Supplementary Tables

| | GDX | DX | CDZ | QXQ | XCZ | ZGT |
|-------------------|-------------|---------------|-------------|-------------|-------------|---------------|
| Gender | Male | Female | Male | Male | Female | Male |
| Age | 55 | 49 | 67 | 86 | 77 | 55 |
| Tumor types | Rectal | Rectal cancer | Rectal | Colon | Colon | Rectal cancer |
| | cancer | | cancer | cancer | cancer | |
| Pathological type | Adenocarcin | Adenocarcin | Adenocarcin | Adenocarcin | Adenocarcin | Adenocarcin |
| | oma | oma | oma | oma | oma | oma |
| Differentiation | Middle | Middle | Middle | Middle | Middle | Middle |
| degree | | | | | | |
| TNM stage | T2N1M0 | T2N1M0 | T3N2M0 | T2N2M0 | T3N1M0 | T2N1M0 |
| Tumor size | 4*3*1 | 2.5*2.5*0.5 | 2.5*2*0.5 | 4.6*3.5*1.7 | 1.7*1.5*1.3 | 3*3*1 |
| Lymph node | Yes | Yes | Yes | Yes | Yes | Yes |
| metastasis | | | | | | |
| Distant | No | No | No | No | No | No |
| metastasis | | | | | | |

Table S1 The clinical data of 6 pairs CRC tissues from patients

Table S2 The short reverse complementary sequences in circ1662 flank sequence

| Score | | Exp | ect | Identities | Gaps | Strand |
|--------|----------|-----------------|-----------|--------------|----------|-----------------------|
| 21.1 b | oits(22) |) 4.4 | | 11/11(100%) | 0/11(0%) | Plus/Minus |
| Query | 717 | ATACAGGTTTC | 727 | | | |
| Sbjct | 206 | ATACAGGTTTC | 196 | | | |
| Coore | | Eve | oct | Identities | Cana | Strand |
| Score | | Exp | ect | Identities | | Sulanu Dhua (Miana |
| 21.11 | oits(22 |) 4.4 | | 11/11(100%) | 0/11(0%) | Plus/Minus |
| Query | 1634 | GTATGTTGGCA | 1644 | | | |
| Sbjct | 1760 | GTATGTTGGCA | 1750 | | | |
| | | | | | | |
| Score | | Evn | oct | Identities | Cane | Strand |
| 22.01 | | LXP | ect | 12/12/1000() | | Suanu Dhua (Miana |
| 22.91 | JILS(24 |) 1.3 | | 12/12(100%) | 0/12(0%) | Plus/Minus |
| Query | 1758 | TAGTAAATAAT | [1769 | | | |
| Sbjct | 2091 | TAGTAAATAAT | 2080 | | | |
| | | | | | | |
| Score | | Exp | ect | Identities | Gaps | Strand |
| 21.1 b | its(22) | 4.4 | | 11/11(100%) | 0/11(0%) | Plus/Minus |
| Query | 1836 | AAGTTTTTTAAC | 1846 | · \ / | - · · / | |
| SUJCT | JZ40 | AAGIIIIAAU | 3Z30 | | | |

