

Supplemental Information

Super-Enhancer-Associated LncRNA *UCA1*

Interacts Directly with AMOT to Activate

YAP Target Genes in Epithelial Ovarian Cancer

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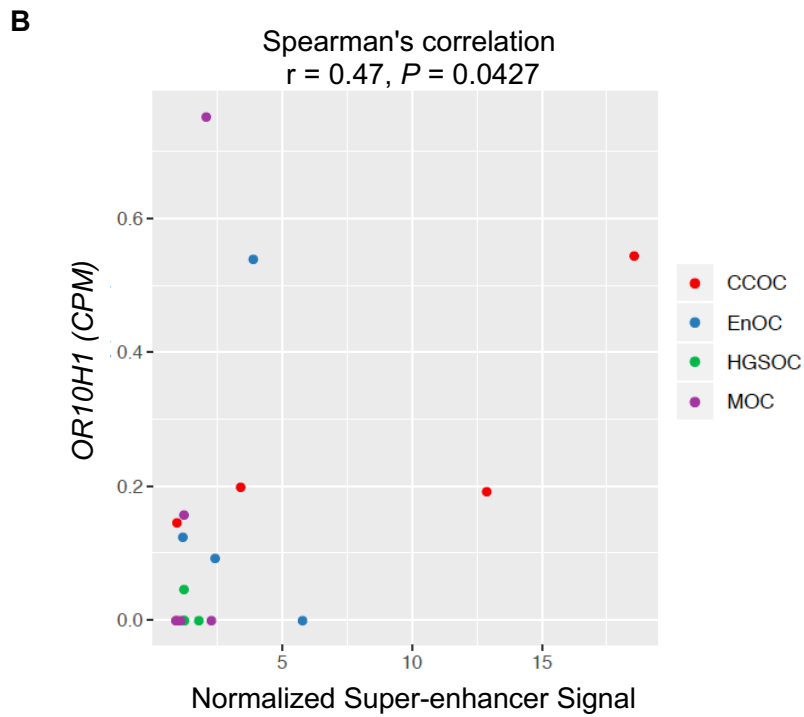
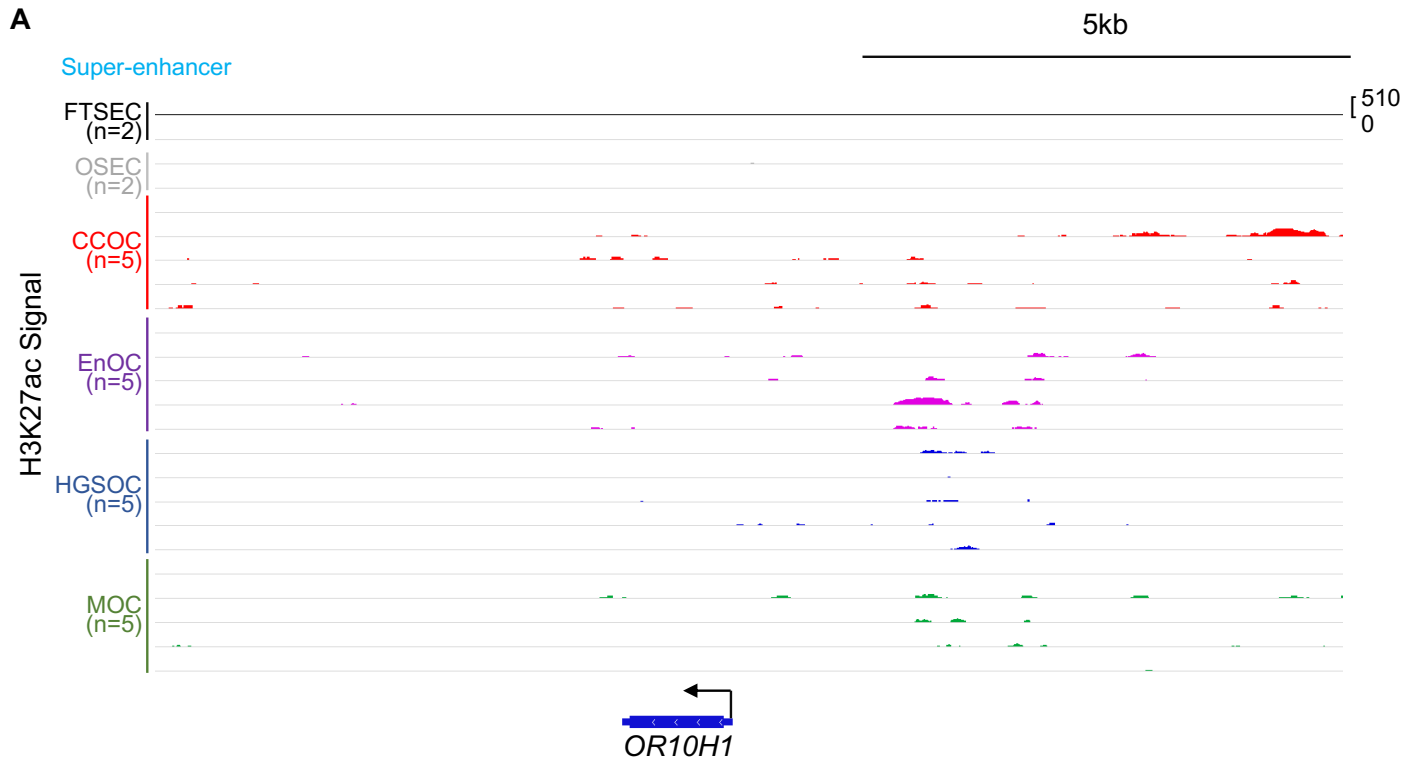


Figure S1. No evidence of super-enhancer activity at the *OR10H1* gene locus, Related to Figure 2

(A) H3K27ac signal at the *OR10H1* gene locus is shown at log scale. (B) Super-enhancer signals positively correlate with *OR10H1* expressions (Spearman's correlation, $r=0.47, P=0.043$). Counts per million (CPM) of *UCA1* from RNA-Seq is shown.

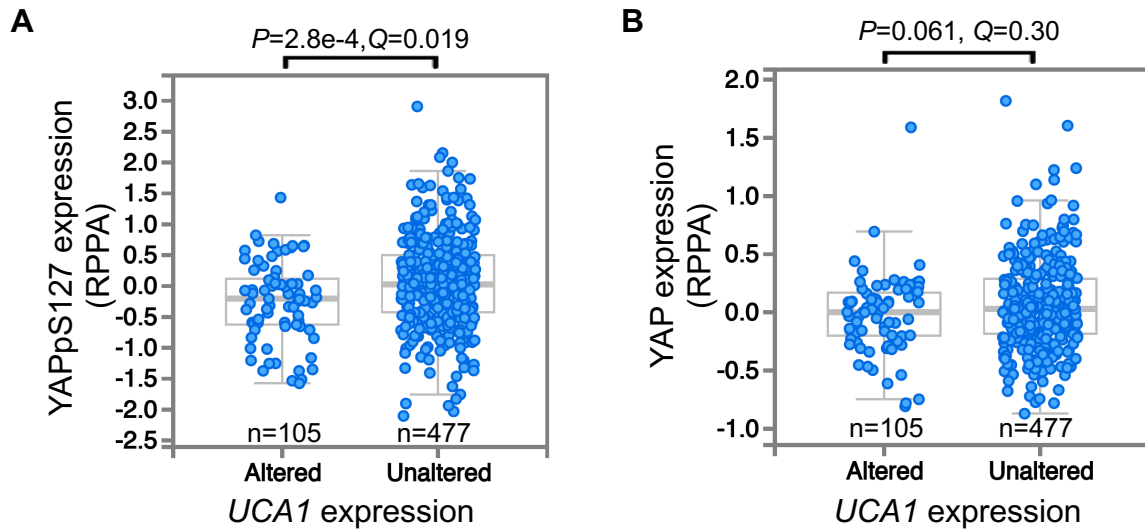


Figure S2. Overexpressed *UCA1* correlates with lower YAP phosphorylation in primary high-grade serous EOCs, Related to Figure 4A

(A) Comparison of RPPA data for YAPpS127 between ovarian cancers with (Altered) or without (Unaltered) *UCA1* amplification. (B) Total YAP is not significantly different between the two groups. Z-score threshold was set at 2. Data are from TCGA (<http://www.cbioportal.org>). *P*-value was determined using Student's *t*-test, while the *Q*-value was derived from Benjamini-Hochberg procedure.

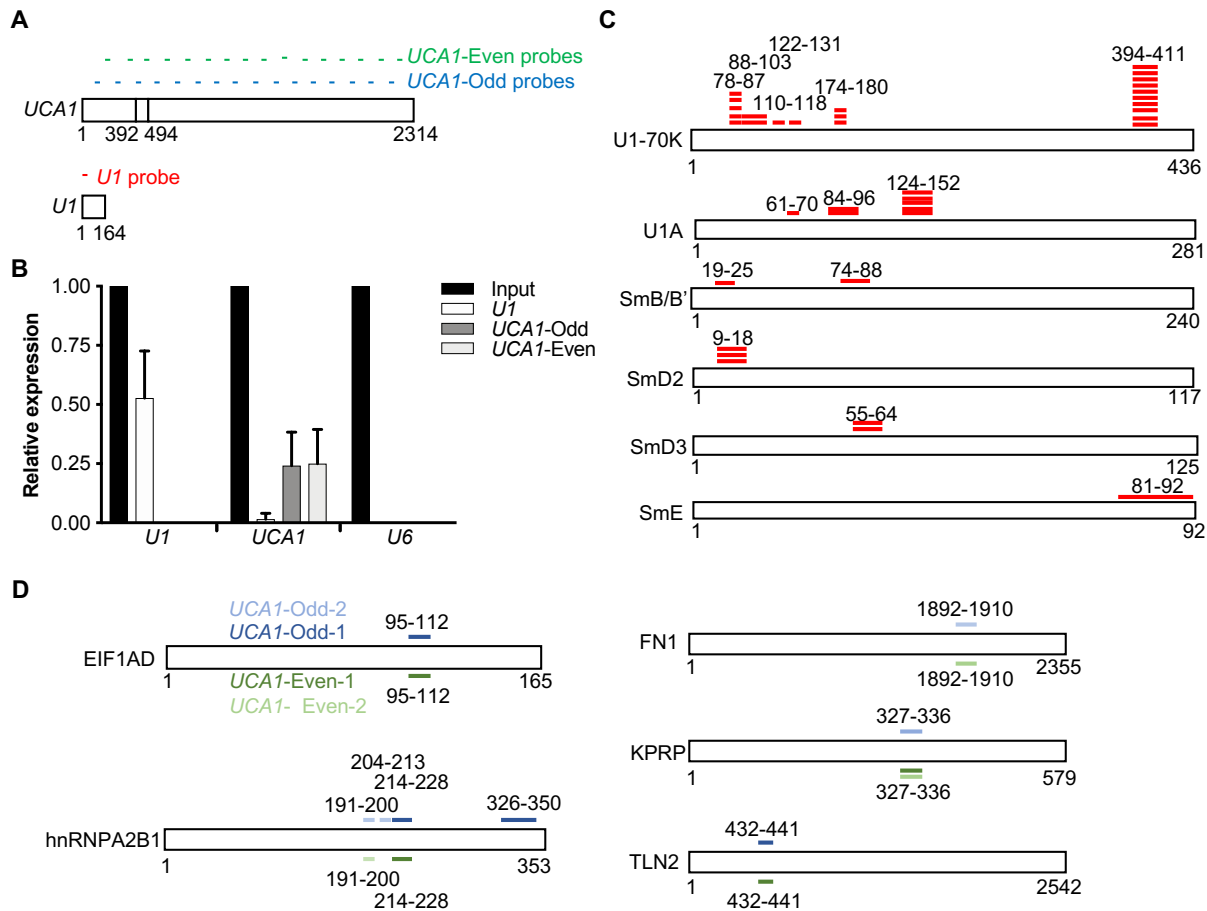


Figure S3. iRAP identifies the direct interacting proteome of *UCA1*, Related to Figure 5A

(A) Probe designing for *UCA1*-iRAP. Two sets of non-overlapping antisense DNA probes for *UCA1* were designed and labeled with biotin at their 3' end. An antisense DNA probe complementary to 1-20 nt of *U1* snRNA was included as a positive control. (B) RT-qPCR analysis of RNA retrieved from iRAP experiments. Data shown are mean \pm SD from 4 independent experiments. (C) Peptides were retrieved from *U1* iRAP-MS for direct binding proteins of *U1* snRNA. Numbers indicate the starting amino acid position and the ending amino acid position of the peptide retrieved or the full length of target protein. Protein length is not drawn in scale. (D) The same peptides were reproducibly retrieved from *UCA1* iRAP-MS experiments. A selection of representative proteins is shown. Numbers indicate the starting amino acid position and the ending amino acid position of the peptide retrieved or the full length of target protein. Protein length is not drawn in scale. Data shown are from 2 independent experiments.

