

Data file S4. Differentially expressed proteins (DEPs) identified by LDA (Prob<0.05) by comparing PSMs from MB49 Bladder cancer model untreated (CTR, n=6), treated with SNFs-OVA (SNFs-OVA, n=6) and treated with SNFs-CpG (SNFs-CpG, n=6). Average PSMs are shown. Pairwise comparisons (CTR vs SNFs-OVA, CTR vs SNFs-CpG) by DAVE index are reported; positive DAVE values (in red) indicate proteins up-regulated in CTR (down-regulated in SNFs treatments), while negative DAVE values (in blue) indicate proteins up-regulated following SNFs treatments (down-regulated in CTR).

ID UNPROT	Gene name	Description	MW [kDa]	calc. pI	Ratio	LDA			P. PSMs (MB49 BLADDER CANCER)		DAVE index	
						Preb	CTR	SNFs-OVA	SNFs-CpG	CTR vs SNFs-OVA	CTR vs SNFs-CpG	
Q288M5	Psmf12	26S proteasome non-ATPase regulatory subunit 12	52.9	7.06	124	4.2E-13	0	0	0	0	-2.00	-2.00
A0A045W94	Myadn	Myeloid-associated differentiation marker (Fragment)	8.6	8.38	65	1.7E-10	2	0	0.2	2.00	1.64	1.64
P17426	Ap2a1	AP-2 complex subunit alpha-1	107.6	7.03	62	2.8E-10	0	1.7	0	0	2.00	2.00
O35955	Psmb10	Proteasome subunit beta-type-10	29	6.87	45	4.5E-09	3.5	1.5	6.9	0.00	-0.65	-0.65
P46935	Nedd4	E3 ubiquitin-protein ligase NEDD4	102.6	5.26	44	5.0E-09	0	1.5	0	0	-2.00	-2.00
E909E1	E4fig1	Eukaryotic translation initiation factor 4 gamma 1	175.2	5.38	25	6.6E-07	0.2	2.8	0.2	0.2	-1.73	-1.73
P17751	Tpi1	Triosephosphate isomerase	26.7	7.3	22	1.5E-06	8.6	11.3	3	0.27	0.97	0.97
P50516	Atp6v1a	V-type proton ATPase catalytic subunit A	68.3	5.58	20	2.6E-06	0.5	3.3	3.2	0.50	-1.66	-1.66
G5E8J2	Ank1	Ankyrin-1	202.4	6.65	19	4.9E-06	2	0.2	0	0	1.64	2.00
P94869	Rip60	60S acidic ribosomal protein P0	34.2	6.25	16	1.8E-05	2.4	5.7	2.3	0.81	2.00	2.00
P23018	Actg2	Actin, gamma-enteric smooth muscle	41.9	5.48	15	2.0E-05	72.4	64	113.5	0	-0.44	-0.44
P01872	Ighm	Immunoglobulin heavy constant mu	90.7	6.6	14	3.4E-05	4.9	1.6	1.8	1.02	0.93	0.93
A0A046V90	Ighg2b	Immunoglobulin heavy constant gamma 2B (Fragment)	44.3	6.52	14	3.7E-05	0.6	0.4	2.8	0.40	-1.29	-1.29
Q61074	Ppm1g	Protein phosphatase 1G	58.7	4.39	13	6.4E-05	0.5	2	0.2	-1.20	0.86	0.86
Q8K297	Colgal1	Procollagen galactosyltransferase 1	71	7.28	13	6.5E-05	0	1.5	0	0	-2.00	-2.00
P68134	Acta1	Actin, alpha skeletal muscle	42	5.39	13	6.9E-05	79.5	71.8	121	0	-0.41	-0.41
Q9R1P1	Psmb3	Proteasome subunit beta-type-3	22.9	6.55	13	7.1E-05	0	1.5	0	0	-2.00	-2.00