| Score Expect Identities Gaps Strand 24.7 bits(26) 0.36 16/18(89%) 0/18(0%) Plus/Minus Query 2036 ATTAAAAATATTTTAAAA 2053 Sbjet 2576 ATAAAAACATATTTTAAAA 2559 Score Expect Identities Gaps Strand 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 11111111111 1111111111 1111111111 11111111111 111111111111 111111111111 1111111111111 11111111111111111 11111111111111111111 111111111111111111111111111111111111 | Score Expect Identities Gaps 24.7 bits(26) 0.36 16/18(89%) 0/18(0 Query 2036 ATTAAAAATATTTTAAAA 2053 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | |
|---|--|------------------|
| 24.7 bits(26) 0.36 16/18(89%) 0/18(0%) Plus/Minus Query 2036 ATTAAAAATATTTTAAAA 2053 111111111111111111111111111111111111 | 24.7 bits(26) 0.36 16/18(89%) 0/18(6 Query 2036 ATTAAAAATATTTTAAAA 2053 Sbjct 2576 ATAAAAACATATTTTAAAA 2559 Score Expect Identities Gaps 23.8 bits(25) 1.3 14/15(93%) 0/15(6 Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTCTATCAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2455 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/17(0 Query 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 111 Sbjct 2640 TGTATTTACTAGAACA 2624 2624 Score Expect Identities Gaps | Strand |
| Query 2036 ATTAAAAATATTTTAAAA 2053 Sbjct 2576 ATAAAACATATTTTAAAA 2559 Score Expect Identities Gaps Strand 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 | Query 2036 ATTAAAAATATTTTAAAA 2053 Sbjct 2576 ATAAAACATATTTTAAAA 2559 Score Expect Identities Gaps 23.8 bits(25) 1.3 14/15(93%) 0/15(0 Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTTCTATAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 111 Sbjct 2640 TGTATTTACTTAGAACA 2602 111 Sbjct 2910 GGAAATTTAAA 2920 111 Sbjct 1052 GGAAATTTAAA 2920 111 Sbjct 1052 GGAAATTTAAA 2640 10/11(Query 2910 < | 0%) Plus/Minus |
| Sbjct 2576 ATAAAACATATTTTAAAA 2559 Score Expect Identities Gaps Strand 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 111111111111111111111111111111111111 | Sbjct 2576 ATAAAACATATTTTAAAAA 2559 Score Expect Identities Gaps 23.8 bits(25) 1.3 14/15(93%) 0/15(0 Query 2144 CCATTTTTCTATCAT 2158 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | |
| Score Expect Identities Gaps Strand 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 1088 CCATTTTTCTATCAT 1074 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2447 GTAATTTGTTA 2457 11111111 111111111 111111111 11110% 0/11(0%) Plus/Minus Query 2445 GTAATTTGTTA 2455 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 111 111111111111 111111111111111111111111111111111111 | Score Expect Identities Gaps 23.8 bits(25) 1.3 14/15(93%) 0/15(0 Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTCTATCAT 2158 Sbjct 1088 CCATTTTCTATTAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 111 Sbjct 2640 TGTATTTACTTAGAACA 2602 111 Sbjct 2640 TGTATTTACTTAGAACA 2602 111 Query 2910 GGAAATTTAAA 2920 111 Sbjct 1052 GGAAATTTAAA 2920 11111100%) 0/110 | |
| Score Expect Identities Gaps Strand 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 111111111111111111111111111111111111 | Score Expect Identities Gaps 23.8 bits(25) 1.3 14/15(93%) 0/15(0 Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTTCTATCAT 2158 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 CTAATTTGTTA 2457 | |
| 23.8 bits(25) 1.3 14/15(93%) 0/15(0%) Plus/Minus Query 2144 CCATTTTTCTATCAT 2158 | 23.8 bits(25) 1.3 14/15(93%) 0/15(0 Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTTCTATTAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Strand |
| Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTCTATTAT 1074 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 111111111111111111111111111111111111 | Query 2144 CCATTTTTCTATCAT 2158 Sbjct 1088 CCATTTTCTATTAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 11111(100%) 0/11(Query 2447 GTAATTTGTTA 2455 2465 Gaps Sbjct 2465 GTAATTTGTTA 2455 2465 Gaps Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0) Query 2586 TGTTTATACTTAGAACA 2602 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(0) Query 2910 GGAAATTTAAA 2920 21.1 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(0) Score Expect Identities Gaps | 0%) Plus/Minus |
| Sbjct 1088 CCATTTTTCTATTAT 1074 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2447 GTAATTTGTTA 2457 1111111111 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 111111111111111111111111111111111111 | Sbjet 1088 CCATTTTCTATTAT 1074 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjet 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTACAACA 2602 Sbjet 2640 TGTATTTACTTAGAACA 2602 Sbjet 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 CGAAATTTAAA 2920 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | |
| Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTACGAACA 2602 | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0) Query 2586 TGTTTATACTTACAACA 2602 Query 2586 TGTATTTACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 111111111 1111 100%) 0/11(Query 2910 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2560 ACTAAAATTA 2560 10/11(| |
| ScoreExpectIdentitiesGapsStrand21.1 bits(22)4.411/11(100%)0/11(0%)Plus/MinusQuery2447GTAATTTGTTA2457Sbjct2465GTAATTTGTTA2455ScoreExpect22.9 bits(24)1.315/17(88%)Query2586TGTTTATACTTAGAACA2602Sbjct2640TGTATTTACTTAGAACA2602ScoreExpectIdentitiesGapsSbjct2640TGTATTTACTTAGAACA2624ScoreExpectIdentitiesGapsStrand21.1 bits(22)4.411/11(100%)Query2910GGAAATTTAAA2920IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0) Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 1111111111 Sbjct 1052 GGAAATTTAAA Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query | |
| 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 | 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0) Query 2586 TGTTTATACTTAGAACA 2602 JIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | Strand |
| Query 2447 GTAATTTGTTA 2457 Sbjet 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 | Query 2447 GTAATTTGTTA 2457 Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0) Query 2586 TGTTTATACTTAGAACA 2602 Suery 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | (0%) Plus/Minus |
| Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 | Sbjct 2465 GTAATTTGTTA 2455 Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(0) Query 2910 GGAAATTTAAA 2920 1000000000000000000000000000000000000 | |
| Score Expect Identities Gaps Strand 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 | Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 CGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 CGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Outery 2550 ACTAAAAAATA 2560 0/11(| |
| ScoreExpectIdentitiesGapsStrand22.9 bits(24)1.315/17(88%)0/17(0%)Plus/MinusQuery2586TGTTTATACTTAGAACA2602Sbjct2640TGTATTTACTTAGAACA2624ScoreExpectIdentitiesGapsStrand21.1 bits(22)4.411/11(100%)0/11(0%)Plus/MinusQuery2910GCAAATTTAAA2920Sbjct1052GGAAATTTAAA1042 | Score Expect Identities Gaps 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(0 Query 2910 GGAAATTTAAA 2920 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | |
| 22.9 bits(24) 1.3 15/17(88%) 0/17(0%) Plus/Minus Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 1000000000000000000000000000000000000 | 22.9 bits(24) 1.3 15/17(88%) 0/17(0 Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2550 ACTAAAAAATA 2560 | Strand |
| Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 111111111111111111111111111111111111 | Query 2586 TGTTTATACTTAGAACA 2602 Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 1000000000000000000000000000000000000 | 0%) Plus/Minus |
| Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 111111111111111111111111111111111111 | Sbjct 2640 TGTATTTACTTAGAACA 2624 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 1000000000000000000000000000000000000 | |
| Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 1111111111 Sbjct 1052 GGAAATTTAAA 1042 | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| |
| Score Expect Identities Gaps Strand 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 111/11(100%) Sbjct 1052 GGAAATTTAAA 1042 | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| |
| 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus Query 2910 GGAAATTTAAA 2920 111111111111111111111111111111111111 | 21.1 bits(22) 4.4 11/11(100%) 0/11(Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(Output 2550 4CTAAAAAATA 2560 | Strand |
| Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 | Query 2910 GGAAATTTAAA 2920 Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| .(0%) Plus/Minus |
| Sbjct 1052 GGAAATTTAAA 1042 | Sbjct 1052 GGAAATTTAAA 1042 Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| |
| | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| |
| | Score Expect Identities Gaps 21.1 bits(22) 4.4 11/11(100%) 0/11(| |
| Score Expect Identities Gaps Strand | 21.1 bits(22) 4.4 11/11(100%) 0/11(| Strand |
| 21.1 bits(22) 4.4 11/11(100%) 0/11(0%) Plus/Minus | | (0%) Plus/Minus |
| Query 2559 AGTAAAAAATA 2569 | Innera 7002 Yelyyyyyyy 7002 | |
| | | |

