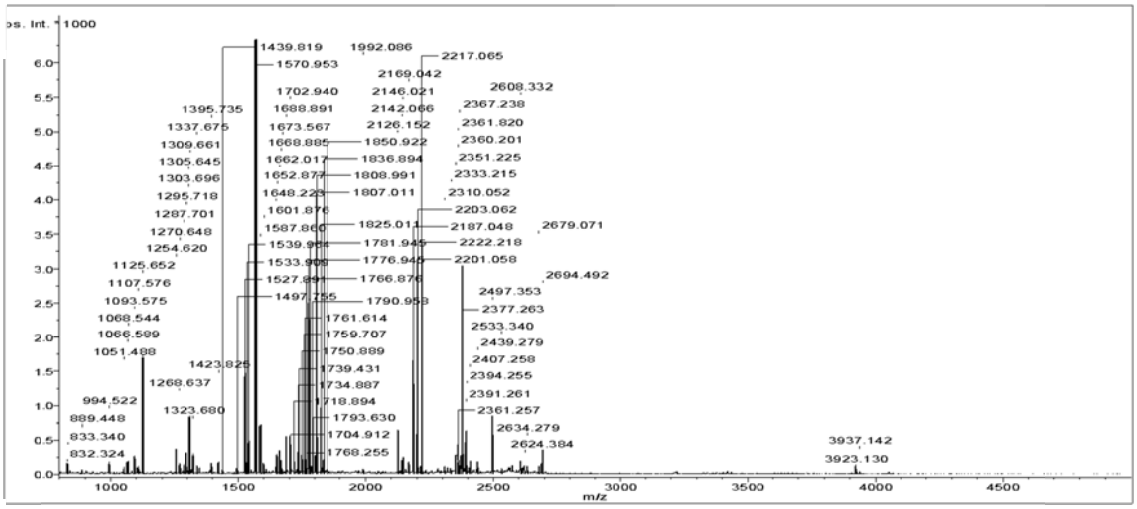
Electronic Supplementary Material (ESI) for Molecular BioSystems.

Figure S1. Identification by PMF and MS/MS of Vimentin, corresponding to spot no. 1 of the 2-DE gel. (A) MALDI peptide mass fingerprint of Vimentin. (B) The product ion spectra of Vimentin tryptic peptide R.ISLPLPNFSSLNLR.E at m/z 1570.9533.

A



B

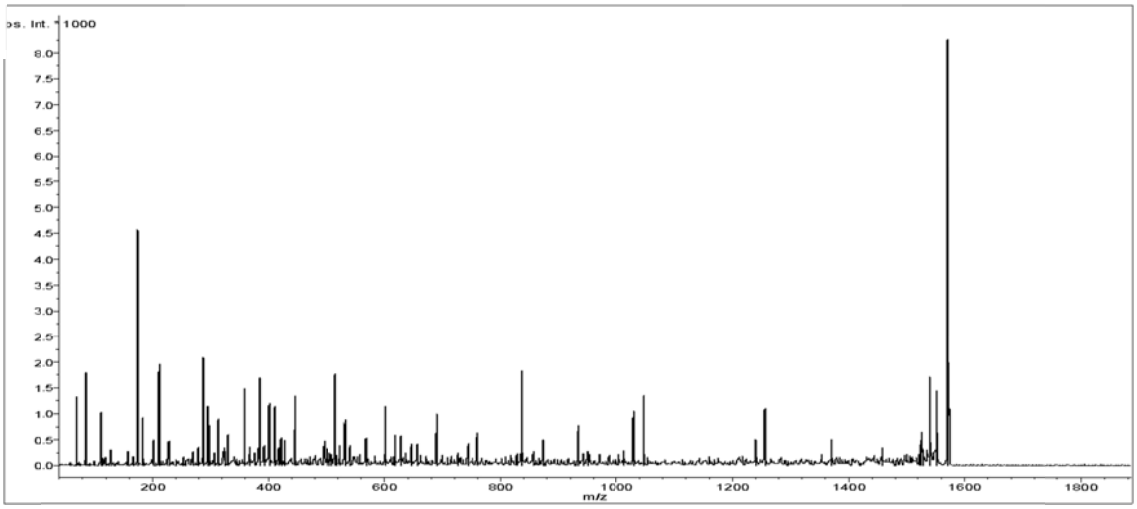


Figure S2. (A) Peptide information for Vimentin based on MALDI-TOF-MS/MS analysis. (B) The amino acid sequences of Vimentin, in which matched peptide sequences are underlined.

