



Supplemental Material to:

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CRISPR adaptive immune systems of Archaea

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Table S1. Comprehensive annotation of CRISPR-cas gene cassettes into functional modules of cas genes with subtype designations, for all archaeal genomes available as of May 2013. Adaptation modules (A) are marked blue, Type I interference modules (1), yellow, Type III interference (3), red, processing (6), orange, regulation (R), green, and non-core cas associated genes (N) are marked purple. Mobilome-associated genes like IS elements and toxin-antitoxin gene pairs were common within or flanking cas gene cassettes, but were mostly omitted from this table. When included, they are marked in grey (M). The genome of *A. brierleyi* is unpublished. Gene calling on *F. acidarmanus* was done using Easygene (<http://cbs.dtu.dk/services/EasyGene/>).

Link to online table:

<http://crispr.archaea.dk/TableS1.html>

Table S2. Non-core *cas* associated genes for the order Thermococcales

name	count	example	gene product
TMPK	5	Py04_0813	thymidylate kinase
reductase	6	CL1_0388	dehydrogenase/reductase
HtpX	6	Py04_0814	Zn(II) dependent protease
nodU	6	Py04_0811	carbomyltransferase
ATPgrasp	6	CL1_0374	ATP-grasp
4Fe4S	5	CL1_0387	ferredoxin domain
Glrx_arch	6	CL1_0385	glutaredoxin domain
HTH	5	CL1_0386	COG1777/HTH
COG5316	6	CL1_0373	no match
?	4	Py04_0812	Unknown
HprK	4	CL1_0384	kinase
lectL	3	TK0467	putative lectine

Figure S1

Dendrogram of all archaeal adaptation modules. The subtype of the associated interference module is indicated to the right. Adaptation modules colour-coded red are susceptible to exchange of Type I interference modules. The light blue rectangle on the left indicates the threshold used for defining the nine classes of adaptation modules summarised in Figure 3. The dendrogram was prepared using the neighbor joining method on module to module distances based on pairwise alignment scores of all constituent protein subunits. The resulting tree was midpoint rooted.

Citation: Vestergaard G, Garrett RA, Shah SA. CRISPR adaptive immune systems of the Archaea. (2014) RNA *biol* 11:3
 Online link: <http://crispr.archaea.dk/FigureS1.pdf>