G3UVV4	Hk1	Hexokinase	101.8	6.67	12	9.4E-05	4.7	0	0.7	2.00	1.48	1.48
I972ML	Nap1a4	Nap1A protein	43.9	4.68	12	9.5E-05	0.5	2.3	0	-1.29	2.00	2.00
Q91518	Atp6v1b	V-type proton ATPase subunit E 1	13.5	5.94	12	1.0E-04	0.2	0.3	1.5	2.00	1.53	1.53
Q62167	Dck3	FACT complex non-ATPase helix DCK3	73.1	7.18	12	1.3E-04	6.8	8.8	5.1	0.26	0.29	0.29
P26883	Fkbp1a	Peptidyl-prolyl cis-trans isomerase FKBP1A	11.9	8.16	11	1.4E-04	1.3	2	0	-0.42	2.00	2.00
P97352	S100A13	Protein S100-A13	11.2	6.13	11	1.9E-04	1.8	0.5	0	1.13	2.00	2.00
P16045	Lgals1	Galectin-1	14.9	5.49	11	2.0E-04	2.7	1.8	0.2	0.40	1.72	1.72
P62849	Rps24	40S ribosomal protein S24	15.4	10.78	11	2.1E-04	0.3	3.2	0	-1.66	2.00	2.00
Q64522	H2ac21	Histone H2A type 2-B	14	10.89	10	2.5E-04	24	35.9	22.4	0.17	0.20	0.20
P60710	Actb	Actin, cytoplasmic 1	41.7	5.48	10	2.7E-04	130.2	110	179.4	-0.40	-0.32	-0.32
P54116	Stom	Stomatin	31.4	6.93	10	3.2E-04	0.6	0	0	0	2.00	2.00
Q9D6Z1	Nop56	Nucleolar protein 56	64.4	9.44	10	3.7E-04	0.2	1.5	0.4	-1.53	-0.67	-0.67
P90573	Pdx5	Thioredoxin-dependent peroxidoreductin	41.9	5.48	15	3.8E-04	4.4	5.5	14.2	-0.22	-1.05	-1.05
A0A14078M1	Igkv1-88	Immunoglobulin kappa chain variable 1-88 (Fragment)	13.2	8.02	10	3.9E-04	0	0	1.6	0	-2.00	-2.00
P62900	Rpl31	60S ribosomal protein L31	14.5	10.54	10	4.1E-04	0.2	2	0.4	-1.64	-0.67	-0.67
P70696	H2bc1	Histone H2B type 1-A	14.2	10.29	9	4.4E-04	17.6	5.7	19.8	1.02	0.74	0.74
A0A79NVR94	Ahnak2	AHNAK nucleoprotein 2	368.2	5.88	9	4.6E-04	5.7	3.8	0.4	0.40	1.74	1.74
P50637	Tspo	Translocator protein	18.8	9.52	9	4.6E-04	0.2	0.3	0	-0.40	2.00	2.00
P09411	Pgk1	Phosphoglycerate kinase 1	44.5	7.9	9	5.0E-04	22.3	16.3	9.9	0.31	0.77	0.77
Q9CZM7	Shmt2	Serine hydroxymethyltransferase, mitochondrial	55.7	8.47	9	5.2E-04	4.2	2.8	0.4	0.40	1.65	1.65
Q8BFZ3	Actb2	Beta-actin-like protein 2	42	5.49	9	5.3E-04	78	63.3	107.8	0.21	-0.32	-0.32
G3UJ22	Syncrip	Heterogeneous nuclear ribonucleoprotein Q	58.7	7.56	9	6.1E-04	4.9	7.1	1.6	-0.37	1.02	1.02
Q91272	Nr5a2	Nuclear receptor 5A2	64.8	5.94	9	6.4E-04	1.1	2	0	0	-2.00	-2.00
Q08943	Srsr1	FACT complex subunit SRSR1	80.8	6.76	9	6.4E-04	0	1.5	0.2	-2.00	-2.00	-2.00
P47911	Rpl6	60S ribosomal protein L6	33.5	10.7	9	6.5E-04	4.9	8.6	1.1	-0.55	1.27	1.27
P68040	Rack1	Receptor of activated protein C kinase 1	35.1	7.69	9	7.2E-04	5.8	7.4	1.5	-0.24	1.18	1.18
Q64475	H2bc3	Histone H2B type 1-B	13.9	10.32	8	8.8E-04	50.8	39.4	58.1	0.25	1.60	1.60
