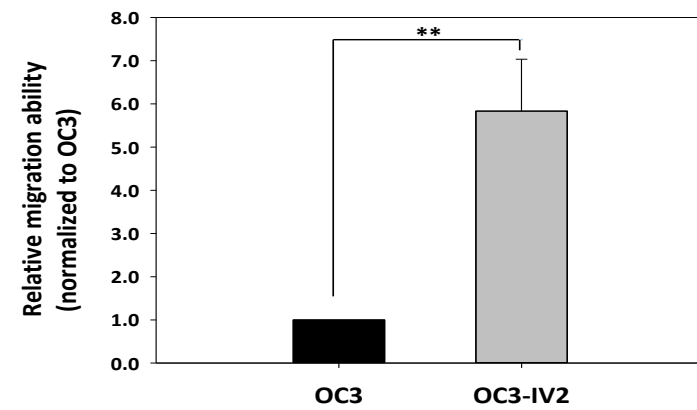
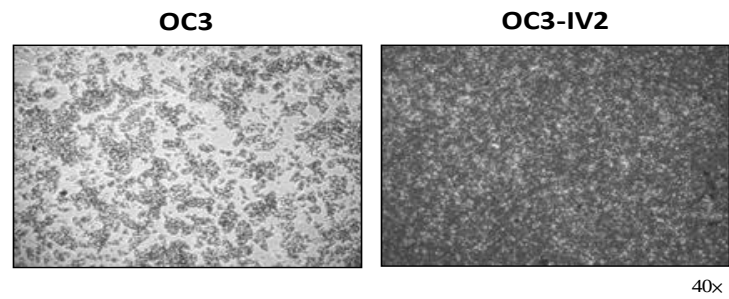


Figure S1

A



B

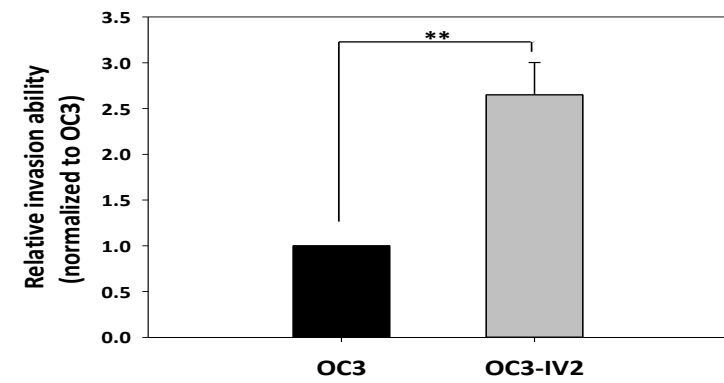
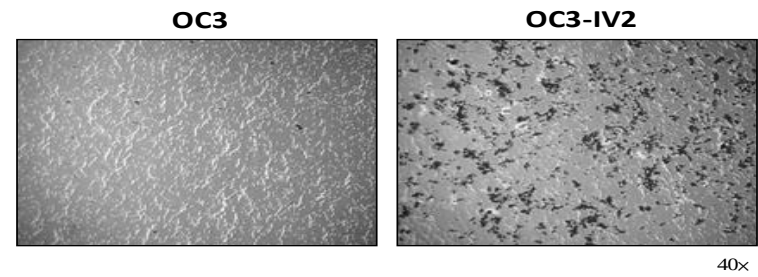


Table S1. Alphabetic List of Identified Differentially Proteins After 2D-DIGE Coupled With MALDI-TOF Mass Spectrometry Analysis between OC3 and OC3-IV2 Cells

Spot No.	Swiss-prot No.	Protein name	MW	pI	No. matched peptides	MO WSE score	Seq cov. (%)	Subcellular location	Functional classification	OC3-IV2/OC3	Representative matched peptides
1149	Q7M4R4	14-3-3protein epsilon	29326	4.63	15	125/56	43%	Cytoplasm	Signal transduction	2.12	K.HLIP AANTGESK.V R.YLAEFATGNDR.K
1081	P31947	14-3-3protein sigma	27871	4.68	23	169/56	57%	Secreted	Signal transduction	4.11	R.YEDMAAFMK.G K.GAVEKGEELSCEER.N
1235	P31947	14-3-3protein sigma	27871	4.68	9	73/56	24%	Secreted	Signal transduction	-2.61	R.VLSSIEQK.S K.MKGDYYR.Y
1116	Q6IN74	14-3-3protein zeta/delta	27899	4.73	18	158/56	46%	Cytoplasm	Signal transduction	2.42	K.LAEQAER.Y K.SVTEQGAELSNEER.N
1107	Q6IN74	14-3-3protein zeta/delta	27899	4.73	12	75/56	27%	Cytoplasm	Signal transduction	2.53	K.SVTEQGAELSNEER.N R.NLLSVAYK.N
1548	P25398	40Sribosomal protein S12	14905	6.81	5	77/56	28%	Cytoplasm	Translation control	7.21	K.TALIH DGLAR.G K.LGEWVGLCK.I
336	P10809	60 kDa heat shock protein, mitochondrial	61187	5.70	7	106/56	18%	Mitochondrion	Protein folding	2.47	R.TVII EQSWGSPK.V R.GYISPYFINTSK.G
343	P10809	60 kDa heat shock protein, mitochondrial	61187	5.70	9	71/56	10%	Mitochondrion	Protein folding	4.85	K.VGLQV VAVK.A K.DRVT DALNATR.A
1110	O95336	6-phosphogluconolactonase	27815	5.70	8	119/56	36%	Cytoplasm	Pentose phosphate pathway	2.42	R.AACCLAGAR.A R.WTLGFCDER.L

