Table S1. **Examples of prokaryotic "lifestyles" in respect to heme and siroheme**

	ALA biosynthesis			**Uro'gen III biosynthesi**			**Siroheme biosynthesis**			**Heme biosynthesis, alternative**				**Heme biosynthesis, transitional and classic pathways**								
	C5 pathway		C4 path	common pathway						siroheme-dependent					coproporphyrin-dependent			protoporphyrin-dependent				
Historic enzyme and gene names:	**GltR**	**GAST**	**ALAS**	**PBS**	**PBD**	**UROS**	**UROM**	**PR2O**	**SIRFC ***	**AhbA**	**AhbB**	**AhbC**	**AhbD**	**UROD**	**Copro'gen OX**	**Copro DC**	**Copro FC**	**Copro'gen DC**		**Pro'gen OX**		**Proto FC**	**Sample organism**
	hemA (C5)	*hemL*	*hemA (C4)*	*hemB*	*hemC*	*hemD*	*(cysG)* *	*CysG*	*CysG, SirB, ChiK*	*ahbA*	*ahbB*	*ahbC*	*ahbD*	*hemE*	*hemY*	*hemQ*	*hemH(c)*	*hemF*	*hemN*	*hemG*	*hemJ*	*hemH(p)*	
Proposed new enzyme nomenclature:	**GtrR**	**GsaM**	**AlaS**	**PbgS**	**HmbS**	**UroS**								**UroD**	**CgoX/PgoX**	**ChdC**	**CpfC**	**CgdC**	**CgdH**	**PgdH1**	**PgdH2**	**PpfC**	
Signature genes for:																							
sirocheme-dependent route >>										🟩	🟩	🟩		**NO**									
coproporphyrin-dependent route >>													🟦	**YES**	🟦	🟦							
protoporphyrin-dependent route >>														**YES**				🟧	🟧	🟧	🟧		
Examples of the 3 basic routes of heme bios:																							
siroheme-dependent >>	+	+		+	+	+	+	+	+	+	+	+	+										*Desulfovibrio vulgaris Hildenborough*
coproporph-dependent (via HemQ) >>	+	+		+	+	+	+	+	+					+	+	+	+						*Bacillus subtilis 168*
coproporph-dependent (via AhbD) >>	+	+		+	+	+	+	+	+				+	+	+		+						*Geobacter sulfurreducens PCA*
protoporphyrin-dependent >>	+	+		+	+	+	+	+	+					+				+	+		+	+	*Escherichia coli K12*
Coexistence of 2 heme routes in one org:																							
two heme routes are present (2 FCs) >>	+	+		+	+	+	+	+	+						+	+	+	+	+	+		+	*Rhodanobacter sp. 2APBS1*
two heme routes are present >>	+	+		+	+	+	+	?	?	+	+	?	+		+	+	+						*Methylomirabilis oxyfera*
Variations in the source of uro'gen III:																							
de novo ALA bios. via C5 pathway >>	+	+		+	+	+	+							+				+	+	+		+	*Synechocystis sp. PCC 6803*
both, C4 and C5 pathways are present >>	+	+	+	+	+	+	+	+	+					+	+			+	+	+		+	*Chromobacterium violaceum*
de novo ALA bios via C4 pathway >>			+	+	+	+	+	+	+					+				+	+	+		+	*Agrobacterium tumefaciens str. C5*
dependence on exogenous ALA >>				+	+	+	+	+	+														*Clostridium botulinum ATCC 3502*
dependence on porphobilinogen >>					+	+	+	+	+														*Buchnera aphidicola str. APS*
dependence on porphobilinogen >>					+	+	+	+	+					+				+			+	+	*Serratia symbiotica 'Cinara cedri'*
dependence on exogenous uro'gen III >>							+	+	+														*Roseburia intestinalis XB6B4*
Dependence on exogenous heme/siroheme? -																							
protoheme ferrochelatase only >>																						+	*Streptococcus pneumoniae R6*
sirocheme ferrochelatase only >>									+														*Treponema denticola ATCC 35405*
Predicted "hybrid" paths for heme or other tetrapyrroles																							
path with archaeal ChdC(long) + AhbCD	+	+		+	+	+	+	+	+			+	+			long							*Halobacterium sp. NRC-1*
path with archaeal ChdC(long) + AhbCD + more	+	+		+	+	+	+	+	+			+	+	+		long					+	+	*Halorhabdus utahensis DSM 1294*
	+	+		+	+	+	+	+	?				+	+			+						*Thermoplasma volcanium GSS1*
path with AhbAB + HemQ	+	+		+	+	+	+	+	+	+	+					+							*Deinococcus geothermalis DSM*
path with AhbAB + classic heme bios	+	+		+	+	+	+	+	+	+	+			+					+	+		+	*Persephonella marina EX-H1*

