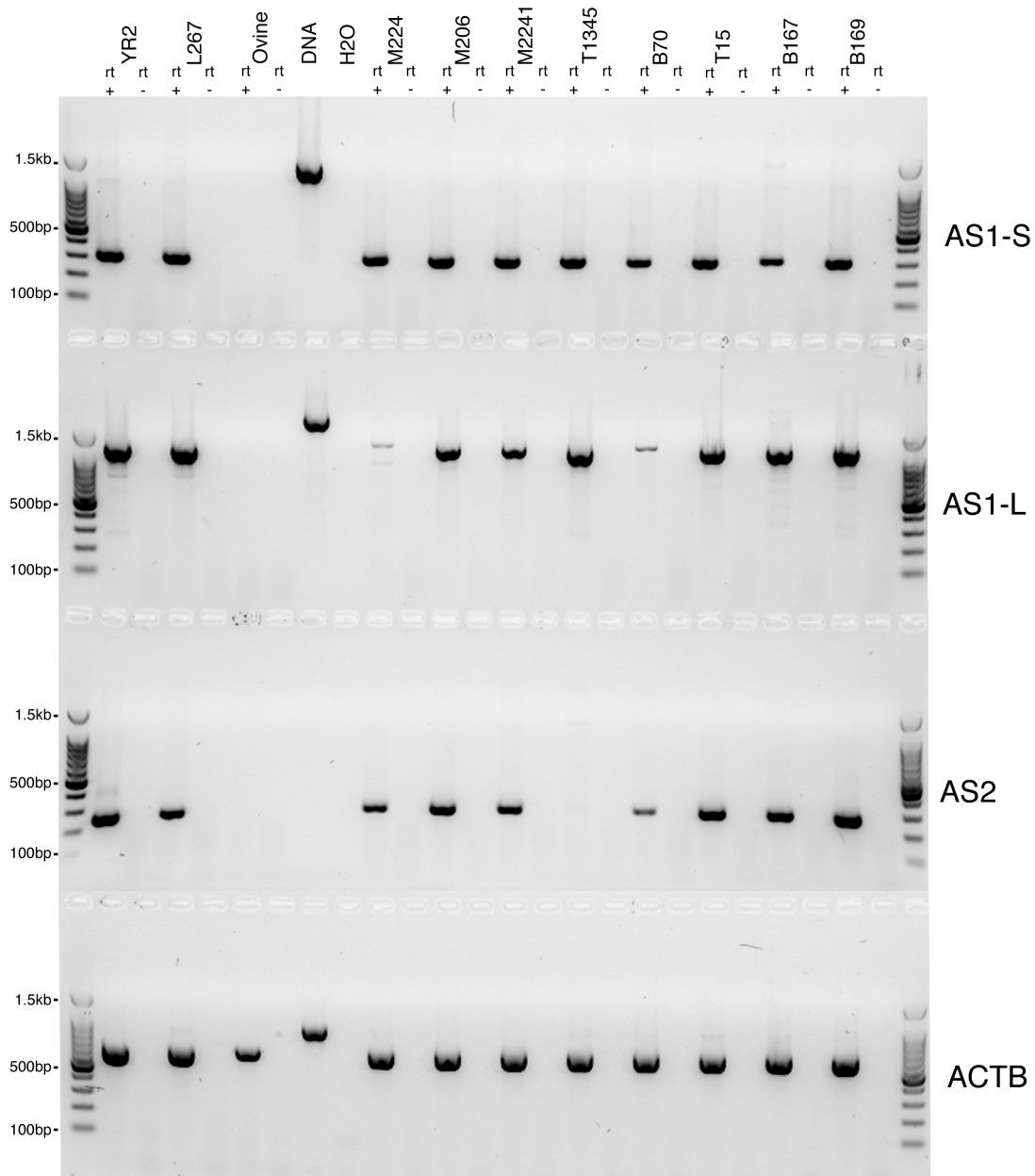


## Supplementary Figures and Tables for

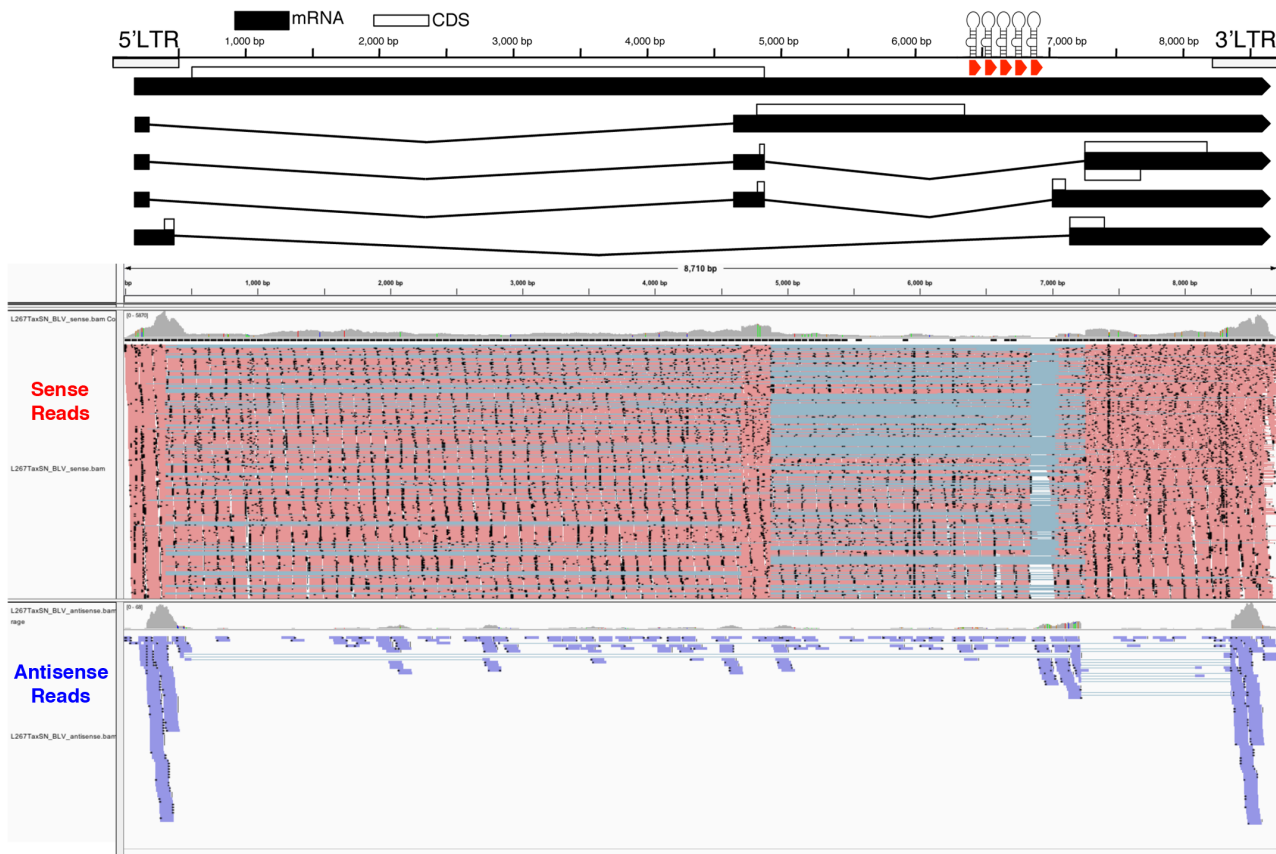
Identification and characterization of novel Bovine Leukemia Virus (BLV) antisense transcripts reveals their constitutive expression in leukemic and pre-leukemic clones

