

ANTICANCER RESEARCH

**Global Analysis of Protein Expression in A549 Cells After Prolonged Nicotine Exposure
by Using Label-Free Quantification**

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Supplementary Table I. *List of up-regulated proteins from the monolayer system.*

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
1	LAP2B_HUMAN	TMPO	Lamina-associated polypeptide 2, isoforms beta/gamma	16	293.84	50639	9.39	3.2	Transcription
2	HSP72_HUMAN	HSPA2	Heat shock-related 70 kDa protein 2	12	604.77	69978	5.56	2.99	Response to stimulus
3	CATD_HUMAN	CTSD	Cathepsin D	12	196.1	44524	6.1	2.38	Proteolysis
4	HNRPC_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	13	438.71	33650	4.95	2.22	mRNA processing
5	LGMN_HUMAN	LGMN	Legumain	9	108.48	49379	6.07	2.22	Proteolysis

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
6	HS90A_HUMAN	HSP90AA1	Heat shock protein HSP 90-alpha	28	43.41	84607	4.94	2.02	Response to stimulus
7	RL15_HUMAN	RPL15	60S ribosomal protein L15	7	159.84	24131	11.62	1.99	Translation
8	H4_HUMAN	HIST1H4F	Histone H4	7	307.19	11360	11.36	1.96	Nucleosome assembly
9	ROA0_HUMAN	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	11	113.08	30822	9.34	1.77	mRNA processing
10	RL37A_HUMAN	RPL37A	60S ribosomal protein L37a	9	208.66	10268	10.44	1.66	Translation
11	TBB5_HUMAN	TUBB	Tubulin beta chain	11	398.09	49639	4.78	1.63	Cell division

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
12	DDX5_HUMAN	DDX5	Probable ATP-dependent RNA helicase DDX5	17	512.82	69105	9.06	1.63	Transcription
13	SUMO2_HUMAN	SUMO2	Small ubiquitin-related modifier 2	3	147.63	10864	6.4	1.63	Metabolic process
14	DDX3Y_HUMAN	DDX3Y	ATP-dependent RNA helicase DDX3Y	26	230.47	73108	7.24	1.62	Transcription
15	LASP1_HUMAN	LASP1	LIM and SH3 domain protein 1	9	140.97	29698	6.61	1.61	Ion transport
16	PRDX5_HUMAN	PRDX5	Peroxiredoxin-5, mitochondrial	11	168.35	22073	8.93	1.6	Response to stimulus
17	PDIA3_HUMAN	PDIA3	Protein disulfide-isomerase A3	14	349.25	56747	5.98	1.59	Response to stimulus

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
18	1433T_HUMAN	YWHAQ	14-3-3 protein theta	5	214.43	27747	4.68	1.58	Protein targeting
19	HMGA1_HUMAN	HMGA1	High mobility group protein HMG-I/HMG-Y	7	111.3	11669	10.32	1.57	Transcription
20	AK1BF_HUMAN	AKR1B15	Aldo-keto reductase family 1 member B15	9	285.66	36514	6.23	1.55	Metabolic process
21	PROF1_HUMAN	PFN1	Profilin-1	11	338.36	15045	8.44	1.54	Metabolic process
22	PTMA_HUMAN	PTMA	Prothymosin alpha	4	105.3	12196	3.69	1.54	Transcription
23	H31T_HUMAN	HIST3H3	Histone H3.1t	6	161.25	15499	11.13	1.54	Nucleosome assembly
24	PIR_HUMAN	PIR	Pirin	7	147.55	32093	6.42	1.53	Transcription
25	H2BFS_HUMAN	H2BFS	Histone H2B type F-S	5	148.61	13936	10.37	1.52	Nucleosome assembly

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
26	LDHB_HUMAN	LDHB	L-lactate dehydrogenase B chain	11	404.15	36615	5.71	1.51	Metabolic process
27	RAB15_HUMAN	RAB15	Ras-related protein Rab- 15	5	149.32	24375	5.53	1.51	Protein transport

Supplementary Table II. *List of down-regulated proteins from the monolayer system.*

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
1	ANM2_HUMAN	PRMT2	Protein arginine N-methyltransferase 2	5	42.97	49010	5.03	2.62	Transcription
2	RS10_HUMAN	RPS10	40S ribosomal protein S10	5	118.1	18886	10.15	2.47	Translation
3	PAIRB_HUMAN	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	9	266.02	44938	8.66	2.17	Apoptotic process
4	CAH12_HUMAN	CA12	Carbonic anhydrase 12	6	92.2	39426	6.73	2.14	Ion transport
5	HGB1A_HUMAN	HMGB1P1	Putative high mobility group protein B1-like 1	5	99.7	24223	5.92	2.07	Transcription
6	RAB10_HUMAN	RAB10	Ras-related protein Rab-10	6	157.54	22527	8.59	2.07	Protein transport

