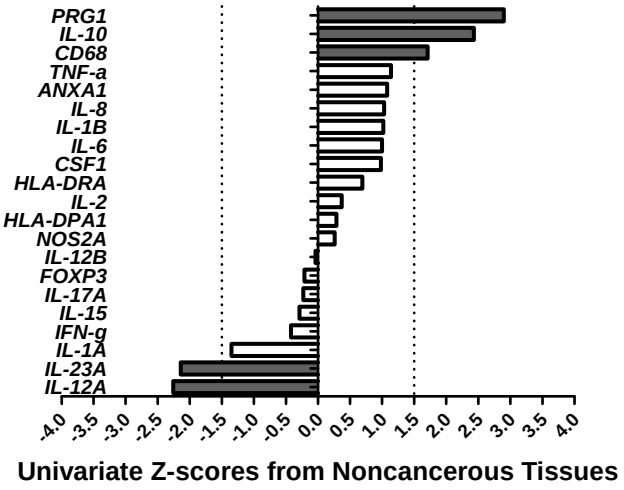
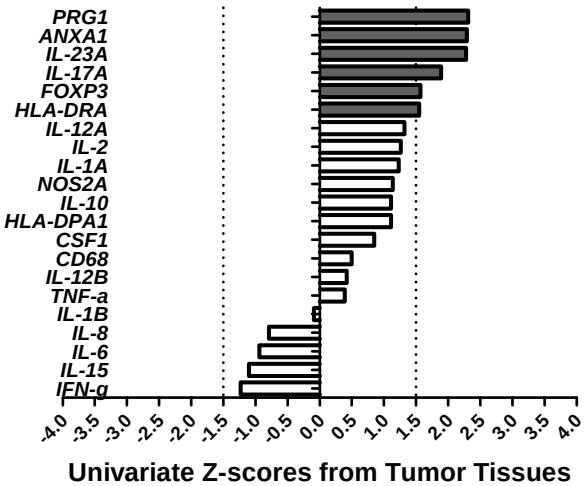
Supplemental Figure 1

Z-scores from univariate Cox regression analysis on expression levels of inflammatory genes in Hong Kong Training Cohort.



Univariate Z-scores from Noncancerous Tissues



Univariate Z-scores from Tumor Tissues

Supplemental figure 1: Univariate analysis of the expression of 23 inflammatory genes in noncancerous or tumor tissue with cancer-specific mortality. The genes are ranked based on their predictive power (univariate Z-score). Dashed lines indicate |Z-score|=1.5. Black bars represent |Z-score|>1.5. This criterion was used for selecting genes to include in the multivariate Cox regression model used to calculate IRS.

Supplemental Table 1: Inflammatory Genes that are differentially expressed in tumors vs. non-cancerous tissue, by cohort or colon adenomas

	Hong Kong Cohort		NCI-Maryland Cohort		Adenoma Study	
Genes Decreased in Tumors	**Fold Change[1]**	**P-value[2]**	**Fold Change[1]**	**P-value[2]**	**Fold Change[1]**	**P-value[2]**
IL-2	0.23	$P < 1 \times 10^{-7}$	0.30	$P < 1 \times 10^{-7}$	0.54	P = 0.007
IL-15	0.42	$P < 1 \times 10^{-7}$	0.67	P = 0.006	0.79	P = 0.27
IL-10	0.46	$P < 1 \times 10^{-7}$	0.74	P = 0.006	0.61	P = 0.09
IL-12A	0.58	$P = 1 \times 10^{-7}$	0.57	$P = 3 \times 10^{-7}$	0.62	P = 0.009
CSF1	0.58	$P < 1 \times 10^{-7}$	0.54	$P = 2 \times 10^{-6}$	0.61	P = 0.01
HLA-DPA1	0.67	$P < 1 \times 10^{-7}$	0.69	$P = 7 \times 10^{-5}$	0.61	P = 0.003
HLA-DRA	0.69	$P < 1 \times 10^{-7}$	0.84	P = 0.03	0.75	P = 0.04
PRG1	0.80	$P = 3 \times 10^{-7}$	1.09	P = 0.19	0.69	P = 0.02
TNF-a	0.83	P = 0.03	0.59	$P = 1 \times 10^{-6}$	0.92	P = 0.60
CD68	0.90	P = 0.02	0.76	P = 0.0005	0.85	P = 0.25
Genes Increased in Tumors	**Fold Change[1]**	**P-value[2]**	**Fold Change[1]**	**P-value[2]**	**Fold Change[1]**	**P-value[2]**
IL-6	2.06	$P = 8 \times 10^{-6}$	2.41	P = 0.0001	1.50	P = 0.44
IFN-γ	2.37	$P < 1 \times 10^{-7}$	1.87	P = 0.005	1.14	P = 0.53
IL-17A	2.71	$P < 1 \times 10^{-7}$	2.22	P = 0.02	4.36	P = 0.01
FOXP3	3.33	$P < 1 \times 10^{-7}$	1.65	P = 0.0003	1.60	P = 0.04
IL-1B	3.36	$P < 1 \times 10^{-7}$	1.88	$P = 1 \times 10^{-5}$	2.00	P = 0.001
IL-1A	5.21	$P < 1 \times 10^{-7}$	3.40	$P < 1 \times 10^{-7}$	6.20	$P = 2.7 \times 10^{-5}$
IL-23A	7.90	$P < 1 \times 10^{-7}$	4.37	$P < 1 \times 10^{-7}$	6.47	$P = 3.7 \times 10^{-4}$
IL-8	13.12	$P < 1 \times 10^{-7}$	11.09	$P < 1 \times 10^{-7}$	7.93	$P = 9.0 \times 10^{-7}$

