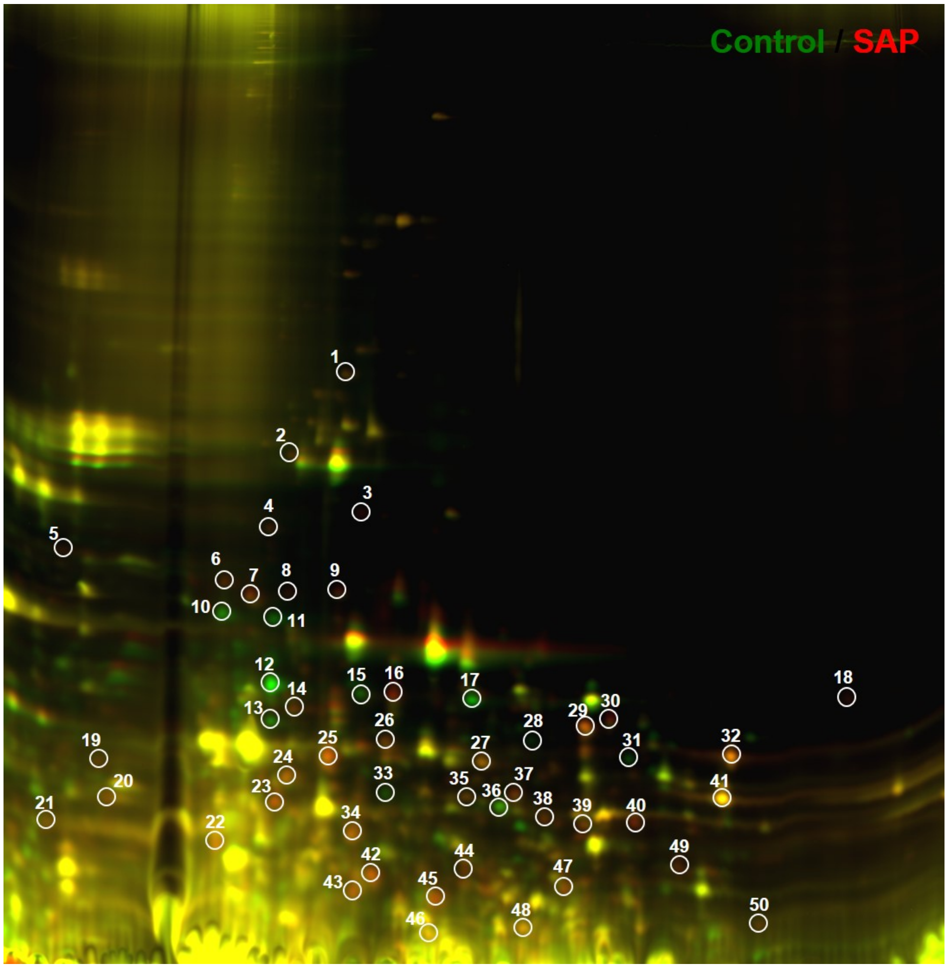
