Figure S1. Association between CFB gene expression and the prognosis of patients with lung adenocarcinoma. (A and B) Patients were divided into three groups based on the tertile expression of CFB, and then the Q1 and Q3 groups were compared in terms of (A) overall survival and (B) disease-free survival. (C and D) Patients were divided into four groups based on the quartile expression of CFB, and then the Q1 and Q4 groups were compared in terms of (C) overall survival and (D) disease-free survival. CFB, complement factor B; HR, hazard ratio.

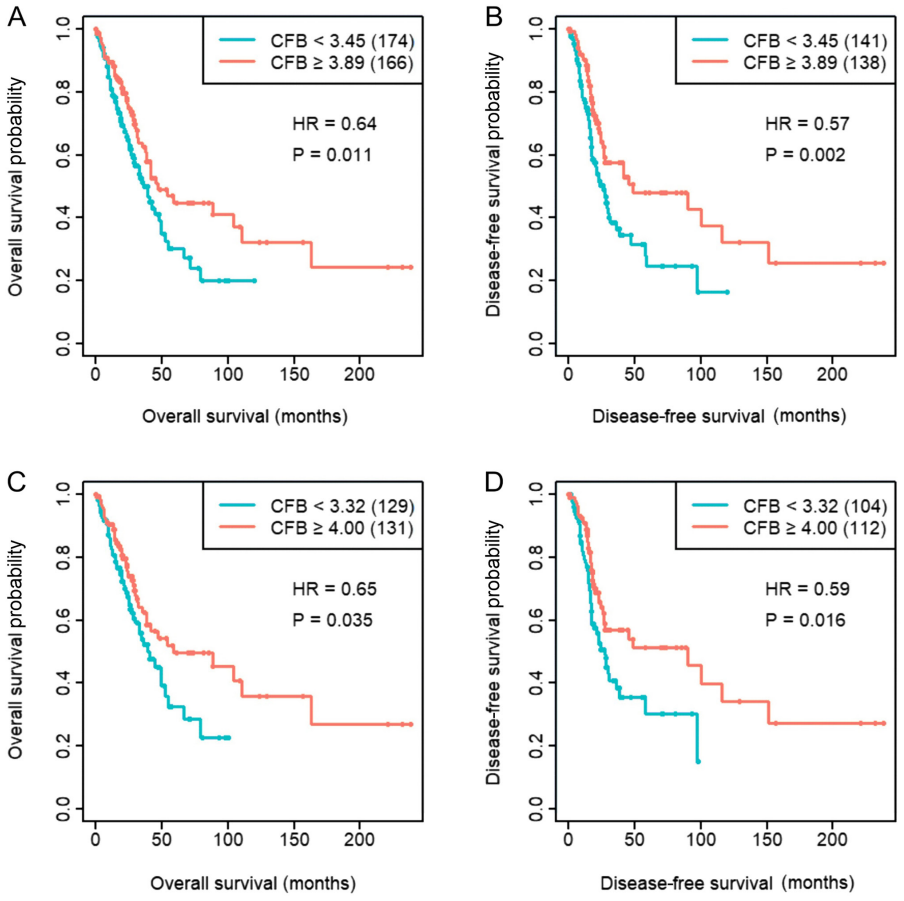

Figure S2. Association between CFB gene expression and the prognosis of patients with lung adenocarcinoma. (A and B) Association between CFB expression and (A) overall survival and (B) disease-free survival in non-smokers. (C and D) Association between CFB expression and (C) overall survival and (D) disease-free survival in former smokers. (E and F) Association between CFB expression and (E) overall survival and (F) disease-free survival in current smokers. The patients were divided into three groups based on the tertile expression of CFB. CFB, complement factor B; HR, hazard ratio.