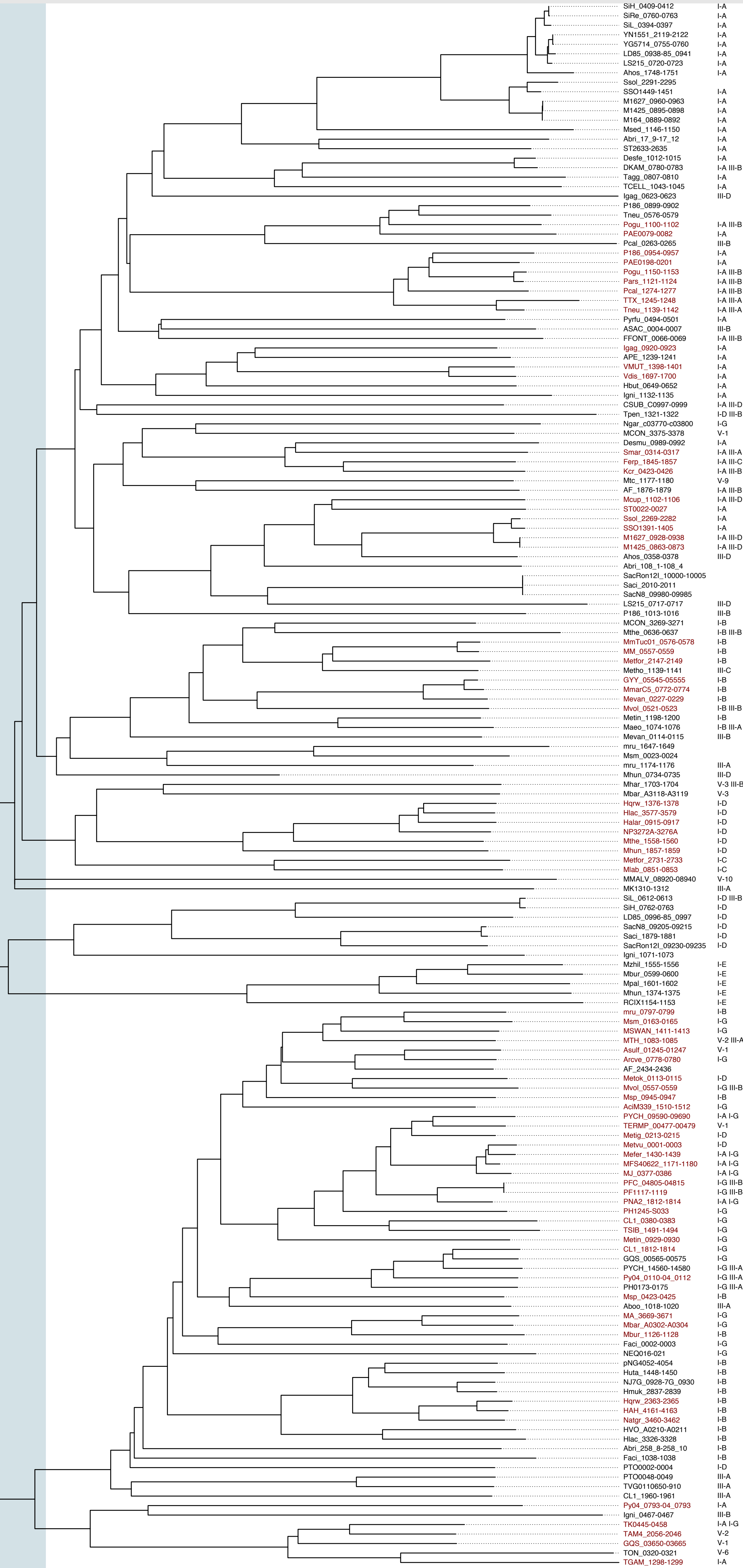


Figure S2

Dendrogram of all archaeal Type I and Type III interference modules. The subtype for each group of interference modules is indicated to the right. Type I modules colour-coded red are susceptible to exchange of adaptation modules. The leftmost vertical line is yellow for Type I systems and red for Type III systems. The wider line following it has different shades for different subtypes. The following blue line is the subtype threshold. Branches occurring before the threshold represent separate subtypes whereas branches initiating after it belong to the same subtype. Branches occurring within it represent separate subtypes if the corresponding modules show consistent changes in gene synteny. If not, they represent deeply diverging variants of the same subtype. The dendrogram was prepared using the neighbor joining method on module to module distances based on pairwise alignment scores of all constituent protein subunits. The resulting tree was midpoint rooted and the subtype threshold was placed so as best to separate the known subtypes defined by the 2011 classification scheme¹⁴.

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 Online link: <http://crispr.archaea.dk/FigureS2.pdf>

