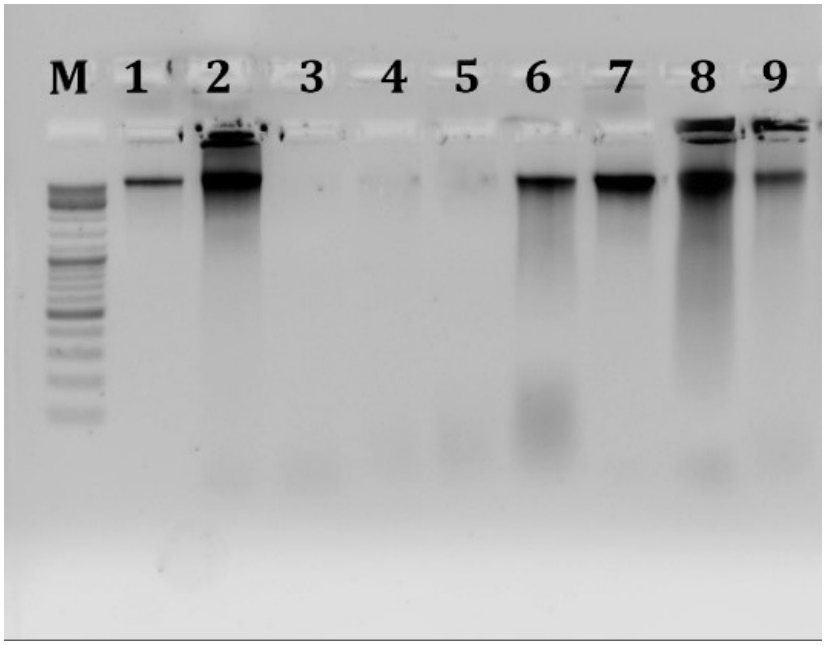
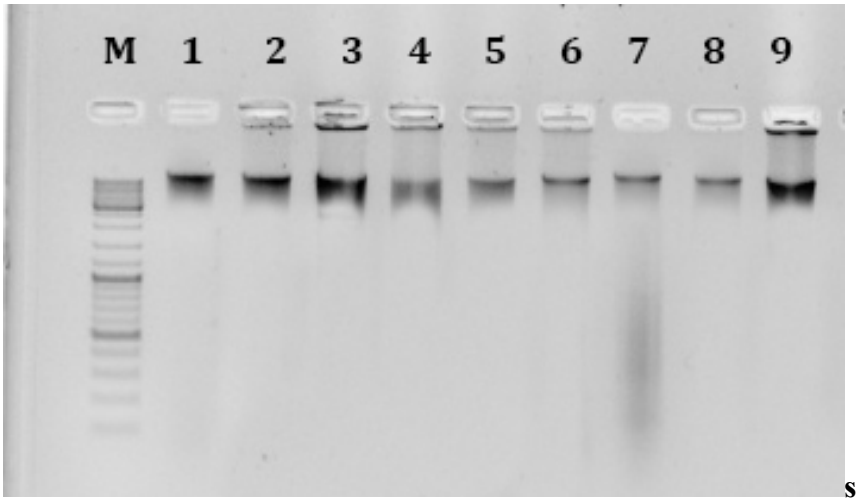


A



s

B

Figure S1. Genomic profile of *Rheum* sp. extracted using CTAB method (A) and with addition of Na2SO3 (1%) and PVP (B)

