Supplementary table 2. RNA polymerase subunit gene copy number in archaeal genomes

RNAP subunits	Cluster Index/ Taxonomy	Crenarchaeota				Euryarchaeota										
		APER	PAER	SSOL	STOK	AFUL	HALO	MACE	MUAN	MKAN	MMAZ	MTHE	PABY	PHOR	TACI	TVOL
A	278 / B-E	2	2	2	2	2	2	2	2	2	2	5	2	2	2	2
В	267/E	1	1	2	- 1	2	2	2	2	2	2	2	1	- 1	1	-1
	277 / B-E		+		+	(4)	-		-	-	-	(+)	-	+		1
	256 / E							- 3		- 1		- 1				
E	226/E	-1	1	-1	1.	1	-1	. 1	1	1	1	1	-1	1	-1	1
	195 / A		10-11	1	1	1		1	1	1	1	1	1	-	1	1
Н	247 / E	. 1	1	1	1	1	-1	- 1	1	1	1	1	1	1	-1	1
К	38 / A	. 4			- 20			5+	1		+	-	4			+-
	239 / E	1	1	1	1	1	-1	1		1	1	1	1	14.5	-1	1
L	180 / E		16-	1	1	- 90	- 1		+)		+	-	-	Ute-1		
	49 / A	1			4	-	3	-	4	+	465	-	34			-
	206 / A		1		-	1	-1	1	1		1	1	1			- 1
N	245/E	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Columns: **RNAP subunits**, RNA polymerase subunit family as determined from the SwissProt functional annotations of the TAP members. (The "A" family contains subunits A' and A", and the "B" families contain subunits B' and B"); **Cluster Index/Taxonomy**, the identifier of the TRIBE-MCL family and which domains of life the TAP reference sequences originate: **A** - Archaea, **B** - Bacteria, **E** - Eukaryota; columns 3-17, the number of archaeal sequences present within a family. The four letter species codes in the second row of these columns are defined in the Methods section.