**Table S4 List of gene involved in four redox-active pathways in *H. thermocellum* ATCC 27405**

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| --- | --- | --- | --- |
| **Gene ID** | **Protein** | **FAs1 vs. CGs1**  **(log2FC)** | **GAs1 vs. CGs1**  **(log2FC)** |
| **[NiFe] hydrogenase** | | | |
| Cthe\_3013 | Hydrogenase expression/formation protein HypE | 1.24 | 1.14 |
| Cthe\_3014 | Hydrogenase expression/formation protein HypD | 0.82 | 1.11 |
| Cthe\_3016 | [NiFe] hydrogenase maturation protein HypF | 1.15 | 0.97 |
| Cthe\_3018 | Hydrogenase expression/synthesis HypA | 1.46 | 1.01 |
| Cthe\_3019 | 4Fe-4S ferredoxin iron-sulfur binding domain-containing protein | 1.15 | 0.8 |
| **Ammonia assimilation** | | | |
| Cthe\_0197 | Glutamine amidotransferase family protein | 2.12 | 3.18 |
| Cthe\_0198 | Glutamate synthase | 3 | 4.11 |
| Cthe\_0199 | Iron-sulfur cluster-binding protein | 2.27 | 4.11 |
| **Porphyrin biosynthesis** | | | |
| Cthe\_2525 | Glutamyl-tRNA reductase | 0.55 | 2.11 |
| Cthe\_2527 | Porphobilinogen deaminase | 0.34 | 1.26 |
| Cthe\_2528 | Uroporphyrinogen-III synthase/Uroporphyrin-III C-methyltransferase | 0.85 | 1.17 |
| Cthe\_2529 | Delta-aminolevulinic acid dehydratase | 1.32 | 1.53 |
| **Sulfate transport & metabolism** | | | |
| Cthe\_2531 | Sulfate ABC transporter, periplasmic sulfate-binding protein | -1.68 | 0.46 |
| Cthe\_2532 | Sulfate ABC transporter, inner membrane subunit CysT | -1.56 | 0.49 |
| Cthe\_2533 | Sulfate ABC transporter, inner membrane subunit CysW | -0.16 | 1.51 |
| Cthe\_2534 | Sulfate ABC transporter, ATPase subunit | -1.22 | 0.35 |
| Cthe\_2536 | Sulfate adenylyltransferase subunit 2 | -1.02 | -0.05 |
| Cthe\_2537 | Sulfate adenylyltransferase, large subunit | -1.17 | 0.48 |
| Cthe\_2538 | Thiamine biosynthesis protein ThiS | -1.36 | 0.37 |