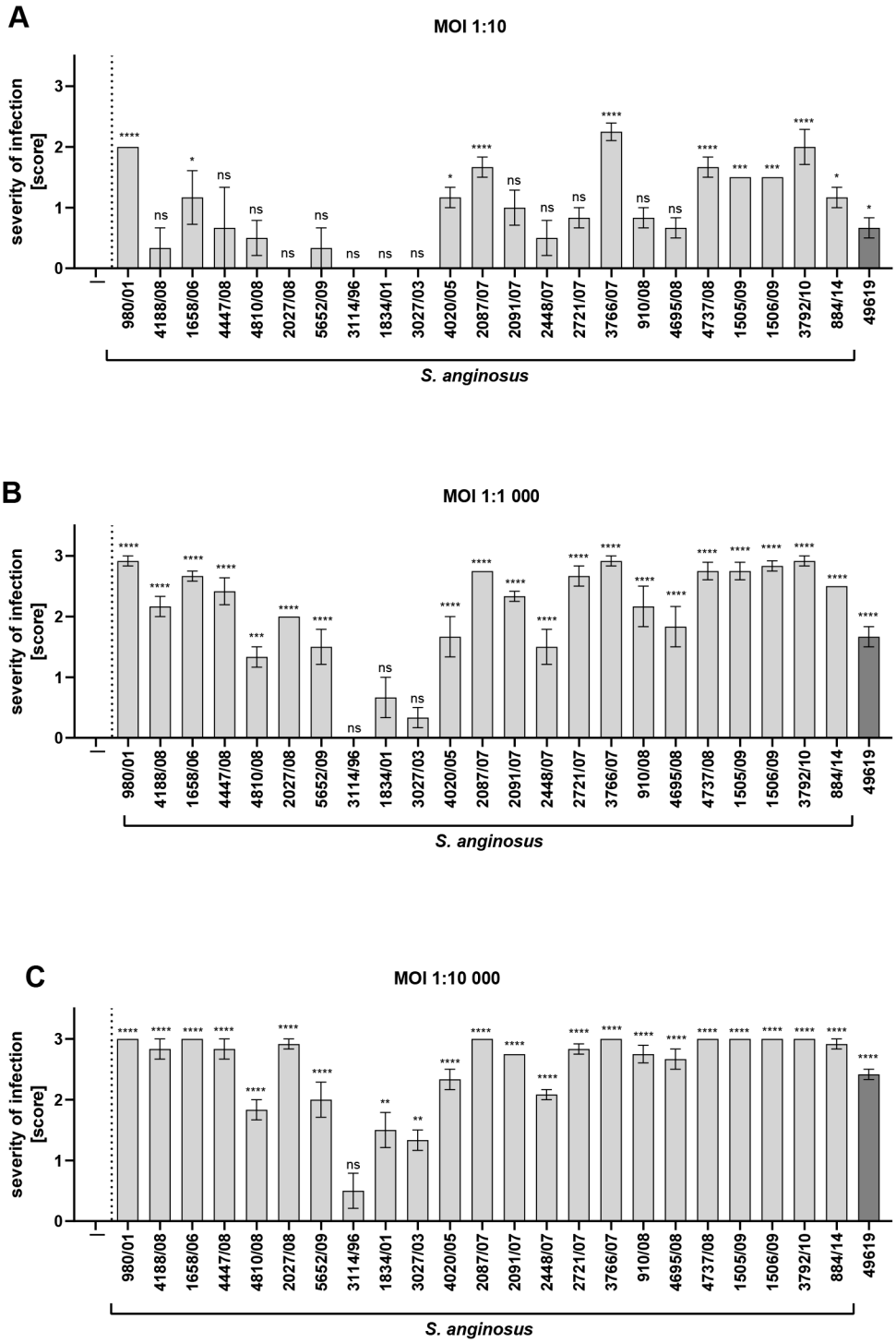
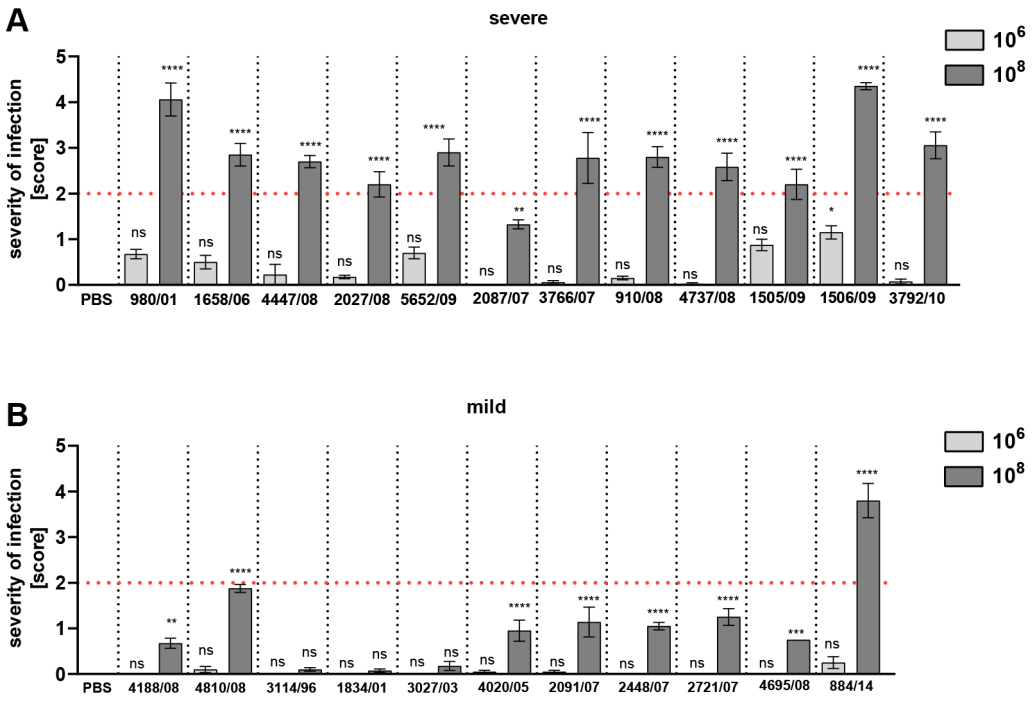
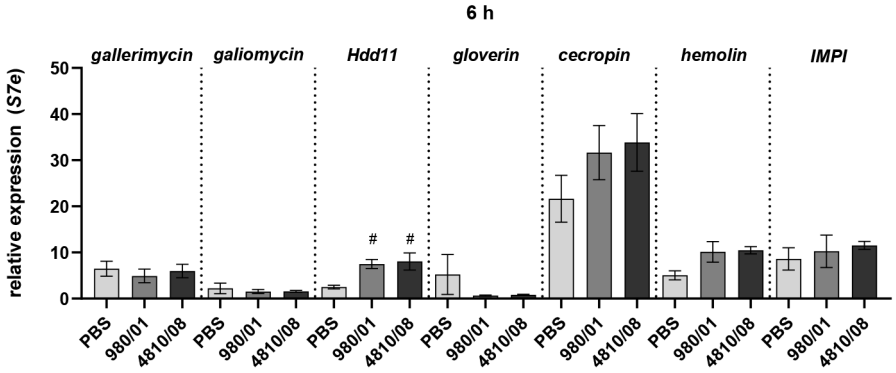
Supplement fig. S1