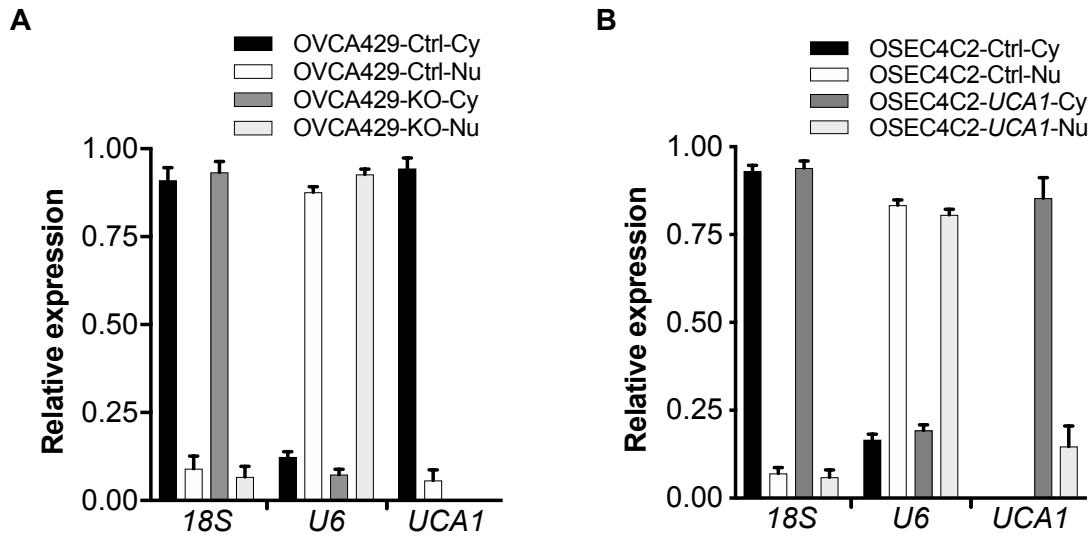


Figure S4. LncRNA *UCA1* predominantly localizes in cytoplasm, Related to Figure 6

(A) RT-qPCR measurement of cytoplasmic *18S* rRNA, nuclear *U6* snRNA and *UCA1* in OVCA429 fractionated samples. (B) RT-qPCR measurement of cytoplasmic *18S* rRNA, nuclear *U6* snRNA and *UCA1* in OSEC4C2 fractionated samples. Data shown are mean \pm SD from 3 independent experiments.

Table S1. Prognostic lncRNAs in high-grade serous EOC, Related to Figure 2A

| LncRNA Name | Importance-score | Raw-score | Chr | Start | End | Width | Strand | Gene Type |
|---------------|------------------|-----------|-------|-----------|-----------|--------|--------|----------------------|
| TTY14 | 1.06572E+13 | 1.723 | chrY | 18872501 | 19077416 | 204916 | - | lincRNA |
| PSMB1 | 99159107045 | 2.907 | chr6 | 170535117 | 170553341 | 18225 | - | protein_coding |
| ZFAS1 | 48072327683 | 2.585 | chr20 | 49278178 | 49295738 | 17561 | + | antisense |
| TUG1 | 40492304785 | 1.923 | chr22 | 30970677 | 30979395 | 8719 | + | antisense |
| FGD5-AS1 | 35063860805 | 2.147 | chr3 | 14920347 | 14948424 | 28078 | - | antisense |
| RP11-554D15.1 | 29197615843 | -1.956 | chr6 | 74069451 | 74690727 | 621277 | + | lincRNA |
| CTB-55O6.12 | 23922544460 | 1.501 | chr19 | 14137179 | 14171267 | 34089 | + | antisense |
| GAS5 | 22959917722 | 3.715 | chr1 | 173863900 | 173868882 | 4983 | - | processed_transcript |
| RP5-1061H20.4 | 22563332287 | 2.269 | chr1 | 229258281 | 229271028 | 12748 | - | lincRNA |
| RP11-64D24.2 | 18447025405 | 2.552 | chr11 | 114210616 | 114356571 | 145956 | - | antisense |
| RP11-6N17.9 | 17963712426 | 1.799 | chr17 | 47945424 | 47974438 | 29015 | + | processed_transcript |
| OIP5-AS1 | 16976708028 | 2.315 | chr15 | 41283990 | 41309737 | 25748 | + | processed_transcript |
| SNHG15 | 16315350372 | 2.006 | chr7 | 44983023 | 44986961 | 3939 | - | lincRNA |
| RP11-865I6.2 | 15818503929 | 1.567 | chr8 | 68848742 | 68852763 | 4022 | - | lincRNA |
| ILF3-AS1 | 15338973685 | 1.479 | chr19 | 10651862 | 10653844 | 1983 | - | lincRNA |
| SNHG8 | 11732839093 | 2.472 | chr4 | 118278709 | 118279823 | 1115 | + | lincRNA |
| NOP14-AS1 | 11574773571 | 1.796 | chr4 | 2934899 | 2961738 | 26840 | + | antisense |
| LINC00662 | 11461006830 | 1.478 | chr19 | 27684580 | 27793940 | 109361 | - | lincRNA |
| AC005083.1 | 10597230777 | 2.135 | chr7 | 20217577 | 20221700 | 4124 | + | processed_transcript |
| LINC00648 | 10263227364 | 2.269 | chr14 | 47764954 | 47795092 | 30139 | - | lincRNA |
| AC004112.4 | 10158300092 | 2.129 | chr7 | 112328189 | 112409623 | 81435 | - | antisense |
| RP4-758J18.2 | 9884322048 | 1.601 | chr1 | 1399522 | 1402046 | 2525 | + | processed_transcript |
| RP11-38J22.3 | 9686546170 | 3.22 | chr1 | 206117783 | 206126805 | 9023 | + | antisense |
| RP11-458F8.4 | 7896100113 | 1.608 | chr7 | 66902857 | 66906297 | 3441 | + | lincRNA |
| SNHG9 | 7431812371 | 1.628 | chr16 | 1964959 | 1965509 | 551 | + | lincRNA |
| AJ006995.3 | 7240196117 | -1.844 | chr21 | 27954922 | 27985295 | 30374 | + | lincRNA |
| LINC00339 | 6936706793 | 2.163 | chr1 | 22024531 | 22031225 | 6695 | + | lincRNA |
| LINC00578 | 6647351610 | 2.907 | chr3 | 177441921 | 177752305 | 310385 | + | lincRNA |
| RP11-47A8.5 | 6296575822 | 2.823 | chr10 | 102642792 | 102644140 | 1349 | - | lincRNA |
| SNHG17 | 6267686164 | 3.08 | chr20 | 38420588 | 38435353 | 14766 | - | processed_transcript |
| LINC00910 | 6258879085 | 2.145 | chr17 | 43369845 | 43389199 | 19355 | - | lincRNA |
| OSER1-AS1 | 6149104986 | 2.444 | chr20 | 44210960 | 44226027 | 15068 | + | lincRNA |
| C8orf31 | 6007255795 | 1.443 | chr8 | 143039209 | 143059942 | 20734 | + | processed_transcript |
| RP5-1132H15.1 | 5980054129 | 1.991 | chr7 | 66119603 | 66165011 | 45409 | - | antisense |

| | | | | | | | | |
|---------------|--------------|-------|-------|-----------|-----------|--------|---|----------------------|
| RP11-430C7.4 | 5776440431 | 2.282 | chr1 | 204603035 | 204616565 | 13531 | + | antisense |
| RP11-191L9.4 | 5456541984 | 1.633 | chr22 | 47631674 | 47855600 | 223927 | + | lincRNA |
| RP11-115C21.2 | 5322360392 | 2.492 | chr8 | 6403551 | 6407142 | 3592 | - | antisense |
| RP11-296I10.3 | 5160521700 | 2.558 | chr16 | 70156340 | 70173448 | 17109 | - | antisense |
| UCA1 | 5062358192 | 1.923 | chr19 | 15828961 | 15836320 | 7360 | + | processed_transcript |
| RP11-799D4.4 | 5028502297 | 1.529 | chr17 | 35231450 | 35242963 | 11514 | - | antisense |
| RP11-526P5.2 | 4914956869 | 4.806 | chr10 | 2501783 | 2567239 | 65457 | + | lincRNA |
| LINC00284 | 4896454541 | 2.783 | chr13 | 43908669 | 44030461 | 121793 | + | lincRNA |
| FAM157C | -4806404688 | 2.891 | chr16 | 90102271 | 90186204 | 83934 | + | lincRNA |
| CTC-444N24.11 | -5585259828 | 1.666 | chr19 | 57304305 | 57308562 | 4258 | + | lincRNA |
| C1orf132 | -5802882217 | 1.689 | chr1 | 207801518 | 207879096 | 77579 | - | lincRNA |
| RMRP | -6118555929 | 1.777 | chr9 | 35657751 | 35658018 | 268 | - | lincRNA |
| RAD51-AS1 | -7420839971 | 1.729 | chr15 | 40686724 | 40695107 | 8384 | - | processed_transcript |
| MIR205HG | -17249780561 | 1.462 | chr1 | 209428820 | 209432838 | 4019 | + | processed_transcript |
| RASSF8-AS1 | -23114357641 | 2.725 | chr12 | 25939329 | 25959765 | 20437 | - | antisense |
| NEAT1 | -29777169121 | 1.896 | chr11 | 65422774 | 65445540 | 22767 | + | lincRNA |

Table S2. Super-enhancer-associated lncRNAs in high-grade serous EOCs, Related to Figure 2A

| LncRNA Name | Chr | Start | End | Width | Strand | Gene Type |
|-------------|-------|-----------|-----------|-------|--------|----------------------|
| ZNF503-AS2 | chr10 | 77160759 | 77168738 | 7980 | + | processed_transcript |
| ZEB2-AS1 | chr2 | 145275664 | 145279058 | 3395 | + | antisense |
| ZBTB11-AS1 | chr3 | 101395274 | 101398061 | 2788 | + | antisense |
| WT1-AS | chr11 | 32457064 | 32480315 | 23252 | + | antisense |
| UNC5B-AS1 | chr10 | 72976981 | 72977985 | 1005 | - | antisense |
| UCA1 | chr19 | 15939771 | 15947130 | 7360 | + | processed_transcript |
| UBXN8 | chr8 | 30589764 | 30624522 | 34759 | + | processed_transcript |
| TMPRSS4-AS1 | chr11 | 117886487 | 117957508 | 71022 | - | antisense |
| TMEM72-AS1 | chr10 | 45306472 | 45455137 | 1E+05 | - | antisense |
| THAP9-AS1 | chr4 | 83814162 | 83822113 | 7952 | - | antisense |
| TFAP2A-AS1 | chr6 | 10409573 | 10416679 | 7107 | + | antisense |
| STK4-AS1 | chr20 | 43592435 | 43595043 | 2609 | - | lincRNA |
| SSSCA1-AS1 | chr11 | 65337131 | 65337744 | 614 | - | antisense |
| SRP14-AS1 | chr15 | 40331512 | 40359491 | 27980 | + | lincRNA |
| SPPL2B | chr19 | 2328614 | 2355099 | 26486 | + | processed_transcript |
| SNORA67 | chr17 | 7476144 | 7485342 | 9199 | + | processed_transcript |
| SNORA59B | chr17 | 19460524 | 19461224 | 701 | + | sense_intronic |
| SNHG9 | chr16 | 2014960 | 2015510 | 551 | + | lincRNA |
| SNHG16 | chr17 | 74553848 | 74561430 | 7583 | + | processed_transcript |
| SNHG15 | chr7 | 45022622 | 45026560 | 3939 | - | lincRNA |
| SNHG10 | chr14 | 95998634 | 96001209 | 2576 | - | antisense |
| SNHG1 | chr11 | 62619460 | 62623386 | 3927 | - | processed_transcript |
| SNAI3-AS1 | chr16 | 88729706 | 88753594 | 23889 | + | antisense |
| SLC2A1-AS1 | chr1 | 43424720 | 43449029 | 24310 | + | lincRNA |
| SEN3-EIF4A1 | chr17 | 7466604 | 7482033 | 15430 | + | processed_transcript |
| SEMA3B | chr3 | 50304990 | 50314977 | 9988 | + | processed_transcript |
| RPS10P7 | chr1 | 201487831 | 201499602 | 11772 | + | lincRNA |
| RNF157-AS1 | chr17 | 74136637 | 74150731 | 14095 | + | antisense |
| PTOV1-AS1 | chr19 | 50341896 | 50354933 | 13038 | - | antisense |
| PSMG3-AS1 | chr7 | 1609709 | 1629262 | 19554 | + | lincRNA |
| PROSER2-AS1 | chr10 | 11891612 | 11936699 | 45088 | - | antisense |
| PLAC4 | chr21 | 42548249 | 42558715 | 10467 | - | antisense |
| PDCD4-AS1 | chr10 | 112629626 | 112631991 | 2366 | - | antisense |
| PCOLCE-AS1 | chr7 | 100187025 | 100201829 | 14805 | - | antisense |
| PCED1B-AS1 | chr12 | 47599681 | 47610239 | 10559 | - | processed_transcript |
| PCBP1-AS1 | chr2 | 70189395 | 70315978 | 1E+05 | - | antisense |
| NEAT1 | chr11 | 65190245 | 65213011 | 22767 | + | lincRNA |
| MYLK-AS1 | chr3 | 123304389 | 123363415 | 59027 | + | antisense |
| MRPL23-AS1 | chr11 | 2004467 | 2011150 | 6684 | - | antisense |
| MIR29B1 | chr7 | 130561495 | 130598069 | 36575 | - | lincRNA |
| MIR22HG | chr17 | 1614805 | 1620468 | 5664 | - | lincRNA |
| MIR210HG | chr11 | 565660 | 568457 | 2798 | - | lincRNA |
| MIR194-2 | chr11 | 64658827 | 64660921 | 2095 | - | lincRNA |
| MIR142 | chr17 | 56408245 | 56409869 | 1625 | - | antisense |
| MIR10A | chr17 | 46656992 | 46659621 | 2630 | - | sense_intronic |
| MEIS1-AS3 | chr2 | 66653867 | 66660602 | 6736 | - | antisense |
| MAP3K14-AS1 | chr17 | 43325292 | 43345997 | 20706 | + | antisense |
| MAP3K14 | chr17 | 43340488 | 43394414 | 53927 | - | processed_transcript |
| LMCD1-AS1 | chr3 | 7994492 | 8653610 | 7E+05 | - | antisense |
| LINC01011 | chr6 | 2988201 | 2991407 | 3207 | + | lincRNA |
| LINC01004 | chr7 | 104590762 | 104653491 | 62730 | - | antisense |

