Figure S1. VL30 retrotransposition frequency values in C127 and J3B1A cells. (A and B) Samples of 15,000 cells from single and massive (Mass.) C127 or J3B1A clone cells were measured for EGFP positivity with FACS using respective normal cells. Columns represent the mean value of net retrotransposition frequencies (calculated as in Fig. 1A) of duplicate samples from three independent experiments with ±SD indicated with bars. There was no statistically significant difference (n.s.) between retrotransposition frequencies of C127 clones 3, 4, 8, 13, as well as 5 and 6 clones. In the remaining clones, multiple comparisons in pairs (Tukey's post hoc test after ANOVA) revealed a statistically significant difference at $P<0.05$. Similarly, in the retrotransposition frequencies of J3B1A clones 1, 10, 13, as well as clones 8, 9 there was no statistically significant difference. In all other relative clones, multiple comparisons in pairs (Tukey's post hoc test after ANOVA) revealed a statistically significant difference at $P<0.05$.

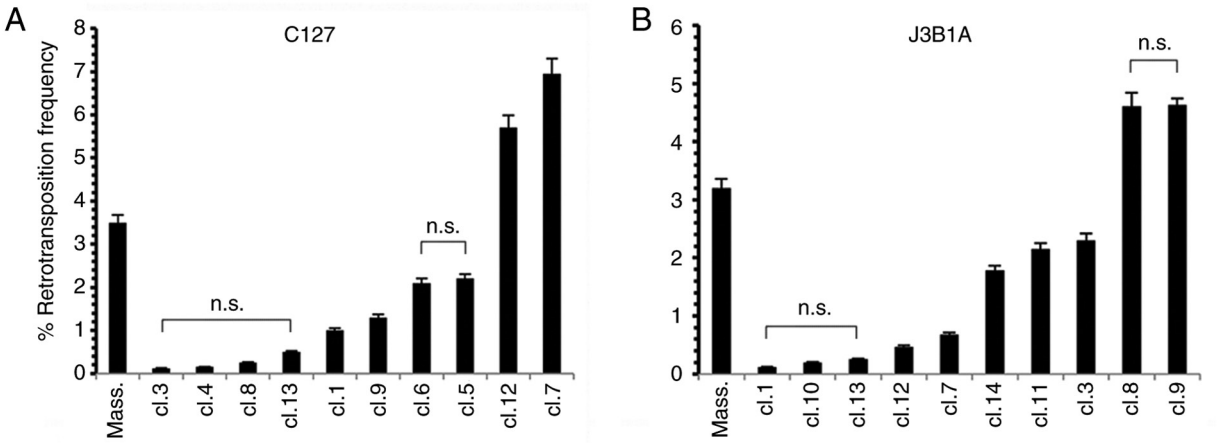

Figure S2. VL30 retrotransposition has no effect on the epithelial phenotype of C127 cells. Control C127 and C127-retrotransposition positive clone 7 cells, respectively, were grown in normal culture dishes and photographed under normal light (magnification, x20).

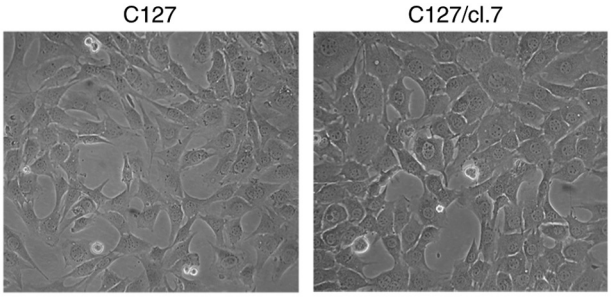

Figure S3. EGFP-N1/G418-resistant HC11 cells retain their epithelial phenotype. Control HC11 and massive EGFP-N1/G418-resistant HC11 clone cells, grown in normal culture dishes, were photographed under normal light (magnification, x20).

