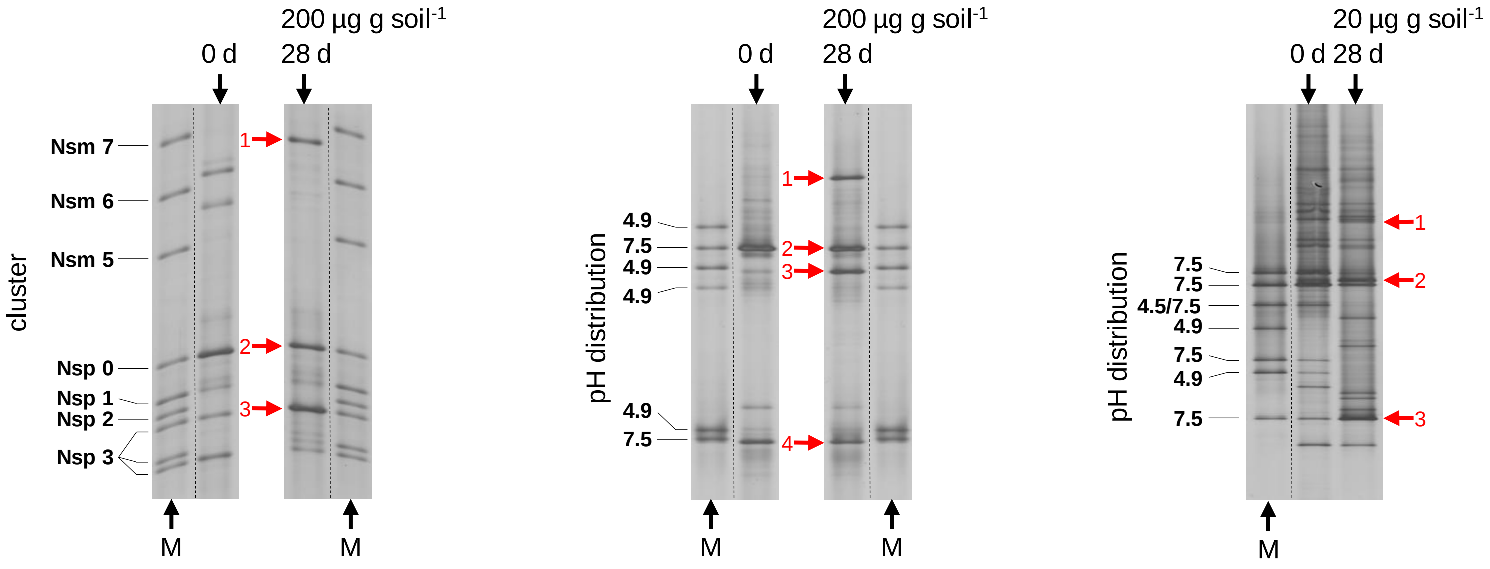

a) AOB 16S rRNA

b) Thaumarchaeal 16S rRNA

c) AOA *amoA*

Supplementary Figure 1. DGGE analysis of individual PCR products derived from single soil microcosms incubated for 0 or 28 days (profiled in Figure 2) alongside marker lanes. (a) M represents a marker composed of 16S rRNA genes sequences from different betaproteobacterial AOB phylogenetic clusters (Purkhold *et al.*, 2003). Numbered arrows indicate migration positions of three band positions (Figure 2e) sequenced and subject to phylogenetic analysis (Supplementary Figure 3a). (b) M represents a marker lane of thaumarchaeal 16S rRNA gene clones amplified from and found in Craibstone soil of pH 4.9 or 7.5 only (Nicol *et al.,* 2008). Numbered arrows indicate four band positions (Figure 2d) sequenced and subject to phylogenetic analysis (Supplementary Figure 2a). (c) M represents a marker lane of thaumarchaeal *amoA* gene clones amplified from and found in Craibstone soil of pH 4.9 or 7.5 only, or both (4.5/7.5). Numbered arrows indicate migration positions of four band positions (Figure 2f) sequenced and subject to phylogenetic analysis (Supplementary Figure 2b).

References

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