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|--------------|-------|-----------|-----------|-------|---|----------------------|
| LINC00974 | chr17 | 39705858 | 39710747 | 4890 | - | lincRNA |
| LINC00938 | chr12 | 46119510 | 46121558 | 2049 | - | lincRNA |
| LINC00899 | chr22 | 46435787 | 46440733 | 4947 | - | processed_transcript |
| LINC00857 | chr10 | 81967466 | 81979413 | 11948 | + | lincRNA |
| LINC00847 | chr5 | 180257957 | 180262726 | 4770 | + | lincRNA |
| LINC00638 | chr14 | 105287538 | 105290055 | 2518 | + | lincRNA |
| LINC00605 | chr14 | 103653558 | 103655365 | 1808 | - | lincRNA |
| LINC00518 | chr6 | 10429488 | 10435107 | 5620 | - | lincRNA |
| LINC00511 | chr17 | 70319264 | 70636611 | 3E+05 | - | lincRNA |
| LINC00336 | chr6 | 33553883 | 33561115 | 7233 | - | antisense |
| LINC00324 | chr17 | 8123960 | 8127361 | 3402 | - | lincRNA |
| LINC00319 | chr21 | 44866481 | 44873773 | 7293 | + | lincRNA |
| LINC00313 | chr21 | 44881974 | 44899414 | 17441 | - | lincRNA |
| LINC00176 | chr20 | 62665697 | 62671315 | 5619 | + | lincRNA |
| LINC00163 | chr21 | 46409779 | 46414001 | 4223 | - | lincRNA |
| LINC00114 | chr21 | 40110945 | 40119384 | 8440 | - | lincRNA |
| LINC00111 | chr21 | 43099341 | 43117496 | 18156 | + | lincRNA |
| KRTAP5-AS1 | chr11 | 1592583 | 1620414 | 27832 | + | antisense |
| ITGB2-AS1 | chr21 | 46340966 | 46349593 | 8628 | + | antisense |
| HPN-AS1 | chr19 | 35549963 | 35597208 | 47246 | - | antisense |
| HOXB-AS3 | chr17 | 46626992 | 46683776 | 56785 | + | antisense |
| HOXB-AS1 | chr17 | 46620913 | 46628610 | 7698 | + | antisense |
| HCG11 | chr6 | 26522076 | 26526807 | 4732 | + | lincRNA |
| GATA6-AS1 | chr18 | 19746859 | 19748929 | 2071 | - | lincRNA |
| FAM13A-AS1 | chr4 | 89630940 | 89651254 | 20315 | + | antisense |
| ENO1-AS1 | chr1 | 8938894 | 8939953 | 1060 | + | antisense |
| EMX2OS | chr10 | 119232726 | 119304579 | 71854 | - | antisense |
| EGOT | chr3 | 4790876 | 4793274 | 2399 | - | lincRNA |
| DLGAP1-AS1 | chr18 | 3593730 | 3598350 | 4621 | + | antisense |
| CYP1B1-AS1 | chr2 | 38302791 | 38408997 | 1E+05 | + | antisense |
| CSNK1G2-AS1 | chr19 | 1952530 | 1954585 | 2056 | - | antisense |
| CPEB2-AS1 | chr4 | 14911585 | 15003669 | 92085 | - | lincRNA |
| COL18A1-AS2 | chr21 | 46827301 | 46829980 | 2680 | - | antisense |
| COL18A1-AS1 | chr21 | 46839631 | 46844985 | 5355 | - | antisense |
| CDKN2B-AS1 | chr9 | 21994777 | 22121096 | 1E+05 | + | antisense |
| CD27-AS1 | chr12 | 6548167 | 6560733 | 12567 | - | antisense |
| BAIAP2-AS1 | chr17 | 79002933 | 79008501 | 5569 | - | lincRNA |
| ASB16-AS1 | chr17 | 42253341 | 42264085 | 10745 | - | antisense |
| ARHGAP26-AS1 | chr5 | 142239169 | 142248487 | 9319 | - | antisense |
| AGAP11 | chr10 | 88752163 | 88769960 | 17798 | + | processed_transcript |
| ACTN1-AS1 | chr14 | 69446399 | 69454180 | 7782 | + | antisense |
| APO | chr9 | 136125788 | 136150617 | 24830 | - | processed_transcript |

Table S3. Differentially expressed proteins caused by disruption of *UCA1*, Related to Figure 4A

| Protein | OVCA4 29-1 | OVCA 429-2 | Contr ol-1 | Contr ol-2 | Contr ol-3 | <i>UCA1</i> KO1-1 | <i>UCA1</i> KO1-2 | <i>UCA1</i> KO1-3 | <i>UCA1</i> KO2-1 | <i>UCA1</i> KO2-2 | Ratio (KO/ WT) | T test |
|---------------------------------------|---------------|---------------|---------------|---------------|---------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------|
| PEA-15-R-V_GBL1116480 | 1.04 | 1.03 | 1.06 | 1.07 | 1.09 | 0.94 | 0.91 | 0.97 | 0.97 | 0.97 | 0.90 | 9.10E-05 |
| UGT1A-M-V_GBL1116415 | 1.12 | 1.11 | 1.05 | 1.11 | 1.13 | 0.93 | 0.91 | 0.89 | 0.97 | 0.98 | 0.85 | 1.66E-04 |
| c-Met_pY1234_Y1235-R- V_GBL1115572 | 1.23 | 1.18 | 1.18 | 1.23 | 1.16 | 0.92 | 0.85 | 0.78 | 0.95 | 0.89 | 0.74 | 1.67E-04 |
| Caveolin-1-R-V_GBL1115521 | 1.14 | 1.16 | 1.18 | 1.15 | 1.28 | 0.78 | 0.75 | 0.72 | 0.85 | 0.83 | 0.66 | 2.07E-04 |
| H2AX_pS139-R-V_GBL1116473 | 1.02 | 1.03 | 1.04 | 1.02 | 1.00 | 0.97 | 0.98 | 0.98 | 0.97 | 0.98 | 0.95 | 9.14E-04 |
| PCNA-M-C_GBL1116373 | 1.03 | 1.06 | 1.07 | 1.07 | 1.01 | 0.92 | 0.86 | 0.87 | 0.90 | 0.95 | 0.86 | 0.01 |
| LDHA-R-C_GBL1115596 | 1.14 | 1.18 | 1.18 | 1.28 | 1.42 | 0.85 | 0.54 | 0.64 | 1.08 | 0.82 | 0.63 | 0.01 |
| Rb_pS807_S811-R- V_GBL1115559 | 1.25 | 1.22 | 1.09 | 1.20 | 1.09 | 0.93 | 0.86 | 0.87 | 1.09 | 0.93 | 0.80 | 0.01 |
| Bcl2A1-R-V_GBL1116330 | 1.11 | 1.04 | 1.11 | 1.00 | 1.03 | 0.98 | 0.93 | 0.95 | 0.95 | 0.96 | 0.90 | 0.01 |
| MSH6-R-C_GBL1115609 | 1.08 | 1.07 | 1.11 | 1.10 | 1.14 | 0.90 | 0.78 | 0.82 | 1.04 | 0.93 | 0.81 | 0.01 |
| Cyclin-B1-R-V_GBL1115524 | 1.07 | 1.10 | 1.05 | 1.07 | 1.03 | 1.01 | 1.00 | 0.95 | 0.88 | 0.83 | 0.88 | 0.01 |
| PYGM-M-C_GBL1116395 | 1.07 | 1.09 | 1.01 | 1.08 | 1.10 | 0.98 | 0.86 | 0.86 | 1.02 | 0.90 | 0.86 | 0.01 |
| Myosin-11-R-V_GBL1115630 | 1.01 | 1.18 | 0.92 | 1.27 | 1.28 | 0.85 | 0.50 | 0.54 | 1.05 | 0.79 | 0.66 | 0.01 |
| CD49b-M-V_GBL1116425 | 0.97 | 0.99 | 0.95 | 1.12 | 1.04 | 0.94 | 0.84 | 0.88 | 1.04 | 0.96 | 0.92 | 0.02 |
| Lck-R-V_GBL1115538 | 1.46 | 1.49 | 1.03 | 1.43 | 1.45 | 0.73 | 0.67 | 0.66 | 1.32 | 1.02 | 0.64 | 0.02 |
| EGFR_pY1173-R-V_GBL1115526 | 1.10 | 1.07 | 1.10 | 0.98 | 1.02 | 0.93 | 0.96 | 0.90 | 0.95 | 0.93 | 0.89 | 0.02 |
| Gys_pS641-R-V_GBL1115603 | 1.08 | 1.12 | 1.05 | 1.05 | 1.03 | 0.95 | 0.97 | 0.90 | 1.03 | 0.96 | 0.90 | 0.02 |
| RBM15-R-V_GBL1115629 | 1.09 | 1.03 | 1.00 | 1.03 | 1.05 | 0.97 | 0.84 | 0.81 | 1.01 | 0.97 | 0.89 | 0.02 |
| PMS2-R-V_GBL1116324 | 1.17 | 1.18 | 1.04 | 1.07 | 1.09 | 0.96 | 0.87 | 0.87 | 1.05 | 0.95 | 0.84 | 0.02 |
| Src_pY416-R-C_GBL1116447 | 1.00 | 1.01 | 1.01 | 1.03 | 1.06 | 0.96 | 1.00 | 0.97 | 0.94 | 1.01 | 0.95 | 0.02 |
| Transglutaminase-M- V_GBL1116383 | 0.87 | 0.96 | 1.11 | 1.05 | 1.09 | 0.51 | 0.55 | 0.56 | 0.95 | 0.96 | 0.69 | 0.02 |
| XPA-M-V_GBL1116419 | 1.09 | 1.15 | 0.99 | 1.07 | 1.01 | 0.92 | 0.99 | 0.94 | 0.96 | 0.99 | 0.90 | 0.02 |
| RPA32-T-C_GBL1116471 | 1.06 | 1.03 | 0.98 | 1.04 | 1.10 | 0.92 | 0.88 | 0.85 | 1.03 | 1.04 | 0.91 | 0.02 |
| Ets-1-R-V_GBL1116361 | 1.24 | 1.18 | 1.36 | 1.01 | 1.24 | 0.95 | 0.69 | 0.73 | 0.99 | 0.90 | 0.70 | 0.03 |
| Axl-R-V_GBL1116474 | 1.47 | 1.09 | 1.14 | 1.08 | 1.13 | 0.83 | 0.89 | 0.91 | 0.88 | 0.93 | 0.75 | 0.03 |
| UQCRC2-M-C_GBL1116412 | 1.04 | 1.04 | 1.01 | 1.00 | 1.04 | 1.02 | 0.93 | 0.94 | 0.96 | 1.01 | 0.95 | 0.03 |
| ERCC5-R-C_GBL1116336 | 1.00 | 1.00 | 1.08 | 1.07 | 1.06 | 0.99 | 0.96 | 0.94 | 0.93 | 0.98 | 0.92 | 0.04 |
| <i>S6_pS240_S244-R-V_GBL1115562</i> | 1.19 | 1.12 | 0.99 | 1.12 | 1.07 | 0.96 | 0.79 | 0.84 | 1.12 | 0.94 | 0.85 | 0.04 |
| Glutaminase-R-C_GBL1116346 | 0.98 | 0.95 | 1.07 | 1.05 | 1.06 | 0.87 | 0.81 | 0.80 | 1.02 | 0.98 | 0.88 | 0.04 |
| Rad50-M-V_GBL1116385 | 1.05 | 1.05 | 1.08 | 0.99 | 1.01 | 1.01 | 1.00 | 0.97 | 0.94 | 1.00 | 0.95 | 0.04 |
| eEF2-R-C_GBL1115607 | 1.05 | 1.08 | 1.15 | 1.07 | 1.23 | 0.87 | 0.43 | 0.46 | 1.04 | 0.83 | 0.65 | 0.04 |
| ERCC1-M-V_GBL1116435 | 1.03 | 1.08 | 0.96 | 1.03 | 1.02 | 0.93 | 0.93 | 0.93 | 1.00 | 0.99 | 0.93 | 0.04 |

