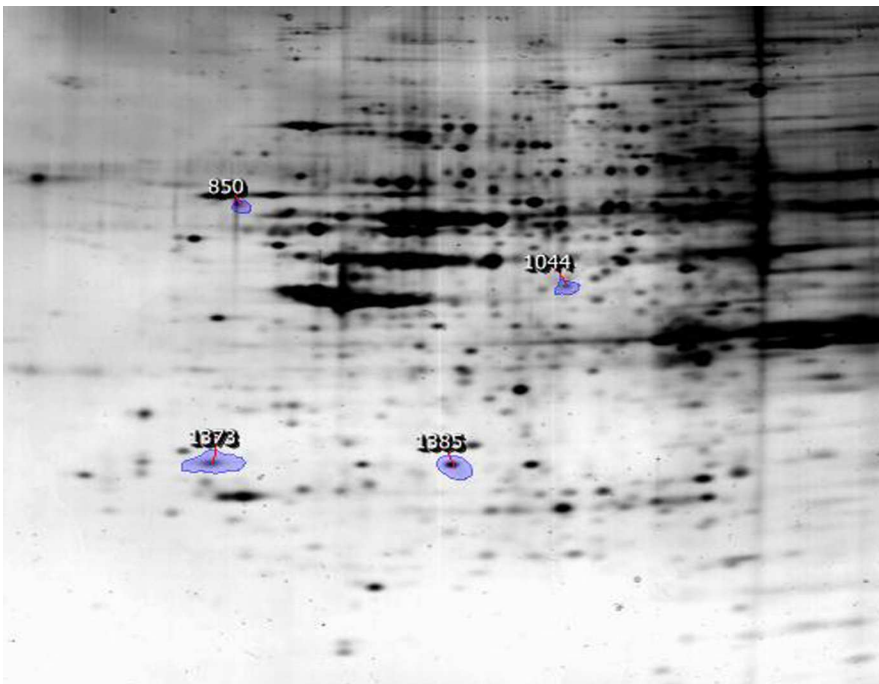


## Dataset S4

### Proteomics Profiles

#### HB2 (Breast Epithelial Cell Line)

	Un-treated	Treated	Passage 1	Passage 3	Passage 5	Passage 7	Passage 10
Replicate 1							
Replicate 2							
Replicate 3							

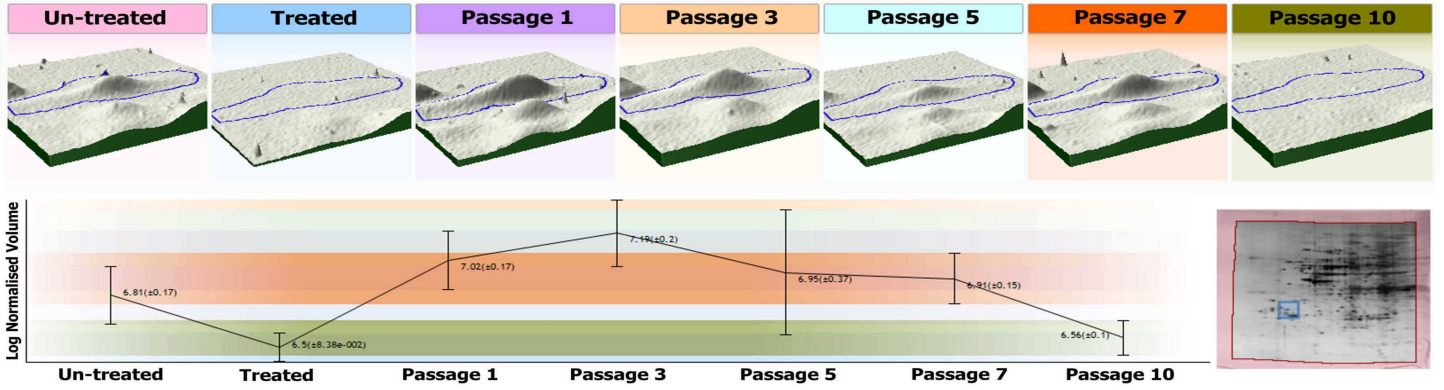


Spot No.	Anova (p)	Fold change	pI
1373	0.022	4.9	5.07
850	0.040	2.0	5.3
1044	0.044	1.6	7.75
1385	0.050	2.4	6.94

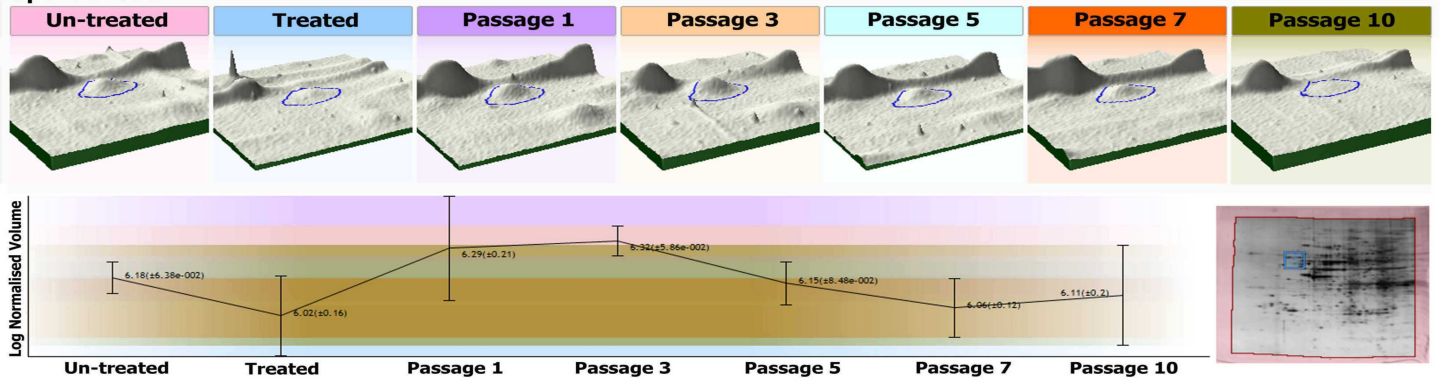
Spot picking gel for significant up/down-regulated intersection proteins.

Expression profile of candidate spots within different treatment passages.