Keith Durkin, Nicolas Rosewick, Maria Artesi, Vincent Hahaut, Philip Griebel, Natasa Arsic, Arsène Burny, Michel Georges & Anne Van den Broeke



### Sup Fig 1. RT-PCR in bovine and ovine tumors

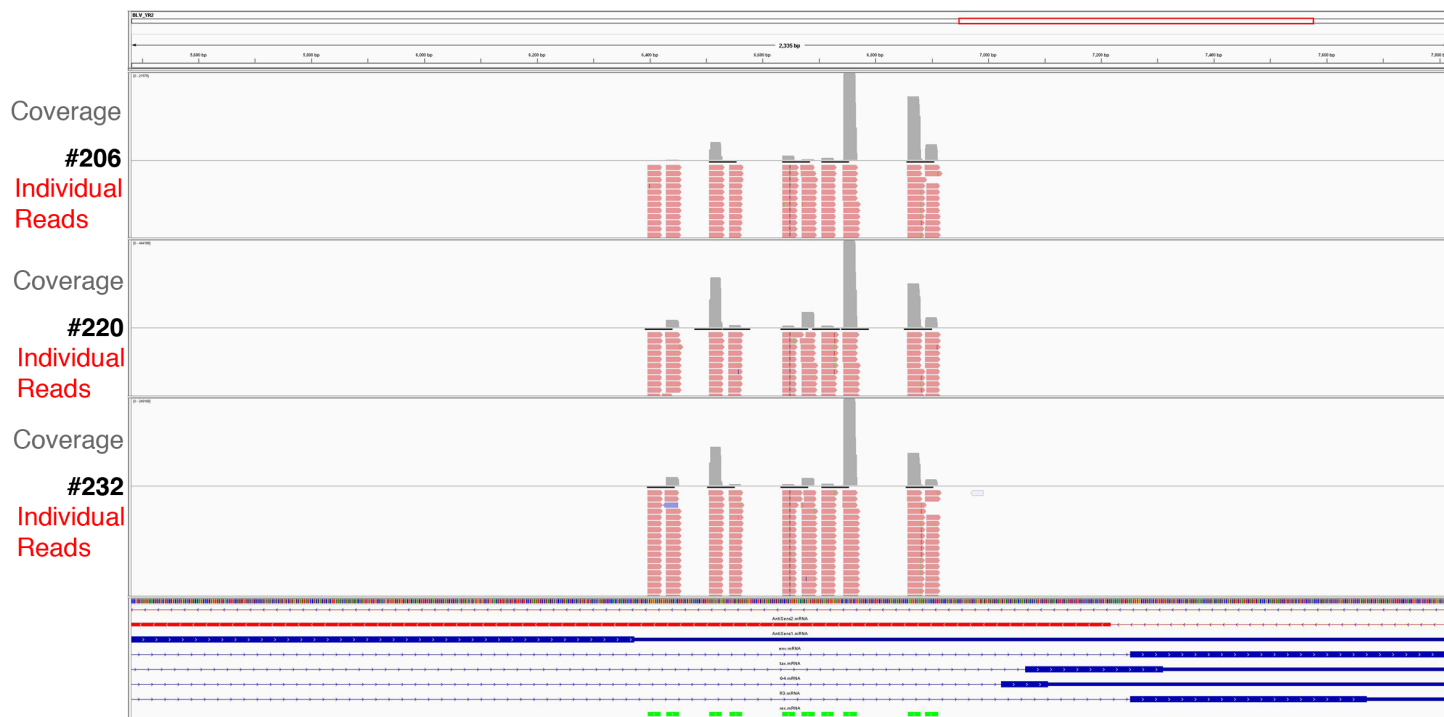
Extended version of Fig 1 B showing RT-PCR results for three ovine (M224, M206, M2241) and five bovine (T1345, B70, T15, B167, B169) tumors. The lack of amplification in T1345 for AS2 is expected as this tumour carries a provirus with a large internal deletion that removes the second exon of AS2 (See Figure 7). (Rt+ reverse transcriptase positive, Rt- reverse transcriptase negative).



## L267<sub>LTaxSN</sub>

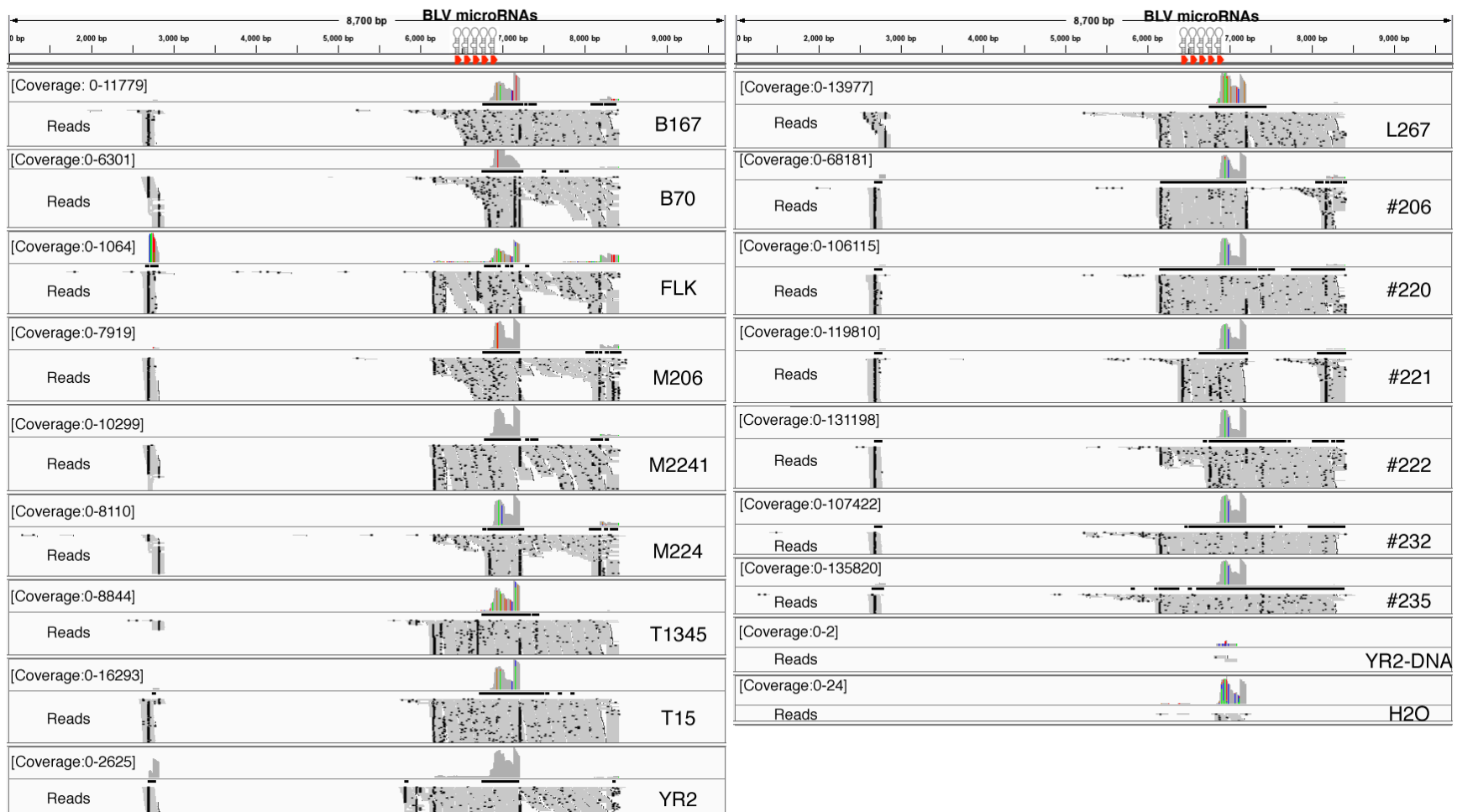
### Sup Fig 2. Sense and antisense transcription from the BLV provirus

Ideogram of the BLV provirus with IGV screenshot showing sense (red) and antisense (blue) reads from a stranded RNA library using the L267<sub>LTaxSN</sub> cell line. Despite robust sense transcription induced by retroviral vector-mediated expression of Tax, antisense transcripts are still present.



