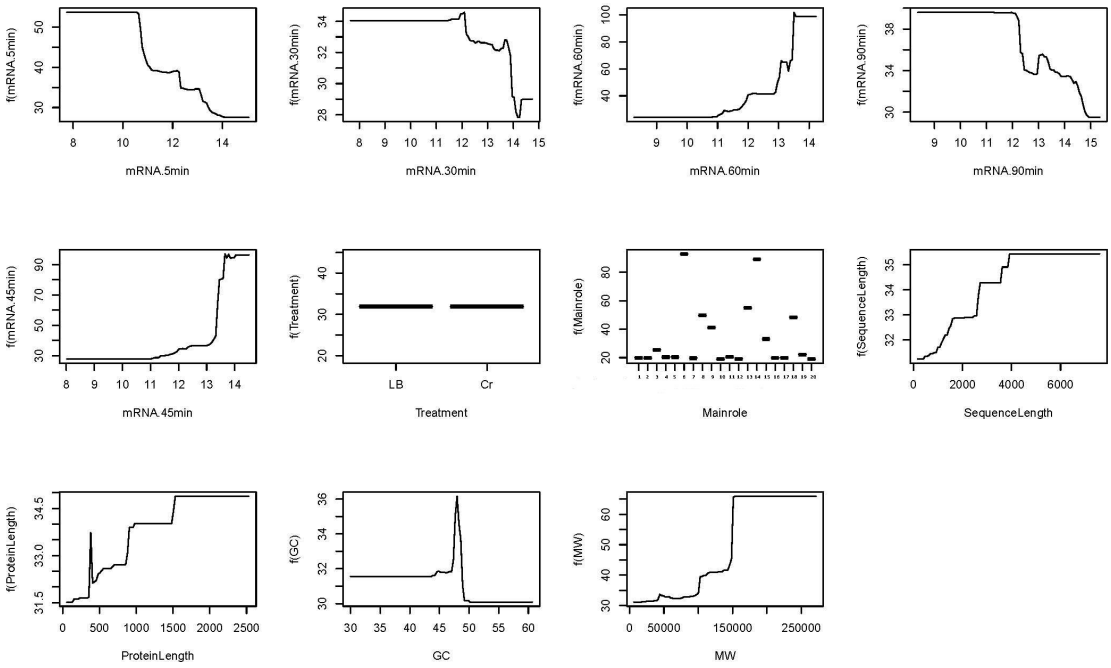
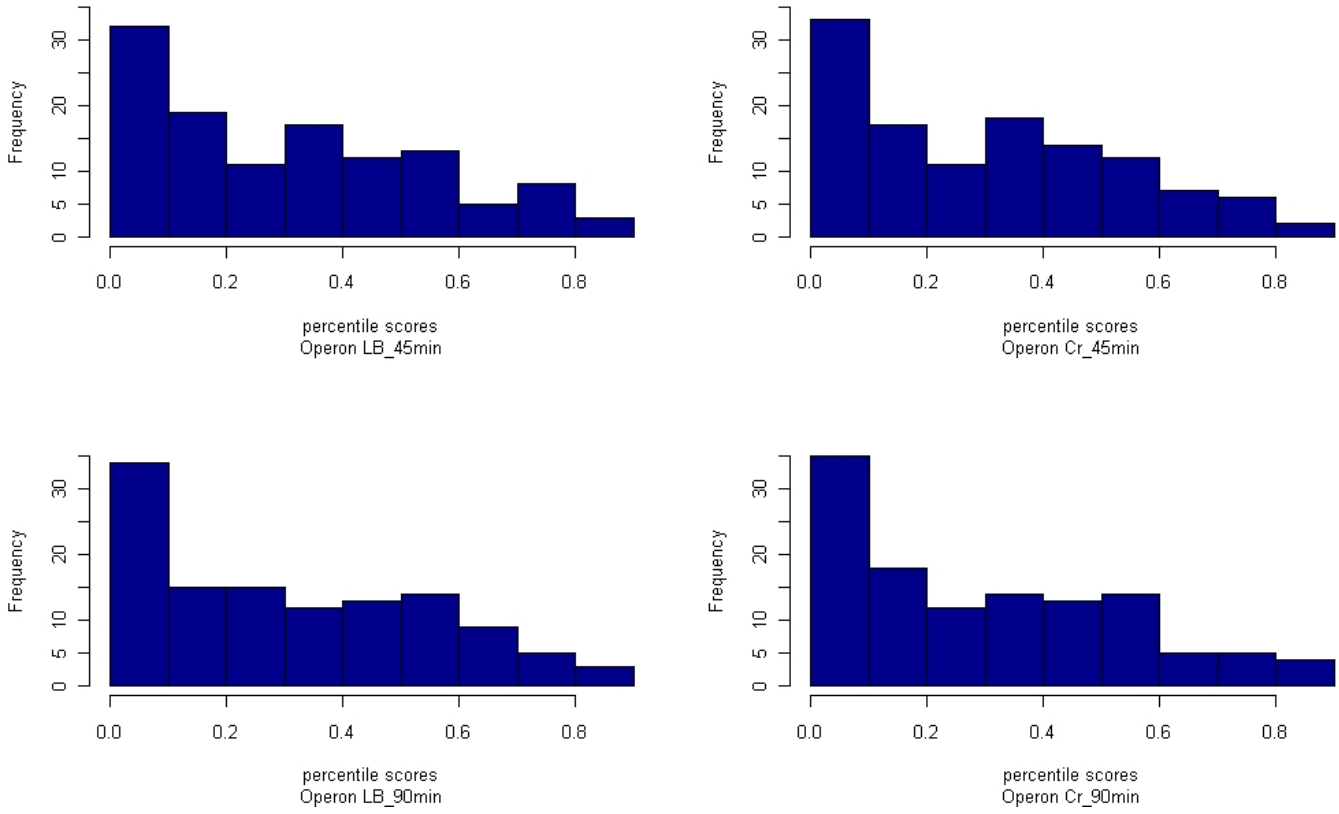


