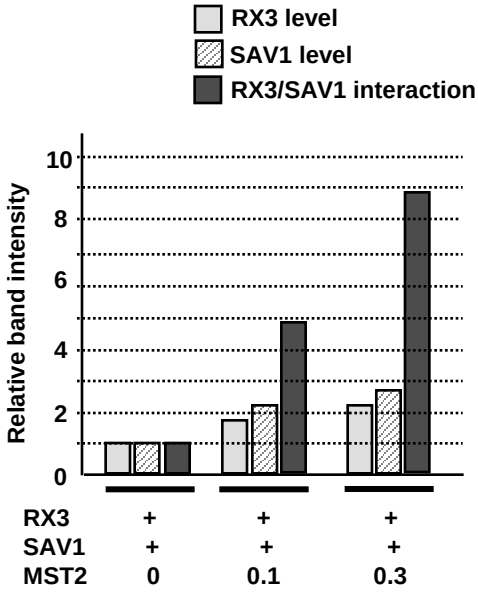
Supplementary Figure 1



Supplementary Figure 1. Densitometric analysis of Fig. 1C.
The band intensities of RUNX3, SAV1 and the interaction of the two proteins (SAV1/RX3) of the Figure 1C were analyzed by Luminescent image analyzer (Fuji film LAS-3000) and the relative intensities are depicted as a bar diagram. .

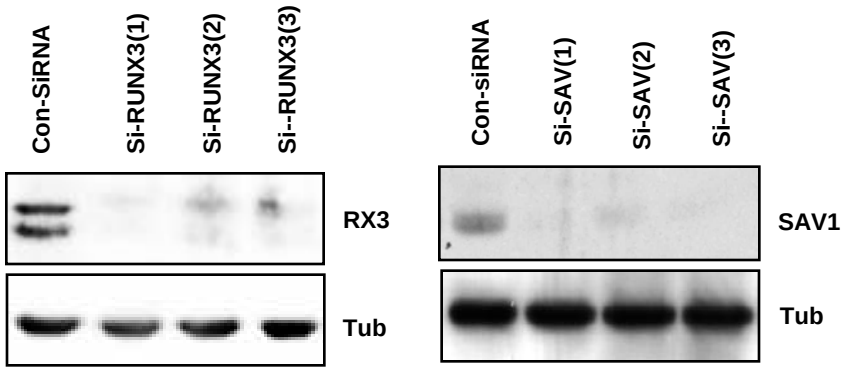
Supplementary Figure 2

Phosphorylation sites	Peptide Scan (Peptide Hits)	Molecular Weight	Charge	Xcor
T69, S77, S81	R.T^DSPNFLCS^VLPS^HWR.C (18/48)	2098.89	1.60	**1**
S71, S77, S81	R.TDS^PNFLCS^VLPS^HWR.C (22/60)	2098.89	1.63	**2**
S153	R.AIKVT^VDGPREPR.R (18/48)	1517.82	1.62	**1**
S17	R.FTPPS^PAFCGGGGGKM (10.30)	1627.69	1.48	**1**

Supplementary Figure 2. Identification of phosphorylation sites by LC-MS/MS HEK293 cells transfected with expression plasmids for *Myc-RUNX3, SAV1* and *MST2* (or MST2-K56R for negative control) and purified by pull down with G-Sepharose-anti-Myc antibody beads. The bounded protein was separated by 10% SDS-PAGE, and the corresponding RUNX3 band was in gel digested by trypsin and analyzed by tandem mass spectrometry (MS/MS) using an LTQ linear ion trap mass spectrometer (Thermo Electron). Assignment of MS/MS data was performed using SEQUEST software (Thermo Electron). Resultant matches were entered and compiled into a MySQL database, and proteomics computational analyses were performed using a Hypertext Preprocessor (PHP)-based program. First, peptide identifications were made based on the following criteria: cross-correlation score > 1.5, 2.0 and 2.5 for charge states +1, +2 and +3, respectively; delta correlation > 0.1; primary score > 200; ranking of the primary score < 3; and percent fragment ions > 30%. Second, protein identifications were assigned when the following criteria were met: the unique peptide match number was greater than or equal to two, the peptides contributing to protein matches were derived from a single gel slice or from adjacent slices, and the protein was identified in at least two vitreous samples.

Supplementary Figure 3

Si-RUNX3(1) -HSS101407	5'-AGU UCU CGU CAU UGC CUG CCA UCA C-3'
Si-RUNX3(2) -HSS101408	5'-UUG GUG AAC ACA GUG AUG GUC AGG G-3'
Si-RUNX3(3) -HSS101409	5'-UGA AGU GGC UUG UGG UGC UGA GUG A-3'
Si-SAV1(1) -HSS127048	5'-AAA UUC GGA UGA CUC AAC UCG UUC C-3'
Si-SAV1(2) -HSS127049	5'-UUC AUG UGC ACG AUC UCC AAG UGG C-3'
Si-SAV1(3) -HSS127050	5'-UAA AUC UUC AGA ACC AUG GUU AGU C-3'



Supplementary Figure 3. Knockdown of *SAV1* and *RUNX3*.
HEK293 cells were transfected with siRNAs against *SAV1* or *RUNX3* and knock down of endogenous *SAV1* and *RUNX3* were measured by IB with anti-SAV1 or anti-RUNX3 antibody.