**Sup Fig 3. BLV microRNA expression is present during the polyclonal stage of infection.**

Small RNA HTS reads derived from three sheep during the polyclonal stage of infection mapped to the BLV genome. The samples used correspond to those in Fig 2.



**Sup Fig 4. Eighteen 3'RACE libraries mapped to the BLV genome**

Screen shot from IGV with the position of the BLV microRNAs indicated, showing reads mapping to the BLV genome for cell lines YR2, L267, FLK, three ovine tumors, four bovine tumors and the 6 asymptomatic BLV infected sheep 17 months post inoculation. In each library, coverage is concentrated just after the BLV microRNA region marking the 3' end of AS1-S. A much smaller fraction of reads extends beyond the BLV microRNA region (AS1-L) or spliced further upstream (AS2). As a negative control, libraries were prepared using YR2 DNA and H2O as template. In both of these libraries a small number of reads were observed, due either to cross contamination between samples during the library preparation or inaccurate demultiplexing. In the case of both negative control libraries, the coverage was orders or magnitude lower than that seen in the BLV positive libraries.





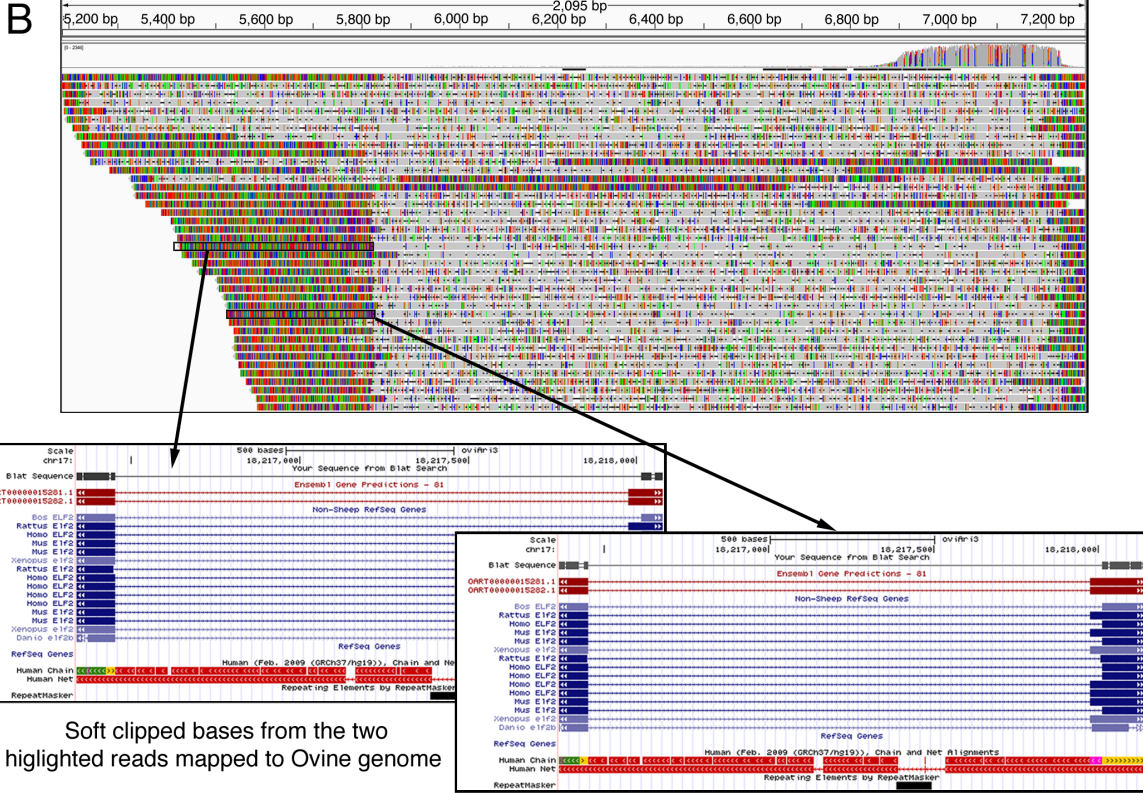
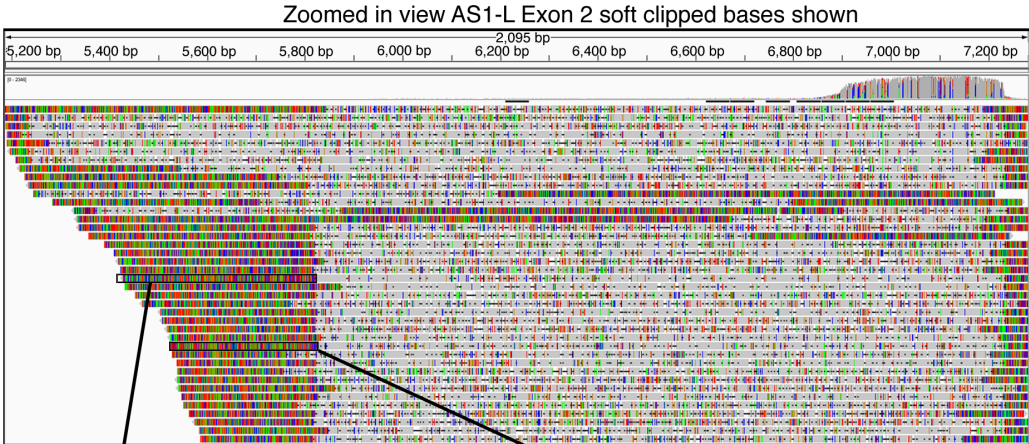
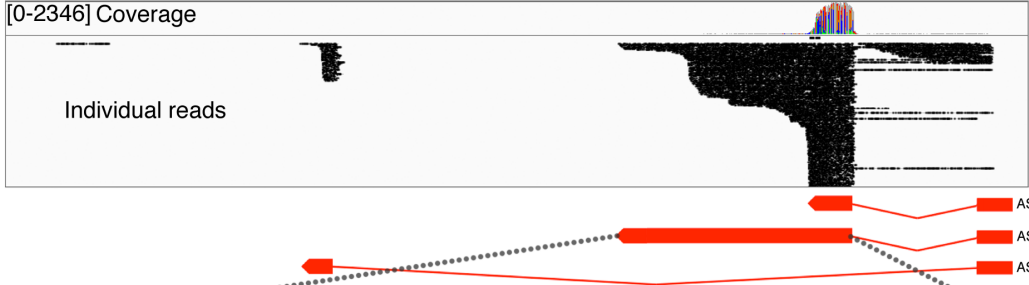
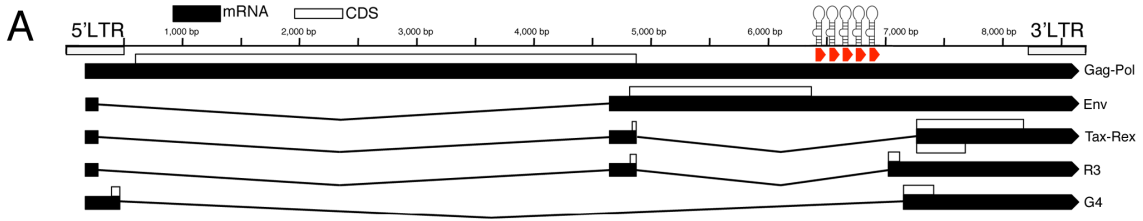
### **Sup Fig 5. Potential 3' ends of BLV antisense transcripts**

