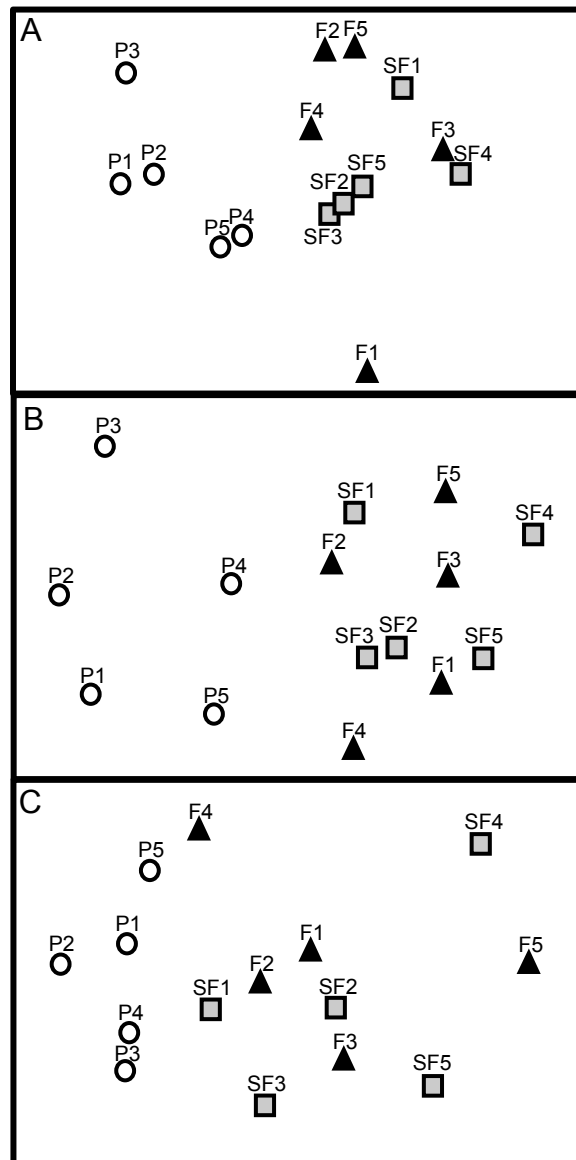
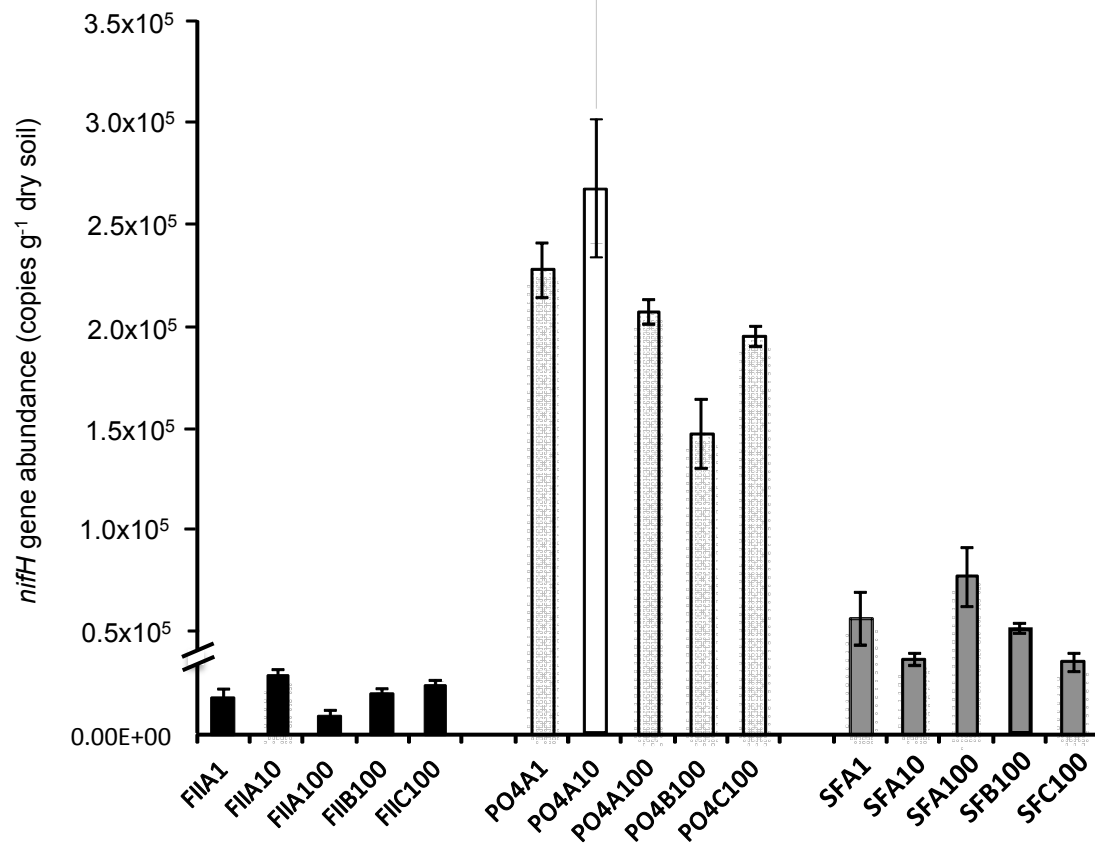


