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Supplemental Table

Reverse phase protein array (RPPA)-generated protein expression in breast tumor tissue at baseline (pre-treatment) and at surgical resection (post-treatment) following the Polyphenon E (Poly E) intervention compared to untreated controls (paired tumor samples from matched historical controls who did not receive Poly E). Includes all protein biomarkers which had a significant change from baseline (p<0.05) in the Poly E-treated group.

Protein Biomarker	Poly E-treated group			Untreated control group			P-value, 2-sample t-test[c]
	Mean protein level at baseline[a] (SD)	Mean protein level at surgical resection[a] (SD)	P-value, paired t-test[b]	Mean protein level at baseline[a] (SD)	Mean protein level at surgical resection[a] (SD)	P-value, paired t-test[b]	
PI3K/AKT pathway							
PRAS40-pT246	0.7703 (0.0632)	0.6289 (0.0808)	<.0001[d]	0.9351 (0.3472)	0.6112 (0.1109)	0.0002[d]	0.0279[e]
mTOR-pS2448	0.3077 (0.0500)	0.2303 (0.0392)	0.0002[d]	0.2832 (0.0708)	0.2320 (0.0585)	0.0045	0.1463
GSK3-alpha-beta-pS21-S9	0.8324 (0.1472)	0.6091 (0.2445)	0.0004	0.8283 (0.2486)	0.5654 (0.2117)	<.0001	0.9939
4EBP1-pT37-T46	1.3924 (0.3584)	0.8818 (0.3557)	0.0005	1.4804 (0.5066)	1.0891 (0.5830)	0.0020	0.8294
Akt	0.7848 (0.1937)	0.9374 (0.1520)	0.0010	0.9490 (0.2447)	1.0129 (0.1476)	0.1930	0.3941
4E-BP1	0.2767 (0.0583)	0.3583 (0.0642)	0.0013	0.2808 (0.0964)	0.4023 (0.2114)	0.0064	0.5229
GAB2	1.7661 (1.0477)	0.9245 (0.2253)	0.0024	1.2675 (0.7749)	0.9485 (0.3143)	0.0386	0.0607
PDK1-pS241	0.6596 (0.1161)	0.8137 (0.1442)	0.0032	0.6744 (0.1740)	0.8034 (0.1661)	0.0081	0.6273
GSK3-pS9	0.6104 (0.1569)	0.4721 (0.2150)	0.0073	0.6225 (0.2473)	0.3580 (0.1531)	<.0001	0.0912
FOXO3a	0.7122 (0.1022)	0.9250 (0.3927)	0.0205	0.7531 (0.1457)	0.9850 (0.3234)	0.0161	0.5673
p27	0.5141 (0.0864)	0.5438 (0.0619)	0.0242	0.5048 (0.1181)	0.5341 (0.0867)	0.3484	0.7773
4E-BP1-pS65	0.5174 (0.1044)	0.4531 (0.0892)	0.0463	0.5189 (0.1599)	0.4201 (0.1112)	0.0006	0.2860
HSP90 Clients							
HER2-pY1248	0.7387 (0.1578)	0.5255 (0.0974)	0.0001[d]	0.5928 (0.1749)	0.4849 (0.1167)	0.0354	0.0744
CDK4	0.7461 (0.4130)	0.2923 (0.1125)	0.0002[d]	0.6288 (0.4713)	0.3344 (0.1662)	0.0220	0.2006
MEK1	0.3725 (0.1364)	0.5398 (0.1057)	0.0002[d]	0.4421 (0.1892)	0.5330 (0.1103)	0.0199	0.1382
MIG-6	0.7612 (0.3202)	0.4555 (0.1952)	0.0002[d]	0.5076 (0.1663)	0.4425 (0.0547)	0.0652	0.0008[e]
EGFR-pY1068	0.0978 (0.0197)	0.0799 (0.0130)	0.0083	0.0998 (0.0569)	0.0790 (0.0144)	0.1635	0.8934
HER3	0.5540 (0.0532)	0.6238 (0.1048)	0.0123	0.6014 (0.1428)	0.6534 (0.1621)	0.6088	0.2483
EGFR-pY1173	1.0172 (0.0933)	1.0713 (0.1206)	0.0273	1.0752 (0.2262)	1.1545 (0.1508)	0.2049	0.9680
Src/STAT Activity							
Src-pY416	0.9064 (0.2800)	0.5850 (0.1683)	<.0001[d]	0.7035 (0.1354)	0.5139 (0.1302)	0.0007	0.0428[e]
Src-pY527	0.5755 (0.1500)	0.2376 (0.1069)	<.0001[d]	0.5357 (0.3102)	0.2304 (0.1289)	0.0029	0.5440
p38-MAPK	0.5673 (0.0754)	0.6841 (0.0901)	0.0001[d]	0.6256 (0.1512)	0.6581 (0.0939)	0.6116	0.0529
MAPK-pT202-Y204	0.3872 (0.1160)	0.2473 (0.0685)	0.0002[d]	0.3763 (0.1160)	0.2258 (0.0632)	0.0001d	0.7778
JNK2	0.6852 (0.0953)	0.8562 (0.1304)	0.0003[d]	0.7379 (0.1993)	0.8513 (0.1573)	0.0282	0.2323
PKC-alpha	0.4080 (0.0398)	0.4743 (0.0419)	0.0004	0.4387 (0.1217)	0.8094 (1.1725)	0.1851	0.3013
Dvl3	0.3986 (0.0348)	0.4631 (0.0796)	0.0026	0.4367 (0.1205)	0.4481 (0.0977)	0.5841	0.0886
STAT3-pY705	0.8014 (0.1938)	0.6918 (0.1098)	0.0037	0.7109 (0.2546)	0.6719 (0.1498)	0.6591	0.4029
FAK	2.5742 (1.4086)	1.7292 (0.6725)	0.0267	1.6977 (0.6868)	1.4399 (0.3911)	0.0705	0.1144
K-Ras	0.1902 (0.0102)	0.1825 (0.0181)	0.0267	0.1857 (0.0129)	0.1814 (0.0179)	0.4420	0.1984
JNK-pT183-T185	0.5489 (0.0498)	0.5261 (0.0441)	0.0269	0.5236 (0.0636)	0.5021 (0.0571)	0.1911	0.8372
C-Raf-pS338	0.9265 (0.1109)	0.8398 (0.0905)	0.0400	0.9764 (0.1790)	0.8350 (0.0900)	0.0093	0.2329
PKC-alpha-pS657	0.2350 (0.0379)	0.2529 (0.0421)	0.0418	0.2263 (0.0368)	0.2540 (0.0379)	0.0255	0.5094

