

RUNX1 knockdown induced apoptosis and impaired EMT in high-grade serous ovarian cancer cells

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Additional file 1: Figure & Table Legends:

Figure.S1. Overall Survival and Disease-Free Survival comparison of RUNX1 altered and unaltered patients in Ovarian Serous Cystadenocarcinoma via the cBioportal Genomics database. Genetically altered of RUNX1 gene occurs in ovarian cancer patients (A). Overall Survival comparison of RUNX1 altered patients and unaltered patients (B). Disease-Free Survival comparison of RUNX1 altered patients and unaltered patients (C).

Figure.S2. Two ovarian cancer cell lines with stable knockdown RUNX1 were established. Western blot confirmed RUNX1 stable knockdown in ovarian cancer cells (SKOV3 and OVCAR3) constructed by plasmids containing RUNX1-targeting shRNA (A and B).

Figure.S3. The quantitative analysis of apoptosis-related molecules proteins after RUNX1 knockdown and Ro5-3335 treatment. The quantitatively analysis of the apoptosis-related molecules in RUNX1 knockdown cell lines (A and B). The quantitative analysis of the apoptosis-related molecules after Ro5-3335 (a RUNX1 inhibitor) treatment (C and D). * $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$ compared to control cells expressing a scramble shRNA control, paired t-test.

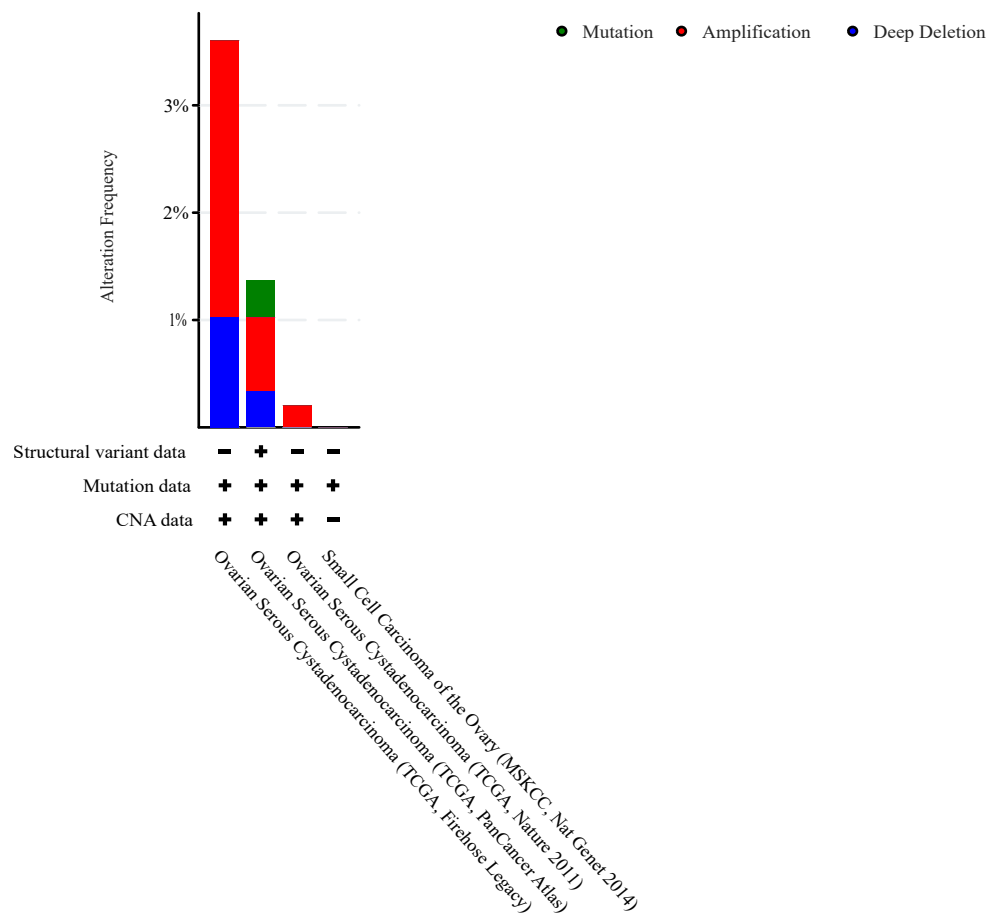
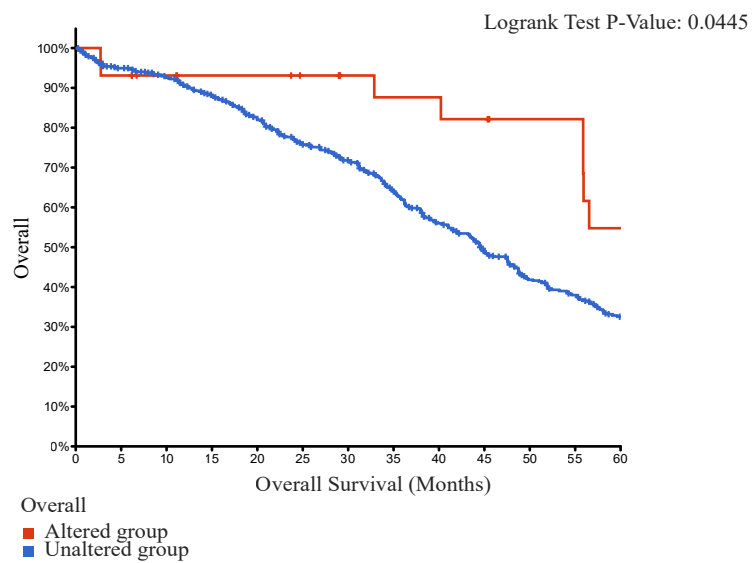
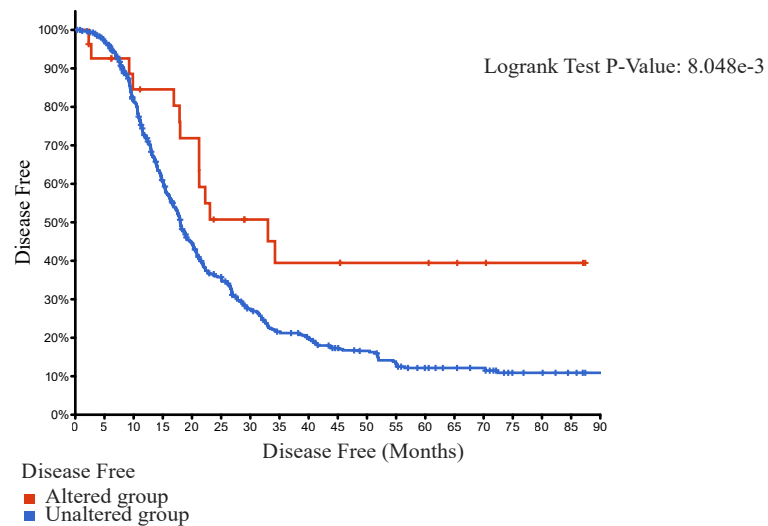
Additional file 1: Figure 4. The quantitative analysis of EMT-related signaling pathway proteins after RUNX1 knockdown and Ro5-3335 treatment. The