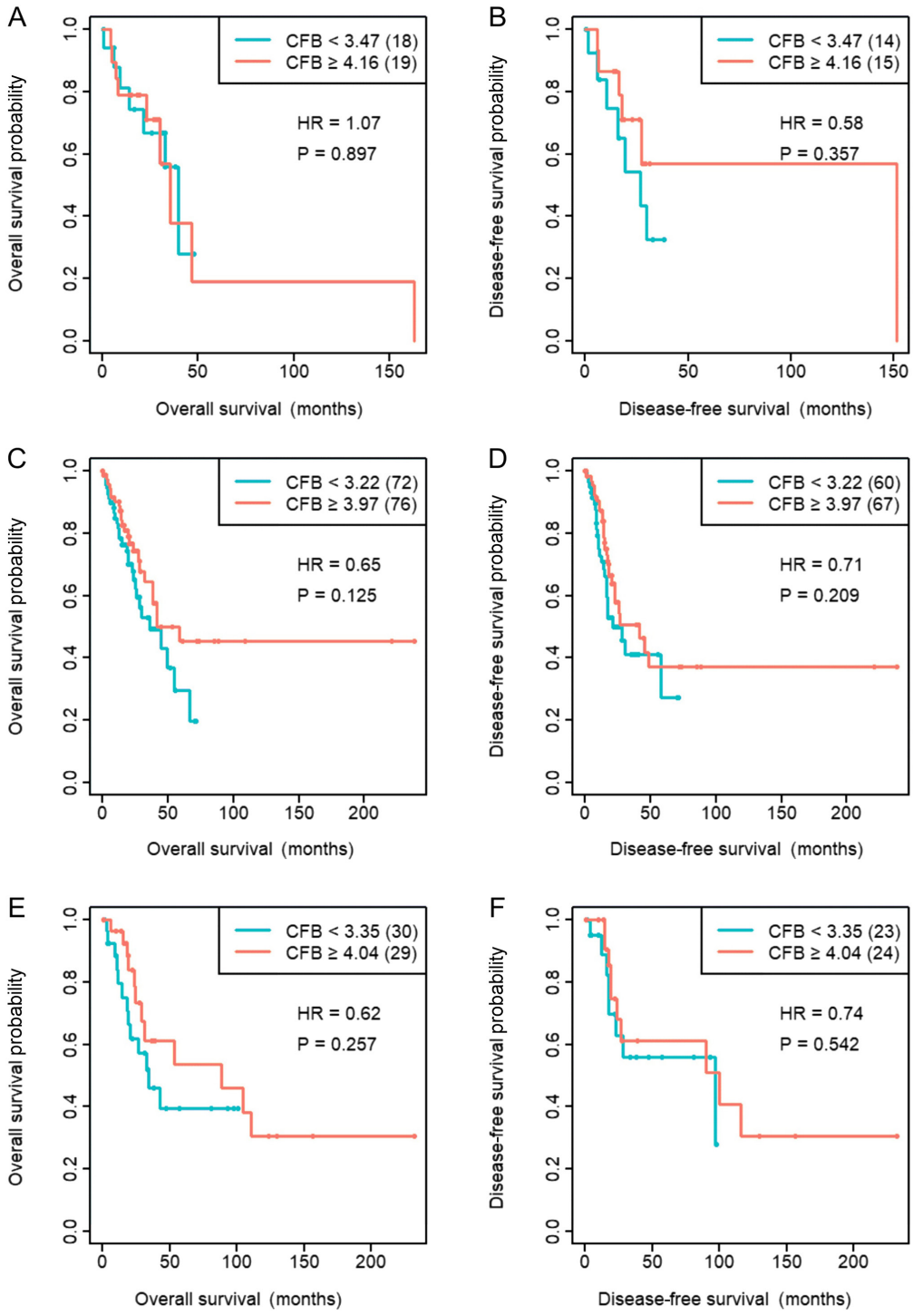

Table SI. Gene set enrichment analysis results of Gene Ontology biological processes in three comparisons.