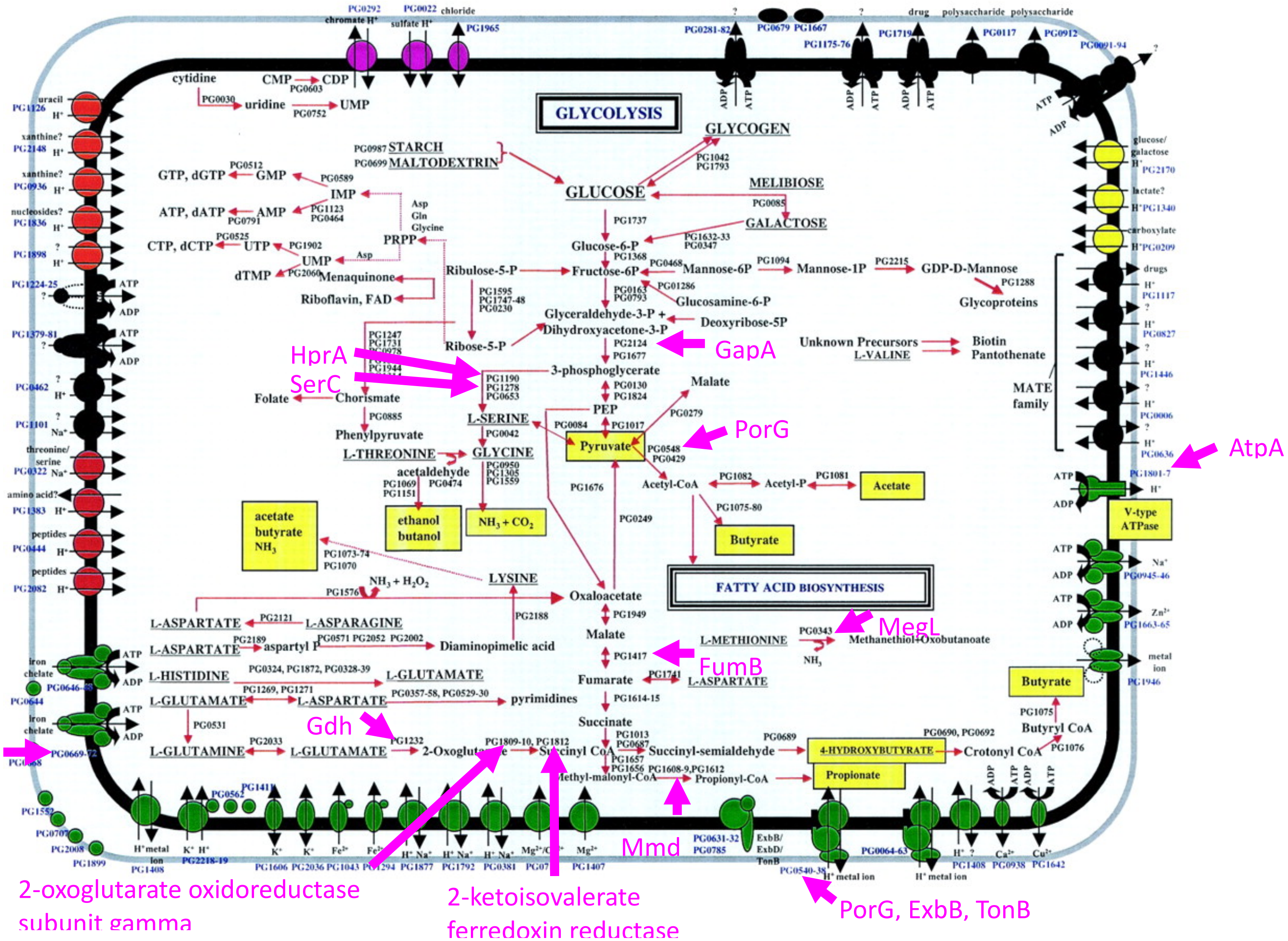


