

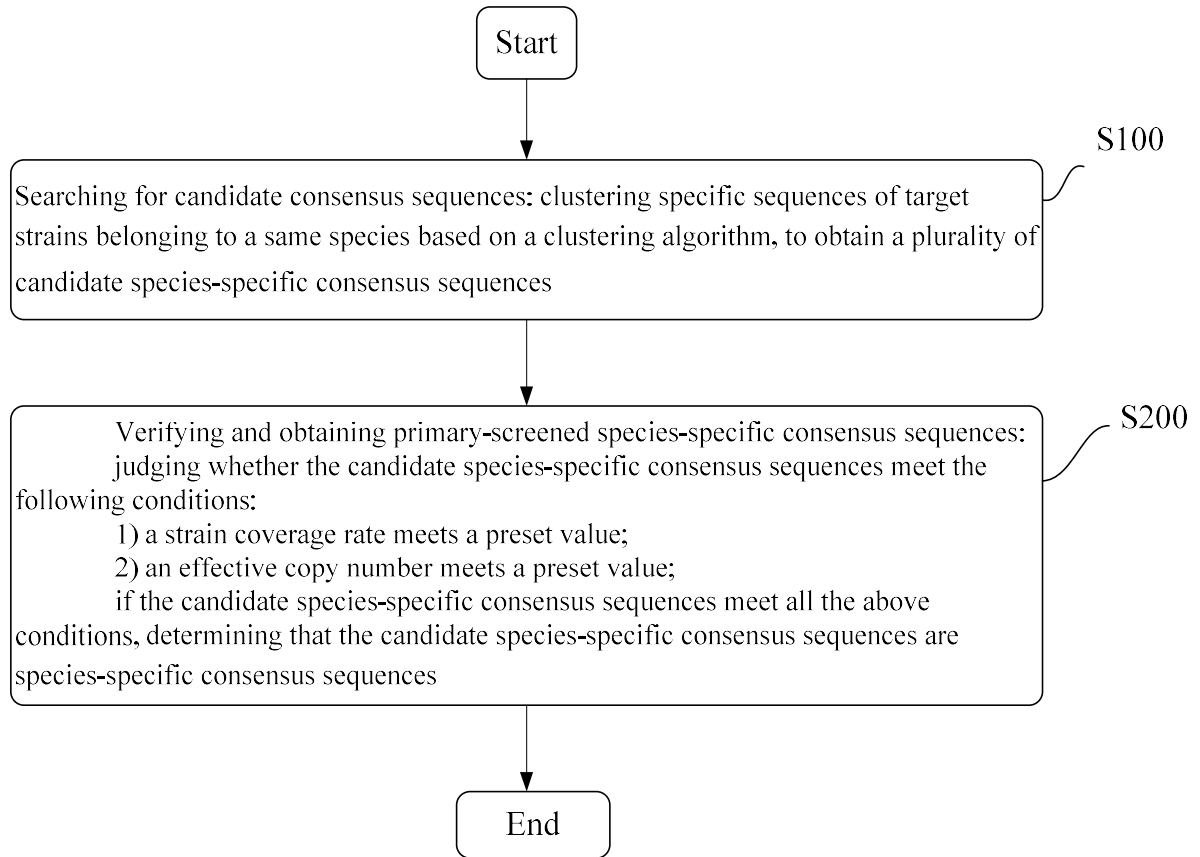


FIG. 1

ClusterID	Distribution	Marker	Percent_of_strains	Weighted_Average_Copy
Cluster43	9(5) *	100.0%[5/5]	9	
Cluster226	7(1) 8(2) 9(2) *	100.0%[5/5]	8.2	
Cluster56	8(5) *	100.0%[5/5]	8	
Cluster36	7(1) 8(3) 9(1) *	100.0%[5/5]	8	
Cluster123	5(1) 8(3) 9(1) *	100.0%[5/5]	7.6	
Cluster5	5(1) 7(1) 8(3) *	100.0%[5/5]	7.2	
Cluster39	6(2) 7(2) 9(1) *	100.0%[5/5]	7	
Cluster194	6(1) 7(3) 8(1) *	100.0%[5/5]	7	
Cluster67	6(2) 7(2) 8(1) *	100.0%[5/5]	6.8	
Cluster10	4(1) 7(2) 8(2) *	100.0%[5/5]	6.8	
Cluster182	3(1) 6(1) 7(2) 8(1) *	100.0%[5/5]	6.2	
Cluster52	4(1) 5(1) 6(1) 7(1) 8(1) *	100.0%[5/5]	6	6
Cluster249	3(1) 6(2) 7(1) 8(1) *	100.0%[5/5]	6	
Cluster47	5(1) 6(4) *	100.0%[5/5]	5.8	
Cluster186	3(1) 5(1) 6(1) 7(1) 8(1) *	100.0%[5/5]	5.8	5.8
Cluster217	3(1) 5(2) 6(1) 7(1) *	100.0%[5/5]	5.2	
Cluster64	3(1) 4(1) 6(3) *	100.0%[5/5]	5	
Cluster94	1(1) 2(1) 5(1) 8(2) *	100.0%[5/5]	4.8	
Cluster214	1(1) 3(1) 6(2) 8(1) *	100.0%[5/5]	4.8	
Cluster148	2(1) 4(1) 5(2) 7(1) *	100.0%[5/5]	4.6	
Cluster93	1(1) 3(1) 5(2) 8(1) *	100.0%[5/5]	4.4	
Cluster234	0(1) 3(1) 6(2) 7(1) *	80.0%[4/5]	4.4	
Cluster66	3(1) 4(2) 5(2) *	100.0%[5/5]	4.2	
Cluster252	1(1) 4(1) 5(2) 6(1) *	100.0%[5/5]	4.2	
Cluster24	3(2) 4(1) 5(1) 6(1) *	100.0%[5/5]	4.2	
