

## S1

Primer pair Spa2f – Spa2r was designed upon an alignment of *Sporidiobolus pararoseus* sequences AF417115.1, FJ999721.1, AB030338.1, AF444604.1, AY015429.1, FJ755245.1, EU409803.1, FJ758388.1, EF505797.1, EF505785.1, EU002958.1, sequences from other *Sporidiobolus* species (EF592111.1, AB030337.1, FJ515195.1, EU276010.1, EF592138.1, AB073255.1) and from relative genera (AB073230.1, FJ515206.1, AB073255.1, AF444510.1, FJ345357.1, AY069991.1, FJ591128.1, AY070005.1, DQ640071.1). Sequences with specificity for *S. pararoseus*, which did not match sequences from other *Sporidiobolus* species or relative genera were selected for the primer pair. BLAST analysis showed a high degree of specificity for *S. pararoseus*, but also sequences from *Sporobolomyces* species were found among the hits (*S. ruberrimus*, *S. phaffi*, *S. patagonicus*).