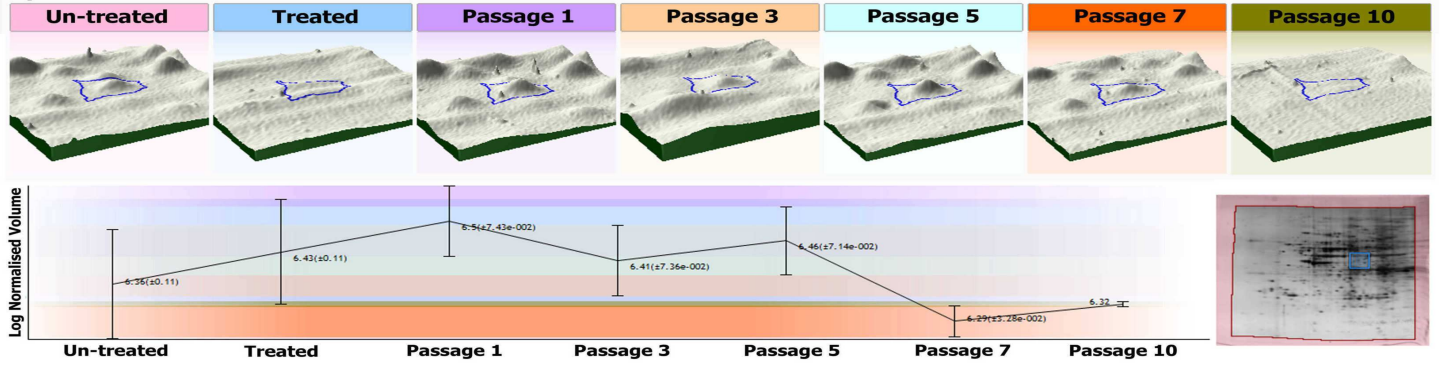
Spot no. 1373



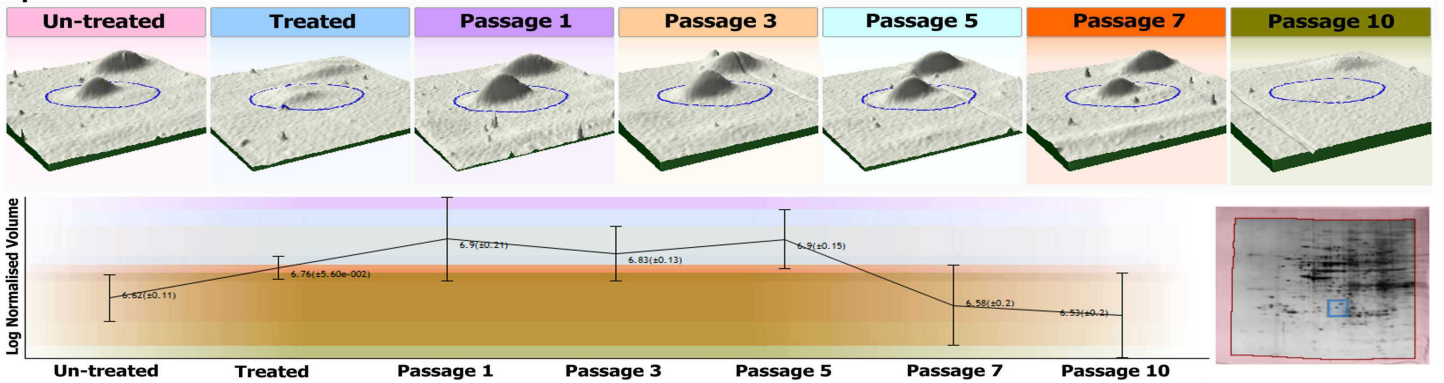
Spot no. 850



Spot no. 1044

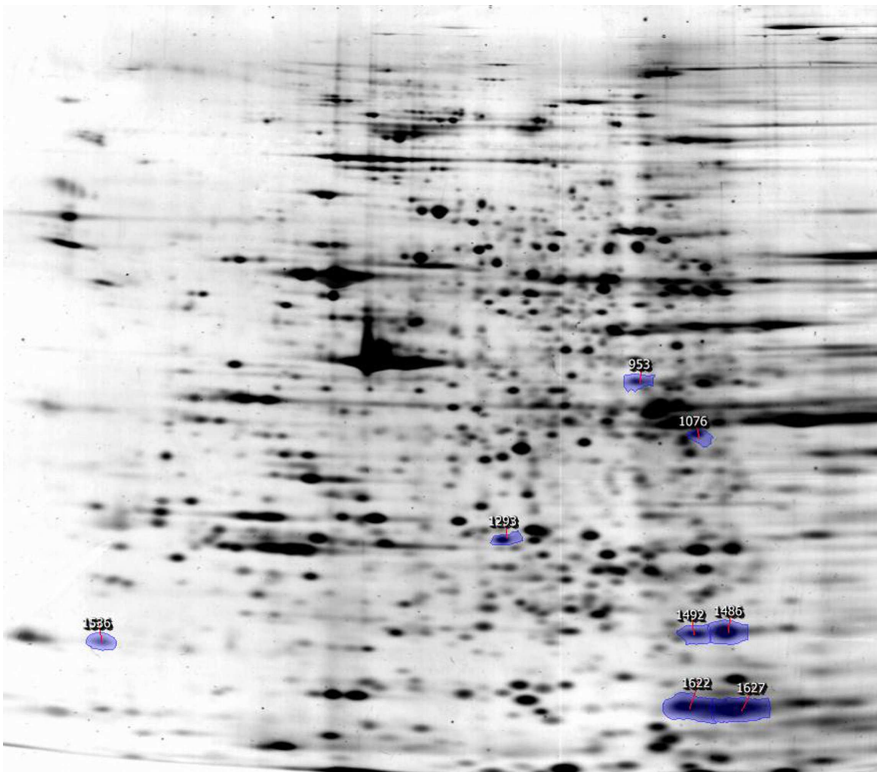


Spot no. 1385



## MDA-MB231 (Highly Aggressive Breast Cancer Cell Line)

	Un-treated	Treated	Passage 1	Passage 3	Passage 5	Passage 7	Passage 10
Replicate 1							
Replicate 2							
Replicate 3							

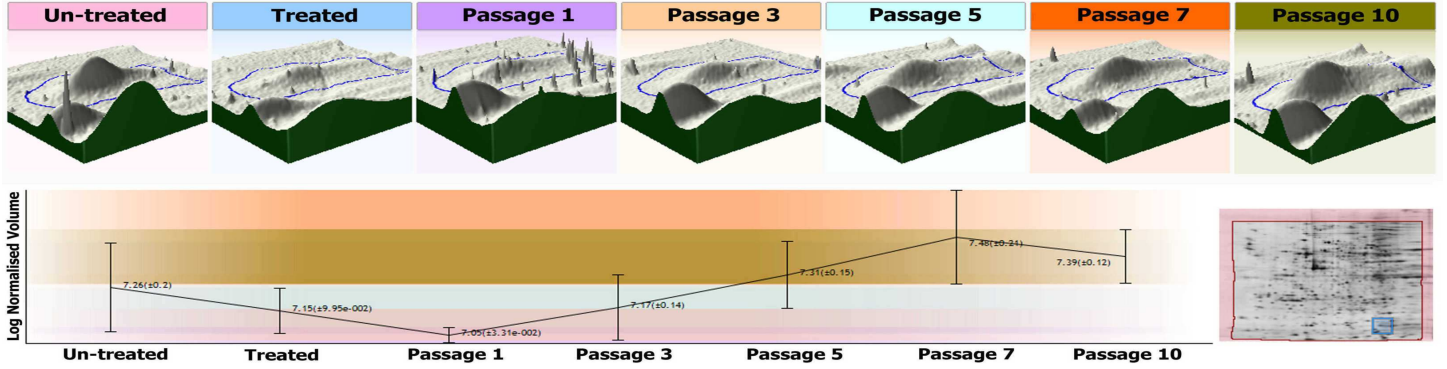


Spot No.	Anova (p)	Fold change	pI
1622	0.007	2.8	8.36
953	0.030	1.6	7.98
1486	0.032	1.9	8.7
1492	0.036	2.0	8.46
1627	0.038	2.6	8.83
1536	0.038	1.6	3.72
1293	0.041	1.7	6.94
1076	0.047	1.9	8.47

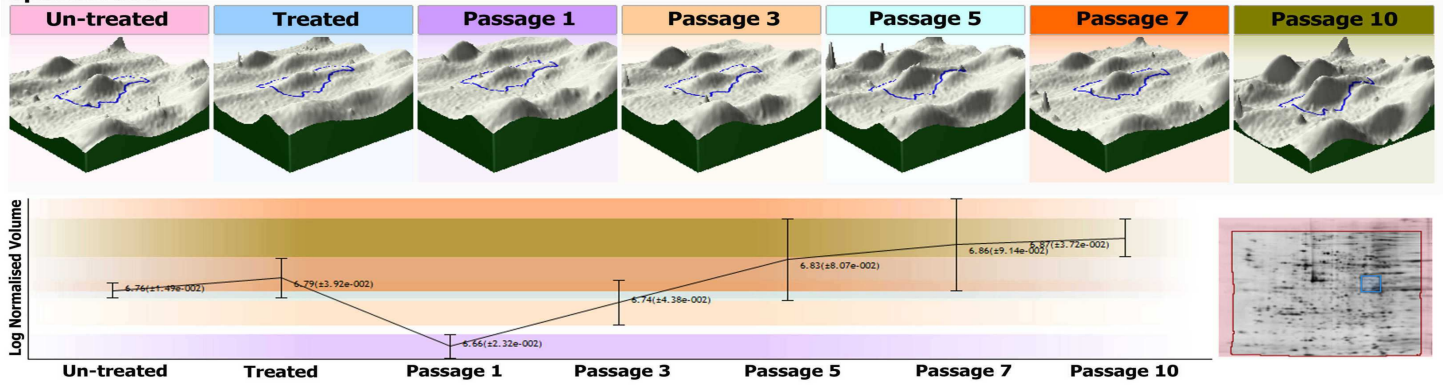
Spot picking gel for significant up/down-regulated intersection proteins.

Expression profile of candidate spots within different treatment passages.