Supplementary Figure 1: Partial Dependency Plots: Every graph depicts the partial dependency prediction values for each of the 11 predictors used in the nonlinear model when predicting protein abundance at 90-min.



Supplementary Figure 2: Model Validation: Percentile Scores for CV values of operon groups

Supplementary Table 1: Model validation: mRNA abundance predictions at 45 minutes in some operons groups

	Operon	mRNA at 45min			
		LB		Cr	
		CV	PCV_{mean}	CV	PCV_{mean}
1:	SO0003-SO0009	0.924	0.573#	0.928	0.574#
2:	SO0023-SO0032	0.458	0.579	0.453	0.579
3:	SO0066-SO0074	0.47	0.579	0.464	0.579
4:	SO0101-SO0109	0.78	0.579#	0.785	0.579#
5:	SO0163-SO0181	0.536	0.619	0.526	0.611
6:	SO0182-SO0189	0.711	0.573#	0.699	0.574#
7:	SO0218-SO0229	0.605	0.608	0.604	0.605
8:	SO0230-SO0257	0.476	0.629	0.454	0.621
9:	SO0258-SO0269	0.435	0.579	0.418	0.579
10:	SO0272-SO0285	0.481	0.593	0.47	0.584
11:	SO0286-SO0300	0.535	0.597	0.532	0.595
12:	SO0311-SO0318	0.787	0.556#	0.772	0.544#
13:	SO0342-SO0346	0.388	0.556	0.39	0.544
14:	SO0395-SO0401	0.29	0.556	0.288	0.544
15:	SO0441-SO0456	0.822	0.579#	0.809	0.579#
16:	SO0476-SO0488	0.349	0.608	0.347	0.605
17:	SO0532-SO0536	0.573	0.556#	0.538	0.544
18:	SO0599-SO0606	0.742	0.594#	0.728	0.583#
19:	SO0608-SO0612	0.364	0.556	0.37	0.544
20:	SO0639-SO0652	0.53	0.579	0.52	0.579
21:	SO0656-SO0672	0.445	0.593	0.432	0.584
22:	SO0674-SO0690	0.839	0.597#	0.856	0.595#
23:	SO0712-SO0718	0.628	0.503#	0.573	0.512
24:	SO0842-SO0849	0.929	0.556#	0.92	0.544#
25:	SO0850-SO0854	0.445	0.556	0.444	0.544
26:	SO0877-SO0883	0.563	0.556#	0.559	0.544#
27:	SO0900-SO0909	0.3	0.573	0.296	0.574
28:	SO1008-SO1021	0.538	0.606	0.536	0.595
29:	SO1103-SO1110	0.703	0.594#	0.719	0.583#
30:	SO1155-SO1163	0.644	0.573#	0.623	0.574#

Coefficient of Variation (CV) is computed by dividing standard deviation by the mean of the prediction values for protein abundance for a specific set of genes (group). The protein prediction values were normalized by molecular weight before CV calculation. More details in Materials and Methods Section.

* CV values of selected operons based on predicted protein abundance from various experimental conditions are listed.

** PCV_{mean} is the mean of CV values computed through permutation test for selected operons.

CV values that is greater than the PCVmean.