Table S3 The sequence of primer, siRNA and probe

| Gene | Primer-sense | Primer-antisense |
|----------|------------------------|-------------------------|
| circ1662 | CAAGAACTGCTTCGGCAGG | GGAGAGGAATGAGCTCGAACA |
| circ1662 | GATGAACTCGGCTTCAGCCAT | GAGACTACTCCAGTGGGGGGT |
| YAP1 | TAGCCCTGCGTAGCCAGTTA | TCATGCTTAGTCCACTGTCTGT |
| METTL3 | GGAGTTGGGGGAGAGAATG | GCGAGTGCCAGGAGATA |
| SMAD3 | ACGACTACAGCCATTCCATCCC | TCATCTGGTGGTCACTGGTTTCT |
| ACVR2A | ACACAGCCCACTTCAAATCC | CAAATGACAATCCCCGCAAT |
| CALM3 | TGGGAACGGGACCATTGACT | GACACGGAACGCCTCTCGGA |
| EGFR | TACTTGGAGGACCGTCGCTTG | ATGGTATTCTTTCTCTTCCGCAC |
| HK2 | GTGCCCGCCAGAAGACATTA | TTGCTCAGACCTCGCTCCAT |
| МҮС | AAGGCCCCCAAGGTAGTTATCC | TCGTCGTTTCCGCAACAAGTC |
| RELA | TACCACCAAGACCCACCCAC | CAGCCTCATAGAAGCCATCCCG |

| SGK1 | TTGACCCCGAGTTTACCGAA | TTGACGCTGGCTGTGACGAG |
|----------------------------|--------------------------|-------------------------|
| SOCS3 | CCCCCAGAAGAGCCTATTACA | TCCGACAGAGATGCTGAAGAGTG |
| TGFBR1 | CTGTGAAGCCTTGAGAGTAATG | CCTGTTGACTGAGTTGCGATA |
| GAPDH | AACGGATTTGGTCGTATTGG | TTGATTTTGGAGGGATCTCG |
| circ1662-convergent | AGCCCTGACTCCACAGCATG | GACCAGAAGATGTCTTTGCC |
| circ1662-intron-upstream | GTTCTTTCACCCCTGCTC | TTAGTCATCGCTTCCCAA |
| circ1662-intron-downstream | ACACCTGTAATCTCAACTTCTC | ACTATGTCCTACTTTCCCCA |
| 1663-up-03 | GAGGTGGGGGTAGAACCG | GCGTTTCAGCCGACTGTAAA |
| 1662-up-06 | ACAAAAACCCGGGTTAAGGA | AACTGCTGGATATAAATTCTTGT |
| 1662-up-07 | ATTCATAAACTATTATAGTTTTGT | GTATTTACAACCTAGATTTG |
| 1662-up-08 | CACAACACAAACTGGTGACTG | AAGCCATCTACAATGAACAGGAT |
| 1662-up-09 | GAACATTTGGGCAGTTCAAA | TTAAGAGGTCAGTGCAGTTAT |
| 1662-up-10 | TAGTTGCCCTTACATGTCTA | CTATTAGGGAATATTAAGATG |
| 1662-down-01 | TAGAAACCAGCCTTCCACTT | GCAATCCACAATTCCATGTAC |
| 1662-down-04 | AGAAGGTACTGTTGGTTTT | AAGAAACTCATAGTTATTTAGGC |
| 1662-down-06 | TAGGGCTGTATTTTAAAAGTATC | TGGAGTATCATTTTCTGAGC |
| 1662-down-07 | ATGGTTCTTTGACAAACTAAG | GGTTAGTAAATAATTCTCTTTGG |
| 1662-down-09 | TATCTGACATAAAAAAGGATG | AAGAACTTTTTTTTTTTAGTTTC |
| 1662-down-11 | CATACTAATAGACTATTTTTAG | CATGGTCTGGCTGTGTAGG |

| siRNA | Target sequence |
|----------------|---------------------------------------|
| si-circ1662-01 | GCCACAGGCCAGTACTGAT |
| si-circ1662-02 | CCACAGGCCAGTACTGATG |
| si-YAP1 | CAGTGGCACCTATCACTCT |
| si-METTL3 | GCTGCACTTCAGACGAATT |
| si-SMAD3 | GAGGCTGTCTACCAGTTGA |
| | |
| Gene | Probe sequence |
| Circ1662(ISH) | 5'-DIG-ATCAGTACTGGCCTGTGGCCTCACCTG-DI |
| | |

| Circ1662(FISH) | 5' Cv3-AGTACTGGCCTGTGGCCTCACCT |
|----------------|--------------------------------|
| |) |

Circ1662(Pull down) 5'-ATCAGTAC+TGGCCTGTGGCC+TCACCTGC-3'

