

Table SI. Clinical characteristics of the patients (n=34).

Clinical index	Patients, n
Sex	
Male	0
Female	34
Age, years	
≤60	18
>60	16
Tumor size, cm ^a	
≤5	11
>5	20
Pathological grade	
I-II	8
III	26
Groups	
Endometrioid adenocarcinoma	34
Others	0

^aInformation was missing for 3 patients.

Table SII. Pathways positively correlated with ISG15 expression.

Name	Gs follow link to MSigDB	Size, bp	Es	Nes	Nom P-value	Fdr q-value	Fwer P-value	Rank at	Leading edge		
									Tags, %	List, %	Signal, %
HALLMARK_INTERFERON_ALPHA_RESPONSE	HALLMARK_INTERFERON_ALPHA_RESPONSE	95	0.8515657	3.7976868	0.000	0.00	0.000	1,167	74	6	78
HALLMARK_INTERFERON_GAMMA_RESPONSE	HALLMARK_INTERFERON_GAMMA_RESPONSE	197	0.7432788	3.7423754	0.000	0.00	0.000	1,435	53	7	56
HALLMARK_ALLOGRAFT_REJECTION	HALLMARK_ALLOGRAFT_REJECTION	200	0.4794209	2.4210489	0.000	0.00	0.000	4,511	49	22	63
HALLMARK_OXIDATIVE_PHOSPHORYLATION	HALLMARK_OXIDATIVE_PHOSPHORYLATION	200	0.4235511	2.1354530	0.000	0.00	0.000	3,054	36	15	41
HALLMARK_MYC_TARGETS_V2	HALLMARK_MYC_TARGETS_V2	58	0.5037472	2.1111012	0.000	0.00	0.000	4,205	50	21	63
HALLMARK_IL6_JAK_STAT3_SIGNALING	HALLMARK_IL6_JAK_STAT3_SIGNALING	86	0.4581528	2.0442474	0.000	0.00	0.000	4,100	42	20	52
HALLMARK_UV_RESPONSE_UP	HALLMARK_UV_RESPONSE_UP	158	0.3962218	1.9225634	0.000	1.67x10 ⁻⁴	0.001	3,835	37	19	46
HALLMARK_INFLAMMATORY_RESPONSE	HALLMARK_INFLAMMATORY_RESPONSE	200	0.3550082	1.8253767	0.000	6.17 x10 ⁻⁴	0.004	4,579	34	23	44
HALLMARK_DNA_REPAIR	HALLMARK_DNA_REPAIR	149	0.3542266	1.7263566	0.000	0.00	0.012	3,923	35	20	43
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	49	0.4366076	1.7259257	0.002	0.00	0.012	3,970	39	20	48
HALLMARK_COMPLEMENT	HALLMARK_COMPLEMENT	199	0.3247297	1.6491816	0.000	0.00	0.028	2,828	24	14	28

HALLMARK_MYOGENESIS	HALLMARK_MYOGENESIS	200	0.3097104	1.5781847	0.000	0.01	0.069	5,432	38	27	52
HALLMARK_KRAS_SIGNALING_DN	HALLMARK_KRAS_SIGNALING_DN	199	0.2659020	1.3470829	0.009	0.07	0.547	6,485	41	32	60
HALLMARK_IL2_STAT5_SIGNALING	HALLMARK_IL2_STAT5_SIGNALING	200	0.2531694	1.2905697	0.023	0.11	0.730	4,428	31	22	39
HALLMARK_COAGULATION	HALLMARK_COAGULATION	138	0.2666506	1.2881562	0.062	0.11	0.737	3,235	20	16	24
HALLMARK_MYC_TARGETS_V1	HALLMARK_MYC_TARGETS_V1	199	0.2471236	1.2437081	0.069	0.15	0.860	4,938	34	25	45
HALLMARK_ADIPOGENESIS	HALLMARK_ADIPOGENESIS	198	0.2436114	1.2364913	0.073	0.15	0.871	3,561	27	18	33
HALLMARK_TNFA_SIGNALING_VIA_NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	199	0.2426767	1.2302164	0.056	0.14	0.881	4,089	25	20	31
HALLMARK_APOPTOSIS	HALLMARK_APOPTOSIS	161	0.2492127	1.2236257	0.062	0.14	0.895	4,623	31	23	40
HALLMARK_P53_PATHWAY	HALLMARK_P53_PATHWAY	200	0.2402054	1.2220846	0.057	0.14	0.896	3,131	23	16	26
HALLMARK_ESTROGEN_RESPONSE_LATE	HALLMARK_ESTROGEN_RESPONSE_LATE	200	0.2141524	1.1045586	0.169	0.31	0.994	3,638	22	18	27
HALLMARK_APICAL_JUNCTION	HALLMARK_APICAL_JUNCTION	200	0.2154999	1.0955664	0.230	0.31	0.996	4,707	32	23	41
HALLMARK_E2F_TARGETS	HALLMARK_E2F_TARGETS	200	0.2102328	1.0677334	0.267	0.37	0.998	2,097	17	10	19
HALLMARK_FATTY_ACID_METABOLISM	HALLMARK_FATTY_ACID_METABOLISM	158	0.2165683	1.0472877	0.316	0.40	0.999	2,968	20	15	23
HALLMARK_GLYCOLYSIS	HALLMARK_GLYCOLYSIS	198	0.2005873	1.0246333	0.385	0.44	0.999	4,363	28	22	36
HALLMARK_CHOLESTEROL_HOMEOSTASIS	HALLMARK_CHOLESTEROL_HOMEOSTASIS	73	0.2411662	1.0244213	0.425	0.42	0.999	2,615	22	13	25

HALLMARK_XENOBIOTIC_METABOLISM	HALLMARK_XENOBIOTIC_METABOLISM	199	0.1904176	0.9650053	0.525	0.56	1.000	3,977	22	20	27
HALLMARK_APICAL_SURFACE	HALLMARK_APICAL_SURFACE	44	0.2315549	0.8984273	0.653	0.72	1.000	4,471	30	22	38

Es, enrichment score; Nes, corrected enrichment score, the average value of ES obtained by random combination of all ES/gene sets of a functional gene set; Nom, P-value, statistical significance of enrichment score obtained for a subset of functional genes; Fdr, false-discovery rate; Fwer, overall error rate.