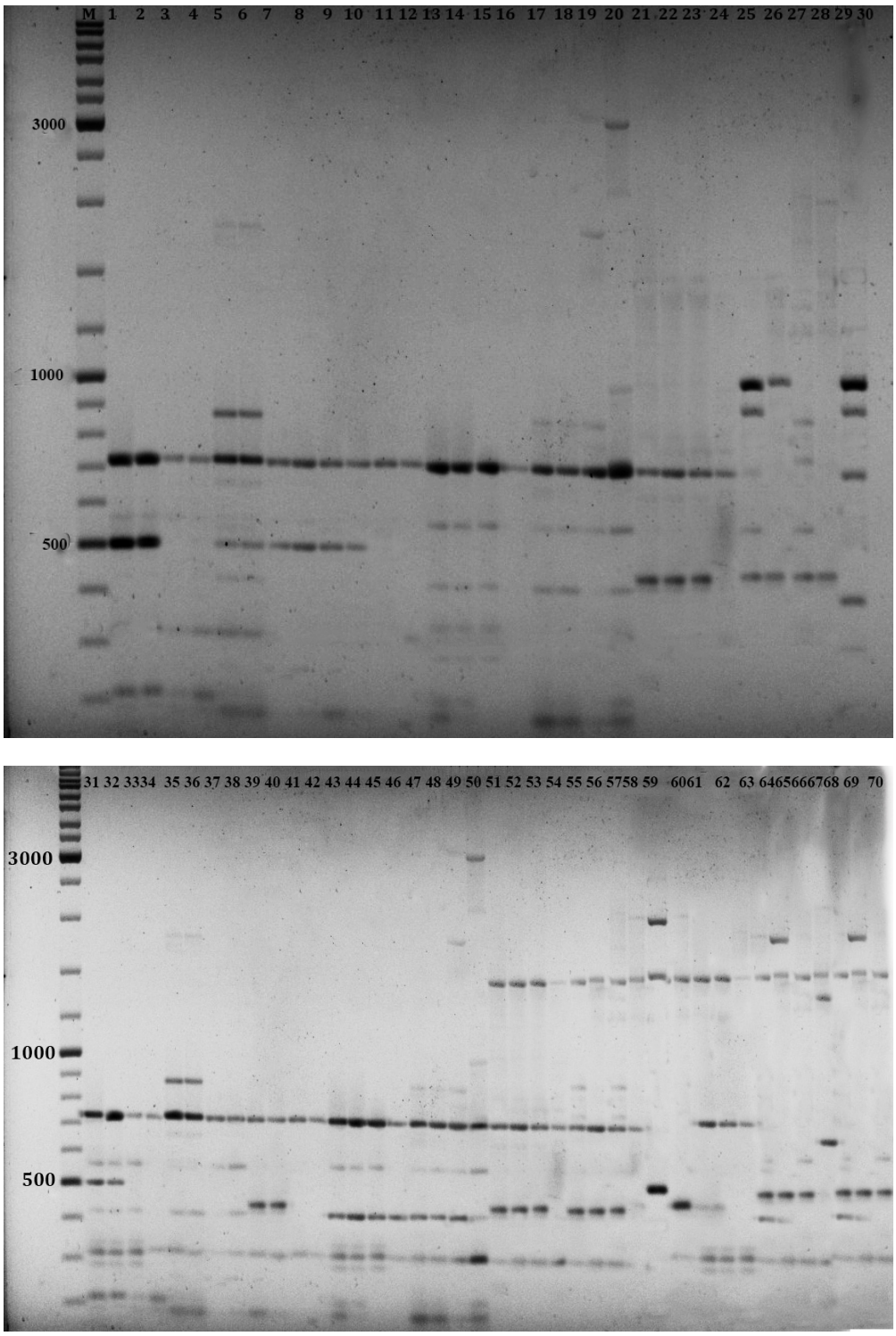
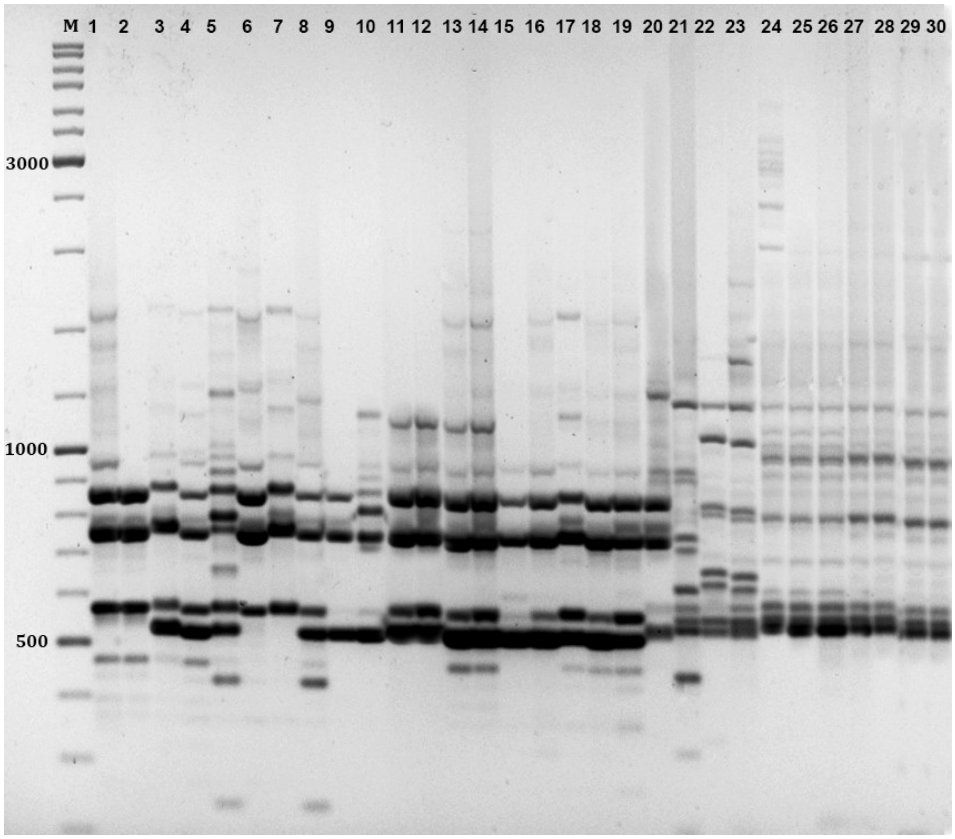


