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