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
7	SRSF4_HUMAN	SRSF4	Serine/arginine-rich splicing factor 4	10	118.09	56645	11.52	2.02	mRNA processing
8	TIF1B_HUMAN	TRIM28	Transcription intermediary factor 1-beta	11	176.84	88493	5.52	1.98	Transcription
9	1433G_HUMAN	YWHAG	14-3-3 protein gamma	8	132.67	28285	4.8	1.98	Protein targeting
10	RS15A_HUMAN	RPS15A	40S ribosomal protein S15a	5	131.82	14830	10.14	1.97	Translation
11	IQGA1_HUMAN	IQGAP1	Ras GTPase-activating-like protein IQGAP1	24	275.35	189134	6.08	1.96	Cell migration
12	ERO1A_HUMAN	ERO1L	ERO1-like protein alpha	4	30.94	54358	5.48	1.95	Apoptotic process
13	RAB1C_HUMAN	RAB1C	Putative Ras-related protein Rab-1C	10	282.58	22003	5.25	1.9	Protein transport

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
14	HMGB1_HUMAN	HMGB1	High mobility group protein B1	7	161.6	24878	5.62	1.84	Response to stimulus
15	PGK2_HUMAN	PGK2	Phosphoglycerate kinase 2	12	388.21	44767	8.74	1.79	Metabolic process
16	DX39B_HUMAN	DDX39B	Spliceosome RNA helicase DDX39B	12	251.09	48960	5.44	1.76	Transcription
17	AL1B1_HUMAN	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial	4	56.98	57170	6.36	1.73	Metabolic process
18	HSP76_HUMAN	HSPA6	Heat shock 70 kDa protein 6	17	444.92	70984	5.81	1.69	Response to stimulus
19	DESM_HUMAN	DES	Desmin	19	461.2	53503	5.21	1.65	Cytoskeleton
20	EF1B_HUMAN	EEF1B2	Elongation factor 1-beta	4	19.76	24748	4.5	1.63	Translation

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
21	COBA1_HUMAN	COL11A1	Collagen alpha-1(XI) chain	17	186.29	180954	5.06	1.6	Extracellular matrix organization
22	LACB2_HUMAN	LACTB2	Endoribonuclease LACTB2	3	78.69	32785	6.32	1.59	Endonucleolytic
23	SRP14_HUMAN	SRP14	Signal recognition particle 14 kDa protein	5	111.7	14561	10.05	1.55	Localization
24	RMXL2_HUMAN	RBMXL2	RNA-binding motif protein, X-linked-like-2	12	174.45	42788	10.33	1.54	mRNA processing
25	PSB3_HUMAN	PSMB3	Proteasome subunit beta type-3	20	192.97	22933	6.14	1.54	Metabolic process
26	RL19_HUMAN	RPL19	60S ribosomal protein L19	3	130.43	23451	11.48	1.53	Translation
27	CX6B1_HUMAN	COX6B1	Cytochrome c oxidase subunit 6B1	2	102.06	10186	6.54	1.52	Metabolic process

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
28	PSB1_HUMAN	PSMB1	Proteasome subunit beta type-1	8	85.08	26472	8.27	1.5	Metabolic process

Supplementary Table III. *List of up-regulated proteins from the invasion system.*

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
1	OLA1_HUMAN	<i>OLA1</i>	Obg-like ATPase 1	2	88.41	44715	7.64	2.03	Metabolic process
2	ETFB_HUMAN	<i>ETFB</i>	Electron transfer flavoprotein subunit beta	2	43.58	27826	8.24	1.92	Metabolic process
3	UCHL1_HUMAN	<i>UCHL1</i>	Ubiquitin carboxyl-terminal hydrolase isozyme L1	2	77.81	24808	5.33	1.86	Response to stimulus
4	ANXA5_HUMAN	<i>ANXA5</i>	Annexin A5	2	70.01	35914	4.94	1.79	Signal transduction
5	ATPB_HUMAN	<i>ATP5B</i>	ATP synthase subunit beta, mitochondrial	4	199.85	56525	5.26	1.71	Metabolic process
6	1433T_HUMAN	<i>YWHAQ</i>	14-3-3 protein theta	5	211.66	27747	4.68	1.65	Protein targeting
7	ALDOA_HUMAN	<i>ALDOA</i>	Fructose-bisphosphate aldolase A	6	107.82	39395	8.3	1.58	Metabolic process

