Figure S11A. Genomic regions surrounding CAGs. Blue columns represent atypical genes (assigned value = 1) whereas blanks between the columns represent non-atypical genes (assigned value = 0). The green horizontal lines above the graphics represent the core genes shared by these elements. Black arrows show the position of integrases and pink columns represent the tRNA genes.

Figure S11B-E. Evolutionary relationship between CAGs of pT26-2 family. pT26-2 (brown), TKV2, TKV3, PHV1, MMPV1, MMC7V1, MMC7V2 and MMC6V1 share core genes and are linked with bold lines. These elements share at least 5, 4, 3 or 2 homologues (according to fixed threshold) with integrated elements detected in other archaea (Euryarchaeota and Crenarchaeota) (Cortez *et al.*, 2009). Each integrated element is represented as a spot colored according to the group the element belongs to: light blue for Thermococcales, pink for Methanococcales, dark blue for Methanosarcinales, green for Halobacteriales, mauve for Thermoplasmatales and dark red for Sulfolobales.

Figure S11A

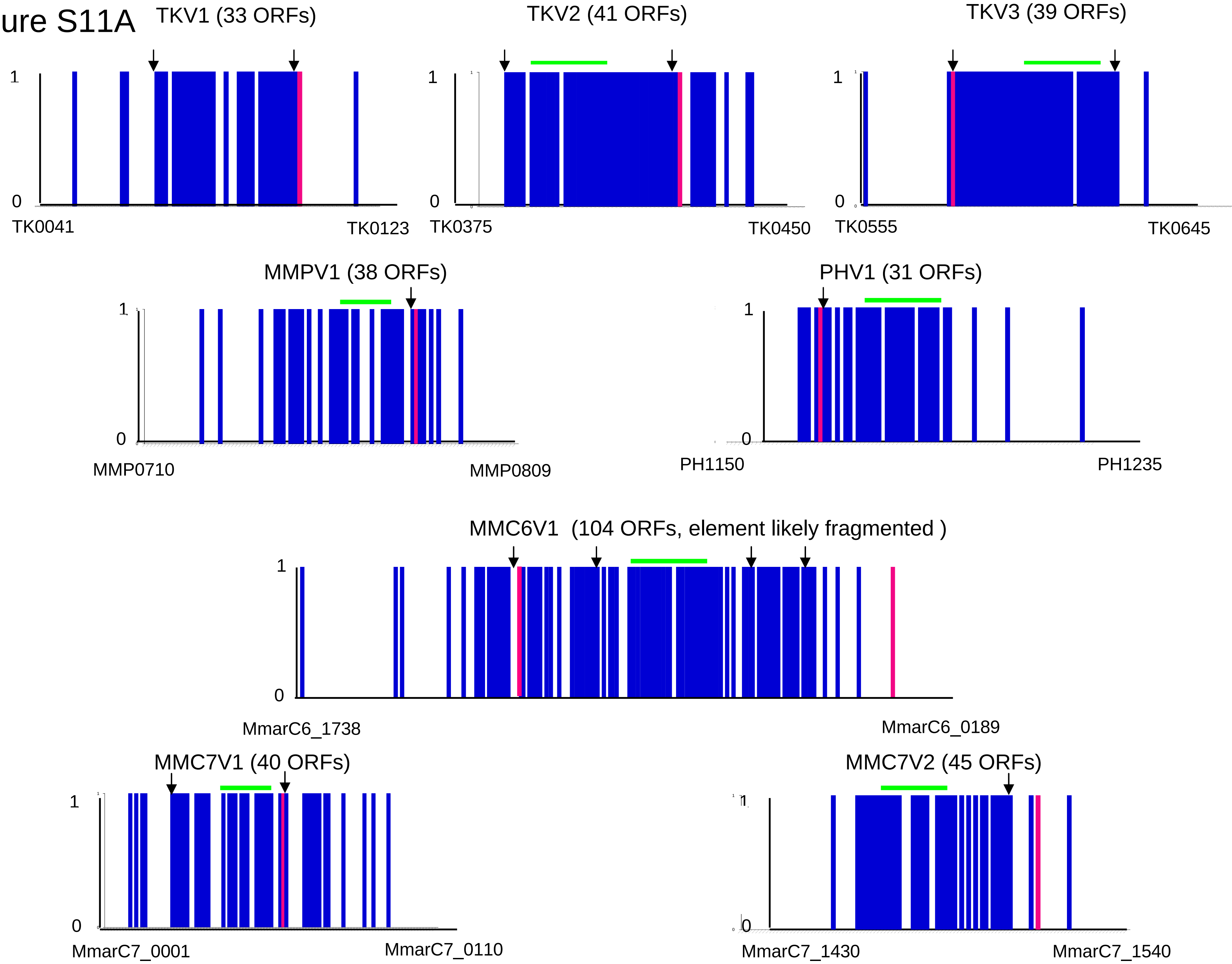

TKV1 (33 ORFs)
1
0
TK0041
TK0123
TKV2 (41 ORFs)
1
0
TK0375
TK0450
TKV3 (39 ORFs)
1
0
TK0555
TK0645
MMPV1 (38 ORFs)
1
0
MMP0710
MMP0809
PHV1 (31 ORFs)
1
0
PH1150
PH1235
MMC6V1 (104 ORFs, element likely fragmented)
1
0
MmarC6_1738
MmarC6_0189
MMC7V1 (40 ORFs)
1
0
MmarC7_0001
MmarC7_0110
MMC7V2 (45 ORFs)
1
0
MmarC7_1430
MmarC7_1540

