Figure S3

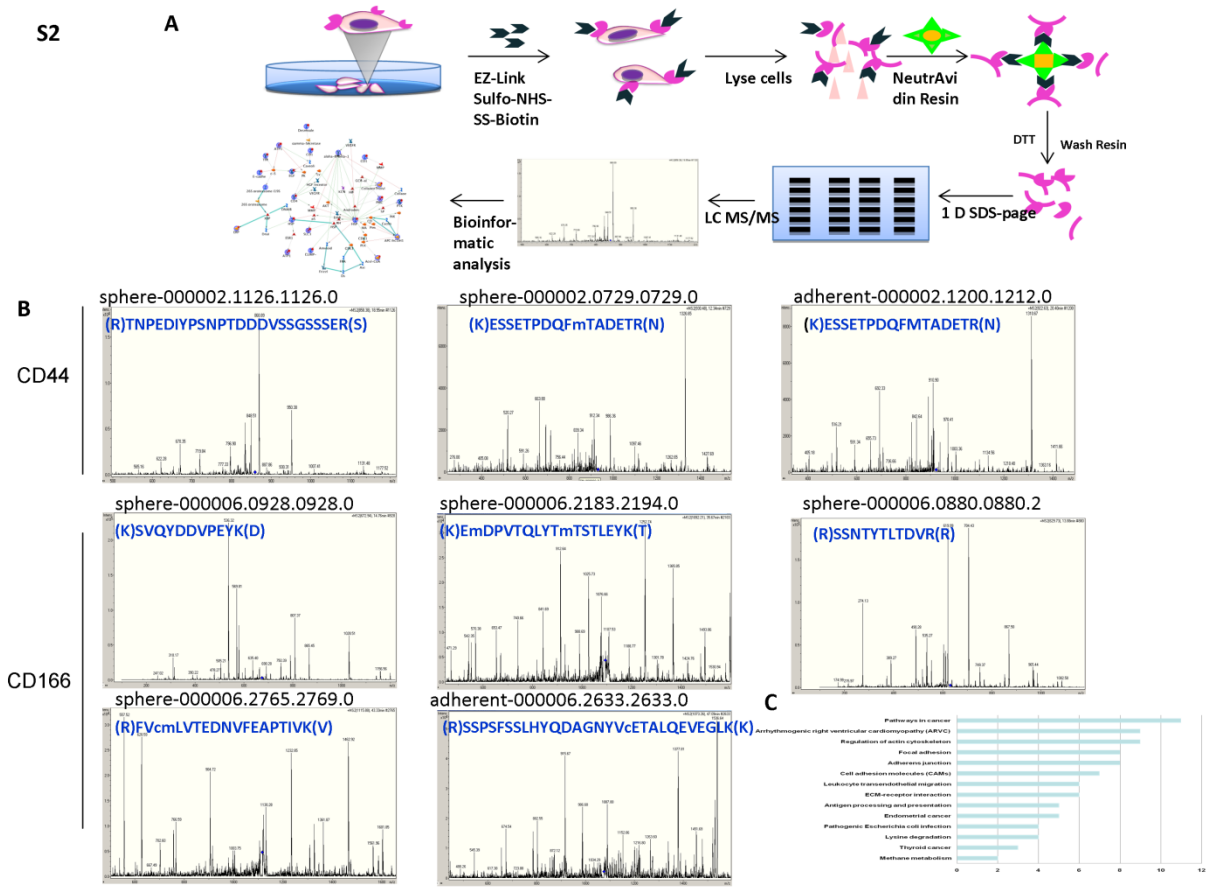

Figure S3. The experimental workflow of the membrane proteomic analysis. A. The membrane proteins were labeled by EZ-Link Sulfo-NHS-SS-Biotin, and then purified with NeutrAvidin Resin from the total protein lysis of labeled cells. The membrane proteins collected from 4 different cell lines were equally mixed and separated by 1 D SDS-PAGE, and analyzed on LC-MS/MS. The proteomics profile data were further analyzed with three bioinformatics tools. B. MS/MS spectrums of CD44 and CD166 identified in sphere and adherent cultured HNSCC cells. C. KEGG pathways analysis with DAVID bioinformatics database. ‘Pathway in cancer’, ‘regulation of actin cytoskeleton’, ‘adherens junction’, ‘focal adhesion’ and ‘cell adhesion molecules (CAMs)’ were identified as the key pathways that were deregulated in microspheres.