Figure S2. Electropherogram of the results of amplification of individual DNA samples from 70 samples of 7 populations of *Rheum* sp. with primer 2221



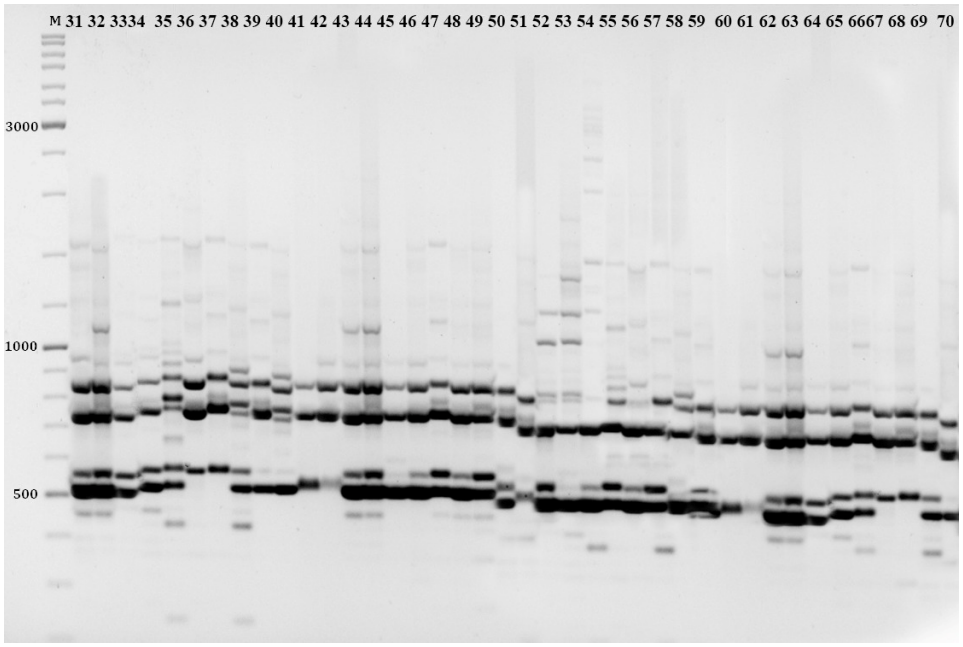


Figure S3. Electropherogram of the results of amplification of individual DNA samples from 70 samples of 7 populations of *Rheum* sp. with primer 2230