Apoptosis							
Bax	0.4565 (0.0880)	0.5547 (0.1146)	0.0010	0.4481 (0.1228)	0.5040 (0.0860)	0.0652	0.1034
Caspase-7-cleavedD198	0.1959 (0.0206)	0.2184 (0.0230)	0.0017	0.2107 (0.0456)	0.2192 (0.0262)	0.6049	0.1090
p53	0.3895 (0.0665)	0.3358 (0.0491)	0.0061	0.4050 (0.1246)	0.3884 (0.0719)	0.8188	0.1489
c-Myc	1.4595 (0.2886)	1.7492 (0.3268)	0.0065	1.4743 (0.3962)	1.6842 (0.3036)	0.0317	0.3719
14-3-3-epsilon	0.9957 (0.2711)	1.0415 (0.1301)	0.0066	0.9339 (0.1856)	1.0450 (0.1367)	0.0008	0.6626
TIGAR	1.0598 (0.1136)	1.1731 (0.1734)	0.0076	1.1517 (0.1635)	1.2189 (0.1490)	0.1839	0.1440
Bid	0.5926 (0.0556)	0.6206 (0.0596)	0.0170	0.5955 (0.0920)	0.5806 (0.0782)	0.4952	0.0943
Rb_pS807_S811	0.7144 (0.1995)	0.5456 (0.2820)	0.0220	0.7793 (0.3024)	0.6364 (0.4089)	0.1071	0.5282
Caspase-9-cleavedD330	1.0385 (0.1699)	1.2068 (0.2492)	0.0290	1.1215 (0.1462)	1.4377 (0.2800)	0.0005	0.3562
cIAP	1.1592 (0.1569)	1.0717 (0.1615)	0.0436	1.1112 (0.1544)	1.0293 (0.1522)	0.0765	0.4541
Other							
NF2	6.0532 (4.0881)	2.4432 (0.5097)	0.0014	4.8234 (5.1089)	2.7004 (1.0296)	0.0905	0.2507
NF-kB-p65-pS536	0.2103 (0.0276)	0.1825 (0.0264)	0.0042	0.2443 (0.1174)	0.1817 (0.0300)	0.0460	0.3177
Smad1	1.1116 (0.1720)	1.2384 (0.1424)	0.0073	1.1745 (0.1609)	1.2045 (0.1725)	0.4675	0.1187
ACC-pS79	0.6589 (0.2610)	0.5290 (0.1273)	0.0085	0.6359 (0.3119)	0.6167 (0.4386)	0.1769	0.5134
Rad50	0.7017 (0.1524)	0.6620 (0.0989)	0.0120	0.6662 (0.0926)	0.5901 (0.0936)	0.0071	0.8237
Tau	0.5326 (0.2320)	0.3486 (0.1515)	0.0135	0.7109 (0.4234)	0.4303 (0.2567)	0.0106	0.4846
VASP	1.4745 (0.2550)	1.6260 (0.3769)	0.0139	1.4861 (0.2811)	1.7727 (0.2844)	0.0040	0.6689
Notch1	0.2776 (0.0351)	0.3053 (0.0392)	0.0190	0.2872 (0.0378)	0.2780 (0.0382)	0.4094	0.0199[e]
Rab25	1.8176 (0.3614)	2.0147 (0.3118)	0.0264	1.9388 (0.5766)	2.2973 (0.5046)	0.0099	0.1136
ER-alpha-pS118	1.2563 (0.4636)	0.9968 (0.2047)	0.0294	0.9239 (0.2087)	0.8240 (0.1944)	0.1473	0.3296
Claudin-7	1.0142 (0.3459)	0.9107 (0.2425)	0.0386	1.2711 (0.8316)	0.8441 (0.3496)	0.0363	0.1841
eEF2	0.9290 (0.1492)	1.1087 (0.3456)	0.0494	0.8566 (0.1836)	1.0547 (0.2462)	0.0166	0.8322

a. Relative protein levels for each sample were derived from the supercurve for each lysate by curve-fitting, were normalized for protein loading, and the log2-scaled protein concentrations were normalized by global sample median normalization.
b. Paired t-tests to evaluate within-group biomarker changes from baseline to surgical resection.
c. Two-sample t-tests to assess differences in biomarker changes between the Poly E-treated and untreated control groups.
d. Statistically significant after Bonferroni correction with a conservative p-value of <0.0003.
e. Statistically significant based upon p<0.05.

***Corresponding Author**:
Katherine D. Crew MD MS,
Assistant Professor of Medicine and Epidemiology, Herbert Irving Comprehensive Cancer Center, Columbia University, 161 Fort Washington Ave, 10-1072, New York, NY 10032, USA.
Tel: 212-305-1732
Fax: 212-305-0178
E-mail: kd59@cumc.columbia.edu

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