Ideogram of the BLV provirus, with 3'RACE reads for L267 mapping to the BLV genome shown below. Potential 3' ends of the BLV antisense transcripts are shown.

**(A)** Zoomed in IGV screen shot showing a large cluster of reads with poly A tails (shown as T in IGV) adjacent to the end of miR-B5-3p. No signal position predominates, although the bulk are found downstream (in the context of the AS transcript) of a canonical AAUAAA polyadenylation signal sequence (PAS). AS1 transcripts ending at this position were given the designation AS1-S.

**(B)** In five of the libraries subjected to 3'RACE a small number of poly A reads were observed at position ~5237. This is located 20bp downstream (in the context of the AS transcript) of a second canonical AAUAAA (PAS). Further, 3'RACE carried out on YR2 with the forward primer adjacent to this potential poly A site rather than the in AS1 exon 1 also showed polyadenylated products matching this position.

**(C)** For AS2, only L267 showed any evidence of a poly A tail, however no canonical PAS was observed and no consistent poly A site was observed. In the remaining samples (also observed in many L267 reads) the AS2 transcript underwent splicing with the host genome. Shown are the soft clipped bases (the bases in the read that did not map to BLV) for YR2 mapped to the ovine genome with BLAT (<http://genome.ucsc.edu/>). The bases correspond to an exon of the ELF2 transcript ~5kb upstream of the YR2 provirus integrated site.