689	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	41838	6.47	7	92/56	19%	Cytoplasm	Lipid metabolism	2.05	K.EIVPVLVSTR.K R.ILVTLLHTLER.M
1653	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	28941	3.94	6	59/56	24%	Nucleus	Cell cycle	2.65	K.LPNLTHLNLSGKN.L K.DISTLEPLKK.L
620	Q96HG5	Actin, cytoplasmic 1	42052	5.29	12	103/56	32%	Cytoplasm	Cytoskeleton	2.43	K.AGFAGDDAPR.A K.DSYVGDEAQSKR.G
616	Q96HG5	Actin, cytoplasmic 1	42052	5.29	13	109/56	29%	Cytoplasm	Cytoskeleton	2.55	K.AGFAGDDAPR.A K.DSYVGDEAQSK.R
657	Q96HG5	Actin, cytoplasmic 1	42052	5.29	9	114/56	28%	Cytoplasm	Cytoskeleton	-2.58	K.AGFAGDDAPR.A K.SYELPDGQVITIGNER.F
658	Q96HG5	Actin, cytoplasmic 1	42052	5.29	12	122/56	36%	Cytoplasm	Cytoskeleton	2.18	K.AGFAGDDAPR.A K.DSYVGDEAQSKR.G
639	Q96HG5	Actin, cytoplasmic 1	42052	5.29	14	125/56	36%	Cytoplasm	Cytoskeleton	2.43	K.AGFAGDDAPR.A K.DSYVGDEAQSK.R
995	Q96HG5	Actin, cytoplasmic 1	42052	5.29	7	68/56	20%	Cytoplasm	Cytoskeleton	-2.3	R.GYSFTTTAER.E K.SYELPDGQVITIGNER.F
695	Q96HG5	Actin, cytoplasmic 1	42052	5.29	7	74/56	26%	Cytoplasm	Cytoskeleton	2.08	K.AGFAGDDAPR.A K.IWHHTFYNELR.V
1140	Q96HG5	Actin, cytoplasmic 1	42052	5.29	10	83/56	23%	Cytoplasm	Cytoskeleton	-4.6	R.GYSFTTTAER.E K.SYELPDGQVITIGNER.F
649	Q96HG5	Actin, cytoplasmic 1	42052	5.29	7	82/56	22%	Cytoplasm	Cytoskeleton	2.33	K.AGFAGDDAPR.A K.IWHHTFYNELR.V

1029	Q96HG5	Actin, cytoplasmic 1	42052	5.29	7	91/56	22%	Cytoplasm	Cytoskeleton	-2.74	R.GYSFTTT AER.E K.SYELPDGQVITIGNER.F
648	P63261	Actin, cytoplasmic 2	42108	5.31	14	103/56	33%	Cytoplasm	Cytoskeleton	2.28	K.AGFAGDDAPR.A R.HQGVMVGMGQK.D
1105	O15144	Actin-related protein 2/3 complex subunit 2	34426	6.84	6	78/56	16%	Cytoplasm	Cytoskeleton regulation	-2.64	K.YFQFQEEGK.E R.ASHTAPQVLFSHR.E
622	P23526	Adenosylhomocysteinase	48255	5.92	8	96/56	17%	Cytoplasm	One-carbon metabolism	3.18	K.AGIPVYAWK.G K.YPQLLPGIR.G
888	Q04828	Aldo-keto reductase family 1 member C1	37221	8.02	6	63/56	12%	Cytoplasm	Redox regulation	-3.1	K.REDIFYTSK.L R.EDIFYTSK.L
853	P15121	Aldose reductase	36230	6.51	13	147/56	36%	Cytoplasm	Redox regulation	-2.24	K.SPPGQVTEAVK.V K.VAIDVGYR.H
1258	Q96IU4	Alpha/beta hydrolase domain-containing protein 14B	22446	5.94	6	100/56	30%	Cytoplasm	Metabolism	3.14	R.EALPGSGQAR.F R.FSVLLLHGIR.F
1042	Q6GMP2	Alpha-enolase	47481	7.01	6	65/56	18%	Cytoplasm	Glycolysis	-2.69	R.IGAEVYHNLK.N R.YISPDQLADLYK.S
985	Q6GMP2	Alpha-enolase	47481	7.01	6	82/56	17%	Cytoplasm	Glycolysis	-2.59	R.IGAEVYHNLK.N R.YISPDQLADLYK.S
1031	Q6GMP2	Alpha-enolase	47481	7.01	7	93/56	19%	Cytoplasm	Glycolysis	-5.17	R.IGAEVYHNLK.N R.YISPDQLADLYK.S
630	Q03154	Aminoacylase-1	46084	5.77	6	74/56	12%	Secreted	Proteolysis	-3.24	K.DSEGYIYAR.G R.TPVLLHDHDER.L