Supplementary Figure 1. 2D-DIGE gel showing *P. gingivalis* protein differences in untreated and sapienic acid-treated samples. Red spots indicate upregulation of proteins in treated samples and green spots indicate downregulation of proteins, relative to the control sample. Yellow spots indicate colocalization, where the same proteins were present in both samples. This previously published figure was included with permission from the Nature Publishing Group (Fischer, et al., Int J Oral Sci 5(3):130-140).

Supplemental Figure 2. Overview of the current state of knowledge of *P. gingivalis* metabolism and transport. This overview of the current state of knowledge of *P. gingivalis* metabolism and transport, published by Dr. Nelson, et. al (Journal of Bacteriology, 2003; 185:5591-5601)^1 has been reprinted with permission from ASM journals. We have annotated it (pink words and arrows) to show where the metabolic pathways involved with sapienic acid treatment of *P. gingivalis* fit within known *P. gingivalis* metabolic data (Nelson KE, et al. 2003. J Bacterol 185:5591-5601).



Supplemental Table 1. Complete list of all proteins differentially expressed and fold changes with sapienic acid treatment (relative to untreated controls).

Spot #	Locus	Gene	Blast result (top hit)	Cellular role, Pathway, Function	Fold Change
Translational activities					
50	PG0314	*rplU*	S1 30S ribosomal protein	Translation – structural constituent of ribosome; binds mRNA and facilitates recognition of translation initiation point	+1.9
42	PG1297	*rpsA*	L21 50S ribosomal protein	Translation – ribonucleoprotein; binds to 23S rRNA	+2.6
Transport systems and associated surface receptors					
43	PG0780	*exbD*	TonB complex protein	Provides energy for transport of heme/other large molecules into bacterial cells; integral membrane protein	+3.6
13	CAA68897	*tlr*	TonB-linked adhesion/receptor	Outer membrane receptor; binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	-3.0
10	PG0185	*ragA*	TonB-linked adhesion/receptor	Temperature-regulated receptor that binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	-9.6
11	PG0185	*ragA*	TonB-linked adhesion/receptor	Temperature-regulated receptor that binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	-6.6
20	PG0185	*ragA*	TonB-linked adhesion/receptor	Temperature-regulated receptor that binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	+2.9
38	PG0185	*ragA*	TonB-linked adhesion/receptor	Temperature-regulated receptor that binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	+2.1
46	PG0185	*ragA*	TonB-linked adhesion/receptor	Temperature-regulated receptor that binds heme/other large molecules for transport into bacterial cells; transport depends upon energy supplied by the TonB complex	+1.6
Central metabolism: glycolysis, gluconeogenesis, and the TCA cycle					
39	PG0548	*porG*	Pyruvate ferredoxin/flavodoxin	Predicted to function in the pyruvate pathway to acetate; electron carrier activity; iron binding; cofactor binding; cation binding	+1.7

23	PG1755	*fba*	Fructose-1,6-bisphosphate aldolase	Glycolysis, gluconeogenesis, TCA cycle; amino acid metabolic processes (anabolic and catabolic)	+2.4
29	PG2124	*gapA*	Glyceraldehyde 3-phosphate dehydrogenase; type 1	Glycolysis; nucleotide binding; phosphorylating activity	+2.5
32	PG2124	*gapA*	Glyceraldehyde 3-phosphate dehydrogenase; type 1	Glycolysis; nucleotide binding; phosphorylating activity	+2.3
34	PG1809		2-oxoglutarate oxidoreductase subunit gamma	Oxidoreductase activity; catalytic activity; microbial metabolism in diverse environments; TCA cycle; metabolic pathways; carbon metabolism	+2.0
44	PGN_1117		Acetyl-CoA synthetase	Cofactor binding	+3.2
21	PG1812		2-ketoisovalerate ferredoxin oxidoreductase	TCA cycle, metabolic pathways, microbial metabolism in diverse environments; carbon metabolism	+1.8
Metabolism of peptides/amino acids					
14	PG1232	*gdh*	NAD-dependent glutamate dehydrogenase	Primary pathway: metabolism of glutamate and aspartate for energy production; reverse (anabolic reaction is also possible under certain conditions – leading to glutamate biosynthesis)	+2.3
16	PG1232	*gdh*	NAD-dependent glutamate dehydrogenase	Primary pathway: metabolism of glutamate and aspartate for energy production; reverse (anabolic reaction is also possible under certain conditions – leading to glutamate biosynthesis)	+3.3
25	PG1232	*gdh*	NAD-dependent glutamate dehydrogenase	Primary pathway: metabolism of glutamate and aspartate for energy production; reverse (anabolic reaction is also possible under certain conditions – leading to glutamate biosynthesis)	+2.3
26	PG1232	*gdh*	NAD-dependent glutamate dehydrogenase	Primary pathway: metabolism of glutamate and aspartate for energy production; reverse (anabolic reaction is also possible under certain conditions – leading to glutamate biosynthesis)	+2.3
	PG1190	*hprA*	Glycerate dehydrogenase	Biosynthesis of secondary metabolites; metabolism of amino acids; microbial metabolism in diverse environments	
24	PG1278	*serC*	Phosphoserine aminotransferase	Microbial metabolism in diverse environments; methane metabolism; amino acid metabolism/biosynthesis	+1.9

