

## Manuscript Title

Circulating mRNA Profiling in Esophageal Squamous Cell Carcinoma Identifies FAM84B  
As A Biomaker In Predicting Pathological Response to Neoadjuvant Chemoradiation

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**Supplementary Table e1.** David (Database for Annotation, Visualization, and Integrated Discovery) functional annotation clustering with differentially expressed genes before and after chemoradiation.

Annotation Cluster 1	Enrichment Score: 8.64			
Category	Term	Count	P Value	Bonferroni
GOTERM_BP_ALL	GO:0002376~immune system process	33	1.2E-14	1.3E-11
GOTERM_BP_ALL	GO:0006955~immune response	24	7.2E-11	7.7E-8
GOTERM_BP_ALL	GO:0050896~response to stimulus	34	1.4E-2	1.0E0
Annotation Cluster 2	Enrichment Score: 2.84			
Category	Term	Count	P Value	Bonferroni
GOTERM_BP_ALL	GO:0048534~hemopoietic or lymphoid organ development	10	5.3E-5	5.5E-2
GOTERM_BP_ALL	GO:0002520~immune system development	10	8.4E-5	8.6E-2
GOTERM_BP_ALL	GO:0046649~lymphocyte activation	8	3.4E-4	3.0E-1
GOTERM_BP_ALL	GO:0048872~homeostasis of number of cells	6	5.1E-4	4.2E-1
GOTERM_BP_ALL	GO:0030097~hemopoiesis	8	9.3E-4	6.3E-1
GOTERM_BP_ALL	GO:0045321~leukocyte activation	8	1.1E-3	6.9E-1
GOTERM_BP_ALL	GO:0042113~B cell activation	5	1.6E-3	8.2E-1
GOTERM_BP_ALL	GO:0046651~lymphocyte proliferation	4	2.6E-3	9.4E-1
GOTERM_BP_ALL	GO:0001775~cell activation	8	2.9E-3	9.5E-1
GOTERM_BP_ALL	GO:0070661~leukocyte proliferation	4	3.0E-3	9.6E-1

GOTERM_BP_ALL	GO:0032943~mononuclear cell proliferation	4	3.0E-3	9.6E-1
GOTERM_BP_ALL	GO:0042100~B cell proliferation	3	3.2E-3	9.7E-1
GOTERM_BP_ALL	GO:0048538~thymus development	3	9.1E-3	1.0E0
GOTERM_BP_ALL	GO:0042110~T cell activation	5	9.6E-3	1.0E0
GOTERM_BP_ALL	GO:0002521~leukocyte differentiation	5	1.1E-2	1.0E0
Annotation Cluster 3	Enrichment Score: 2.61			
Category	Term	Count	P Value	Bonferroni
GOTERM_BP_ALL	GO:0002682~regulation of immune system process	11	2.2E-4	2.1E-1
GOTERM_BP_ALL	GO:0050776~regulation of immune response	8	7.2E-4	5.4E-1
GOTERM_BP_ALL	GO:0002684~positive regulation of immune system process	8	9.8E-4	6.5E-1
GOTERM_BP_ALL	GO:0002768~immune response-regulating cell surface receptor signaling pathway	4	2.6E-3	9.4E-1
GOTERM_BP_ALL	GO:0050778~positive regulation of immune response	6	2.7E-3	9.4E-1
GOTERM_BP_ALL	GO:0002253~activation of immune response	5	3.4E-3	9.7E-1
GOTERM_BP_ALL	GO:0048583~regulation of response to stimulus	10	3.5E-3	9.8E-1
GOTERM_BP_ALL	GO:0048584~positive regulation of response to stimulus	7	4.7E-3	9.9E-1
GOTERM_BP_ALL	GO:0002764~immune response-regulating signal transduction	4	6.0E-3	1.0E0
GOTERM_BP_ALL	GO:0050851~antigen receptor-mediated signaling pathway	3	2.0E-2	1.0E0
Annotation Cluster 4	Enrichment Score: 2.09			
Category	Term	Count	P Value	Bonferroni
GOTERM_BP_ALL	GO:0042440~pigment metabolic process	4	3.2E-3	9.7E-1
GOTERM_BP_ALL	GO:0006783~heme biosynthetic process	3	5.5E-3	1.0E0
GOTERM_BP_ALL	GO:0033014~tetrapyrrole biosynthetic process	3	7.6E-3	1.0E0
GOTERM_BP_ALL	GO:0006779~porphyrin biosynthetic process	3	7.6E-3	1.0E0
GOTERM_BP_ALL	GO:0042168~heme metabolic process	3	9.1E-3	1.0E0
GOTERM_BP_ALL	GO:0033013~tetrapyrrole metabolic process	3	1.6E-2	1.0E0
GOTERM_BP_ALL	GO:0006778~porphyrin metabolic process	3	1.6E-2	1.0E0
Annotation Cluster 5	Enrichment Score: 1.96			
Category	Term	Count	P Value	Bonferroni
GOTERM_BP_ALL	GO:0006959~humoral immune response	5	1.8E-3	8.6E-1

ALL				
GOTERM_BP_ ALL	GO:0006952~defense response	11	7.2E-3	1.0E0
GOTERM_BP_ ALL	GO:0042592~homeostatic process	12	1.0E-2	1.0E0
GOTERM_BP_ ALL	GO:0019725~cellular homeostasis	9	1.2E-2	1.0E0
GOTERM_BP_ ALL	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	6	1.7E-2	1.0E0
GOTERM_BP_ ALL	GO:0006879~cellular iron ion homeostasis	3	1.8E-2	1.0E0
GOTERM_BP_ ALL	GO:0055066~di-, tri-valent inorganic cation homeostasis	6	2.1E-2	1.0E0
GOTERM_BP_ ALL	GO:0055072~iron ion homeostasis	3	2.3E-2	1.0E0