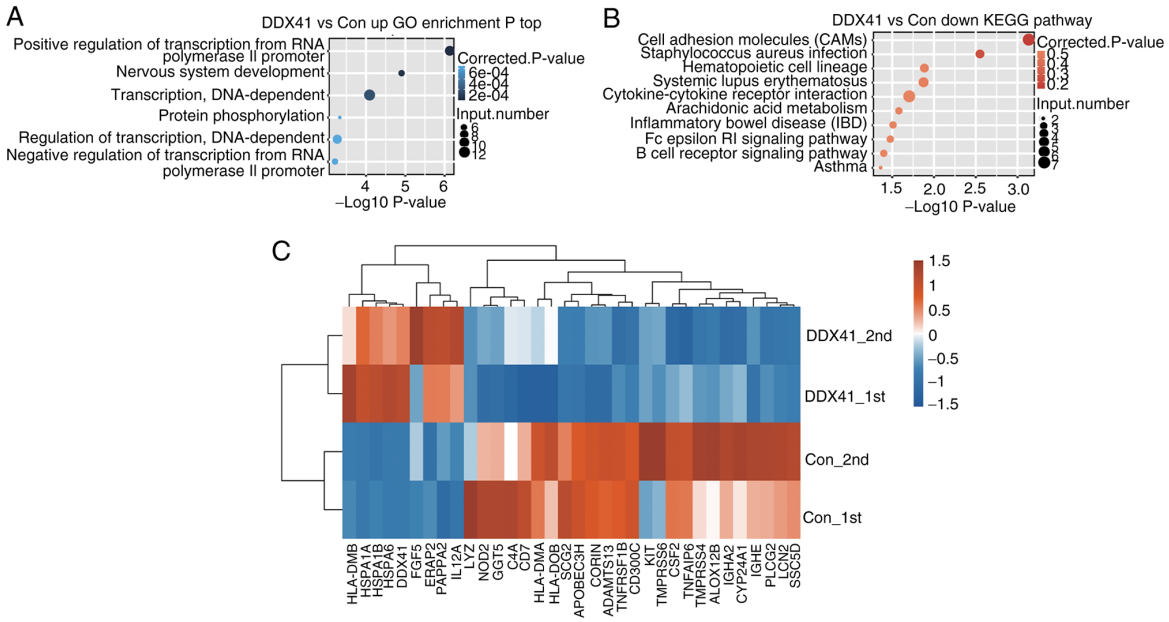

Figure S1. Analysis of immune-associated gene expression levels regulated by DDX41. (A) Top ten GO terms of upregulated gene sets. (B) Top ten KEGG pathways of downregulated gene sets. (C) Hierarchical clustering of the expression of immune-associated differentially expressed genes regulated by DDX41 overexpression in HeLa cells compared with Ctrl. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; DDX41, DEAD-box helicase 41; Ctrl, control.