Cluster114	0(1) 3(1) 4(1) 7(2) *	80.0%[4/5]	4.2	
Cluster203	0(1) 3(1) 5(2) 7(1) *	80.0%[4/5]	4	
Cluster62	2(1) 3(1) 4(1) 5(2) *	100.0%[5/5]	3.8	
Cluster46	2(1) 3(1) 4(1) 5(2) *	100.0%[5/5]	3.8	
Cluster32	3(1) 4(4) *	100.0%[5/5]	3.8	
Cluster235	1(1) 3(1) 5(3) *	100.0%[5/5]	3.8	
Cluster205	3(1) 4(4) *	100.0%[5/5]	3.8	
Cluster201	1(1) 3(1) 4(1) 5(1) 6(1) *	100.0%[5/5]	3.8	3.8
Cluster107	1(1) 4(2) 5(2) *	100.0%[5/5]	3.8	
Cluster2	1(1) 3(1) 4(2) 6(1) *	100.0%[5/5]	3.6	
Cluster141	0(1) 3(1) 4(2) 7(1) *	80.0%[4/5]	3.6	
Cluster87	2(2) 3(1) 5(2) *	100.0%[5/5]	3.4	
Cluster72	3(3) 4(2) *	100.0%[5/5]	3.4	
Cluster246	3(3) 4(2) *	100.0%[5/5]	3.4	

FIG. 1-1



FIG. 1-2

Sequence 1	Sequence 2	Sequence matching rate	Alignment length	Mismatch length	Length of gap openings	Starting value of sequence 1	End value of sequence 1	Starting value of sequence 2	End value of sequence 2	e value	Score
Query id	Subject id	% identity	alignment length	mismatches	gap openings	q. start	q. end	s. start	s. end	e-value	bit score
A	B	98.4	187	3	0	1	187	1170	1356	1.90E-98	356
Sequence coverage rate = (alignment length / end value of sequence 1 - starting value of sequence 1 + 1)											
Similarity = sequence coverage rate * sequence matching rate											