quantitative analysis of the signaling molecules changes pattern in the RUNX1 KD cells involved in the EMT-related signaling pathway (A&B). The quantitative analysis of the signaling molecules changes pattern after Ro5-3335 (a RUNX1 inhibitor) treatment involved in the EMT-related signaling pathway (C and D). The quantitatively analysis of EMT-related molecules in RUNX1 knockdown cell lines (E and F). The quantitative analysis of EMT-related molecules after Ro5-3335 treatment (G and H). * $p < 0.05$, ** $p < 0.01$ and *** $p < 0.001$ compared to control cells expressing a scramble shRNA control, paired t-test.

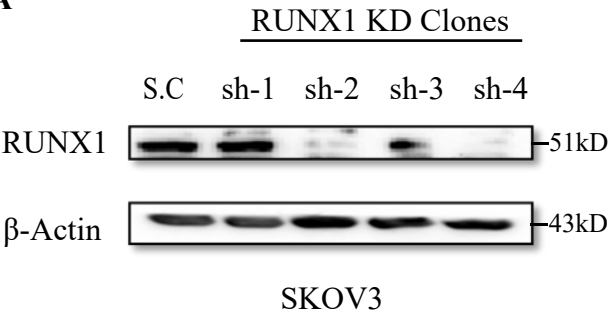
Additional file 1: Figure 5. The effect of RUNX1 knockdown on the WNT signaling pathway. GSEA identified the enrichment plot of WNT signaling-related genes in RUNX1 KD compared to control cells (A). Western blot detected the critical molecule of WNT signaling in RUNX1 knockdown cell lines (B and C).

Table S1. ShRNA constructions and information for RUNX1.

