|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **M8** | **Gene name** | **Region** | **Selected Sites** | **Pr (w>1)** | **Number of Sites** |
| BEB | *psbA* | LSC | 445 N, 556 N, 707 N, 861 F | 0.983\*, 0.985\*, 0.983\*, 0.986\* | 4 |
| *psbK* | LSC | 3095 W | 0.988\* | 1 |
| *atpA* | LSC | 4289 Q | 0.984\* | 1 |
| *rpoC2* | LSC | 9581 A, 9639 V, 9778 I, 9799 M, 9803 I, 9991 E, 9997 A, 10127 Q, 10143 N, 10503 K, 10504 M, 10505 I, 10639 K | 0.984\*, 0.984\*, 1.000\*\*, 0.986\*, 0.985\*, 0.987\*, 0.987\*, 0.987\*, 0.983\*, 0.985\*, 1.000\*\*, 0.984\*, 0.984\* | 13 |
| *rpoC1* | LSC | 11841 R, 12162 E | 0.985\*, 0.985\* | 2 |
| *rpoB* | LSC | 13888 M, 13889 K, 13890 E, 13891 L, 13893 N, 13894 V, 14259 T, 14268 I, 14323 S, 15159 K, 15283 G | 0.988\*, 0.983\*, 1.000\*\*, 0.987\*, 1.000\*\*, 1.000\*\*, 0.985\*, 0.983\*, 1.000\*\*, 0.984\*, 0.987\* | 11 |
| *psbD* | LSC | 16748 K, 16857 Q | 0.984\*, 0.988\* | 2 |
| *psbC* | LSC | 18626 F | 0.983\* | 1 |
| *psbZ* | LSC | 19201 L, 19227 F | 0.988\*, 0.984\* | 2 |
| *psaB* | LSC | 20234 A, 21317 Y, 21363 K, 21496 F, 21573 Q, 21577 L, 21818 K | 0.987\*, 0.985\*, 0.984\*, 0.984\*, 0.986\*, 0.987\*, 0.984\* | 7 |
| *psaA* |  | 21903 R, 21936 I, 21940 I, 22436 P, 22439 Q, 22441 N, 22442 L, 22444 F, 22516 Q, 22707 Y, 23578 K, 23702 G | 0.999\*\*, 0.985\*, 0.984\*, 0.986\*, 0.986\*, 0.999\*\*, 1.000\*\*, 0.985\*, 1.000\*\*, 0.984\*, 0.984\*, 0.987\* | 12 |
| *rps4* |  | 25167 K | 0.984\* | 1 |
| *ndhJ* |  | 25276 Q | 0.988\* | 1 |
|  | *ndhK* |  | 26215 F, 26219 L , 26220 T | 0.999\*\*, 0.964\*, 0.996\*\* | 3 |

**Table S11. Positive selected sites detected in the cp genome of *Polygonatum* + *Heteropolygonatum***

\*: P>95%; \*\*: P>99%)