Supplement fig. S2



Suplement fig. S3



Supplement fig. S4

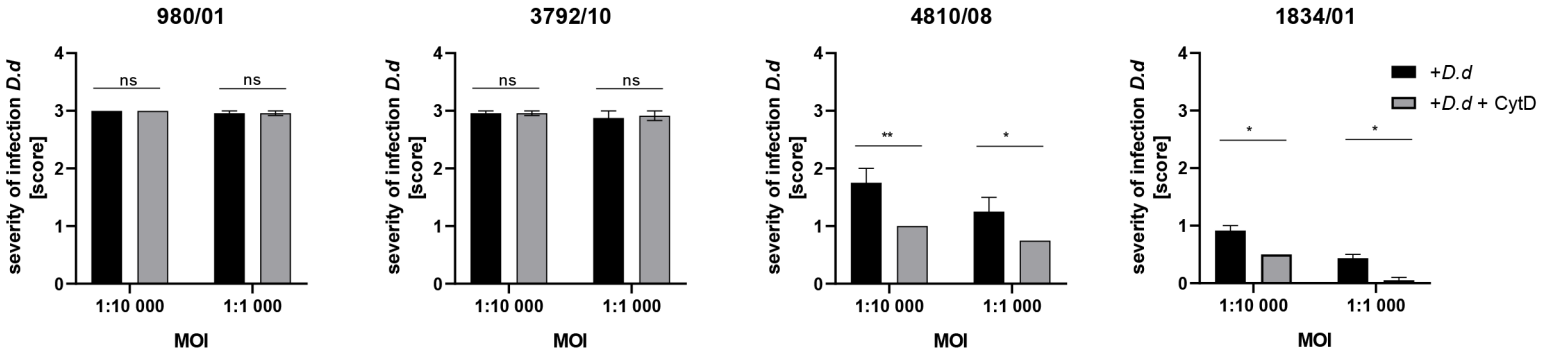


Table S1. Oligonucleotide sequences used in quantitative reverse transcription-PCR (qRT-PCR).