1120	P00918	Carbonic anhydrase 2	29285	6.87	4	60/56	15%	Plasma membrane	Homeostasis	2.77	K.GGPLDGT YRL K.SADFTNFDPR.G
486	P07339	Cathepsin D	45037	6.10	9	95/56	14%	Secreted	Proteolysis	2.78	K.QPGITFIAAK.F K.FDGILGMAYPR.I
512	P07339	Cathepsin D	45037	6.10	10	98/56	16%	Secreted	Proteolysis	-3.23	K.QPGITFIAAK.F K.GSLSYLNVTRK.A
1048	O00299	Chloride intracellular channel protein 1	27248	5.09	6	85/56	24%	Plasma membrane	Transport	2.23	K.IGNCPFSQR.L K.GVTFNVTTVDTK.R
1534	Q14019	Coactosin-like protein	16049	5.54	7	80/56	30%	Plasma membrane	Protein folding	2.15	K.EFVISDRK.E K.ELEEDFIK.S
1454	P23528	Cofilin-1	18719	8.22	6	80/56	31%	Cytoplasm	Cytoskeleton regulation	14.68	K.AVLFCLSEDKK.N K.NIILEEGK.E
1471	P23528	Cofilin-1	18719	8.22	7	90/56	45%	Cytoplasm	Cytoskeleton regulation	7.21	K.AVLFCLSEDKK.N R.YALYDATYETK.E
1024	P12109	Collagen alpha-1(VI) chain	1E+05	5.26	9	62/56	7%	Secreted	Cell adhesion	-3.27	R.LKPYGALVDK.V K.RFIDNLR.D
839	P00736	Complement C1r subcomponent	81606	5.82	8	106/56	12%	Secreted	Immuno response	4.18	R.LPVANPQACENWLR.G K.VLNYVDWIK.K
1555	P01034	Cystatin-C	16017	9.00	7	96/56	36%	Secreted	Proteolysis	2.2	R.RALDFAVGEYNK.A R.ALDFAVGEYNK.A
1158	O43237	Cytoplasmic dynein 1 light intermediate chain 2	54351	5.97	6	59/56	10%	Cytoplasm	Cytoskeleton regulation	-6.65	K.NLDLLYK.Y K.ELAAEDEQVFLMK.Q

886	Q6P179	Endoplasmic reticulum aminopeptidase 2	1E+05	6.25	11	72/56	8%	Endoplasmic Reticulum	Immuno response	-7.3	K.VSIYASPDK.R K.EMMTTWTLQK.G
1111	P30040	Endoplasmic reticulum resident protein 29	29032	6.77	8	96/56	30%	Endoplasmic Reticulum	Protein folding	4.32	K.GALPLDVTTFYK.V K.FDTQYPYGEK.Q
35	P14625	Endoplasmin	92696	4.76	8	92/56	10%	Endoplasmic Reticulum	Protein folding	3.47	K.FAFQAEVNR.M K.SILFVPT SAPR.G
566	P60842	Eukaryotic initiation factor 4A-I	46353	5.32	14	119/56	28%	Nucleus	Transcription control	5.74	K.GYDVIAQAQSGTGK.T K.ATQALVLAPTR.E
1133	P56537	Eukaryotic translation initiation factor 6	27095	4.56	6	101/56	42%	Cytoplasm	Translation control	-4.17	R.ASFENNCEIGCFAK.L R.NSLPDT VQIR.R
911	P52907	F-actin-capping protein subunit alpha-1	33073	5.45	8	76/56	22%	Cytoplasm	Cytoskeleton regulation	2.27	R.LLLNNDNLLR.E R.ESCDSALR.A
1552	Q01469	Fatty acid-binding protein, epidermal	15497	6.60	8	109/56	55%	Cytoplasm	Transport	2.37	K.TTQFSC TLGEK.F K.FEETTADGR.K
1397	P02794	Ferritin heavy chain	21383	5.30	8	108/56	35%	Cytoplasm	Homeostasis	2.16	R.QNYHQDSEAAINR.Q K.YFLHQSHEER.E
1187	Q6PIW4	Fidgetin-like protein 1	74829	8.07	6	77/56	8%	Nucleus	DNA repair	-2.58	R.TQDFPESNR.L K.EDSSLPTFK.T
121	Q8N475	Follistatin-related protein 5	97002	5.61	9	77/56	10%	Secreted	Growth regulation	-2.29	K.HLALEEFYR.A R.EPGVTASLR.C
606	P07954	Fumarate hydratase, mitochondrial	54773	8.85	7	61/56	14%	Mitochondrion	TCA cycle	3.11	K.VPNDKYYGAQTVR.S K.YYGAQTVR.S