		CFB-high vs. Control		CFB-low vs. Control		CFB-high vs. CFB-low	
Name	Gene counts	NES	P-value	NES	P-value	NES	P-value
Regulation of heart contraction	17	1.85	0.004	1.85	0.002	1.23	0.200
Bicellular tight junction assembly	23	1.75	0.005	1.76	0.002	0.98	0.458
Ventricular trabecula myocardium morphogenesis	35	1.75	0.004	1.71	0.009	1.15	0.287
Maturation of SSU-rRNA	21	1.74	0.006	1.73	0.008	1.49	0.046
Response to γ radiation	24	1.73	0.006	1.76	0.000	1.05	0.380
'*De novo*' protein folding	18	1.71	0.007	1.61	0.037	-1.00	0.454
piRNA metabolic process	15	1.70	0.009	1.76	0.008	1.55	0.027
Embryonic hindlimb morphogenesis	43	1.70	0.007	1.56	0.039	1.09	0.330
Golgi to endosome transport	15	1.69	0.008	1.69	0.010	0.67	0.909
Skin development	17	1.68	0.009	1.55	0.009	0.88	0.641
MyD88-independent toll-like receptor signaling pathway	30	1.66	0.011	1.55	0.038	1.59	0.025
Regulation of neurogenesis	107	1.64	0.021	1.66	0.011	-1.20	0.222
Gene silencing by RNA	32	1.62	0.025	1.58	0.037	1.67	0.012
Epoxygenase P450 pathway	27	1.60	0.020	1.49	0.047	-0.86	0.665
Phototransduction	15	1.60	0.019	1.37	0.094	0.78	0.819
Generation of precursor metabolites and energy	27	1.60	0.013	1.66	0.008	1.06	0.375
Phospholipid translocation	120	1.58	0.021	1.65	0.014	1.20	0.220
Negative regulation of transposition	15	1.58	0.027	1.50	0.051	-0.71	0.862
Linoleic acid metabolic process	117	1.57	0.029	1.57	0.028	1.27	0.165
Response to zinc ion	64	1.57	0.025	1.52	0.039	1.43	0.063
Mitochondrial fission	20	1.57	0.023	1.51	0.059	0.93	0.534
Fibroblast growth factor receptor signaling pathway	16	1.57	0.005	1.54	0.007	1.38	0.042
DNA demethylation	62	1.56	0.030	1.48	0.057	1.29	0.178
Establishment or maintenance of cell polarity	29	1.56	0.022	1.50	0.032	1.17	0.240
Regulation of cell morphogenesis	24	1.56	0.026	1.58	0.012	0.91	0.584
Positive regulation of G2/M transition of mitotic cell cycle	18	1.56	0.031	1.63	0.024	-0.63	0.934
Negative regulation of apoptotic signaling pathway	20	1.55	0.026	1.45	0.061	1.00	0.472
Positive regulation of G1/S transition of mitotic cell cycle	15	1.55	0.024	1.46	0.059	1.08	0.356
Positive regulation of T cell differentiation	36	1.55	0.059	1.56	0.045	-0.68	0.844
Epithelial cell morphogenesis	52	1.54	0.030	1.45	0.057	0.89	0.615