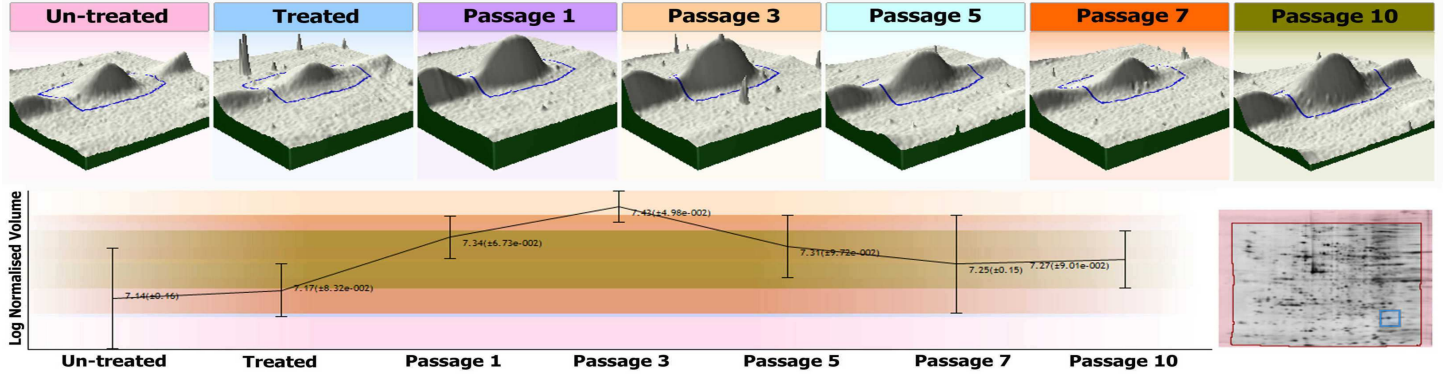
**Spot no. 1622**



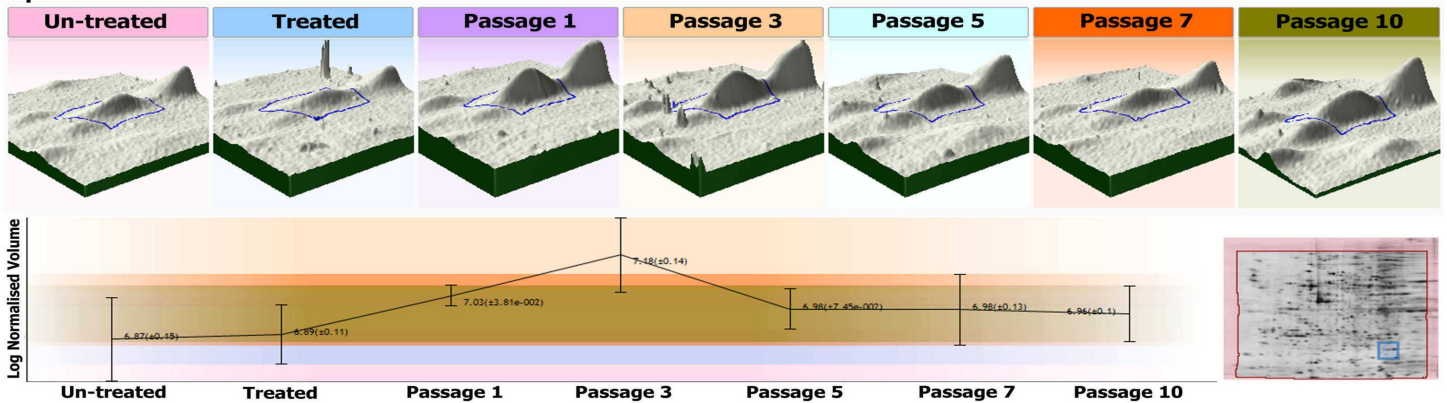
**Spot no. 953**



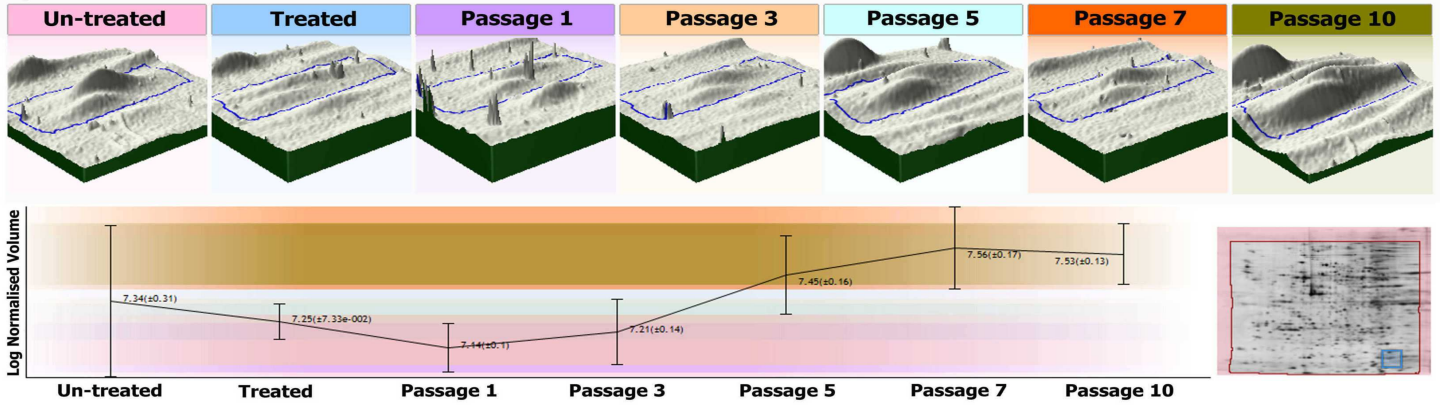
**Spot no. 1486**



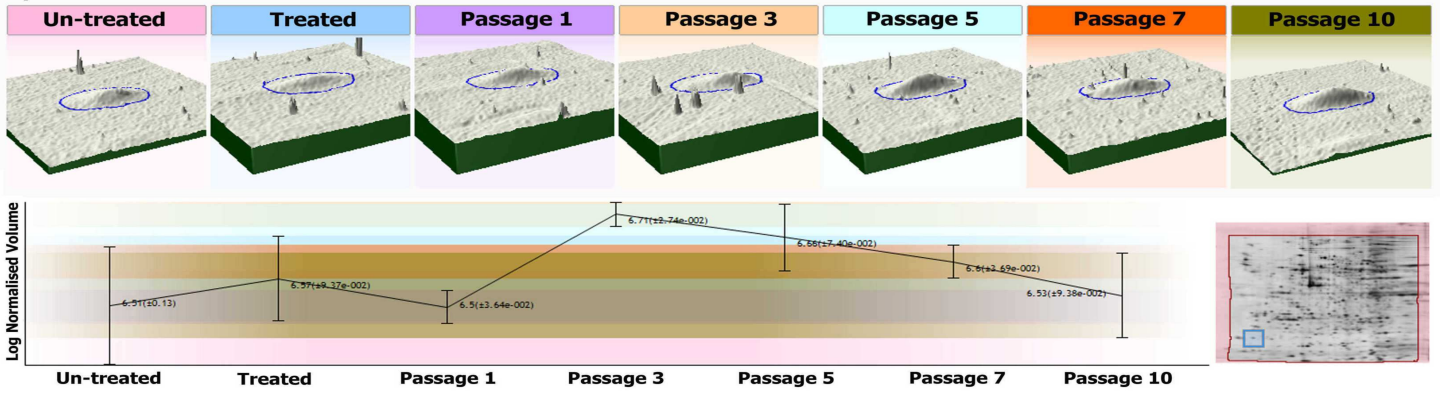
**Spot no. 1492**



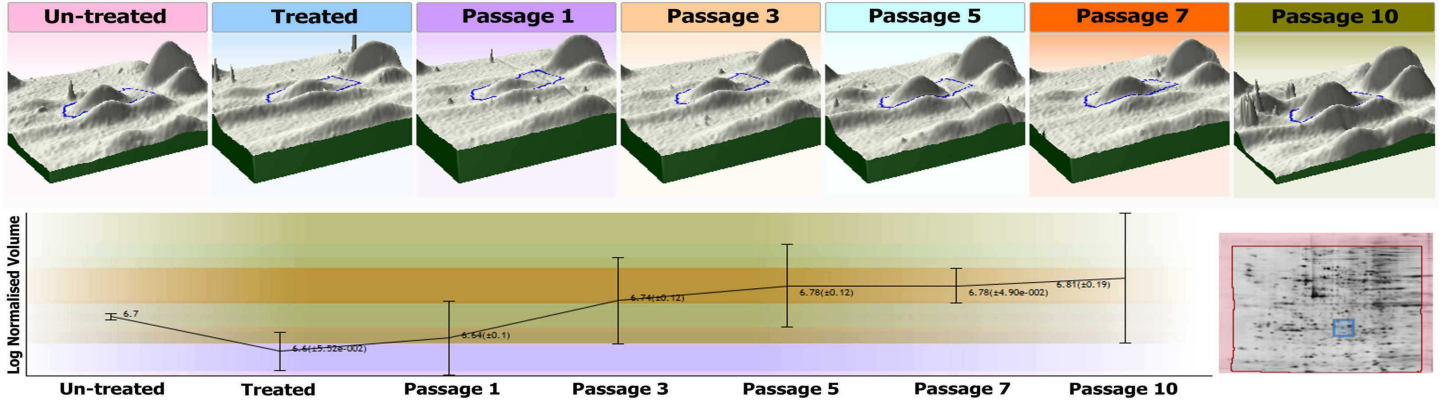
**Spot no. 1627**



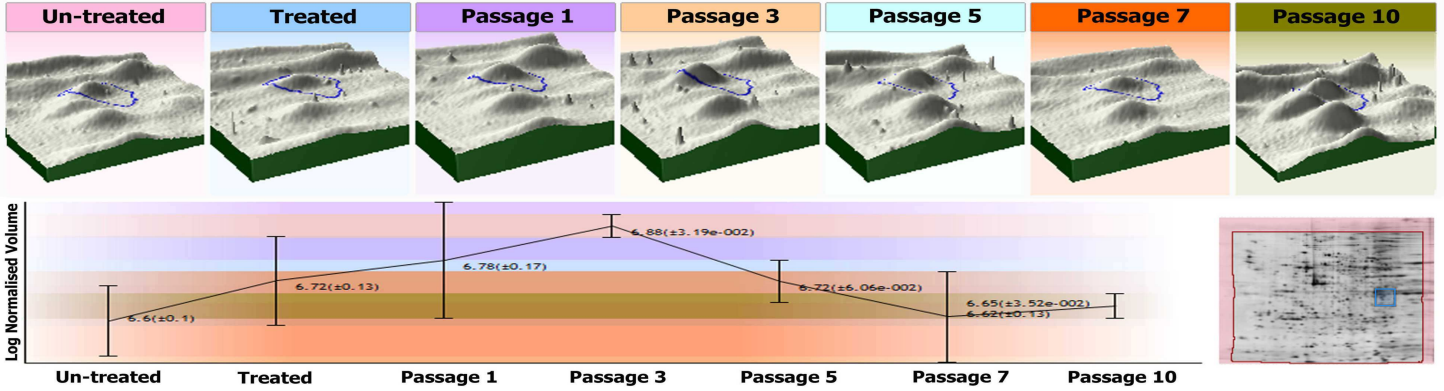
**Spot no. 1536**



**Spot no. 1293**

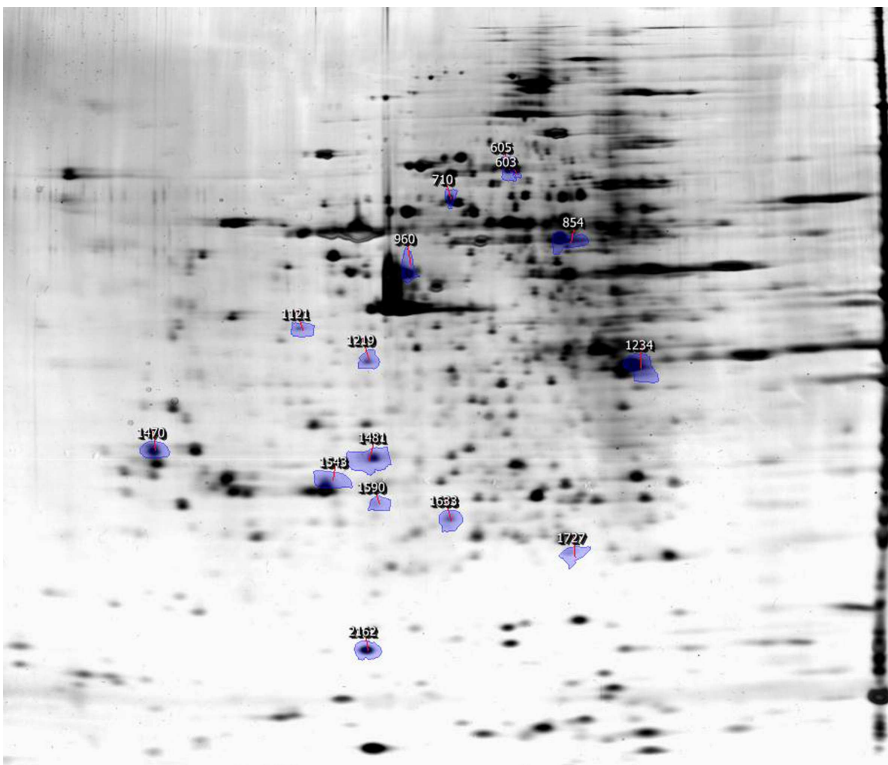


**Spot no. 1076**



## SKBR3 (Non- aggressive Breast Cancer Cell Line)

	Un-treated	Treated	Passage 1	Passage 3	Passage 5	Passage 7	Passage 10
Replicate 1							