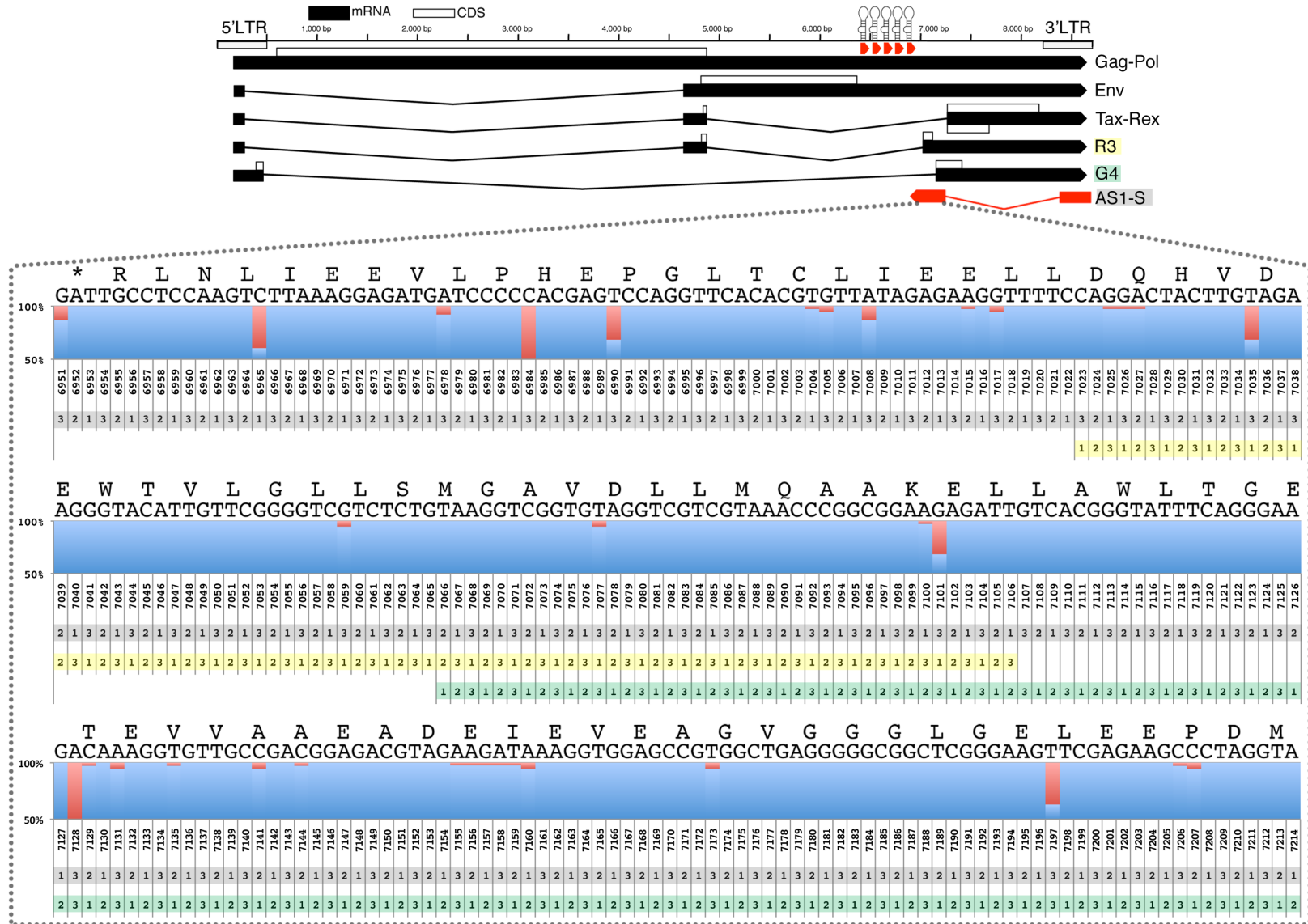


Soft clipped bases from the two highlighted reads mapped to Ovine genome

**Sup Fig 6. AS1-L 3'RACE long reads**

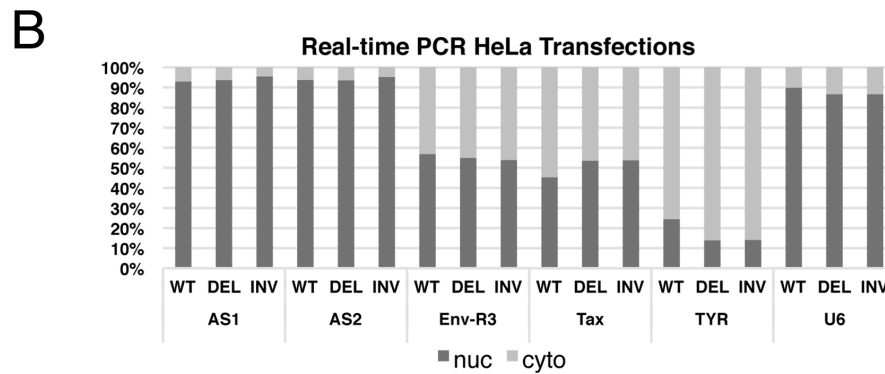
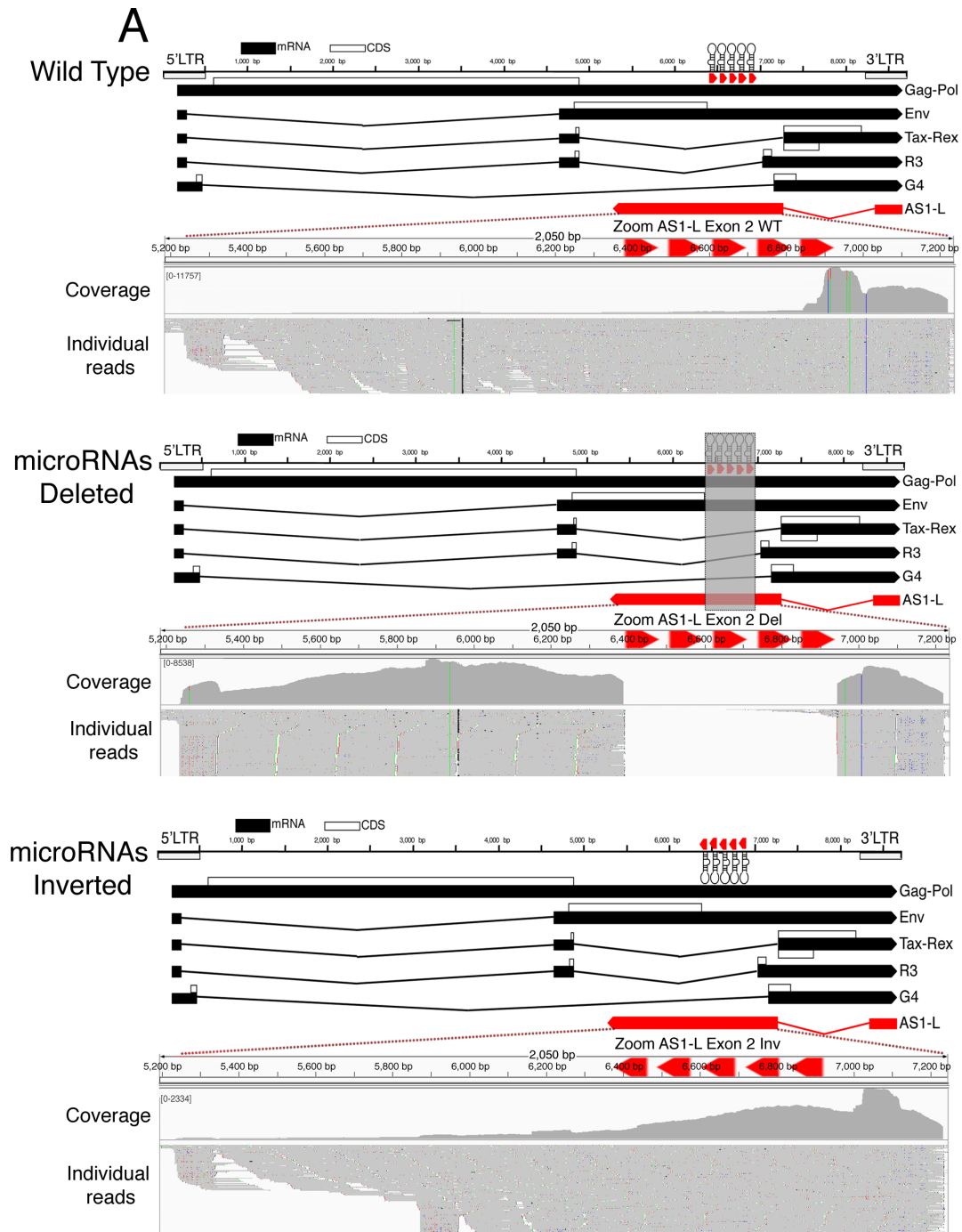
**(A)** Ideogram of the BLV provirus, with 3'RACE products from YR2 sequenced on a MinION (Oxford Nanopore Technologies) and mapping back to the BLV genome. Location of antisense transcripts is also shown. Like the case of the Illumina sequencing the majority of the reads take the form of the shorter AS1-S, some reads do extend to the postulated end of AS1-L at position ~5237. A number of long reads end before this position.

**(B)** Mapping of the soft clipped reads with BLAT (<http://genome.ucsc.edu/>) showed that many of these transcripts had undergone splicing with the ELF2 transcript. The large number of polymorphisms observed in the mapped reads are due to the high error rate observed in Nanopore reads.



**Sup Fig 7. BLV AS1 potential open reading frame**

Potential amino acid sequence and the underlying nucleotide sequence. Shown below is the percentage conservation for each base calculated using the consensus sequence of the ovine and bovine tumours sequenced by us, as well as six BLV genomes available in NCBI. The amount of red at each position indicates the degree that a particular base varies in the samples examined. Below each base is indicated whether it corresponds to the 1<sup>st</sup>, 2<sup>nd</sup> or 3<sup>rd</sup> position of the relevant ORF. Shown ORFs include the potential AS1 ORF (grey), the sense R3 (yellow) and G4 (green) ORFs.

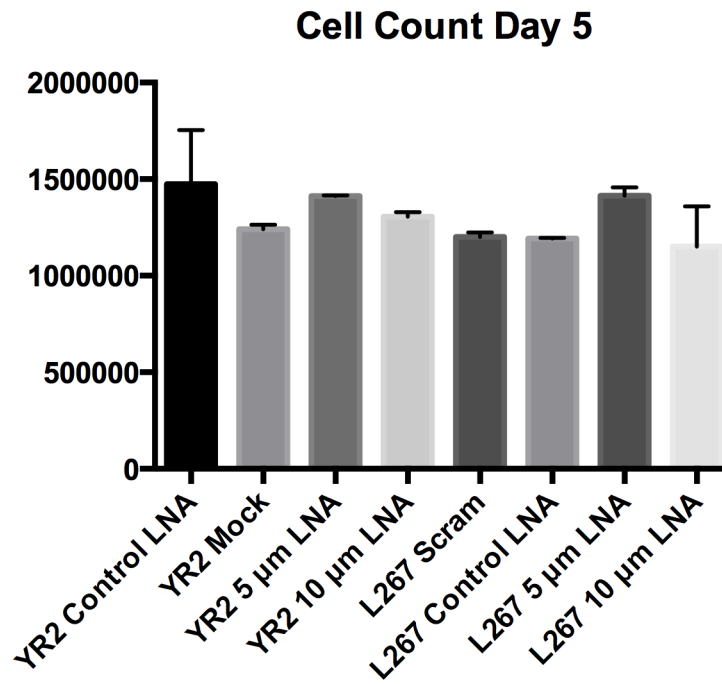




**Sup Fig 8. Effect of removal and inversion of BLV microRNAs**

**(A)** Ideograms showing the three proviruses used in transfections, the first a wild-type, the second where the microRNAs were deleted (grey box indicates the region removed), the third where the BLV microRNAs are inverted. 3'RACE on total RNA from HeLa cells transfected with the three constructs shows that the microRNA deletion/inversion increases the fraction of AS1-L reads. In the case of the wild type provirus and the microRNA deleted provirus, reads were mapped to the wild type provirus sequence. In the case of the microRNA inverted provirus, they are mapped to a proviral genome with microRNAs inverted to match the provirus used.