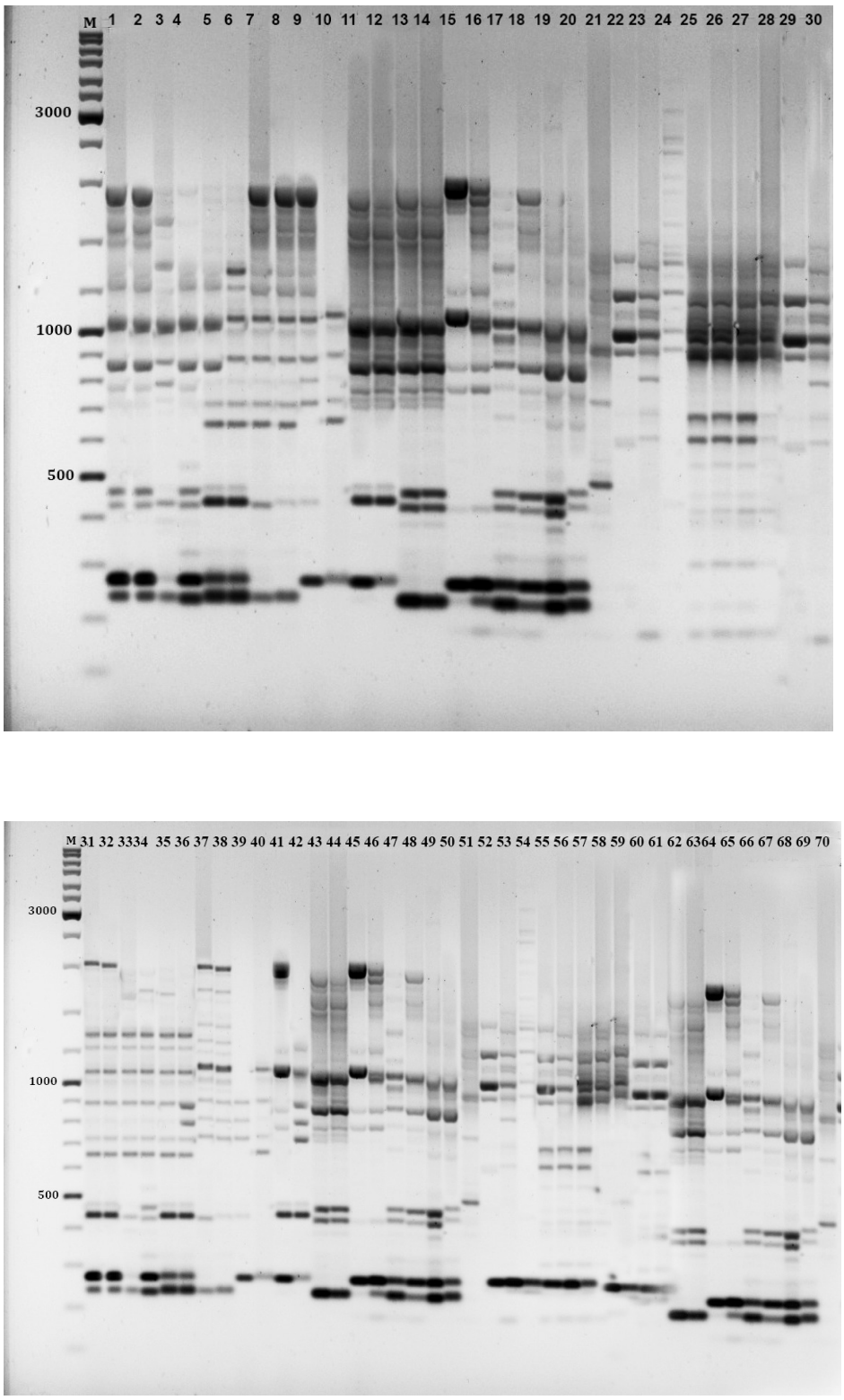


Figure S4. Electropherogram of the results of amplification of individual DNA samples from 70 samples of 7 populations of *Rheum* sp. with primer 2232