Q91XL1	Lrg1	Leucine-rich HEV glycoprotein	37.4	6.61	8	8.9E-04	1.8	0	0.2	2.00	1.60	1.60
D3Z2M0	Ctuz	Cytoplasmic tRNA 2-thiolation protein 2 (Fragment)	27.3	8.19	8	9.6E-04	1.5	1	0.8	0.40	0.61	0.61
Q9CZU6	Cs	Citrate synthase, mitochondrial	51.7	8.57	8	9.9E-04	1.6	4	1.7	-0.86	-0.40	-0.40
Q9EPB4	Pycard	Apoptosis-associated speck-like protein containing a CARD	110.4	5.43	8	1.1E-03	0	0.2	4.6	-2.00	-2.00	-2.00
Q80X19	Col4a19	Collagen alpha-1(XIV) chain	219.2	5.1	8	1.1E-03	0	3.3	13.3	-2.00	-2.00	-2.00
Q64525	H2ac2b	Histone H2Ac type 2-B	13.9	10.32	7	1.2E-03	53.3	39.4	58.3	0.30	1.29	1.29
Q8VDM4	Psm22	26S proteasome non-ATPase regulatory subunit 22	100.1	8.2	7	1.2E-03	0	2	0.2	-0.67	1.33	1.33
P14483	H2-Ab1	H-2 class II histocompatibility antigen, A beta chain	30.1	7.24	8	1.3E-03	0.5	1.5	5.1	-0.60	-1.64	-1.64
Q54218	Igtb2	Integrin beta	84.8	7.05	8	1.3E-03	1.5	2.5	5.1	-0.50	-1.09	-1.09
A0A384DV79	Hmgal1	High mobility group protein HMG-1/HMG-Y	10.5	10.43	8	1.4E-03	1.3	0	0	2.00	2.00	2.00
Q923D2	Eno1	Flavin reductase (NADPH)	22.2	7.01	8	1.4E-03	1.7	0.9	2.3	0.62	-0.30	-0.30
P17182	Bnr1	Alpha-enolase	47.1	6.8	8	1.5E-03	43.5	29.2	26.4	0.39	0.49	0.49
A62144	Aldoa	Fructose-bisphosphate aldolase	45.1	7.91	7	1.5E-03	17.9	11.6	8.5	0.43	0.71	0.71
E9QLG3	Mga	MAX gene-associated protein	332.9	7.58	7	1.6E-03	0	1.8	0.2	-2.00	-2.00	-2.00
Q9J126	Hic2	Hypermethylated in cancer 2 protein	66.7	6.35	7	1.6E-03	0	1	0	0	-2.00	-2.00
P91R04	Ctss	Cathepsin S	38.6	7.15	7	1.7E-03	0	0.2	3.7	0	-2.00	-2.00
A0A081282	Kcd12f	BTB/Poz domain-containing protein KCD12f	35.9	8.81	7	1.8E-03	0	1.6	0.4	-0.67	2.00	2.00
A0A046Y53	Ighg2c	Immunoglobulin heavy constant gamma 2C (Fragment)	36.5	8.02	7	1.8E-03	0	0	4.5	-2.00	-2.00	-2.00
Q14A46	L700009N14Rk	GTP-binding nuclear protein Ran	24.3	7.97	7	1.9E-03	0	1.3	0	-2.00	-2.00	-2.00
Q99K94	Stat1	Signal transducer and activator of transcription	87.1	6.02	7	1.9E-03	0	0.8	7.7	-2.00	-2.00	-2.00
A0A498WGD8	Txn1l	Thioredoxin-like protein 1	32.7	5.07	7	2.1E-03	0.9	1.4	0.2	-0.43	1.27	1.27
P14733	Lmnb1	Lamin-B1	66.7	5.16	7	2.2E-03	6.6	0.7	3.2	1.62	0.69	0.69
P62814	Atp6v1b2	V-type proton ATPase subunit B, brain isoform	56.5	5.81	7	2.2E-03	0	0	2.2	-2.00	-2.00	-2.00
Q9WV77	Myo1c	Unconventional myosin-1c	121.9	9.35	7	2.2E-03	0	0.2	1.6	0.40	-1.37	-1.37
Q61937	Npm1	Nucleophosmin	32.5	4.77	7	2.3E-03	5.8	7.5	1.2	-0.26	1.31	1.31
