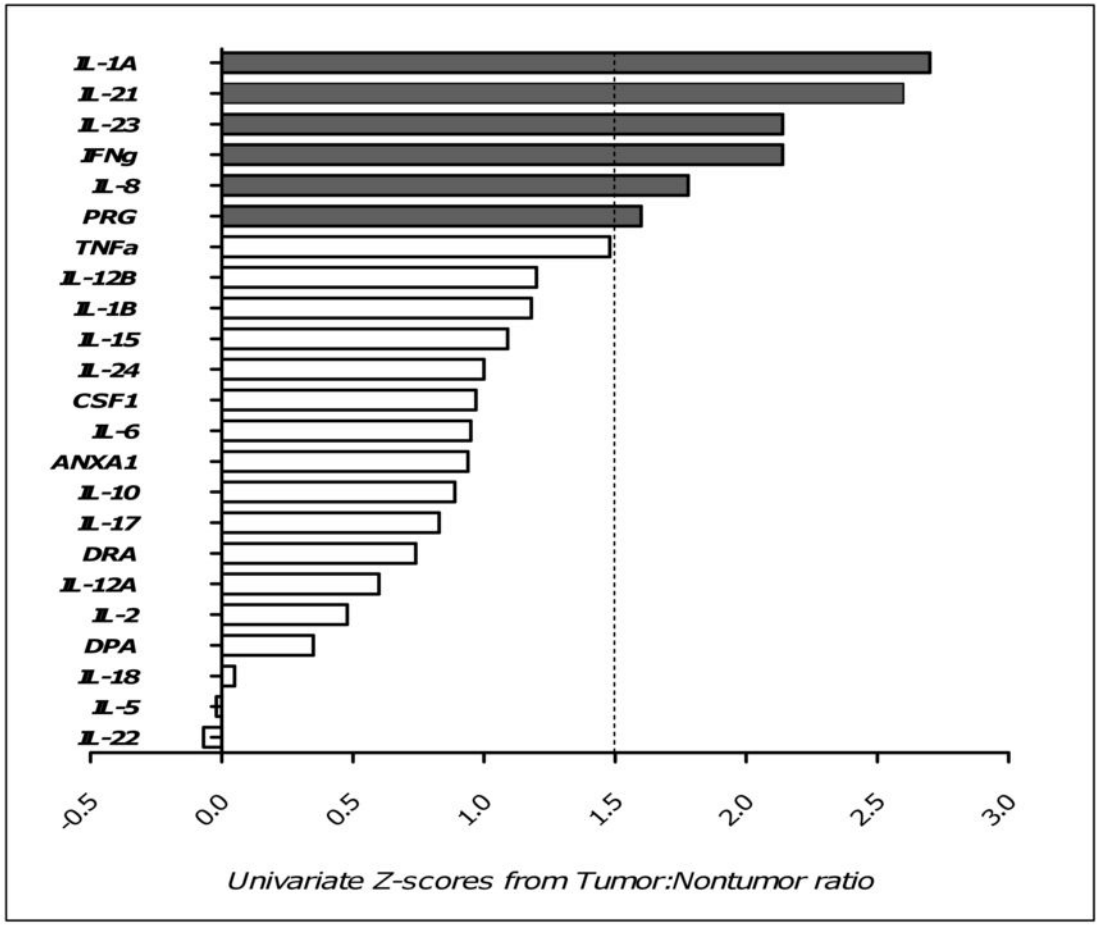
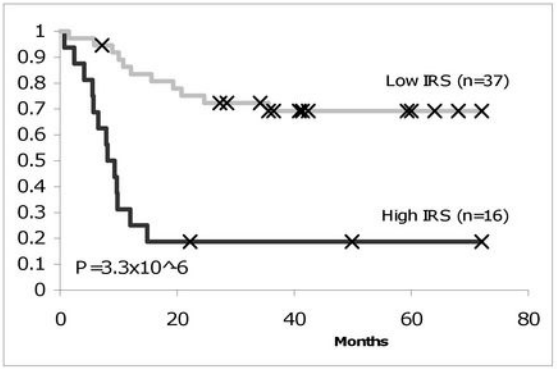
Supplemental Figure S1. Z-scores for Univariate Cox Regression Analysis on Expression Levels of All Genes in the Training Cohort (n=47)

