

## Supplementary materials

### Supplementary Table Legends

**Table S1.** Methodological quality of the included studies based on the Newcastle-Ottawa Scale.

**Table S2.** (A) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* amplification and overall survival; (B) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* amplification and progression free survival.

**Table S3.** (A) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and overall survival; (B) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and progression free survival; (C) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and recurrence free survival; (D) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and cancer specific survival. (E) Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and distant metastasis free survival.

**Table S1.** Methodological quality of the included studies based on the Newcastle-Ottawa Scale

Study	Design	Selection	Comparability	Outcome/exposure	Overall quality(max=9)
Ayhan A(2016)	Cohort	★★★ <sup>a</sup>	★★	★★	8
Nakayama K(2015)	Cohort	★★★★	★★	★★	8
Pils D(2014)	Cohort	★★★	★★	★★	7
TCGA(2011)	Cohort	★★★	★★	★★★	8
Nakayama N(2010)	Cohort	★★★	★★	★	6
Luhtala S(2016)	Cohort	★★★	★	★★	6
Zhou Z(2014)	Cohort	★★★★	★★	★★	8
Wu S(2014)	Cohort	★★★	★★	★★★	8
Farley J(2003)	Cohort	★★★	★★	★	6
Shariat SF(2006)	Cohort	★★★★	★★	★★	8
Chappuis PO(2005)	Cohort	★★★	★	★★	6
Lotan Y(2013)	Cohort	★★★★	★★	★★	8
Lundgren C(2015)	Case-control	★★★★	★★	★	7
Matsushita R(2015)	Cohort	★★★	★★	★	6
Marchini S(2008)	Cohort	★★★★	★★	★	7
Sieuwerts AM(2006)	Cohort	★★★	★★	★★★	8
Jansen MP(2011)	Cohort	★★★	★	★★	6
Kreike B(2010)	Cohort	★★★	★★	★★★	8
Desmedt C(2006)	Cohort	★★★	★	★★★	7
Fredholm H(2017)	Cohort	★★★	★★	★★★	8

a: each asterisk represents if individual criterion within the subsection was fulfilled.

**Table S2A.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* amplification and overall survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of involved Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.59	1.05 to 2.40	0.027	75%	0.003	5
<b>Tumor type</b>						
<b>ovarian cancer</b>	1.46	0.98 to 2.18	0.064	76.5%	0.005	4
<b>endometrial carcinomas</b>	3.80	1.02 to 14.22	0.047	/	/	1
<b>Analysis methods</b>						
<b>Univariate analysis</b>	1.22	0.90 to 1.65	0.193	61.8%	0.073	3
<b>Multivariate analysis</b>	3.45	1.76 to 6.77	< 0.001	0	0.867	2
<b>Method</b>						
<b>FISH</b>	2.46	1.33 to 4.56	0.004	23.8%	0.269	3
<b>PCR</b>	1.03	0.90 to 1.17	0.659	/	/	1
<b>Microarray</b>	1.49	1.10 to 2.01	0.009	/	/	1
<b>Region</b>						
<b>North America</b>	1.49	1.10 to 2.01	0.009	/	/	1
<b>Europe</b>	1.03	0.90 to 1.17	0.659	/	/	1
<b>Asia</b>	3.45	1.76 to 6.77	< 0.001	0	0.867	2
<b>Mixed</b>	1.42	0.61 to 3.30	0.415	/	/	1
<b>Source of HR</b>						
<b>Survival curve</b>	1.49	1.10 to 2.01	0.009	/	/	1
<b>Reported</b>	1.83	0.91 to 3.67	0.090	75.7%	0.006	4
<b>Research center</b>						
<b>Single</b>	3.45	1.76 to 6.77	< 0.001	0	0.867	2
<b>Multicenter</b>	1.22	0.90 to 1.65	0.193	61.8%	0.073	3
<b>Quality</b>						
<b>&gt; 7</b>	1.54	1.17 to 2.04	0.002	0	0.390	3
<b>&lt;=7</b>	1.73	0.55 to 5.44	0.345	88.1%	0.004	2