A0A045V32	Serp1	Plasminogen activator-inhibitor 1 RNA-binding protein	93.9	9.66	7	2.3E-03	0.6	2.3	0.6	-1.17	1.29	1.29
A0A180G53	Bax	Apoptosis regulator BAX (Fragment)	12.6	12.94	7	2.4E-03	1.2	1.5	0.5	-0.64	1.29	1.29
Q8RDW0	Epk1	Eplakin	77.6	6.07	7	2.5E-03	1.8	3.5	0.7	0.42	1.89	1.89
P25444	Rps2	40S ribosomal protein S2	31.2	10.24	7	2.6E-03	2.5	5.6	0.8	-0.77	1.03	1.03
I7HLV2	Rpl10	60S ribosomal protein L10 (Fragment)	23.1	10.01	7	2.7E-03	2.1	1.5	0.2	0.33	1.65	1.65
P99026	Psmb4	Proteasome subunit beta-type-4	29.1	5.64	7	2.8E-03	0.2	0.3	1.5	-0.40	-1.53	-1.53
Q9D1A2	Cndp2	Cytosolic non-specific dipeptidase	52.7	5.66	7	2.8E-03	0.8	2.8	14	-1.11	-1.78	-1.78
Q8BSH9	Nap11	Nucleosome assembly protein 1-like 1	44.6	4.56	7	2.8E-03	1.5	3.8	0.4	-0.87	1.16	1.16
Q9DBJ1	Pgam1	Phosphoglycerate mutase 1	28.8	7.18	7	2.8E-03	8.9	8	3.9	0.78	0.78	0.78
Q8BG07	Pld4	5'-3' exonuclease (PLD4)	56.1	7.31	7	2.9E-03	0	0	2.5	0	-2.00	-2.00
Q92181	Prs11	Protease, serine 1 (Prs11)	26.1	4.94	7	2.9E-03	0.3	1.8	0.6	-1.43	-0.67	-0.67
P19324	SerpinH1	Serpin H1	46.5	8.82	6	3.0E-03	6.3	17.6	15.4	-0.37	-1.28	-1.28
Q62433	Ndr1g	Protein NDRG1	43	6.1	6	3.4E-03	1.3	0	0.4	2.00	1.06	1.06
Q09131	Gsto1	Glutathione S-transferase omega-1	27.5	7.36	6	3.6E-03	2.4	0.2	0	1.69	2.00	2.00
P97351	Rps3a	40S ribosomal protein S3a	29.9	9.73	6	3.7E-03	1	0	0	2.00	2.00	2.00
E9PWS2	Serpinf1	Pigment epithelium-derived factor	15.8	5.77	6	3.7E-03	0.3	0.2	2.6	0.40	-1.59	-1.59
Q61233	Lcp1	Plastin-2	70.1	5.33	6	3.8E-03	2.9	3.3	22	-1.53	-1.53	-1.53
P58252	Eef2	Elongation factor 2	95.3	6.83	6	3.8E-03	15.2	18.7	9.9	-0.21	0.42	0.42
P62855	Rps26	40S ribosomal protein S26	13	11	6	3.8E-03	5.4	4.1	0.9	0.27	1.43	1.43
E9Q5L2	Ith4	Inter alpha-trypsin inhibitor, heavy chain 4	102.8	6.37	6	3.9E-03	1.5	0	0	2.00	2.00	2.00
P55771	Idh2	Isocitrate dehydrogenase [NADP], mitochondrial	50.9	8.69	6	3.9E-03	0	1.2	0	0	-2.00	-2.00
Rps16	Rps16	40S ribosomal protein S16	16.4	10.21	6	4.0E-03	4.6	8	5.4	-0.16	-0.16	-0.16
A0A040M0A5	Tub4a	Tubulin alpha chain (Fragment)	52.9	5.19	6	4.3E-03	30.8	26.1	22.9	0.17	0.29	0.29
Q9ERD7	Tubb3	Tubulin beta-3 chain	50.4	4.93	6	4.3E-03	38	44.9	38.2	-0.17	-2.00	-2.00
P28654	Dcn	Decorin	39.8	8.68	6	4.3E-03	0	4.3	3.1	-2.00	-2.00	-2.00
P28063	Psmb8	Proteasome subunit beta-type-8	30.2	6.68	6	4.3E-03	0	0	1.2	0	-2.00	-2.00
P51150	Rab7a	Ras-related protein Rab-7a	23.5	6.7	6	4.5E-03	2.7	7.6	3.8	-0.95		