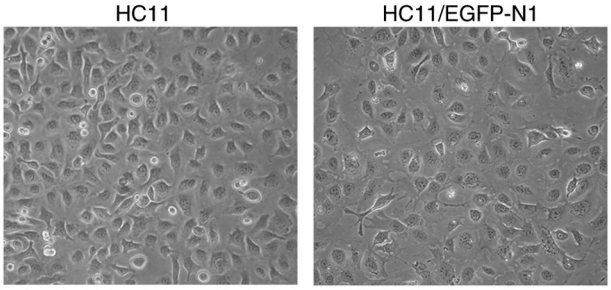

Figure S4. Target sequencing analysis of clone 7 and clone 19 DNAs. (A) Basic structure of the NVL-3*/EGFP-INT VL30 recombinant element. 5' and 3' LTRs are shown with black blocks. Green blocks are parts of sequences of the EGFP gene interrupted by a γ-globin intron shown with a yellow block. Light blue block corresponds to sequences of the human cytomegalovirus immediate-early (CMV-IE) promoter. Block arrowheads show transcriptional orientations. (B) Schematic mapped reads corresponding to both 3'LTR and extending genomic sequences obtained after sequencing of clone 7 (cl.7) and clone 19 (cl.19) DNAs. Both-side arrowhead shows '3 LTR sequences.

