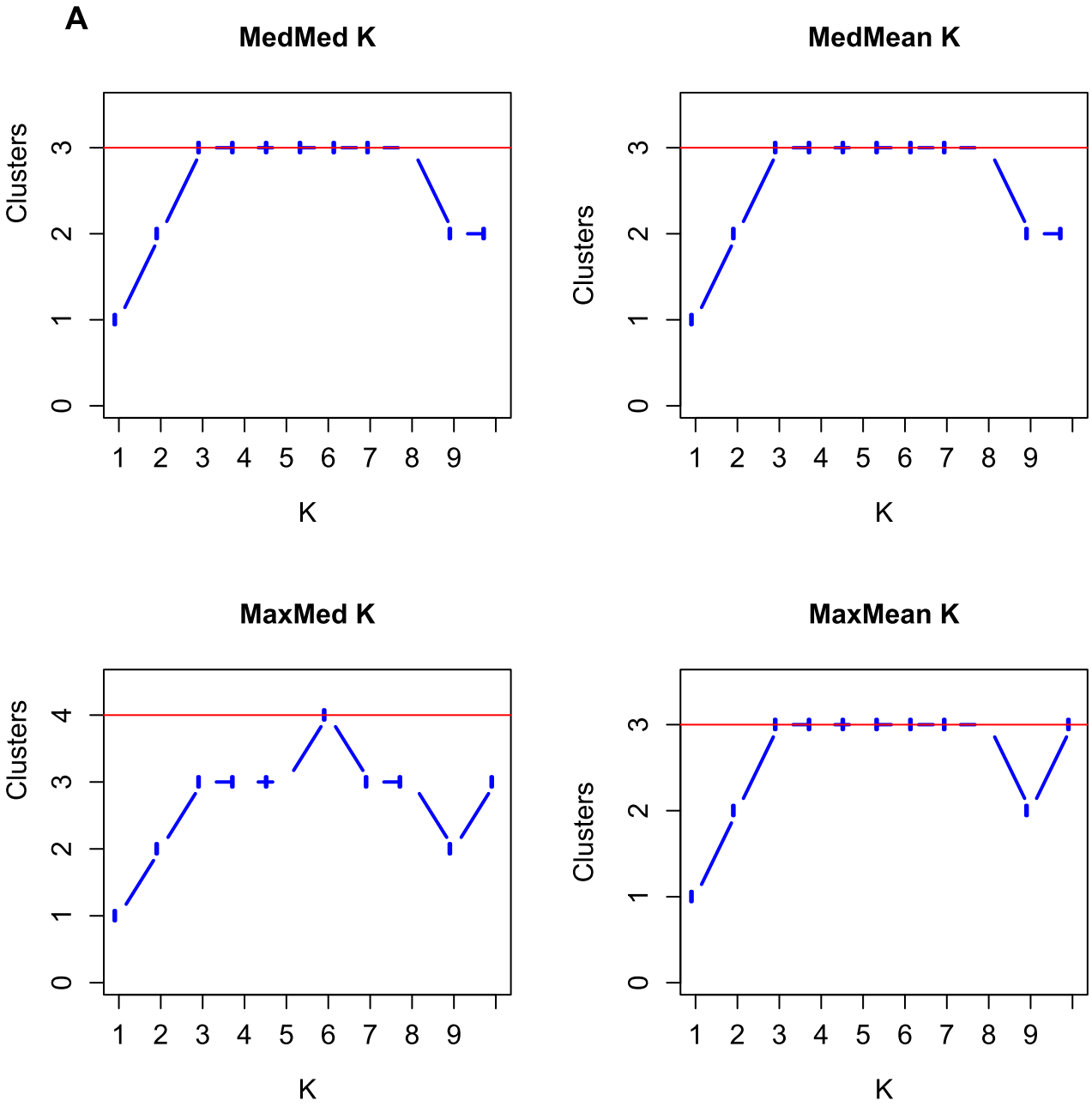
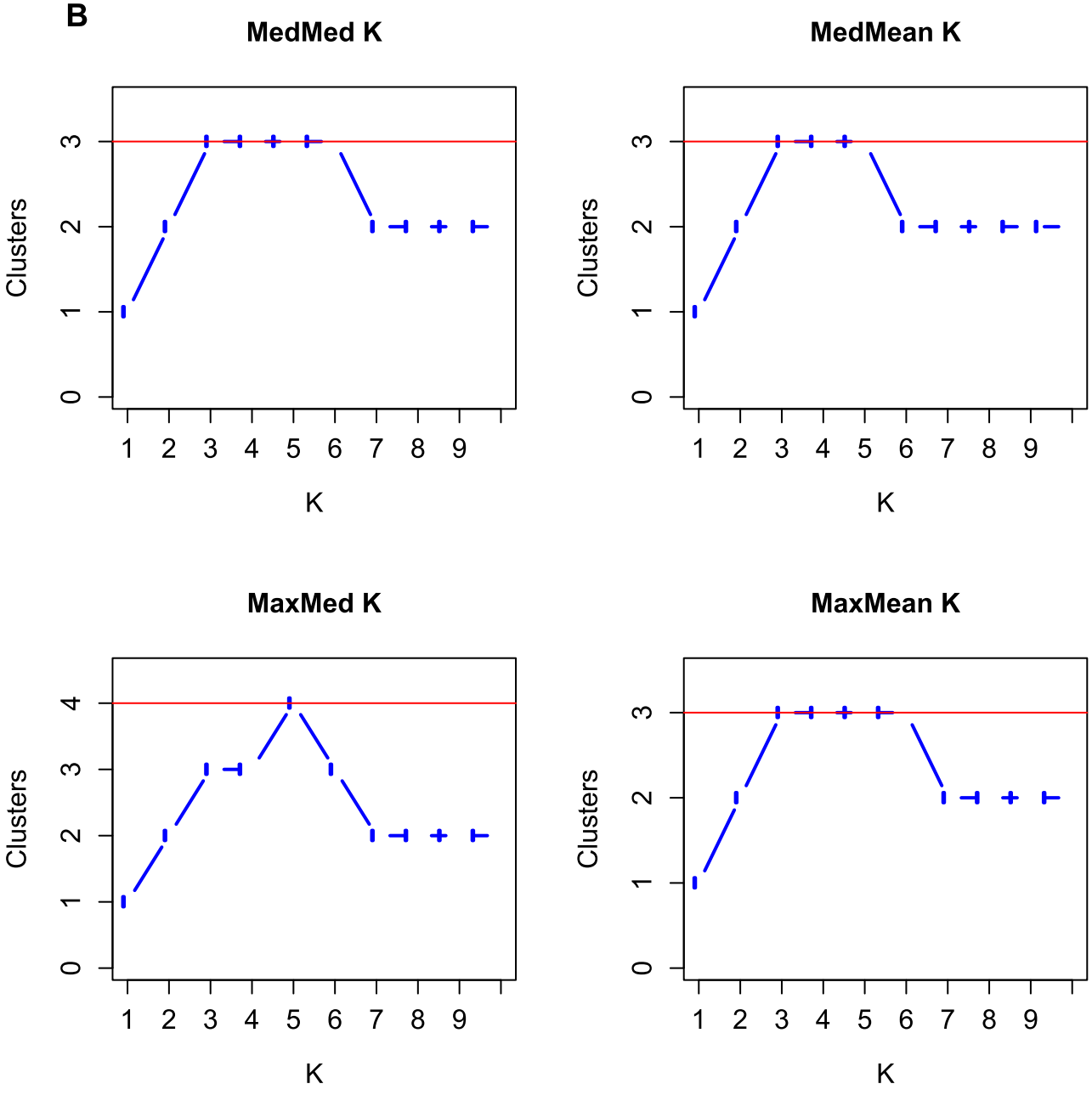
Supplementary Figure S1
to the article “Population genomics reveals speciation processes in the Mallard lineage”
I.V.Kulikova, S.V. Shedko

Number of robust genetic clusters identified by the Puechmaille method (threshold = 0.5) for each tested K value (K = 1–10) based on: (a) 2,164 autosomal ddRAD-seq loci; (b) 104 Z-linked ddRAD-seq loci. The four estimators — MedMed (median of medians), MedMean (median of means), MaxMed (maximum of medians), and MaxMean (maximum of means) — are shown. The horizontal red line indicates the overall optimal K value.



B


MedMed K
Clusters
0
1
2
3
1 2 3 4 5 6 7 8 9
K
MedMean K
Clusters
0
1
2
3
1 2 3 4 5 6 7 8 9
K
MaxMed K
Clusters
0
1
2
3
4
1 2 3 4 5 6 7 8 9
K
MaxMean K
Clusters
0
1
2
3
1 2 3 4 5 6 7 8 9
K