

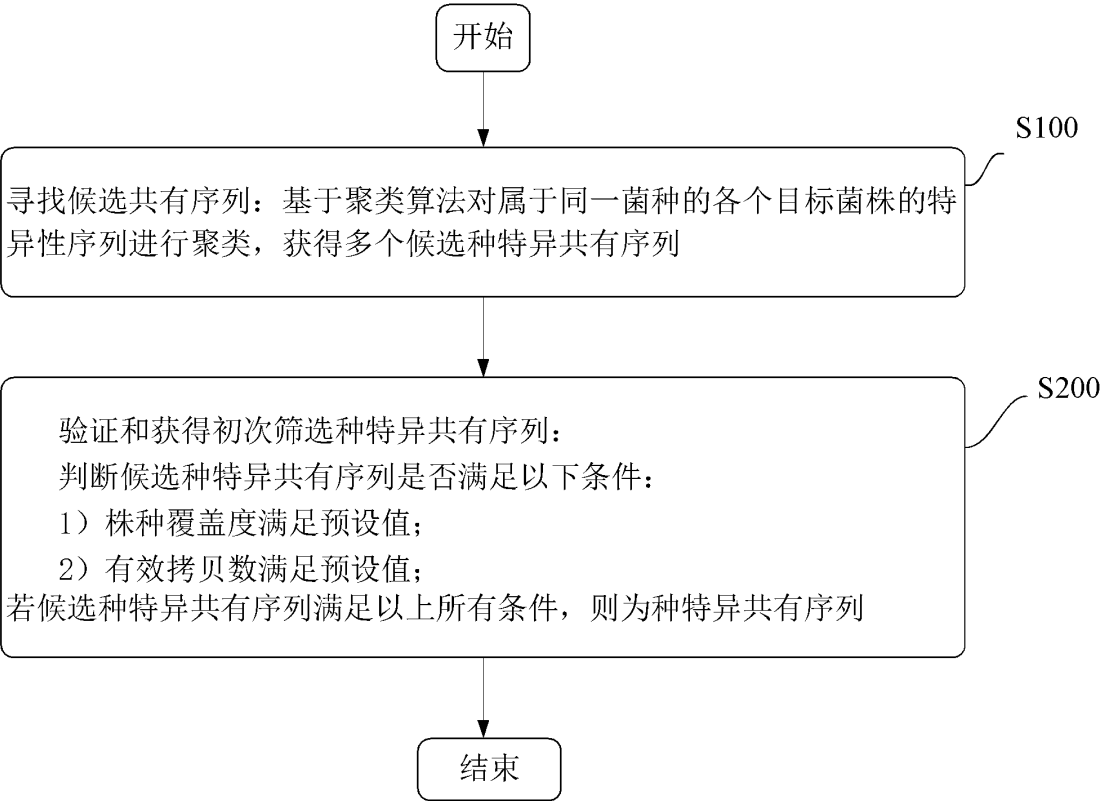


图 1

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
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
Cluster106	3(1) 5(1) 6(1) 7(1) 8(1)	*	100.0%[5/5]	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
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

图 1-1

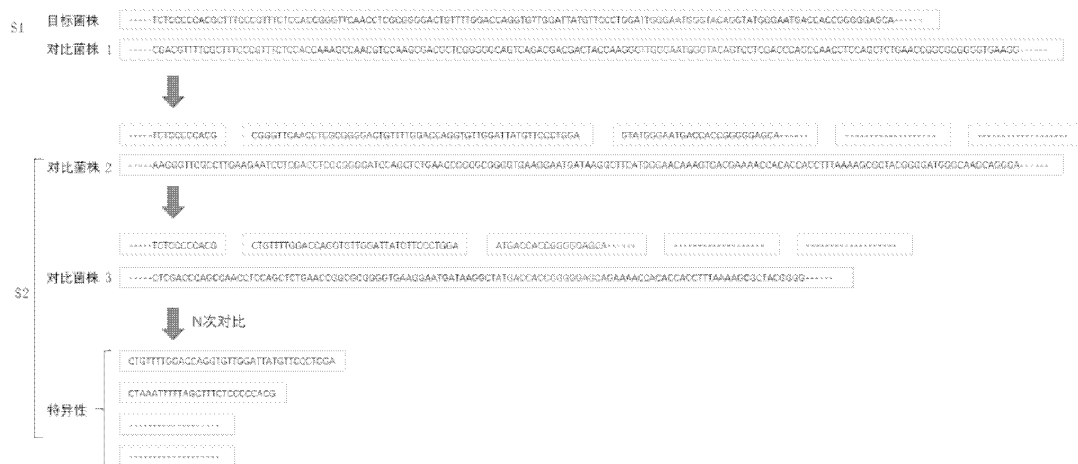


图 1-2

序列1	序列2	序列匹配率	比对长度	错配长度	缺口长度	序列1起始值	序列1末端值	序列2起始值	序列2末端值	e值	打分
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
序列覆盖率= (比对长度/ (序列1末端值-序列1起始值+1)) 相位性= 序列覆盖率*序列匹配率											