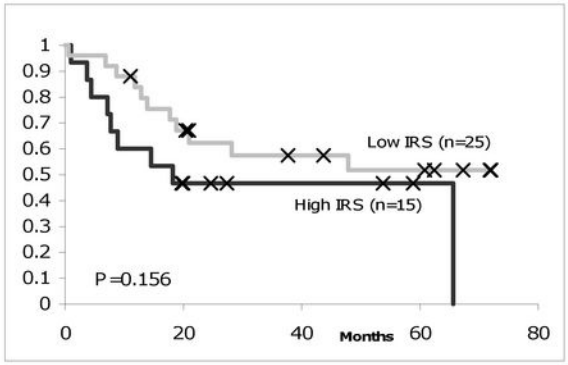


NOTE: Univariate analysis based on gene expression of all 23 genes used in the training cohort with cancer-specific mortality. The genes are ranked based on their predictive power (univariate Z-score). Z-scores > 1.5 are highlighted with a black box. The dashed line represents Z-score >1.5. For the 6 genes shown, an elevated level of expression in either one of them is consistent with poor prognosis. These genes were included in the multivariate Cox regression model used to calculate Inflammatory Risk Score (IRS). See Results section for details.

Supplemental Figure S2. High IRS is associated with poor prognosis in patients without neoadjuvant thereapy

A. Neoadjuvant therapy naive patients (n=53) **B. Neoadjuvant treated patients (n=40)**





A, High IRS expression was classified based on highest tertile using tumor and notumor ratio. The association between IRS and prognosis in nontreated patients. B, Kaplan-Meir graph showed the association between IRS and prognosis in neoadjuvant patients.

Supplemental Table S1. 24 Inflammation Associated Genes Used in the Study			
Gene	Gene Symbol	Source	Function
Annexin A1	ANXA1	Many, not limited to hematopoietic cells	Intracellular phospholipid binding protein; Anti-inflammatory activity
Colony stimulating factor 1	CSF1	Many, including endothelial cells	Production and differentiation of macrophages
Interferon γ	IFNγ	T cells, NK cells, and others	Hallmark of the Th1 immune response; Has antiviral and antitumor properties; Activates macrophages
Interleukin 1α/β	IL-1α/β	Macrophages and others	Important mediator of inflammation, proliferation, hematopoiesis, and cell injury/apoptosis; Pyrogenic
Interleukin 2	IL-2	T cells	Growth and differentiation of T, B, and NK cells
Interleukin 4	IL-4	T cells and mast cells	Induction of the Th2 immune response; B cell activation and IgE class switching; T cell proliferation and associated with allergy
Interleukin 5	IL-5	T cells	Th2 cytokine; Stimulates B cells and is a major regulator of eosinophil biology; Associated with allergy
Interleukin 6	IL-6	Macrophages and others	Important mediator of fever and acute phase response; Differentiation of B cells and hematopoiesis; Drives Th17 response when combined with TGFβ
Interleukin 8	IL-8	Macrophages and others	Major chemokine and angiogenic factor; Recruitment of neutrophils
Interleukin 10	IL-10	Macrophages, T cells, and others	Major immunoregulatory cytokine with numerous effects; Blocks Th1/Th2/Th17 responses; B cell proliferation
Interleukin 12, p35/p40	IL-12 A/B	Macrophages, dendritic cells, and others	Subunit of IL-12; Important inducer of Th1 cell development; Also acts on NK cells
Interleukin 15	IL-15	Many hematopoietic cells	IL-2 family; Regulates activation and proliferation of T cells and NK cells
Interleukin 17A	IL-17A	T cells and others	Associated with multiple chronic inflammatory diseases including rheumatoid arthritis, psoriasis, and multiple sclerosis; Neutrophil chemotaxis
Interleukin 18	IL-18	Macrophages and others	IL-1 family; Proinflammatory cytokine that stimulates NK and T cells; Induces IFNg by T cells
Interleukin 21	IL-21	T cells	IL-2 family; Proliferation and maturation of T, B, and NK cells
Interleukin 22	IL-22	T cells and NK cells	IL-10 family; Induces acute phase response in hepatocytes; Antimicrobial
Interleukin 23	IL-23	Macrophages, dendritic cells, and others	IL-12 family; Proinflammatory cytokine involved in Th17 response
Interleukin 24	IL-24	T cells, monocytes, and others	IL-10 family; Induces apoptosis in various cancer cells
HLA-DPα1	HLA-DPA1	Antigen presenting cells	Major histocompatibility complex, class II
HLA-DRα1	HLA-DRA1	Antigen presenting cells	Major histocompatibility complex, class II
Platelet Proteoglycan	PRG or SRGN	Mast cells, T cells, and others	Proteoglycan found in hematopoietic cell granules, including mast cells and cytotoxic T lymphocytes
Tumor necrosis factor	TNF	Macrophages and others	Proinflammatory cytokine with a broad spectrum of biological activities; Implicated in inflammation associated with many diseases including cancer

Supplemental Table S2. Differentially Expressed Genes in Tumors Compared with Its NonTumor Tissues

