

Supplementary Information

Movie DR1 Movie file consisting of 105 individual frames representing 100 nm thick slices, of a FIB milled region of the initial formation of a polymorphic layer. The images show abundant void areas surrounded by bacterioform Au(1) as well as bacterioform Au(2) occurring in the last 34 frames in the lower left region of the layer.

(See: MovieDR1.mov)

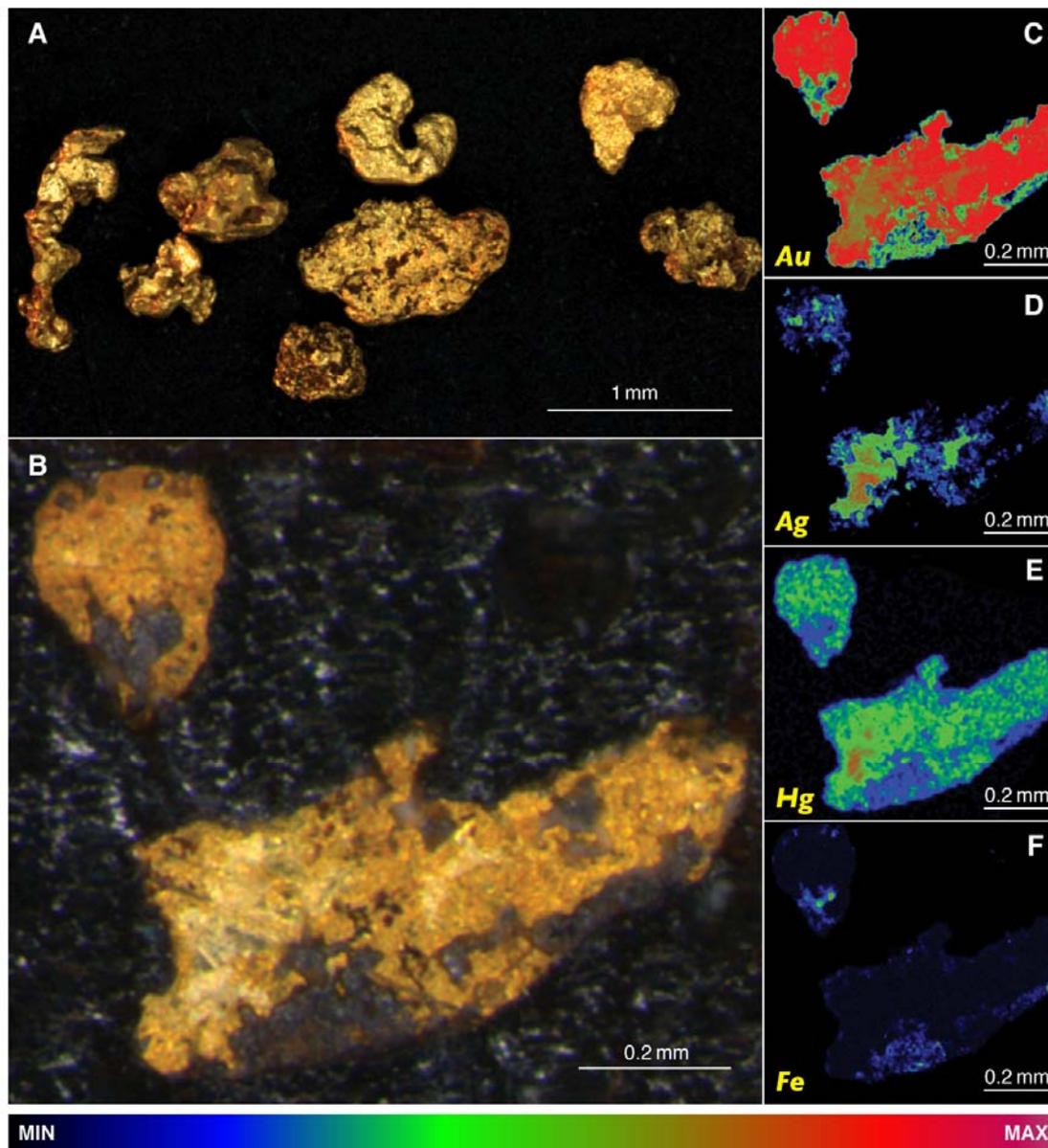


Figure DR1 Optical micrographs and electron microprobe analyses of Au grains from the Prophet Gold Mine, Qld., Australia. **(A)** Typical sizes and morphologies of grains. **(B)** Optical micrograph of polished section of and quantitative analyses of Au **(C)**, max. conc. 99.9 wt.%), Ag **(D)**, maximum conc. 13.5 wt.%), Hg **(E)**, max. conc. 4.3 wt.%), and Fe **(F)**, maximum conc. 3.0 wt.%).