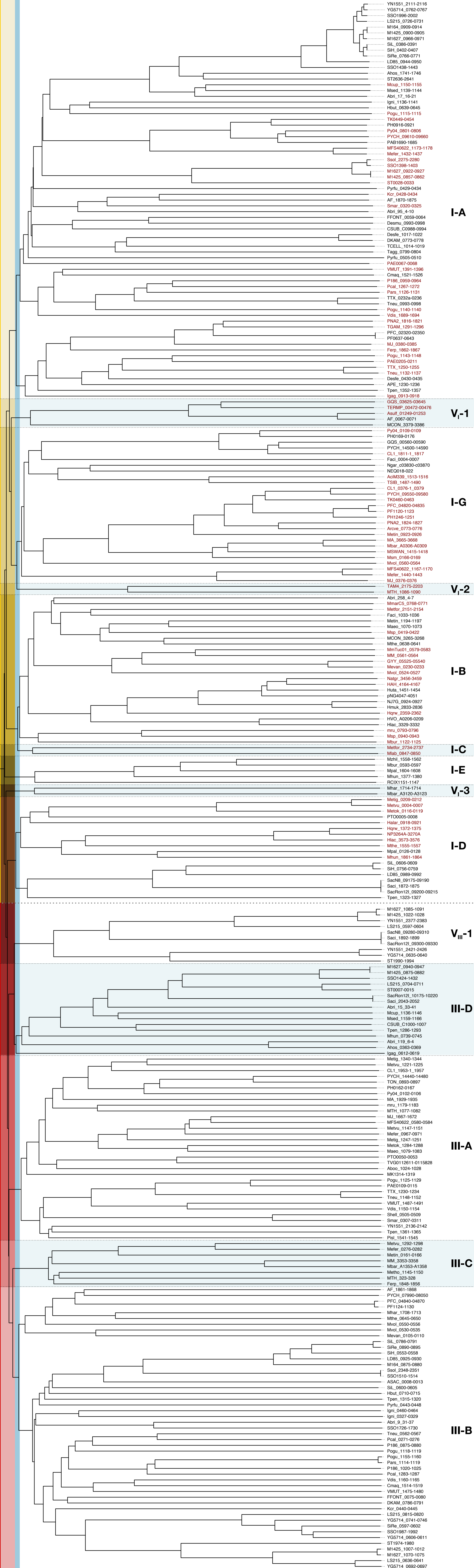
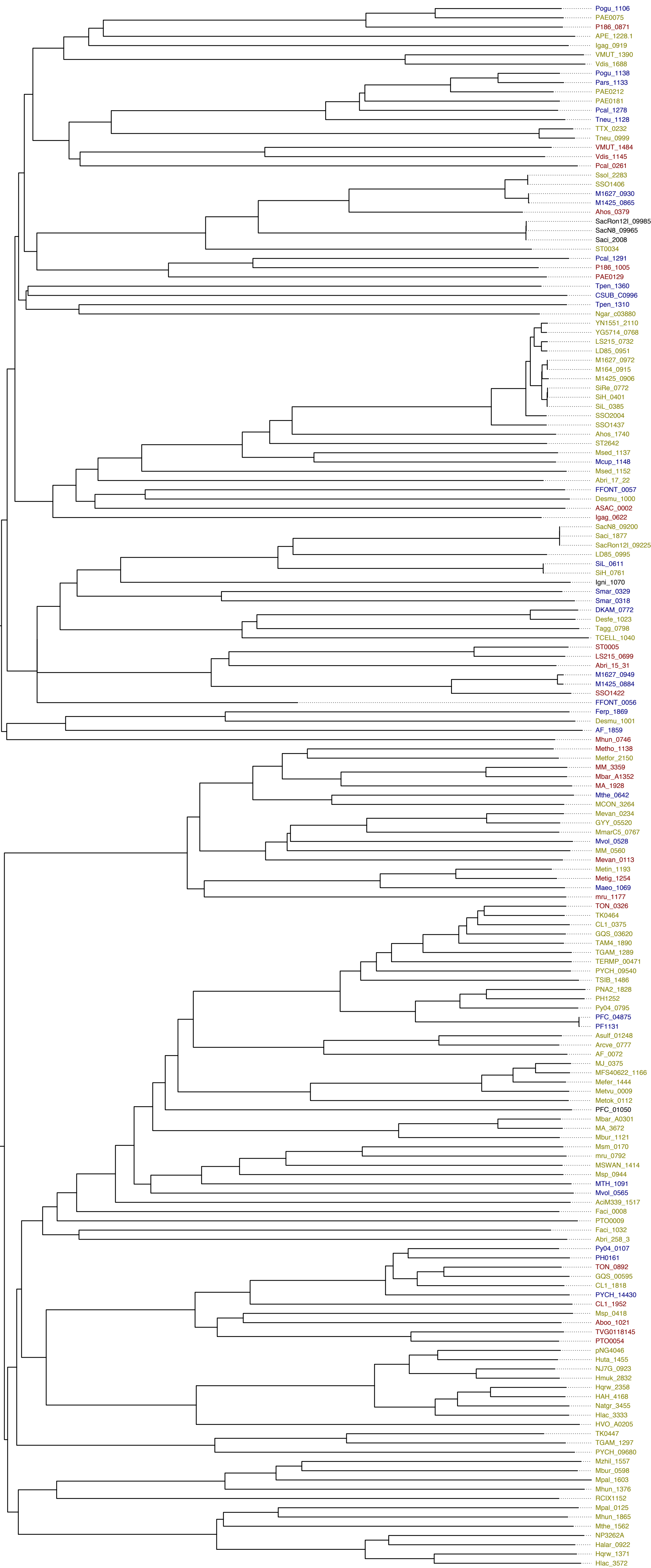


Figure S3

Dendrogram of all archaeal Cas6 sequences which are a part of archaeal cas cassettes (Table S1). Genes colour-coded yellow are associated with Type I interference modules and those colour-coded red are associated with Type III interference modules, while blue cas6 genes are shared between physically linked Type III and Type I interference modules.

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