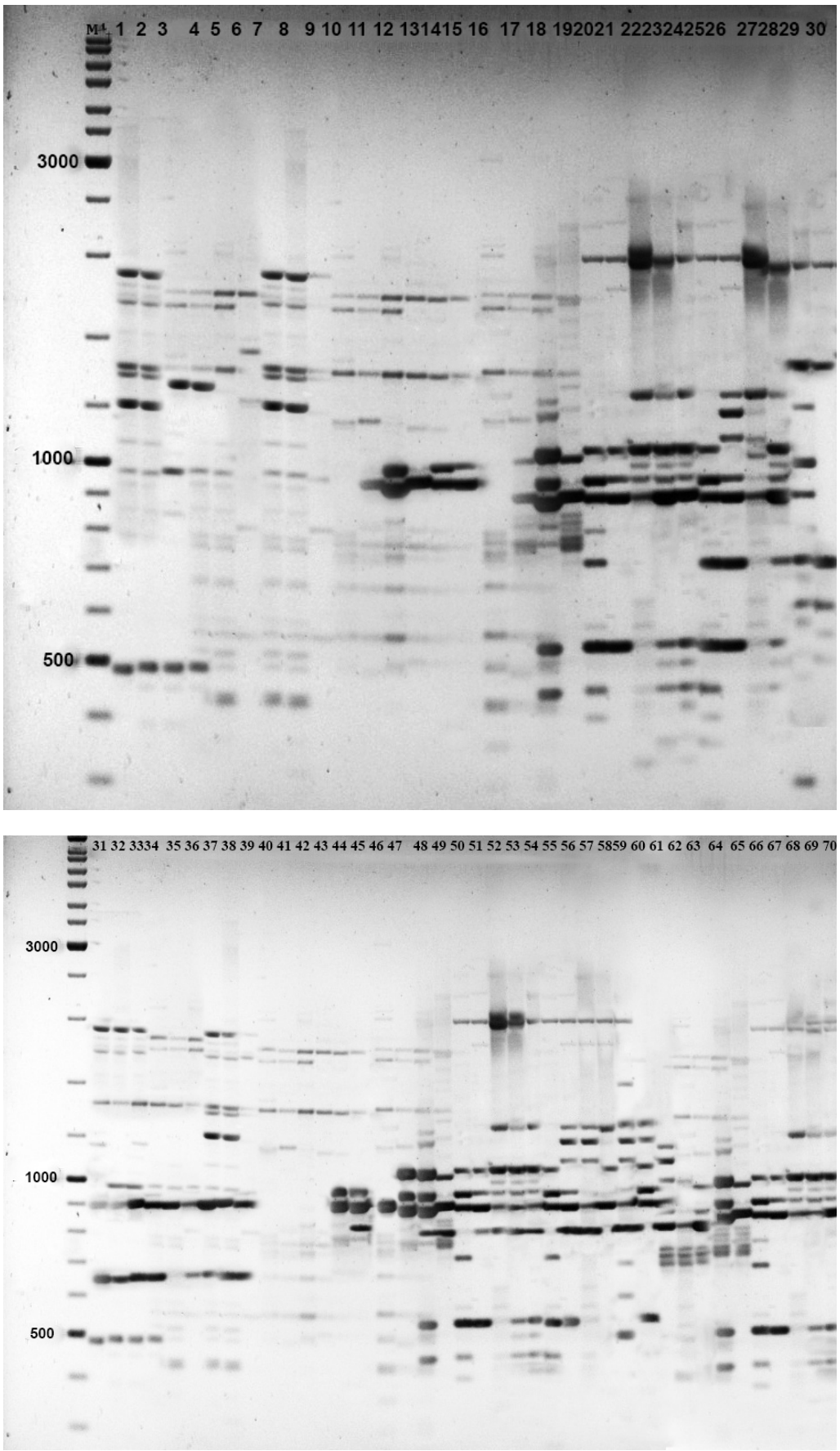


Figure S5. Electropherogram of the results of amplification of individual DNA samples from 70 samples of 7 populations of *Rheum* sp. with primer 2240

```
# File generated at 2025-07-18 11:47:31 CST
# Generated by StructureSelector
# http://lmme.qdio.ac.cn/StructureSelector/
# https://lmme.ac.cn/StructureSelector/
# Contact: Yulong Li <liyulong12@mails.ucas.ac.cn>
# Citation: Li YL, Liu JX (2018) StructureSelector: A web based software
to select and visualize the optimal number of
# clusters using multiple methods.Molecular Ecology Resources, 18:176-
177.
#
# Evanno method:
# Citation:
# Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters
of individuals using the software structure:
# a simulation study. Molecular Ecology, 14: 2611-2620.
# K    Reps    Mean LnP(K)    Stdev LnP(K)    Ln'(K)    |Ln''(K)|
Delta K
1     10    -2671.590000.50211    NA    NA    NA
2     10    -1941.260000.34383    730.33000   572.25000   1664.31774
3     10    -1783.180009.78841    158.08000   3.70000    0.37800
4     10    -1628.8000031.00642   154.38000   1.86000    0.05999
5     10    -1472.5600018.08795   156.24000   140.05000   7.74273
6     10    -1456.37000290.44048  16.19000    142.44000   0.49043
7     10    -1297.7400091.44260   158.63000   127.42000   1.39344
8     10    -1266.53000226.74166  31.21000    74.76000    0.32971
9     10    -1160.56000222.33306  105.97000   23.50000    0.10570
10    10    -1031.0900032.66627   129.47000   NA    NA
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Figure S6. The results of K value determination by the Evanno method

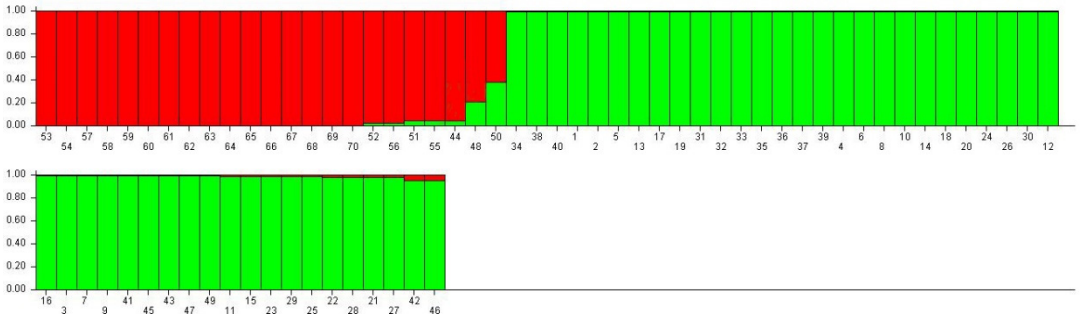


Figure S7. The calculated by STRUCTURE impurity fraction (Q)

Table S1. Estimates of admixture proportions of 7 populations of Rheum sp. based on Q values (K = 2)

Populations, species	Interferred ancestry of individuals