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
8	RL6_HUMAN	<i>RPL6</i>	60S ribosomal protein L6	11	291.02	32708	10.59	1.50	Translation
9	IMA1_HUMAN	<i>KPNA2</i>	Importin subunit alpha-1	3	67.15	57826	5.25	1.40	Metabolic process
10	1433G_HUMAN	<i>YWHAG</i>	14-3-3 protein gamma	5	187.96	28285	4.8	1.37	Protein targeting
11	CISY_HUMAN	<i>CS</i>	Citrate synthase, mitochondrial	2	58.56	51680	8.45	1.33	Metabolic process
12	SAHH_HUMAN	<i>AHCY</i>	Adenosylhomocysteinase	3	41.89	47685	5.92	1.33	Metabolic process
13	ASNS_HUMAN	<i>ASNS</i>	Asparagine synthetase [glutamine-hydrolyzing]	2	51.26	64329	6.39	1.32	Metabolic process
14	RS21_HUMAN	<i>RPS21</i>	40S ribosomal protein S21	2	41.98	9106	8.68	1.29	Translation
15	LGMN_HUMAN	<i>LGMN</i>	Legumain	1	55.43	49379	6.07	1.28	Proteolysis

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
16	NONO_HUMAN	<i>NONO</i>	Non-POU domain-containing octamer-binding protein	5	160.71	54197	9.01	1.28	mRNA processing
17	WDR36_HUMAN	<i>WDR36</i>	WD repeat-containing protein 36	2	34.02	105255	7.32	1.28	Response to stimulus
18	PUR9_HUMAN	<i>ATIC</i>	Bifunctional purine biosynthesis protein PURH	2	55.38	64616	6.27	1.28	Metabolic process
19	1433Z_HUMAN	<i>YWHAZ</i>	14-3-3 protein zeta/delta	4	311.6	27728	4.73	1.26	Protein targeting
20	ROA2_HUMAN	<i>YWHAZ</i>	Heterogeneous nuclear ribonucleoproteins A2/B1	25	946.49	37407	8.97	1.26	mRNA processing
21	K1C19_HUMAN	<i>KRT19</i>	Keratin, type I cytoskeletal 19	2	62.05	44079	5.04	1.26	Cytoskeleton

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
22	SAP_HUMAN	<i>PSAP</i>	Prosaposin	6	98.47	58074	5.06	1.25	Metabolic process
23	EIF3A_HUMAN	<i>EIF3A</i>	Eukaryotic translation initiation factor 3 subunit A	4	92.05	166468	6.38	1.25	Translation
24	ETFHA_HUMAN	<i>ETFHA</i>	Electron transfer flavoprotein subunit alpha, mitochondrial	6	142.12	35058	8.62	1.25	Metabolic process

Supplementary Table IV. *List of down-regulated proteins from the invasion system.*

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
1	AT2A2_HUMAN	<i>ATP2A2</i>	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	2	35.72	114683	5.23	1.85	Localization
2	MCM7_HUMAN	<i>MCM7</i>	DNA replication licensing factor MCM7	2	33.79	81257	6.08	1.74	DNA replication
3	LRC59_HUMAN	<i>LRRC59</i>	Leucine-rich repeat-containing protein 59	3	49.47	34909	9.61	1.74	Signal transduction
4	PA2G4_HUMAN	<i>PA2G4</i>	Proliferation-associated protein 2G4	4	61.65	43759	6.13	1.70	Translation
5	COR1C_HUMAN	<i>CORO1C</i>	Coronin-1C	2	37.73	53215	6.65	1.68	Cell division
6	RCC2_HUMAN	<i>RCC2</i>	Protein RCC2	4	128.44	56049	9.02	1.67	Cell division

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
7	DAZP1_HUMAN	<i>DAZAPI</i>	DAZ-associated protein 1	3	59.83	43356	8.73	1.66	mRNA processing
8	MBB1A_HUMAN	<i>MYBBP1A</i>	Myb-binding protein 1A	2	32.41	148762	9.34	1.66	Transcription
9	ENOA_HUMAN	<i>ENO1</i>	Alpha-enolase	17	1201.93	47139	7.01	1.66	Transcription
10	RS26_HUMAN	<i>RPS26</i>	40S ribosomal protein S26	3	57	13007	11.01	1.62	Translation
11	EF1B_HUMAN	<i>EEF1B2</i>	Elongation factor 1-beta	3	95.39	24748	4.5	1.61	Translation
12	HMGB2_HUMAN	<i>HMGB2</i>	High mobility group protein B2	3	51.06	24019	7.62	1.60	Transcription
13	DSRAD_HUMAN	<i>ADAR</i>	Double-stranded RNA-specific adenosine deaminase	3	62.37	135981	8.86	1.54	mRNA processing
14	RS16_HUMAN	<i>RPS16</i>	40S ribosomal protein S16	3	67.2	16435	10.21	1.52	Translation