**Table S2B.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* amplification and progression free survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of involved Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.49	0.83 to 2.67	0.177	62.3%	0.07	3
<b>Tumor type</b>						
<b>ovarian cancer</b>	1.41	0.71 to 2.80	0.328	75.5%	0.043	2
<b>endometrial carcinomas</b>	2.20	0.63 to 7.73	0.219	/	/	1
<b>Analysis methods</b>						
<b>Univariate analysis</b>	1.07	0.98 to 1.17	0.134	/	/	1
<b>Multivariate analysis</b>	2.20	1.20 to 4.04	0.011	0	1	2
<b>Method</b>						
<b>FISH</b>	2.20	1.20 to 4.04	0.011	0	1	2
<b>PCR</b>	1.07	0.98 to 1.17	0.134	/	/	1
<b>Region</b>						
<b>Europe</b>	1.07	0.98 to 1.17	0.134	/	/	1
<b>Asia</b>	2.20	1.20 to 4.04	0.011	0	1	2
<b>Source of HR</b>						
<b>Survival curve</b>	/	/		/	/	0
<b>Reported</b>	1.49	0.83 to 2.67	0.177	62.3%	0.07	3
<b>Research center</b>						
<b>Single</b>	2.20	1.20 to 4.04	0.011	0	1	2
<b>Multicenter</b>	1.07	0.98 to 1.17	0.134	/	/	1
<b>Quality</b>						
<b>&gt; 7</b>	2.20	0.63 to 7.73	0.219	/	/	1
<b>&lt;=7</b>	1.41	0.83 to 2.67	0.328	75.5%	0.043	2

**Table S3A.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and overall survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of involved Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.52	1.05 to 2.20	0.027	78.5%	<0.001	10
<b>Tumor type</b>						
<b>bladder cancer</b>	1.65	0.69 to 3.95	0.261	/	/	1
<b>ovarian cancer</b>	1.28	0.81 to 2.03	0.283	80.3%	<0.001	5
<b>breast cancer</b>	1.95	1.43 to 2.65	< 0.001	/	/	1
<b>endometrial carcinomas</b>	1.90	0.68 to 5.28	0.218	/	/	1
<b>esophageal adenocarcinoma</b>	0.96	0.49 to 1.89	0.906	/	/	1
<b>upper tract urothelial carcinoma</b>	36.27	4.24 to 310.09	0.001	/	/	1
<b>Analysis methods</b>						
<b>Univariate analysis</b>	1.44	0.97 to 2.14	0.069	0	0.545	4
<b>Multivariate analysis</b>	1.59	0.95 to 2.67	0.076	87.3%	<0.001	6
<b>Method</b>						
<b>IHC</b>	1.97	1.14 to 3.40	0.015	64.3%	0.016	6
<b>RT-qPCR</b>	1.19	0.69 to 2.06	0.529	87.8%	<0.001	4
<b>Microarray</b>	/	/	/	/	/	0
<b>Expression level</b>						
<b>protein</b>	1.97	1.14 to 3.40	0.015	64.3%	0.016	6
<b>mRNA</b>	1.19	0.69 to 2.06	0.529	87.8%	<0.001	4
<b>Region</b>						
<b>North America</b>	1.28	0.93 to 1.78	0.133	0	0.338	2
<b>Europe</b>	1.11	0.59 to 2.09	0.736	91.6%	<0.001	3
<b>Asia</b>	2.46	1.10 to 5.49	0.029	58.8%	0.064	4
<b>Mixed</b>	4	1.42 to 11.28	0.009	/	/	1
<b>Source of HR</b>						
<b>Survival curve</b>	1.18	0.69 to 2.01	0.552	0	0.337	2
<b>Reported</b>	1.62	1.05 to 2.50	0.029	82.9%	<0.001	8
<b>Research center</b>						
<b>Single</b>	1.58	0.98 to 2.56	0.063	59.9%	0.029	6
<b>Multicenter</b>	1.47	0.76 to 2.81	0.250	89.8%	<0.001	4
<b>Quality</b>						
<b>&gt; 7</b>	1.52	1.05 to 2.20	0.013	69.6%	0.011	5
<b>&lt;=7</b>	1.15	0.78 to 1.70	0.473	73.3%	0.005	5

