SUPPLEMENTARY TABLES

Suppl. Table I. Primers used in this study.

Primer	Name	Sequence (5'’→3'’)	Applications
1	Spyo/HEF-Hup	ACATATGATTACAGTATATTCC	Linkage RT-PCR
2	Spyo/HEF-Eintlw	GGAACGGTAATCCCTAGTGAC	Linkage RT-PCR
3	Spyo/HEF-Eintup	GGATGATGGGGAAGAAGTGGGCG	Linkage RT-PCR
4	Spyo/HEF-Fintlw	GAGGAGTGCGAACATCAGCACG	Linkage RT-PCR
5	Spyo/FIE-Fintup	GACCGTGCCCGTGTCTTGATTCC	Linkage RT-PCR
6	Spyo/FIE-Eintlw	CCAATTGATGGAGCGCAACTG	Linkage RT-PCR
7	Spyo/I2up	CATATGCCTCAGATTACCCTTG	Linkage RT-PCR
8	Spyo/I2lw	GGATCCATGGACTGTCTAGCTG	Linkage RT-PCR
9	Spyo/HEF-Fup	ACATATGACTACATATTATGAAGC	Protein overproduction
10	Spyo/HEF-Flw	AGGATCCTGAGCACTATTAGAGTC	Protein overproduction
11	Spyo/HEF-Eup	ACATATGAGTCTCAAAGATCTTGG	Protein overproduction
12	Spyo/HEF-Elw	AGGATCCTTACTTCTTAACCAATTAAATG	Protein overproduction
13	Spyo/FIE-Fup	ACATATGACCCAACATTATTATG	Protein overproduction
14	Spyo/FIE-Flw	AGGATCCATTTCTTAAAACTCCC	Protein overproduction
15	Spyo/FIE-Eup	ACATATGTCACAAACCAATGCG	Protein overproduction
16	Spyo/FIE-Elw	GGATCCGATAGGGGACACGAGAG	Protein overproduction
17	Spyo/RBS-HEFup	GAGCTCAAGGAGAACAAGACATGATTACAG	Heterologous complementation

Primer	Name	Sequence (5'’→3'’)	Applications
18	Spyo/RBS-HEFlw	CTGCAGAGCACTATTAGAGTCC	Heterologous complementation
19	Spyo/RBS-FIEup	GAGCTCAAGGAGAGAGACAAATGACCCAAC	Heterologous complementation
20	Spyo/RBS-FIElw	CTGCAGGAGAGCTTTCTAGTAGC	Heterologous complementation
21	Spyo/RBS-I2up	GAGCTCAAGGAGAGACACTTATGCCTCAGA	Heterologous complementation
22	Spyo/RBS-I2lw	CTGCAGATGGACTGTCTAGCTG	Heterologous complementation
23	Spn/RBS-HEFup	TCTAGAAGGAGATTACACAATGGTAACCG	Heterologous complementation
24	Spn/RBS-HEFlw	CTGCAGTGAGAGTGATGGAGAATTAG	Heterologous complementation
25	Spn/RBS-I2up	TCTAGAAGGAGAGGTACATATGAAGAC	Heterologous complementation
26	Spn/RBS-I2lw	CTGCAGCATTGAGTATTAATTCTCC	Heterologous complementation
27	Spyo/RBS-I*up	GAGCTCAAGGAGATTAAGAAATGGCAGAGC	Heterologous complementation
28	Spyo/RBS-I*lw	CTGCAGGTGCATTTAATGAGAGG	Heterologous complementation
29	Spyo/RBS-E*up	GAGCTCAAGGAGCACACCCATGTCACAAACC	Heterologous complementation
30	Spyo/RBS-E*lw	CTGCAGATAGGGGACACGAGAG	Heterologous complementation

Suppl. **Table II.** Important residues in NrdE and NrdA subunits.

E. coli **NrdA**	***S. typhimurium*** **NrdE**	***S. pyogenes*** **NrdE**	***S. pyogenes*** **NrdE***	***S. pneumoniae*** **NrdE**	**Function**
S224	S168	S171	S169	S171	Active site
C225	C169	C172	C170	C172	Active site, redox active cysteine
D232	D176	D179	D177	D179	Allosteric specificity site
R262	R206	R209	R207	R209	Allosteric specificity site
I268	I212	I215	I213	I215	Allosteric specificity site
R329	R271	R276	R274	R276	R2 interaction area
N437	N377	N380	N380	N380	Active site
L438	L378	L381	L381	L381	Active site
C439	C379	C382	C382	C382	Active site, transient thiyl radical
E441	E381	E384	E384	E384	Active site, base in the catalysis
C462	C406	C409	C409	C409	Active site, redox active cysteine
L464	L408	L411	L411	L411	Active site
P621	P579	P580	P582	P580	Active site
Y730	Y683	Y697	Y687	Y697	Electron transfer chain
Y731	Y684	Y698	Y688	Y698	Electron transfer chain
C754	C700	C714	C721	C714	Redox active cysteine, Trx/Grx interaction
C759	C703	C717	C724	C717	Redox active cysteine, Trx/Grx interaction

Suppl. **Table III.** Important residues in NrdF and NrdB subunits.

E. coli **NrdB**	***S. typhimurium*** **NrdF**	***S. pyogenes*** **NrdF**	***S. pyogenes*** **NrdF***	***S. pneumoniae*** **NrdF**	**Function**
W48	W31	W30	W49	W30	Electron transfer chain
D84	D67	D66	D85	D66	Iron ligand, electron transfer chain
E115	E98	E97	**V116**	E97	**Iron ligand**
H118	H101	H100	H119	H100	Iron ligand, electron transfer chain
Y122	Y105	Y104	Y123	Y104	Stable tyrosyl radical
E204	E158	E157	**P176**	E157	**Iron ligand**
F208	F162	F161	**L180**	F161	**Hydrophobic pocket, radical stability**
Y209	Y163	Y162	Y181	Y162	Channel to hydrophobic pocket
S211	G165	G164	G183	G164	Channel to hydrophobic pocket
F212	F166	F165	F184	F165	Hydrophobic pocket
I234	I188	I187	I206	I187	Hydrophobic pocket
R236	R190	R189	R208	R189	R1 interaction, radical transport?
D237	D191	D190	D209	D190	Electron transfer chain
E238	E192	E191	**K210**	E191	**Iron ligand**
H241	H195	H194	H213	H194	Iron ligand
E350	S298	S296	S316	S296	R1 interaction
Y356	Y304	Y302	Y322	Y302	Electron transfer chain