Figure S11B

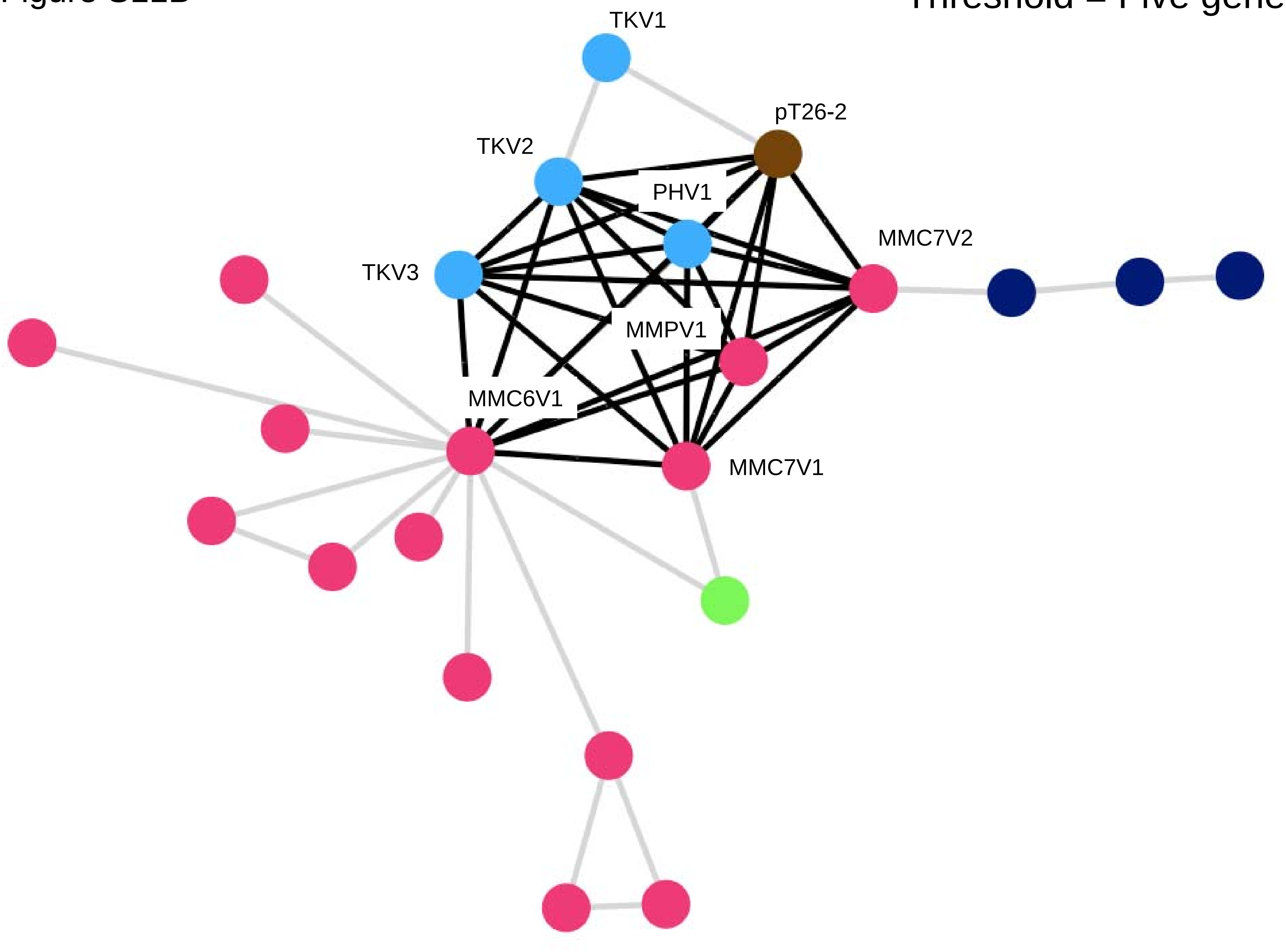

Threshold = Five genes
TKV1
pT26-2
TKV2
PHV1
MMC7V2
TKV3
MMPV1
MMC6V1