**Table S3B.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and progression free survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of involved Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.20	1.07 to 1.34	0.001	41%	0.148	5
<b>Tumor type</b>						
ovarian cancer	1.14	0.97 to 1.34	0.109	65.6%	0.055	3
breast cancer	1.24	1.06 to 1.45	0.006	/	/	1
endometrial carcinomas	1.70	0.60 to 4.81	0.317	/	/	1
<b>Analysis methods</b>						
Univariate analysis	1.01	0.82 to 1.24	0.958	5.3%	0.348	3
Multivariate analysis	1.29	1.13 to 1.47	< 0.001	0	0.377	2
<b>Method</b>						
IHC	1.49	0.83 to 2.65	0.178	0	0.761	2
RT-qPCR	1.19	1.06 to 1.33	0.003	67.4%	0.047	3
<b>Microarray</b>	/	/	/	/	/	0
<b>Expression level</b>						
protein	1.49	0.83 to 2.65	0.178	0	0.761	2
mRNA	1.19	1.06 to 1.33	0.003	67.4%	0.047	3
<b>Region</b>						
Europe	1.19	1.06 to 1.33	0.003	67.4%	0.047	3
Asia	1.49	0.83 to 2.65	0.178	0	0.761	2
<b>Source of HR</b>						
Survival curve	/	/	/	/	/	0
Reported	1.20	1.07 to 1.34	0.001	41%	0.148	5
<b>Research center</b>						
Single	1.29	1.14 to 1.47	< 0.001	0	0.776	4
Multicenter	0.95	0.76 to 1.18	0.648	/	/	1
<b>Quality</b>						
> 7	1.70	0.60 to 4.81	0.317	/	/	1
<=7	1.19	1.07 to 1.33	0.002	52.7%	0.096	4

**Table S3C.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and recurrence free survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of involved Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.68	0.81 to 3.50	0.164	83%	<0.001	5
<b>Tumor type</b>						
breast cancer	2.01	1.08 to 3.71	0.027	48.4%	0.144	3
bladder cancer	1.25	0.29 to 5.43	0.766	86.6%	0.006	2
<b>Analysis methods</b>						
Univariate analysis	1.68	0.81 to 3.50	0.164	83%	<0.001	5
Multivariate analysis	/	/	/	/	/	0
<b>Method</b>						
IHC	1.19	0.53 to 2.67	0.672	78%	0.011	3
RT-qPCR	2.26	1.44 to 3.56	<0.001	/	/	1
Microarray	7.22	1.09 to 47.83	0.040	/	/	1
<b>Expression level</b>						
protein	1.19	0.53 to 2.67	0.672	78%	0.011	3
mRNA	2.77	1.17 to 6.58	0.021	27%	0.242	2
<b>Region</b>						
Europe	2.01	1.08 to 3.71	0.027	48.4%	0.144	3
North America	1.25	0.29 to 5.43	0.766	86.6%	0.006	2
<b>Source of HR</b>						
Survival curve	0.63	0.42 to 0.94	/	/	/	1
Reported	2.10	1.31 to 3.36	0.002	30.8%	0.228	4
<b>Research center</b>						
Single	1.68	0.81 to 3.50	0.164	83%	<0.001	5
Multicenter	/	/	/	/	/	0
<b>Quality</b>						
> 7	1.93	0.46 to 8.08	0.366	84.1%	0.002	3
<=7	1.78	1.02 to 3.11	0.042	50%	0.157	2