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
15	H2AV_HUMAN	<i>H2AFV</i>	Histone H2A.V	7	193.91	13501	10.58	1.52	Nucleosome assembly
16	H4_HUMAN	<i>HIST1H4F</i>	Histone H4	16	482.92	11360	11.36	1.51	Nucleosome assembly
17	RPN1_HUMAN	<i>RPN1</i>	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	3	82.55	68527	5.96	1.50	Protein glycosylation
18	THOC4_HUMAN	<i>ALYREF</i>	THO complex subunit 4	4	98.35	26872	11.15	1.48	mRNA processing
19	RL23_HUMAN	<i>RPL23</i>	60S ribosomal protein L23	2	97.64	14856	10.51	1.46	Translation

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
20	HNRL1_HUMAN	<i>HNRNPUL1</i>	Heterogeneous nuclear ribonucleoprotein U-like protein 1	3	114.27	95679	6.49	1.45	mRNA processing
21	XRCC6_HUMAN	<i>XRCC6</i>	X-ray repair cross-complementing protein 6	14	373.74	69799	6.23	1.45	Transcription
22	PTBP1_HUMAN	<i>PTBP1</i>	Polypyrimidine tract-binding protein 1	10	265.16	57186	9.22	1.45	mRNA processing
23	RL24_HUMAN	<i>RPL24</i>	60S ribosomal protein L24	2	50.82	17768	11.26	1.40	Translation
24	RRP5_HUMAN	<i>PDCD11</i>	Protein RRP5 homolog	2	47.33	208570	8.99	1.40	mRNA processing
25	TXD17_HUMAN	<i>TXNDC17</i>	Thioredoxin domain-containing protein 17	2	72.27	13932	5.4	1.39	Metabolic process

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
26	SND1_HUMAN	<i>SND1</i>	Staphylococcal nuclease domain-containing protein 1	3	43.17	101934	6.74	1.39	Transcription
27	API5_HUMAN	<i>API5</i>	Apoptosis inhibitor 5	3	86.99	58968	6.99	1.39	Apoptotic process
28	G3P_HUMAN	<i>GAPDH</i>	Glyceraldehyde-3-phosphate dehydrogenase	20	802.92	36030	8.57	1.37	Translation
29	TAGL2_HUMAN	<i>TAGLN2</i>	Transgelin-2	6	202.4	22377	8.41	1.37	Epithelial cell differentiation
30	ICAL_HUMAN	<i>CAST</i>	Calpastatin	2	36.4	76526	4.97	1.37	Protease inhibitor
31	PARP1_HUMAN	<i>PARP1</i>	Poly [ADP-ribose] polymerase 1	5	198.26	113012	8.99	1.37	Transcription

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
32	LAP2A_HUMAN	<i>TMPO</i>	Lamina-associated polypeptide 2, isoform alpha	7	102.07	75446	7.56	1.37	Transcription
33	TOP1_HUMAN	<i>TOP1</i>	DNA topoisomerase 1	2	35.76	90669	9.33	1.37	DNA replication
34	RS6_HUMAN	<i>RPS6</i>	40S ribosomal protein S6	2	56.56	28663	10.85	1.37	Translation
35	U2AF2_HUMAN	<i>U2AF2</i>	Splicing factor U2AF 65 kDa subunit	3	43.95	53467	9.19	1.36	mRNA processing
36	IF4A1_HUMAN	<i>EIF4A1</i>	Eukaryotic initiation factor 4A-I	4	98.46	46125	5.32	1.35	Translation
37	RBM14_HUMAN	<i>RBM14</i>	RNA-binding protein 14	4	86.34	69449	9.68	1.35	Transcription
38	PEBP1_HUMAN	<i>PEBP1</i>	Phosphatidylethanolamine-binding protein 1	8	272.83	21044	7.01	1.35	Protease inhibitor