653	P07954	Fumarate hydratase, mitochondrial	54773	8.85	8	74/56	18%	Mitochondrion	TCA cycle	-3.07	R.AAAAEVNQDYGLDPK.I K.IPVHPNDHVNK.S
1573	P09382	Galectin-1 (LGALS1)	15048	5.34	10	137/56	71%	Secreted	Apoptosis	2.42	K.DSNNLCLHFNPR.F R.FNAHGDANTIVCNSK.D
9	Q08380	Galectin-3-binding protein	66202	5.13	6	74/56	8%	Secreted	Cell adhesion	3.28	R.LADGGATNQGR.V R.STHTLDLSR.E
21	Q08380	Galectin-3-binding protein	66202	5.13	10	135/56	16%	Secreted	Cell adhesion	2.79	R.LADGGATNQGR.V R.ELSEALGQIFDSQR.G
1384	O75223	Gamma-glutamylcyclotransferase	21222	5.07	6	80/56	37%	Cytoplasm	Apoptosis	-2.43	R.NPSAAFFCVAR.L K.LDFGNSQ GK.T
822	P07093	Glia-derived nexin	44202	9.35	7	78/56	11%	Secreted	Proteolysis	-2.23	R.NKDV FQCEVR.N K.DVFQCEVR.N
97	P14314	Glucosidase 2 subunit beta	60357	4.33	8	81/56	17%	Endoplasmic Reticulum	Glycan processing	2.26	K.LWEEQLAAAK.A K.AQQEQELAADA FK.E
723	O76003	Glutaredoxin-3	37693	5.31	6	65/56	18%	Cytoplasm	Redox regulation	3.11	R.HASSGSFLPSANEHLK.E K.GELVGGLDIVK.E
960	P04406	Glyceraldehyde-3-phosphate dehydrogenase	36201	8.57	6	82/56	18%	Cytoplasm	Glycolysis	5.16	K.VGVNGFGR.I R.VPTANVSVDLT CR.L
965	P04406	Glyceraldehyde-3-phosphate dehydrogenase	36201	8.57	6	89/56	21%	Cytoplasm	Glycolysis	2.75	K.AGAHLQGGAK.R R.VPTANVSVDLT CR.L
1053	Q6FH47	Guanine nucleotide-binding protein subunit beta-2-like 1	35511	7.60	6	84/56	19%	Plasma membrane	Signal transduction	2.1	R.DETNYGIPQR.A R.LWDLTTGTTTR.R

458	P07900	Heat shock protein HSP 90-alpha	85006	4.94	8	88/56	10%	Cytoplasm	Protein folding	-3	K.SLTNDWEDHLAVK.H R.APFDLFENR.K
1370	P09651	Heterogeneous nuclear ribonucleoprotein A1	38837	9.17	7	58/56	17%	Nucleus	Transcription control	-2.81	K.SESPKEPEQLR.K K.EPEQLRK.L
1365	P09651	Heterogeneous nuclear ribonucleoprotein A1	38837	9.17	7	61/56	17%	Nucleus	Transcription control	-4.42	K.SESPKEPEQLR.K R.EDSQRPGAHLTVK.K
1546	P08476	Inhibin beta A chain	48210	8.30	8	59/56	9%	Secreted	Growth regulation	-2.31	K.KQFFVSEFK.D R.GHSPFANLK.S
991	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	10	111/56	25%	Cytoplasm	Glycolysis	5.71	K.DYNVTANSK.L R.VIGSGCNLDSAR.F
902	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	8	112/56	22%	Cytoplasm	Glycolysis	2.72	K.DYNVTANSK.L K.LVIITAGAR.Q
928	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	8	116/56	22%	Cytoplasm	Glycolysis	4.04	K.LVIITAGAR.Q R.VIGSGCNLDSAR.F
1069	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	12	134/56	33%	Cytoplasm	Glycolysis	-2.78	K.DYNVTANSK.L K.LVIITAGAR.Q
969	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	10	149/56	29%	Cytoplasm	Glycolysis	3.34	K.DYNVTANSK.L R.VIGSGCNLDSAR.F
996	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	10	149/56	29%	Cytoplasm	Glycolysis	2.49	K.DYNVTANSK.L K.LVIITAGAR.Q
993	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	15	149/56	30%	Cytoplasm	Glycolysis	3.05	K.DYNVTANSK.L K.LVIITAGAR.Q

