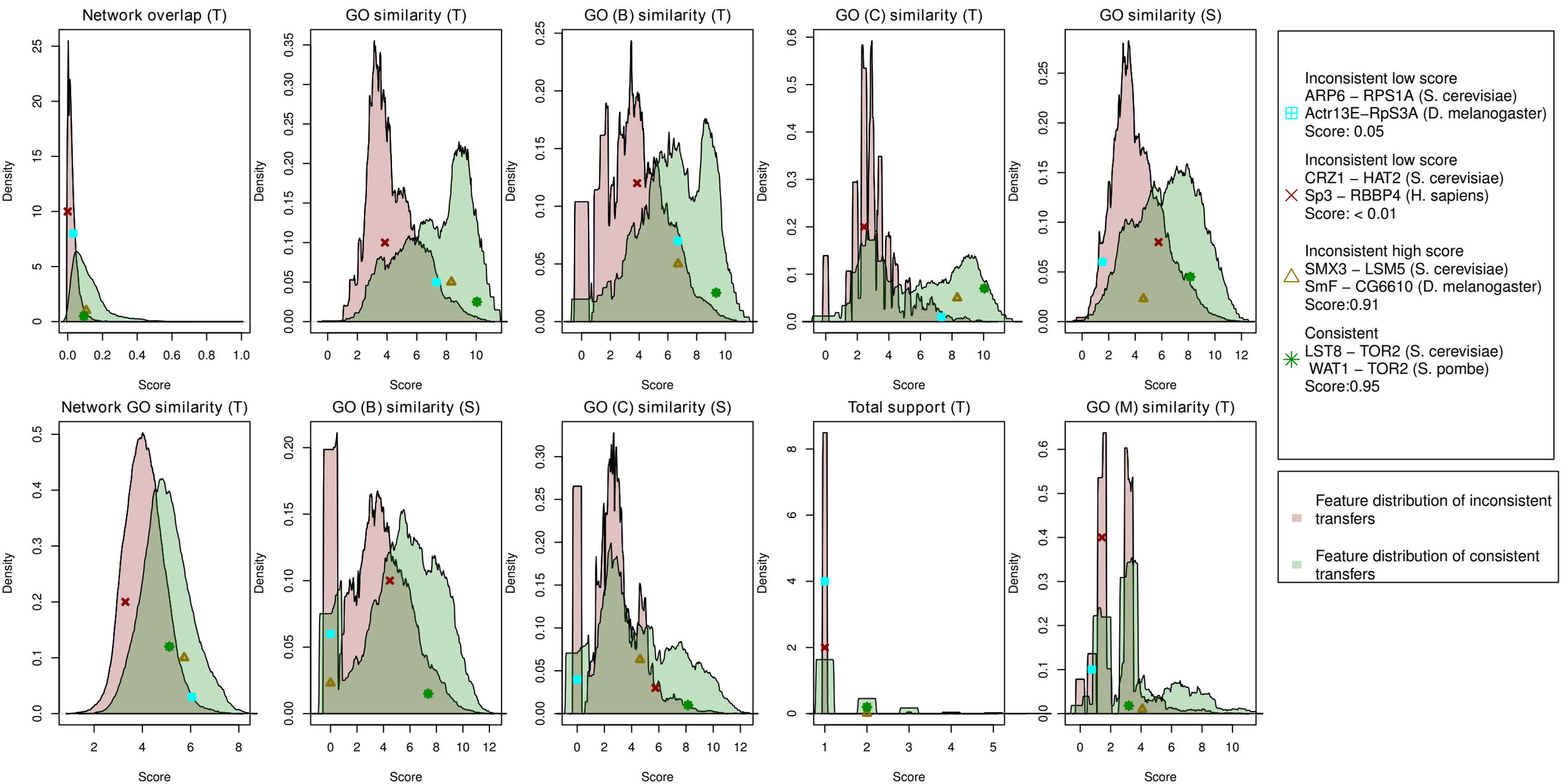
Network overlap (T)
GO similarity (T)
GO (B) similarity (T)
GO (C) similarity (T)
GO similarity (S)
Network GO similarity (T)
GO (B) similarity (S)
GO (C) similarity (S)
Total support (T)
GO (M) similarity (T)
Density
Score
Inconsistent low score
ARP6 – RPS1A (S. cerevisiae)
Actr13E–RpS3A (D. melanogaster)
Score: 0.05
Inconsistent low score
CRZ1 – HAT2 (S. cerevisiae)
Sp3 – RBBP4 (H. sapiens)
Score: < 0.01
Inconsistent high score
SMX3 – LSM5 (S. cerevisiae)
SmF – CG6610 (D. melanogaster)
Score:0.91
Consistent
LST8 – TOR2 (S. cerevisiae)
WAT1 – TOR2 (S. pombe)
Score:0.95
Feature distribution of inconsistent transfers
Feature distribution of consistent transfers