Supplemental Table 1: *RAB31* Oligonucleotide primer sequences used for PCR in ChIP analysis.

Primers	Position	Strand	Nucleotide sequence
Site I	-858/-800	Forward	-858/-839 5'- GGGATCTCCACGTTTCTACCT-3'
		Reverse	-779/-800 5'- TTTCTCAGTAGAGCAAATCCTG-3'
Site II	-978/-867	Forward	-979/-960 5'- GAGTGGATGAGGTGCTCTAG-3'
		Reverse	-867/-886 5'-CCTGCATCGTTCCTAACTGG-3'
Site III	-1502/-1337	Forward	-1502/-1483 5'-TGCCCACATAGAAGACTCTG-3'
		Reverse	-1337/-1356 5'-ATTAAATTCCCCAGAAGAGC-3'
Site IV	-2019/-1874	Forward	-2019/-2001 5'-ATGAGACACAAATGAGGTC-3'
		Reverse	-1855/-1874 5'-CTGCTCTCTTCTCCACTAGA-3'

Supplemental Table 2. Infra-red (IR) labeled *RAB31* nucleotide probes for EMSA analysis.

Primers	Position	Nucleotide sequence	Strand
Site I	-816/-797	5'/5IRD700/CTGCCCACACGAGTTGCAGG-3'	Forward
		5'/5IRD700/GACGGGTGTGCTCAACGTCC-3'	Reverse
Site II	-976/-957	5'/5IRD700/TGGATGAGGTGCTCTAGGCC-3'	Forward
		5'/5IRD700/ACCTACTCCACGAGATCCGG-3'	Reverse
Site III	-1506/ -1487	5'/5IRD700/ACCTCGTCCACGAGATCCGG-3'	Forward
		5'/5IRD700/TGGAGCAGGTGCTCTAGGCC-3'	Forward
Site IV	-2016/ -1997	5'/5IRD700/AGACACAAATGAGGTCATTT-3'	Forward
		5'/5IRD700/TCTGTGTTTACTCCAGTAAA-3'	Reverse

Supplemental Table 3. Primers used to generate various *RAB31* promoter elements.

Constructs (-2023/+41 bp)	**No.**	**Primers with restriction sites (5'-3')**	**Position**	**Strand**
Wild type*	1	aat *acgcgt* CAGAATGAGACACAAATGAGGTC	-2023/ -2001	Forward
	2	aat *gctagc* CAGTCCTCAGAGGTACAGGTAGA AACGTGGAGATCCC	-858/ -822	Reverse
	3	ggg *gctagc* GGTTTCTGCCCACACGAGTTGCAG GATTTGCTCTACTG	-821/ -784	Forward
	4	ggg *aagctt* ACCCCGAGAAGGCACACTTTGAGC TCCCGTATCG	+41/-9	Reverse
Site I mutant	1	Same as above in wild type construct		
	2	Same as above in wild type construct		
	3	aat *gctagc* GGTTTCTG**C<u>AAGTA</u>**CGAGTTGCAG GATTTGCTCTACTG Substitutions underlined in *RUNX1* site I (bold)	-821/ -784	Forward
	4	Same as above in wild type construct		
Site II mutant	1	Same as above in wild type construct		
	2	aat *gctagc* CGTGTGGGCAGAAACCCAGTCCTC AGAGGTACA …… GAGC**A<u>TAGAA</u>**TCC Substitutions underlined in RUNX1 site II (bold)	-975/ -806	Reverse
	3	ggg *gctagc* AGTTGCAGGATTTGCTCTACTGAG AAAAAGAC	-805/ -765	Forward
	4	Same as above in wild type construct		
Site III mutant	1	Same as above in wild type construct		
	2	aat *gctagc* CAGAGTCTTCTA**T<u>ACA</u>TG**CAG Substitutions underlined in RUNX1 site III (bold)	-1503/ -1483	Reverse
	3	aat *gctagc* CTTTGGATACAGAGTCAAGGAC	-1482/ -1461	Forward
	4	Same as above in wild type construct		
Site IV mutant	1	aat *acgcgt* CAGAATGAGACACAAA**<u>CACTTG</u>**C Substitutions underlined in RUNX1 site IV (bold)	-2023/ -2001	Forward
	2	Same as above in wild type construct		
	3	Same as above in wild type construct		
	4	Same as above in wild type construct		

The position numbering shown is from the ATG site. Appropriate restriction sites introduced at the 5' end of the primers indicated in italics. *acgcgt*= Mlu I site; *gctagc*=Nhe I site and *gctagc*=Hind III site.

* Wild type promoter regions were generated by PCR using the primer set 1 and 2 or 3 and 4 separately with the restriction site (s) incorporated and cloned into TOPO TA vectors. The recombinants were digested with same restriction enzymes and the genomic inserts were ligated and subcloned into pGL3 basic with appropriate sites.

Mutant promoter regions were also generated using primers as indicated above.

Supplemental Table 4. Antibodies used in this manuscript.

WB: western blot; IF: immunofluorescence

Antigen	Catalogue	Vendor	Application
RUNX1(N-20)	sc-8563	Santa Cruz Biotechnology	WB/IF
RUNX1	sc-365644	Santa Cruz Biotechnology	WB
IgG	sc-2028	Santa Cruz Biotechnology	WB/IF
RAB31	ARP61983-P050	Aviva System Technology	WB/IF
CD-MPR (H-7)	sc-365196	Santa Cruz Biotechnology	WB/IF
β-actin	sc-1616	Santa Cruz Biotechnology	WB
VWF	ab6994	Abcam	WB/IF
mPR alpha	PA5-61376	Invitrogen/Thermo Scientific	WB/IF
CD63(Mx49.129.5)	sc-5275	Santa Cruz Biotechnology	WB/IF
EGFR	4267	Cell Signaling Technology	IF
EEA1	2411	Cell Signaling Technology	IF
CD-M6PR	ab134153	Abcam	WB/IF