Figure S1 Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the phylogenetic position of strain M28T among related strains.

 *Microbacterium keratanolyticum* DSM 8606 T

 *Microbacterium phyllosphaerae* DSM 13468 T

 *Microbacterium profundi* Shh49T

 *Microbacterium murale* CCM 7640T

 *Microbacterium diaminobutyricum* KU843548 T

 *Microbacterium pullorum* Sa4CUA7T

 *Microbacterium oleivorans* NBRC 103075T

 *Microbacterium paraoxydans* DSM 15019T

 *Microbacterium algeriense* G1 DSM 109018T

 *Microbacterium saperdae* DSM 20169T

 *Microbacterium oxydans* DSM 2057 T

 *Microbacterium maritypicum* AJ85391 T

 *Microbacterium azadirachtae* DSM 23848T

 *Microbacterium arabinogalactanolyticum* JCM 9171T

 *Microbacterium resistens* NBRC 103078T

 *Microbacterium testaceum* NBRC 12675T

 ***Microbacterium triticisoli* M28**T

 *Microbacterium aquimaris* DSM 19713T

 *Microbacterium allomyrinae* NBRC 115127T

 *Microbacterium ureisolvens* DSM 103157T

 *Microbacterium aureliae* KF793922T

 *Microbacterium sulfonylureivorans* LAM7116T

 *Microbacterium fluvii* AB286028T

 *Microbacterium binotii* JCM 16365T

 *Microbacterium neimengense* JN408293T

 *Agromyces aureus strain* AR33T

99

83

87

53

97

63

85

64

64

73

70

0.0050