NC (Pull down) 5'-GCTACGCAGCCGTCTCTCGTATGTACCG-3'

Supplementary figures



Supplementary Figure 1. (A) The design of si-circ1662 which was across the junction site. (B) Overexpressed vector of circ1662. (C, D) Transwell assay of HCT116 and SW480 transfected circ1662 vector for evaluating migration and invasion. The number of migration and invasion was counted in HCT116 and SW480. (E) The cell morphology of HCT116 and SW480 transfected circ1662 overexpression plasmids after 72h. The effect of YAP1 (F) and SMAD3 (G) siRNA in HCT116 and SW480 using qPCR analysis. (H, I) Transwell assay of HCT116 and SW480 transfected SMAD3 siRNA. The number of migration and invasion was counted in HCT116 and SW480 transfected SMAD3 siRNA. (K) The effect of METTL3 siRNA in HCT116 and SW480 transfected SMAD3 siRNA. (K) The effect of METTL3 siRNA in HCT116 and SW480 using qPCR analysis. GAPDH is the negative control. Student's t test was use to determined the *P* value (**P* < 0.05, 0.001 < ** P < 0.01, *** *P* < 0.001), Mean ±SEM.



Supplementary Figure 2. (A) GEO data (GSE9348) analyzing SMAD3 expression in CRC tissues (n = 12) compared normal tissues (n = 70). (B) H-score of YAP1 in 54 pairs CRC tissuea compared to normal tissues from tissue chip. (C) UALCAN showing the pan-cancer of SMAD3 expression which data from TCGA. (D) GEO data (GSE23878) analyzing SMAD3 expression in CRC tissues (n = 35) compared normal tissues (n = 24). GEO data (GSE32323) analyzing SMAD3 expression in CRC tissues (n = 17) compared normal tissues (n = 17). GEO data (GSE9348) analyzing SMAD3 expression in CRC tissues (n = 17) compared normal tissues (n = 70). (E) Survival analyzing SMAD3 expression compared to low SMAD3 expression in rectal cancer via KM-plotter online tool. Then it was assessed by log-rank test. (F, G) GEO data (GSE41328, GSE9348) analyzing the correlation between YAP1 and SMAD3 in CRC tissues. Student's t test was use to determined the *P* value (**P* < 0.05, 0.001 < ** *P* < 0.01, *** *P* < 0.001), Mean \pm SEM.





Supplementary Figure 3. The squence alignment and qPCR production identified by agarose gel electrophoresis. (A) The up-and down flank sequences of circ1662 were aligned in the UCSC Genome Browser. MIRc element, MIR family; AluSz6 and FLAM C elements, Alu family. (b) Circ1662-up-03, 06, 07, 08, 09, 10 and circ1662-down-01, 04, 06, 07, 09, 11 in HCT116 and SW480 were detected by MeRIP-qPCR. (C) Circ1662-up-03, 06, 08, 09 and circ1662-down-04, 06 were pulled down by METTL3 antibody using RIP-qPCR in HCT116. Circ1662-up-06, 08, 09, 10 and circ1662-down by METTL3 antibody using RIP-qPCR in SW480. Input group was the positive control and IgG group was the negative control.



Supplementary Figure 4. The role of METTL3 in CRC (A) UALCAN showing the pan-cancer of METTL3 expression which data from TCGA. (B) IHC image of METTL3 expression in CRC tissue chip. (C) H-score of METTL3 in CRC tissues (n = 26) compared to normal tissues (n = 33) from tissue chip. (D) Survival analysis of high METTL3 expression compared to low METTL3 expression in CRC tissues from CRC tissue chip. Then it was assessed by log-rank (Mantel-Cox) test. (E, F) The migrated and invasive ability of HCT116 transfected METTL3 siRNA using wound healing assays and transwell assays. The migration area was counted by image J. (G, H) The migrated and invasive ability of SW480 transfected METTL3 siRNA using wound healing assays. The migration area was counted by image J. Statistical significance was calculated by Student's t test, *P < 0.05, 0.001 < **P < 0.01, ***P < 0.001, Mean ±SEM.