Replicate 2							
Replicate 3							

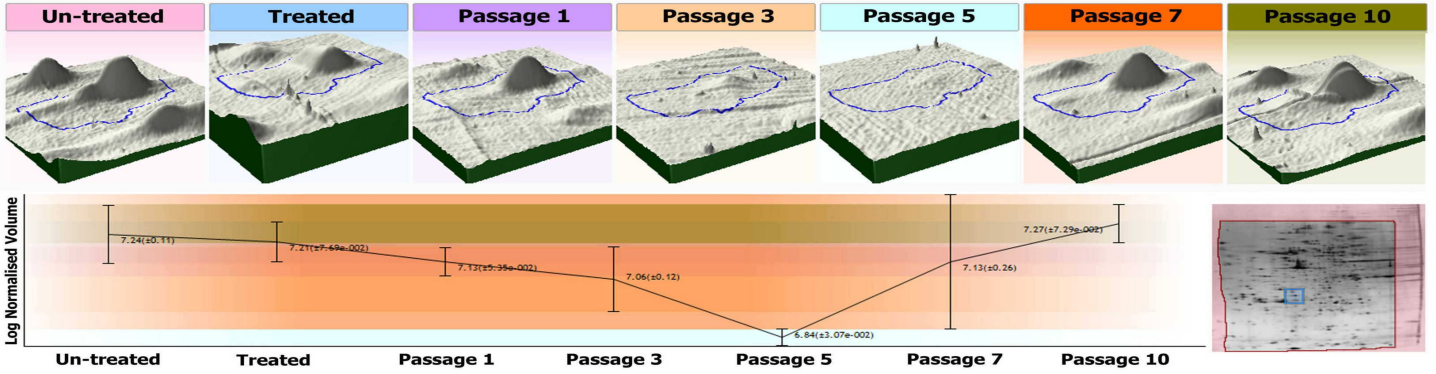


Spots No.	Anova (p)	Fold change	pI
710	0.005	3.1	7.2
1543	0.013	2.2	6.11
2162	0.016	2.6	6.42
1727	0.016	1.9	8.24
603	0.017	7.3	7.76
1470	0.021	6.6	4.67
1121	0.025	3.2	5.87
854	0.030	1.9	8.16
1633	0.030	2.9	7.18
960	0.038	2.7	6.8
1219	0.041	2.2	6.47
1234	0.045	2.0	8.78
605	0.047	3.3	7.7
1590	0.047	2.5	6.53
1481	0.048	2.7	6.53

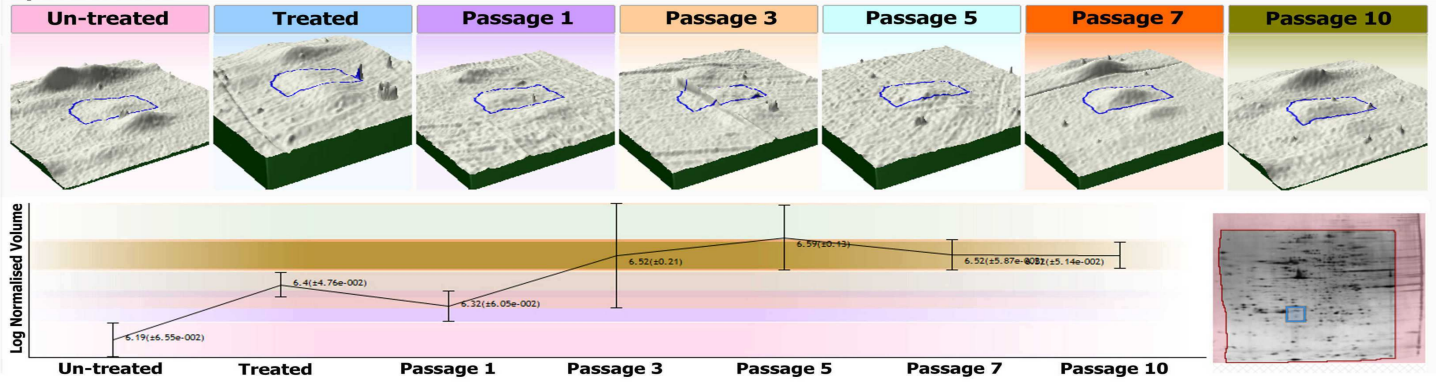
Spot picking gel for significant up/down-regulated intersection proteins.

expression profile of candidate spots within different treatment passages.

