

Table S1. Primers for QPCR.

| GeneID | Function | | Sequence (5'-3') |
|------------------|---|-----------|--|
| HMPREF0421_20131 | subunit A of gyrase | | F: TGACACTTGGTCGTATGGC R: TCCGTATAACGCATTGCTGC |
| HMPREF0421_20660 | sensor kinase | histidine | F: GTGGTACTGGCTTAGGTATGTCT R: ATCACTGCTGGCCTAGATGC |
| HMPREF0421_20990 | sensor kinase | histidine | F: CGAAATGGCTGAAGAACTAGAGC R: TAGCTTGTAAATGCACTAACAGGTG |
| HMPREF0421_20118 | thioredoxin-disulfide reductase | | F: GCAAGAATACTCTGGACGAGGT R: CAAAAGCTGAATGCCCTCCG |
| HMPREF0421_21330 | glutaredoxin | | F: GCGTCAATTCACTAACGCTAGGC R: GAGTAATCACCACTGGCGCT |
| HMPREF0421_21015 | 3-oxoacyl-ACP reductase | | F: ACGCAACAAACCATGCTTTAT R: GCGTATGCTGCTGTTCTAG |
| HMPREF0421_21022 | sensor kinase | histidine | F: GCCTTATTGTTGCAGCAATAGC R: CCTTGATCCCATTGCTGC |
| HMPREF0421_21221 | sulfonate transporter permease | ABC | F: TATTCGTCATTGCATGCCG R: GTGAACCTGTGCGTCCGAAT |
| HMPREF0421_20219 | major facilitator superfamily (MFS) transporter | | F: ACCAGCAAGCACAAATAGC R: ACTCCTAAGACTATTAACCATGGTGT |
| HMPREF0421_20303 | actinobacterial surface-anchored domain protein | | F: CGAAAGAAACTAAAACCACTAATACTG R: TCCCGTTCTTAACAACAGAC |
| HMPREF0421_20991 | transferring glycosyl groups | | F: TATTCGTGCTCAACTTATGTAGG R: CCAAATATGAAAAAGGCTTATCG |
| HMPREF0421_20208 | hydroxyethylthiazole kinase | | F: GCAGAAGAAGCTGAAGTCTTGC R: CGAATCGCAGCATCCATAGATTC |
| HMPREF0421_21089 | type IV prepilin peptidase | | F: TGTGCCTAGACTTGGTTGT R: TACTGCAAAAGCCAGCCAC |

Table S2. Unique genes in the Venn analysis.

| Unique genes | GeneID | Function |
|--------------|------------------|--|
| Control | HMPREF0421_20665 | integral component of membrane |
| | HMPREF0421_20284 | hypothetical protein |
| | HMPREF0421_20681 | hypothetical protein |
| | HMPREF0421_20017 | hypothetical protein |
| | HMPREF0421_20419 | hypothetical protein |
| | HMPREF0421_21040 | inclusion membrane protein F |
| | HMPREF0421_21316 | hypothetical protein |
| Lac | HMPREF0421_20047 | hypothetical protein |
| | HMPREF0421_21359 | type I restriction enzyme, R subunit |
| | HMPREF0421_20088 | hypothetical protein |
| LacHyd | HMPREF0421_20371 | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase |

Table S3. List of the genes with fold changes above two among the differentially expressed genes in *G. vaginalis* cultured under lactate. All *P* values were less than 0.02.

| GeneID | Log2Fold Change | <i>P</i> value | <i>P</i> adj | Function |
|------------------|-----------------|-------------------------|-------------------------|---|
| Upregulated | | | | |
| HMPREF0421_21022 | 3.65 | 5.42×10^{-166} | 1.51×10^{-164} | Sensor histidine kinase |
| HMPREF0421_21024 | 3.24 | 1.31×10^{-18} | 4.20×10^{-18} | ABC transporter |
| HMPREF0421_20927 | 3.15 | 0 | 0 | ABC transporter substrate-binding protein |
| HMPREF0421_20219 | 2.97 | 4.12×10^{-71} | 4.02×10^{-70} | major facilitator superfamily (MFS) transporter |
| HMPREF0421_21023 | 2.96 | 1.88×10^{-14} | 5.23×10^{-14} | Hypothetical protein |
| HMPREF0421_21015 | 2.90 | 1.27×10^{-91} | 1.64×10^{-90} | 3-oxoacyl-ACP reductase |
| HMPREF0421_21026 | 2.73 | 5.07×10^{-21} | 1.72×10^{-20} | ABC transporter ATP-binding protein |
| HMPREF0421_21025 | 2.70 | 6.04×10^{-33} | 2.94×10^{-32} | ABC transporter ATP-binding protein |
| HMPREF0421_20844 | 2.59 | 0 | 0 | Cobalt ABC transporter |
| HMPREF0421_20843 | 2.36 | 5.32×10^{-206} | 2.16×10^{-204} | Membrane protein |
| HMPREF0421_20839 | 2.20 | 0 | 0 | NADH dehydrogenase |
| HMPREF0421_20940 | 2.17 | 0 | 0 | oligoribonuclease |
| HMPREF0421_21014 | 2.05 | 1.04×10^{-120} | 2.04×10^{-119} | 2-keto-3-deoxygluconate permease |
| Downregulated | | | | |
| HMPREF0421_20991 | -3.24 | 7.95×10^{-28} | 3.39×10^{-27} | Transferring glycosyl groups |
| HMPREF0421_21002 | -2.86 | 9.73×10^{-82} | 1.06×10^{-80} | Cell division protein FtsK |
| HMPREF0421_20208 | -2.75 | 0 | 0 | Hydroxyethylthiazole kinase |
| HMPREF0421_21089 | -2.51 | 4.12×10^{-12} | 1.06×10^{-11} | Type IV prepilin peptidase |
| Novel C3 | -2.46 | 9.40×10^{-20} | 3.08×10^{-19} | Transcription regulator |
| HMPREF0421_20331 | -2.24 | 5.36×10^{-58} | 4.22×10^{-57} | Serine/threonine protein kinase |
| HMPREF0421_20303 | -2.21 | 8.22×10^{-223} | 4.08×10^{-221} | Actinobacterial surface-anchored domain protein |
| HMPREF0421_20304 | -2.04 | 1.31×10^{-77} | 1.38×10^{-76} | Hypothetical protein |

Table S4. List of the differentially expressed genes in the Lac group compared to the LacHyd group. All *P* values were less than 0.02.

| Gene ID | Fold change | <i>P</i> value | <i>P</i> adj | Function |
|------------------|-------------|-------------------------|-------------------------|---|
| HMPREF0421_20956 | 1.42 | 7.96×10^{-156} | 3.55×10^{-153} | Trimeric autotransporter adhesin |
| HMPREF0421_20499 | -1.37 | 8.86×10^{-11} | 7.95×10^{-10} | LPXTG-motif cell wall anchor domain protein |
| HMPREF0421_20990 | -1.17 | 1.35×10^{-33} | 5.84×10^{-32} | Sensor histidine kinase |
| HMPREF0421_20489 | -1.26 | 7.72×10^{-200} | 1.03×10^{-196} | ABC transporter ATP-binding protein |
| HMPREF0421_20488 | -1.09 | 1.28×10^{-177} | 8.58×10^{-175} | ABC transporter substrate-binding protein |

Figure S1. The expressional level of response markers after adding lactate and H₂O₂. Bars represent the mean and the error bars the standard error of the mean (mean \pm SEM).

