

Figure S1. Enrichr web server-based gene set enrichment analysis for upregulated cancer progression genes in LNCaP cells treated with bacteriophages (A) MS2 and (B) T4 and M13 through GO biological processes, predicted 'caveolin-mediated endocytosis' for MS2 bacterial virus. Similarly, the 'integrin-mediated signaling pathway' and 'caveolin-mediated endocytosis' were predicted for both bacteriophages T4 and M13. Also, based on GO cellular component prediction focal adhesion, cell-substrate junction, caveola, plasma membrane raft, early and late endosomes were predicted for MS2, T4, as well as M13 phages further validating the caveolin-mediated endocytosis for these phages. [Here, The q-value is defined as the minimum false discovery rate at which an observed score is deemed significant. Thus, the q-value attempts to control the percentage of false positives among a collection of scores].

A Table of top 10 significant p-values and q-values for GO Biological Process 2021					B Table of top 10 significant p-values and q-values for GO Biological Process 2021				
	term	p-value	q-value	overlap_genes		term	p-value	q-value	overlap_genes
	Caveolin-mediated endocytosis (GO:0072584)	0.000001	0.000221	[MAPK1, MAPK3]		Integrin-mediated signaling pathway (GO:0007229)	3.764491e-08	0.000014	[ITGB1, ITGB5, ITGB3, ITGA5]
	Positive regulation of macrophage proliferation (GO:0120041)	0.000001	0.000221	[MAPK1, MAPK3]		Heterotypic cell-cell adhesion (GO:0034113)	3.628342e-07	0.000069	[ITGB1, ITGB3, ITGA5]
	Regulation of macrophage proliferation (GO:0120040)	0.000002	0.000221	[MAPK1, MAPK3]		Caveolin-mediated endocytosis (GO:0072584)	2.248131e-06	0.000169	[MAPK1, MAPK3]
	Modulation by symbiont of host apoptotic process (GO:0052150)	0.000003	0.000221	[MAPK1, MAPK3]		Positive regulation of macrophage proliferation (GO:0120041)	2.248131e-06	0.000169	[MAPK1, MAPK3]
	Negative regulation by symbiont of host apoptotic process (GO:0033668)	0.000004	0.000221	[MAPK1, MAPK3]		Extracellular structure organization (GO:0043062)	2.640600e-06	0.000169	[ITGB1, ITGB5, ITGB3, ITGA5]
	Negative regulation by symbiont of host programmed cell death (GO:0052041)	0.000004	0.000221	[MAPK1, MAPK3]		External encapsulating structure organization (GO:0045229)	2.689539e-06	0.000169	[ITGB1, ITGB5, ITGB3, ITGA5]
	CD40 signaling pathway (GO:0023035)	0.000005	0.000236	[ITGB1, ITGA5]		Regulation of macrophage proliferation (GO:0120040)	3.371314e-06	0.000182	[MAPK1, MAPK3]
	Response to dopamine (GO:1903350)	0.000006	0.000236	[MAPK1, MAPK3]		modulation by symbiont of host apoptotic process (GO:0052150)	4.718600e-06	0.000223	[MAPK1, MAPK3]
	Cellular response to dopamine (GO:1903351)	0.000006	0.000236	[MAPK1, MAPK3]		Negative regulation by symbiont of host apoptotic process (GO:0033668)	6.289809e-06	0.000238	[MAPK1, MAPK3]
	Regulation of cytoplasmic transport (GO:1903649)	0.000008	0.000236	[MAPK1, MAPK3]		Negative regulation by symbiont of host programmed cell death (GO:0052041)	6.289809e-06	0.000238	[MAPK1, MAPK3]
Table of top 10 significant p-values and q-values for GO Cellular Component 2021					Table of top 10 significant p-values and q-values for GO Cellular Component 2021				
	term	p-value	q-value	overlap_genes		term	p-value	q-value	overlap_genes
	Focal adhesion (GO:0005925)	0.000009	0.000146	[ITGB1, MAPK1, ITGA5, MAPK3]		Focal adhesion (GO:0005925)	9.932333e-09	2.376701e-07	[ITGB1, ITGB5, ITGB3, MAPK1, ITGA5, MAPK3]
	Cell-substrate junction (GO:0030055)	0.000010	0.000146	[ITGB1, MAPK1, ITGA5, MAPK3]		Cell-substrate junction (GO:0030055)	1.105442e-08	2.376701e-07	[ITGB1, ITGB5, ITGB3, MAPK1, ITGA5, MAPK3]
	Caveola (GO:0005901)	0.000245	0.002449	[MAPK1, MAPK3]		Filopodium (GO:0030175)	3.664175e-04	4.215544e-03	[ITGB1, ITGB3]
	Plasma membrane raft (GO:0044853)	0.000458	0.003432	[MAPK1, MAPK3]		Caveola (GO:0005901)	3.921436e-04	4.215544e-03	[MAPK1, MAPK3]
	Late endosome (GO:0005770)	0.002396	0.014375	[MAPK1, MAPK3]		Plasma membrane raft (GO:0044853)	7.314649e-04	6.290598e-03	[MAPK1, MAPK3]
	Early endosome (GO:0005769)	0.004680	0.020952	[MAPK1, MAPK3]		Late endosome (GO:0005770)	3.802922e-03	2.725428e-02	[MAPK1, MAPK3]
	Endoplasmic reticulum lumen (GO:0005788)	0.005354	0.020952	[MAPK1, MAPK3]		Microvillus membrane (GO:0031528)	5.487568e-03	2.801406e-02	[ITGB3]
	Glial cell projection (GO:0097386)	0.005587	0.020952	[ITGB1]		Filopodium membrane (GO:0031527)	5.985094e-03	2.801406e-02	[ITGB3]
	Neuromuscular junction (GO:0031594)	0.015102	0.050339	[ITGB1]		Glial cell projection (GO:0097386)	6.979474e-03	2.801406e-02	[ITGB1]
	Sarcolemma (GO:0042383)	0.020615	0.057424	[ITGB1]		Early endosome (GO:0005769)	7.390943e-03	2.801406e-02	[MAPK1, MAPK3]

Figure S2. Network of protein-protein interactions in LNCaP cells according to their interaction with bacteriophages T4 and M13. The strong link between SRC kinases and other associated proteins and integrins is evident through the highest level of confidence (0.7-0.9) across all proteins based on interactions.