| | | | | | | | | | | | | |
|----------------------------------|------|------|------|------|------|------|------|------|------|------|------|----------|
| Dvl3-R-V_GBL1116454 | 1.02 | 1.03 | 0.91 | 1.04 | 1.05 | 0.99 | 0.91 | 0.90 | 0.99 | 0.96 | 0.94 | 0.04 |
| Myosin-IIa_pS1943-R-V_GBL1115635 | 1.23 | 1.43 | 1.02 | 1.28 | 1.50 | 0.82 | 0.17 | 0.26 | 1.30 | 0.90 | 0.54 | 0.05 |
| FAK-R-C_GBL1115530 | 1.11 | 1.08 | 1.03 | 1.06 | 1.09 | 1.08 | 0.89 | 0.96 | 1.04 | 0.94 | 0.91 | 0.05 |
| Chk1_pS296-R-V_GBL1116335 | 1.11 | 1.11 | 1.03 | 1.00 | 0.99 | 1.04 | 1.09 | 1.03 | 0.95 | 0.96 | 0.97 | 0.05 |
| p53-R-C_GBL1115545 | 0.88 | 0.93 | 0.91 | 0.89 | 0.91 | 1.01 | 1.03 | 1.03 | 0.99 | 1.04 | 1.13 | 1.89E-04 |
| NDRG1_pT346-R-V_GBL1116491 | 0.84 | 0.90 | 0.82 | 0.84 | 0.81 | 1.20 | 1.22 | 1.25 | 1.07 | 1.18 | 1.41 | 4.42E-04 |
| Gab2-R-V_GBL1115594 | 0.88 | 0.91 | 0.82 | 0.80 | 0.80 | 1.06 | 1.05 | 1.05 | 0.93 | 0.99 | 1.20 | 7.12E-04 |
| PDK1_pS241-R-V_GBL1115550 | 0.93 | 0.88 | 0.94 | 0.87 | 0.92 | 1.14 | 1.08 | 1.05 | 1.02 | 1.04 | 1.17 | 1.49E-03 |
| Claudin-7-R-V_GBL1115586 | 0.85 | 0.86 | 0.82 | 0.99 | 0.98 | 1.06 | 1.32 | 1.16 | 1.45 | 1.32 | 1.40 | 1.52E-03 |
| Tuberin_pT1462-R-V_GBL1116448 | 0.91 | 0.92 | 0.80 | 0.84 | 0.85 | 1.01 | 1.04 | 1.02 | 0.96 | 0.99 | 1.16 | 2.48E-03 |
| INPP4b-R-V_GBL1115611 | 0.90 | 0.90 | 0.96 | 0.96 | 0.96 | 1.13 | 1.03 | 1.07 | 1.10 | 1.09 | 1.16 | 2.57E-03 |
| p27_pT198-R-V_GBL1115587 | 0.97 | 0.95 | 1.00 | 0.94 | 0.95 | 1.01 | 1.03 | 1.04 | 0.99 | 0.98 | 1.05 | 2.92E-03 |
| ACVRL1-R-C_GBL1116458 | 0.98 | 0.98 | 0.96 | 0.95 | 1.01 | 1.04 | 1.02 | 0.99 | 0.97 | 1.04 | 1.04 | 3.58E-03 |
| Pdcd4-R-C_GBL1115583 | 0.85 | 0.89 | 0.88 | 0.93 | 0.97 | 1.02 | 1.07 | 1.09 | 1.04 | 1.04 | 1.17 | 4.02E-03 |
| Tuberin-R-V_GBL1115566 | 0.96 | 0.95 | 0.88 | 0.98 | 0.97 | 1.14 | 1.04 | 1.02 | 1.08 | 1.04 | 1.12 | 4.51E-03 |
| Caspase-3-R-C_GBL1115519 | 0.93 | 0.91 | 0.96 | 0.92 | 0.91 | 1.02 | 1.05 | 1.04 | 0.98 | 0.96 | 1.09 | 0.01 |
| Tyro3-R-V_GBL1116457 | 0.95 | 0.96 | 0.93 | 0.92 | 0.93 | 1.04 | 1.06 | 1.00 | 0.99 | 1.11 | 1.11 | 0.01 |
| c-Abl-R-V_GBL1116347 | 1.00 | 0.99 | 1.04 | 0.99 | 0.95 | 1.04 | 1.02 | 1.05 | 1.02 | 0.99 | 1.03 | 0.01 |
| ER-R-V_GBL1116352 | 0.91 | 0.89 | 0.95 | 0.91 | 0.91 | 1.10 | 1.04 | 1.06 | 0.97 | 1.11 | 1.15 | 0.01 |
| HER2-M-V_GBL1116406 | 0.92 | 0.92 | 0.93 | 0.91 | 0.95 | 1.04 | 1.06 | 1.03 | 0.94 | 1.06 | 1.11 | 0.01 |
| A-Raf-R-V_GBL1116314 | 0.98 | 0.95 | 0.92 | 0.92 | 0.89 | 1.02 | 1.04 | 1.08 | 1.01 | 0.97 | 1.10 | 0.01 |
| MMP2-R-V_GBL1115540 | 0.91 | 0.93 | 0.95 | 0.92 | 0.91 | 1.06 | 1.03 | 1.03 | 0.95 | 1.00 | 1.10 | 0.01 |
| D-alpha-Tubulin-R-V_GBL1116339 | 1.01 | 0.98 | 0.94 | 0.91 | 0.93 | 1.14 | 1.05 | 1.04 | 0.96 | 0.97 | 1.08 | 0.01 |
| CXCR4-R-C_GBL1116362 | 0.94 | 0.95 | 0.96 | 0.94 | 0.90 | 1.02 | 1.03 | 1.03 | 1.01 | 1.09 | 1.11 | 0.01 |
| Cyclophilin-F-M-V_GBL1116413 | 0.92 | 0.97 | 0.91 | 0.93 | 0.90 | 1.03 | 1.02 | 1.04 | 0.96 | 1.01 | 1.09 | 0.01 |
| P-Cadherin-R-C_GBL1116446 | 0.97 | 1.00 | 0.91 | 0.95 | 0.92 | 1.05 | 1.04 | 0.94 | 1.03 | 1.05 | 1.08 | 0.02 |
| PDGFR-beta-R-V_GBL1116319 | 1.00 | 0.94 | 0.96 | 0.94 | 0.86 | 1.01 | 1.06 | 1.06 | 1.00 | 0.95 | 1.08 | 0.02 |
| MEK2-R-V_GBL1116323 | 1.03 | 1.00 | 0.98 | 0.95 | 0.95 | 1.13 | 1.05 | 1.01 | 1.07 | 1.10 | 1.09 | 0.02 |
| TFAM-R-V_GBL1116333 | 0.88 | 0.95 | 0.89 | 0.89 | 0.91 | 0.98 | 1.13 | 1.10 | 0.95 | 0.97 | 1.13 | 0.02 |
| IGFBP5-G-C_GBL1116469 | 0.93 | 0.91 | 0.93 | 0.94 | 0.91 | 0.98 | 1.06 | 1.01 | 0.97 | 0.99 | 1.08 | 0.02 |
| Bad_pS112-R-V_GBL1115511 | 1.00 | 0.88 | 1.01 | 0.89 | 0.94 | 1.14 | 1.11 | 1.06 | 1.06 | 0.99 | 1.14 | 0.02 |
| Notch3-R-C_GBL1116354 | 0.89 | 0.88 | 0.99 | 0.94 | 0.97 | 1.02 | 1.06 | 1.04 | 1.00 | 1.03 | 1.10 | 0.02 |
| mTOR_pS2448-R-C_GBL1115542 | 0.99 | 0.99 | 0.91 | 1.04 | 0.98 | 1.08 | 1.01 | 1.01 | 1.06 | 1.06 | 1.06 | 0.02 |
| eIF4E-R-V_GBL1115571 | 0.88 | 0.92 | 1.01 | 0.95 | 0.98 | 0.98 | 0.98 | 1.05 | 0.99 | 1.00 | 1.05 | 0.02 |
| MDM2_pS166-R-V_GBL1116306 | 0.96 | 0.94 | 1.00 | 1.01 | 1.01 | 1.09 | 1.02 | 1.01 | 1.08 | 1.07 | 1.07 | 0.02 |

| | | | | | | | | | | | | |
|------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|
| Notch1-R-V_GBL1115610 | 0.99 | 1.02 | 0.91 | 0.89 | 0.91 | 1.08 | 1.03 | 1.03 | 1.08 | 1.03 | 1.11 | 0.03 |
| ATM-R-V_GBL1116337 | 0.91 | 0.89 | 0.79 | 0.92 | 0.87 | 1.05 | 1.12 | 1.11 | 0.94 | 1.00 | 1.19 | 0.03 |
| Rictor_pT1135-R-V_GBL1115627 | 0.93 | 0.92 | 0.90 | 0.99 | 0.91 | 1.04 | 1.03 | 1.03 | 0.98 | 0.98 | 1.09 | 0.03 |
| Rictor-R-C_GBL1115626 | 0.95 | 0.94 | 0.92 | 0.97 | 0.94 | 1.03 | 1.03 | 1.04 | 0.97 | 0.98 | 1.07 | 0.04 |
| Src-M-V_GBL1116378 | 1.01 | 0.93 | 0.93 | 0.88 | 0.81 | 1.04 | 1.13 | 0.99 | 1.02 | 1.11 | 1.16 | 0.04 |
| YAP_pS127-R-E_GBL1115578 | 0.83 | 0.89 | 0.99 | 0.96 | 1.00 | 1.41 | 1.12 | 1.11 | 1.37 | 1.08 | 1.30 | 0.04 |
| Puma-R-C_GBL1116329 | 0.89 | 0.92 | 0.91 | 0.91 | 0.90 | 1.01 | 1.02 | 1.04 | 1.30 | 1.01 | 1.18 | 0.04 |
| Pdcd-1L1-G-C_GBL1116468 | 0.91 | 0.96 | 0.81 | 0.80 | 0.97 | 0.96 | 1.04 | 1.02 | 1.00 | 0.99 | 1.13 | 0.05 |
| CD29-M-V_GBL1116426 | 0.89 | 0.93 | 0.96 | 0.95 | 0.95 | 0.95 | 1.06 | 1.02 | 0.94 | 1.02 | 1.07 | 0.05 |

The differentially expressed proteins with $P \leq 0.05$ are shown.

