Supplementary materials S1. Characterizing the status of energetic metabolism of dinoflagellate resting cysts under mock conditions of marine sediments via physiological and transcriptomic measurements

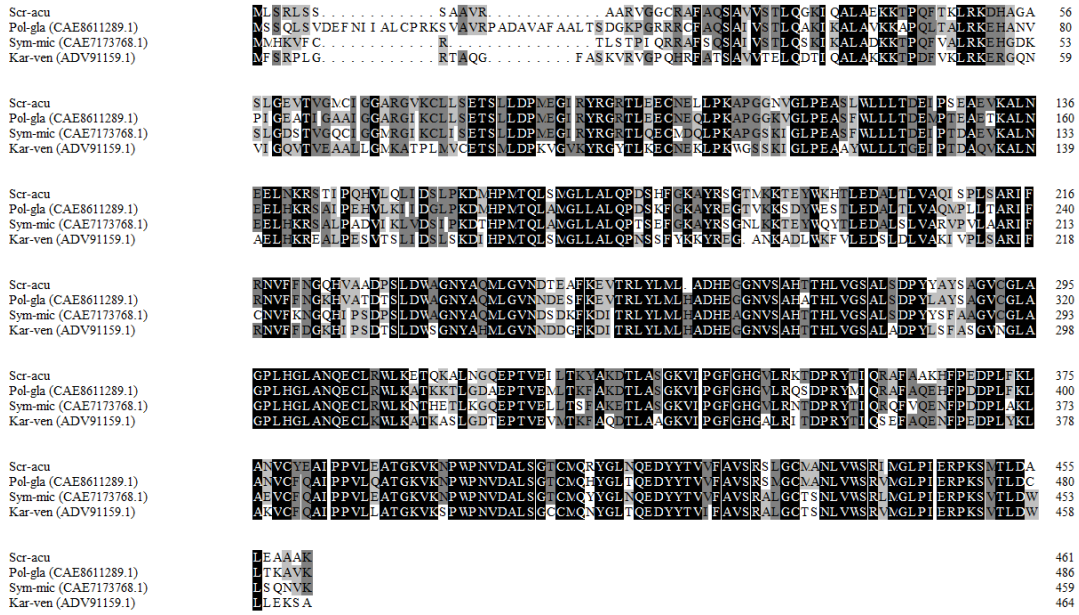


Figure S1-1 Multiple sequence alignment of *SaCS* amino acid sequences with other known dinoflagellate species.The shaded areas indicated similarities. Scr-acu=*S. acunimata*, Pol-gla=*Polarella glacialis*, Sym-mic= *S. microadriaticum*, Kar-ven=*K. veneficum*.

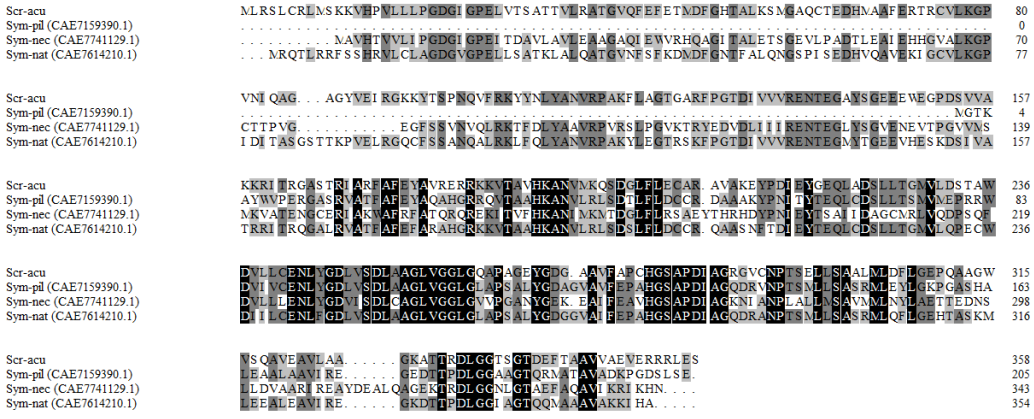


Figure S1-2 Multiple sequence alignment of *SaIDH* amino acid sequences with other known dinoflagellate species. The shaded areas indicate similarities. Scr-acu= *S. acuminata*, Sym-pil= *S. pilosum*, Sym-nat= *S. natans*, Sym-nec= *S. necroappetens*.