Immune system process	33	1.54	0.035	1.46	0.042	1.11	0.317
Response to UV	20	1.53	0.034	1.44	0.068	1.38	0.081
Negative regulation of insulin receptor signaling pathway	87	1.53	0.022	1.48	0.047	0.90	0.624
Muscle cell cellular homeostasis	54	1.52	0.034	1.53	0.041	1.20	0.233
Regulation of ERK1 and ERK2 cascade	19	1.52	0.032	1.59	0.018	0.66	0.927
Blood circulation	116	1.51	0.022	1.50	0.026	0.86	0.693
Positive regulation of heart rate	48	1.51	0.029	1.58	0.019	0.90	0.600
Regulation of centrosome duplication	20	1.51	0.076	1.59	0.022	1.06	0.371
Multivesicular body assembly	15	1.51	0.042	1.37	0.058	1.37	0.071
Positive regulation of axon extension	45	1.50	0.024	1.48	0.030	1.07	0.369
Proteolysis involved in cellular protein catabolic process	79	1.50	0.033	1.58	0.022	1.32	0.105
Positive regulation of canonical Wnt signaling pathway	39	1.49	0.003	1.48	0.014	1.00	0.442
Glucose homeostasis	26	1.49	0.013	1.28	0.089	1.39	0.031
Stem cell differentiation	97	1.48	0.042	1.36	0.101	0.93	0.563
3'-phosphoadenosine 5'-phosphosulfate metabolic process	19	1.48	0.042	1.52	0.035	1.00	0.481
Positive regulation of telomerase RNA localization to Cajal body	20	1.48	0.046	1.37	0.139	-0.63	0.935
TRIF-dependent toll-like receptor signaling pathway	64	1.47	0.054	1.39	0.079	1.48	0.048
Tesponse to muscle activity	40	1.47	0.055	1.58	0.044	0.77	0.777
Negative regulation of anoikis	95	1.47	0.057	1.48	0.046	1.39	0.085
Positive regulation of interleukin-10 production	32	1.46	0.072	1.50	0.043	0.76	0.814
Androgen receptor signaling pathway	30	1.46	0.032	1.33	0.114	1.59	0.014
Embryonic forelimb morphogenesis	19	1.45	0.040	1.40	0.068	-0.82	0.748
Retina development in camera-type eye	15	1.45	0.039	1.41	0.065	1.50	0.040
Endocytic recycling	108	1.45	0.049	1.57	0.017	0.53	0.986
Substrate adhesion-dependent cell spreading	19	1.45	0.042	1.44	0.067	1.12	0.281
Glutamine metabolic process	24	1.44	0.096	1.51	0.043	-1.09	0.377
Positive regulation of osteoblast differentiation	39	1.42	0.049	1.41	0.057	1.46	0.035
Viral life cycle	18	1.41	0.047	1.25	0.176	1.71	0.016
cGMP biosynthetic process	25	1.40	0.105	1.31	0.161	1.49	0.048
Negative regulation of viral genome replication	29	1.40	0.076	1.36	0.087	1.49	0.033