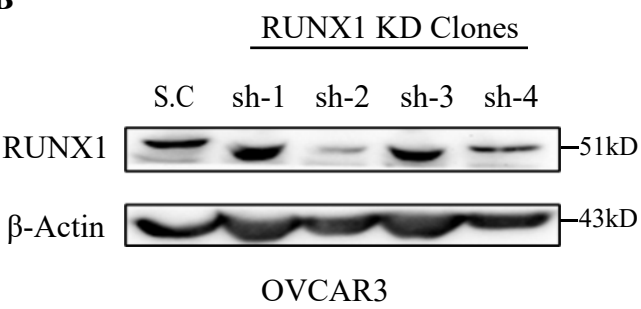
Table S2. Six clinical drug treatment responses with or without RUNX1.

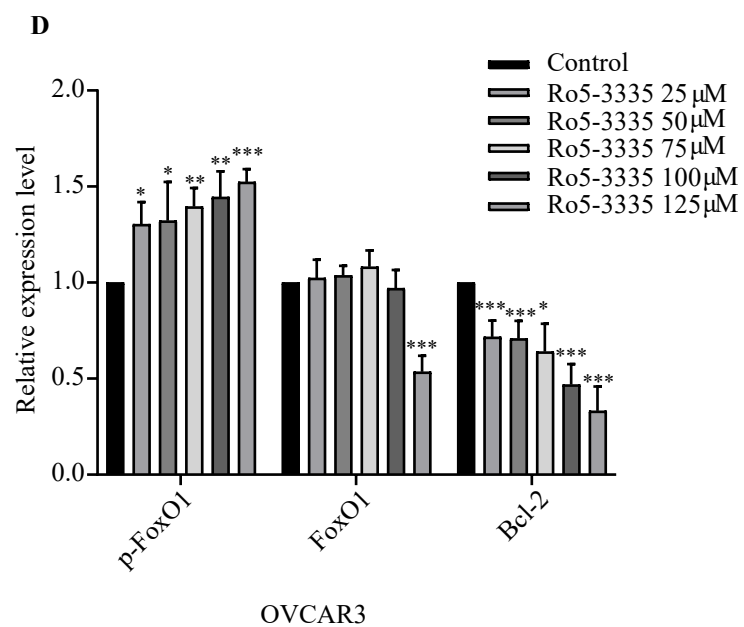