36	PG0343	*megL*	Methionine gamma-lyase	Cofactor-binding enzyme involved in multiple amino acid metabolic pathways; catalyzes the committed step of methionine biosynthesis	-3.3
Lipid biosynthesis and metabolism					
6	PG1764	*fabF*	3-oxoacyl-(acyl-carrier protein) synthase II	Thermal regulation of membrane fatty acid composition; elongates fatty acid chains during synthesis	+2.4
7	PG1764	*fabF*	3-oxoacyl-(acyl-carrier protein) synthase II	Thermal regulation of membrane fatty acid composition; elongates fatty acid chains during synthesis	+2.2
12	PG1764	*fabF*	3-oxoacyl-(acyl-carrier protein) synthase II	Thermal regulation of membrane fatty acid composition; elongates fatty acid chains during synthesis	-20.6
8	PG2124	*fabH*	3-oxoacyl-(acyl-carrier protein) synthase III	ACP synthase initiates and controls the rate of fatty acid biosynthesis; determines whether fatty acids are branched/straight-chain; only reversible step in the fatty acid elongation process	+1.9
Respiration					
27	PG1417	*fumB*	Fumarate hydratase, Class 1	Fumarate respiratory chain: Reversibly catalyzes the hydration/dehydration of fumarate to malate	+1.9
35	PG1803	*atpA*	V-type ATP synthase, subunit A	Fumarate respiratory chain: V-type ATP synthase function – transport Na^+ or H^+ ions into the bacterial cells in an energy-dependent fashion; can also reverse direction to export Na^+ out of bacterial cells	+1.7
4	PG1609	*mmdA*	Methylmalonyl-CoA	Fumarate respiratory chain: helps generate transmembrane Na^+ gradient; helps regulate cellular homeostasis by transport of H^+ and Na^+ across the membrane	+2.1
19	PGN_0503	*mmdC*	Biotin carboxyl carrier protein	Fumarate respiratory chain: helps generate transmembrane Na^+ gradient; helps regulate cellular homeostasis by transport of H^+ and Na^+ across the membrane	+2.1
30	PG0304	*rnfC*	RnfABCDGE type electron transport complex subunit C	Fumarate respiratory chain: Part of Complex I, helps transport electrons to a nitrogenase via ferredoxin	+2.4
Iron acquisition and processing/Virulence					

28	PG0669	*fetB*	Heme-binding protein FetB	Heme binding protein involved in the anaerobic cobalamin biosynthetic process	+1.8
9	PGN_1970	*rgpA*	Arginine-specific cysteine proteinase RpgA	Acquire and degrade heme-containing molecules for acquisition of heme/peptides needed for growth; virulence factor	+2.3
40	PGN_1970	*rgpA*	Arginine-specific cysteine proteinase RpgA	Acquire and degrade heme-containing molecules for acquisition of heme/peptides needed for growth; virulence factor	+3.2
1	PG0506	*rpgB*	Arginine-specific cysteine proteinase RpgB	Acquire and degrade heme-containing molecules for acquisition of heme/peptides needed for growth; virulence factor	+1.7
22	PG0506	*rpgB*	Arginine-specific cysteine proteinase RpgB	Acquire and degrade heme-containing molecules for acquisition of heme/peptides needed for growth; virulence factor	+2.2
41	PGN_1728	*kgp*	Lysine-specific cysteine proteinase Kgp	Acquire and degrade heme-containing molecules for acquisition of heme/peptides needed for growth; virulence factor	+1.7
2	PG0181	*fimA*	Fimbrial protein, type II	Adhesion to host tissues and salivary molecules	+3.9
31	PG1844	*hagD*	Hemagglutinin D	Adhesion for colonization and nutritional purposes	-2.9
33	PG1844	*hagD*	Hemagglutinin D	Adhesion for colonization and nutritional purposes	-3.5
15	PG2024	*hagE*	Hemagglutinin E	Adhesion for colonization and nutritional purposes	-3.2
18	PG0443		Hemagglutinin-like protein		+2.0
17	PG1385	*tprA*	Tpr domain protein	Tetratricopeptide repeat-containing protein	-13.8
Stress					
45	PG1545	*sod*	Superoxide dismutase	Confers tolerance to oxidative stress	+1.8
Unknown function					
49	PGN_1023	*olpA*	Acid phosphatase OlpA	Acid phosphatase (Class B); 5’ nucleotidase lipoprotein 3(P4)	+1.8
5	PG1486	*traA*	Putative conjugate transposon protein TraA		+2.2

37	PG1486	*traA*	Putative conjugate transposon protein TraA		+1.9
47	PGN_1950		Hypothetical protein		+1.9
48	PG1684		Hypothetical protein		+2.1