**Table S3D.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and cancer specific survival

	HR	95%CI	<i>p</i> value	Degree of heterogeneity		No. of included Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.54	0.74 to 3.18	0.246	90.4%	<0.001	4
<b>Tumor type</b>						
<b>bladder cancer</b>	1.14	0.20 to 6.50	0.884	87.1%	0.005	2
<b>breast cancer</b>	2.10	1.03 to 4.25	0.040	84.6%	0.011	2
<b>Analysis methods</b>						
<b>Univariate analysis</b>	1.54	0.74 to 3.18	0.246	90.4%	<0.001	4
<b>Multivariate analysis</b>	/	/	/	/	/	0
<b>Method</b>						
<b>IHC</b>	1.54	0.74 to 3.18	0.246	90.4%	<0.001	4
<b>RT-qPCR</b>	/	/	/	/	/	0
<b>Microarray</b>	/	/	/	/	/	0
<b>Expression level</b>						
<b>protein</b>	1.54	0.74 to 3.18	0.246	90.4%	<0.001	4
<b>mRNA</b>	/	/	/	/	/	0
<b>Region</b>						
<b>North America</b>	1.63	0.40 to 6.61	0.495	93.1%	<0.001	3
<b>Europe</b>	1.53	1.33 to 1.77	< 0.001	/	/	1
<b>Source of HR</b>						
<b>Survival curve</b>	1.26	0.21 to 7.58	0.800	96.2%	<0.001	2
<b>Reported</b>	1.66	1.07 to 2.57	0.022	21.8%	0.258	2
<b>Research center</b>						
<b>Single</b>	1.63	0.40 to 6.61	0.495	93.1%	<0.001	3
<b>Multicenter</b>	1.53	1.33 to 1.77	< 0.001	/	/	1
<b>Quality</b>						
<b>&gt; 7</b>	1.14	0.20 to 6.50	0.884	87.1%	0.005	2
<b>&lt;=7</b>	2.10	1.03 to 4.25	0.040	84.6%	0.011	2



**Table S3E.** Subgroup analyses stratified by some of the baseline characteristics for associations between *CCNE1* overexpression and distant metastasis free survival.

	HR	95% CI	<i>p</i> value	Degree of heterogeneity		No. of included Studies
				I <sup>2</sup> statistics	<i>p</i> value (Q test)	
<b>Total</b>	1.62	1.09 to 2.40	0.017	86.6%	0.001	3
<b>Tumor type</b>						
<b>breast cancer</b>	1.62	1.09 to 2.40	0.017	86.6%	0.001	3
<b>Analysis methods</b>						
<b>Univariate analysis</b>	1.33	1 to 1.77	0.051	69.8%	0.069	2
<b>Multivariate analysis</b>	2.65	1.89 to 3.71	< 0.001	/	/	1
<b>Method</b>						
<b>IHC</b>	1.33	1 to 1.77	0.051	69.8%	0.069	2
<b>RT-qPCR</b>	2.65	1.89 to 3.71	< 0.001	/	/	1
<b>Expression level</b>						
<b>protein</b>	1.33	1 to 1.77	0.051	69.8%	0.069	2
<b>mRNA</b>	2.65	1.89 to 3.71	< 0.001	/	/	1
<b>Region</b>						
<b>Europe</b>	1.62	1.09 to 2.40	0.017	86.6%	0.001	3
<b>Source of HR</b>						
<b>Reported</b>	1.62	1.09 to 2.40	0.017	86.6%	0.001	3
<b>Research center</b>						
<b>Single</b>	1.15	0.84 to 1.48	0.455	/	/	1
<b>Multicenter</b>	1.95	1.12 to 3.40	0.018	89.2%	0.002	2
<b>Quality</b>						
<b>&gt; 7</b>	1.71	0.73 to 4.00	0.215	93.2%	< 0.001	2
<b>&lt;=7</b>	1.50	1.30 to 1.73	< 0.001	/	/	1