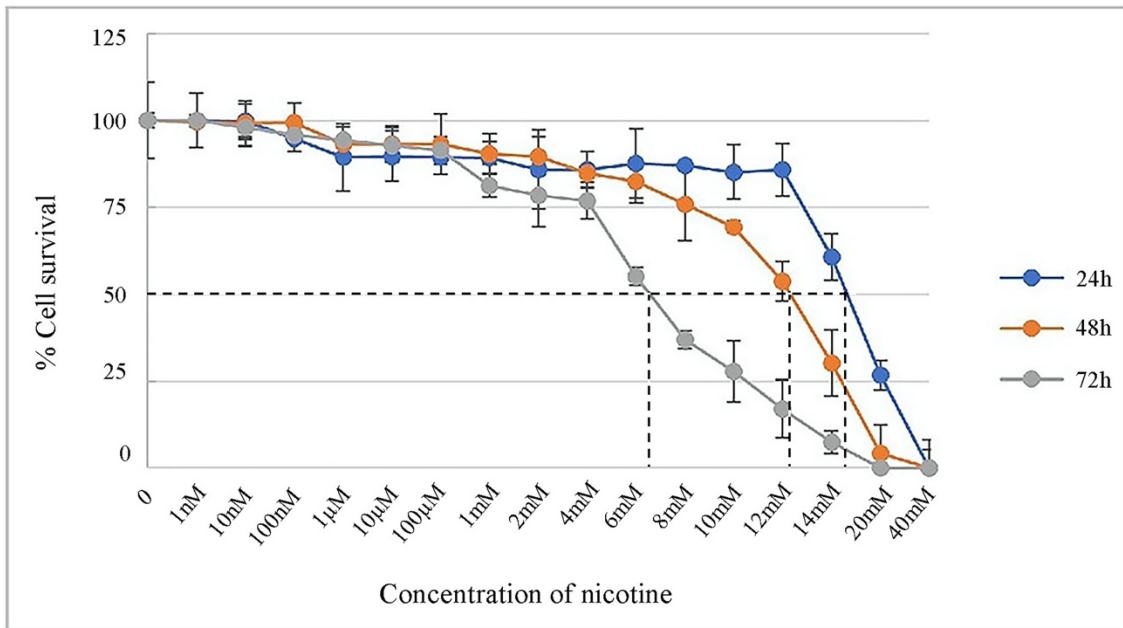
No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
39	RSSA_HUMAN	<i>RPSA</i>	40S ribosomal protein SA	9	249.39	32833	4.79	1.35	Translation
40	TOP2A_HUMAN	<i>TOP2A</i>	DNA topoisomerase 2-alpha	6	250.02	174276	8.82	1.35	Apoptotic process
41	K2C7_HUMAN	<i>KRT7</i>	Keratin, type II cytoskeletal 7	20	1372.11	51354	5.4	1.34	Cytoskeleton
42	HNRH1_HUMAN	<i>HNRNPH1</i>	Heterogeneous nuclear ribonucleoprotein H	11	389.81	49198	5.89	1.34	mRNA processing
43	EFTU_HUMAN	<i>TUFM</i>	Elongation factor Tu, mitochondrial	7	204.84	49510	7.26	1.34	Translation
44	PCBP1_HUMAN	<i>PCBP1</i>	Poly(rC)-binding protein 1	7	206.6	37474	6.66	1.34	mRNA processing
45	CAVN1_HUMAN	<i>PTRF</i>	Caveolae-associated protein 1	2	43.86	43450	5.51	1.34	Transcription

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
46	ANXA1_HUMAN	<i>ANXA1</i>	Annexin A1	24	779.9	38690	6.57	1.34	Cell migration
47	RUVB1_HUMAN	<i>RUVBL1</i>	RuvB-like 1	2	43.96	50196	6.02	1.33	Cell division
48	PAIRB_HUMAN	<i>SERBP1</i>	Plasminogen activator inhibitor 1 RNA-binding protein	6	187.57	44938	8.66	1.33	Apoptotic process
49	PRDX1_HUMAN	<i>PRDX1</i>	Peroxiredoxin-1	2	64.8	22096	8.27	1.32	Response to stimulus
50	NUCL_HUMAN	<i>NCL</i>	Nucleolin	4	39.86	76568	4.6	1.32	Transcription
51	BUB3_HUMAN	<i>BUB3</i>	Mitotic checkpoint protein BUB3	4	96.17	37131	6.36	1.32	Cell division
52	K2C8_HUMAN	<i>KRT8</i>	Keratin, type II cytoskeletal 8	17	979.99	53671	5.52	1.31	Cytoskeleton
53	LMNA_HUMAN	<i>LMNA</i>	Prelamin-A/C	12	735.27	74095	6.57	1.31	Cell migration