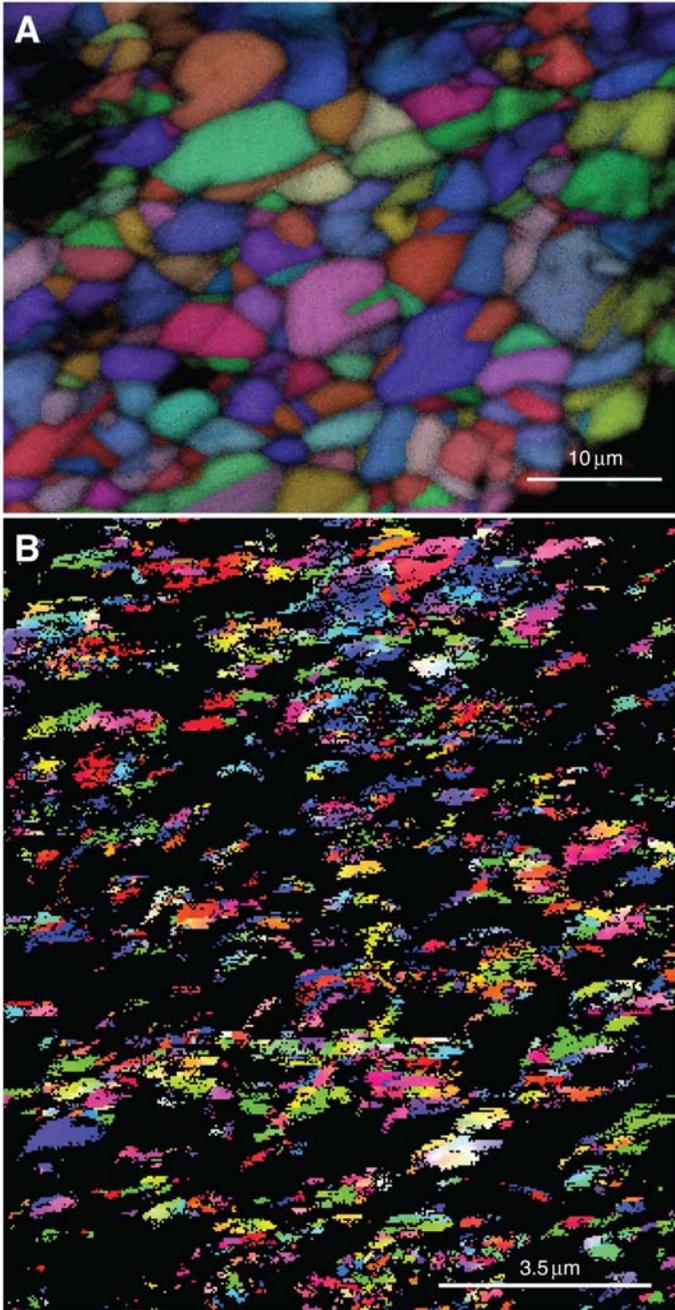


Figure DR2 EBSD maps of an unpolished bacterioform Au grain surface (A) and a polished centre (B) of a Au grain from the Prophet Gold Mine, Qld., Australia.