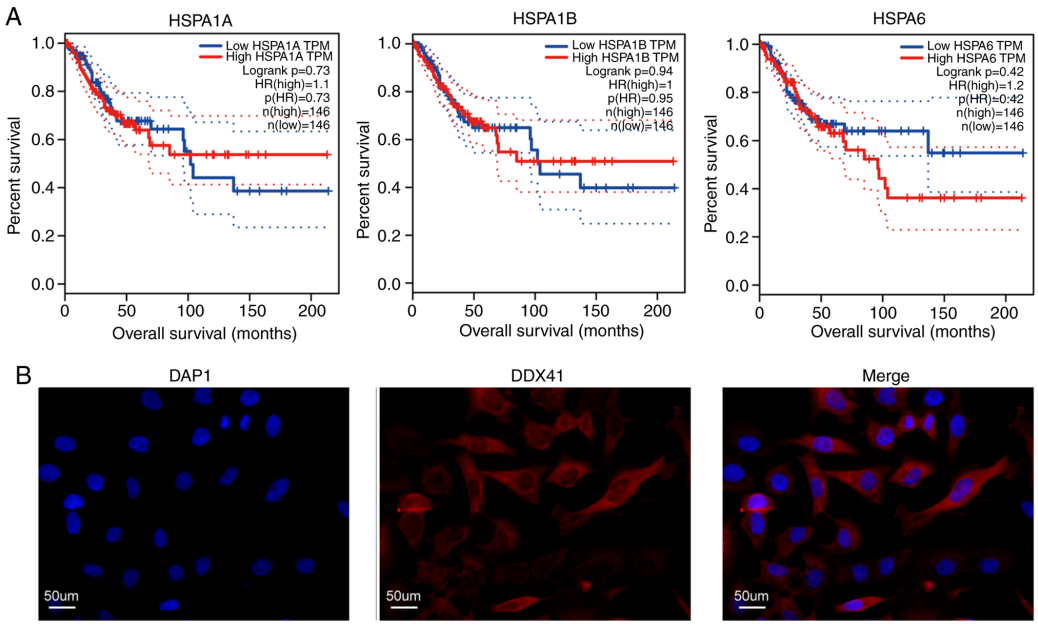

Figure S2. Kaplan-Meier curves of DDX41 upregulated genes in patients with cervical cancer. (A) Survival analysis of two genes in the Gene Expression Profiling Interactive Analysis databases of cervical and endocervical squamous carcinoma (cut-off point based on the median method). (B) Images of the DDX41 distribution (n=3). DDX41, DEAD-box helicase 41; HR, hazard ratio.

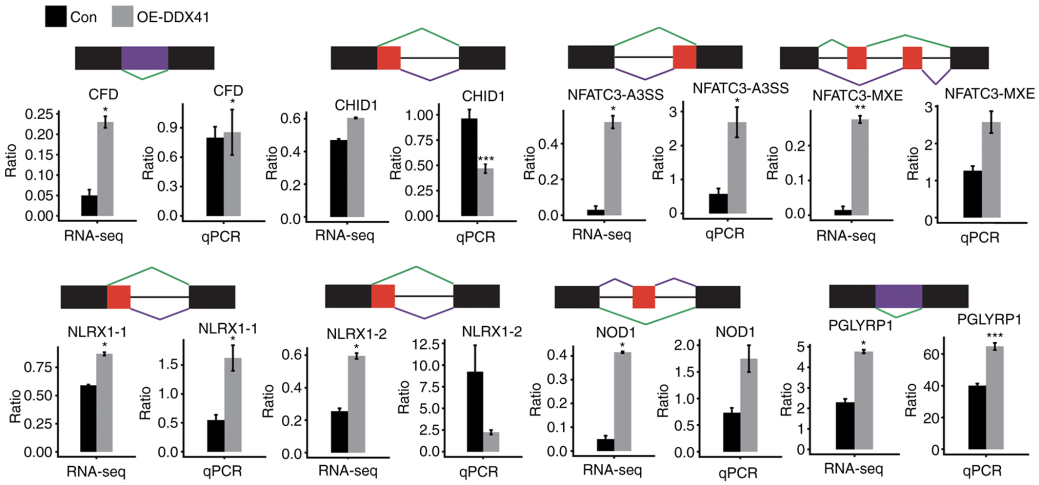

Figure S3. Schematic diagrams depicting the structures of AS1 (purple) and AS2 (green). Boxes indicate exon sequences; horizontal line indicates intron sequences. RNA-seq quantification and qPCR validation of ASEs. The changed ratio of ASEs in RNA-seq were calculated using the formula: AS1 junction reads/AS1 junction reads + AS2 junction reads. The altered ratio of ASEs in qPCR was calculated using the formula: AS1 transcripts level/AS2 transcripts level. Con, control; OE-DDX41, overexpression DEAD-box helicase 41; RNA-seq, RNA-sequencing; qPCR, quantitative PCR.

Table SI. Primers used in reverse transcription-quantitative PCR.

A, Overexpression

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
DDX41	GTATCCCACCACCCATCAAG	ACCAGTGTCTTGCCTGAACC

B, Differentially expressed genes

Gene	Forward primer	Reverse primer
IL12A	ATTGAGATGGGAGGATTG	CAGACATATTGTCCAGGCT
CD22	GGCCTTTTCCACCTCATA	GGATCGGATACCCATAGC
CD177	ACGGAGGCCAAGGACCAG	CCAAAGCGGGAGGGAGTT
CSF2	GACCTGCCTACAGACCCG	GGCCCTTGAGCTTGGTGA
SELPLG	GCCGTCAGTCGAGTTGTC	CAGCAGCTATGGAGATACAG
TNFRSF1B	GCACTCGGGAACAGAACC	GCACCCCTCCTGCTTGCT
HSPA1A	CGTTGTCCCAAGGCTTCC	CTGTCGGCTCCGCTCTGA
HSPA1B	GCTGAACCCGCAGAACAC	TCCTCGGGGTAGAATGCC
HSPA6	CGGTGCAGTCGGACATGA	TCTCCTCGGGGTAGAACG
HLA-DMB	GCCATCTTATTCTCCTCTG	TGGAAAGCACCTGTCTGT
HLA-DOB	ATCCACGGCCTGTCTGCT	GTGATGTGGGGATGTTTG
HLA-G	TCTACCCTGCGGAGATCA	CTCCAGAAGGCACCACCA
HPV18-E6	ATAAGGTGCCTGCGGTGCC	TGCGTCGTTGGAGTCGTTC
HPV18-E7	GAGCACGACAGGAACGACT	GGGCTGGTAAATGTTGATGAT
HPV18-L1	CAGGTGGTGGCAATAAGCAGGA	TGGCGGCATGGGAACTTTCAG
GAPDH	GGTCGGAGTCAACGGATTTG	GGAAGATGGTGATGGGATTTC

