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# **Supplemental Information**

# A 70-Gene Signature for Predicting Treatment

#### **Outcome in Advanced-Stage Cervical Cancer**

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Figure S1. Validation of the 70-gene signature in independent data sets. (A-B) Incorporation of 70-gene signature into patients with RNA-seq of TCGA (A), microarray of GSE39001 and GSE52904 (B). Each group was classified by 70-gene signature into low- and high-risk, and evaluated by Kaplan-Meier analysis. The p values were computed by the log-rank test. (C). Heatmap of median centered 70-gene expression profiles between high- and low-risk groups in TCGA data sets (red, relative high expression; green, relative low expression). (D). Heatmap of median centered 70-gene expression profiles between high- and low-risk groups in TCGA data sets (red, relative high expression; green, relative low expression).

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### Figure S2. Survival analysis of patients under 65 years old by the 70-gene signature. (A-C)

The 70-gene signature was applied to patients under 65 years old (**A**), early-stage (**B**), advanced-stage (**C**). Each group was classified by 70-gene signature into low- and high-risk, and evaluated by Kaplan-Meier analysis. The p values were computed by the log-rank test.

# Figure S3.



Figure S3. Survival analysis by the treatment methods in patients with early-stage. (A) Patients were separated according to the conventional therapies; hysterectomy and/or radiotherapy. (B) Effect of additional chemotherapy with hysterectomy and radiotherapy. The p values were computed by the log-rank test. CT, chemotherapy; HT, hysterectomy; RT, radiotherapy

Figure S4.



# Advanced stage – chemoradation therapy

#### Figure S4. Survival analysis of advanced-stage patients treated with chemoradiation therapy

by the 70-gene signature. Incorporation of 70-gene signature into patients with chemoradiation therapy. Each group was classified by 70-gene signature into low- and high-risk, and evaluated by Kaplan-Meier analysis. The p values were computed by the log-rank test.

Figure S5.



# Figure S5. Work flowchart of the applied analysis

Table S1. Univariate and multivariate Cox proportional hazard regression of prognosiswith stage.

Variables -	Univariate			Multivariate		
	HR	95%CI	p value	HR	95%CI	<i>p</i> value
Stage (Stage IIB-IV)	3.547	2.466 - 5.103	8.8e-12	3.691	2.564 - 5.313	2.2e-12
Signature (High risk)	2.265	1.566 - 3.275	1.4e-05	2.369	1.637 – 3.428	4.8e-06

HR, Hazard Ratio; CI, Confidence Interval; the Wald test was used to estimate *p*-values. All

statistical tests were two-sided.

Variables _	Univariate			Multivariate		
	HR	95%CI	p value	HR	95%CI	p value
Size	3 703	1.917 - 7.152	0.70.05	2 724	1.397 – 5.311	0 00326
(≥4 cm)	5.705		9.76-05	2.724		0.00320
Signature	6760	2.632 -17.409	7 2 . 05	5 401	2.108 - 14.304	0.00040
(High-risk)	0.769		7.3e-05	5.491		0.00049

Table S2. Univariate and multivariate Cox proportional hazard regression analysis ofprognosis with size.

HR, Hazard Ratio; CI, Confidence Interval; the Wald test was used to estimate *p*-values. All

statistical tests were two-sided.

Variables	Univariate			Multivariate		
	HR	95%CI	<i>p</i> value	HR	95%CI	p value
Age under 65year (Advanced Stage)	2.144	1.346-3.416	0.0013	2.048	1.284-3.265	0.0033
Signature(high)	2.134	1.328 -3.432	0.0017	2.095	1.303 - 3.368	0.0023

 Table S3. Univariate and multivariate Cox proportional hazard regression analysis of prognosis.

HR, Hazard Ratio; CI, Confidence Interval; the Wald test was used to estimate p-values. All

statistical tests were two-sided.

## Table S5. Cervical cancer RNA expression data sets.

GEO Number	Origin /Year	Chip type	References
TCGA		IlluminaHiSeq	
GSE39001	Mexico 2013	Affymetrix Human HG-Focus Target Array	Espinosa et al.
GSE44001	Korea 2013	Illumina HumanHT-12 WG-DASL V4.0 R2 expression beadchip	Lee et al.
GSE52904	Mexico 2015	Affymetrix Human Gene 1.0 ST Array [transcript (gene) version]	Medina- Martinez et al.