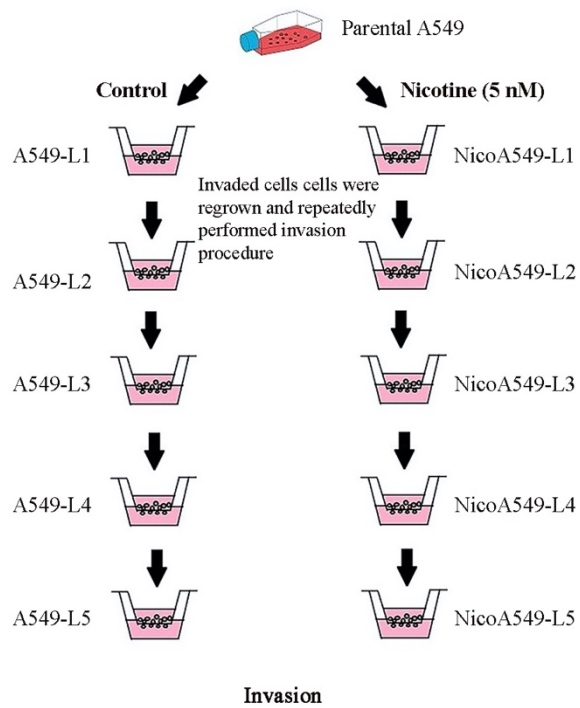
No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
54	RL19_HUMAN	<i>RPL19</i>	60S ribosomal protein L19	3	130.86	23451	11.48	1.31	Translation
55	TBB5_HUMAN	<i>TUBB</i>	Tubulin beta chain	10	397	49639	4.78	1.31	Cell division
56	H2A2B_HUMAN	<i>ST2H2AB</i>	Histone H2A type 2-B	5	104.73	13987	10.88	1.31	Nucleosome assembly
57	S10A4_HUMAN	<i>SI00A4</i>	Protein S100-A4	2	44.71	11721	5.85	1.31	Cell migration
58	UBA1_HUMAN	<i>UBA1</i>	Ubiquitin-like modifier-activating enzyme 1	4	108.03	117774	5.49	1.31	Response to stimulus
59	K1C18_HUMAN	<i>KRT18</i>	Keratin, type I cytoskeletal 18	25	817.92	48029	5.34	1.30	Cytoskeleton
60	PRS6A_HUMAN	<i>PSMC3</i>	26S proteasome regulatory subunit 6A	3	77.22	49172	5.13	1.30	Transcription
61	EWS_HUMAN	<i>EWSR1</i>	RNA-binding protein EWS	4	87.32	68436	9.37	1.29	Transcription

No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
62	PRP8_HUMAN	<i>PRPF8</i>	Pre-mRNA-processing-splicing factor 8	3	83.55	273427	8.95	1.28	mRNA processing
63	SRP09_HUMAN	<i>SRP9</i>	Signal recognition particle 9 kDa protein	2	50.6	10105	7.76	1.28	Translation
64	STIP1_HUMAN	<i>STIP1</i>	Stress-induced-phosphoprotein 1	3	96.86	62599	6.4	1.28	Response to stimulus
65	HNRL2_HUMAN	<i>HNRNPUL2</i>	Heterogeneous nuclear ribonucleoprotein U-like protein 2	2	50.33	85052	4.85	1.28	mRNA processing
66	LA_HUMAN	<i>SSB</i>	Lupus La protein	2	40.48	46808	6.68	1.27	tRNA processing
67	NOP56_HUMAN	<i>NOP56</i>	Nucleolar protein 56	4	97.52	66009	9.24	1.27	rRNA processing
68	GLU2B_HUMAN	<i>PRKCSH</i>	Glucosidase 2 subunit beta	3	54.97	59388	4.33	1.26	Metabolic process