Table S4. iRAP antisense DNA probe sequences, Related to Figure 5

| Target Sequence Access # | Probe Sequence | Length | Start | End | Gene ID | Gene Name | Note |
|-----------------------------|------------------------|--------|-------|------|---------|--------------|------|
| NR_015379 | GGA CT CATTGTCCAGAAGAA | 20 | 6 | 25 | 652995 | UCA1 | Odd |
| NR_015379 | GTTATCTGTTGT CAGCAGAG | 20 | 61 | 80 | 652995 | UCA1 | Odd |
| NR_015379 | GAGATAGGAGAGGGGCAGCT | 20 | 124 | 143 | 652995 | UCA1 | Odd |
| NR_015379 | AAGCATGTCCGTATAGAAGA | 20 | 231 | 250 | 652995 | UCA1 | Odd |
| NR_015379 | ACGGAATGAGGGCCAGGACA | 20 | 305 | 324 | 652995 | UCA1 | Odd |
| NR_015379 | GAGGAGATCCGATTTGAAAT | 20 | 381 | 400 | 652995 | UCA1 | Odd |
| NR_015379 | TGGTCCAAGGGGCTTCTGAG | 20 | 436 | 455 | 652995 | UCA1 | Odd |
| NR_015379 | CAGCTAGGGTGTCTTCATAT | 20 | 505 | 524 | 652995 | UCA1 | Odd |
| NR_015379 | AATGACCGGGTAGGGTCTGG | 20 | 579 | 598 | 652995 | UCA1 | Odd |
| NR_015379 | TGGGCATGGCTTTATTCTGG | 20 | 654 | 673 | 652995 | UCA1 | Odd |
| NR_015379 | GTTTGTCTGATCGGCTCTCG | 20 | 727 | 746 | 652995 | UCA1 | Odd |
| NR_015379 | GCATGCTGGGATGGCCATTT | 20 | 813 | 832 | 652995 | UCA1 | Odd |
| NR_015379 | TTTTATAGGCGGCAGGTCTT | 20 | 875 | 894 | 652995 | UCA1 | Odd |
| NR_015379 | GACTTTTGACCCAGAGATTT | 20 | 949 | 968 | 652995 | UCA1 | Odd |
| NR_015379 | GTTGTCCATTT CATGAGAGT | 20 | 1023 | 1042 | 652995 | UCA1 | Odd |
| NR_015379 | CCCTCTAACAAACAACAACA | 20 | 1111 | 1130 | 652995 | UCA1 | Odd |
| NR_015379 | CTTTGTCTCCTGGATTAAGC | 20 | 1161 | 1180 | 652995 | UCA1 | Odd |
| NR_015379 | TCCCATAGGTGTGAGTGGCG | 20 | 1249 | 1268 | 652995 | UCA1 | Odd |
| NR_015379 | AGCCTTTTGTCCCATTTC | 20 | 1320 | 1339 | 652995 | UCA1 | Odd |
| NR_015379 | CAGTAATCAGGCATATTAGC | 20 | 1399 | 1418 | 652995 | UCA1 | Odd |
| NR_015379 | GCTAACAAAGGTGCCAGTTAG | 20 | 1467 | 1486 | 652995 | UCA1 | Odd |
| NR_015379 | GACTGCGTGGACACCTTAAA | 20 | 1541 | 1560 | 652995 | UCA1 | Odd |
| NR_015379 | AGTTCCTTCTGGGGATTACT | 20 | 1606 | 1625 | 652995 | UCA1 | Odd |
| NR_015379 | GACGGATATGTGCAGGTCAC | 20 | 1724 | 1743 | 652995 | UCA1 | Odd |
| NR_015379 | CTGTTTCACTTCTTTGTGGT | 20 | 1786 | 1805 | 652995 | UCA1 | Odd |
| NR_015379 | CATAATGGTGGAATGTCGTA | 20 | 1837 | 1856 | 652995 | UCA1 | Odd |
| NR_015379 | GATGGGACTCATTGTCCAGG | 20 | 1925 | 1944 | 652995 | UCA1 | Odd |
| NR_015379 | TAGGCGTGGAAAGTTACAGT | 20 | 2000 | 2019 | 652995 | UCA1 | Odd |
| NR_015379 | CTGTTAATTCAC TTGGGTGC | 20 | 2089 | 2108 | 652995 | UCA1 | Odd |
| NR_015379 | AGGTTCTGT CACGCGTGTC | 20 | 2151 | 2170 | 652995 | UCA1 | Odd |
| NR_015379 | AGGTGCATGGTGGAGAGATG | 20 | 29 | 48 | 652995 | UCA1 | Even |
| NR_015379 | ATAGGGCTGGGGTAGGCTGT | 20 | 102 | 121 | 652995 | UCA1 | Even |
| NR_015379 | TGTTAATTCAC TTGGGTGCA | 20 | 178 | 197 | 652995 | UCA1 | Even |

| | | | | | | | |
|-------------|-----------------------|----|------|------|--------|------|------|
| NR_015379 | AGATTTTGGCACCAAGTGTC | 20 | 251 | 270 | 652995 | UCA1 | Even |
| NR_015379 | GGTCGCAGGTGGATCTCTTC | 20 | 325 | 344 | 652995 | UCA1 | Even |
| NR_015379 | CAGTCTTCAGCCACTAAGCC | 20 | 401 | 420 | 652995 | UCA1 | Even |
| NR_015379 | CCGTAAGAGTTACCCGAAGC | 20 | 469 | 488 | 652995 | UCA1 | Even |
| NR_015379 | GTTTGAGGGGTCAGACTTTT | 20 | 542 | 561 | 652995 | UCA1 | Even |
| NR_015379 | AGAGGGTCCTGCAGATGGAC | 20 | 617 | 636 | 652995 | UCA1 | Even |
| NR_015379 | GAAGAGGAGAGATCAAGCTG | 20 | 683 | 702 | 652995 | UCA1 | Even |
| NR_015379 | TGGAAGCATGGCCTTGCTG | 20 | 778 | 797 | 652995 | UCA1 | Even |
| NR_015379 | AGGAACGGATGAAGCCTGCT | 20 | 838 | 857 | 652995 | UCA1 | Even |
| NR_015379 | GAGGATAGGGTCTCAAGATA | 20 | 902 | 921 | 652995 | UCA1 | Even |
| NR_015379 | ACCATGGGCAAGGATCTGAT | 20 | 991 | 1010 | 652995 | UCA1 | Even |
| NR_015379 | TGCCAAATATGTGGAAGTGG | 20 | 1060 | 1079 | 652995 | UCA1 | Even |
| NR_015379 | GGCAAAGAGTGAAATGTCCC | 20 | 1134 | 1153 | 652995 | UCA1 | Even |
| NR_015379 | ATAGTTCTGATTGCAGATCC | 20 | 1210 | 1229 | 652995 | UCA1 | Even |
| NR_015379 | CCCTGTTGCTAAGCCGATGA | 20 | 1282 | 1301 | 652995 | UCA1 | Even |
| NR_015379 | GTAGGTGGCGATGAGTTTTT | 20 | 1373 | 1392 | 652995 | UCA1 | Even |
| NR_015379 | CTTGGAAGTGCCTAATAAAA | 20 | 1435 | 1454 | 652995 | UCA1 | Even |
| NR_015379 | TCTAGTAAGTTTCGGGTCTA | 20 | 1504 | 1523 | 652995 | UCA1 | Even |
| NR_015379 | GCTGATATTTCTCCGGACTG | 20 | 1578 | 1597 | 652995 | UCA1 | Even |
| NR_015379 | CTTCAGCTCACAGGCCTGAC | 20 | 1685 | 1704 | 652995 | UCA1 | Even |
| NR_015379 | CTGCTCCAGACTTCTTGCT | 20 | 1759 | 1778 | 652995 | UCA1 | Even |
| NR_015379 | GTGGGTAAATTAGTTAAGGC | 20 | 1815 | 1834 | 652995 | UCA1 | Even |
| NR_015379 | GATTGATCAGTTGGGGCAGG | 20 | 1886 | 1905 | 652995 | UCA1 | Even |
| NR_015379 | GTCACAAGGTGCATGGTGGGA | 20 | 1950 | 1969 | 652995 | UCA1 | Even |
| NR_015379 | GGGCAGCTTTATAGGGCTTG | 20 | 2022 | 2041 | 652995 | UCA1 | Even |
| NR_015379 | CCAATCAGGCTTTGTGTGAG | 20 | 2117 | 2136 | 652995 | UCA1 | Even |
| NR_015379 | AGGAAAGGAAAACCATGA | 20 | 2244 | 2263 | 652995 | UCA1 | Even |
| NR_004430.2 | CTCCCCTGCCAGGTAAGTAT | 20 | 1 | 20 | 26871 | U1 | |

All the antisense DNA probes are labeled with biotin at the 3' end.