**(B)** Nuclear vs. cytoplasmic enrichment for BLV sense and antisense transcripts obtained via real-time RT-PCR with nuclear and cytoplasmic enriched RNA from HeLa cells transfected with either the wild type BLV pBLV344 provirus, the provirus with the BLV microRNAs removed or with the orientation of the BLV microRNAs inverted. Removing or inverting the BLV microRNAs had no apparent effect on the localisation of the sense or antisense transcripts. TYR = cytoplasmic enriched control, U6 = nuclear enriched control.



**Sup Fig 9. Locked nucleic acid AS knock down does not affect cell viability**

Following five days of incubation there was no obvious difference in the cell count among the different treatment conditions for both cell lines (numbers represent average, error bar shows maximum cell count).



**Table S1 Counts per million reads (CPM) for RNA sequencing**

BLV cell lines	Antisense reads	Sense reads	Uniquely mapped reads	Antisense CPM	Sense CPM	AS CPM / S CPM
L267	732	49	98989055	7.4	0.5	14.9
YR2	526	9	54121243	9.7	0.2	58.4

BLV cell lines Constitutive Tax expressing	Antisense reads	Sense reads*	Uniquely mapped reads	Antisense CPM	Sense CPM*	AS CPM / S CPM*
L267_TaxSN	149	40918	40848268	4	1002	0
YR2_TaxSN	766	2126142	26093199	29	81483	0

\*As these cells have been transduced with a lentiviral vector containing the BLV Tax gene, the sense read count will be somewhat artificially elevated.

Ovine Tumors	Antisense reads	Sense reads	Uniquely mapped reads	Antisense CPM	Sense CPM	AS CPM / S CPM
M107	149	1	49133967	3	0	149
M108	10176	96	89870131	113	1	106
M126	416	0	54523313	8	0	na
M138	9734	113	78184059	125	1	86
M155	4922	124	47933750	103	3	40
M160	303	1	26665476	11	0	303
M161	27	1	60630935	0	0	27
M206	323	69	72283867	4	1	5
M20PS	134	0	64457064	2	0	na
M210	531	152	98718132	5	2	3
M21PS	261	0	88207690	3	0	na
M2233	10826	1894	98091530	110	19	6
M2241	333	96	116416582	3	1	3
M224	200	52	123827745	2	0	4
M2311RM	51	1	18352207	3	0	51
M251	476	2	57534668	8	0	238
M2531T	77	23	22379496	3	1	3
M2532PS	90	43	27152057	3	2	2
M28PS	153	2	27420479	6	0	77
M31Leu	134	49	44855981	3	1	3
M32Leu	154	34	43549560	4	1	5
M33Leu	80	177	27828214	3	6	0
M344t0	113	6	26399373	4	0	19
M360	95	11	31508541	3	0	9
M395t0	118	14	25704049	5	1	8
M41Leu	248	99	59025661	4	2	3
M51	145	26	43602381	3	1	6
M5578	154	1	56526611	3	0	154

Bovine Tumors	Antisense reads	Sense reads	Uniquely mapped reads	Antisense CPM	Sense CPM	AS CPM / S CPM
B167	466	104	58806726	7.9	1.8	4.5
B169	372	13	45113265	8.2	0.3	28.6
B3171	358	7	66728945	5.4	0.1	51.1
B3191	736	14	66654840	11.0	0.2	52.6
B3198	212	104	57163314	3.7	1.8	2.0
B3261	270	315	27374722	9.9	11.5	0.9
B70	27	0	45802524	0.6	0.0	na
B76SUS	84	1	81850287	1.0	0.0	84.0
LB120	94	4	43108562	2.2	0.1	23.5
T1345	171	60	37133243	4.6	1.6	2.9
T15	171	60	37133243	4.6	1.6	2.9
B1351	775	1222	147025250	5.3	8.3	0.6

Bovine negative control	Antisense reads	Sense reads	Uniquely mapped reads	Antisense CPM	Sense CPM	AS CPM / S CPM
B78t0	0	0	64282590	0.0	0.0	na

Pre-leukemic ovine samples	Antisense reads	Sense reads	Uniquely mapped reads	Antisense CPM	Sense CPM	AS CPM / S CPM	Proviral Load	Number of clones
#206	31	5	50636602	0.6	0.1	6.2	5.3	1044
#220	32	14	39135557	0.8	0.4	2.3	6.4	810
#221	76	16	41934579	1.8	0.4	4.8	15.5	2118
#222	34	8	38819095	0.9	0.2	4.3	7.4	1522
#232	64	10	40063428	1.6	0.2	6.4	11.2	1368
#235	354	24	58371371	6.1	0.4	14.8	40.6	446

**BLV microRNA levels in three Pre-leukemic ovine samples**

	#206		#220		#232		Average CPM
	Reads	CPM	Reads	CPM	Reads	CPM	
<b>BLV-miR-1-3p</b>	155	79.31	39998	2859.1	24854	1926.96	<b>1621.79</b>
<b>BLV-miR-1-5p</b>	68	34.79	902	64.48	691	53.57	<b>50.95</b>
<b>BLV-miR-2-3p</b>	31	15.86	10598	757.56	3834	297.25	<b>356.89</b>
<b>BLV-miR-2-5p</b>	4544	2325.08	246282	17604.51	107735	8352.81	<b>9427.47</b>
<b>BLV-miR-3-3p</b>	267	136.62	79434	5678.03	21722	1684.13	<b>2499.59</b>
<b>BLV-miR-3-5p</b>	1148	587.41	9333	667.13	3680	285.31	<b>513.28</b>
<b>BLV-miR-4-3p</b>	20887	10687.49	441945	31590.73	248436	19261.52	<b>20513.25</b>
<b>BLV-miR-4-5p</b>	595	304.45	9210	658.34	5739	444.95	<b>469.25</b>
<b>BLV-miR-5-3p</b>	3848	1968.95	51727	3697.5	17401	1349.12	<b>2338.52</b>
<b>BLV-miR-5-5p</b>	15422	7891.15	220195	15739.79	91538	7097.04	<b>10242.66</b>

**Table S2 5'RACE**

<b>Start position</b>	<b>AS1 %</b>	<b>AS2 %</b>
<b>8661</b>	<u>3.33</u>	<u>0.00</u>
<b>8659</b>	<u>1.13</u>	<u>0.00</u>
<b>8657</b>	<u>1.53</u>	<u>0.00</u>
<b>8656</b>	<u>0.51</u>	<u>1.80</u>
<b>8655</b>	<u>1.42</u>	<u>0.74</u>
<b>8653</b>	<u>0.00</u>	<u>2.21</u>
<b>8650</b>	<u>42.26</u>	<u>45.88</u>
<b>8649</b>	<u>3.29</u>	<u>4.36</u>
<b>8645</b>	<u>1.95</u>	<u>0.00</u>
<b>8640</b>	<u>0.00</u>	<u>2.39</u>
<b>8638</b>	<u>0.62</u>	<u>0.00</u>
<b>8626</b>	<u>0.64</u>	<u>0.00</u>
<b>8622</b>	<u>0.01</u>	<u>2.03</u>
<b>8621</b>	<u>0.67</u>	<u>0.00</u>
<b>8614</b>	<u>0.52</u>	<u>0.00</u>
<b>8598</b>	<u>2.23</u>	<u>0.00</u>
<b>8593</b>	<u>0.90</u>	<u>5.98</u>
<b>8591</b>	<u>27.35</u>	<u>20.76</u>
<b>8590</b>	<u>3.68</u>	<u>0.00</u>
<b>8588</b>	<u>3.69</u>	<u>3.65</u>
<b>8586</b>	<u>2.58</u>	<u>5.98</u>
<b>8578</b>	<u>0.88</u>	<u>4.24</u>
<b>8563</b>	<u>0.80</u>	<u>0.00</u>