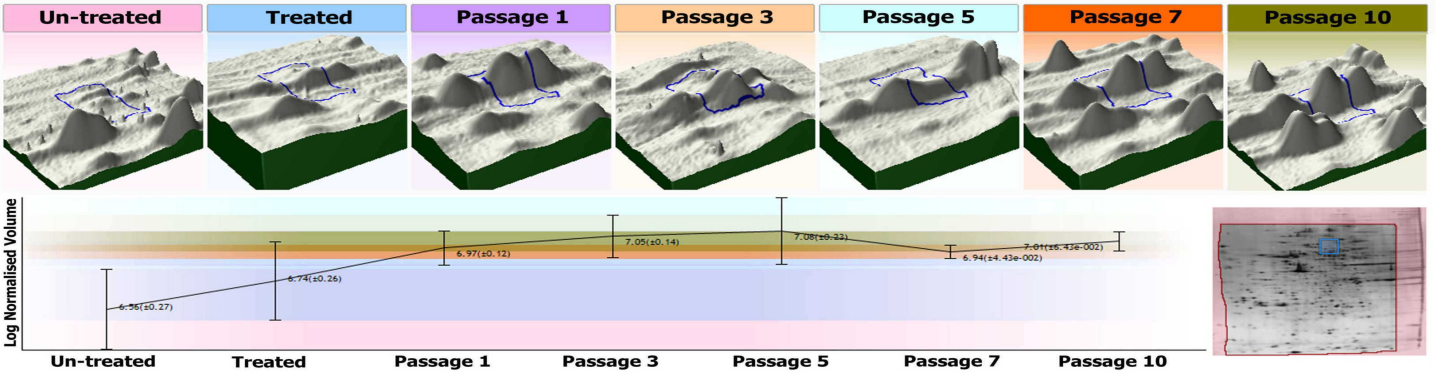
**Spot no. 1481**



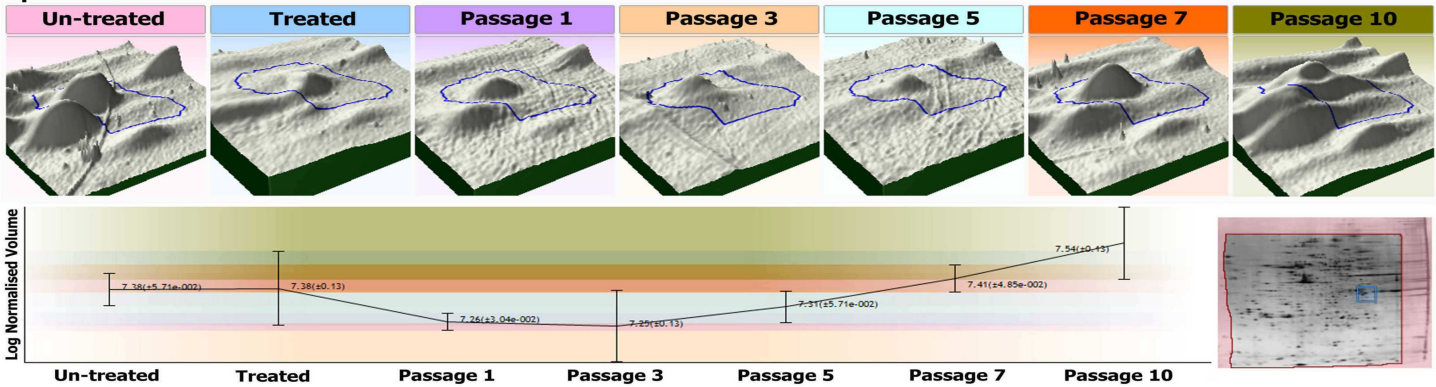
**Spot no. 1590**



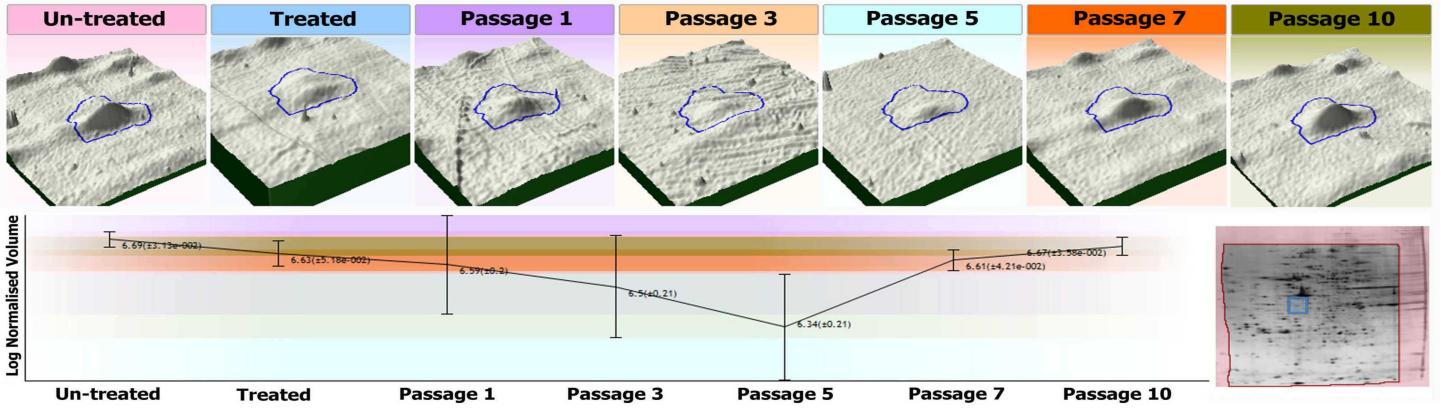
**Spot no. 605**



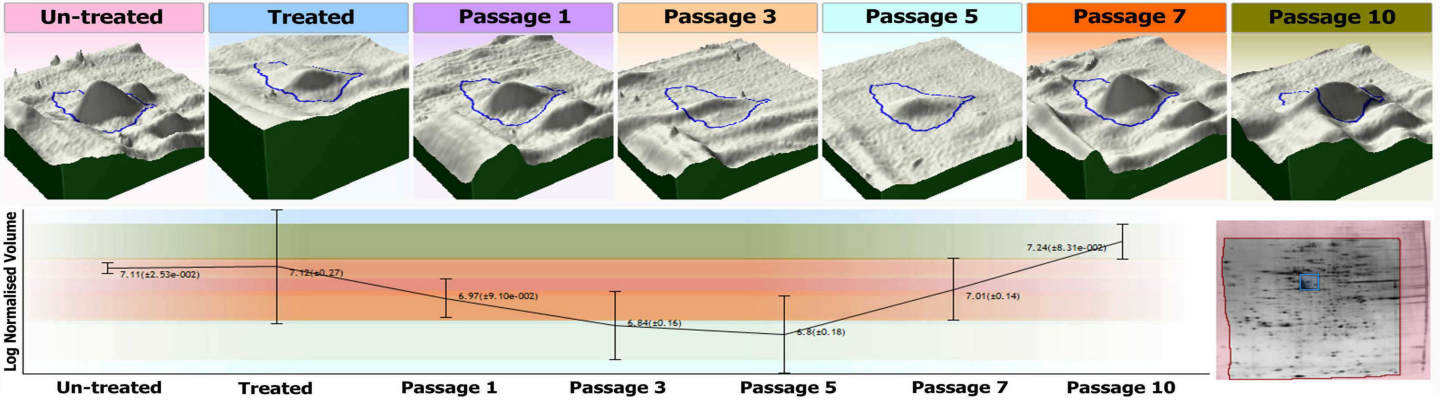
**Spot no. 1234**



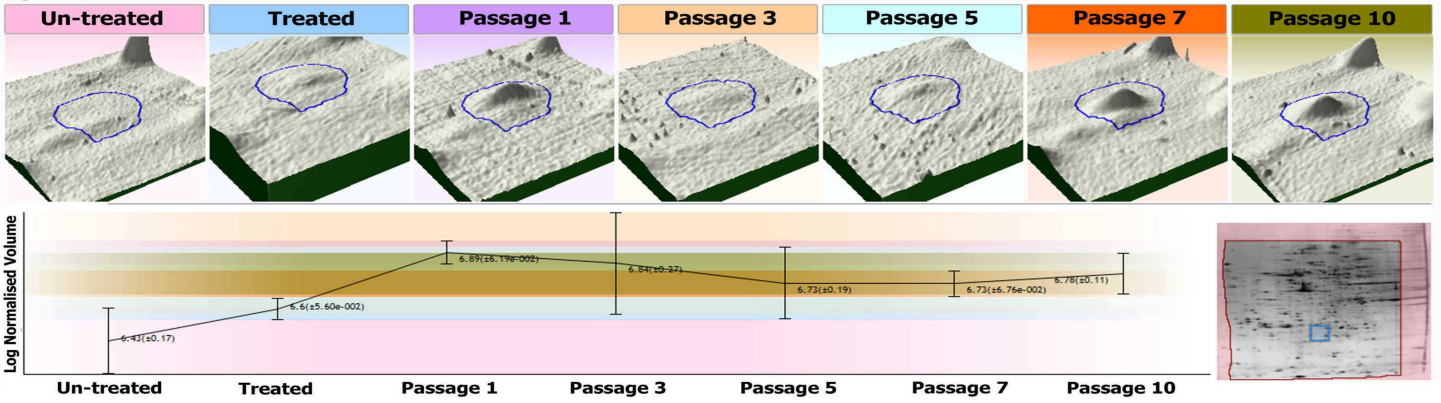
**Spot no. 1219**



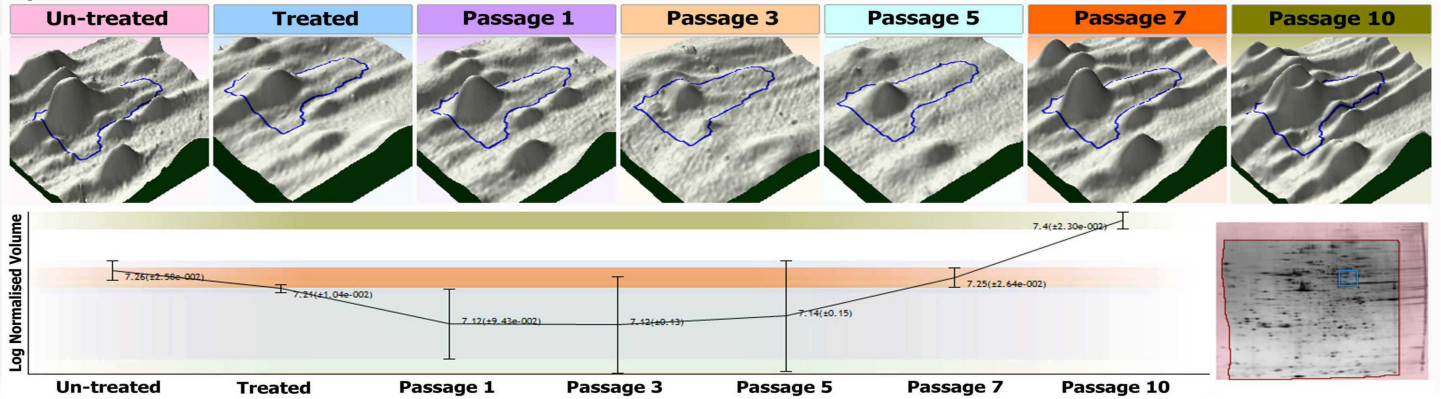
**Spot no. 960**



**Spot no. 1633**

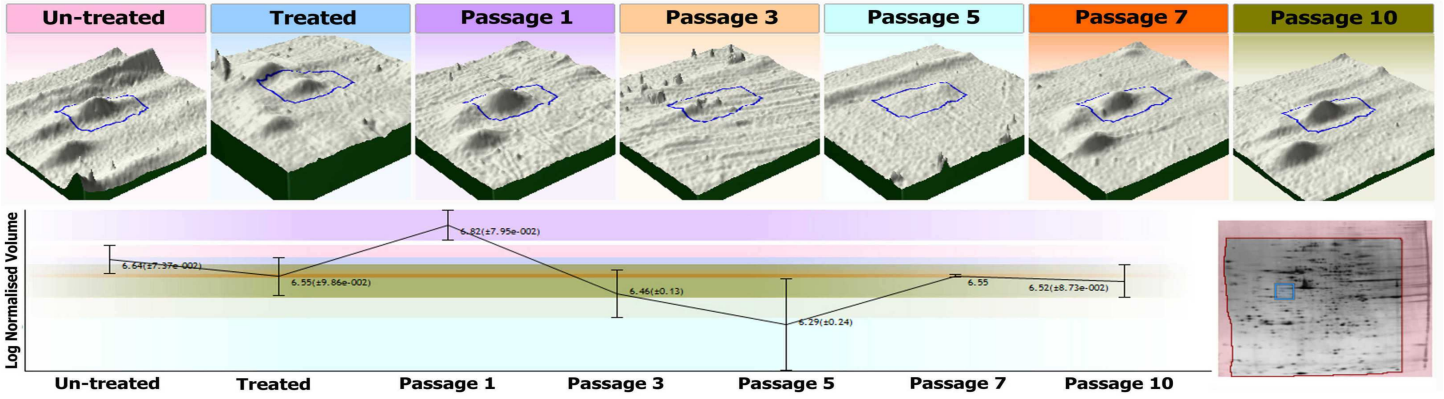


**Spot no. 854**

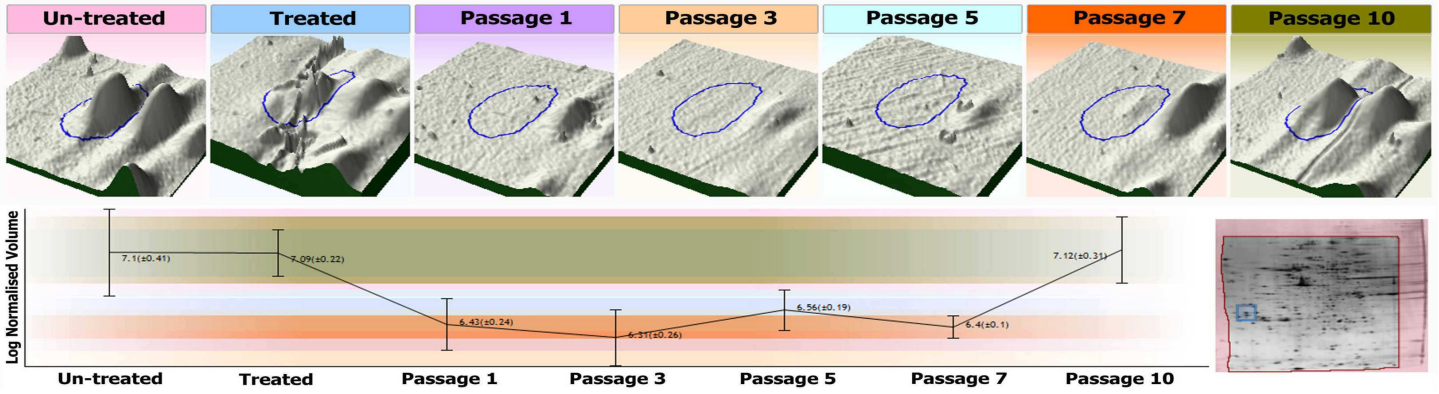




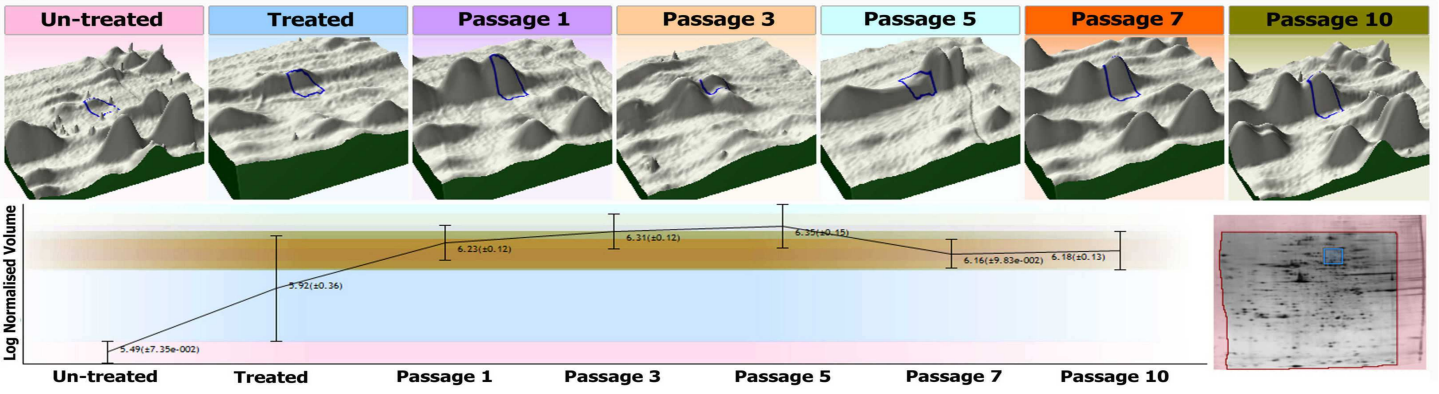
