

Supplementary table 1:

Z-statistics of differentially glycosylated proteins detected by lectins together with fold changes both in log 2 and non-log 2 form

ConA										
Protein ID (Access #)	N/A ^a	log 2	Fold difference	N/C ^b	log 2	Fold difference	A/C	log 2	Fold difference	
<i>Proteins that are significantly different in cancer than those in adenoma and normal</i>										
Complement C3 (P01024)	CONA	0.6	0.17	1.13	-0.09	-0.02	0.99	-1.93	-0.19	0.88
	AAL	-1.9	-0.17	0.89	-4.19	-0.6	0.66	-3.35	-0.43	0.74
	MAL	-2.91	-0.1	0.93	-5.38	-0.45	0.73	-4.05	-0.35	0.78
	SNA	-1.72	-0.27	0.83	-5.77	-0.85	0.55	-3.35	-0.58	0.67
	PNA	-1.51	-0.26	0.84	-6.21	-1.18	0.44	-4.61	-0.92	0.53
Kininogen-1 (P01042)	CONA	-4.86	-0.38	0.77	-6.48	-0.38	0.77	0.01	0	1.00
	AAL	-5.04	-0.3	0.81	-7.22	-0.61	0.66	-3.44	-0.3	0.81
	MAL	-2.73	-0.19	0.88	-7.64	-0.69	0.62	-4.75	-0.5	0.71
	SNA	-6.68	-0.8	0.57	-10	-1.29	0.41	-3.24	-0.5	0.71
	PNA	-1.26	-0.41	0.75	-4.67	-1.29	0.41	-2.94	-0.88	0.54
Histidine-rich glycoprotein (P04196)	CONA	-1.25	-0.1	0.93	-2.23	-0.14	0.91	-0.53	-0.04	0.97
	AAL	-0.55	-0.08	0.95	-4.03	-0.54	0.69	-3.64	-0.47	0.72
	MAL	0.75	0.01	1.01	-1.89	-0.02	0.99	-2.86	-0.02	0.99
	SNA	-1.37	-0.18	0.88	-3.33	-0.45	0.73	-2.44	-0.27	0.83
	PNA	0.84	0.1	1.07	-0.98	-0.12	0.92	-2.52	-0.22	0.86
<i>Proteins that are significantly different in cancer and adenoma than those in normal</i>										
Alpha-1B-glycoprotein (P04217)	CONA	-3.29	-0.21	0.86	-3.94	-0.26	0.84	-0.75	-0.05	0.97
	AAL	-3.04	-0.28	0.82	-6.94	-0.4	0.76	-1.43	-0.12	0.92
	MAL	-1.65	-0.01	0.99	-2.65	-0.01	0.99	-0.93	-0.01	0.99
	SNA	-3.24	-0.24	0.85	-5.13	-0.38	0.77	-1.65	-0.14	0.91
	PNA	0.04	0	1.00	-5.17	-0.13	0.91	-4.69	-0.13	0.91
Hemopexin (P02790)	CONA	-6.41	-0.41	0.75	-5.86	-0.3	0.81	1.32	0.1	1.07
	AAL	-6.68	-0.51	0.70	-5.77	-0.49	0.71	0.18	0.02	1.01
	MAL	-2.95	-0.01	0.99	-3.03	-0.01	0.99	-0.12	0	1.00
	SNA	-7.62	-0.48	0.72	-7.01	-0.43	0.74	0.58	0.05	1.04
	PNA	-1.28	-0.04	0.97	-2.57	-0.07	0.95	-0.8	-0.03	0.98
Complement factor I (P05156)	CONA	-2.57	-0.55	0.68	-3.89	-0.69	0.62	-0.52	-0.14	0.91
	AAL	-2.32	-0.39	0.76	-3.28	-0.63	0.65	-1.07	-0.25	0.84
	MAL	-0.98	-0.01	0.99	-2.09	-0.02	0.99	-1.11	-0.01	0.99
	SNA	-3.48	-0.66	0.63	-5.6	-0.94	0.52	-1.15	-0.28	0.82
	PNA	-0.44	-0.03	0.98	-4.28	-0.29	0.82	-2.81	-0.25	0.84
Ceruloplasmin (P00450)	CONA	-4.61	-0.36	0.78	-4.3	-0.32	0.80	0.5	0.05	1.04
	AAL	-4.06	-0.42	0.75	-4.57	-0.56	0.68	-0.94	-0.14	0.91
	MAL	-3	-0.01	0.99	-2.52	-0.01	0.99	-0.3	0	1.00
	SNA	-5.06	-0.47	0.72	-6.65	-0.45	0.73	0.24	0.02	1.01
	PNA	-0.01	0	1.00	-4.02	-0.1	0.93	-3.61	-0.1	0.93

Afamin (P43652)	CONA	<u>-4.47</u>	-0.45	0.73	<u>-4.35</u>	-0.35	0.78	0.82	0.1	1.07
	AAL	<u>-3.86</u>	-0.38	0.77	<u>-4.8</u>	-0.75	0.59	-2.04	-0.37	0.77
	MAL	-0.29	0	1.00	-2.11	-0.15	0.90	-2.09	-0.14	0.91
	SNA	<u>-4.19</u>	-0.35	0.78	<u>-4.34</u>	-0.44	0.74	-0.74	-0.09	0.94
	PNA	-2.38	-0.1	0.93	-1.64	-0.47	0.72	-1.3	-0.37	0.77
Alpha-1- antichymotrypsin (P01011)	CONA	<u>-4.21</u>	-0.68	0.62	<u>-5.96</u>	-0.52	0.70	0.89	0.16	1.12
	AAL	-3.14	-0.54	0.69	<u>-5.32</u>	-0.49	0.71	0.27	0.05	1.04
	MAL	-1.13	-0.01	0.99	-1.05	-0.01	0.99	0.47	0	1.00
	SNA	<u>-4.07</u>	-0.59	0.66	<u>-5.82</u>	-0.42	0.75	1.08	0.17	1.13
	PNA	-1.34	-0.06	0.96	0.48	0.02	1.01	1.68	0.08	1.06
Complement C4 precursor (P01028)	CONA	<u>-3.8</u>	-1.33	0.40	<u>-5.95</u>	-1.31	0.40	0.07	0.02	1.01
	AAL	<u>-3.42</u>	-0.89	0.54	<u>-6.05</u>	-0.72	0.61	0.69	0.18	1.13
	MAL	-2.56	-0.07	0.95	-2.34	-0.03	0.98	1.59	0.04	1.03
	SNA	<u>-4.22</u>	-1.05	0.48	<u>-6.09</u>	-0.83	0.56	0.95	0.22	1.16
	PNA	-1.88	-0.2	0.87	-2.25	-0.15	0.90	0.41	0.05	1.04

^{a, b}: N: normal; A: adenoma; C: cancer. The highlighted ($Z \geq 3.2$ or $Z \leq -3.2$) correspond to 95% significant level with multiple testing correction.