Table SIII. Pathways negatively correlated with ISG15 expression.

Name	Gs follow link to MSigDB	Size, bp	Es	Nes	Nom P-value	Fdr q-value	Fwer P-value	Rank at	Leading edge		
									Tags, %	List, %	Signal, %
HALLMARK_PROTEIN_SECRETION	HALLMARK_PROTEIN_SECRETION	96	-0.5493212	-2.4794745	0.000	0.00	0.000	4,001	59	20	74
HALLMARK_UV_RESPONSE_DN	HALLMARK_UV_RESPONSE_DN	143	-0.4830128	-2.2644274	0.000	0.00	0.000	5,814	59	29	82
HALLMARK_ANDROGEN_RESPONSE	HALLMARK_ANDROGEN_RESPONSE	99	-0.4523616	-1.9953578	0.000	2.82x10 ⁻⁴	0.001	5,806	57	29	79
HALLMARK_TGF_BETA_SIGNALING	HALLMARK_TGF_BETA_SIGNALING	54	-0.4620373	-1.8210695	0.006	0.00	0.013	2,501	35	12	40
HALLMARK_MITOTIC_SPINDLE	HALLMARK_MITOTIC_SPINDLE	197	-0.3674066	-1.8008875	0.000	0.00	0.013	4,710	41	23	53
HALLMARK_WNT_BETA_CATENIN_SIGNALING	HALLMARK_WNT_BETA_CATENIN_SIGNALING	42	-0.3814488	-1.4363021	0.0462	0.06	0.351	5,230	43	26	58
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	112	-0.2928085	-1.3363515	0.040	0.12	0.647	3,388	30	17	36
HALLMARK_G2M_CHECKPOINT	HALLMARK_G2M_CHECKPOINT	198	-0.2658793	-1.3072953	0.022	0.13	0.737	3,904	28	19	35
HALLMARK_PEROXISOME	HALLMARK_PEROXISOME	103	-0.2844669	-1.2861072	0.064	0.15	0.811	3,155	28	16	33
HALLMARK_ESTROGEN_RESPONSE_EARLY	HALLMARK_ESTROGEN_RESPONSE_EARLY	199	-0.2592949	-1.2816657	0.054	0.14	0.829	5,345	33	27	45
HALLMARK_HEME_METABOLISM	HALLMARK_HEME_METABOLISM	195	-0.2557984	-1.2581391	0.035	0.15	0.883	3,881	27	19	33
HALLMARK_HEDGEHOG_SIGNALING	HALLMARK_HEDGEHOG_SIGNALING	36	-0.3437583	-1.2443161	0.155	0.16	0.912	6,296	53	31	77
HALLMARK_MTORC1_SIGNALING	HALLMARK_MTORC1_SIGNALING	199	-0.2316023	-1.1308786	0.198	0.35	0.999	3,882	29	19	35
HALLMARK_BILE_ACID_METABOLISM	HALLMARK_BILE_ACID_METABOLISM	112	-0.2435439	-1.1045178	0.261	0.38	1.000	3,214	23	16	27
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	199	-0.2231496	-1.1021316	0.202	0.36	1.000	6,217	41	31	58
HALLMARK_PI3K_AKT_MTOR_SIGNALING	HALLMARK_PI3K_AKT_MTOR_SIGNALING	105	-0.2316563	-1.0348167	0.364	0.52	1.000	3,954	28	20	34
HALLMARK_NOTCH_SIGNALING	HALLMARK_NOTCH_SIGNALING	32	-0.28804523	-1.0320185	0.416	0.49	1.000	3,212	22	16	26

NALING	NG										
HALLMARK_ANGIOGENESIS	HALLMARK_ANGIOGENESIS	36	-0.2739750	-0.9956932	0.463	0.56	1.000	5,591	39	28	54
HALLMARK_KRAS_SIGNALING_UP	HALLMARK_KRAS_SIGNALING_UP	200	-0.2013213	-0.9860147	0.490	0.56	1.000	3,863	23	19	28
HALLMARK_HYPOXIA	HALLMARK_HYPOXIA	200	-0.1917463	-0.9539720	0.591	0.62	1.000	6,139	36	31	51
HALLMARK_SPERMATOGENESIS	HALLMARK_SPERMATOGENESIS	133	-0.1693886	-0.7913756	0.919	0.96	1.000	3,507	15	17	18
HALLMARK_PANCREAS_BETA_CELLS	HALLMARK_PANCREAS_BETA_CELLS	40	-0.1850622	-0.6785498	0.935	0.99	1.000	6,463	33	32	48

Es, enrichment score; Nes, corrected enrichment score, the average value of ES obtained by random combination of all ES/gene sets of a functional gene set; Nom, P-value, statistical significance of enrichment score obtained for a subset of functional genes; Fdr, false-discovery rate; Fwer, overall error rate.