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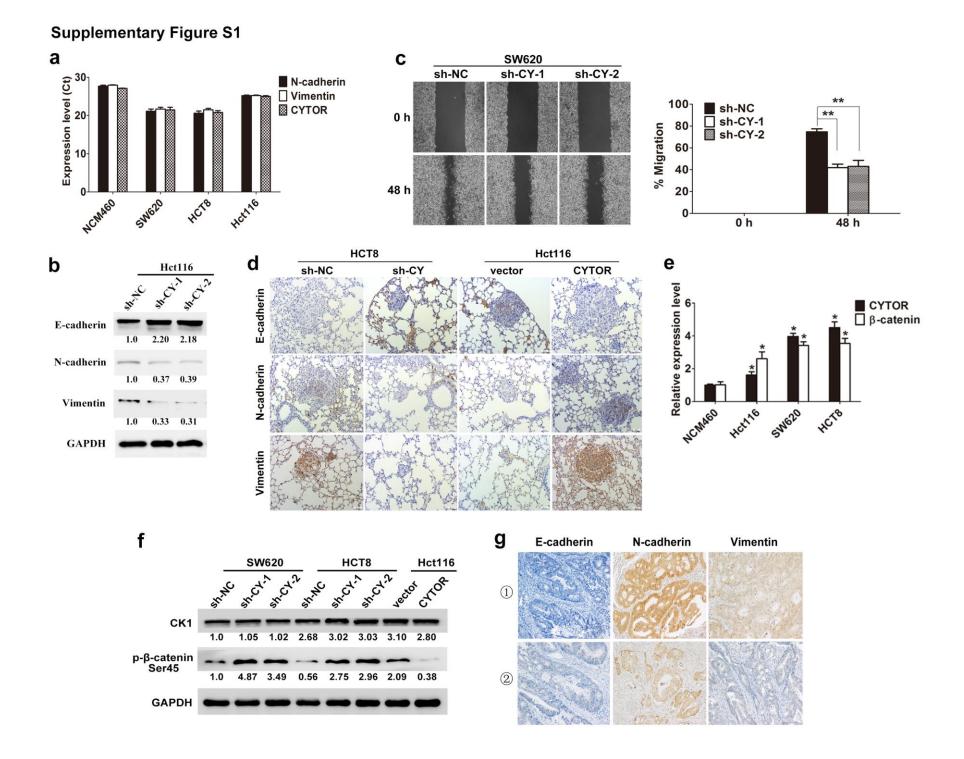
Supplemental Information

A Positive Feed-Forward Loop between

LncRNA-CYTOR and Wnt/β-Catenin Signaling

Promotes Metastasis of Colon Cancer

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Supplementary Fig S1. (a) The endogenous levels of CYTOR and mesenchymal markers N-cadherin and Vimentin were comparable in human colon mucosal epithelial cell line NCM460 and colon cancer cell lines. (b) Knockdown of CYTOR resulted in a significant upregulation of E-cadherin, accompanied by a prominent downregulation of N-cadherin and Vimentin in Hct116 cells. (c) Knockdown of CYTOR significantly decreased cells' migratory ability in SW620 cell line. (d) N-cadherin and Vimentin were reduced, and E-cadherin was upregulated in the lung metastatic tumor tissues with CYTOR knockdown. N-cadherin and Vimentin were upregulated, and E-cadherin was reduced in the lung metastatic tumor tissues with CYTOR overexpression. (e) β -catenin levels are relatively higher with concurrent elevated CYTOR in colon cancer cell lines. (f) Increased phosphorylation levels of β -catenin at Ser45 was observed in cells transfected with CYTOR shRNA, whereas overexpression of CYTOR significantly decreased phospho- β -catenin^{Ser45} expression. CK1 levels showed no obvious changes in the subgroups of every cell line. (g) ① CYTOR^{high}/ β -catenin^{nuc} group, ②CYTOR^{low}/ β -catenin^{cyto} tumor tissues. **P*<0.05, ***P*<0.01.

| Variable | n=100 | Expression | P value | |
|-----------------|-------|-------------|------------|----------|
| | | High (n=50) | Low (n=50) | |
| Age (years) | | | | 0.829 |
| <65 | 31 | 16 | 15 | |
| ≥65 | 69 | 34 | 35 | |
| Gender | | | | 0.841 |
| Male | 47 | 24 | 23 | |
| Female | 53 | 26 | 27 | |
| Location | | | | 0.216 |
| Right | 38 | 16 | 22 | |
| Others | 62 | 34 | 28 | |
| pT stage | | | | 0.033* |
| T1 | 3 | 1 | 2 | |
| T2 | 11 | 2 | 9 | |
| Т3 | 40 | 18 | 22 | |
| T4 | 46 | 29 | 17 | |
| pN stage | | | | < 0.001* |
| NO | 32 | 7 | 25 | |
| N1 | 40 | 23 | 17 | |
| N2 | 28 | 20 | 8 | |
| pM stage | | | | 0.006* |
| MO | 92 | 42 | 50 | |
| M1 | 8 | 8 | 0 | |
| TNM stage | | | | < 0.001* |
| I / II | 32 | 7 | 25 | |
| III/IV | 68 | 43 | 25 | |
| Differentiation | | | | 0.111 |
| Well | 47 | 21 | 26 | |
| Moderate | 40 | 19 | 21 | |
| Poor | 13 | 10 | 3 | |
| Vessel invasion | | | | 0.317 |
| No | 90 | 43 | 47 | |
| Yes | 10 | 7 | 3 | |

Supplementary Table S1. Association between clinicopathologic features and CYTOR expression

p<0.05 indicates a significant association among the variables.