Table S5. iRAP peptide sequences, Related to Figure 5

| Sequence | Proteins | Start | End | UI | UCA1 -Odd1 | UCA1- Even1 | UCA1 -Odd2 | UCA1- Even2 |
|--------------------------------|------------------------------|-------|------|----|---------------|----------------|---------------|----------------|
| GGGGGQDNGLEGLGNSR | sp P08621 RU17_HUMAN | 394 | 411 | 5 | 2 | | | |
| ASMQQQQQLASAR | sp Q9Y3Y2 CHTOP_HUMAN | 39 | 51 | 4 | | | | |
| AVQGGGATPVVGVAVQGPVPMPPMTQAP | sp P09012 SNRPA_HUMAN | 124 | 152 | 4 | 1 | | | |
| EEEEIALVIDNGSGMCK | sp P63261 ACTG_HUMAN | 2 | 18 | 3 | | | 1 | |
| MMLGTGEGGEGFVVK | sp P31943 HNRH1_HUMAN | 1 | 14 | 3 | | | | |
| NMGGPYGGGNYGPGGSGGSGGYGGR | sp P22626 ROA2_HUMAN | 326 | 350 | 3 | 1 | | | |
| QEMQEVQSSR | sp P22626 ROA2_HUMAN | 191 | 200 | 3 | | | | |
| QEVETELK | sp P08621 RU17_HUMAN | 79 | 87 | 3 | 2 | | | |
| RGGADVNR | sp P08621 RU17_HUMAN | 201 | 209 | 3 | 1 | | | |
| RQQEVETELK | sp P08621 RU17_HUMAN | 78 | 87 | 3 | | | | |
| STVHEILCK | sp P07355 ANXA2_HUMAN;sp A | 2 | 10 | 3 | 1 | | 1 | |
| ESTGAQVQVAGDMLPNSTER | sp Q15365 PCBP1_HUMAN;sp Q1 | 125 | 144 | 2 | | | | |
| SEMTPEELQK | sp P62316 SMD2_HUMAN | 9 | 18 | 2 | | | | |
| TDYNASVSVDPSSGPER | sp P61978 HNRPK_HUMAN | 70 | 86 | 2 | | | | |
| DSYVGDAAQSKR | sp P60709 ACTB_HUMAN;sp P63 | 51 | 62 | 2 | | | | |
| VEADRP GK | sp P38159 RBMX_HUMAN;sp Q9 | 2 | 9 | 2 | | | | |
| DSYESYGNSR | sp P38159 RBMX_HUMAN;sp Q9 | 283 | 292 | 2 | | | | |
| DGMDNQGGYGSVGR | sp P31942 HNRH3_HUMAN | 288 | 301 | 2 | | | | |
| NQGGYGGSSSSSYGSGR | sp P09651 ROA1_HUMAN | 353 | 370 | 2 | | | | 1 |
| MWDPHNDPNAQGDFAK | sp P08621 RU17_HUMAN | 88 | 103 | 2 | | | | |
| VNYDTTESKLR | sp P08621 RU17_HUMAN | 110 | 120 | 2 | | | | |
| MIAGQVLDINLAAEPK | sp P07910 HNRPC_HUMAN | 74 | 89 | 2 | | | | |
| SLKLQASNVTKNDPK | sp Q9UKM9 RALY_HUMAN | 2 | 17 | 1 | | | | |
| HRSCNTDDCPPGSQDFREVQCSEFDSIPFR | sp Q9H324 ATS10_HUMAN | 593 | 622 | 1 | | | | |
| MSATSVDTQR | sp Q9BYJ9 YTHD1_HUMAN | 1 | 10 | 1 | 1 | 1 | | |
| VADLTEQYNEQYGA VR | sp Q9BWF3 RBM4_HUMAN | 183 | 198 | 1 | | | | |
| EVYQQQQYGS GGR | sp Q99729 ROAA_HUMAN | 233 | 245 | 1 | | | | |
| EGSIEIDIPV PK | sp Q96RQ3 MCCA_HUMAN | 624 | 635 | 1 | | | | |
| IIEEAPAPGK | sp Q96RQ3 MCCA_HUMAN | 285 | 295 | 1 | | | | |
| YLVSSVSSQETQGGPLAPMTGTIEK | sp Q96RQ3 MCCA_HUMAN | 636 | 659 | 1 | 1 | | | |
| TMFENVTR | sp Q96QA5 GSDMA_HUMAN | 2 | 9 | 1 | | | | 1 |
| AGGGPTLQCPPSSPEK | sp Q96N66 MBOA7_HUMAN | 272 | 288 | 1 | | | | |
| KIQNDAGVR | sp Q92945 FUBP2_HUMAN;sp Q9 | 347 | 355 | 1 | | | | |
| DAFADAVQR | sp Q92945 FUBP2_HUMAN | 72 | 80 | 1 | | | | |
| IGGGIDVPVPR | sp Q92945 FUBP2_HUMAN | 321 | 331 | 1 | | | | |
| IGQQPQQPGAPPQQDYTK | sp Q92945 FUBP2_HUMAN | 629 | 646 | 1 | | | | |
| SDYSTGGPPPGPPAGGGGAGGGGPP | sp Q92945 FUBP2_HUMAN | 2 | 40 | 1 | | | | |
| SVSLTGAPESVQK | sp Q92945 FUBP2_HUMAN | 191 | 203 | 1 | | | | |
| VQISPDSSGGLPER | sp Q92945 FUBP2_HUMAN | 178 | 190 | 1 | | | | |
| APILIATDVASR | sp Q92841 DDX17_HUMAN;sp P1 | 469 | 480 | 1 | | | | |
| DMVGIAQTGSGK | sp Q92841 DDX17_HUMAN | 210 | 221 | 1 | | | | |
| SSQSSSQFSGIGR | sp Q92841 DDX17_HUMAN | 671 | 684 | 1 | | | | |
| VLEEANQAINPK | sp Q92841 DDX17_HUMAN | 536 | 547 | 1 | | | | |
| EQMEKVEADLTR | sp Q8N8E3 CE112_HUMAN | 623 | 634 | 1 | | | | |
| QDNTPKR | sp Q8N118 CP4X1_HUMAN | 275 | 281 | 1 | | | | 1 |
| RLASPSEETWITCDNK | sp Q86VB7 C163A_HUMAN | 913 | 928 | 1 | | | | |
| DLQEONKK | sp Q5TB80 CE162_HUMAN | 733 | 740 | 1 | 1 | | 1 | |
| VAPDEHPILLTEAPLNPK | sp Q562R1 ACTBL_HUMAN | 97 | 114 | 1 | | | | 1 |
| GGSYSQAASSDSAQGS DVSLTA | sp Q31612 1B73_HUMAN | 342 | 363 | 1 | | | | |
| VLVDQTTGLSR | sp Q15717 ELAV1_HUMAN | 137 | 147 | 1 | | | | |
| QKNKSGETVVLK | sp Q15652 JHD2C_HUMAN | 2249 | 2260 | 1 | | | | |
| INISEGNCPER | sp Q15365 PCBP1_HUMAN;sp Q1 | 47 | 57 | 1 | | | | |
| MQSNKTFNLEK | sp Q15233 NONO_HUMAN | 1 | 11 | 1 | | | | |
| SSSVGSSSSYPISPAVSR | sp Q15149 PLEC_HUMAN | 4384 | 4401 | 1 | | | | |
| AAAAVQGGR | sp Q15005 SPCS2_HUMAN | 2 | 10 | 1 | | | | |
| IFVGGLSPTDPEEK | sp Q14103 HNRPD_HUMAN | 184 | 197 | 1 | | | | |
| SSGGSYRDSYDSYATHNE | sp Q14011 CIRBP_HUMAN | 155 | 172 | 1 | | | | |
| AASAAAASAAAASAASGSPGPEGGSAGGE | sp Q13263 TIF1B_HUMAN | 2 | 32 | 1 | | | | |
| VLVNDQAK | sp Q13263 TIF1B_HUMAN | 312 | 319 | 1 | | | | |
| AATASAGAGGIDGKPR | sp Q02978 M2OM_HUMAN | 2 | 17 | 1 | | | | |
| GDATVSYEDPPTAK | sp Q01844 EWS_HUMAN | 411 | 424 | 1 | | | | |
| ATVQLEGR | sp Q01469 FABP5_HUMAN | 2 | 10 | 1 | 1 | | | |
| SSGPTSLFAVTVAPPGAR | sp Q00839 HNRPU_HUMAN | 187 | 204 | 1 | | | | |
| IQTQPGYANTLR | sp Q00325 MPCP_HUMAN | 190 | 201 | 1 | | | | |
| MIQVYFPK | sp P82650 RT22_HUMAN | 192 | 199 | 1 | | | | |
| AADPPAENSSAPEAEQGGAE | sp P67809 YBOX1_HUMAN | 305 | 324 | 1 | | | | |
| GAEAAVNTGPGGVPVQGSK | sp P67809 YBOX1_HUMAN | 119 | 137 | 1 | | | | |
| GENLVSM TVEGPPPKDTGIAR | sp P63162 RSMN_HUMAN;sp P14 | 74 | 94 | 1 | | | | |
| TITLEVPSDTIENVK | sp P62987 RL40_HUMAN;sp P629 | 12 | 27 | 1 | | | | |
| AAQGE PQVQFK | sp P62826 RAN_HUMAN | 2 | 12 | 1 | | | | |
| ECTIEATA | sp P62633 CNBP_HUMAN | 170 | 177 | 1 | | | | |
| SSNECFKCGR | sp P62633 CNBP_HUMAN | 2 | 11 | 1 | | | | |
| VAQLEQVYIR | sp P62318 SMD3_HUMAN | 55 | 64 | 1 | | | | |
| GDNITLLQSVSN | sp P62304 RUXE_HUMAN | 81 | 92 | 1 | | | | |
| ADIQTER | sp P62280 RS11_HUMAN | 2 | 8 | 1 | | | 1 | |
| EITALAPSTMK | sp P60709 ACTB_HUMAN;sp P63 | 316 | 326 | 1 | | | | |
| AGFAGDDAPR | sp P60709 ACTB_HUMAN;sp P63 | 19 | 28 | 1 | 1 | | 1 | 1 |

| | | | | | | | | |
|-------------------------------|-----------------------------|------|------|---|--|---|--|---|
| DDDIAALVVDNGSGMCK | sp P60709 ACTB_HUMAN | 2 | 18 | 1 | | | | |
| HTGPNSPDTANDGFVR | sp P55795 HNRH2_HUMAN;sp P3 | 99 | 114 | 1 | | | | |
| MMLSTEGR | sp P55795 HNRH2_HUMAN | 1 | 8 | 1 | | | | |
| MLGPEGGEFVVK | sp P52597 HNRPF_HUMAN | 2 | 14 | 1 | | | | |
| MGPAMGPALGAGIER | sp P52272 HNRPM_HUMAN | 592 | 606 | 1 | | | | |
| QGGGGGGGSSVPGIER | sp P52272 HNRPM_HUMAN | 389 | 403 | 1 | | | | |
| SSGSPYGGGYGSGGGSGGYGSR | sp P51991 ROA3_HUMAN | 355 | 376 | 1 | | | | |
| ALVDGPCTQVR | sp P50914 RL14_HUMAN | 36 | 46 | 1 | | | | |
| ATTATMATSGSAR | sp P38919 IF4A3_HUMAN | 2 | 14 | 1 | | | | 1 |
| DDGYSTKDSYSSRDYPSR | sp P38159 RBMX_HUMAN;sp Q9 | 211 | 229 | 1 | | | | |
| DVYLSPR | sp P38159 RBMX_HUMAN;sp Q9 | 204 | 210 | 1 | | | | |
| YDDYSSSR | sp P38159 RBMX_HUMAN;sp Q9 | 310 | 317 | 1 | | | | |
| RGPPPPR | sp P38159 RBMX_HUMAN | 94 | 101 | 1 | | | | |
| SDLYSSGR | sp P38159 RBMX_HUMAN | 332 | 339 | 1 | | | | |
| GEATVSFDDPPSAK | sp P35637 FUS_HUMAN;sp Q928 | 335 | 348 | 1 | | | | |
| GLPWSCADEVQR | sp P31943 HNRH1_HUMAN | 17 | 29 | 1 | | | | |
| MLGTEGGEFVVK | sp P31943 HNRH1_HUMAN | 2 | 14 | 1 | | | | |
| MLGTEGGEFVVKVR | sp P31943 HNRH1_HUMAN | 2 | 16 | 1 | | | | |
| STGEAFVQFASK | sp P31942 HNRH3_HUMAN | 56 | 67 | 1 | | | | |
| DTSSSTVVSTQR | sp P31483 TIA1_HUMAN | 90 | 101 | 1 | | | | |
| FGQGGAGPVGGQGR | sp P23246 SFPQ_HUMAN | 667 | 681 | 1 | | | | |
| MEKTLETVPLER | sp P22626 ROA2_HUMAN | 1 | 12 | 1 | | | | |
| TLETVPLER | sp P22626 ROA2_HUMAN | 4 | 12 | 1 | | | | |
| SISLYYTGEK | sp P19338 NUCL_HUMAN | 458 | 467 | 1 | | | | |
| AGEAPTENPAPTQSSAE | sp P16989 YBOX3_HUMAN | 354 | 372 | 1 | | | | |
| SEAGEATTTTTTLQPAPTEAAAAAPQDPA | sp P16989 YBOX3_HUMAN | 2 | 33 | 1 | | | | |
| DNEETGFGSGTR | sp P15144 AMPN_HUMAN | 924 | 935 | 1 | | | | |
| AEAEAQAEELSFPR | sp P11498 PYC_HUMAN | 929 | 942 | 1 | | | | |
| ALAVSDLNR | sp P11498 PYC_HUMAN | 1062 | 1070 | 1 | | | | |
| SKSESPKEPEQLR | sp P09651 ROA1_HUMAN | 2 | 14 | 1 | | | | |
| DGGAWGTEQR | sp P09382 LEG1_HUMAN | 65 | 74 | 1 | | | | 1 |
| EVSSATNALR | sp P09012 SNRPA_HUMAN | 61 | 70 | 1 | | | | |
| IQYAKTDSHIAK | sp P09012 SNRPA_HUMAN | 84 | 96 | 1 | | | | |
| KAVQGGGATPVVGAVQGPVGMPPMTQA | sp P09012 SNRPA_HUMAN | 123 | 152 | 1 | | 1 | | 1 |
| TDSHIAK | sp P09012 SNRPA_HUMAN | 89 | 96 | 1 | | | | |
| AETREEMER | sp P08621 RU17_HUMAN | 60 | 69 | 1 | | | | |
| DPIPYLPPLEK | sp P08621 RU17_HUMAN | 17 | 27 | 1 | | | | |
| GGADVNR | sp P08621 RU17_HUMAN | 202 | 209 | 1 | | | | |
| GSEGRDEAR | sp P08621 RU17_HUMAN | 384 | 393 | 1 | | | | |
| IHMVYSK | sp P08621 RU17_HUMAN | 132 | 138 | 1 | | | | |
| KEELRGGGGDMAEPSEAGDAPPDDGPPGE | sp P08621 RU17_HUMAN | 306 | 346 | 1 | | 1 | | |
| VLVDVER | sp P08621 RU17_HUMAN | 174 | 180 | 1 | | 1 | | |
| AAVAGEDGR | sp P07910 HNRPC_HUMAN;sp P0 | 65 | 73 | 1 | | | | |
| ASNVTNKTDPR | sp P07910 HNRPC_HUMAN | 2 | 12 | 1 | | | | |
| VPPPPPIAR | sp P07910 HNRPC_HUMAN | 143 | 151 | 1 | | | | |
| AMGEQAVALAR | sp P05165 PCCA_HUMAN | 315 | 325 | 1 | | | | |
| MADALDNYVIR | sp P05165 PCCA_HUMAN | 466 | 476 | 1 | | | | |
| MADEAVCVGAPTSTK | sp P05165 PCCA_HUMAN | 105 | 119 | 1 | | | | |
| VVEEAPSIFLDAETR | sp P05165 PCCA_HUMAN | 299 | 313 | 1 | | | | |
| SGAQASSTPLSPTR | sp P02545 LMNA_HUMAN | 12 | 25 | 1 | | | | |
| MEDSASASLSSAAATGTSTSTPAAPTAR | sp O76021 RLID1_HUMAN | 1 | 28 | 1 | | | | |
| TGYTLDTVTGQR | sp O60506 HNRPQ_HUMAN;sp O | 131 | 142 | 1 | | | | |
| MEKENQLEASR | sp O60343 TBCD4_HUMAN | 856 | 867 | 1 | | | | |
| PAASITSKPATLTTTSATSK | sp O43670 ZN207_HUMAN | 343 | 362 | 1 | | | | |
| NDNQETAAMKPENLKK | sp A2A2Z9 AN18B_HUMAN | 266 | 281 | 1 | | | | |
| QMEELLFLK | tr Q8WYG7 Q8WYG7_HUMAN | 12 | 21 | | | | | 1 |
| STILQQFNR | sp Q9Y4G6 TLN2_HUMAN | 432 | 441 | 1 | | 1 | | |
| QTDAQSASSPKK | sp Q9Y3R0 GRIP1_HUMAN | 754 | 765 | | | 1 | | |
| GVLQQGAGALGSSAQGVK | sp Q9H8X9 ZDH11_HUMAN | 297 | 314 | | | 1 | | |
| GGGEQETQELASK | sp Q96QR8 PURB_HUMAN | 25 | 37 | | | 1 | | |
| SSGQMAQKFSFSK | sp Q96Q89 KI20B_HUMAN | 105 | 117 | | | | | 1 |
| MKQKQEVMFQSR | sp Q96LM1 CL037_HUMAN | 1 | 12 | | | | | 1 |
| DGAILCQPYITNGSLSLGVCGPQGR | sp Q96BF3 TMIG2_HUMAN | 62 | 86 | | | | | 1 |
| STEPKMETMR | sp Q8WTQ4 CP078_HUMAN | 197 | 206 | | | | | 1 |
| SLQKEGFWPEAFSEVAEK | sp Q8N9N8 EIF1A_HUMAN | 95 | 112 | | | 1 | | 1 |
| DQAEQWLR | sp Q8N4X5 AF1L2_HUMAN | 257 | 264 | | | 1 | | 1 |
| FYEMYLLINK | sp Q8IZJ1 UNC5B_HUMAN | 577 | 586 | | | 1 | | |
| NSLSSIMKNKDK | sp Q8IY51 TIGD4_HUMAN | 51 | 62 | | | | | 1 |
| KNDQALQLTQMDKMHK | sp Q86Z20 CC125_HUMAN | 337 | 352 | | | | | 1 |
| GSGSGQSPSYGR | sp Q86YZ3 HORN_HUMAN;CON | 897 | 908 | | | | | 1 |
| HGSSSGSSSR | sp Q86YZ3 HORN_HUMAN;CON | 2149 | 2158 | | | | | 1 |
| QGSSAGSSSYGQHGSGSR | sp Q86YZ3 HORN_HUMAN;CON | 507 | 525 | | | | | 1 |
| YGQQGSGSGQSPSR | sp Q86YZ3 HORN_HUMAN;CON | 649 | 662 | | | | | 1 |
| FEVNAKFLGVDMER | sp Q86VI3 IQGA3_HUMAN | 1575 | 1588 | | | 1 | | |
| DVDAAYYSK | sp Q7Z794 K2C1B_HUMAN;CON | 274 | 282 | | | | | 1 |
| VTVQTDSSNK | sp Q6ZP68 ATPUN_HUMAN | 105 | 114 | | | | | 1 |
| SGTNNHVTVAIEN | sp Q5W0Z9 ZDH20_HUMAN | 353 | 365 | | | | | 1 |
| QESTSKADLNCSSKNK | sp Q5W0B1 RN219_HUMAN | 328 | 342 | | | 1 | | |
| IQSSQPMCLK | sp Q5U4N7 GDF50_HUMAN | 2 | 11 | | | | | 1 |
| IEISSPCCPR | sp Q5T749 KPRP_HUMAN | 327 | 336 | | | 1 | | 1 |
| CQEEFWIR | sp Q5FWF4 ZRAB3_HUMAN | 940 | 947 | | | | | 1 |

