,Dear Dr Eisen

My name is Adit Naor, a PhD student at Dr. Uri Gophna's lab at Tel-Aviv University in Israel, also working closely with prof. Moshe .Mevarech from our department

I would first like to thank you for allowing us to access to the .recently sequenced genome of Haloferax mediterranei

.I have worked on this organism during my M.Sc studies at prof .Mevarech's lab and have recently done some further work on H .mediterranei

When comparing the genomic location of several genes from Haloferax volcanii to their H. mediterranei homologs, using the database you provided, I noticed that while the gene order was very similar from million bp, the region between 1.8 million to 3 million seemed 0-1.8 to be inverted. To examine whether this inversion occurred at the genome level or whether this inversion represents an error in the assembly procedure, I designed two PCR primers located: about 300 bp a reverse primer), and 1.8mil region (a forward primer). We received) a PCR fragment of about 500 bp which was then sequenced and was shown
in a blast to H. mediterranei to contain the nucleotides positions and then nucleotides positions 1,854,112 to 1,854,288. I 1-352 therefore believe that this "inversion" is actually an error at the scaffold level, probably due to the duplication of the gene coding for 5S rRNA, which has copies both at the 1.8 million region and 3 million .region

,I am attaching a word document containing a schematic illustration the primers and the sequence of the PCR fragment. If more .information/PCR-based verification is required please let me know

Regards
Adit

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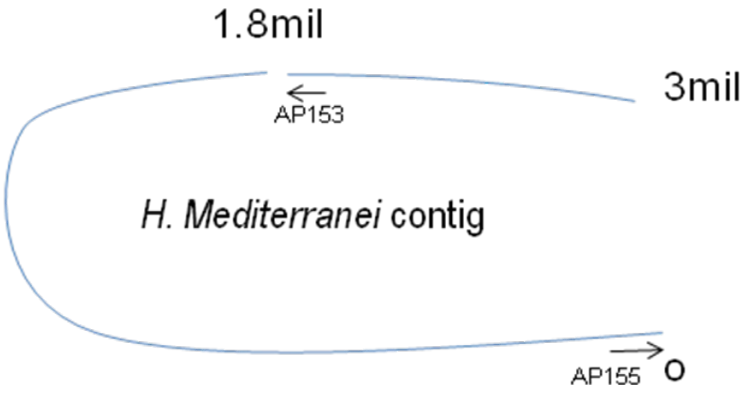

AP153: Med 1.8mil gcaatcgcggtgtgtcgttc

AP155: Med 0mil tcctgtgtgcgatagacgagac

Gatagacgagacctgggaagttatcggggttgaaatccgcaccggggaggtcgtccgcgagggctt
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