A

Spots No.	1
Protein Name	vimentin [Homo sapiens]
Accession No.	gi|62414289

Peptide Information

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1068.5438	1067.5366	1067.4996	34.7	314	321	1	---	K.QESTEYRR.Q
1093.5747	1092.5674	1092.5200	43.5	295	304	0	---	K.FADLSEAANR.N
1125.6521	1124.6448	1124.5978	41.8	114	122	1	66	R.FANYIDKVR.F
1254.6203	1253.6131	1253.5598	42.5	146	155	0	---	R.LGDLYEEEMR.E
1270.6485	1269.6412	1269.5547	68.1	146	155	0	---	R.LGDLYEEEMR.E + Oxidation (M)
1287.7014	1286.6941	1286.6579	28.2	160	170	1	---	R.QVDQLTNDKAR.V
1295.7177	1294.7105	1294.6591	39.7	391	401	0	---	K.MALDIEIATYR.K
1303.6962	1302.6889	1302.6601	22.1	187	196	1	---	R.EKLQEEMLQR.E
1309.6608	1308.6535	1308.5986	42.0	283	292	0	---	K.NLQEAEEWYK.S
1323.6804	1322.6731	1322.6102	47.5	197	207	0	---	R.EEAENTLQSFR.Q
1423.8246	1422.8173	1422.7540	44.5	391	402	1	---	K.MALDIEIATYRK.L
1439.8193	1438.8120	1438.7490	43.8	391	402	1	---	K.MALDIEIATYRK.L + Oxidation (M)
1497.7550	1496.7477	1496.6929	36.6	144	155	1	---	K.SRLGDLYEEEMR.E
1527.8911	1526.8838	1526.8205	41.5	379	390	1	47	R.HLREYQDLLNVK.M
1533.9089	1532.9017	1532.8450	37.0	224	236	1	---	K.VESLQEEIAFLKK.L
1539.9643	1538.9570	1538.9032	35.0	130	143	1	---	K.ILLAELEQLKGQGK.S
1570.9533	1569.9460	1569.8878	37.1	411	424	0	104	R.ISLPLPNFSSLNLR.E
1587.8601	1586.8528	1586.7900	39.6	101	113	1	---	R.TNEKVELQELNDR.F
1652.8770	1651.8697	1651.7875	49.8	146	158	1	---	R.LGDLYEEEMRELR.R
1668.8851	1667.8778	1667.8366	24.7	425	439	0	---	R.ETNLDSLPLVDTHSK.R
1688.8911	1687.8839	1687.8199	37.9	171	184	1	---	R.VEVERDNLAEDIMR.L
1704.9117	1703.9044	1703.8148	52.6	171	184	1	---	R.VEVERDNLAEDIMR.L + Oxidation (M)
1734.8874	1733.8801	1733.8076	41.8	365	378	1	---	R.LQDEIQNMKEEMAR.H
1750.8895	1749.8822	1749.8025	45.5	365	378	1	---	R.LQDEIQNMKEEMAR.H + Oxidation (M)
1766.8761	1765.8688	1765.7974	40.4	365	378	1	---	R.LQDEIQNMKEEMAR.H + 2 Oxidation (M)
1776.9448	1775.9375	1775.8550	46.5	295	310	1	71	K.FADLSEAANRNNDALR.Q
1825.0114	1824.0041	1823.9377	36.4	425	440	1	---	R.ETNLDSLPLVDTHSKR.T
1836.8939	1835.8866	1835.7922	51.4	451	466	0	---	R.DGQVINETSQHHDDLE.-
2126.1515	2125.1443	2125.0579	40.6	79	97	0	---	R.LLQDSVDFSLADAINTEFK.N
2187.0479	2186.0406	2185.9586	37.5	346	364	0	177	R.EMEENFAVEAANYQDTIGR.L
2203.0624	2202.0551	2201.9535	46.1	346	364	0	---	R.EMEENFAVEAANYQDTIGR.L + Oxidation (M)
2351.2248	2350.2175	2350.1223	40.5	189	207	1	---	K.LQEEMLQREEAENTLQSFR.Q
2367.2377	2366.2304	2366.1172	47.9	189	207	1	---	K.LQEEMLQREEAENTLQSFR.Q + Oxidation (M)
2377.2626	2376.2553	2376.1591	40.5	322	342	1	119	R.QVQSLTCEVDALKGTNESLER.Q
2391.2607	2390.2535	2390.2190	14.4	29	50	1	---	R.SYVTTSTRTYSLGSALRPSTSR.S

