

**Table S1.** Oligonucleotides used in this work.

Target	Name	Sequence 5'-3'	Product Length (bp)
<i>tfp1*</i>	pTfp1-F	AAGGTTTCGGTCCTCTATGC	151
	pTfp1-R	TGAATGGAGTGACGTTGAGC	
<i>tfp2*</i>	pTfp2-F	CTGGTAATGGTTGATTTCTGGG	104
	pTfp2-R	GGAATGCCCATGACCTGATAT	
<i>tfp3*</i>	pTfp3-F	TGTTCTGATCCGGAAAAACC	184
	pTfp3-R	GTCGACCAGAACGACTTTC	
<i>tfp4*</i>	pTfp4-F	CTGGATTTGGGAAAACTGC	113
	pTfp4-R	TCTATTTGACGGGACAGACG	
<i>tfp5*</i>	pTfp5-F	CATTGATCAGAATGGTGTGG	109
	pTfp5-R	CGTCTTTGGTCCTTTGTC	
<i>tfp6*</i>	pTfp6-F	GACGGACGACACCTTTCAGA	138
	pTfp6-R	AGTCTCCCGTGGTACTTTCG	
<i>tfp7*</i>	pTfp7-F	AGTTTGAGAGCCGTGAAGC	163
	pTfp7-R	AAGCCGTGAACCTTTGTATGC	
<i>tfp8*</i>	pTfp8-F	AAGAAAAATATCCCGACAGC	107
	pTfp8-R	GATGGCATAACGTTCAATGG	
<i>tfp9*</i>	pTfp9-F	CGATTTCTCTCCGCGATGA	81
	pTfp9-R	GCAATGTCTTTCAGAACGGG	
<i>tfp10*</i>	pTfp10-F	TATCCGAGAGAAGGTTGTGC	119
	pTfp10-R	TGATCTTCCCAAGTTTGACC	
<i>tfp11*</i>	pTfp11-F	AGAGTCTGCAGGACAGAAGC	138
	pTfp11-R	TCCTGCTTTCCAAGAATACG	
<i>tfp12*</i>	qTfp12-F	TCGAAACGGCAGATAATACCT	80
	qTfp12-R	TTTGACCTGACCACCGACAA	
<i>tfp13*</i>	ptfp13-F	TTGCGATTCCGGACCC	108
	ptfp13-R	CTCCRCCAACGACMACG	
pBadTOPO	pBadTopo-R	GATTTAATCTGTATCAGGCTG	335
	pBadTopo-F	ATGCCATAGCATTTTTATCCAT	
<i>rrsB*</i>	pRrsB-F	TACAAGCTTCCGCTCCTG	288
	pRrsB-R	CCGGGCAAAAGTGGTTTACA	
<i>tfp1*</i>	pBad_Tfp1-F	ATGGCCAAGGTTTCGGTC	252
	pBad_Tfp1-R	CTTAAGCGTTTTTCAGGAGGTG	
<i>tfp2*</i>	pBad_Tfp2-F	GTGGAAGTAAATGCTCCGGA	318
	pBad_Tfp2-R	GGACTTGAGAAGAGAGTCAAT	
<i>tfp6*</i>	pBad_Tfp6-F	ATGGATGAGGATATTCTGATGA	471
	pBad_Tfp6-R	GGAAGGGAGCGGGCTGCT	
<i>tfp10*</i>	pBad_Tfp10-F	ATGGCTGCTGAAATAAAAGTGGG	462
	pBad_Tfp10-R	CTATTTCAACTGTTCAAGCGC	
<i>tfp12*</i>	pBad_Tfp12-F	ATGCAAAAGGTCCCATT	765
	pBad_Tfp12-R	CTACTTCTTTTGTCGGAG	
<i>tfpA**</i>	pTfpA-F	ATGAGCGATAAAATTATTCACCT	330
	pTfpA-R	TTACGCCAGGTTAGCGTC	

(\*) *Leptospirillum* sp. CF-1; (\*\*) *E. coli* K-12.**Table S2.** Relative fold change in mRNA levels of *tfp* genes from *Leptospirillum* sp. CF-1 exposed to oxidative stress with ferric ion or diamide.

Gene	Ferric Ion	Diamide	
	Increase	Increase	Decrease
<i>tfp1</i>	-	2.43 ± 0.48	
<i>tfp2</i>	7.33 ± 4.74	2.62 ± 0.39	
<i>tfp3</i>	2.25 ± 0.69	-	-
<i>tfp4</i>	-	5.17 ± 0.24	

<i>tfp5</i>	8.44 ± 3.38	-	-
<i>tfp6</i>	5.4 ± 1.36		0.13 ± 0.01
<i>tfp7</i>	4.12 ± 0.29		0.21 ± 0.02
<i>tfp8</i>	2.78 ± 0.14		0.17 ± 0.05
<i>tfp9</i>	10.2 ± 2.27		0.57 ± 0.12
<i>tfp10</i>	-	1.84 ± 0.26	
<i>tfp11</i>	5.38 ± 1.30		0.32 ± 0.07
<i>tfp12</i>	-		0.33 ± 0.07
<i>tfp13</i>	18.51 ± 4.95		0.49 ± 0.13

(-), no significant changes.

**Table S3.** Percentage of growth recovering of stressed respect to non-stressed cultures of *tfp*-complemented cells.

Strain	Ferric Ion	Diamide
<i>E. coli</i> K-12	14.20 ± 2.10	12.62 ± 0.77
Jem-136	15.29 ± 3.25	1.35 ± 0.15
Jem-136 / <i>tfp1</i>	67.50 ± 1.10	66.48 ± 12.26
Jem-136 / <i>tfp2</i>	21.47 ± 1.36	41.48 ± 1.76
Jem-136 / <i>tfp6</i>	54.28 ± 0.32	10.47 ± 1.01
Jem-136 / <i>tfp10</i>	56.70 ± 0.58	9.30 ± 1.15
Jem-136 / <i>tfp12</i>	63.70 ± 0.75	6.92 ± 0.54
Jem-136 / <i>trxA</i>	25.69 ± 2.02	5.69 ± 1.04

Growth of non-stressed cells was considered 100%. JEM-136 genotype:  $\Delta trxA \Delta trxC$ .