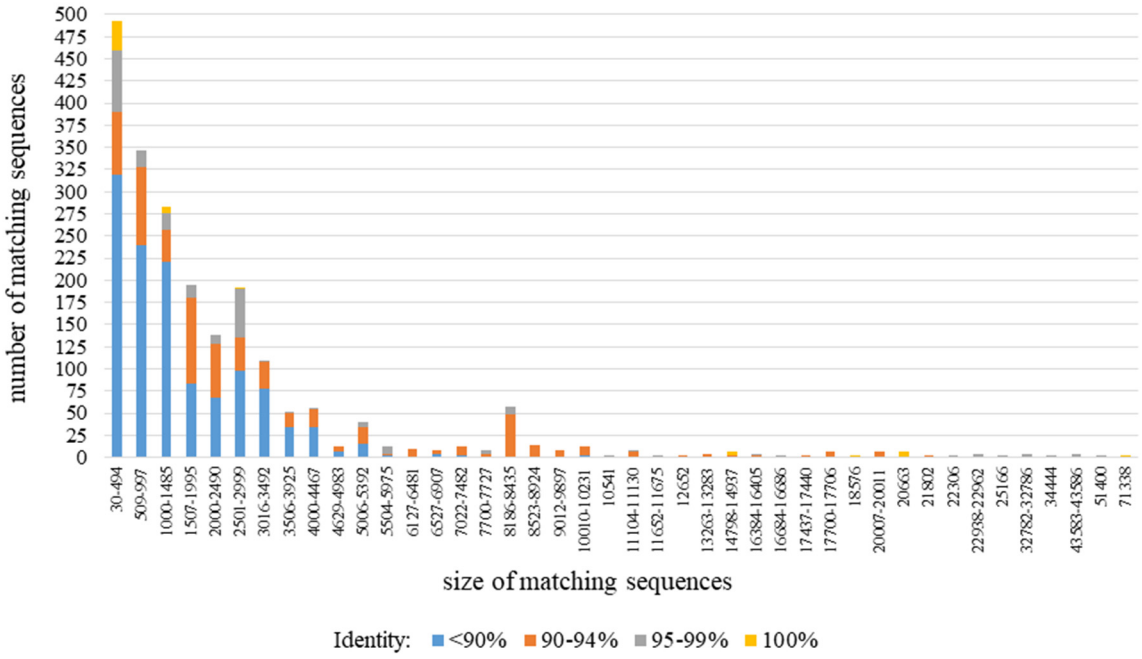


Figure S1. Number and identity (%) of matched sequences between 91 PRSs integrated into tRNA genes of *S. meliloti*. Matched sequences were identified by pairwise alignment of 91 PRSs using BLASTn (see materials and methods).