MMC7V1

Figure S11C

Threshold = Four genes

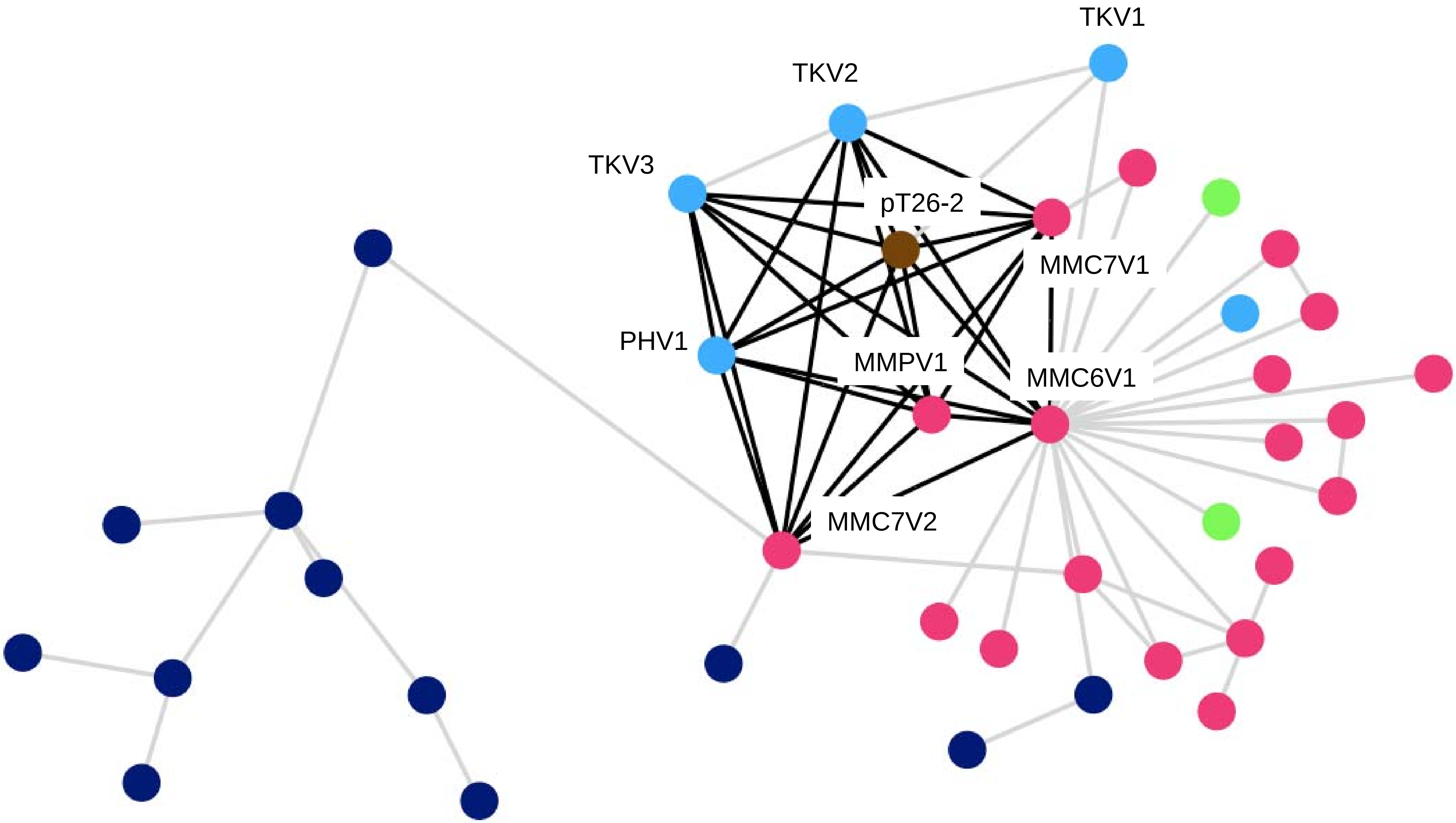


Figure S11D

Threshold = Three genes