Gene name	Unique ID	Chromosomal location	Adenocarcinomas (n=93)		
			Fold change	P value	FDR
Interleukin 24	IL-24	1q32	9.10	2.4×10^{-6}	1.4×10^{-5}
Interleukin 8	IL-8	4q13-q21	4.08	9.9×10^{-5}	3.8×10^{-4}
Interleukin 21	IL-21	4q26-q27	2.67	0.01	0.03
Interferon γ	IFNγ	12q14	2.05	0.04	0.08
Interleukin 5	IL-5	5q31.1	1.64	0.35	0.61
MHC class II antigen	HLA-DPA1	6p21.3	1.54	0.14	0.27
Platelet proteoglycan	PRG	19q13.2	1.35	0.42	0.63
MHC class II antigen	HLA-DRA1	6p21.3	1.33	0.38	0.62
Interleukin 17	IL-17	6p12	1.28	0.61	0.74
Interleukin 1, β	IL-1β	2q14	1.21	0.54	0.68
Interleukin 23	IL-23	12q13.2	1.09	0.80	0.91
Colony stimulating factor	CSF1	1p21-p13	1.04	0.91	0.95
Interleukin 6	IL-6	7p21	1.03	0.95	0.95
Interleukin 10	IL-10	1q31-q32	0.95	0.85	0.93
Interleukin 15	IL-15	4q31	0.86	0.47	0.63
Interleukin 12, p40	IL-12B	5q31.1-q33.1	0.80	0.43	0.63
Interleukin 22	IL-22	12q15	0.47	0.10	0.22
Tumor necrosis factor	TNFα	6p21.3	0.39	2.0×10^{-3}	5.0×10^{-3}
Interleukin 2	IL-2	4q26-q27	0.38	1.0×10^{-3}	4.0×10^{-3}
Interleukin 18	IL-18	11q22.2-q22.3	0.33	1.8×10^{-5}	8.2×10^{-5}
Interleukin 12, p35	IL-12A	3q25.33-q26	0.13	$<1.0 \times 10^{-7}$	$<1.0 \times 10^{-7}$
Interleukin 1, α	IL-1α	2q14	0.12	1.0×10^{-7}	8.0×10^{-7}
Annexin A1	ANXA1	9q12-q21.2	0.08	$<1.0 \times 10^{-7}$	$<1.0 \times 10^{-7}$

NOTE: Shaded areas show significant p values for differentially expressed genes.
Abbreviations: FDR, False Discovery Rate; P value, Parametric p values

Supplemental Table S3. Differentially Expressed Genes in Tumors Compared with Its NonTumor Tissues for Barrett's (BA) vs.Sporadic (NB) Adenocarcinoma

Gene name	Unique ID	Barrett's Adenocarcinoma samples (n=58)			Sporadic Adenocarcinma samples (n=35)			P value *
		Fold change	P value	FDR	Fold change	P value	FDR	
Annexin A1	ANXA1	0.08	2.1×10^{-6}	2.6×10^{-5}	0.08	2.5×10^{-4}	1.0×10^{-3}	0.91
Colony stimulating factor	CSF1	0.92	0.86	0.86	1.28	0.65	0.75	0.72
MHC class II antigen	DPA	1.43	0.35	0.62	1.77	0.23	0.52	0.39
MHC class II antigen	DRA	1.27	0.57	0.78	1.43	0.46	0.73	0.86
Interferon γ	IFNg	2.29	0.08	0.19	1.71	0.27	0.53	0.91
Interleukin 10	IL-10	0.81	0.55	0.78	1.24	0.61	0.75	0.38
Interleukin 12, p35	IL-12A	0.14	2.3×10^{-6}	2.6×10^{-5}	0.14	7.2×10^{-6}	1.6×10^{-4}	0.84
Interleukin 12, p40	IL-12B	0.60	0.20	0.42	1.24	0.62	0.75	0.20
Interleukin 15	IL-15	0.88	0.65	0.78	0.83	0.51	0.73	0.64
Interleukin 17	IL-17	1.29	0.68	0.78	1.24	0.78	0.79	0.48
Interleukin 18	IL-18	0.41	0.01	0.03	0.23	3.0×10^{-3}	1.4×10^{-3}	0.15
Interleukin 1, α	IL-1A	0.13	5.4×10^{-5}	4.0×10^{-4}	0.12	2.2×10^{-4}	1.4×10^{-3}	0.79
Interleukin 1, β	IL-1B	1.18	0.68	0.78	1.27	0.64	0.75	0.38
Interleukin 2	IL-2	0.39	0.02	0.07	0.36	0.02	0.07	0.86
Interleukin 21	IL-21	1.82	0.23	0.44	5.06	0.01	0.05	0.08
Interleukin 22	IL-22	0.36	0.08	0.19	0.73	0.68	0.75	0.48
Interleukin 23	IL-23	1.25	0.59	0.78	0.86	0.79	0.79	0.18
Interleukin 24	IL-24	5.68	2.3×10^{-3}	0.01	19.55	2.2×10^{-4}	1.4×10^{-3}	0.10
Interleukin 5	IL-5	1.26	0.72	0.79	2.59	0.30	0.53	0.60
Interleukin 6	IL-6	0.76	0.63	0.78	1.70	0.49	0.73	0.19
Interleukin 8	IL-8	3.38	0.01	0.03	5.56	3.0×10^{-3}	0.01	0.44
Platelet proteoglycan	PRG	1.12	0.82	0.85	1.85	0.29	0.53	0.54
Tumor necrosis factor	TNFa	0.41	0.02	0.07	0.37	0.03	0.09	0.94