Underlined in the U5 portion of the LTR

Non Underlined in the R portion of the LTR

**Table S3 Output of Coding Potential Assessment Tool (CPAT) for Human and Mouse models.**

Sequence Name	RNA size	ORF size	Fickett Score Human	Hexamer Score Human	Coding Probability Human	Coding Label Human	Fickett Score Mouse	Hexamer Score mouse	Coding Probability Mouse	Coding Label Mouse	Full description
BLV_ENV_CDS	1548	1548	0.4913	0.0524733	1.000	yes	0.4913	0.054735	0.999	yes	AY078387.1 Bovine leukemia virus envelope glycoprotein polyprotein precursor gPr72 mRNA, complete cds
BLV_TAX_CDS	1323	930	0.7419	0.07244925	0.991	yes	0.7419	0.061266	0.955	yes	M26772.1 BLVTAP Bovine leukemia virus transactivator protein (XBL-1) mRNA, complete cds
AS1-L_BLV	2279	264	1.2074	0.20939568	0.449	yes	1.2074	0.18289	0.386	no	YR2 Region included: 5237-7217 & 8353-8650
AS1-S_BLV	621	264	1.2074	0.20939568	0.474	yes	1.2074	0.18289	0.393	no	YR2 Region included: 6895-7217 & 8353-8650
AS2_BLV	475	24	0.6636	-0.0202475	0.003	no	0.6636	0.043919	0.022	no	YR2 Region included: 2653-2829 & 8353-8650
HTLV1_TAX_CDS	1062	1062	0.6939	0.09265053	0.998	yes	0.6939	0.0917	0.983	yes	AB038239.1 Human T-cell lymphotropic virus type 1 proviral gene for TAX, complete cds
HBZ-SI	1088	621	0.9541	0.3919547	0.984	yes	0.9541	0.388948	0.919	yes	AB219938.1 Human T-lymphotropic virus 1 HBZ-SI mRNA for bZIP factor splicing isoform, complete cds
HBZ	2271	621	0.9541	0.39313014	0.983	yes	0.9541	0.39132	0.918	yes	DQ273132.1 Human T-lymphotropic virus 1 bZIP factor (HBZ) mRNA, complete cds
URS0000627204	126	75	0.8738	0.05856478	0.015	no	0.8738	0.106084	0.060	no	Bos taurus FMR1 antisense RNA 1 conserved region 2
URS0000629A5A	74	39	0.814	0.27273758	0.035	no	0.814	0.26024	0.071	no	Bos taurus ST7 overlapping transcript 3 conserved region 1
URS000062C20C	267	54	0.702	-0.4533927	0.000	no	0.702	-0.40761	0.006	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 7
URS000062D38D	173	96	0.8215	-0.1728042	0.004	no	0.8215	-0.20799	0.021	no	Bos taurus SMAD5 antisense RNA 1 conserved region 4
URS000062E2FC	184	42	1.0161	0.39283106	0.134	no	1.0161	0.391101	0.159	no	Bos taurus Pvt1 oncogene conserved region 2
URS00006358D2	122	0	0	0	0.000	no	0	0	0.004	no	Bos taurus WT1 antisense RNA conserved region 6
URS000063C6A6	69	60	1.2062	0.31121489	0.167	no	1.2062	0.294404	0.181	no	Bos taurus HOTAIR conserved region 2
URS000063F560	75	66	1.0881	0.31642329	0.132	no	1.0881	0.320309	0.167	no	Bos taurus Six3os1 conserved region 3
URS0000646539	135	21	0.8415	-0.4974953	0.000	no	0.8415	-0.48419	0.005	no	Bos taurus TTC28 antisense RNA 1 conserved region 2
URS000064CDD2	76	12	0.6466	-1.2066197	0.000	no	0.6466	-1.21027	0.000	no	Bos taurus Ghrelin opposite strand RNA conserved region
URS000064D724	91	0	0	0	0.000	no	0	0	0.004	no	Bos taurus SPRY4-IT1 conserved region 1
URS00006510A8	128	0	0	0	0.000	no	0	0	0.004	no	Bos taurus HOX antisense intergenic RNA myeloid 1 conserved region 1
URS0000654C49	128	108	1.0217	-0.1023593	0.012	no	1.0217	-0.12115	0.045	no	Bos taurus ZEB2 antisense RNA 1 conserved region 1
URS0000656B63	196	66	0.9235	-0.4407478	0.001	no	0.9235	-0.50966	0.007	no	Bos taurus DLG2 antisense RNA 1 conserved region 1
URS000065971F	198	132	1.0106	0.38695776	0.279	no	1.0106	0.413437	0.281	no	Bos taurus FTX transcript, XIST regulator conserved region 5
URS000065978A	129	6	0.3621	0.5274011	0.032	no	0.3621	0.478289	0.052	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 5
URS00006599B8	410	63	0.463	-0.2440055	0.001	no	0.463	-0.22584	0.008	no	Bos taurus Prostate cancer antigen RNA 3 conserved region 2
URS000067674B	226	54	0.9351	-0.209365	0.003	no	0.9351	-0.24973	0.016	no	Bos taurus KCNQ1 overlapping transcript 1 conserved region 5
URS0000677082	362	192	0.6974	0.06993743	0.033	no	0.6974	0.086216	0.090	no	Bos taurus HOXA transcript at the distal tip, conserved region 3
URS0000677825	110	0	0	0	0.000	no	0	0	0.004	no	Bos taurus WT1 antisense RNA conserved region 1
URS00006791CF	71	24	0.8356	-0.2796512	0.001	no	0.8356	-0.26156	0.011	no	Bos taurus FTX transcript, XIST regulator conserved region 1
URS000067BA49	69	27	0.7868	-0.0096499	0.004	no	0.7868	0.012107	0.026	no	Bos taurus SOX2 overlapping transcript exon 2
URS000067BA92	143	9	0.3728	-1.3586378	0.000	no	0.3728	-1.36827	0.000	no	Bos taurus HOX antisense intergenic RNA myeloid 1 conserved region 5
URS000067C9B9	110	0	0	0	0.000	no	0	0	0.004	no	Bos taurus SOX2 overlapping transcript exon 4
URS000067F6F2	95	36	0.7352	-0.4349202	0.000	no	0.7352	-0.48489	0.004	no	Bos taurus Pvt1 oncogene conserved region 3
URS00006863C9	465	132	0.6392	-0.1553791	0.003	no	0.6392	-0.16905	0.022	no	Bos taurus KCNQ1 overlapping transcript 1 conserved region 1
URS0000692A75	272	75	1.0068	-0.3422251	0.002	no	1.0068	-0.35497	0.015	no	Bos taurus ST7 overlapping transcript 4 conserved region 3