[1]Fold change in tumors vs. non-cancerous tissues or adenoma vs. nonadenoma tissue where appropriate.

[2]Paired T-test. Genes included in this table were differentially expressed ($P < 0.01$) in at least one cohort and are organized from low to high based on fold change in the Hong Kong Cohort. Patient samples used included all that passed qRT-PCR quality control (n=113 for Hong Kong Cohort, n=73 for NCI-Maryland Cohort and n=18 for adenoma study)

Supplemental Table 2: Association of *miR-21* expression with inflammatory genes *IL-6, IL-12a, IL-8, IL-10,* and *NOS2a* .

	Nontumor Tissue (n=113)		Tumor Tissue (n=113)		Combined (n=226)	
	Regression Coefficent	p-value	Regression Coefficent	p-value	Regression Coefficent	p-value
IL-6	0.13	0.004	0.13	0.01	**0.13**	**<0.0005 ***
IL-12a	-0.26	0.018	-0.19	<0.0005	**-0.21**	**<0.0005 ***
IL-8	0.21	<0.0005	0.05	0.209	**0.13**	**<0.0005 ***
IL-10	0.32	0.012	0.14	0.053	**0.21**	**0.002 ***
NOS2a	-0.30	0.001	-0.06	0.105	**-0.12**	**0.003 ***
IL-1b	0.29	0.001	0.02	0.616	0.12	0.006
IL-17a	-0.04	0.645	-0.12	0.001	-0.10	0.012
PRG1	0.39	0.040	0.15	0.207	0.26	0.019
ANXA1	0.05	0.742	0.20	0.012	0.15	0.063
IL2	-0.21	0.050	-0.04	0.509	-0.11	0.065
CD68	-0.22	0.187	0.11	0.385	-0.27	0.140
CSF1	-0.33	0.043	0.11	0.359	-0.12	0.241
TNF	0.51	0.489	0.12	0.273	0.06	0.264
IL23a	-0.21	0.071	0.00	0.960	-0.05	0.315
IFNG	0.02	0.817	-0.09	0.090	-0.05	0.331
HLADRA	-0.41	0.043	0.12	0.300	-0.09	0.408
IL1a	0.07	0.435	0.00	0.934	0.02	0.651
IL15	0.11	0.401	-0.01	0.877	0.03	0.653
FOXP3	-0.02	0.850	-0.02	0.808	-0.02	0.768
HLADPA1	-0.10	0.563	0.11	0.354	0.00	0.985

* = statistically signficant with Holm-Bonferonni method of adjustment for multiple comparisons. Coeffiencients are shown for linear regression models of miR-21 expression in nontumor tissue and tumor tissue separately with the expression of inflammatory genes. Combined models include both nontumor and tumor tissue and are adjusted for tumor status. Only the combined models are evaluated for significance.