1010	Q9UDE8	L-lactate dehydrogenase A chain	36950	8.44	7	79/56	20%	Cytoplasm	Glycolysis	4.63	K.DYNVTANSK.L K.LVIITAGAR.Q
903	P07195	L-lactate dehydrogenase B chain	36900	5.71	9	100/56	25%	Cytoplasm	Glycolysis	2.54	K.DDEVAQLKK.S K.SADTLWDIQK.D
910	P07195	L-lactate dehydrogenase B chain	36900	5.71	12	140/56	34%	Cytoplasm	Glycolysis	3.53	K.LIAPVAEEEEATVPNNK.I K.IVADKDYSVTANSK.I
890	P07195	L-lactate dehydrogenase B chain	36900	5.71	15	147/56	34%	Cytoplasm	Glycolysis	4.02	K.IVADKDYSVTANSK.I K.DYSVTANSK.I
1014	P07195	L-lactate dehydrogenase B chain	36900	5.71	7	99/56	19%	Cytoplasm	Glycolysis	-4.5	R.VIGSGCNLDSAR.F K.DDEVAQLKK.S
943	P07195	L-lactate dehydrogenase B chain	36900	5.71	13	138/56	27%	Cytoplasm	Glycolysis	3.28	K.IVADKDYSVTANSK.I K.DYSVTANSK.I
1063	P07195	L-lactate dehydrogenase B chain	36900	5.71	6	72/56	16%	Cytoplasm	Glycolysis	-4.32	K.IVVVTAGVR.Q R.VIGSGCNLDSAR.F
1004	P07195	L-lactate dehydrogenase B chain	36900	5.71	6	80/56	17%	Cytoplasm	Glycolysis	-5.81	R.VIGSGCNLDSAR.F K.DDEVAQLKK.S
1655	P01033	Metalloproteinase inhibitor 1	23840	8.46	6	100/56	36%	Secreted	Protease inhibitor	2.27	K.GFQALGDAADIR.F R.SEEFLIAGK.L
1231	P01033	Metalloproteinase inhibitor 1	23840	8.46	4	70/56	18%	Secreted	Protease inhibitor	2.34	K.GFQALGDAADIR.F R.SEEFLIAGK.L
1157	P01033	Metalloproteinase inhibitor 1	23840	8.46	4	72/56	18%	Secreted	Protease inhibitor	2.01	K.GFQALGDAADIR.F R.SEEFLIAGK.L

1242	P01033	Metalloproteinase inhibitor 1	23840	8.46	5	79/56	26%	Secreted	Protease inhibitor	2.56	K.GFQALGDAADIR.F R.EPGLCTWQSLR.S
1220	P01033	Metalloproteinase inhibitor 1	23840	8.46	5	92/56	26%	Secreted	Protease inhibitor	2.26	K.GFQALGDAADIR.F R.SEEFLIAGK.L
1190	P01033	Metalloproteinase inhibitor 1	23840	8.46	4	71/56	22%	Secreted	Protease inhibitor	2.61	K.GFQALGDAADIR.F R.HLACLPRE
1217	P01033	Metalloproteinase inhibitor 1	23840	8.46	5	72/56	26%	Secreted	Protease inhibitor	2.58	K.GFQALGDAADIR.F R.EPGLCTWQSLR.S
1569	P02795	Metallothionein-2	7178	8.23	3	64/56	65%	Cytoplasm	Metal binding	3.18	K.SCCSCCPVCGAK.C K.CAQGCICK.G
749	P28482	Mitogen-activated protein kinase 1	41762	6.50	6	88/56	17%	Cytoplasm	Signal transduction	3.56	R.GQVFDVGPR.Y K.ISPFEHQTYCQRT
1131	Q8TCH0	Nebulin-related-anchoring protein	2E+05	9.24	11	63/56	7%	Cytoplasm	Cytoskeleton regulation	-4.17	K.MMLSVNNFVSHQK.K K.AQTLASDLDYR.K
375	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4	52057	5.35	6	76/56	12%	Cytoplasm	Protein folding	3.98	K.FQIPPNAELK.Y K.LEQSTIVK.E
377	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4	52057	5.35	8	80/56	12%	Cytoplasm	Protein folding	2.99	K.FSFDLGK.G K.FQIPPNAELK.Y
1317	Q06830	Peroxiredoxin-1	22324	8.27	10	147/56	45%	Cytoplasm	Redox regulation	-5.54	K.IGHAPAPNFK.A K.DISLSDYK.G
1254	Q06830	Peroxiredoxin-1	22324	8.27	10	155/56	41%	Cytoplasm	Redox regulation	2.19	R.TIAQDYGVLK.A R.QITVNDLPVGR.S