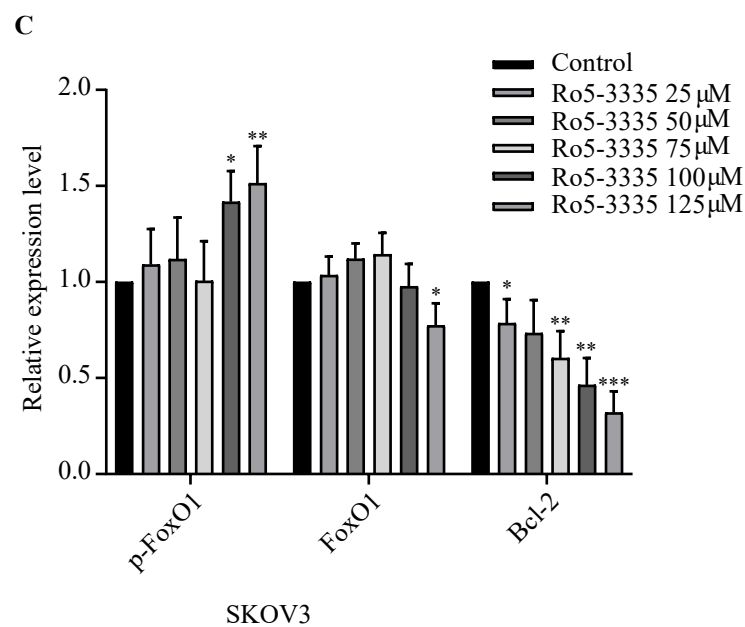
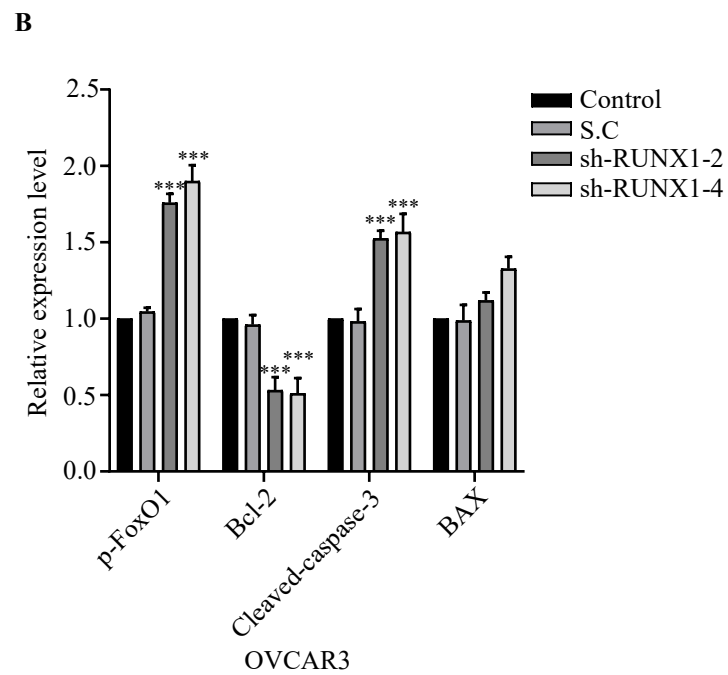
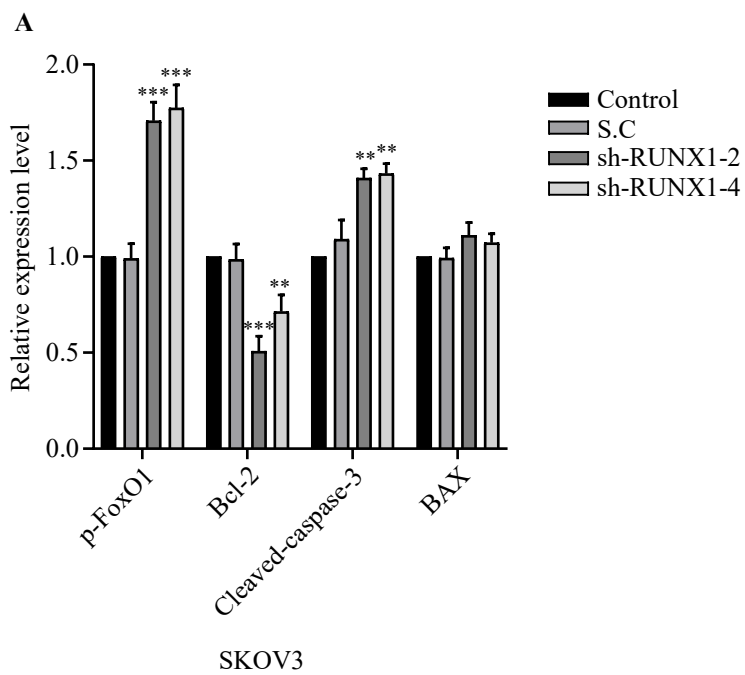
A**B****C**