| | | | | | | | | |
|---------------------|-----------------------------|------|------|---|---|---|---|---|
| FSNSSSSNEFSK | sp Q5D862 FILA2_HUMAN;CON | 404 | 415 | | | | | 1 |
| AGSLQLSSMSAGNSSLR | sp Q53SF7 COBL1_HUMAN | 380 | 396 | | | 1 | 1 | |
| IQKEEEEILMANKR | sp Q4VCS5 AMOT_HUMAN | 727 | 740 | 1 | 1 | | | 1 |
| DMLMQER | sp Q3ZCV2 CA177_HUMAN | 391 | 397 | | | 1 | 1 | 1 |
| MEPIYFARPMNTR | sp Q15468 STIL_HUMAN | 1 | 15 | 1 | 1 | | | |
| ERDAALK | sp Q14980 NUMA1_HUMAN | 598 | 604 | | | | | 1 |
| NEWRMITAMNTIR | sp Q14145 KEAP1_HUMAN | 495 | 507 | 1 | | | | |
| KPEYDLEEDDQEVLK | sp Q13416 ORC2_HUMAN | 52 | 66 | 1 | | | | |
| MQLDNPSK | sp Q13085 ACACA_HUMAN | 818 | 825 | 1 | | | | |
| NVLLNNEK | sp Q08J23 NSUN2_HUMAN | 569 | 577 | 1 | 1 | | | |
| ENAGEDPGLAR | sp P81605 DCD_HUMAN | 43 | 53 | 1 | 1 | | | 1 |
| DSYVGDEAQSK | sp P60709 ACTB_HUMAN;sp P63 | 51 | 61 | | | | 1 | 1 |
| MNALDLNMKTK | sp P30519 HMOX2_HUMAN | 206 | 216 | | | 1 | | |
| GGGGNFGPGPSNFR | sp P22626 ROA2_HUMAN | 214 | 228 | 1 | 1 | | | |
| NLKNSQMCQK | sp P21439 MDR3_HUMAN | 670 | 679 | | | | 1 | |
| NMLSQVNYRVNMR | sp P19174 PLCG1_HUMAN | 179 | 192 | 1 | 1 | | | |
| RQQLNEMLK | sp P11532 DMD_HUMAN | 2572 | 2580 | | | | 1 | |
| KNSYMNPEKK | sp P08473 NEP_HUMAN | 737 | 746 | | | 1 | | |
| AQGYSGLSVK | sp P07996 TSP1_HUMAN;CON | 1055 | 1064 | | | | 1 | |
| GDPSSPAFR | sp P07996 TSP1_HUMAN;CON | 51 | 60 | | | | 1 | |
| GTSQNDPNWVVR | sp P07996 TSP1_HUMAN;CON | 969 | 980 | | | | 1 | |
| SSPVVIDASTAIDAPSNLR | sp P02751 FINC_HUMAN | 1892 | 1910 | | | | 1 | 1 |
| TSLDEALQWR | sp O15539 RGS5_HUMAN | 53 | 62 | 1 | 1 | | | |
| VAASIGNAQK | sp O00151 PDLI1_HUMAN | 247 | 256 | 1 | | | | |

The numbers under each probe are the peptide hits obtained by mass spectrometry for iRAP protein samples.

Table S6. Antibody information used in this study, Related to Figure 4, 5, & 6

| ANTIBODY | SOURCE | IDENTIFIER | NOTE |
|-------------------|---------------------------|----------------------------------|-----------------|
| β -tubulin | Sigma Aldrich | Cat#T8328, RRID: AB_1844090 | 1:2,000 |
| U1-70k | EMD Millipore | Cat#05-1588, RRID: AB_10805959 | 1:1,000 |
| AMOT | Bethyl laboratories | Cat#A303-305A, RRID: AB_10951678 | 1:500 |
| AXL | R&D Systems | Cat#AF-154, RRID: AB_354852 | 1:1,000 |
| CYR61 | Cell Signaling Technology | Cat#14479S, RRID: N/A | 1:1,000 |
| CTGF | Abcam | Cat# ab6992, RRID: AB_305688 | 1:1,000 |
| YAP | Santa Cruz | Cat#sc-15407, RRID: AB_2273277 | 1:100-1,000, WB |
| YAP | Cell Signaling Technology | Cat#4912S, RRID: AB_2218911 | IP |
| YAP (phosphoS127) | Abcam | Cat#ab76252, RRID: AB_1524578 | 1:1,000 |
| Phospho-LATS1 | Cell Signaling Technology | Cat#8654S, RRID: AB_10971635 | 1:100 |
| LATS1 | Cell Signaling Technology | Cat#3477T, RRID: AB_2133513 | 1:500 |
| GFP | Santa Cruz | Cat#sc-9996, RRID: AB_627695 | 1:2,000 |
| GAPDH | Fitzgerald Antibody | Cat#10R-G109A, RRID: AB_1285808 | 1:2,000 |
| β -actin | Santa Cruz | Cat#sc-47778, RRID: AB_626632 | 1:2,000 |
| Rabbit IgG | Thermo Fisher Scientific | Cat#10500C, RRID: AB_2532981 | IP |

Transparent Methods

Cell Culture. FTSEC33 and FTSEC246 cells were grown in DMEM/F12 media supplied with 10% FBS (HyClone, catalogue number: SH3007103) and L-glutamine. OSEC4 and OSEC11 were cultured in NOSE-CM media consisting of MCDB105: Medium 199 (1:1), 15% FBS, 10 ng/mL epidermal growth factor (Sigma Aldrich, catalogue number: E9644-2MG), 0.5 mg/mL hydrocortisone (Sigma Aldrich, catalogue number: H0888), 5 mg/mL insulin (Sigma, catalogue number: I1882-100MG), and 34 mg protein/mL bovine pituitary extract (Thermo Fisher Scientific, catalogue number: 13028014). CaOV3 cells were grown in RPMI1640 supplied with 10% FBS and L-glutamine. OVCA429 cells were cultured in EMEM supplied with 10% FBS, L-glutamine, sodium pyruvate (Lonza, catalogue number: 13-115E), and nonessential amino acids (Lonza, catalogue number: 13-114E). UWB1.289 cells were grown in mammary epithelial growth medium (MEGM): RPMI1640 (1:1) supplied with 3% FBS. HEK293T cells were cultured in DMEM supplied with 10% FBS.

H3K27ac ChIP-Seq and Super-enhancer Identification. H3K27ac ChIP-Seq and data analysis for primary ovarian cancer specimens were performed as described previously (Lawrenson et al., 2018). H3K27ac ChIP-Seq data for FTSEC33, FTSEC246, OSEC4, and OSEC11 are publicly available (Coetzee et al., 2015). The AQUAS pipeline (https://github.com/kundajelab/chipseq_pipeline) was used to process ChIP-Seq data. Reads were aligned to the reference human genome (hg19), filtered by read quality and duplicate reads removed. MACS2 (<https://pypi.python.org/pypi/MACS2>) was used for peak calling. For the cell lines, two technical replicates were generated and the final peaks were obtained using a naive overlap approach, where the peaks are included if they overlap more than 50% between the two technical replicates. After alignment, homer (<http://homer.ucsd.edu/homer/>) was used to identify super-enhancers, using a super slope parameter of 2 and a minimum distance of ten thousand base pairs. For defining a set of high-grade serous ovarian cancer super-enhancers, we selected super-enhancers that were called in at least two high-grade serous ovarian cancer samples. For the FTSEC and OSEC sets of super-enhancers, super-enhancers were called individually in each technical replicate, then all the super-enhancers that overlapped both technical replicates within the same cell

line were selected to get the union set. To identify super-enhancer-associated lncRNAs, we directly overlapped the expressed lncRNAs with super-enhancers in high-grade serous EOC.

Survival and Super-enhancer-association Analysis. We used the `superpc` R package to perform the survival analysis using data from profiling of high-grade serous EOCs performed by TCGA (Cancer Genome Atlas Research, 2011). As training set 80% of the samples were randomly selected (377 samples) and the other 20% (77 samples) were used as the test set. Information about vital status was obtained from TCGA. We defined the threshold parameter as 1.4, `n.components=3` and `prediction.type="continuous"`. The significant genes were obtained in order of decreasing importance score. Super-enhancer domains in each cell line were identified using published procedures (Lovén et al., 2013; Whyte et al., 2013). To associate super-enhancers to lncRNAs we used the `GenomicFeatures` package (version 1.28.4) to manipulate the enhancer and lncRNAs genomic annotations. Gene coordinates were obtained using `TxDb.Hsapiens.UCSC.hg19.knownGene` (version 3.2.2) and `org.Hs.eg.db` (version 3.4.1) libraries.

