

Table S2

TableS2. Summary of 5'RACE sequencing results.

vector	counts	frequency of SA usage
unique fusion transcripts	20	
SA4	13	62% ^{a)}
SA3	5	24%
B	1	5% ^{a)}
SA ^{pbs}	1	5% ^{a)}
LTR transcripts	7	
read-through transcripts	1	
putative fusion transcripts	3	
redundant reads	18	
unspecific/ not mappable	15	
total clones/sequences	64	
alpha unspecific	6	
no sequence retrieved	8	
total clones/sequences	14	

Nomenclature of splice acceptors according to previous publications (Cesana et al. 2012, Moiani et al. 2012). SA^{pbs} indicates a splice acceptor that had not been described previously. ^{a)} Additionally one putative fusion transcript was identified.