Supplementary figure SF1. Operational taxonomic unit (OTU) accumulation curves for three land uses in the Amazon. Panels: (A) a total of 275 *nifH* gene clone sequences were combined per treatment. A total of 55 *nifH* gene clones sequenced per replicate sample for (B) forest, (C) pasture, and (D) secondary forest. The observed number of OTUs were calculated at 3% dissimilarity.



Supplementary Figure SF2. Non-metric multidimensional scaling representation of the *nifH* gene sequence composition based on Bray-Curtis indices at (A) 95% (B) 90% (C) 80% DNA identity for three different land use systems in the Amazon: Black triangles = forest samples (F), white circle = pasture samples (P), and grey squares = secondary forest samples (SF). The 2D stress for panels A, B, and C were 0.11, 0.12, 0.14, respectively.



Supplementary figure SF3. Copy numbers of the *nifH* gene per gram of soil determined for three different land use systems in the Amazon. Each bar represents the average of the three technical replicates. F= forest, P= pasture and SF= secondary forest.

Supplementary table ST1. Sampling site coordinates and soil physiochemical characteristics for three land use systems in the Amazon.

Sample	Latitude	Longitude	Soil moisture (%)	N	C	C/N	pH	P	S	K	Ca	Mg	Al	H ⁺	CEC	V (%)	Al ⁺ sat (m)
FIIA1	10° 10' 18.74"S	62° 47' 15.60"W	13.80	0.1379	1.728	12.53	5.69	12	4	1.6	48	8	-1	22	79.6	72	-1
FIIA10	10° 10' 18.37"S	62° 47' 15.79"W	17.43	0.2082	2.457	11.80	5.82	18	7	2.2	59	7	1	31	99.2	69	1
FIIA100	10° 10' 15.76"S	62° 47' 17.04"W	13.33	0.173	2.093	12.16	5.42	14	4	4.1	31	11	-1	25	71.1	65	-1
FIIIB100	10° 10' 15.14"S	62° 47' 13.75"W	16.11	0.078	0.9281	11.84	5.15	6	3	2.0	10	5	1	31	48.0	35	6
FIIIC100	10° 10' 18.17"S	62° 47' 12.76"W	13.32	0.1192	1.2025	10.08	5.48	6	3	1.4	26	4	1	25	56.4	56	3
P04A1	10° 09' 44.42"S	62° 47' 58.34"W	14.34	0.082	0.99	12.01	5.27	3	8	3.2	5	4	1	25	37.2	33	8
P04A10	10° 09' 44.06"S	62° 47' 58.42"W	9.68	0.057	0.67	11.79	5.32	2	4	2.8	5	3	1	22	32.8	33	8
P04A100	10° 09' 41.18"S	62° 47' 58.24"W	19.09	0.188	2.79	14.86	5.78	6	4	1.2	40	11	-1	25	77.2	68	-1
P04B100	10° 09' 40.86"S	62° 47' 55.39"W	17.76	0.121	1.90	15.71	5.48	4	3	0.9	15	5	1	31	51.9	40	5
P04C100	10° 09' 44.17"S	62° 47' 55.07"W	9.56	0.099	1.16	11.74	5.23	3	23	1.6	23	4	1	28	56.6	51	3
SCA1	10° 09' 38.16"S	62° 47' 52.62"W	18.10	0.15	1.71	11.68	4.96	5	6	1.4	19	9	1	38	67.4	44	3
SCA10	10° 09' 36.58"S	62° 47' 51.36"W	20.76	0.15	1.77	11.67	5.16	6	5	1.5	24	10	1	42	77.5	46	3
SCA100	10° 09' 34.92"S	62° 47' 53.38"W	14.40	0.15	1.74	11.67	4.88	6	6	1.3	9	6	2	38	54.3	30	11
SCB100	10° 09' 34.70"S	62° 47' 50.14"W	10.37	0.09	1.00	11.18	4.59	6	5	0.6	10	5	3	38	53.6	29	16
SCC100	10° 09' 37.94"S	62° 47' 49.45"W	15.47	0.14	1.86	13.37	4.8	6	3	1.1	13	6	3	58	78.1	26	13

