

Supplementary Table

pKT2/FAHIL//SB		
Genomic Sequence	Chromosome	Refseq
<<FAHIL>>TATGCTCCAAATGAGAGGAC	3	Nearest gene ~300kb
<<FAHIL>>TATCAGTCCCTCCAGAACAC	2	Intron of NM_028747
<<FAHIL>>TATGAATGTATGCTATGCCA	3	Intron of Amy2
<<FAHIL>>TAACACGAGGCCAGTACAAG	7	Nearest gene ~300kb
<<FAHIL>>TAGGTCTGCTGAATACCAGA	9	Intron of Senp6
<<FAHIL>>TATATGTGCCATTTTATATG	10	Nearest gene ~20kb
<<FAHIL>>TACATGGAACCTCCAAGCTGT	11	Nearest gene ~130kb
<<FAHIL>>TAGGCCTATTAGGGAGAAGA	11	Nearest gene ~250kb
<<FAHIL>>TATAATACACACAAGACACA	16	Intron of Runx

pKT2/FAH-hAAT//SB		
Genomic Sequence	Chromosome	Refseq
<<FAH-hAAT>>TATCCCTGGCTGTCCATGGG	15	Intron of Krt1-18
<<FAH-hAAT>>TACCGGGTAGGGGAGGCGCT	X	nearest gene 130 kb
<<FAH-hAAT>>TACTACTCCCTATTTCAGTCC	1	Intron of Ddr2

pKT2/FAHIL-NRAS or pT2/sh.p53-GFP		
Genomic Sequence	Chromosome	Refseq
<<Onc>>TATGTCTCCTGGTAACATCA	3	Nearest gene ~15kb
<<Onc>>TATGTATTGGATATTAGACC	7	Nearest gene ~2.5kb
<<Onc>>TAAATGAGGATCAGGCTAAT	7	Nearest gene ~120kb
<<Onc>>TATATTCCCGAAAAGGGTT	X	Nearest gene ~140kb
<<Onc>>TACCTTCAATCCCAGCACTT	2	Intron of Slc9a8
<<Onc>>TACCTATCTCAGTCAACAAG	2	Intron of C20orf67
<<Onc>>TAGGTATAGACTTGACTGCC	8	Nearest gene ~6kb

Supplementary Table Genomic insertion sites of co-expression constructs were recovered from mouse liver DNA extracts. The first 20 nucleotides of genomic sequence are shown, as well as the corresponding chromosome and Refseq information. All integration sites had a TA dinucleotide flanking the terminus of the transposon, a hallmark of SB transposition.

Methods For pKT2/FAHIL//SB and pKT2/FAH-hAAT//SB insertion sites were recovered by inverse PCR as described¹. For oncogene insertion site recovery linker mediated PCR was used as described². The sequence results were analyzed by nucleotide-nucleotide BLAST (<http://www.ncbi.nlm.nih.gov/BLAST>) and the genomic context was further defined using mouse BLAT (<http://genome.ucsc.edu>).

1. A. Wilber, Wangenstein, K. J., Chen, Y., Zhou, L., Frandsen, J. L., Bell, J. B., Zongyu, J. C., Ekker, S. C., McIvor, R. S., Wang, X., *Mol Ther* (2007).
2. V. W. Keng, K. Yae, T. Hayakawa et al., *Nat Methods* **2** (10), 763 (2005).