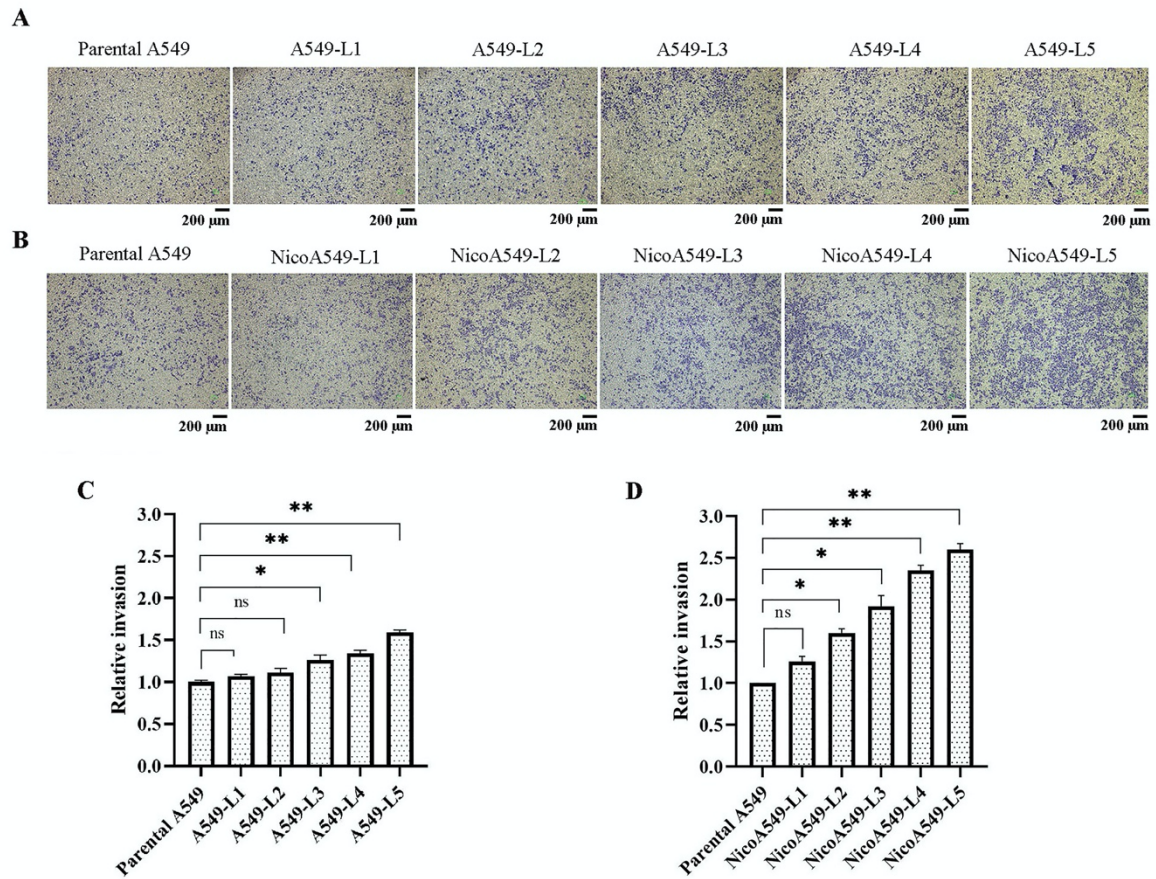
No.	Accession	Gene	Protein name	Peptide count	Score	Mass	pI	Protein fold change	Protein function
69	MDHC_HUMAN	<i>MDHI</i>	Malate dehydrogenase, cytoplasmic	2	67.37	36403	6.91	1.26	Metabolic process
70	PADI1_HUMAN	<i>PADI1</i>	Protein-arginine deiminase type-1	2	41.54	74618	6.07	1.26	Chromatin organization
71	HNRPF_HUMAN	<i>HNRNPF</i>	Heterogeneous nuclear ribonucleoprotein F	6	174.75	45643	5.38	1.26	mRNA processing
72	RL3_HUMAN	<i>RPL3</i>	60S ribosomal protein L3	3	65.62	46080	10.19	1.25	Translation
73	RS5_HUMAN	<i>RPS5</i>	40S ribosomal protein S5	4	176.77	22862	9.73	1.25	Translation
74	RLA0_HUMAN	<i>RPLP0</i>	60S acidic ribosomal protein P0	2	51.81	34252	5.71	1.25	Translation
75	RAB7A_HUMAN	<i>RAB7A</i>	Ras-related protein Rab-7a	2	58.11	23475	6.4	1.25	Protein transport
76	RS28_HUMAN	<i>RPS28</i>	40S ribosomal protein S28	2	86.98	7836	10.7	1.25	Translation



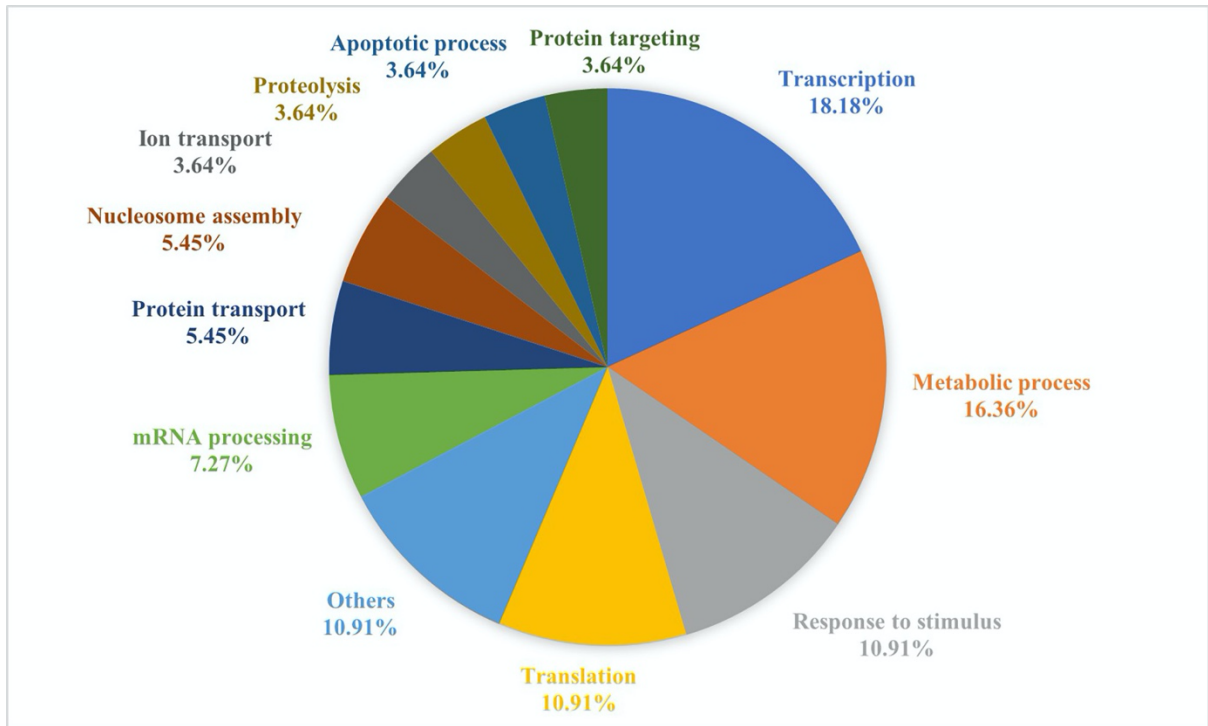
Supplementary Figure 1. *The cytotoxic effects of nicotine on A549 lung cancer cells by MTT assay. The results are expressed as mean \pm SD of three independent experiments.*