Measured soil variables: C, carbon; N, nitrogen; pH, potential activity of hydrogen; P, phosphorus; S, sulfur; K, potassium; Ca, calcium; Mg, magnesium; Al, aluminum; H⁺, hydrogen; CEC, potential cation exchange capacity; V, base saturation; Al⁺ sat, aluminum saturation.

C and N are expressed in g.Kg⁻¹ soil; P and S are expressed as mg dm⁻³; K, Ca, Mg, Al and CEC are expressed in mmol c.dm⁻³.

Supplementary table ST2. Operational protein units (OPUs) and the closest matched sequences obtained through NCBI BlastP search of few randomly selected *nifH* amino acid sequences from each OPU. The right most column represents the taxonomic grouping assigned based on the Blast search.

OPU No.	Closest relative (Accession number)	% Similarity	Taxonomic description
OPU1	<i>Geobacter daltonii</i> (YP_002538026), <i>Anaeromyxobacter</i> sp.(YP_001380211), <i>Pelobacter propionicus</i> (YP_903117), uncultured bacterium (AY601069), uncultured bacterium (AY601072), <i>Geobacter uraniireducens</i> (NC_009483)	94-99	Delta-proteobacteria
OPU2	uncultured bacterium (ABF66505), uncultured bacterium (ACI32206), uncultured bacterium (ADD48906)	89-99	Uncultured
OPU4	<i>Nostoc azollae</i> (YP_003720733), <i>Anabaena</i> sp. (NC_003272)	97-98	Cyanobacteria
OPU5	<i>Azospirillum</i> (DQ787332), <i>Burkholderia</i> sp. JPY422 (FN544022), <i>Methylocapsa aurea</i> (FN433472), <i>Methylobacterium nodulans</i> (AY312969), <i>Azorhizobium doebereineriae</i> (FJ223129), <i>Bradyrhizobium japonicum</i> (EF394157), <i>Bradyrhizobium</i> sp. SEMIA (HQ259566), <i>Burkholderia tuberum</i> (FN908431), <i>Bradyrhizobium yuanmingense</i> (EF394167), uncultured bacterium (EU912866)	93-100	Alpha/Beta-Proteobacteria
OPU7	<i>Methanocella arvoryzae</i> (YP_686176), <i>Methanocella conradii</i> (YP_005379432)	89-93	Archaea
OPU9	<i>Methanosphaerula palustris</i> (YP_002465657), <i>Methanoregula boonei</i> (YP_001404303)	93	Archaea
OPU10	<i>Diplosphaera colitermitum</i> TAV2 (ZP_03723745), <i>Opitutaceae</i> bacterium TAV5(ZP_09596372)	93-94	Verrucomicrobia
OPU11	uncultured bacterium (EU912903), uncultured bacterium (ACO36751)	85-89	Uncultured
OPU16	uncultured bacterium (EU913014), Uncultured bacterium (EU090292), Uncultured Bacterium (FJ807383)	94-95	Uncultured
OPU19	uncultured bacterium (EU913008) <i>Spirochaeta zuelzeriae</i> (AF325795), Uncultured bacterium (AFK30407)	97-90	Uncultured/ <i>Spirochaetes</i>
OPU51	<i>Syntrophobotulus glycolicus</i> (YP_004267124), uncultured bacterium (AEO13465), <i>Heliobacterium gestii</i> (BAD80876)	90-94	Firmicutes/ <i>Clostridia</i>
OPU56	<i>Paenibacillus sabiniae</i> (HM583799) <i>Paenibacillus sabiniae</i> (HM583798)	92-95	Firmicutes
OPU63	uncultured bacterium (AB273365), <i>Syntrophothermus lipocalidus</i> (YP_003703438), Uncultured bacterium (AB273365)	87-90	Firmicutes/ <i>Clostridia</i>
OPU72	<i>Clostridium kluyveri</i> (YP_001394435), uncultured low G+C Gram-positive bacterium (AAN78187)	97	<i>Clostridia</i>