Supplementary Figures

Comparison of traditional and new generation DNA markers declares high genetic diversity and differentiated population structure of wild almond species

Karim Sorkheh[b1*], Mehrana Koohi Dehkordi[b2], Sezai Ercisli[b3], Attila Hegedus[4]& Júlia Halász[4]

[1]Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahid Chamran University of Ahvaz, P.O. Box 61355/144, Iran
[2]Department of Agronomy, Faculty of Agriculture, Payame-Noor University, P.O. Box 19395-3697, Tehran, Iran
[3]Department of Horticulture, Agricultural Faculty, Ataturk University, 25240 Erzurum, Turkey
[4]Department of Genetics and Plant Breeding, Szent István University, H-1118 Budapest, Villányiút29-43

[b]these authors contributed equally to this work.

Corresponding author: Prof. Dr. Karim Sorkheh
Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahid Chamran University of Ahvaz, P.O. Box 61355/144, Iran
E-mail address: karimsorkheh@gmail.com

Supplementary Figure S1

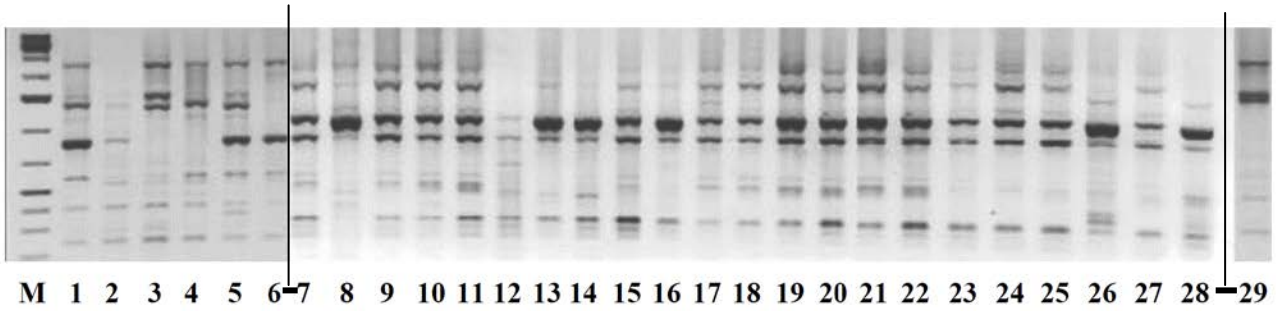

Fig. S1. Polymorphism detected by IRAP primer combination. Lanes from left to right: M: 1 kb+DNA marker (Fermentas); 1 to 10: individuals from Euamygdalus section; 11 to 20: individuals from Lycioides section and 21 to 29: individuals from Spartioides section. Black line between lanes showed that were not run together on the original gel. Vertical lines delineate where the gel is cut.

Supplementary Figure S2

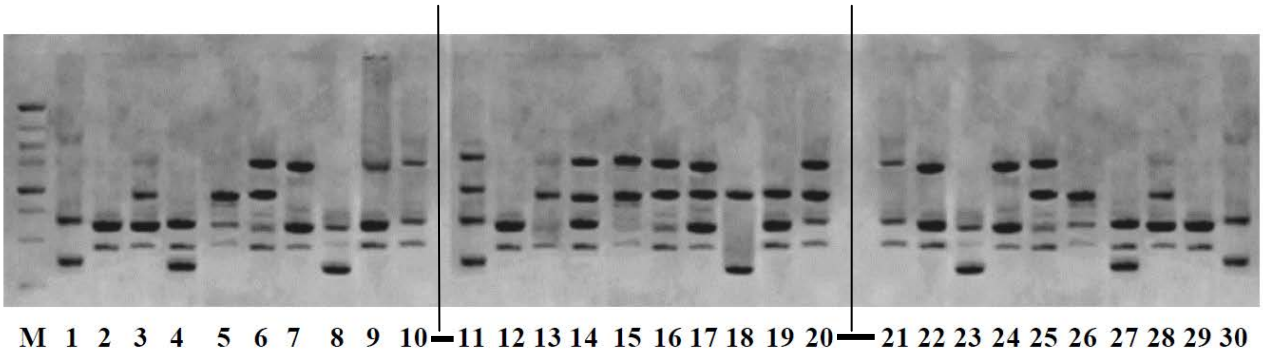

Fig. S2. Polymorphism detected by REMAP primer combination. Lanes from left to right: M: 1 kb+DNA marker (Fermentas); 1 to 10: individuals from Euamygdalus section; 11 to 20: individuals from Lycioides section and 21 to 30: individuals from Spartioides section. Black line between lanes showed that were not run together on the original gel. Vertical lines delineate where the gel is cut.