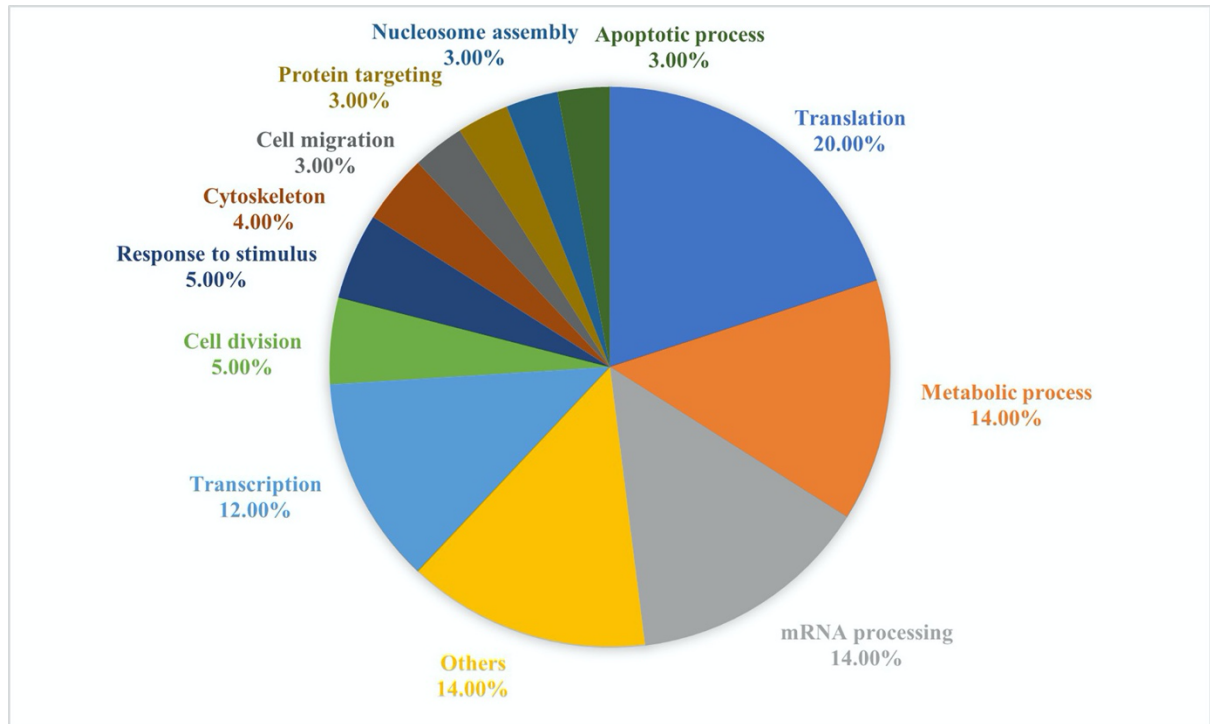
Supplementary Figure 2. *Scheme for selecting an invasive subpopulation from A549 lung cancer cell lines with and without continuous exposure to 5 nM of nicotine.*



Supplementary Figure 3. *Prolonged nicotine exposure enhances the invasive capability of A549 lung cancer cells. Representative images of the invasion assay using five sublines of A549 cells untreated (A) and treated (B) with 5 nM of nicotine. Scale bar, 200 μ m. Bar graphs represent the relative invasion of sublines with (D) and without (C) nicotine treatment. Data points represent the mean \pm SD. (* p <0.05, ** p <0.01).*



Supplementary Figure 4. *The differentially expressed proteins in cells growing as monolayers were analyzed based on biological processes.*



Supplementary Figure 5. *The differentially expressed proteins from the invasion system were analyzed for biological processes.*