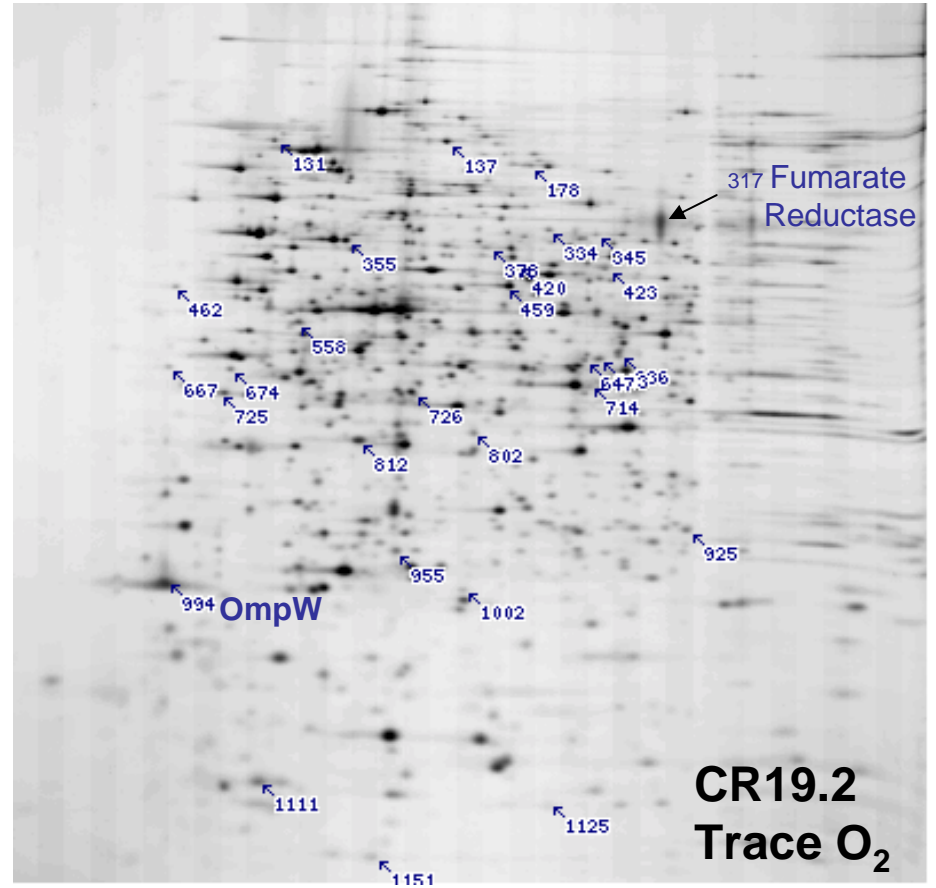
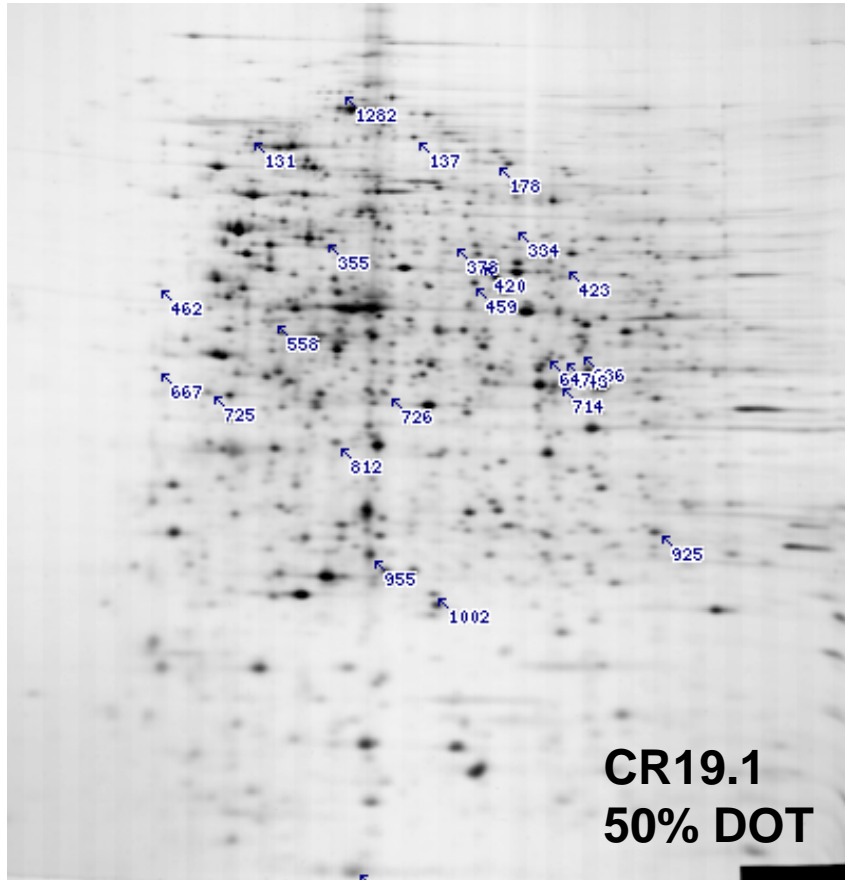