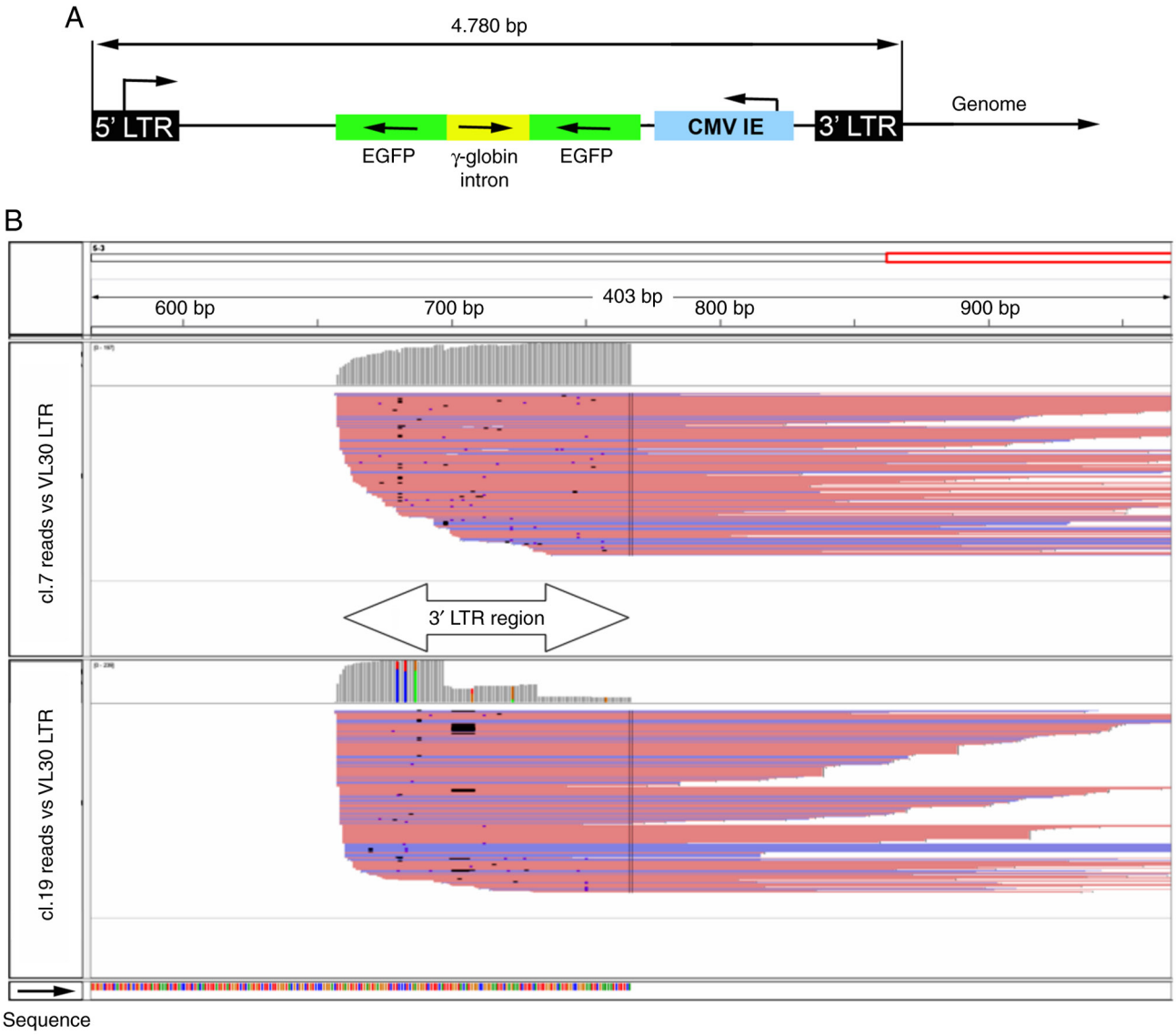

Figure S5. Comparison of mRNA expression of VL30 elements and enRTs genes in NIH3T3 fibroblasts and HC11 cells. Total RNA isolated from NIH3T3 or HC11 cells was reverse transcribed and subjected to RT-qPCR analysis (for primers please see Materials and methods). Indicated grey and blue columns represent mRNA expression levels, after control GAPDH cDNA template normalization, as mean values of duplicate samples from three independent experiments with ±SD indicated with bars. P1 and P2 correspond to statistically significance values of 0.0045 and 0.0134, respectively (paired sampler Student's t-test).

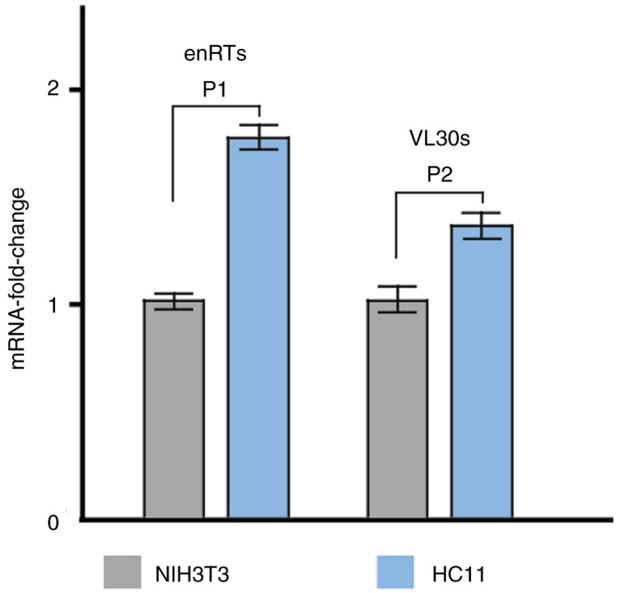

Table SI. High-confidence new VL30 integrations in HC11 clone cells.

