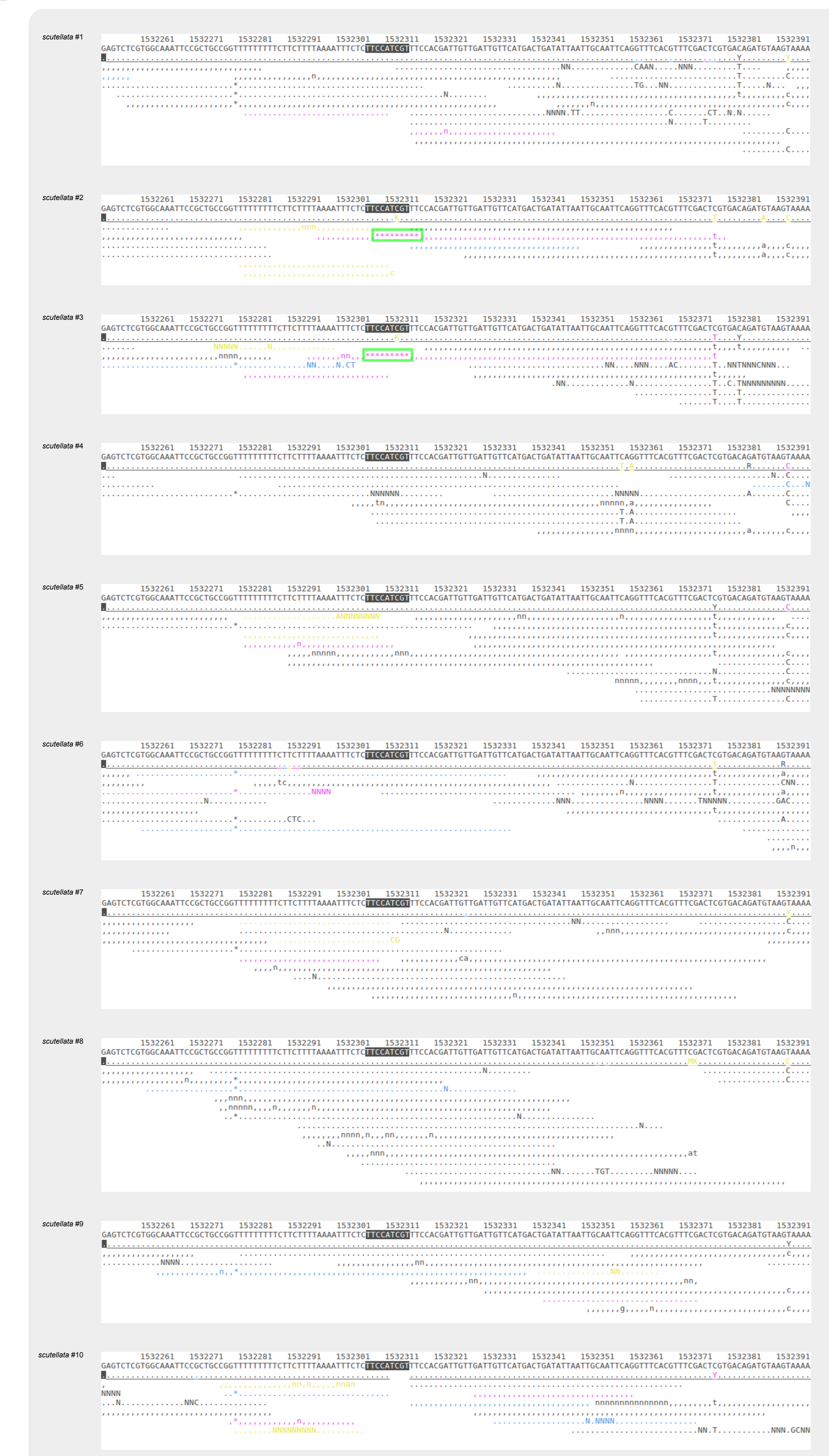
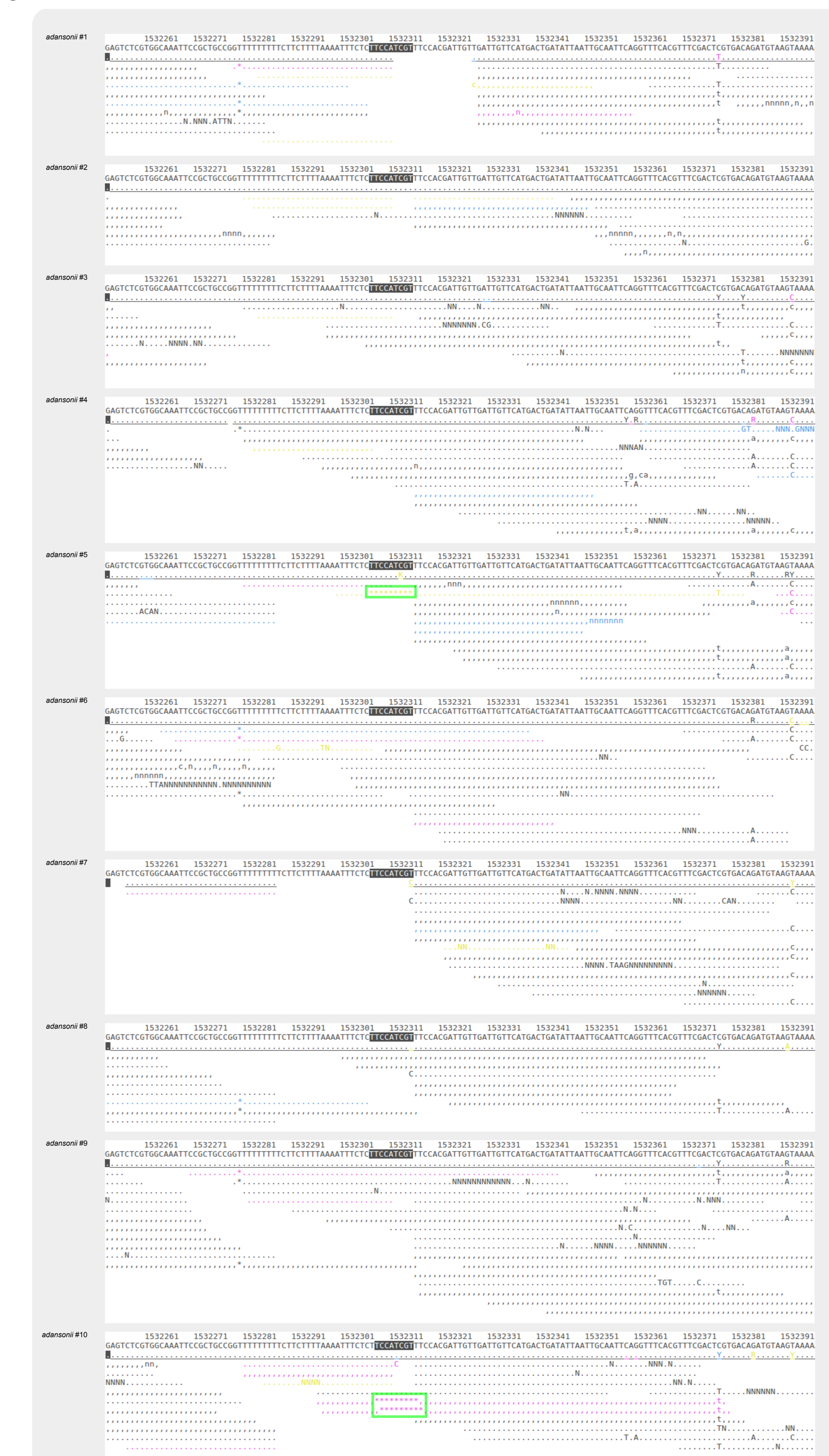


A**B****C****D**

| Subspecies | Sample | Deletion evidence | Putative genotype (D=deletion, d=no deletion) |
|----------------------|--------|--------------------------------|---|
| <i>capensis</i> | 1 | well mapped reads w/o deletion | d |
| | 2 | no mapped reads | D |
| | 3 | no mapped reads | D |
| | 4 | alignment gap | D |
| | 5 | alignment gap | D |
| | 6 | well mapped reads w/o deletion | d |
| | 7 | well mapped reads w/o deletion | d |
| | 8 | well mapped reads w/o deletion | d |
| | 9 | well mapped reads w/o deletion | d |
| | 10 | well mapped reads w/o deletion | d |
| <i>scutellata</i> | 1 | well mapped reads w/o deletion | d |
| | 2 | alignment gap | D |
| | 3 | alignment gap | D |
| | 4 | well mapped reads w/o deletion | d |
| | 5 | well mapped reads w/o deletion | d |
| | 6 | well mapped reads w/o deletion | d |
| | 7 | well mapped reads w/o deletion | d |
| | 8 | well mapped reads w/o deletion | d |
| | 9 | well mapped reads w/o deletion | d |
| | 10 | no mapped reads | D |
| <i>adansonii</i> | 1 | no mapped reads | D |
| | 2 | well mapped reads w/o deletion | d |
| | 3 | well mapped reads w/o deletion | d |
| | 4 | well mapped reads w/o deletion | d |
| | 5 | alignment gap | D |
| | 6 | well mapped reads w/o deletion | d |
| | 7 | no mapped reads | D |
| | 8 | well mapped reads w/o deletion | d |
| | 9 | well mapped reads w/o deletion | d |
| | 10 | alignment gap | D |
| Population frequency | | | 40% |
| Population frequency | | | 30% |
| Population frequency | | | 40% |