1348	Q06830	Peroxiredoxin-1	22324	8.27	11	184/56	49%	Cytoplasm	Redox regulation	-3.57	R.TIAQDYGVLK.A K.DISLSDYK.G
1656	Q06830	Peroxiredoxin-1	22324	8.27	19	224/56	68%	Cytoplasm	Redox regulation	2.51	K.RTIAQDYGVLK.A R.TIAQDYGVLK.A
1334	Q06830	Peroxiredoxin-1	22324	8.27	7	138/56	33%	Cytoplasm	Redox regulation	-2.32	R.TIAQDYGVLK.A R.QITVNDLPVGR.S
1269	Q06830	Peroxiredoxin-1	22324	8.27	14	172/56	55%	Cytoplasm	Redox regulation	2.34	K.IGHPAPNFK.A R.TIAQDYGVLK.A
1349	P32119	Peroxiredoxin-2	22049	5.66	8	114/56	28%	Cytoplasm	Redox regulation	3.81	K.ATAVVDGAFK.E R.RLSEDYGVLK.T
1363	P32119	Peroxiredoxin-2	22049	5.66	8	124/56	28%	Cytoplasm	Redox regulation	3.58	R.IGKPAPDFK.A R.RLSEDYGVLK.T
1338	P32119	Peroxiredoxin-2	22049	5.66	8	110/56	28%	Cytoplasm	Redox regulation	5.59	R.RLSEDYGVLK.T R.LSEDYGVLK.T
1546	Q9UJU4	Peroxiredoxin-5, mitochondrial	22301	8.93	8	76/56	28%	Mitochondrion	Redox regulation	-2.31	K.VNLAELFK.G K.GVLFGVPGAFTPGCSK.T
1510	Q9UJU4	Peroxiredoxin-5, mitochondrial	22301	8.93	6	80/56	29%	Mitochondrion	Redox regulation	4.55	K.GVLFGVPGAFTPGCSK.T R.FSMVVQDGIVK.A
1154	P30041	Peroxiredoxin-6	25133	6.00	9	112/56	30%	Cytoplasm	Redox regulation	4.26	R.DFTPVCTTELGR.A R.AAKLAPEFAK.R
1161	P30041	Peroxiredoxin-6	25133	6.00	6	83/56	26%	Cytoplasm	Redox regulation	2.36	R.DFTPVCTTELGR.A R.AAKLAPEFAK.R

583	P05121	Plasminogen activator inhibitor 1	45088	6.68	14	142/56	28%	Secreted	Protease inhibitor	3.59	R.VFQQVAQASK.D K.ELMGPWNK.D
1651	P07737	Profilin-1	15216	8.44	7	94/56	47%	Cytoplasm	Cytoskeleton regulation	2.22	K.DSPSVWAAVPGK.T K.STGGAPT FNVTVTK.T
1590	P07737	Profilin-1	15216	8.44	6	97/56	47%	Cytoplasm	Cytoskeleton regulation	2.04	K.DSPSVWAAVPGK.T K.STGGAPT FNVTVTK.T
1583	P07737	Profilin-1	15216	8.44	9	118/56	57%	Cytoplasm	Cytoskeleton regulation	3.17	K.DSPSVWAAVPGK.T R.SSFYVNGLT LGGQK.C
768	Q9UQ80	Proliferation-associated protein 2G4	44101	6.13	7	97/56	18%	Cytoplasm	Growth regulation	-2.47	K.AAHLCAEAALR.L K.TIIQNPTDQK.K
1236	P61289	Proteasome activator complex subunit 3	29602	5.69	5	64/56	19%	Nucleus	Apoptosis	2.99	K.SNQLVDIEK.V K.YPHVEDYRR.T
1130	O14818	Proteasome subunit alpha type-7	28041	8.60	10	84/56	31%	Cytoplasm	Proteolysis	2.85	R.GRDIVVLGVEK.K K.SVAKLQDER.T
1353	Q86T01	Proteasome subunit beta type-5	28633	6.43	8	111/56	22%	Cytoplasm	Proteolysis	3.4	K.FRHGIVAAADSR.A R.HGVIVAADSR.A
419	P30101	Protein disulfide-isomerase A3	57146	5.98	12	91/56	18%	Endoplasmic Reticulum	Protein folding	-2.41	R.LAPEYEAAATR.L K.YGVSGYPTLK.I
415	P30101	Protein disulfide-isomerase A3	57146	5.98	9	106/56	16%	Endoplasmic Reticulum	Protein folding	-3.2	R.LAPEYEAAATR.L K.YGVSGYPTLK.I
420	P30101	Protein disulfide-isomerase A3	57146	5.98	11	128/56	20%	Endoplasmic Reticulum	Protein folding	-4.38	R.LAPEYEAAATR.L K.YGVSGYPTLK.I