Table SI. Continued.

Name	Gene counts	CFB-high vs. Control		CFB-low vs. Control		CFB-high vs. CFB-low	
		NES	P-value	NES	P-value	NES	P-value
Error-free translesion synthesis	121	1.39	0.093	1.25	0.198	1.67	0.021
Cation transport	89	1.37	0.110	1.18	0.223	1.75	0.021
Regulation of hematopoietic stem cell differentiation	39	1.35	0.072	1.42	0.048	1.10	0.313
Cellular response to interleukin-4	16	1.35	0.107	1.42	0.055	1.50	0.040
Regulation of peptidyl-tyrosine phosphorylation	24	1.34	0.118	1.45	0.044	1.28	0.158
Negative regulation of nucleic acid-templated transcription	68	1.33	0.104	1.32	0.093	1.45	0.036
Osteoclast differentiation	37	1.33	0.109	1.49	0.041	0.71	0.859
Embryonic cranial skeleton morphogenesis	33	1.30	0.104	1.14	0.284	1.47	0.049
Embryonic limb morphogenesis	15	1.30	0.125	1.21	0.191	1.57	0.012
Translesion synthesis	74	1.28	0.138	1.24	0.158	1.84	0.000
Regulation of tumor necrosis factor-mediated signaling pathway	16	1.27	0.132	1.13	0.278	1.70	0.002
ATP hydrolysis coupled proton transport	19	1.25	0.178	1.25	0.182	1.70	0.012
Intracellular transport of virus	48	1.24	0.151	1.22	0.168	1.60	0.008
Nuclear-transcribed mRNA catabolic process	20	1.24	0.216	1.19	0.234	1.58	0.018
Anterograde synaptic vesicle transport	19	1.23	0.201	1.07	0.373	1.55	0.045
Error-prone translesion synthesis	15	1.22	0.203	1.09	0.331	1.55	0.031
Zinc ion transmembrane transport	27	1.22	0.219	1.10	0.341	1.74	0.002
Regulation of lipid metabolic process	37	1.20	0.166	1.22	0.141	1.50	0.017
Chaperone cofactor-dependent protein refolding	15	1.19	0.238	0.84	0.667	1.67	0.008
Negative regulation of transforming growth factor β receptor signaling pathway	23	1.18	0.225	1.05	0.389	1.68	0.004
Cellular response to cAMP	337	1.17	0.211	1.24	0.148	1.52	0.031
Negative regulation of focal adhesion assembly	34	1.17	0.284	1.03	0.432	1.69	0.008
Positive regulation of myoblast differentiation	18	1.16	0.269	1.24	0.184	1.60	0.027
Respiratory gaseous exchange	80	1.15	0.249	1.02	0.415	1.55	0.033
C-terminal protein lipidation	24	1.15	0.237	1.25	0.123	1.39	0.028
RNA metabolic process	15	1.14	0.249	1.12	0.274	1.45	0.028
B cell differentiation	17	1.13	0.248	0.99	0.475	1.48	0.029
Regulation of immune response	24	1.12	0.242	1.02	0.417	1.49	0.016
Cell surface receptor signaling pathway	32	1.12	0.256	1.09	0.274	1.37	0.032
Negative regulation of viral entry into host cell	46	1.11	0.313	0.95	0.525	1.58	0.021
Negative regulation of T cell proliferation	31	1.11	0.305	1.02	0.427	1.51	0.043
Leukocyte cell-cell adhesion	18	1.10	0.324	1.02	0.422	1.58	0.020
Bone development	15	1.10	0.322	1.06	0.363	1.50	0.030
G-protein coupled purinergic nucleotide receptor signaling pathway	29	1.10	0.338	1.09	0.340	1.59	0.024
Cellular zinc ion homeostasis	19	1.10	0.347	0.83	0.697	2.11	0.000
Spindle assembly	15	1.08	0.333	0.91	0.570	1.49	0.046
Positive regulation of focal adhesion assembly	21	1.07	0.366	1.12	0.289	1.54	0.033
Transcription by RNA polymerase III	21	1.07	0.352	1.05	0.394	1.47	0.045
Protein ubiquitination	170	1.06	0.332	0.98	0.528	1.42	0.008
Cellular protein metabolic process	31	1.05	0.350	-1.11	0.249	1.37	0.034
Positive regulation of I-κB kinase/NF-κB signaling	39	1.04	0.364	1.02	0.403	1.43	0.024
SRP-dependent cotranslational protein targeting to membrane	67	1.04	0.420	1.08	0.323	1.48	0.021
Intracellular receptor signaling pathway	25	1.01	0.430	0.94	0.541	1.52	0.036
Insulin receptor signaling pathway	31	1.01	0.431	0.93	0.546	1.59	0.002
Positive regulation of innate immune response	20	1.00	0.456	0.83	0.761	1.66	0.008
Translation	85	0.99	0.480	0.99	0.468	1.53	0.004
Cell division	37	0.97	0.539	0.91	0.656	1.30	0.041
Mesoderm formation	81	0.97	0.481	0.98	0.493	1.55	0.028
Acute-phase response	157	0.97	0.510	0.94	0.560	1.64	0.010
Adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	75	0.96	0.529	0.83	0.767	1.47	0.037
Regulation of signaling receptor activity	23	0.96	0.543	0.91	0.646	1.32	0.042
Positive regulation of autophagy	16	0.95	0.550	0.91	0.604	1.49	0.034
Fatty acid biosynthetic process	76	0.94	0.550	0.99	0.473	1.58	0.020
Regulation of macroautophagy	23	0.94	0.589	0.85	0.754	1.42	0.030
Multicellular organism development	24	0.93	0.626	0.89	0.713	1.46	0.002
mRNA transport	22	0.92	0.575	-0.95	0.550	1.57	0.023
miRNA metabolic process	60	0.91	0.580	0.70	0.860	1.70	0.013
Response to ionizing radiation	26	0.90	0.645	0.94	0.509	1.59	0.008

Table SI. Continued.

