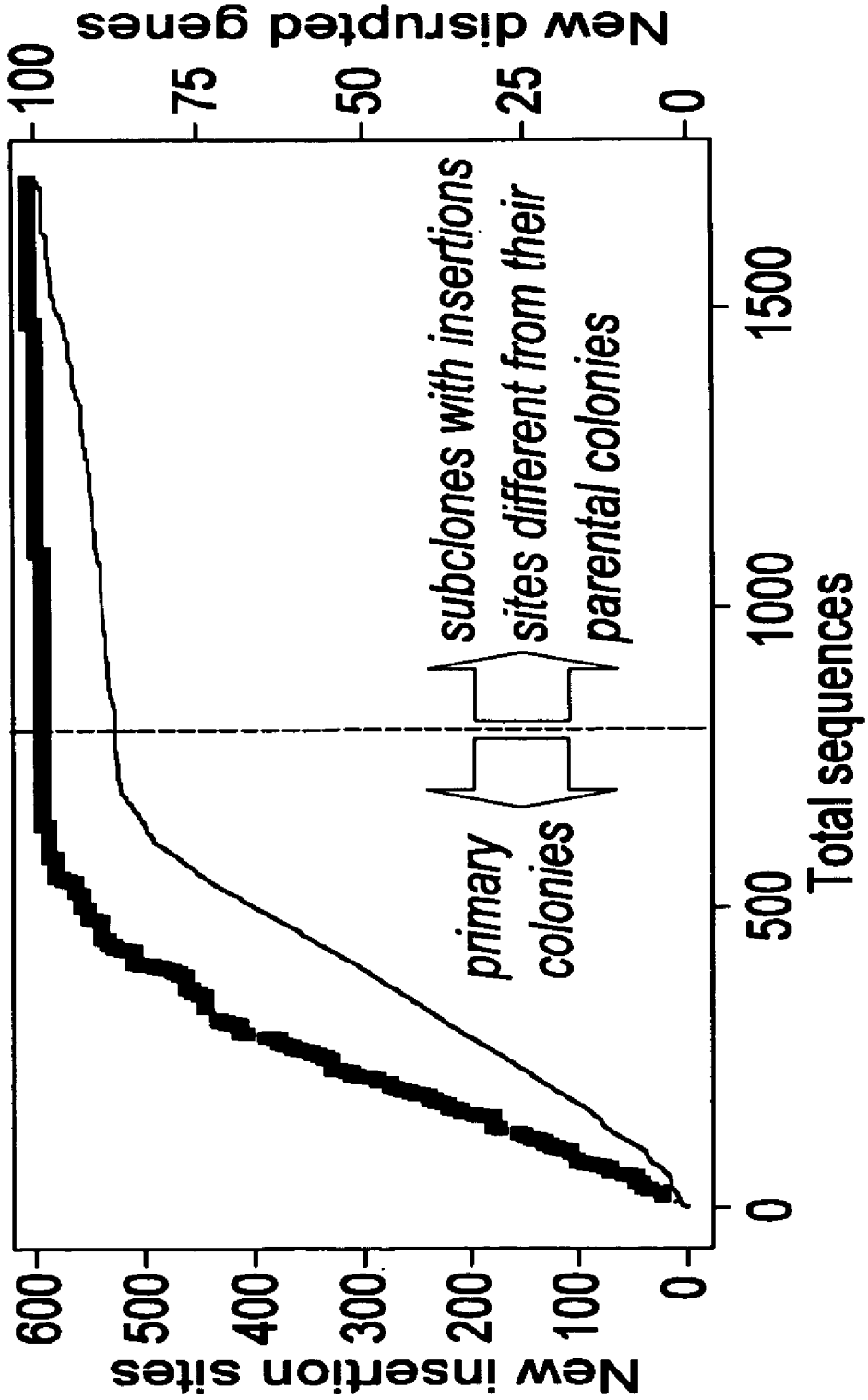
New insertion sites
600
500
400
300
200
100
0
New disrupted genes
100
75
50
25
0
0
500
1000
1500
Total sequences
primary colonies
subclones with insertions sites different from their parental colonies

FIG. 1