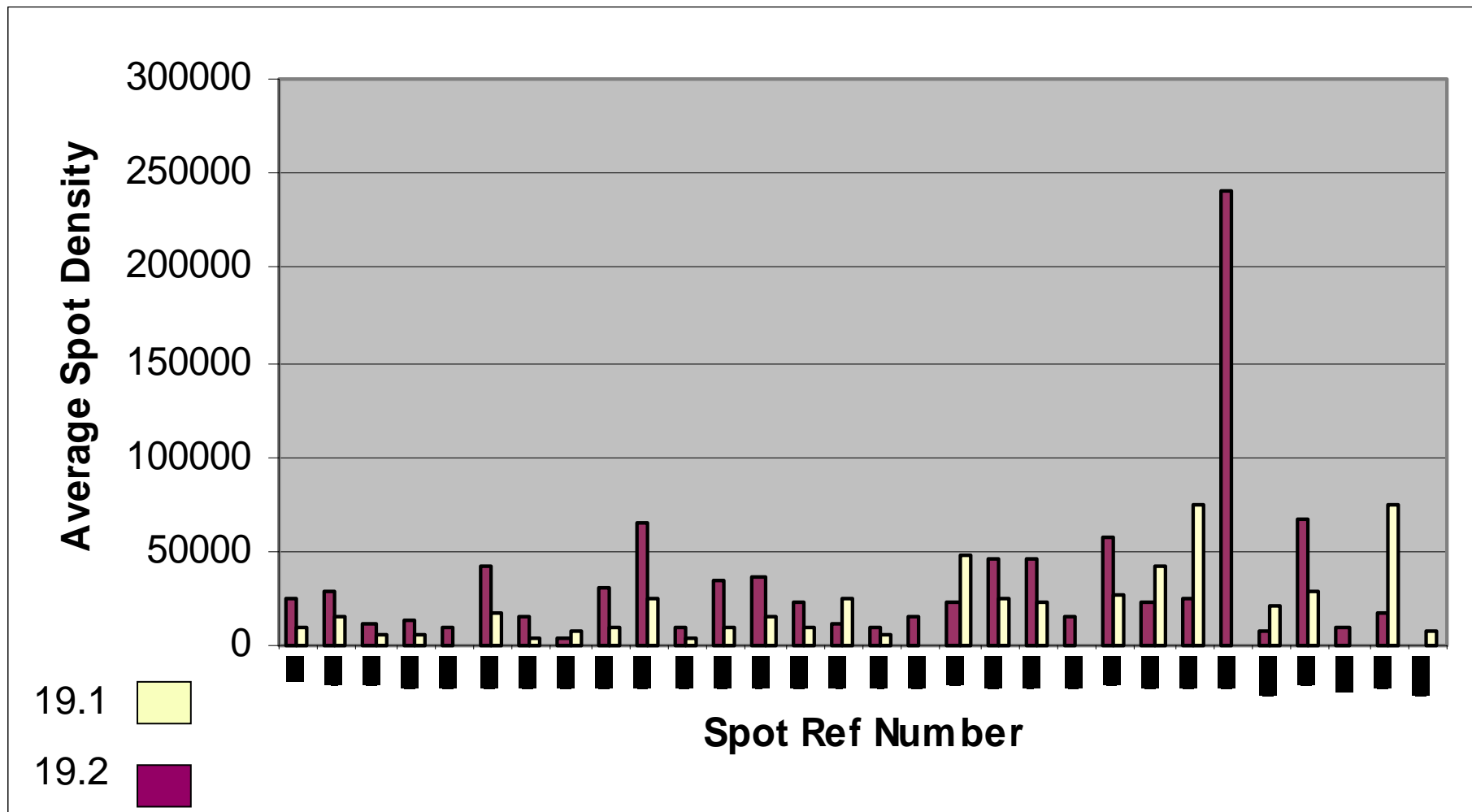
2DE Proteomics for Shewanella Federation

- 13 experiments (BR1,2; CR2, 3, 5, 6, 7, 8,16,17,19, 20, 21)
- 20 samples
- 240 analyses (pH 4-7; >pH 7, heme stain)
- Sample annotation and 2DE images: <http://Proteomes2.bio.anl.gov>
- **5 days** from sample receipt to images on website
- Some protein identifications from MGP database; some newly determined

CR19 Experiment



Differential Protein Expression with Oxygen Limitation



Some *S. oneidensis* Proteins Varying in Abundance in CR19.1 vs. CR19.2

Spot	CR19.1*	CR19.2*	Identification	GI #
131	10400	23900	Bacterial surface antigen	24373205
137	15400	29100	clpB protein	24375079
178	5100	12100	Formate acetyltransferase	24374439
317	ND	155000	Fumarate reductase FAD precursor	24372557
334	5000	12700	Threonine dehydrase	24375825
355	16400	42500	Glutamine synthetase, I	24375890
459	24200	65300	Aspartokinase III	24375473
925	42700	22600	thiG protein	24373988
955	73700	24600	Purine nucleoside phosphorylase	24372802
994	ND	241000	Outer membrane protein OmpW	24373241
1282	7300	ND	DNA-directed RNA polymerase, beta'	24372802

Abundance significantly ($P < 0.001$) increased with oxygen deprivation.

*Average integrated density of protein spots

- AMT and 2DE are complementary approaches to proteome analysis:
 - providing a more comprehensive view of protein expression
 - 2DE: Rapid visualization of complex protein populations with identification of major differences (Assessment of experimental response)
 - AMT tag: Comprehensive identification of proteins in complex protein mixtures
 - Validation of new methodology with “gold standard”
- Comparison of proteome measurements with microarray to elucidate regulatory mechanisms
- Integrative data analysis