Name	Gene counts	CFB-high vs. Control		CFB-low vs. Control		CFB-high vs. CFB-low	
		NES	P-value	NES	P-value	NES	P-value
T cell differentiation in thymus	45	0.89	0.627	0.95	0.532	1.48	0.039
Negative regulation of endopeptidase activity	57	0.89	0.670	-0.92	0.667	1.69	0.002
I-κB kinase/NF-κB signaling	88	0.88	0.674	0.81	0.816	1.67	0.002
Regulation of mRNA stability	17	0.88	0.711	0.86	0.743	1.71	0.000
Innate immune response	21	0.88	0.718	0.90	0.691	1.39	0.012
BMP signaling pathway	358	0.86	0.707	0.81	0.803	1.61	0.004
Cellular protein modification process	19	0.83	0.775	-0.81	0.845	1.48	0.008
Protein localization	23	0.82	0.770	-0.94	0.571	1.47	0.022
Histone acetylation	22	0.81	0.732	1.01	0.453	1.50	0.039
Eye development	27	0.81	0.756	0.85	0.703	1.63	0.019
Negative regulation of fat cell differentiation	83	0.81	0.780	-0.88	0.609	1.53	0.025
Fat cell differentiation	87	0.78	0.851	0.76	0.878	1.45	0.023
Histone H3-K4 trimethylation	70	0.78	0.744	0.79	0.767	1.46	0.043
Positive regulation of gene expression	61	0.78	0.915	0.81	0.866	1.37	0.039
Proton transmembrane transport	62	0.76	0.845	0.72	0.922	1.40	0.043
Detection of chemical stimulus involved in sensory perception of bitter taste	46	0.76	0.841	-0.72	0.893	1.52	0.024
Adult behavior	20	0.70	0.899	-0.65	0.936	1.53	0.035
Glycogen metabolic process	215	0.68	0.925	-0.48	1.000	1.70	0.016
Platelet formation	15	0.66	0.926	0.71	0.852	1.54	0.032
Apoptotic cell clearance	66	-1.80	0.002	-1.75	0.005	0.91	0.584
Mitotic sister chromatid segregation	17	-1.77	0.003	-1.86	0.002	0.99	0.478
Response to lead ion	136	-1.70	0.008	-1.76	0.006	1.14	0.292
Cellular defense response	17	-1.69	0.004	-1.69	0.004	1.17	0.213
Regulation of translation	16	-1.65	0.000	-1.74	0.000	-0.83	0.772
Positive regulation of cardiac muscle hypertrophy	74	-1.65	0.008	-1.53	0.035	0.94	0.531
Innate immune response in mucosa	20	-1.64	0.025	-1.64	0.020	0.98	0.475
Modulation of chemical synaptic transmission	27	-1.62	0.019	-1.62	0.033	-0.64	0.876
Motor neuron axon guidance	45	-1.61	0.034	-1.55	0.023	-0.78	0.740
Smooth muscle contraction	56	-1.61	0.014	-1.39	0.084	-0.85	0.671
Positive regulation of activated T cell proliferation	23	-1.61	0.011	-1.57	0.032	0.81	0.723
Regulation of microtubule cytoskeleton organization	24	-1.60	0.009	-1.51	0.046	-0.71	0.863
Filopodium assembly	48	-1.60	0.027	-1.60	0.032	1.48	0.079
ATP-dependent chromatin remodeling	18	-1.60	0.025	-1.58	0.028	-0.66	0.919
Positive regulation of cytokine secretion	23	-1.60	0.026	-1.64	0.025	-0.87	0.648
Positive regulation of protein kinase activity	28	-1.60	0.014	-1.62	0.013	0.83	0.754
Substantia nigra development	27	-1.59	0.010	-1.61	0.008	-0.99	0.449
Retinoic acid receptor signaling pathway	17	-1.58	0.043	-1.52	0.064	-0.79	0.733
Cellular response to glucose starvation	19	-1.58	0.018	-1.55	0.033	-0.74	0.823
Myeloid cell differentiation	16	-1.56	0.031	-1.56	0.032	-0.86	0.686
Response to peptide hormone	72	-1.55	0.012	-1.53	0.011	-0.77	0.848
Positive regulation of synaptic transmission, glutamatergic	16	-1.55	0.043	-1.50	0.056	0.63	0.942
Cellular response to nerve growth factor stimulus	15	-1.55	0.020	-1.56	0.032	1.09	0.317
Negative regulation of signal transduction	42	-1.55	0.027	-1.49	0.020	-0.90	0.632
Peptide hormone processing	19	-1.54	0.036	-1.65	0.018	-0.70	0.868
Response to endoplasmic reticulum stress	38	-1.54	0.019	-1.52	0.017	1.10	0.315
Positive regulation of cellular protein metabolic process	153	-1.52	0.044	-1.50	0.043	0.99	0.464
Negative regulation of neuron projection development	23	-1.52	0.019	-1.56	0.002	1.13	0.257
Positive regulation of release of sequestered calcium ion into cytosol	20	-1.50	0.028	-1.53	0.037	1.13	0.262
Action potential	45	-1.50	0.037	-1.62	0.023	-0.65	0.929
Response to vitamin D	28	-1.49	0.037	-1.58	0.030	1.33	0.136
Positive regulation of macrophage derived foam cell differentiation	17	-1.49	0.052	-1.52	0.047	0.63	0.920
Regulation of actin cytoskeleton organization	82	-1.48	0.041	-1.51	0.030	1.39	0.090
Positive regulation of cell growth	23	-1.46	0.034	-1.56	0.013	1.19	0.210
Negative regulation of tumor necrosis factor production	31	-1.46	0.050	-1.42	0.047	0.72	0.882
Negative regulation of cell-substrate adhesion	45	-1.46	0.080	-1.46	0.048	1.43	0.100
Ribosome biogenesis	75	-1.46	0.038	-1.41	0.084	0.95	0.507
Microtubule-based process	39	-1.44	0.044	-1.50	0.037	0.50	1.000