FIG. 1-3

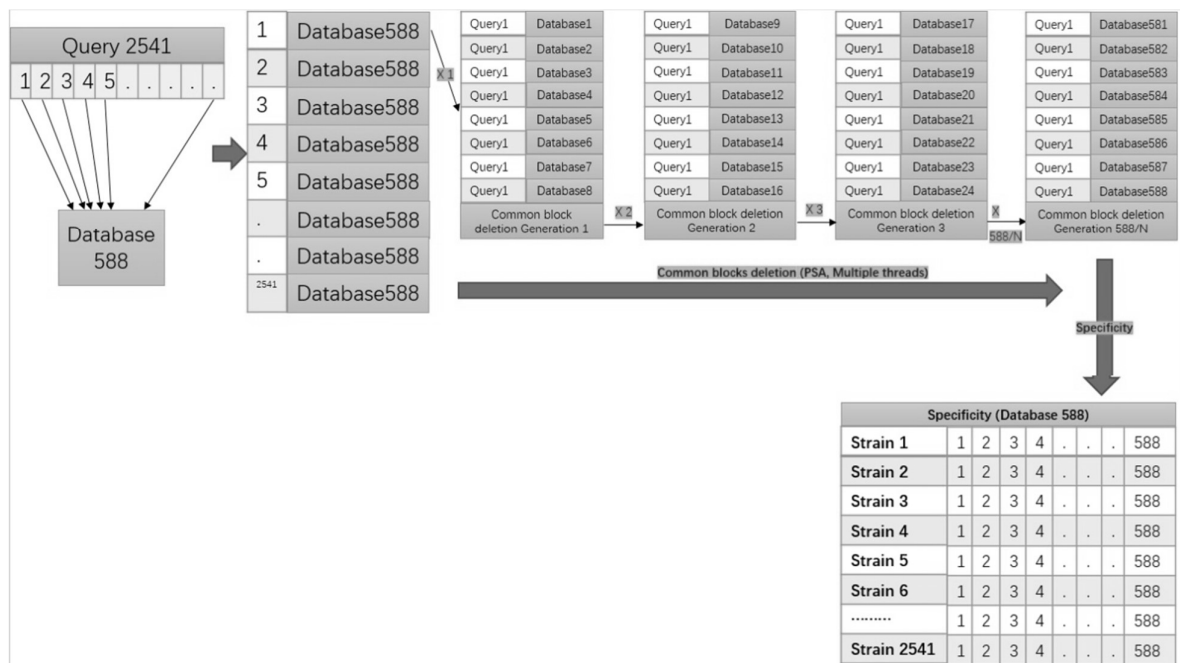


FIG. 1-4

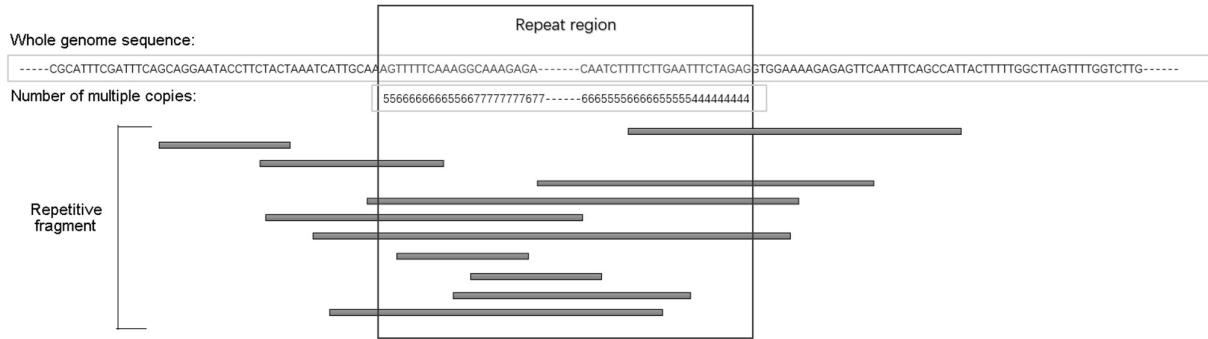


FIG. 1-5

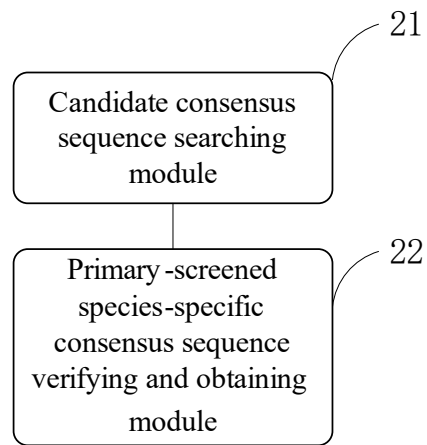


FIG. 2

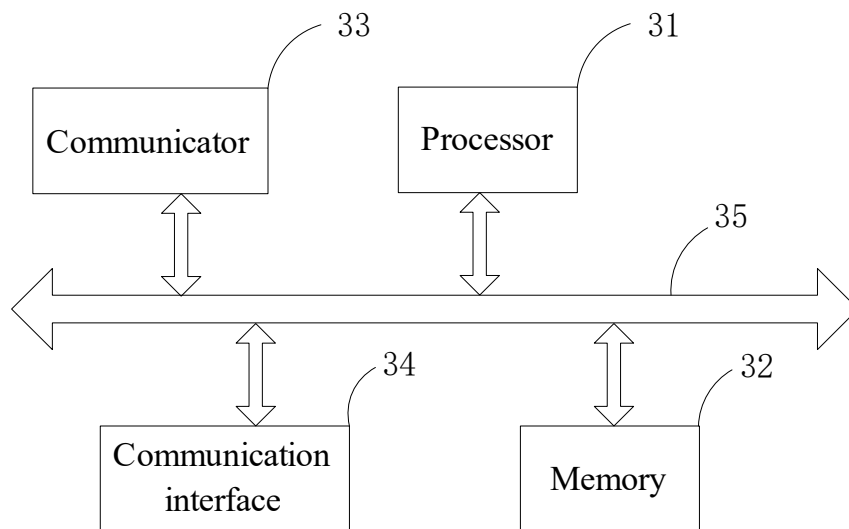


FIG. 3