Oligonucleotide	Sequence	ref	Temperature program[1]
S7e forward F	5'-ATGTGCCAATGCCCAAGTTG-3'	(87)	1. 95˚C, 15 s 2. 60˚C, 15 s 3. 72˚C, 1 min
S7e reverse R	5'-GTGGCTAGGCTTGGGAAG AAT-3'		
gallerimycin F	5'-TATCATTGGCCTTCTTGGCTG-3'		
gallerimycin R	5'-GCACTCGTAAAATACACATCCGG-3'		
galiomycin F	5'-TCGTATCGTCACCGCAAAATG-3'		
galiomycin R	5'-GCCGCAATGACCACCTTTATA-3'		
gloverin F	5'-GTGTTGAGCCCGTATGGGAA -3'	(53)	
gloverin R	5'-CCGTGCATCTGCTTGCTAAC-3'		
cecropin F	5'-CTGTTCGTGTTCGCTTGTGT-3'		
cecropin R	5'-GTAGCTGCTTCGCCTACCAC-3'		
hemolin F	5'-CTCCCTCACGGAGGACAAAC-3'		
hemolin R	5'-GCCACGCACATGTATTCACC-3'		
IMPI F	5'-TAGTAAGCAGTAGCATAGTCC-3'	(88)	
IMPI R	5'-GCCATCTTCACAGTAGCA-3'		
Hdd11 F	5'-TCGGCTTGTGAGTTCGTTGT-3'	(65)	1. 95˚C, 15 s 2. 58˚C, 15 s 3. 72˚C, 1 min
Hdd11 R	5'-GGCACTAGAAGGAGCACCAC-3'		

[1]Denaturation (1); annealing (2); extension (3).

Supplemental Figure Legends

Fig. S1 Inhibition of the growth of *D. discoideum* induced by *S. anginosus.* *S. anginosus* was seeded in SM medium along with *D. discoideum* at an MOI of **(A)** 1:10, **(B)** 1:1 000, or **(C)** 1:10 000. Cultures were carried out for 10 days at room temperature under aerobic conditions. *D. discoideum* plated on SM medium without bacteria was used as the control. After 5 days of co-culture, the growth of *D. discoideum* was assessed both alone and in the presence of bacteria, and growth was scored according to the number and morphology of colonies. Data represent mean values of three independent experiments ± SEM (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant).

Fig. S2 Use of the *G. mellonella* model to assess the virulence of different strains of *S. anginosus* isolated from severe (A) and mild (B) clinical infections. Health index scores of *G. mellonella* larvae (infected with 10^6 and 10^8 CFU/larva) after 6 h p.i. The control group was injected with PBS. Each tested group contained 10 larvae (n = 10). The values represent the mean ± SEM (*, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$; ns, not significant).

Fig. S3 Activation of innate immune response in *G. mellonella* infected with S. anginosus strains. qRT-PCR analysis of *G. mellonella* gene expression was measured at 6 h.p.i. The larvae were frozen in liquid nitrogen and then lysed in TRIzol. RNA was isolated and qRT-PCR was performed. Relative expression of *gallerimycin*, *galiomycin*, *Hdd11*, *gloverin*, *cecropin*, *hemolin*, and *IMPI* is shown. The ribosomal protein *S7e* (a housekeeping gene) was used for normalization. Data represent mean values from three independent experiments ± SEM (#$P<0.05$, vs Control).

Fig. S4.

Quantification of *D. discoideum* deterioration after *S. anginosus* infection in the presence of Cytochalasin D. *S. anginosus* was seeded in SM medium along with *D. discoideum* with or without Cytochalasin D (5 μM) at an MOI of 1:10 000 and 1:1 000. Cultures were monitored for 5 to 10 days. *D. discoideum* plated on SM medium in the absence of bacteria was used as a control. After 5 days of co-culture at room temperature under aerobic conditions, *D. discoideum* growth was assessed and scored for the number and morphology of colonies. Data represent mean values of two independent experiments ± SEM (*, $P < 0.05$; **, $P < 0.01$; ns, not significant.).

Table S1. Oligonucleotide sequences used in quantitative reverse transcription-PCR (qRT-PCR). [1]Denaturation (1); annealing (2); extension (3).