图 1-3

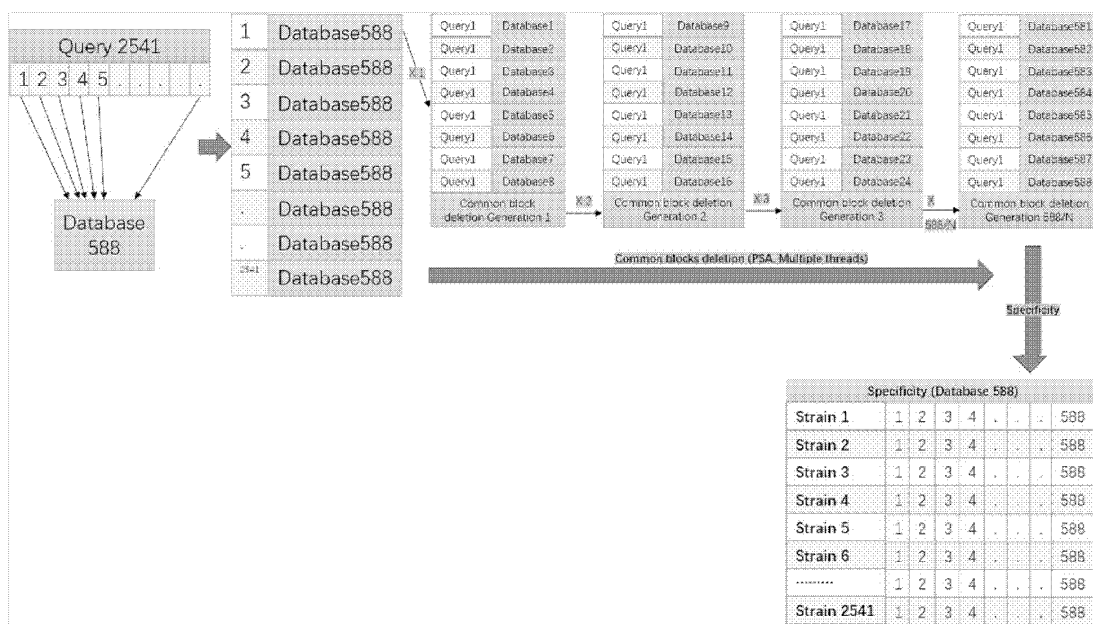


图 1-4

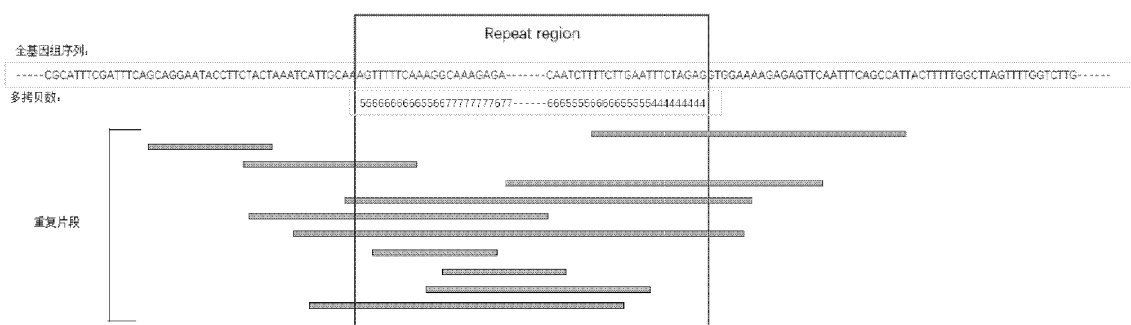


图 1-5

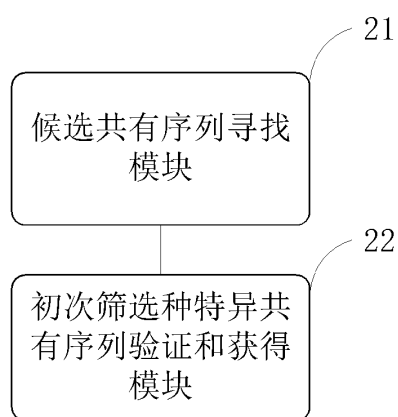


图 2

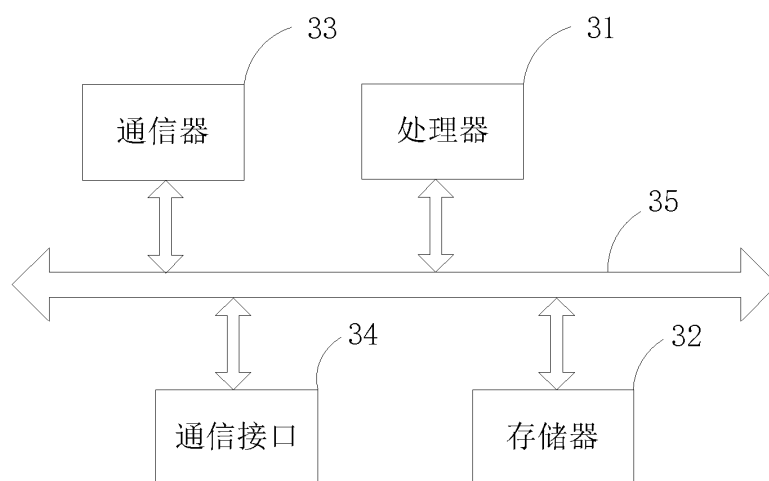


图 3