

Takua: FNE warrior
 Heartgrave: ? shaman works

ie. something in the algorithm?

1 Why would I find primers in the syn.0 anc?
 What could cause that aside from true biology
 It has 57 primers according to bresseq or 10 mutns
 according to GATK (8 are heterozygous in GATK)

2 Is this just definitely x-contamination?

- We know "same" and here is the evidence:
- There are also signatures of parallel evolv.

syn.0 ftsZ ~~Eg~~ ~~1~~ 2 3 4 5
 Q349* 1.0 Q349* .29 Q346* .08 Δ16p 6246051.0 Δ16p 6246051.0
 Δ16p 624254 .05
 G64E .72
 6
 G17C 1.0

→ ipdA: 5/G, have ~~E~~557G (1: .93), and G has 1546N
 Not called in anc.

3b
 → ftsZ 9 10 11 13 14
 E352* 1.0 +ct1062 at 1.0 E315* E315*
 V190I 1.0

→ huaN 9 10 11 13 14
G318R 1.0 G243W 1.0 A31D 1.0 G318R G318R
 R244 K 1.0

→ pgrG 9 10 11 13 14
 V248L G297D D47Y P48L G105V
 EG47* .07

→ pteG 9 10 11 13 14
 EG74* .24 EG64* .54 EG80* 1.0
 Q688* .11 EG84* .40

3. breeding is one thing. > Do you know abt its drawbacks?
> For clones, what programs would you next use for annotation (plus getting the effect on translation, etc?) given > I now have .vcf files ready (from GATK)

- GATK - don't use for pops

- Population2

Does Xpmap - SNPs showed up that weren't in ref strain - MMH xp suggests > mutants do crop up in lab strains

- at least a few xfers, not so worrying

- freezer stock is polymorphic

- SNP eff