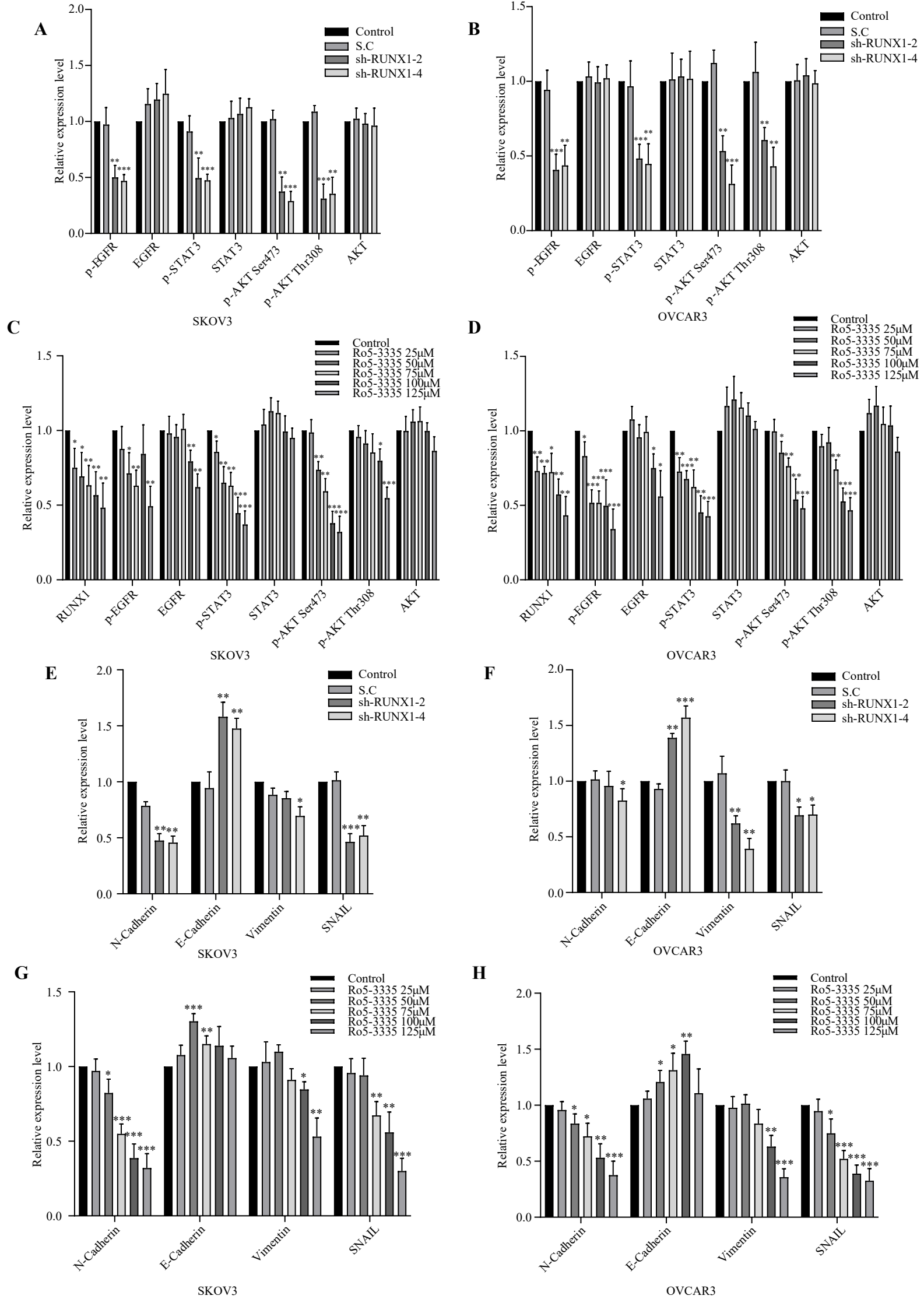
A



B







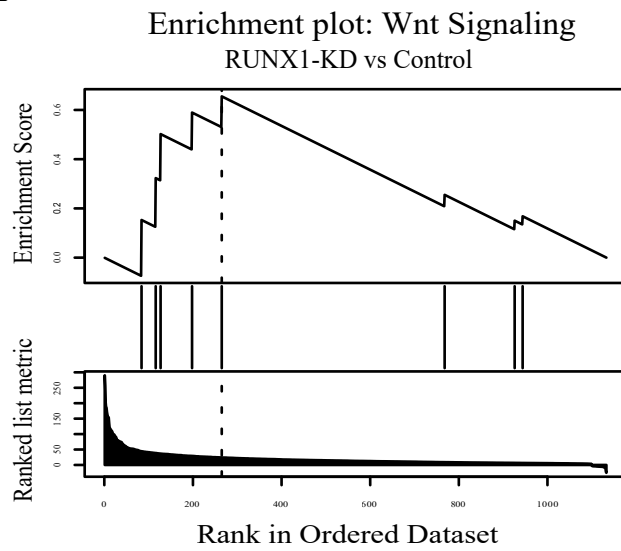
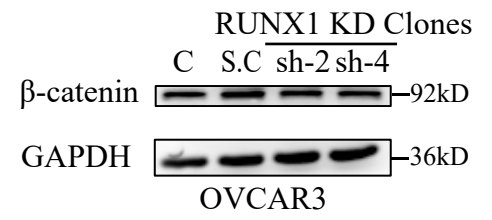
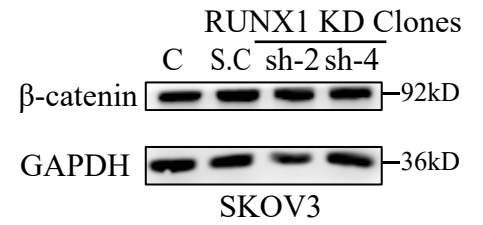
A**B****C**

Table.S1 ShRNA constructions and information for RUNX1.

Gene name	TRC numbers	shRNA sequnces
RUNX1-shRNA-1	TRCN0000338428	CCGGCTACGATCAGTCCTACCAATACTCGAGTATTGGTAGGACTGATCGTAGTTTTTT
RUNX1-shRNA-2	TRCN0000338490	CCGGGAACCACTCCACTGCCTTTAACTCGAGTTAAAGGCAGTGGAGTGGTTCTTTTTT
RUNX1-shRNA-3	TRCN0000338427	CCGGGAACCAGGTTGCAAGATTTAACTCGAGTTAAATCTTGCAACCTGGTTCTTTTTT
RUNX1-shRNA-4	TRCN0000013658	CCGGGCCTTGAAATACCTGTTTCTTCTCGAGAAGAAACAGGTATTTCAAGGCTTTTTT