412	P30101	Protein disulfide-isomerase A3	57146	5.98	6	61/56	10%	Endoplasmic Reticulum	Protein folding	-3.54	R.LAPEYEAAATR.L K.YGVSGYPTLK.I
1306	Q99497	Protein DJ-1	20050	6.33	7	68/56	26%	Plasma membrane	Protein folding	2.45	K.EILKEQENR.K K.VTTHPLAK.D
1311	Q99497	Protein DJ-1	20050	6.33	10	118/56	41%	Plasma membrane	Protein folding	7.61	R.VEKDGLILTSR.G R.DVVICPDASLEDAKK.E
1521	Q5JXB2	Putative ubiquitin-conjugating enzyme E2 N-like	17366	5.66	5	67/56	32%	Cytoplasm	Proteolysis	5.63	R.LLAEPVPGIK.A K.AEPDESNAR.Y
1245	P52565	Rho GDP-dissociation inhibitor 1	23250	5.02	6	58/56	14%	Plasma membrane	Signal transduction	2.47	K.YIQHTYR.K K.IDKTDYMGVSGYGPRA
1264	P52565	Rho GDP-dissociation inhibitor 1	23250	5.02	8	82/56	29%	Plasma membrane	Signal transduction	2.92	K.TDYMGVSGYGPRA K.IDKTDYMGVSGYGPRA
1043	Q5TZA2	Rootletin	2E+05	5.45	19	60/56	9%	Cytoplasm	Cell cycle	-4.74	R.LVAQLEEEKSALQGR.Q R.EEQERLEELR.L
677	Q9NV66	S-adenosyl-L-methionine-dependent tRNA 4-demethylwyosine synthase	84732	6.42	6	57/56	6%	Cytoplasm	tRNA processing	-5.99	K.TQGKNLQEK.S K.TFSAKDYMART
474	Q12765	Secernin-1	46980	4.66	7	72/56	18%	Cytoplasm	Exocytosis	-2.08	K.VECTYISIDQVPR.T R.SSPCIHYFTGTPDPSR.S
708	P36952	Serpin B5	42530	5.72	11	167/56	37%	Secreted	Proteolysis	4.3	K.DVPFGFQTVTSDVKNK.L K.SLNLSTEFISSTK.R
1005	P09486	SPARC	35465	4.73	7	70/56	20%	Secreted	Growth regulation	-3.65	K.TFDSSCHFFATK.C K.LHLDYIGPCK.Y

987	P09486	SPARC	35465	4.73	9	79/56	28%	Secreted	Growth regulation	-2.94	K.TFDSSCHFFATK.C K.LHLDYIGPCK.Y
1001	P09486	SPARC	35465	4.73	10	86/56	24%	Secreted	Growth regulation	-4.07	K.TFDSSCHFFATK.C K.LHLDYIGPCK.Y
751	P09486	SPARC	35465	4.73	10	105/56	26%	Secreted	Growth regulation	3.51	K.TFDSSCHFFATK.C K.LHLDYIGPCK.Y
772	P09486	SPARC	35465	4.73	16	139/56	40%	Secreted	Growth regulation	2.19	K.TFDSSCHFFATK.C K.LHLDYIGPCK.Y
362	P31948	Stress-induced-phosphoprotein 1	63227	6.40	13	91/56	19%	Cytoplasm	Protein folding	2.25	K.LDPHNVLYSNR.S K.TVDLKPDWGK.G
935	Q9Y405	Sulfatase-modifying factor 2	33936	7.78	7	81/56	22%	Endoplasmic Reticulum	Metabolism	-2.36	R.FLMGTNSPDSR.D R.QPAGPGSGIR.E
959	Q9Y405	Sulfatase-modifying factor 2	33936	7.78	8	94/56	25%	Endoplasmic Reticulum	Metabolism	-2.8	R.QPAGPGSGIR.E R.GASWIDTADGSANHR.A
1579	Q9BRA2	Thioredoxin domain-containing protein 17	14217	5.40	6	94/56	39%	Cytoplasm	Redox regulation	3.14	R.AVEQHNGK.T K.TIFAYFTGSK.D
868	P37837	Transaldolase	37688	6.36	8	76/56	18%	Cytoplasm	Pentose phosphate pathway	2.56	K.DAMVARARR.L K.LSSTWEGIQAGK.E
1507	Q15370	Transcription elongation factor B polypeptide 2	13239	4.73	7	92/56	38%	Nucleus	Transcription control	-2.44	K.TTIFTDAK.E K.ESSTVFELKR.I
340	O43219	Transforming growth factor-beta-induced protein ig-h3	75261	7.62	11	110/56	14%	Secreted	Cell adhesion	-4.51	K.STVISYECCPGYEK.V K.IPSETLNR.I