RNA-Seq Data Generation and Analysis. Primary ovarian cancer specimens were homogenized and total RNA was extracted using TRIzol LS (Thermo Fisher Scientific, catalogue number: 10296028). Ribosomal RNA (rRNA) was depleted using RiboMinus Transcriptome Isolation Kit (Thermo Fisher Scientific, catalogue number: K155002). Poly (A)⁺ RNA was then isolated using Dynabeads Oligo (dT)₂₅ (Thermo Fisher Scientific, catalogue number: 61002). Twenty nanograms rRNA-poly (A)⁺ RNA was used to prepare each RNA-Seq library. External RNA Controls Consortium (ERCC) spike-ins (Thermo Fisher Scientific, catalogue number: 4456740) were added as control for normalization of the samples. Strand-specific RNA-Seq libraries were constructed using the NEBNext Ultra Directional RNA Library Prep Kit (NEB, catalogue number: E7420). The resulting library concentrations were quantified using the Nanodrop. Libraries were sequenced to generate paired-end 75 bp reads on NextSeq 500 platform (Illumina) in high output running mode. Sequencing was performed at the Molecular Genomics Core facility at the University of Southern California. RNA-Seq data were analyzed using Partek Flow and Partek Genomics Suite software after mapping reads to reference lncRNA gene mode (Gencode V16) with Tophat2.

Data Availability. H3K27ac ChIP-Seq data for normal precursor cells and primary tumors as well as RNA-Seq data for primary tumors have been deposited in the Gene Expression Omnibus database (GEO: GSE121103).

(+)-JQ1 treatment of the ovarian cancer cells. CaOV3 or UWB1.289 cells were treated with 10 nM (+)-JQ1 (Tocris, catalogue number: 4499) or an equal volume of DMSO (Sigma Aldrich, catalogue number: D2650) for 16 h before harvesting for RNA extraction.

Reverse transcription and real time quantitative PCR (RT-qPCR). RNA was extracted using TRIzol LS (Thermo Fisher Scientific, catalogue number: 10296028). M-MLV reverse transcriptase (Promega, catalogue number: M5301) and random hexamers (Promega, catalogue number: C1181) were used for reverse transcription. Gene expression was quantified by RT-qPCR using iQ SYBR Green supermix (Bio-Rad, catalogue number: 170-8886). The relative gene expression was calculated using the $2^{-\Delta\Delta C_t}$ method (Schmittgen and Livak, 2008). Two hundred and fifty nanograms cDNA was used for RT-qPCR analysis on CFX96 Touch Real-Time PCR Detection System (Bio-Rad) using the following primer pairs. *UCA1*-F:

5'CTTCTGCATAGGATCTGCAATCAG3', *UCA1*-R: TTTTGTCCCCATTTTCCATCATACG. *UI*-F:

CCAGGGCGAGGCTTATCCATT, *UI*-R: GCAGTCCCCCACTACCACAAAT. *U6*-F:

GCTTCGGCAGCACATATACTAAAAT, *U6*-R: CGCTTCACGAATTTGCGTGTCAT. *AXL*-F:

GGTGGCTGTGAAGACGATGA, *AXL*-R: CTCAGATACTCCATGCCACT. *CYR61*-F:

AAACCCGGATTTGTGAGGT, *CYR61*-R: GCTGCATTTCTTGCCCTTT. *OR10H1*-F:

CCCAAAGTCCCCAGTCTCT, *OR10H1*-R: CTCCTTGTTCTGAGGCTGA. *GAPDH*-F:

TGCCAAATATGATGACATCAAGAA, *GAPDH*-R: GGAGTGGGTGTCGCTGTTG, *18S*-F:

CAGCCACCCGAGATTGAGCA, *18S*-R: TAGTAGCGACGGGCGTGTG, *β -actin*-F:

TCACCCACACTGTGCCCATCTACGA, *β -actin*-R: CAGCGGAACCGCTCATTGCCAATGG.

CRISPR/Cas9 KO of *UCA1*. Guide RNAs (gRNAs) were designed using the CRISPR design tool

(<http://crispr.mit.edu/>). Two gRNAs were cloned into PX458 (Addgene plasmid number 48138) - *UCA1*

promoter: GGTTTCCTTTTAGATGACGG, *UCA1* intron: GGCTAGAATATTTGCAGGCG, following the methods of the Zhang laboratory (Ran et al., 2013). Target cells were co-transfected with the two gRNAs

expressing plasmids or the vector backbone only as a control, using the BioT transfection reagent (Bioland Scientific, catalog number: B01-01). Positive cells were isolated using an Aria II flow cytometer (BD Biosciences) to sort single cells into 96 well plates. For validation of the deletion, PCR was performed using Sequel Prep™ Long PCR Kit with the following primers - Forward: GACACTGCATTGTGTGCGTT, Reverse: TCCCTGTTGCTAAGCCGATG.

Mouse xenografts. All *in vivo* work was performed with the approval of the USC Institutional Animal Care and Use Committee. Ten million cells were injected with 25% Matrigel subcutaneously into female nu/nu mice (aged 6-8 weeks). Tumor growth was measured by digital caliper measurement and animals euthanized when tumor diameter reached >1.5 cm, or after 8 weeks.

RPPA. Cells were plated into 6 well plates overnight. Cells were washed with PBS and lysed for 20 minutes in buffer containing 1% Triton X-100, 50 mM HEPES, pH 7.4, 150 mM NaCl, 1.5 mM MgCl₂, 1 mM EGTA, 100 mM NaF, 10 mM Na pyrophosphate, 1 mM Na₃VO₄, 10% glycerol, plus PhosSTOP Protease Inhibitor Cocktail (Roche, catalog number: 4906837001) and Protease Inhibitor Cocktail (Roche, catalog number: 11873580001). Insoluble proteins were removed by centrifugation and normalized proteins denatured by boiling in 4× SDS sample buffer (40% Glycerol, 8% SDS, 0.25 M Tris-HCl, pH 6.8 plus 10% 2-mercaptoethanol).

iRAP. Two sets of UCA1 antisense DNA probes with 3' biotin labels were ordered from siTOOLS Biotech GmbH. A U1 antisense probe (Chu et al., 2015) was included as a positive control. OVCA429 were cultured on 150 mm tissue culture plates and used at 90% confluency 96 h after seeding. Cells were washed with 10 mL ice-cold PBS and crosslinked in the presence of 10 mL ice-cold PBS using a Stratalinker (UV Stratalinker 1800, Stratagene) at 254 nm wavelength with 0.8 J/cm². Cells were collected and centrifuged at 1,000 g for 5 min at 4 °C. The supernatant was removed and cells used directly for iRAP or snap frozen in liquid nitrogen and stored at -80 °C until use. Cells were lysed in Lysis Buffer (10× the mass of pellet, 10 mM Tris-HCl, pH7.0, 50 mM EDTA, 1% SDS) containing freshly added PhosSTOP Protease Inhibitor Cocktail (Roche, catalog number: 4906837001) and Protease Inhibitor Cocktail (Roche, catalog number: 11873580001), PMSF (Sigma Aldrich, catalog number: 93482) and Superase-in (Ambion, catalog number: AM2696). Crosslinked cells were lysed

using a Covaris E220 evolution Focused-Ultrasonicator at 4 °C, 20% output, 200 burst cycles, for 15 min for each 20 million cells in 1 mL lysate buffer. Sonicated samples were centrifuged at 16,000 g for 10 min at 4 °C. Cell lysates representing 400 million cells were combined with 2 nM U1 or UCA1-odd/even probe sets in two volumes of hybridization buffer (750 mM NaCl, 1% SDS, 50 mM Tris-HCl pH 7.0, 1 mM EDTA, 15% formamide, with fresh PMSF, phosphatase inhibitor, proteinase inhibitor cocktail, and Suprase-in). Hybridization was performed at 37 °C with rotation overnight. RNA-protein complexes were precipitated by adding 2 mL Streptavidin Dynabeads M-270 (Thermo Fisher Scientific, catalog number: 65036) for 30 min at 37 °C. Dynabeads were washed with 2×NaCl and sodium citrate (SSC), 0.5% SDS, and fresh PMSF for 5×5 min.

RIP. Twelve microliter Dynabeads Protein A (Thermo Fisher Scientific, catalog number: 10001D) were washed with 200 µL HBS (150 mM NaCl, 10 mM HEPES, pH7.5 by KOH and incubated with 2 µg AMOT antibody, 2 µg YAP antibody or 2 µg rabbit IgG isotype control in the presence of 80 µL HBS buffer at room temperature for 1 h. Eight million CaOV3, OVCA429, or UWB1.289 cells were lysed with 800 µL cell lysis buffer (10 mM HEPES, pH7.5 by KOH, 150 mM NaCl, 0.1% NP-40, 5 mM EGTA, supplemented with 1× protease inhibitor cocktail and Suprase-in) at 4°C for 1 h. Cell debris and insoluble proteins were removed by centrifugation at 4°C, 12,000 g for 10 min, and the supernatants were incubated with antibody-conjugated Dynabeads at 4°C for 1 h. The Dynabeads were then washed 3 times with wash buffer (150 mM NaCl, 10 mM HEPES, pH7.5 by KOH, 0.1% NP-40). Half of the sample was eluted with 12 µL 1×Laemmli sample buffer (Bio-Rad, catalog number: 1610747) and used for Western blotting, TRIzol LS was added to the other half before proceeding with RNA extraction (Thermo Fisher Scientific, catalog number: 10296028).

Plasmids. Lenti GFP-AMOT p80 and lenti GFP-AMOT p130 were gifts from Dr. Kun-Liang Guan (Addgene plasmid numbers 32830 & 32828). To generate a *UCA1* overexpression plasmid, the full cDNA sequence for *UCA1* was purchased from Genewiz and cloned into the LeGO-iT vector. LeGO-iT was a gift from Dr. Boris Fehse (Addgene plasmid number 27361). Lentiviral particles were produced from co-transfecting HEK293T cells with LeGO-iT+*UCA1*, Lenti GFP-AMOT p80, or Lenti GFP-AMOT p130 together with lentiviral

packaging plasmids pMD2.G and psPAX2 (Gifts from Dr. Didier Trono, Addgene plasmid numbers 12259 & 12260). LeGO-iT has an IRES-tdTomato marker that was used for flow cytometric selection on Aria II cell sorter (BD Biosciences) after transduction.

Transfection. Pooled siRNAs targeting human *UCA1* (Dharmacon, catalog number: R-188002-00-0005), AMOT (Dharmacon, catalog number: L-015417-01-0005), YAP (Dharmacon, catalog number: L-012200-00-0005) or non-targeting scramble controls (Dharmacon, catalog number: D-001810-01-20) were transfected into CaOV3, UWB1.289, or OVCA429 cells using Lipofectamine RNAiMAX transfection reagent (Thermo Fisher Scientific, catalog number: 13778075), DharmaFECT 3 (Dharmacon, catalog number: T-2003-03), or DharmaFECT 1 transfection reagent (Dharmacon, catalog number :T-2001-03), respectively.

Cellular fractionation. Cells were fractionated as previously described (Bahn et al., 2015) with some modifications. Six million OVCA429 cells were treated with the plasma membrane lysis buffer (10 mM Tris-HCl, pH 7.5, 0.15% Nonidet P-40, 150 mM NaCl) on ice for 5 min after homogenization by flicking. For CaOV3 and UWB1.289 cells, six million cells were lysed for 4 min with lysis buffer and for OSEC4C2 cells, eight million cells were treated with lysis buffer for 2 min. Centrifuge at 15,000 g for 10 min at 4°C after loading the lysate onto 24% sucrose cushion (24% RNase-free sucrose in plasma membrane lysis buffer) using large orifice tips. The supernatant (cytoplasmic fraction) was retained after centrifugation, and the pellet (nuclear fraction) was washed with 1×PBS/1 mM EDTA and resuspended in 200 µL of 1×PBS/1 mM EDTA.

Western Blotting. Protein samples were run on 4-20% gradient precast protein gel (Bio-Rad, catalogue number: 456-1096) and transferred onto PVDF membrane (Bio-Rad, catalogue number: 1704157). After 1 h blocking, membranes were incubated with corresponding antibody at 4°C overnight. Membranes were washed three times with Tris-buffered saline containing 0.5% Tween 20 (TBST) before incubating with HRP-conjugated secondary antibody or Clean-Blot IP detection reagent (Thermo Fisher Scientific, catalogue number: 21230) for IP samples at room temperature for 2 h. Then the membranes were incubated briefly with ECL Western Blotting substrate (Thermo Fisher Scientific, catalogue number: 32106) after three times wash with

TBST. The membranes were exposed to HyBlot Autoradiography Film (Denville Scientific, catalogue number: E3018). Antibody information is listed in Supplementary Table 6.

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