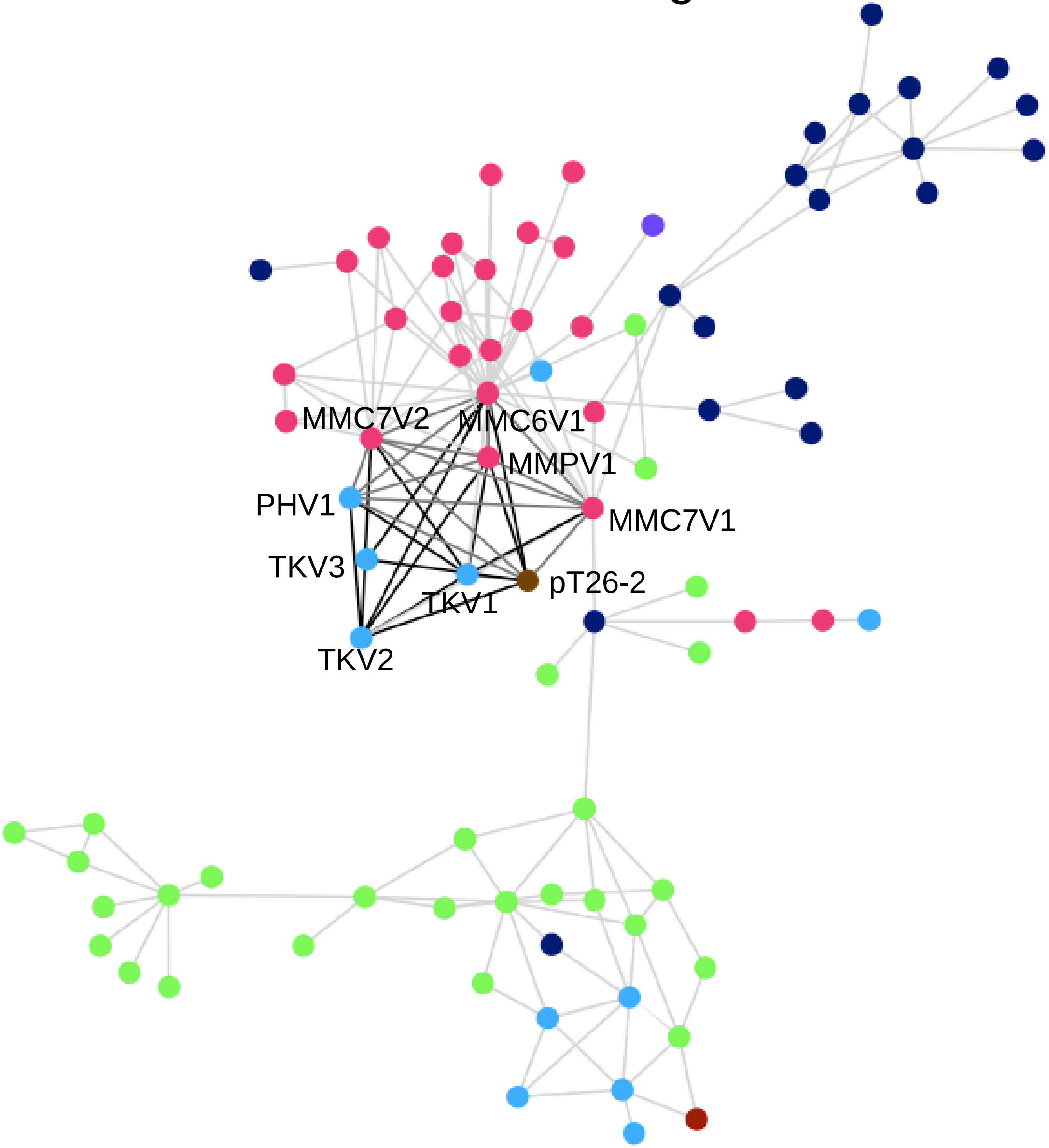


Figure S11E

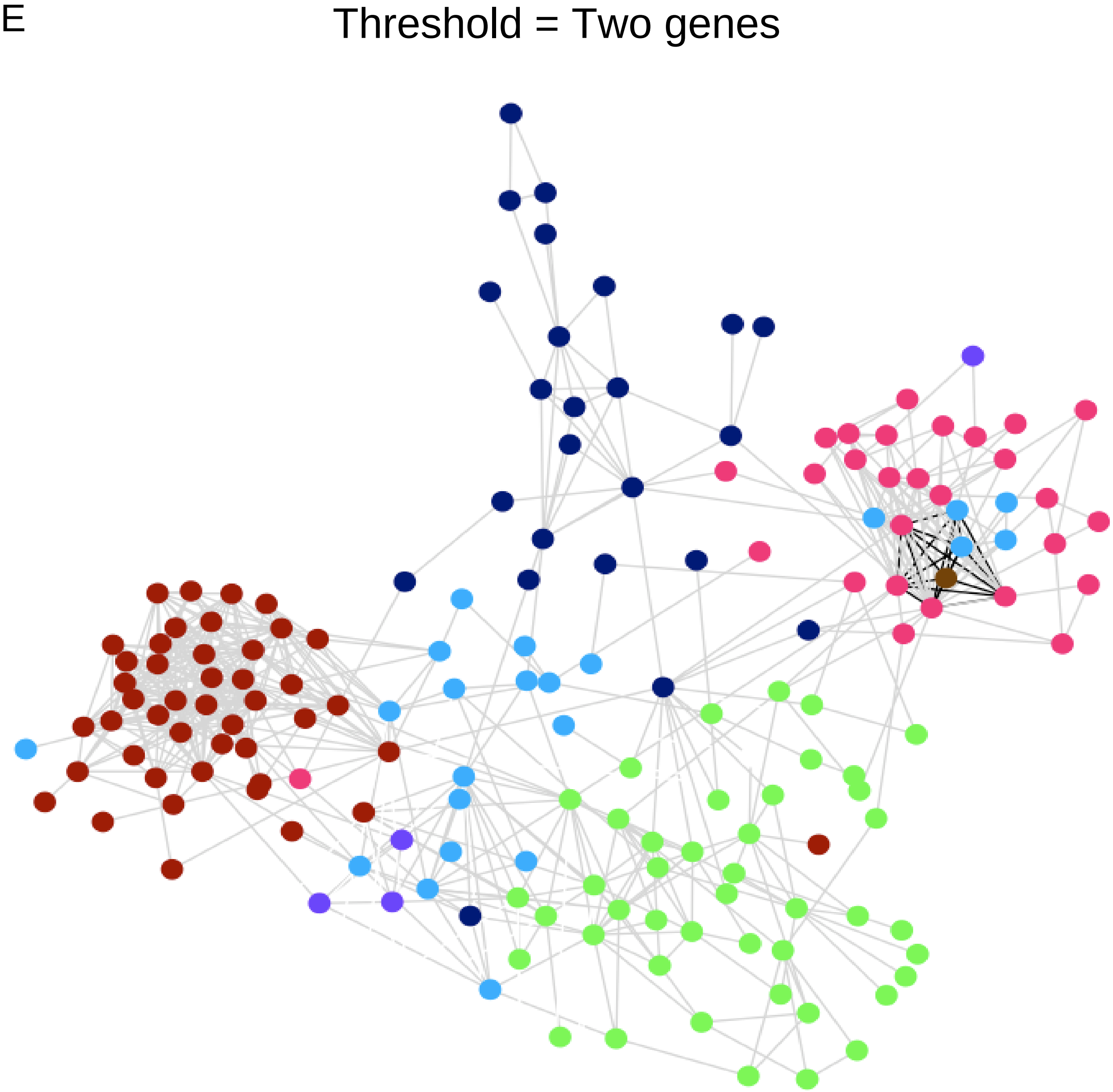


Figure S12