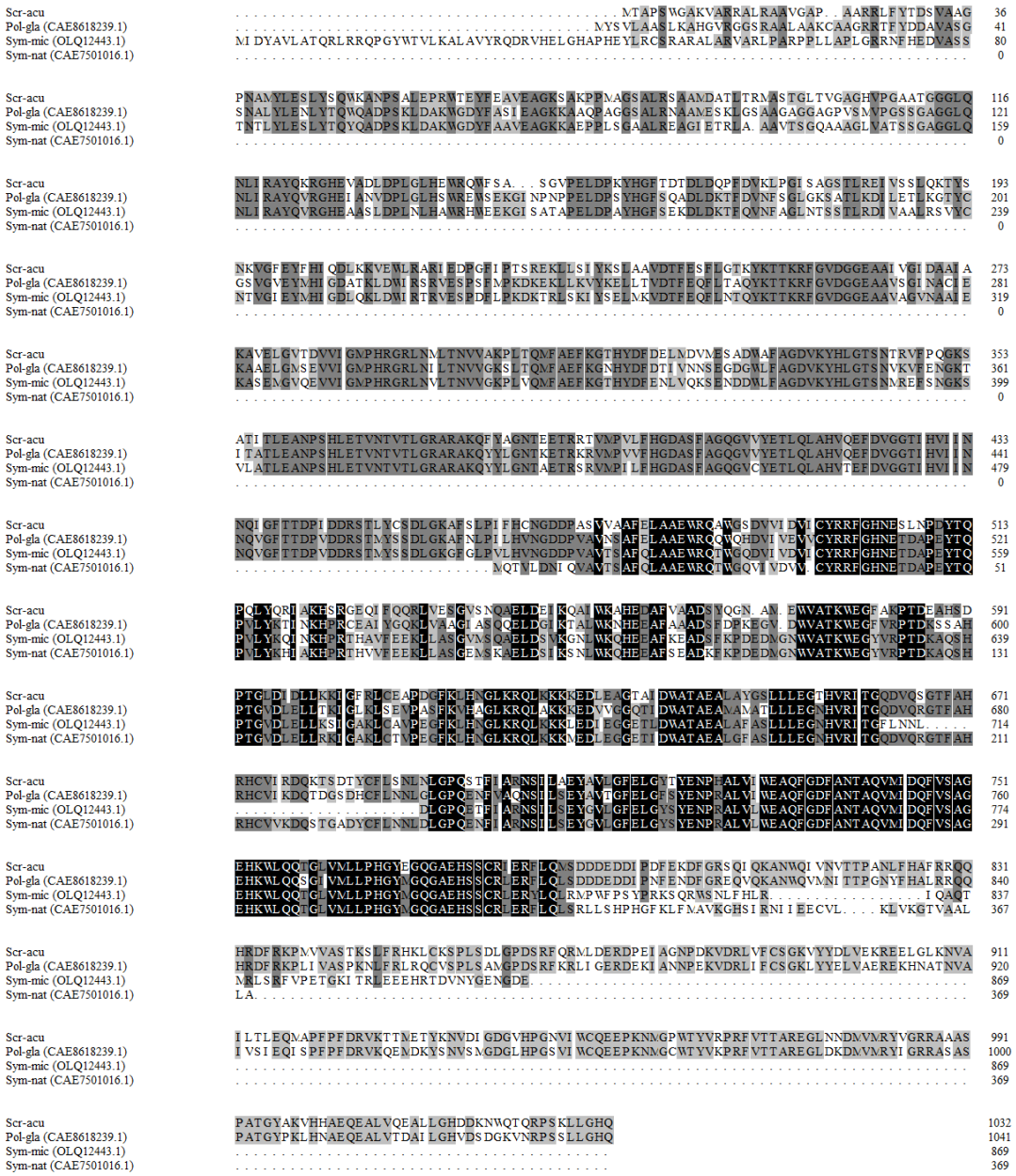


Figure S1-3 Multiple sequence alignment of *Saα-KGDH* amino acid sequences with other known dinoflagellate species. The shaded areas indicate similarities. Scr-acu= *S. acuminata*, Pol-gla= *P. glacialis*, Sym-mic= *S. microadriaticum*, Sym-nat= *S. natans*.