# Meeting with Mado 04.10.

Fixed mutation: either mutation is present in whole population or it dies out

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| --- | --- | --- | --- | --- |
| **Microbe.Replicon** | **Microcosme.Replicate** | **Position** | **Ref** | **Alt** |
| AGTU.c01 | 1.1 | 703340 | C | T |
| Replicon: c= Chromosome; p= Plasmid; with Number | Microcosme: Growth in with community  Replicate: Nr. of replicate | Position / Coordinate of SNP; Nr. of nuclotide | Nucleotide in Reference sequence | Alternate nucleotide (SNP) |

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| --- | --- | --- | --- | --- |
| **CHRM\_00001** | **1** | **1461** | **D CDS AGTU.c01\_000010** | **Valid dnaA\_1** |
| Ignore | Nucleotide Start nr. of Gene | Nucleotide Start nr. of Gene | Ignore | Name of Gene (and if Validated or not |

|  |  |  |  |
| --- | --- | --- | --- |
| **replicon AGTU.c01** | **P05648** | **NA** | **Chromosomal replication initiator protein DnaA** |
| Replicon | Uniprot ID (Uniprot: store infomation about protein) | Ignore (is a classification/database ID) | Function of protein |

SNP1 encodes for this protein: CHRM\_00001 703145 704191 D CDS AGTU.c01\_006770 Valid ropA\_2 | replicon AGTU.c01 | Q05811 | NA | Outer membrane protein IIIA 🡪 found manually!!

12.10

3) Based on the Protein sequence (alltogether\_modified.prt): define the consequence of the SNP: synonymous or nonsynonymous ? Calculate dN/dS (if applicable, because few SNPs but the code can be ready for more data)