Gene name	Distance to gene/chromosome no.	Function, disease and cancer type	(Refs.)
Clone 19 integrations			
Accb1a	+94142/17	Low expression involved in colorectal cancer	(1)
Ahctf1	-130748/1	Related to cancer through histone LSD1 demethylase	(2,3)
Calm2	-154014/17	Prognostic biomarker for gastric cancer	(4)
Cd38	+42731/5	Suppression of the immune system in breast cancer	(5)
Cdc42bpa	-26157/1	Regulated by miR-515-5p in breast cancer	(6)
Dgke	+22081/11	Silenced in non-adherent HT-29 colon cancer cells	(7)
Eif2ak1	-35707/5	Inhibitor kinase responding to heme deprivation	(8)
Epcam	-35030/17	Linked with Lynch syndrome (retrotransposon Alu)	(9)
		CSCs marker in solid cancers including breast cancer	(10)
Fbxo33	-7540/12	Involved in cancer development & progression & EMT	(11)
Fgfbp1	+70222/5	Associated with several types of cancer including pancreatic and colorectal adenocarcinomas	(12)
Ganab	+932/19	Associated with polycystic kidney and liver disease	(13)
Gm3604	+86570/13	Unknown function	-
Gm6614	-161544/6	Unknown function	-
Gspt2	-15268/X	Related to translational control in mammary tumors	(14)
		Hypothesis: Generated by retrotransposition of GPT1's RNA	(15)
Maged1	-78658/X	Down-regulated in breast carcinoma cell lines	(16)
Ndufa6	-4910/15	Down-regulated in response to drugs in rheumatoid arthritis	(17)
Pbx1	-169721/1	Regulates EGF-ERα genes expressed in aggressive breast tumors	(18)
Rbm12b1	-7309/4	Unknown to be linked with disease	OMIM database https://www.omim.org
Rbm12b2	+43567/4	Unknown to be linked with disease	OMIM database https://www.omim.org
Slco1a6	+13195/6	Broadly affects gene expression in mouse pancreatic islets	(19)
Trim25	+45393/11	Overexpressed in breast and ovarian cancer	(20,21)
Try4	-105197/6	A maturation marker in pancreas	(22)
Usp42	-49801/5	Involved in modulation of transcription	(23)
		Stabilizes p53 in response to stress	(24)
Zfp808	+135344/13	Zinc finger proteins are related to *Epithelial to mesenchymal transition and cancer progression*	(25)
Clone 7 integrations			
Aarsd1	+10804/11	Co-chaperone, required for muscle differentiation	(26)
Abcf2	+3545/5	Related to chemo-resistance in breast cancer	(27)
Akap2	-65048/4	Required for regulation of β-catenin/Wnt signaling	(28)
Asb14	-140846/14	Related to metabolic syndrome	(29)
Col5a1	+109009/2	Might be a key gene for human breast cancer	(30)
Dnahc12	+60437/14	Unknown to be linked with disease	OMIM database https://www.omim.org
Fam49a	+222800/12	Modulates the PTEN pathway	(31)
		The PTEN/Akt/mTOR pathway is involved in breast cancer	(32)
Fcnb	+89451/2	Marks apoptotic & necrotic cell death	(33)
G6pc	+39250/11	Glucose metabolism and cell cycle control in *ovarian cancer*	(34)
Gm13151	-692/4	Zinc finger proteins are related to *Epithelial to mesenchymal transition and cancer progression*	(25)
Gm20459	+151288/4	Links the Palm2 and Akap2 anchor protein 2 genes	OMIM database https://www.omim.org
Gpr68	+104086/12	Mediates interaction of *cancer fibroblasts and cancer cells*	(35)
Pet2	+398507/X	Not related to disease	OMIM database https://www.omim.org
Rpl36-ps3	-427047/12	Pseudogene 3	OMIM database https://www.omim.org

Table SI. Continued.

Gene name	Distance to gene/chromosome no.	Function, disease and cancer type	(Refs.)
Slc28a1	-29880/7	Associates with prognosis of *pancreatic cancer*	(36)
Il1rapl1	-895537/X	Lower expression in breast cancer cell lines and primary tumors	(37)
Rragc	+376884/4	Regulates the mammalian target rapamycin complex 1 (mTORC1)	(38)
Rragc		mTORC1/RRAGC mutations are related with *follicular lymphoma*	(39)
		Activated AKT-mTOR signaling is involved in breast cancer metastasis	(40)
		mTOR activation drives *epithelial to mesenchymal transition*	(41)

New VL30 genomic integrations of clones 19 and 7. The list shows horizontally the name of a gene accompanied by: Its molecular distance from the nearest new VL30 integration, chromosome number of integration, as well as gene property, function, and related disease/non-disease or cancer type. Symbols (-) or (+) denote integrations upstream or downstream of genes, respectively. Genes involved in various types of cancer are presented in italics, while those in breast cancer are underlined. The numbered references of the genes are presented in the Reference list.

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