Supplementary Table 2. Model Validation: Protein abundance predictions at 45 and 90 minutes in some operons groups *

Operon		Protein 45 min				Protein 90 min			
		LB		Cr		LB		Cr	
		CV	PCV_{mean}	CV	PCV_{mea}	CV	PCV_{mea}	CV	PCV_{mea}
1:	SO0003-SO0009	0.759	0.699#	0.908	0.705#	0.824	0.675#	0.88	0.674#
2:	SO0023-SO0032	0.618	0.807	0.559	0.772	0.627	0.786	0.555	0.738
3:	SO0066-SO0074	0.419	0.951	0.425	0.907	0.402	0.889	0.406	0.883
4:	SO0163-SO0181	0.624	0.951	0.64	0.907	0.559	0.889	0.561	0.883
5:	SO0182-SO0189	0.416	0.878	0.418	0.833	0.432	0.826	0.432	0.792
6:	SO0218-SO0229	0.537	1.188	0.547	1.101	0.524	1.132	0.522	1.059
7:	SO0230-SO0257	0.401	1.37	0.425	1.308	0.418	1.315	0.471	1.205
8:	SO0258-SO0269	0.447	1.092	0.463	1.022	0.474	1.06	0.497	0.976
9:	SO0272-SO0285	0.374	1.022	0.377	0.983	0.395	0.99	0.398	0.937
10:	SO0286-SO0300	0.703	1.092	0.637	1.022	0.731	1.06	0.67	0.976
11:	SO0311-SO0318	0.786	0.807	0.786	0.772	0.781	0.786	0.781	0.738#
12:	SO0342-SO0346	0.282	0.699	0.265	0.705	0.219	0.675	0.212	0.674
13:	SO0395-SO0401	0.774	0.807	0.512	0.772	0.77	0.786	0.572	0.738
14:	SO0441-SO0456	0.585	1.092	0.585	1.022	0.537	1.06	0.537	0.976
15:	SO0476-SO0488	0.651	0.577#	0.651	0.556#	0.654	0.565#	0.654	0.551#
16:	SO0532-SO0536	0.859	0.951	0.829	0.907	0.795	0.889	0.762	0.883
17:	SO0599-SO0606	0.374	0.699	0.382	0.705	0.405	0.675	0.415	0.674
18:	SO0608-SO0612	0.226	0.878	0.226	0.833	0.224	0.826	0.224	0.792
19:	SO0639-SO0652	0.35	0.577	0.35	0.556	0.352	0.565	0.352	0.551
20:	SO0656-SO0672	0.862	0.878	0.862	0.833#	0.855	0.826#	0.856	0.792#
21:	SO0674-SO0690	0.621	0.577#	0.621	0.556#	0.609	0.565#	0.609	0.551#
22:	SO0842-SO0849	0.233	0.807	0.209	0.772	0.218	0.786	0.213	0.738
23:	SO0850-SO0854	0.405	0.577	0.45	0.556	0.437	0.565	0.453	0.551
24:	SO0877-SO0883	0.474	0.699	0.474	0.705	0.392	0.675	0.392	0.674
25:	SO0900-SO0909	0.564	1.01	0.583	0.92	0.556	0.969	0.571	0.922
26:	SO1008-SO1021	0.453	1.092	0.463	1.022	0.422	1.06	0.441	0.976
27:	SO1103-SO1110	1.158	0.807#	1.158	0.772#	0.867	0.786#	0.867	0.738#
28:	SO1155-SO1163	0.33	0.577	0.33	0.556	0.334	0.565	0.334	0.551

Coefficient of Variation (CV) is computed by dividing standard deviation by the mean of the prediction values for protein abundance for a specific set of genes (group). The protein prediction values were normalized by molecular weight before CV calculation. More details in Methods section.

* CV values of selected operons based on predicted protein abundance from various experimental conditions are listed.

** PCV_{mean} is the mean of CV values computed through permutation test for selected operons.

\# CV values that is greater than the PCVmean.

Supplementary Table 3. Description of the dataset used in this study

Organism	*Shewanella oneidensis*
Conditions	LB (Control) and Cr (Chromate Stress)
Number of Variables	12
{Variables}	{mRNA at 5-,30-,45-,60-,90-min, Mainrole, GC, MW, Sequence Length, Protein Length, Treatment, Dye}
Number of replicates (mRNA abundance)	6/gene (2 dyes ea. per condition)
Number of genes analyzed	4516 for both conditions
Quality of mRNA replicates {Pearson Correlation}	{0.85-0.98}
Number of replicates (protein abundance)	2/gene per condition
Number of genes analyzed	2447 for both conditions
Quality of protein replicates {Pearson Correlation}	{0.91-0.99}