Table SI. Continued.

Name	Gene counts	CFB-high vs. Control		CFB-low vs. Control		CFB-high vs. CFB-low	
		NES	P-value	NES	P-value	NES	P-value
Response to glucocorticoid	81	-1.43	0.036	-1.31	0.102	1.10	0.305
Interleukin-12-mediated signaling pathway	49	-1.43	0.037	-1.49	0.023	0.80	0.809
Positive regulation of protein binding	129	-1.42	0.032	-1.44	0.028	0.83	0.772
Regulation of synaptic plasticity	24	-1.42	0.071	-1.53	0.032	0.74	0.869
Oligodendrocyte development	32	-1.41	0.072	-1.53	0.027	-0.85	0.694
Receptor internalization	118	-1.41	0.062	-1.46	0.038	0.90	0.632
SMAD protein signal transduction	60	-1.38	0.046	-1.43	0.052	1.32	0.113
Response to vitamin A	63	-1.38	0.101	-1.49	0.043	1.55	0.027
Cell cycle arrest	147	-1.37	0.031	-1.38	0.075	1.13	0.260
Negative regulation of neuron differentiation	25	-1.37	0.058	-1.41	0.032	-0.89	0.648
Hippocampus development	16	-1.37	0.068	-1.45	0.016	0.97	0.522
Positive regulation of gene expression, epigenetic	21	-1.37	0.091	-1.47	0.026	1.40	0.072
Positive regulation of DNA replication	23	-1.36	0.094	-1.46	0.044	1.07	0.377
Melanosome organization	85	-1.36	0.122	-1.37	0.103	1.68	0.016
Positive regulation of stress-activated MAPK cascade	27	-1.35	0.103	-1.39	0.112	1.66	0.017
Cholesterol biosynthetic process	49	-1.35	0.062	-1.44	0.045	0.99	0.428
Inositol phosphate metabolic process	45	-1.35	0.083	-1.44	0.028	0.88	0.688
Ovarian follicle development	476	-1.34	0.080	-1.27	0.133	1.46	0.029
Inactivation of MAPK activity	15	-1.32	0.118	-1.21	0.205	-1.53	0.032
Orotein dephosphorylation	124	-1.32	0.049	-1.34	0.048	1.33	0.080
Cellular response to epidermal growth factor stimulus	23	-1.30	0.101	-1.43	0.049	1.04	0.396
Protein homooligomerization	42	-1.29	0.047	-1.33	0.053	1.14	0.220
Positive regulation of fibroblast proliferation	32	-1.29	0.143	-1.44	0.042	0.93	0.576
Ubiquitin-dependent protein catabolic process	51	-1.27	0.078	-1.38	0.029	1.44	0.013
Actin cytoskeleton organization	56	-1.23	0.111	-1.26	0.096	1.69	0.000
Regulation of autophagy	62	-1.23	0.170	-1.20	0.190	1.43	0.041
Astrocyte development	63	-1.21	0.191	-1.18	0.221	1.48	0.043
Regulation of endocytosis	53	-1.20	0.192	-1.35	0.088	1.52	0.026
Electron transport chain	15	-1.16	0.227	-1.18	0.174	1.59	0.010
Regulation of proteasomal protein catabolic process	19	-1.16	0.247	-1.18	0.214	1.73	0.002
Fatty acid β-oxidation using acyl-CoA dehydrogenase	20	-1.15	0.266	-1.27	0.143	1.74	0.004
Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	54	-1.11	0.273	-1.13	0.239	1.60	0.011
Transforming growth factor β receptor signaling pathway	27	-1.09	0.315	-1.10	0.292	1.48	0.014
Mitotic cell cycle	15	-1.08	0.290	-1.10	0.278	1.58	0.008
Nucleocytoplasmic transport	17	-1.06	0.351	-1.07	0.369	1.85	0.002
Macroautophagy	19	-1.03	0.407	-1.13	0.200	1.57	0.004
Potassium ion transmembrane transport	16	-1.03	0.399	-1.02	0.410	1.38	0.019
Protein folding	32	-1.01	0.415	-1.09	0.288	1.39	0.028
Antimicrobial humoral response	42	-1.01	0.429	-1.16	0.225	1.64	0.014
mRNA splicing, via spliceosome	20	-1.01	0.413	-1.00	0.424	1.34	0.048
Positive regulation of peptidyl-threonine phosphorylation	15	-1.00	0.444	-1.20	0.215	1.50	0.038
Neural crest cell migration	19	-0.99	0.458	-0.95	0.528	-1.98	0.000
Regulation of sodium ion transmembrane transporter activity	24	-0.97	0.508	0.97	0.485	-1.57	0.016
Negative regulation of transcription, DNA-templated	15	-0.93	0.609	-1.00	0.457	1.38	0.027
Cytoplasmic translation	15	-0.91	0.614	-0.85	0.716	1.73	0.002
Negative regulation of telomere maintenance via telomerase	35	-0.89	0.620	-1.15	0.251	1.58	0.012
Potassium ion transport	15	-0.88	0.706	-0.90	0.673	1.43	0.034
Sister chromatid cohesion	110	-0.83	0.823	-0.92	0.630	1.54	0.002
Branching morphogenesis of an epithelial tube	40	-0.82	0.724	-0.91	0.573	1.54	0.045
Negative regulation of peptidyl-serine phosphorylation	15	-0.81	0.752	-0.90	0.622	1.67	0.022
Antigen processing and presentation	15	-0.80	0.753	-0.79	0.769	1.61	0.010
Somatic stem cell population maintenance	69	-0.80	0.828	-0.83	0.800	1.57	0.006
Circadian regulation of gene expression	73	-0.78	0.853	-0.88	0.685	1.46	0.020
Positive regulation of long-term synaptic potentiation	19	-0.71	0.860	-0.75	0.812	1.73	0.010
Calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules	15	-0.65	0.927	-0.69	0.883	1.80	0.004