NOTE:Table indicating the fold-change levels in gene expression between tumors and nontumor samples between Barrett's and sporadic adenocarcinoma. P value, parametric p values; FDR, false discovery rate

*Mann-Whitney test was used to calculate the differences between the fold changes in Barrett's vs. sporadic adenocarcinoma.

Supplemental Table S4. Differentially Expressed Genes in Tumors Compared with Its NonTumor Tissues for Therapy treated (NAT) vs.Non-treated (NAT-naive) Esophageal Adenocarcinoma Patients

Gene name	Unique ID	NAT samples (n=40)			NAT-naive samples (n=53)			P value *
		Fold change	P value	FDR	Fold change	P value	FDR	
Annexin A1	ANXA1	0.16	4.2×10^{-5}	4.1×10^{-4}	0.05	4.0×10^{-7}	4.6×10^{-6}	0.17
Colony stimulating factor	CSF1	1.34	0.35	0.54	0.86	0.78	0.82	0.30
MHC class II antigen	DPA	1.56	0.13	0.25	1.50	0.34	0.63	0.54
MHC class II antigen	DRA	1.39	0.38	0.54	1.28	0.59	0.75	0.42
Interferon γ	IFNg	3.00	0.06	0.17	1.55	0.27	0.57	0.10
Interleukin 10	IL-10	1.24	0.59	0.68	0.78	0.47	0.68	0.08
Interleukin 12, p35	IL-12A	0.19	5.3×10^{-5}	4.1×10^{-4}	0.11	1.0×10^{-7}	2.3×10^{-6}	0.34
Interleukin 12, p40	IL-12B	0.95	0.90	0.94	0.71	0.38	0.63	0.33
Interleukin 15	IL-15	0.81	0.48	0.62	0.90	0.70	0.82	0.54
Interleukin 17	IL-17	1.00	1.00	1.00	1.47	0.59	0.75	0.83
Interleukin 18	IL-18	0.26	3.0×10^{-4}	2.2×10^{-3}	0.40	7.6×10^{-3}	0.03	0.54
Interleukin 1, α	IL-1A	0.23	3.6×10^{-3}	0.02	0.08	1.0×10^{-6}	7.7×10^{-6}	0.45
Interleukin 1, β	IL-1B	1.32	0.52	0.63	1.14	0.75	0.82	0.36
Interleukin 2	IL-2	0.56	0.20	0.33	0.29	9.0×10^{-3}	5.2×10^{-3}	0.14
Interleukin 21	IL-21	2.39	0.08	0.20	2.77	0.06	0.14	0.25
Interleukin 22	IL-22	1.12	0.85	0.93	0.21	0.03	0.07	0.33
Interleukin 23	IL-23	0.71	0.42	0.56	1.49	0.38	0.63	0.05
Interleukin 24	IL-24	14.99	7.3×10^{-6}	1.6×10^{-4}	6.43	3.3×10^{-3}	0.01	0.14
Interleukin 5	IL-5	3.27	0.14	0.25	0.81	0.76	0.82	0.20
Interleukin 6	IL-6	1.97	0.14	0.25	0.63	0.47	0.68	0.02
Interleukin 8	IL-8	3.28	0.03	0.09	4.80	1.0×10^{-3}	6.0×10^{-3}	0.51
Platelet proteoglycan	PRG	1.86	0.14	0.25	1.06	0.91	0.91	0.42
Tumor necrosis factor	TNFa	0.42	0.01	0.04	0.37	9.0×10^{-3}	0.03	0.22

NOTE: Table indicating the fold-change levels in gene expression between tumors and nontumor samples between therapy treated patients versus nontreated patients. P value, parametric p values; FDR, false discovery rate

* Mann-Whitney test was used to calculate the differences between the fold changes in therapy treated vs. nontreated patients.