

SUPPLEMENTARY MATERIAL

***Thermococcus henrietii* sp. nov., a novel extreme thermophilic and piezophilic sulfur-reducing archaeon isolated from a deep-sea hydrothermal chimney (EPR 9°N)**

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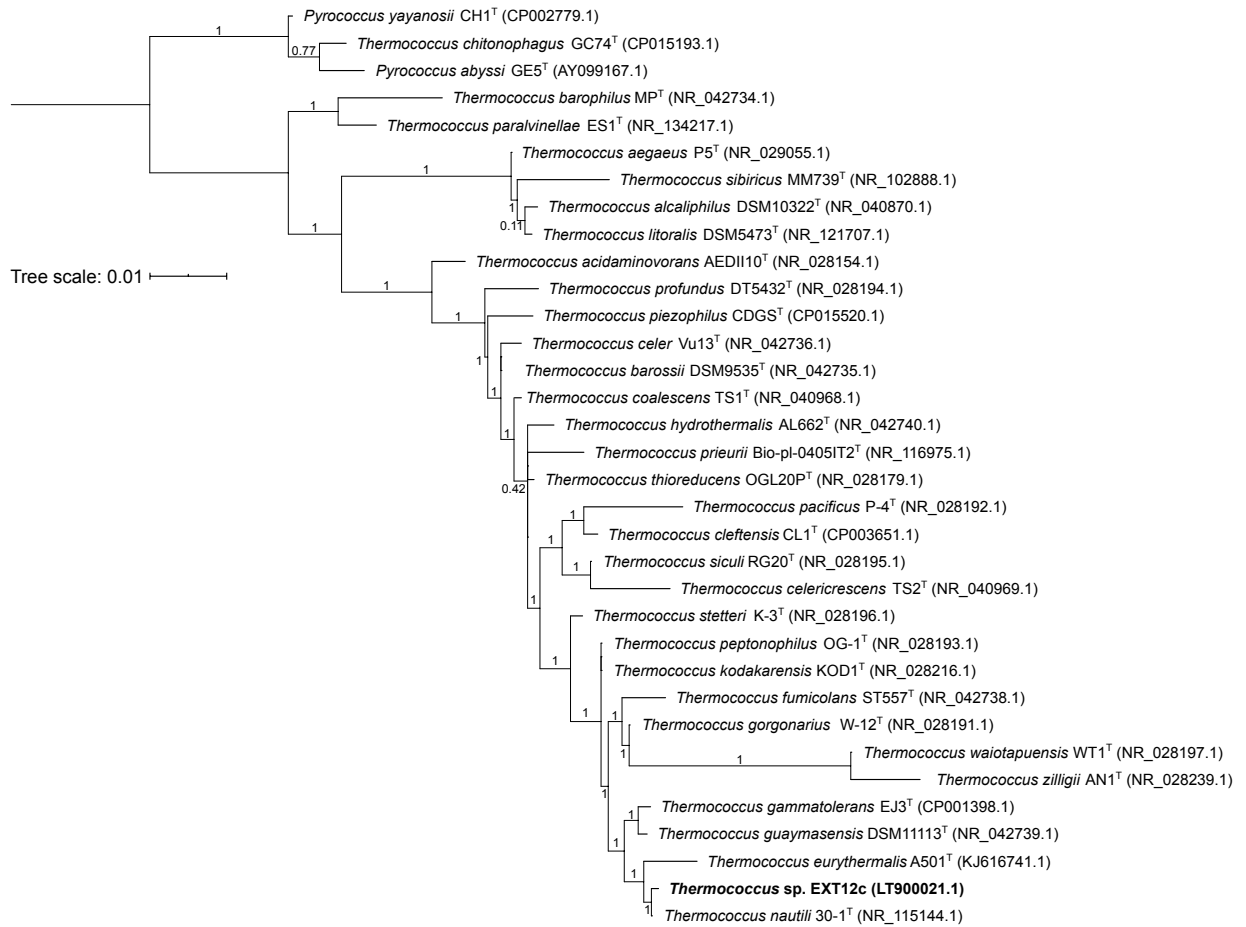


Fig. S1. PhyML phylogenetic tree showing the phylogenetic positions of strain EXT12c^T and representatives of some other related taxa, based on 16S rRNA gene sequences. This phylogenetic reconstruction was calculated by using *Pyrococcus* species as outgroup. Branch supports, computed with the aLTR SH-like method, are shown at branch nodes. Bar, 0.01 nucleotide substitution rate (K_{nuc}) units.

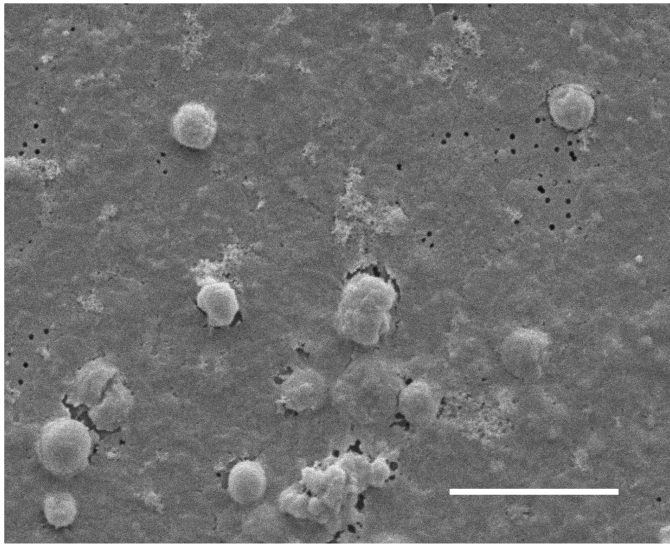


Fig. S2. Scanning electron micrograph of cells of strain EXT12c^T. Bar, 5 μm.

Table S1. Overall genome relatedness indexes between strain EXT12c^T and its closest relatives. Shaded boxes correspond to unavailable genomes. Average Nucleotide Identity scores were calculated using the ANI calculator tool provided by the EzBioCloud web server (<https://www.ezbiocloud.net/tools/ani>). Digital DNA-DNA hybridization (dDDH) estimate values were determined using the formula 2 of the genome-to-genome distance calculator GGDC v2.1.

	16S rRNA gene sequence similarity	OrthoANIu (%)	dDDH (%)
<i>T. henrietii</i> EXT12c ^T (this study)	100	100	100
<i>T. nautili</i> 30-1 ^T	99.93	91.54	43.60
<i>T. gammatolerans</i> EJ3 ^T	99.66	82.84	29.40
<i>T. guaymasensis</i> DSM 1113 ^T	99.40	80.63	25.50
<i>T. eurythermalis</i> A501 ^T	99.38	82.30	25.50
<i>T. peptonophilus</i> OG-1 ^T	99.60	77.02	20.40
<i>T. kodakarensis</i> KOD1 ^T	99.60	76.97	20.70
<i>T. gorgonarius</i> W-12 ^T	99.26	77.16	21.90
<i>T. marinus</i> EJ1 ^T	99.24		
<i>T. fumicolans</i> ST557 ^T	99.10		
<i>T. coalescens</i> TS1 ^T	98.99		
<i>T. stetteri</i> K-3 ^T	99.04		
<i>T. barossii</i> SHCK-94 ^T	98.92	77.64	21.90
<i>T. onnurineus</i> NA1 ^T	98.92	75.89	20.30
<i>T. celer</i> DSM 2476 ^T	98.86		
<i>T. thioeducens</i> DSM 14981 ^T	98.79		
<i>T. cleftensis</i> CL1 ^T	98.79	78.64	22.20