***Rh. tataricum* (ZH)**	Label (%Miss) : Inferred clusters 1 1 (0) : 0.002 0.998 2 2 (0) : 0.002 0.998 3 3 (0) : 0.006 0.994 4 4 (0) : 0.003 0.997 5 5 (0) : 0.002 0.998 6 6 (0) : 0.003 0.997 7 7 (0) : 0.006 0.994 8 8 (0) : 0.003 0.997 9 9 (0) : 0.006 0.994 10 10 (0) : 0.003 0.997
***Rh. tataricum* (TUR)**	Label (%Miss) : Inferred clusters 11 11 (0) : 0.008 0.992 12 12 (0) : 0.004 0.996 13 13 (0) : 0.002 0.998 14 14 (0) : 0.003 0.997 15 15 (0) : 0.008 0.992 16 16 (0) : 0.004 0.996 17 17 (0) : 0.002 0.998 18 18 (0) : 0.003 0.997 19 19 (0) : 0.002 0.998 20 20 (0) : 0.003 0.997
Rh. cordatum	Label (%Miss) : Inferred clusters 21 21 (0) : 0.020 0.980 22 22 (0) : 0.015 0.985 23 23 (0) : 0.010 0.990 24 24 (0) : 0.003 0.997 25 25 (0) : 0.011 0.989 26 26 (0) : 0.003 0.997 27 27 (0) : 0.020 0.980 28 28 (0) : 0.015 0.985 29 29 (0) : 0.010 0.990 30 30 (0) : 0.003 0.997
Rh. turkestanicum	Label (%Miss) : Inferred clusters 31 31 (0) : 0.002 0.998 32 32 (0) : 0.002 0.998 33 33 (0) : 0.002 0.998 34 34 (0) : 0.001 0.999 35 35 (0) : 0.002 0.998 36 36 (0) : 0.002 0.998 37 37 (0) : 0.002 0.998 38 38 (0) : 0.001 0.999 39 39 (0) : 0.002 0.998 40 40 (0) : 0.001 0.999

Rh. altaicum	Label (%Miss) : Inferred clusters 41 41 (0) : 0.006 0.994 42 42 (0) : 0.043 0.957 43 43 (0) : 0.007 0.993 44 44 (0) : 0.969 0.031 45 45 (0) : 0.006 0.994 46 46 (0) : 0.043 0.957 47 47 (0) : 0.007 0.993 48 48 (0) : 0.819 0.181 49 49 (0) : 0.007 0.993 50 50 (0) : 0.619 0.381
Rh. nanum	Label (%Miss) : Inferred clusters 51 51 (0) : 0.967 0.033 52 52 (0) : 0.973 0.027 53 53 (0) : 0.998 0.002 54 54 (0) : 0.998 0.002 55 55 (0) : 0.967 0.033 56 56 (0) : 0.972 0.028 57 57 (0) : 0.998 0.002 58 58 (0) : 0.998 0.002 59 59 (0) : 0.998 0.002 60 60 (0) : 0.998 0.002
Rh. compactum	Label (%Miss) : Inferred clusters 61 61 (0) : 0.998 0.002 62 62 (0) : 0.998 0.002 63 63 (0) : 0.998 0.002 64 64 (0) : 0.998 0.002 65 65 (0) : 0.998 0.002 66 66 (0) : 0.998 0.002 67 67 (0) : 0.998 0.002 68 68 (0) : 0.998 0.002 69 69 (0) : 0.998 0.002 70 70 (0) : 0.998 0.002