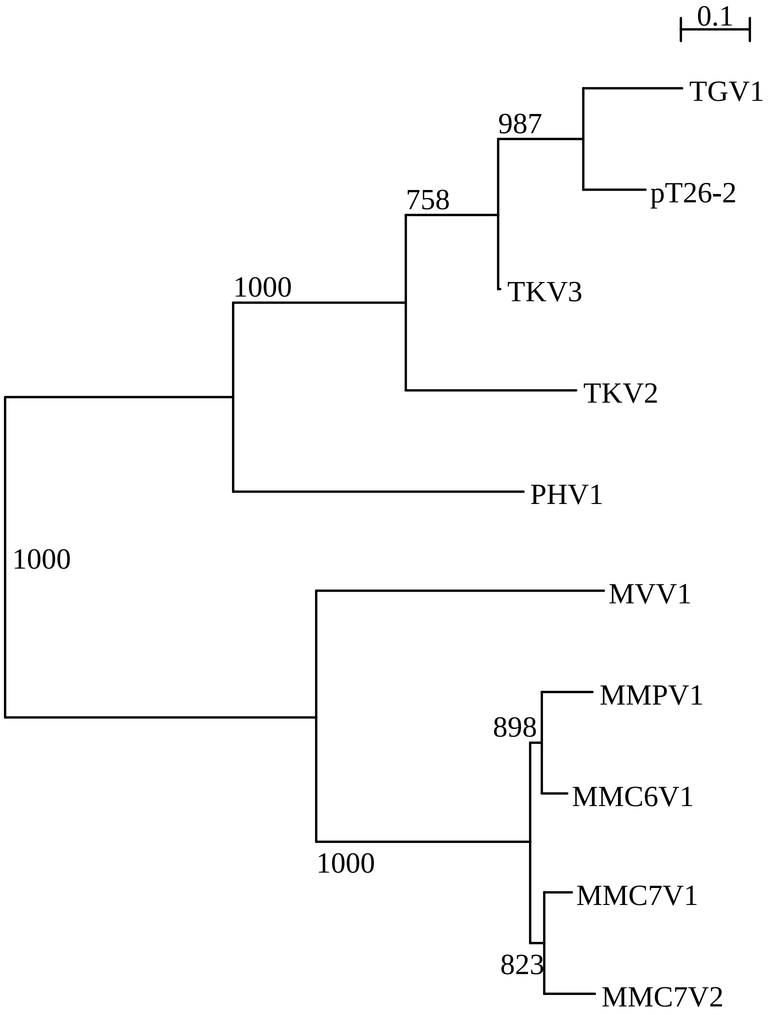
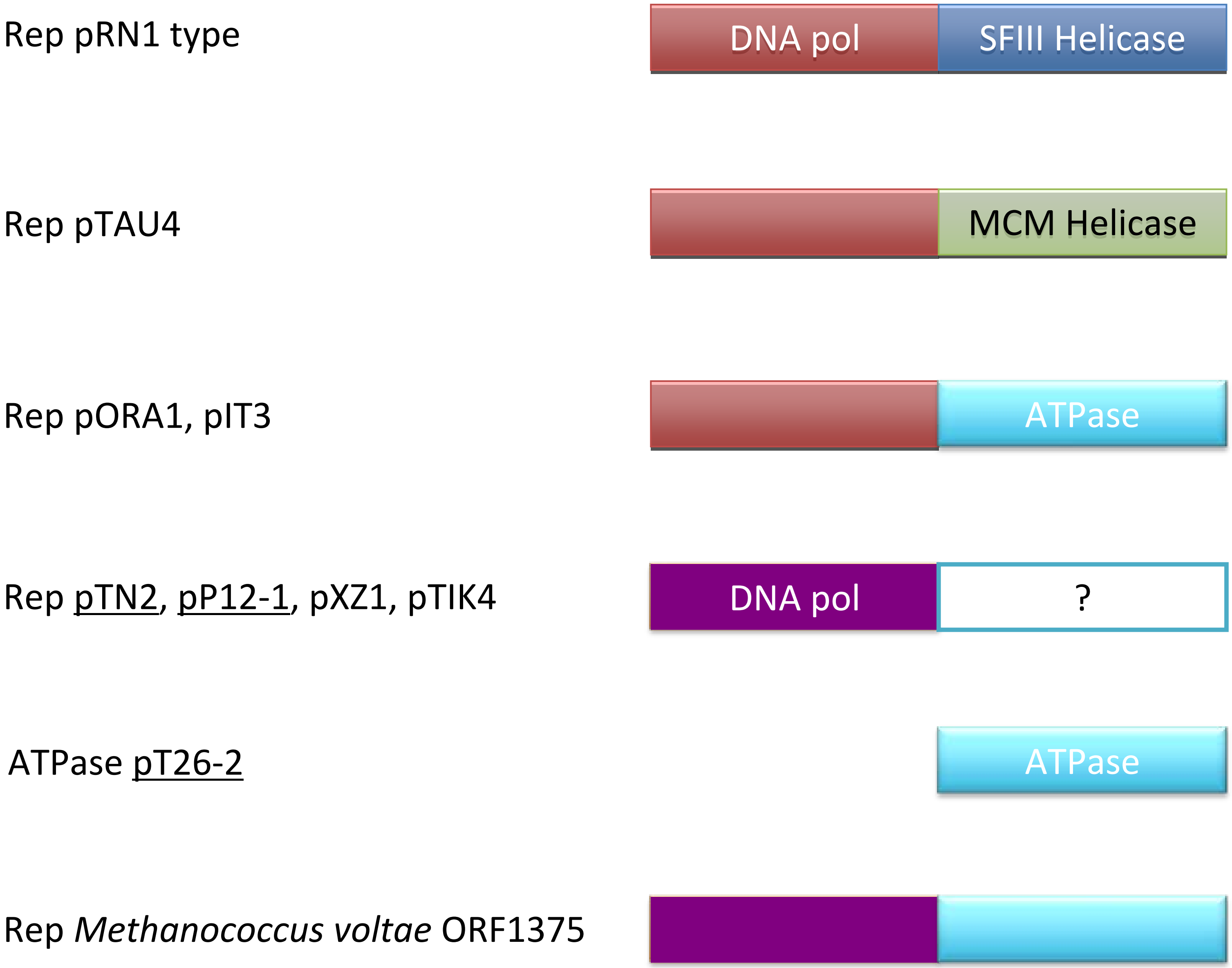

0.1
TGV1
987
pT26-2
758
TKV3
1000
TKV2
PHV1
1000
MVV1
MMPV1
898
MMC6V1
1000
MMC7V1
823
MMC7V2

Figure S13


Rep pRN1 type
DNA pol
SFIII Helicase
Rep pTAU4
MCM Helicase
Rep pORA1, pIT3
ATPase
Rep pTN2, pP12-1, pXZ1, pTIK4
DNA pol
?
ATPase pT26-2
ATPase
Rep *Methanococcus voltae* ORF1375