| | | Overall survival | | | Disease-free survival | | | |
|-----------------|---------------------|------------------|--------------------|---------|-----------------------|---------|-------------------|----------------|
| Variable | Univariate | | Multivariate | | Univariate | | Multivariate | |
| | HR (95% CI) | <i>P</i> value | HR (95% CI) | P value | HR (95% CI) | P value | HR (95% CI) | <i>P</i> value |
| Age | 1.09 (0.54, 2.21) | 0.810 | | | 1.01 (0.51, 1.99) | 0.982 | | |
| Gender | 1.12 (0.59, 2.14) | 0.732 | | | 1.09 (0.58, 2.05) | 0.788 | | |
| Location | 0.97 (0.77, 1.23) | 0.800 | | | 1.02 (0.81, 1.28) | 0.878 | | |
| T stage | 1.73 (1.06, 2.82) | 0.028* | | | 1.89 (1.16, 3.08) | 0.011* | | |
| N stage | 3.69 (2.23, 6.11) | <0.001* | 2.93 (1.71, 5.04) | <0.001* | 3.57 (2.20, 5.79) | <0.001* | 2.73 (1.61, 4.64) | < 0.001* |
| M stage | 10.60 (4.31, 26.01) | <0.001* | 5.34 (2.07, 13.77) | 0.001* | 7.62 (3.33, 17.42) | <0.001* | 3.47 (1.44, 8.33) | 0.005* |
| TNM stage | 6.24 (3.07, 12.67) | <0.001* | | | 4.65 (2.51, 8.64) | <0.001* | | |
| Differentiation | 1.28 (0.81, 2.03) | 0.286 | | | 1.40 (0.90, 2.17) | 0.131 | | |
| Vessel invasion | 2.93 (1.28, 6.71) | 0.011* | | | 3.52 (1.61, 7.72) | 0.002* | 2.45 (1.10, 5.47) | 0.029* |
| CYTOR | 3.89 (1.88, 8.05) | < 0.001* | 2.32 (1.08, 4.98) | 0.031* | 3.86 (1.88, 7.94) | <0.001* | 2.22 (1.04, 4.73) | 0.039* |

Supplementary Table S2. Univariate and multivariate analysis of overall survival and disease-free survival after surgery

*P < 0.05 indicated that 95% CI of HR was not including. HR, hazard ratio; 95% CI, 95% confidence interval

| Supplementary Table S3 | 3. The correlation between ex | pression levels of CYTOR and | β -catenin in 100 cases of colon cancer tissues |
|------------------------|-------------------------------|------------------------------|---|
|------------------------|-------------------------------|------------------------------|---|

| Expression of CYTOR | | | |
|---------------------|-----------------------|---------------------------------|--|
| High | Low | <i>p</i> -value | |
| | | 0.006* | |
| 46 | 34 | | |
| 4 | 16 | | |
| | | 0.008* | |
| 36 | 17 | | |
| 10 | 17 | | |
| | High 46 4 36 | High Low 46 34 4 16 36 17 | |

p<0.05 indicates a significant association among the variables.

Supplementary Table S4. Detailed sequence (5'-3') information

| OVTOD | F | |
|------------|------------|---|
| CYTOR | Forward | TGGGAATGGAGGGAAATAAA |
| | Reverse | CCAGGAACTGTGCTGTGAAG |
| E-cadherin | Forward | GCCCC ATCAG GCCTC CGTTT |
| | Reverse | ACCTT GCCTT CTTTG TCTTT GTTGG A |
| GAPDH | Forward | GGAGCGAGATCCCTCCAAAAT |
| | Reverse | GGCTGTTGTCATACTTCTCAGG |
| | Forward | TGGACCATCACTCGGCTTA |
| N-cadherin | Reverse | ACACTGGCAAACCTTCACG |
| | Forward | CGAAACTTCTCAGCATCACG |
| Vimentin | Reverse | GCAGAAAGGCACTTGAAAGC |
| | Forward | TCATGCACCTTTGCGTGAGC |
| β-catenin | Reverse | GGCGCTGGGTATCCTGATGT |
| | Forward | TTCGGGTAGTGGAAAACCAG |
| c-myc | Reverse | CAGCAGCTCGAATTTCTTCC |
| | Forward | GTGCTGCGAAGTGGAAACC |
| cyclin D1 | Reverse | ATCCAGGTGGCGACGATCT |
| | sense | TGTCTGCATCCCTCGAATAACTTTCAAGAGAAGTTATTCGAGGGATGCAGACTTTTTTC |
| sh-CYTOR-1 | anti-sense | TCGAGAAAAAAGTCTGCATCCCTCGAATAACTTCTCTTGAAAGTTATTCGAGGGATGCAGACA |
| sh-CYTOR-2 | sense | TGACTCTGAGGCCTCTGCATTTCAAGAGAATGCAGAGGCCTCAGAGTCTTTTTTC |
| | anti-sense | TCGAGAAAAAAGACTCTGAGGCCTCTGCATTCTCTTGAAATGCAGAGGCCTCAGAGTCA |
| | Forward | CGCAAATGGGCGGTAGGCGTG |
| LV-CYTOR | Reverse | CATAGCGTAAAAGGAGCAACA |

Supplementary Table S5. Detailed sequence of Primers used for ChIP-PCR

| | Forward | TTCTAGTGGGGCTGCCACA |
|------|---------|----------------------|
| TBE1 | Reverse | AGCCTGCTGGTTTTCCAGAA |
| | Forward | AGGCTCCAAGGGCACCATTG |
| TBE2 | Reverse | GCCTCCCACAGCTTCAAGCA |
| | Forward | AATGATCCAGAAGGCTCCTA |
| Neg | Reverse | GCCAGCCTTTACCTTCTTTA |