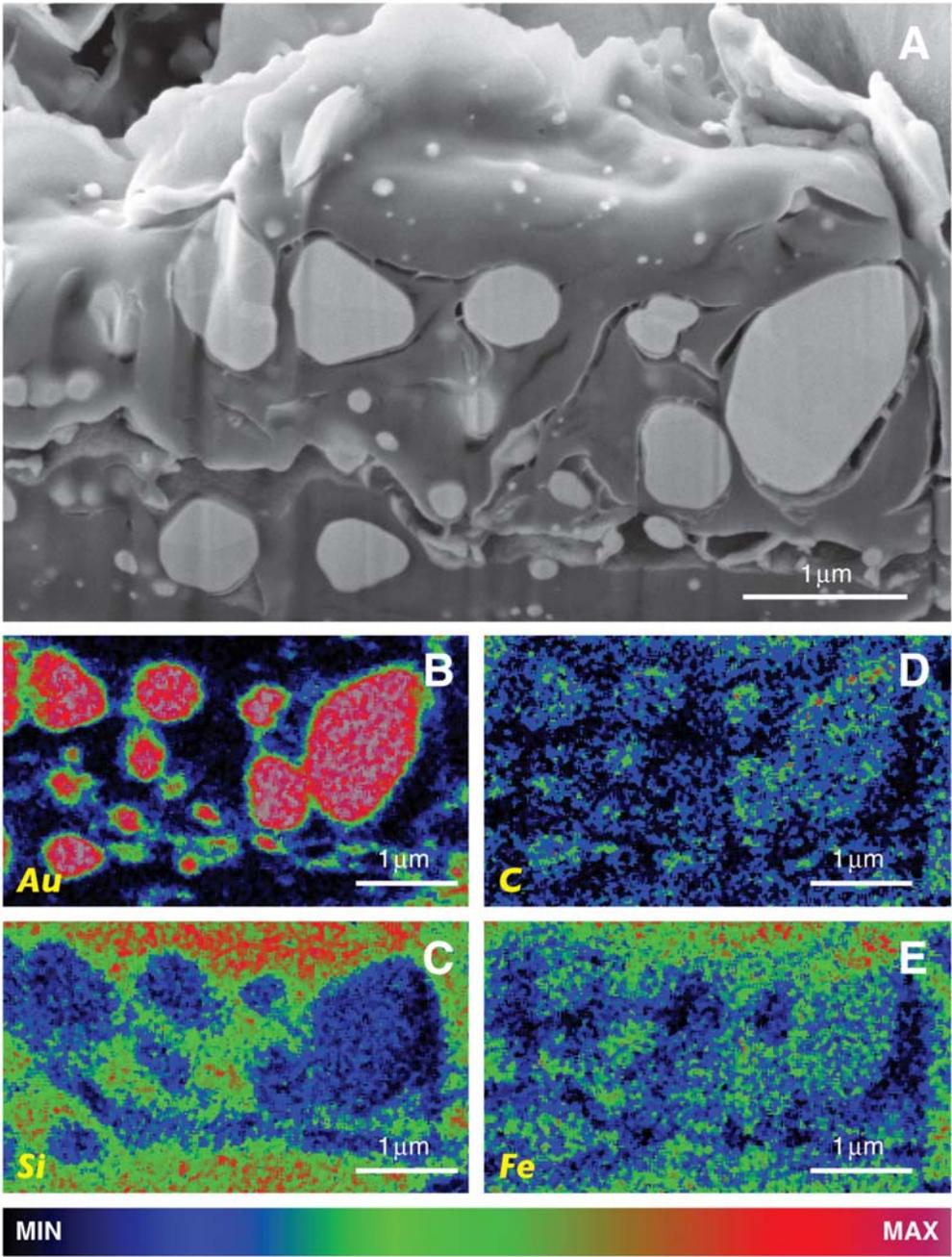
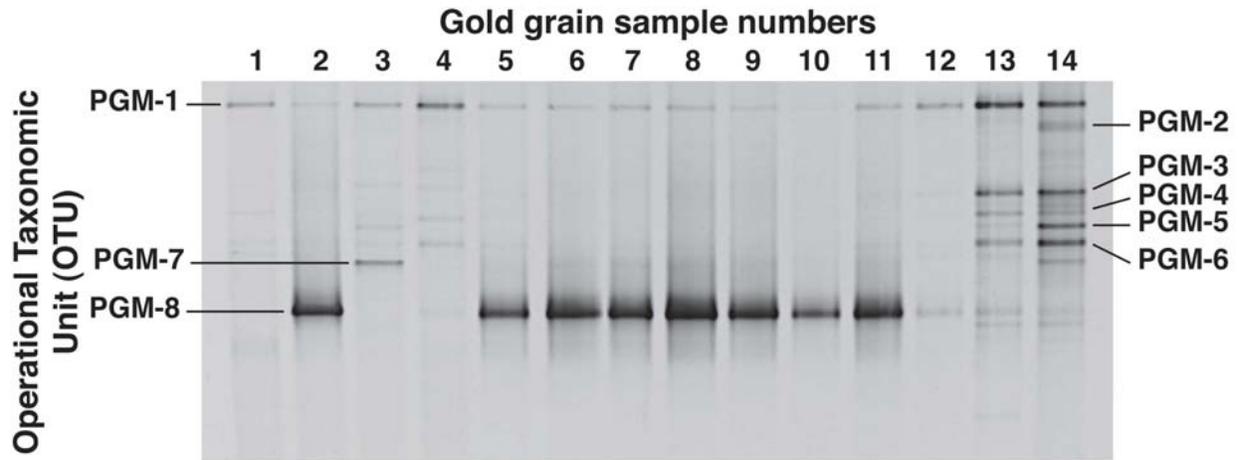


Figure DR3 Secondary electron micrographs (A) and Au, Si, C and Fe maps (B, C, D, E) of a FIB milled section of the polymorphic layer, showing solid buds consisting of high purity Au possibly formed by a combination of biotically-mediated processes.



Representative clone	Phylogenetic affiliation	Most similar sequence in database	Sequenced basepairs [bp]	Percent identity [%]
PGM-1	<i>Delftia</i>	CP000884 - <i>Delftia acidovorans</i> SPH-1	520	100.0
PGM-2	Caulobacteraceae	AY360619 - Uncultured Caulobacteraceae	469	98.1
PGM-3	<i>Burkholderia</i>	GQ359110 - <i>Burkholderia cepacia</i>	524	99.6
PGM-4	<i>Alcaligenes</i>	AJ551119 - <i>Alcaligenes xylooxidans</i>	522	99.2
PGM-5	<i>Hydrogenophaga</i>	AJ585992 - <i>Hydrogenophaga atypica</i> BSB 41.8T	522	99.0
PGM-6	<i>Stenotrophomonas</i>	EU034540 - <i>Stenotrophomonas maltophilia</i> DN1.1	528	100.0
PGM-7	beta-proteobacterium	AF351227 - Uncultured beta proteobacterium	459	98.7
PGM-8	<i>Cupriavidus</i>	<i>Cupriavidus metallidurans</i> strain G1	522	100.0

Figure DR4 (A) PCR-DGGE patterns obtained after amplifying the V3 region of the 16S rRNA amplified directly from Au grains from the Prophet Gold Mine. Bands designated with acronyms were excised from the gels, re-amplified and sequenced. (B) Phylogenetic affiliation of sequenced 16S rRNA OTUs.