**Spot no. 1121**



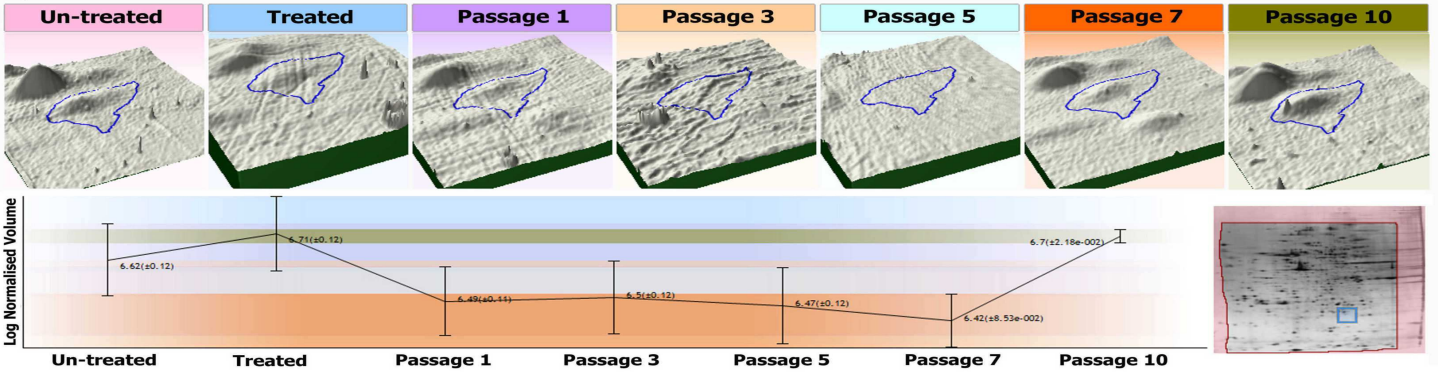
**Spot no. 4070**



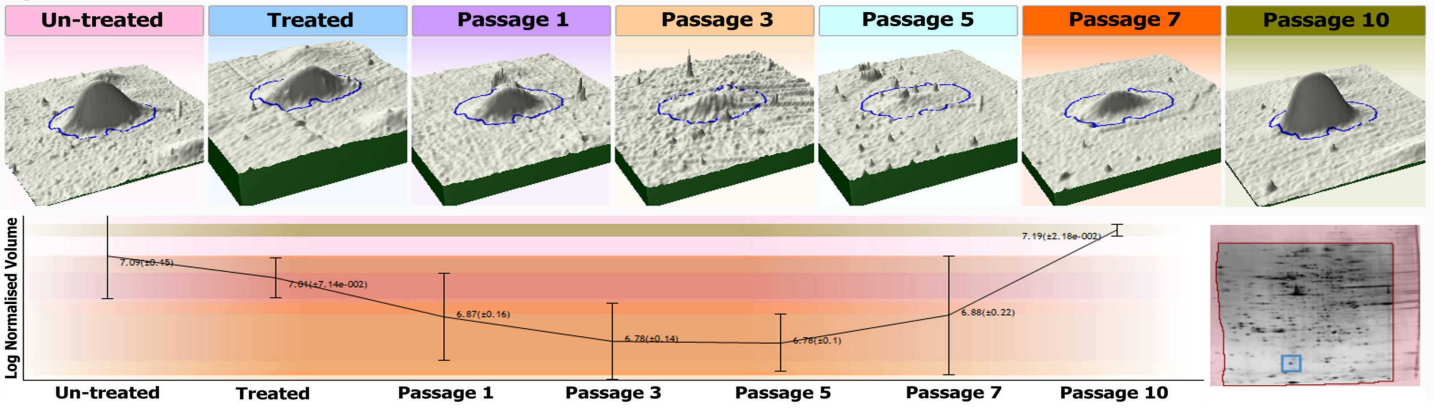
**Spot no. 603**



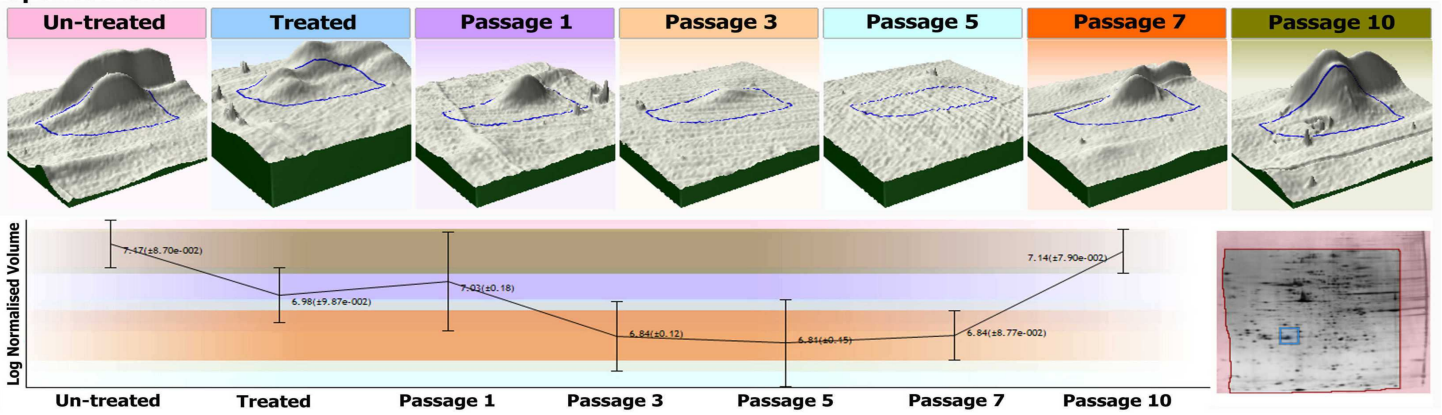
**Spot no. 1727**



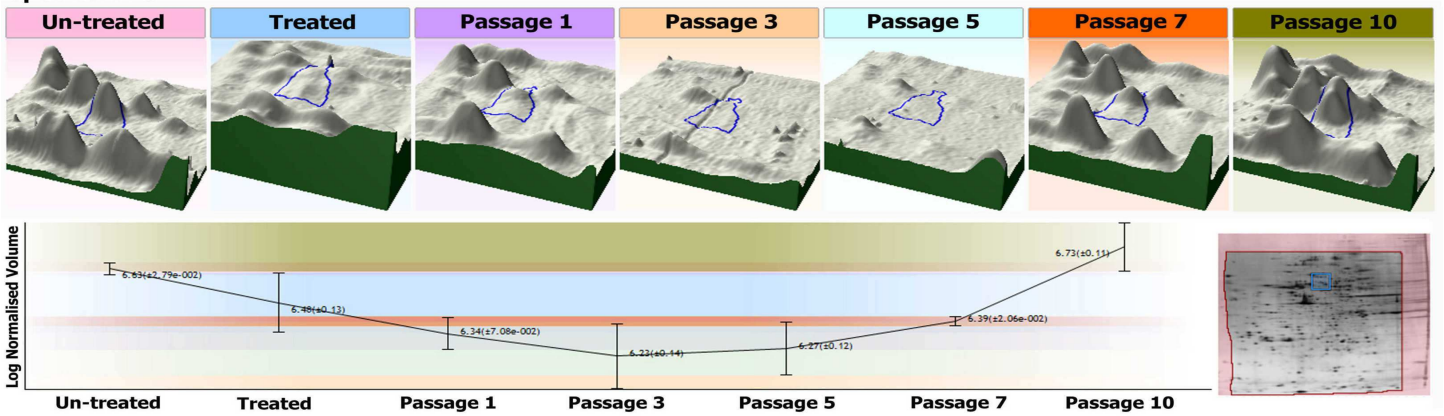
**Spot no. 2162**

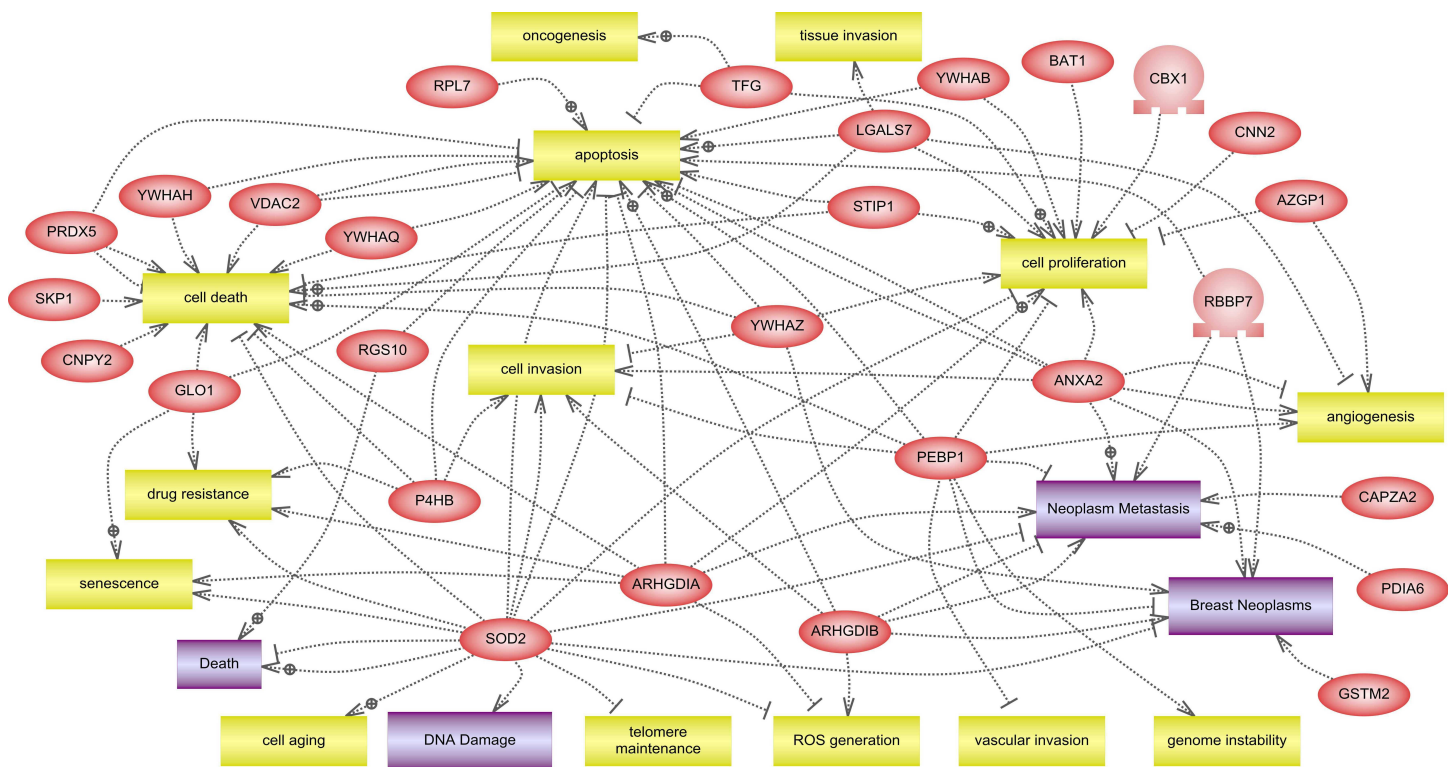


**Spot no. 1543**

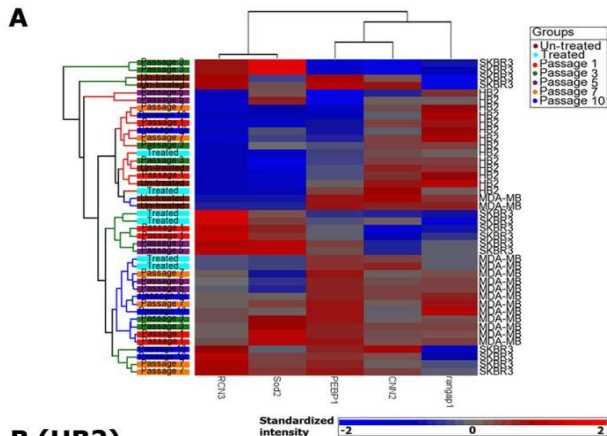


**Spot no. 710**

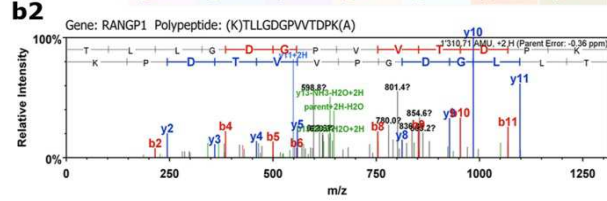
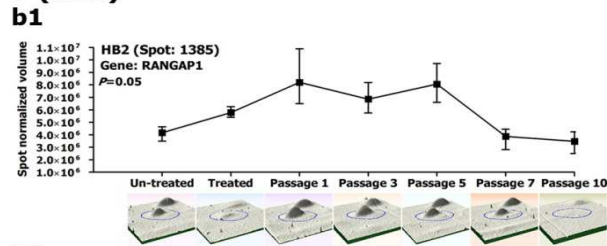




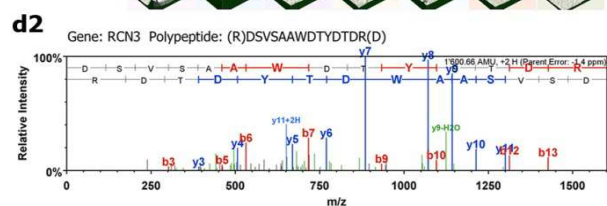
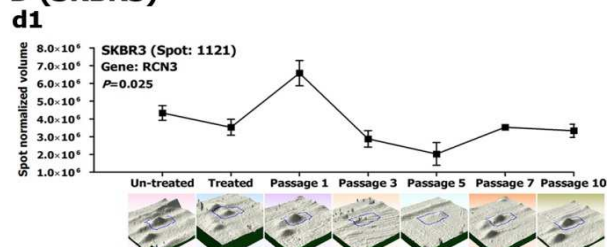
