

Supplementary Table 1: Sequencing Quality of RNA-seq Samples: Number of raw and cleaned (trimmed for quality) reads are presented for each sample. Q20 score represents the probability of one incorrect base call in 100 bases.

Sample name	Raw Reads	Clean Reads	Q20 score
<i>WT+Fe R1 2 h</i>	8.1 x 10 ⁷	7.9 x 10 ⁷	98.8
<i>WT+Fe R2 2 h</i>	8.9 x 10 ⁷	8.6 x 10 ⁷	98.6
<i>WT+Fe R3 2 h</i>	7.0 x 10 ⁷	6.8 x 10 ⁷	98.8
<i>WT+Fe R1 26 h</i>	10.0 x 10 ⁷	9.8 x 10 ⁷	98.3
<i>WT+Fe R2 26 h</i>	7.2 x 10 ⁷	7.0 x 10 ⁷	98.8
<i>WT+Fe R3 26 h</i>	8.8 x 10 ⁷	8.5 x 10 ⁷	98.7
<i>WT-Fe R1 2 h</i>	7.0 x 10 ⁷	6.8 x 10 ⁷	98.7
<i>WT-Fe R2 2 h</i>	9.0 x 10 ⁷	8.7 x 10 ⁷	98.7
<i>WT-Fe R3 2 h</i>	9.2 x 10 ⁷	9.0 x 10 ⁷	98.8
<i>WT-Fe R1 26 h</i>	7.1 x 10 ⁷	6.9 x 10 ⁷	98.7
<i>WT-Fe R2 26 h</i>	6.8 x 10 ⁷	6.6 x 10 ⁷	98.7
<i>WT-Fe R3 26 h</i>	8.4 x 10 ⁷	8.2 x 10 ⁷	98.7
<i>sufb2-2+Fe R1 2 h</i>	7.5 x 10 ⁷	7.2 x 10 ⁷	98.7
<i>sufb2-2 +Fe R2 2 h</i>	7.5 x 10 ⁷	7.4 x 10 ⁷	98.6
<i>sufb2-2+Fe R3 2 h</i>	8.2 x 10 ⁷	8.1 x 10 ⁷	98.7
<i>sufb2-2+Fe R1 26 h</i>	7.1 x 10 ⁷	7.0 x 10 ⁷	98.6
<i>sufb2-2 +Fe R2 26 h</i>	7.2 x 10 ⁷	7.1 x 10 ⁷	98.5
<i>sufb2-2+Fe R3 26 h</i>	6.1 x 10 ⁷	6.0 x 10 ⁷	98.1
<i>average:</i>	7.7 x 10 ⁷	7.5 x 10 ⁷	98.6