Supplemental Table 1. Complete quantitative comparison of MS/MS spectral counts of all 249 proteins found in the proximal fluid from seven breast cancer cell lines. Spectral counts were quantitated in Scaffold and each cell line is the total of 3 separate experiments (Acc. Num.=Accession Number; MW=Molecular Weight; T.P.=Total Peptides; Avg.=Average; S.D.=Standard Deviation; R=Replicate).

Supplemental Table 2. One at a time mean intensity comparisons across the 4 cancer cell groups (triple negative, HER 2 positive-hormone negative, HER2 negative-hormone positive, MCF7 HER2 transected) were carried out using one way analysis of variance (ANOVA) methods. The overall F statistic and corresponding p value under this method is reported. A separate comparison is done for each of the 229 proteins. In this table a listing of the 229 proteins ranked by the strength of the mean intensity differences across the four groups. Using all four groups including MCF7HER2, 145 of the 229 proteins are significantly different in at least one group.

Supplemental Table 3. Quantitative comparison of a select group of proximal fluid proteins to their presence in the nucleocytoplasmic fraction of 7 breast cancer cell lines. The average spectral counts of the proximal fluid (PF) was compared to the average spectral counts found in their respective nucleocytoplasmic (NC) fraction. The proteins chosen are mostly metabolic proteins important to glucose metabolism and cancer growth (Warburg effect). In addition, keratin 19 (Tree test) and keratin 8, potential candidate biomarkers for hormone positive breast cancers were also included for comparison. Interestingly, the number 1 protein identified at the highest quantity in nucleocytoplasmic fractions of all 7 breast cancer cell lines, 60kDa heat shock protein, was significantly lower in the proximal fluid suggesting minimal cell death.

Supplemental Figure 1. Pie diagram demonstrating the cellular localization of all 249 proximal fluid proteins. Each protein may be found in multiple locations and there may be significant overlap for an individual protein.

Supplemental Figure 2. Pie diagram demonstrating the biological process of all 249 proximal fluid proteins. Each protein may have multiple biological processes and there may be significant overlap for an individual protein.

Supplemental Figure 3. Pie diagram demonstrating the biological function of all 249 proximal fluid proteins. Each protein may have multiple biological functions and there may be significant overlap for an individual protein.

Supplemental Figure 4. Blood samples were collected from advanced breast cancer patients who enrolled in an IRB approved clinical trial. Concentrations of serum CK19 were detected in 50ul of 10 serum samples of each subtype of breast cancer patients (TNBC, HER2+/HR- and HER2-/HR+) were quantified using Human Cytokeratin 19 ELISA Kit. All samples were tested in duplicate.