Table S2. Signature genes for detection of the 3 main routes of heme biosynthesys in prokaryotic genomes

	Heme biosynthesis, alternative				Heme biosynthesis, transitional and classic pathways									
	siroheme-dependent					coproporphyrin-dependent			protoporphyrin-dependent					
Historic enzyme/gene names:	**AhbA**	**AhbB**	**AhbC**	**AhbD**	**UROD**	**Copro'gen OX**	**Copro DC**	**Copro FC**	**Copro'gen DC**		**Pro'gen OX**		**Proto FC**	**Sample organisms**
	ahbA	*ahbB*	*ahbC*	*ahbD*	*hemE*	*hemY*	*hemQ*	*hemH(c)*	*hemF*	*hemN*	*hemJ*	*hemG*	*hemH(p)*	
Proposed new enzyme nomenclature:					UroD	CgoX/PgoX	ChdC	CpfC	CgdC	CgdH	PgdH1	PgdH2	PpfC	
sirocheme-dependent route	🟩	🟩	🟩		**NO**									*Desulfovibrio vulgaris; Sulfolobus tokodaii*
coproporphyrin-dependent route				🟦	**YES**	🟦	🟦							*Geobacter sulfurreducens; Bacillus subtilis*
protoporphyrin-dependent route					**YES**				🟧	🟧	🟧	🟧		*Escherichia coli K12; Neisseria meningitidis*

Table S3. Phylogenetic distribution of the siro-, copro-, and proto- dependent routes of heme biosynthesis among the 983 representative prokaryotic genomes. See SEED subsystem for details: http://pubseed.theseed.org//SubsysEditor.cgi?page=ShowSubsystem&subsystem=Heme_Biosynthesis%3A_protoporphyrin-_and_coproporphyrin-dependent_pathways

	Major taxa analysed	**Total genomes from taxon** included in the 983 set	**Number of organisms per taxon encoding each of the 3 main heme biosynthesis pathways**				**Fraction of organisms per taxon with each of the 3 heme biosynthesis pathways (%)**			
			NO heme bios	**AhbABCD**	**CPD**	**PPD**	NO heme	**AhbABCD**	**CPD**	**PPD**
			Total cases among the 983 orgs:							
			233	**76**	**166**	**471**				
			24%	8%	17%	48%				
Archaea	**Archaea**									
	Crenarchaeota	17	3	12	-	-				
	Euryarchaeota	35	19	8	-	-				
	Korarchaeota	1	-	-	-	-				
	Nanoarchaeota	1	1							
Eubacteria	Actinobacteria	99	13	3	81	-				
Monoderm	**Firmicutes:**									
	Bacillales	36	-	1	34	-				
	Clostridia	91	62	25	4	-				
	Lactobacillales	42	42	-	-	-				
	Erysipelotrichales	7	7	-	-	-				
	Negativicutes	3	2	1	-	-				
	Chloroflexi (green non-sulfur bacteria)	11	2	1	6	2				
	Thermotogae*	10	10	-	-	-				
Transitional	Deinococcus-Thermus	10	-	-	8	1				
Eubacteria	**Proteobacteria:**									
Diderm	Alphaproteobacteria	109	4	-	-	106				
	Betaproteobacteria	62	1	-	-	61				
	Gammaproteobacteria	174	11	-	4	159				
	Epsilonproteobacteria	27	-	-	-	27				
	Zetaproteobacteria	1	-	-	-	1				
	Deltaproteobacteria	38	-	19	13	5				
	Acidobacteria	4	-	1	3	-				
	Aquificae (class)	9	-	-	2	7				
	Armatimonadetes	1	-	-	-	-				
	Bacteroidetes/Chlorobi; Bacteroidetes	70	15	-	-	51				
	Bacteroidetes/Chlorobi; Chlorobi (green sulfu	9	-	-	-	9				
	Chlamydiae/Verrucomicrobia group	12		1	-	9				
	Cyanobacteria	25	-	-	-	25				
	Deferribacteres	2	-	-	2	-				
	Fusobacteria*	6	6	-	-	-				
	Gemmatimonadetes	1	-	-	-	1				
	Nitrospira	3	-	-	2	1				
	Planctomycetes	7	-	-	7	-				
	Spirochaetes	18	13	-	-	5				
	Synergistetes	9	7	2	-	-				
	Thermodesulfobacteria	2	-	2	-	-				
	Chrysiogenetes	1	-	-	1	-				
	Tenericutes; Mollicutes*	17	17	-	-	-				
	Caldithrix	1	-	-	-	1				
	Thermobaculum	1	-	-	-	-				

Phyla that include photosynthetic organisms are highlighted in green

*: no heme biosynthetic genes detected in any representatives of this taxon with sequenced genomes