C, Alternative splicing events

Gene		Forward primer	Reverse primer
CFD	AS1	TGGAGGACGCGGCCGACGGG	AGCAGGAGGTCGTGGTCG
	AS2	GGTCCCCAGGGGCCGACGGG	
PGLYRP1	AS1	CCAATTCTGGATGAGGTGGTA	AACTACATGGATCGGGTGCC
	AS2		CCTCCTCCAGATCGGGTGCC
NEATC3_A3SS	AS1	CAGCACTCAACTCAAGCA	GTAAACAAATCATCATCTAA
	AS2		TAGGTCTCAACATCATCTAA
NEATC3_MEX	AS1		
	AS2	CAGCACTCAACTCAAGCA	ATAAATTGGTCATCATCTAA
			TAGGTCTCAACATCATCTAA

Table SI. Continued.

C, Alternative splicing events

Gene		Forward primer	Reverse primer
NOD1	AS1	TACGCTGAGTCTGAGAACAG	CTACTGCAACGCCTGCTC
	AS2	GACCTCTGCCCTGAGAACAG	
ZC3HAV1	AS1	AAGCGGACAACCCTTACA	CTTGTTAACGATTCTTTATC
	AS2	TCTGCTCAGTATTCTTTATC	
IFITM1	AS1	GACAAGTGAGCCAGAAGATG	TTGAACAGGGACCAGACG
	AS2	TCCCCAAAGCCCAGAAGATG	
TANK	AS1	TGGAGAAGAGACCTGTCATT	CTGCCGGAAGGCTTCATA
	AS2	CAAACGAGAGACCTGTCATT	
NLRX1-1	AS1	CTGCCTGAAGGACAGAAGTC	TCGCTGGAGTGCTCTTCT
	AS2	GCAGCCGCGGGACAGAAGTC	
NLRX1-2	AS1	CCGCTGCCAGGACAGAAGTC	TCGCTGGAGTGCTCTTCT
	AS2	GCGGGCGGAGGACAGAAGTC	
CHID1	AS1	GTCCAGAGGGCTGCATGTCA	AGCCCTGCCCAGTCCCCTGT
	AS2	GGGTGGAAATCTGCATGTCA	

Table SII. Summary of RNA-sequencing reads used.

Sample	Raw reads	Clean reads	Paired-end reads	Total mapped[a]	Total uniquely mapped[b]	Splice reads[c]
DDX41_1st	82863280	79800968	36767980	69908587 (90.62%)	67381207 (96.38%)	27164706 (40.31%)
DDX41_2nd	87014568	83839108	36659857	73033917 (90.06%)	70304018 (96.26%)	27599947 (39.26%)
Ctrl_1st	79477058	76304335	38572300	67176989 (91.35%)	64837664 (96.52%)	26594525 (41.02%)
Ctrl_2nd	79182390	76036977	40548512	66508088 (90.71%)	64019512 (96.26%)	25577536 (39.95%)

[a]Percentage of paired-end reads mapped to the genome. [b]Percentage of unique reads mapping out of the total mapped reads. [c]Percentage of uniquely mapped reads mapped to splice site. DDX41, DEAD-box helicase 41; Ctrl, control.

Table SIII. Numbers of genes expressed in each sample.

	Expressed genes	
Sample	FPKM>0	FPKM≥1
OECtrl_1st	24,499	13,173
OECtrl_2nd	25,045	13,164
DDX41_1st	24,618	12,892
DDX41_2nd	24,440	12,885
Total genes	28,914	

OE, overexpression; Ctrl, control; DDX41, DEAD-box helicase 41; FPKM, fragments per kilobase of transcript per million.