Supplemental Table 1: Primers used for Real-Time PCR

Gene	Strand	Primers (5'-3')
RAB1B	Forward	5'- CCTTGCAGCT GGAGAGAATC -3'
RAB1B	Reverse	5'- CTGTCGGGTTGAAAGAGAGC -3'
RAB1A	Forward	5'- AACTATGATGCCATGGGCTC -3'
RAB1A	Reverse	5'- CACCTGACTGCTTGACTGGA -3'
GAPDH	Forward	5'-AACTGTGTGGTCTTGAACCTCCGT -3'
GAPDH	Reverse	5'-ACACACTCTCATGCAGCTACCAT -3'

Supplemental Table 2. Oligonucleotide primer sequences used in PCR for ChIP analysis

Primers	Position	Strand	Nucleotide sequence
Site 1	-400/-480	F	-480/-461 5'-CGAAGAACCCTGGAC AAATG-3'
		R	-400/-419 5'-CCAATACCCACGTTGTGAAC-3'
Sites 2 & 3	-785/-576	F	-658/-639 5'-GCCCACAAGTCAGGCTTTCC-3'
		R	-576/-597 5'-TTTGTG AGGAGCAGAGCTCATA-3'
Site 4	-785/-686	F	-785/-766 5'-CCAGCGTCTCTAGACTGG GG-3'
		R	-766/-785 5'-AATATCTGGGCCCAGCTGCG-3'

ChIP-PCR was performed using Go Taq Green Master Mix with one cycle at 95°c for 2 minutes followed by 32 cycles of 95°c for 30 sec, 62°c for 45 sec, and 72°c for 60 sec. Amplified products were analyzed by agarose gel electrophoresis.

Supplemental Table 3. IR labeled *RAB1B* nucleotide probes for EMSA analysis

Primers	Position	Strand	Nucleotide sequence
Site 1	-445/-426	Sense	5'-/5IRD700/TACTAGAACCCACATTCTCA-3'
		Anti-sense	5'-/5IRD700/ATGATCTTGGGTGTAAGAGT-3'
Site 2	-630/-611	Sense	5'-/5IRD700/CTCACTTGTGGGGTTCTGGA-3'
		Anti-sense	5'-/5IRD700/GAGTGAACACCCCAAGACCT-3'
Site 3	-659/-640	Sense	5'-/5IRD700/GGCCCACAAGTCAGGCTTTC-3'
		Anti-sense	5'-/5IRD700/CCGGGTGTTCAGTCCGAAAG-3'
Site 4	-778/-759	Sense	5'-/5IRD700/CTCTAGACTGGGGTGGAGCC-3'
		Anti-sense	5'-/5IRD700/GAGATCTGACCCCACCTCGG-3'

Supplemental Table 4. Primers used to generate various *RAB1B* promoter elements.

Constructs +15/-785 (bp)	Primers with restriction sites (5'-3')	Strand	Position
Wild Type	aaa *ctcgag* CCAGCGTCTCTAGACTGGG	Forward	-785/-767
	ttt *aagcgt* ATATTCGGGGTTCATGGCGG	Reverse	+15/-5
*Site 1 mutant	aaa *ctcgag* CCAGCGTCTCTAGACTGGG	Forward	-785/-767
	aaa *acgcgt* CATTAAATGAGAATATTTATT (*Nested primer with substitutions underlined*)	Reverse	-419/-440
	ata *acgcgt* TTCACAAACGTGGGTATTGGGA	Forward	-418/-398
	ttt *aagcg*t ATATTCGGGGTTCATGGCGG	Reverse	+15/-5
Site 2 mutant	aaa *ctcgag* CCAGCGTCTCTAGACTGGGGT GGAGCCGGGAAGGGTCGTGCGTGAGTG GGGGACAGTGTGTCTCGCTCAACCGCTG TCCGCGCAGCTGGGCCCAGATATTGTGC CCCACCCCGGAATTGCGTGAGGGGCCCA CAAGTCAGGCTTTCCCTAAAACACTCAC T TCT - - - - CT TCT.	Forward	-785/-614
	ttt *aagcgt* ATATTCGGGGTTCATGGCGG	Reverse	+15/-5
Site 3 mutant	aaa *ctcgag* CCAGCGTCTCTAGACTGGGGTG GAGCCGGGAAGGGTCGTGCGTGAGTGGG GGACAGTGTGTCTCGCTC……TATTG TGCCCCACCCCGGAATTGCGTGAGGGG CTTAAA AGTC.	Forward	-785/-648
	ttt *aagcgt* ATATTCGGGGTTCATGGCGG	Reverse	+15/-5
Site 4 mutant	aaa *ctcgag* CCAGCGTCTCTAGTCTAGTGTGG	Forward	-785/-763
	ttt *aagcgt* ATATTCGGGGTTCATGGCGG	Reverse	+15/-5

The position numbering shown is from the ATG site. Nucleotide substitutions are underlined and deletions are indicated by dashes in RUNX1 sites.

Appropriate restriction sites introduced at the 5'end of the primers indicated in italic.

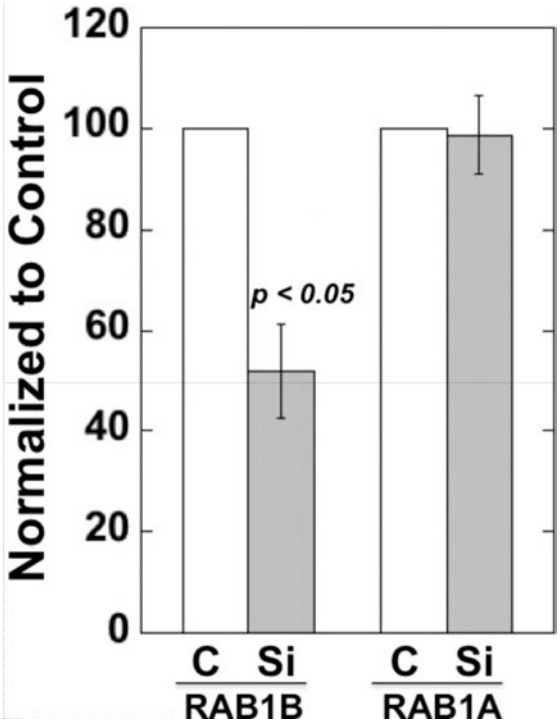
*Site 1 mutant was generated by PCR using the same forward primer as in the case of wild type construct and a reverse nested primer carrying mutated RUNX1 site incorporated with Mlu I restriction site. Site 1 mutation (CCCACA to TAAATA) was incorporated into the nested reverse primer at -419/-440 with a Mlu I site at 5' end (aaa

acgcgt): CATTAAATGAGAATATTTATT. These primers were used to amplify the sequence from -419 bp to the upstream -785 bp.

The sequence -418 bp to the +15 bp was amplified with a forward primer with Mlu I site incorporated next to the nucleotide -418 (-418/ -398 5'- ata *acgcgt* TTCACAAACGTGG GTATTGGGA) and the same reverse primer as used in the generation of the wild type construct.

The above regions were amplified, cloned into TOPO TA vectors, digested based on the restriction sites and the inserts isolated. The genomic inserts Xho -785/ -419 Mlu I and Mlu I -418/ +15 Hind III were ligated and subcloned into pGL3 basic with appropriate sites.

Supplemental Figure 1



RAB1B and RAB1A mRNA in HEL cells transfected with RAB1B siRNA for 48 hours. Shown (mean±SEM, N=5) are levels relative to GAPDH and normalized to the levels in the control siRNA treated cells.