B

1 MSTRSVSSSS YRRMFGGPGT ASRPSSSRSY VTTSTRTYSL GSALRPSTSR
51 SLYASSPGGV YATRSSAVRL RSSVPGVRLL QDSVDFSLAD AINTEFKNTR
101 TNEKVELQEL NDRFANYIDK VRFLEQQNKI LLAELEQLKG QGKSRLGDLY
151 EEEMRELRRQ VDQLTNDKAR VEVERDNLAE DIMRLREKLQ EEMLQREEAE
201 NTLQSFRQDV DNASLARLDL ERKVESLQEE IAFLKKLHEE EIQELQAQIQ
251 EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEEW YKSKFADLSE
301 AANRNNDALR QAKQESTEYR RQVQSLTCEV DALKGTNESL ERQMREMEEN
351 FAVEAANYQD TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY
401 RKLLEGEESR ISLPLPNFSS LNLRETNLDS LPLVDTHSKR TLLIKTVETR
451 DGQVINETSQ HHDDLE

Figure S3. Western blot analysis of the selective differential expression proteins in H460 lung cells.

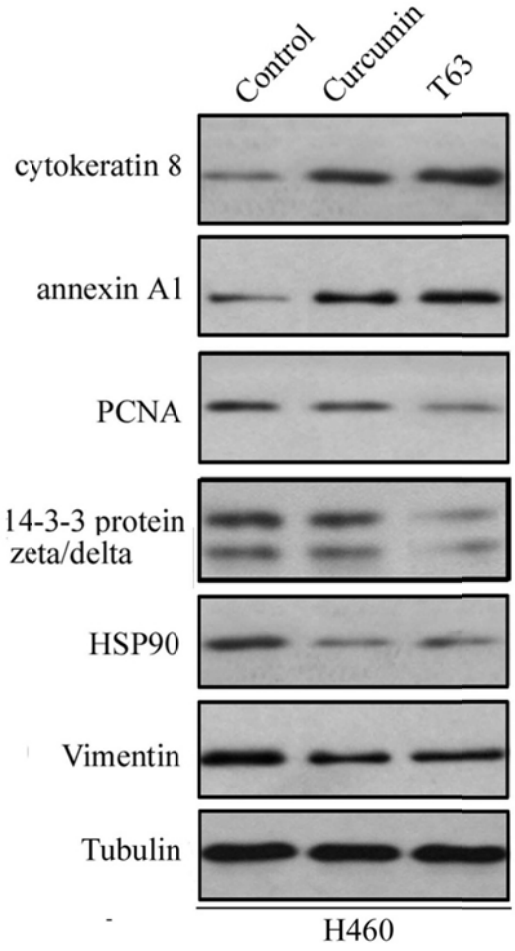


Figure S4. Effect of T63 on expression of p53 in A549 cells. A549 cells were treated with various concentrations (0, 0.25, 0.5, 1, 2 μmol/L) of T63 for 12 h. (A) p53 protein expression levels were analyzed by Western blot. (B) p53 mRNA levels were determined by real-time RT-PCR using GAPDH as an internal control. Data were presented as means ± SD of three independent experiments. Gene-specific primer pairs were as follows, p53-sense 5'-GCGCACAGAGGAAGAGAATCTCCG-3' and p53-antisense 5'-TTTGGCTGGGGAGAGGAGCTG-3', GAPDH-sense 5'-CACCCAGAAGACTGTGGATGG-3' and GAPDH-antisense 5'- GTCTACATGG CAACTGTGAGG-3'.