CFB, complement factor B; NES, normalized enrichment score.

Table SII. Gene set enrichment analysis results of hallmark pathways in three comparisons.

		CFB-high vs. Control		CFB-low vs. Control		CFB-high vs. CFB-low	
Name	Gene counts	NES	P-value	NES	P-value	NES	P-value
Adipogenesis	95	1.13	0.229	1.10	0.264	1.35	0.039
Cholesterol homeostasis	199	1.25	0.174	1.42	0.045	1.11	0.275
Estrogen response late	200	1.05	0.364	0.98	0.498	1.46	0.006
Fatty acid metabolism	198	-1.52	0.032	-1.47	0.047	0.64	0.936
Glycolysis	112	-1.35	0.048	-1.38	0.037	1.23	0.137
Heme metabolism	199	-1.00	0.459	-0.99	0.451	1.38	0.018
Hypoxia	36	1.26	0.072	1.31	0.046	1.39	0.020
KRAS signaling up	42	-0.93	0.591	-0.99	0.457	1.59	0.002
Mitotic spindle	198	1.19	0.236	1.30	0.127	1.50	0.024
Myogenesis	109	0.98	0.512	0.92	0.650	1.38	0.027
Oxidative phosphorylation	193	-1.38	0.014	-1.37	0.025	1.14	0.218
TNFA signaling via NF-κB	98	1.51	0.022	1.55	0.011	1.10	0.291
Unfolded protein response	197	0.90	0.661	0.84	0.791	1.31	0.039
Wnt/β-catenin signaling	196	1.19	0.169	1.20	0.149	1.44	0.023

CFB, complement factor B; NES, normalized enrichment score.