345	O43219	Transforming growth factor-beta-induced protein ig-h3	75261	7.62	13	146/56	17%	Secreted	Cell adhesion	-4.72	K.STVISYECCPGYEK.V K.IPSETLNR.I
332	O43219	Transforming growth factor-beta-induced protein ig-h3	75261	7.62	9	80/56	13%	Secreted	Cell adhesion	-2.04	K.STVISYECCPGYEK.V R.ILGDPEALR.D
347	O43219	Transforming growth factor-beta-induced protein ig-h3	75261	7.62	6	85/56	9%	Secreted	Cell adhesion	-6.28	K.IPSETLNR.I R.QAGLGNHLSGSR.L
78	P55072	Transitional endoplasmic reticulum ATPase	89950	5.14	10	89/56	11%	Cytoplasm	Vesicle transport	3.15	R.GILLYGPPGTGK.T R.EVDIGIPDATGR.L
1173	P60174	Triosephosphate isomerase	31057	5.65	11	171/56	49%	Cytoplasm	Glycolysis	2.46	K.FFVGGNWK.M K.IAVAAQNCYK.V
1184	P60174	Triosephosphate isomerase	31057	5.65	8	84/56	33%	Cytoplasm	Glycolysis	2.11	R.LGSSAMAPSR.K K.DCGATWVVLGHSE.R
431	Q9GZM7	Tubulointerstitial nephritis antigen-like	53721	6.54	6	99/56	17%	Secreted	Proteolysis	-2.1	R.ELAPGLHLR.G R.IYPVLGT YWDNCNR.C
1248	P61086	Ubiquitin-conjugating enzyme E2 K	22507	5.33	8	96/56	37%	Cytoplasm	Proteolysis	2.39	K.VDLVDENFTELR.G K.IPETYPFNPPK.V
1521	P61088	Ubiquitin-conjugating enzyme E2 N	17184	6.13	6	80/56	33%	Cytoplasm	Proteolysis	5.63	R.LLAEPVPGIK.A K.TNEAQAIETARA
1553	P05161	Ubiquitin-like protein ISG15	17933	6.84	6	103/56	33%	Secreted	Growth regulation	3.73	M.GWDLTVK.M K.IGVHAFQQR.L
980	P00749	Urokinase-type plasminogen activator	49901	8.78	10	100/56	22%	Secreted	Proteolysis	2.12	K.KEDYIVYLGR.S K.EDYIVYLGR.S

1673	Q8N850	Vimentin	53676	5.06	32	220/56	43%	Cytoplasm	Cytoskeleton	2.58	R.RMFGGPGTASRPSSSR.S R.TNEKVELQELNDR.F
1412	Q8N850	Vimentin	53676	5.06	15	85/56	19%	Cytoplasm	Cytoskeleton	3.09	K.VELQELNDR.F R.FANYIDKVR.F
1394	Q8N850	Vimentin	53676	5.06	11	96/56	15%	Cytoplasm	Cytoskeleton	6.65	K.VELQELNDR.F R.LGDLYEEEMR.E
1402	Q8N850	Vimentin	53676	5.06	15	97/56	19%	Cytoplasm	Cytoskeleton	10.29	R.TNEKVELQELNDR.F K.VELQELNDR.F
1672	Q8N850	Vimentin	53676	5.06	28	219/56	43%	Cytoplasm	Cytoskeleton	4.55	R.RMFGGPGTASRPSSSR.S R.TNEKVELQELNDR.F
1015	Q8ND82	Zinc finger protein 280C	84867	9.29	8	64/56	8%	Nucleus	Transcription control	-7.76	R.FMNHMK.H R.SSTFSDVEAHFR.A

Table S2. Clinicopathologic characteristics in oral tissue specimens from tissue microarray

		Normal	Tumor	Metastasis
Age	Mean $\pm$ SEM	45.2 $\pm$ 3.6	58.5 $\pm$ 1.9	62.0 $\pm$ 8.4
	$\leq$ 40 y	3 (30%)	3 (7%)	1 (25%)
	41 - 50 y	5 (50%)	10 (24%)	0 (0%)
	51 - 60 y	1 (10%)	15 (36%)	1 (25%)
	$\geq$ 61 y	1 (10%)	14 (33%)	2 (50%)
Sex	Male	6 (60%)	28 (67%)	1 (25%)
	Female	4 (40%)	14 (33%)	3 (75%)
T stage (Primary tumor)				
	T1 - T2		40 (95%)	
	T3 - T4		2 (5%)	
N stage (Lymph node metastasis)				
	0		42 (100%)	
	> 0		0 (0%)	
M stage (Distant metastasis)				
	0		38 (90%)	
	> 0		4 (10%)	
Overall stage				
	I - II		36 (86%)	
	III - IV		6 (14%)	
Total		10 (100%)	42 (100%)	4 (100%)