Pathway analysis of 28 out of 41 detected proteins/ isoforms in three analyzed cell lines (HB2, MDA-MB231, SKBR3) that are linked to neoplasms, metastasis or carcinogenesis.



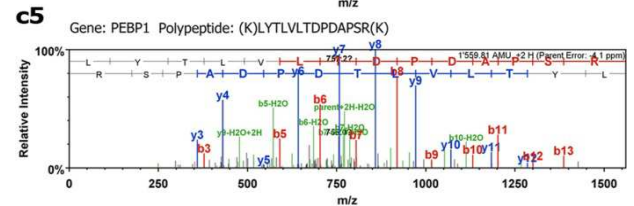
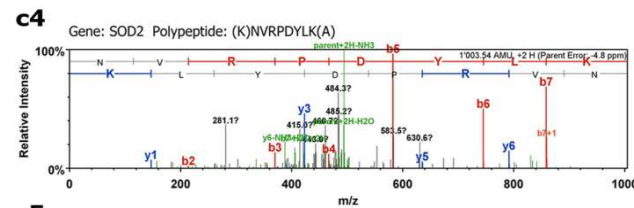
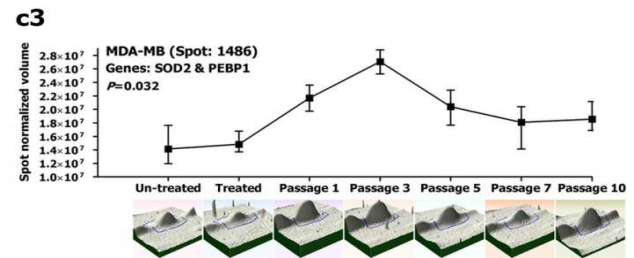
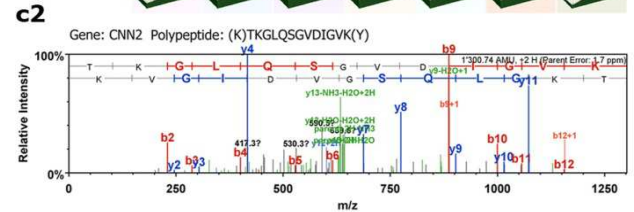
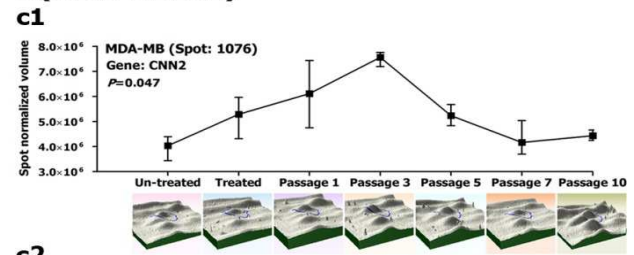
**B (HB2)**



**D (SKBR3)**



**C (MDA-MB231)**



Expression profiles of five genes/proteins that were detected similarly in both transcriptomic and proteomic analysis. A) Expression profiles of five differentially expressed genes in transcriptomic analysis. B-D) Expression profiles of five proteins as significant changing markers in proteomic analysis for the HB2, MDA-MB231 and SKBR3 cell lines. b1-2) Proteomic profile of Rangp1 protein including expression pattern and LC/MS/MS detection. c1-2) Proteomic profile of Cnn2 protein including expression pattern and LC/MS/MS detection. c3-5) Proteomic profiles of Sod2 and Pebp1 proteins including expression pattern and LC/MS/MS detection. d1-2) Proteomic profile of Rnc3 protein including expression pattern and LC/MS/MS detection.