URS00006940C3	350	48	1.0193	0.22573242	0.052	no	1.0193	0.219188	0.095	no	Bos taurus Six3os1 conserved region 4
URS0000696811	244	75	0.8859	-0.1532851	0.004	no	0.8859	-0.1798	0.022	no	Bos taurus MEST intronic transcript 1, antisense RNA conserved region
URS000069B56D	77	0	0	0	0.000	no	0	0	0.004	no	Bos taurus MER1 repeat containing imprinted transcript 1 conserved region 1
URS00006B0AAD	142	126	0.5035	-0.1773767	0.002	no	0.5035	-0.22026	0.013	no	Bos taurus Embryonic ventral forebrain-2 long ncRNA
URS00006B3397	139	0	0	0	0.000	no	0	0	0.004	no	Bos taurus T-cell leukemia/lymphoma 6 conserved region 3
URS00006B4586	96	57	0.8308	-0.0128911	0.007	no	0.8308	-0.00722	0.033	no	Bos taurus FTX transcript, XIST regulator conserved region 2
URS00006B4E0E	85	0	0	0	0.000	no	0	0	0.004	no	Bos taurus X-chromosome inactivation gene exon 1
URS00006B5CAE	87	84	0.9455	-0.0385016	0.011	no	0.9455	-0.00353	0.050	no	Bos taurus Six3os1 conserved region 1
URS00006BA2BF	113	45	1.2098	-0.5166496	0.001	no	1.2098	-0.47865	0.012	no	Bos taurus FAM13A antisense RNA 1 conserved region 2
URS00006BE61D	90	42	0.7436	-0.1707097	0.002	no	0.7436	-0.25714	0.010	no	Bos taurus Deleted in lymphocytic leukemia 2 conserved region 2
URS00006C4A69	55	24	0.9172	-0.5042849	0.000	no	0.9172	-0.53981	0.004	no	Bos taurus Deleted in lymphocytic leukemia 2 conserved region 4
URS00006C6BE4	97	15	0.3752	-0.5360566	0.000	no	0.3752	-0.64961	0.001	no	Bos taurus Maternally expressed 8 exon 1
URS00006CA376	106	48	1.2192	0.05717137	0.033	no	1.2192	0.020792	0.071	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 4
URS00006CB17F	70	6	0.4615	0.5002443	0.036	no	0.4615	0.45189	0.057	no	Bos taurus H19 conserved region 1
URS00006CC536	168	9	0.876	-1.8762211	0.000	no	0.876	-1.53144	0.000	no	Bos taurus FAS antisense RNA 1 conserved region
URS00006CDA32	281	30	0.4802	-0.1819694	0.001	no	0.4802	-0.22201	0.006	no	Bos taurus Highly up-regulated in liver cancer conserved region
URS00006CF3EB	105	9	0.6632	-0.9039742	0.000	no	0.6632	-0.98346	0.000	no	Bos taurus Maternally expressed 3 conserved region 2
URS00006D1977	127	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Nuclear enriched abundant transcript 1 conserved region 2
URS00006D2BA2	108	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Maternally expressed 8 exon 2
URS00006D5400	231	69	0.9188	-0.4056706	0.001	no	0.9188	-0.43784	0.009	no	Bos taurus HOXA11 antisense RNA 1 conserved region 4
URS00006D9004	237	9	0.6218	-1.8230951	0.000	no	0.6218	-1.55709	0.000	no	Bos taurus Hydatidiform mole associated and imprinted conserved region
URS00006DB21C	229	57	0.9927	-0.1059787	0.006	no	0.9927	-0.10886	0.031	no	Bos taurus SOX2 overlapping transcript exon 1
URS00006DD07E	129	114	1.0023	-0.0866744	0.013	no	1.0023	-0.08125	0.052	no	Bos taurus SMAD5 antisense RNA 1 conserved region 2
URS00006DEB8C	288	57	1.1384	-0.2507425	0.004	no	1.1384	-0.14768	0.036	no	Bos taurus WT1 antisense RNA conserved region 7
URS00006E1889	103	39	0.9909	0.21341658	0.041	no	0.9909	0.264031	0.099	no	Bos taurus T-cell leukemia/lymphoma 6 conserved region 1
URS00006E497F	91	87	0.6421	0.08119545	0.010	no	0.6421	0.064335	0.037	no	Bos taurus ZNFX1 antisense RNA 1 conserved region 2
URS00006E59D7	144	72	0.9981	-0.1669965	0.005	no	0.9981	-0.14338	0.031	no	Bos taurus Taurine upregulated gene 1 conserved region 1
URS00006EA6C7	180	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Embryonic ventral forebrain RNA 1 conserved region 1
URS00006EA80E	115	0	0	0	0.000	no	0	0	0.004	no	Bos taurus FAM13A antisense RNA 1 conserved region 1
URS00006EEA29	135	42	1.0223	-0.1295657	0.005	no	1.0223	-0.09857	0.031	no	Bos taurus Myocardial infarction associated transcript exon 1
URS00006F4484	68	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Maternally expressed 8 exon 3
URS00006F60BE	92	78	1.1896	-0.0083285	0.027	no	1.1896	0.019669	0.082	no	Bos taurus ZNFX1 antisense RNA 1 conserved region 2
URS00006F7F53	154	48	1.1266	-0.0075192	0.016	no	1.1266	0.045069	0.065	no	Bos taurus NPPA antisense RNA 1 conserved region 2
URS00006FE4FF	171	75	0.779	-0.3315217	0.001	no	0.779	-0.36448	0.009	no	Bos taurus ST7 overlapping transcript 4 conserved region 2
URS00006FF6E6	143	99	0.8323	0.11958267	0.026	no	0.8323	0.150557	0.076	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 8
URS00006FFF5E	262	114	1.014	0.05805101	0.035	no	1.014	0.042241	0.081	no	Bos taurus SMAD5 antisense RNA 1 conserved region 1
URS00007035F2	132	18	0.408	-0.0844732	0.001	no	0.408	-0.18755	0.006	no	Bos taurus Pvt1 oncogene conserved region 5
URS00007036C6	141	57	0.6862	0.02145747	0.006	no	0.6862	0.067528	0.033	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 2
URS0000708ABD	586	120	0.8006	0.07255146	0.021	no	0.8006	0.115562	0.073	no	Bos taurus Vax2os1 conserved region 2
URS0000717AE7	102	0	0	0	0.000	no	0	0	0.004	no	Bos taurus ZEB2 antisense RNA 1 conserved region 3

URS0000717FE0	101	0	0	0	0.000	no	0	0	0.004	no	Bos taurus ZEB2 antisense RNA 1 conserved region 3
URS0000719B0F	77	48	1.1266	-0.0075192	0.016	no	1.1266	0.045069	0.065	no	Bos taurus NPPA antisense RNA 1 conserved region 2
URS00007259BA	104	75	1.0494	-0.2156819	0.004	no	1.0494	-0.21204	0.027	no	Bos taurus Metastasis associated lung adenocarcinoma transcript 1
URS0000726CC0	118	12	1.0582	-0.380929	0.001	no	1.0582	-0.48892	0.007	no	Bos taurus GNAS antisense RNA 1 conserved region 2
URS000072850B	247	45	1.1273	-0.2826858	0.003	no	1.1273	-0.28376	0.020	no	Bos taurus Prostate androgen-regulated transcript 1 conserved region 2
URS000072AE6B	54	27	0.867	-0.7723672	0.000	no	0.867	-0.8099	0.002	no	Bos taurus FMR1 antisense RNA 1 conserved region 1
URS000072B940	215	192	1.0975	0.05917406	0.100	no	1.0975	0.060013	0.165	no	Bos taurus DLG2 antisense RNA 1 conserved region 2
URS000072CEB9	330	141	0.9852	-0.0307435	0.024	no	0.9852	-0.01007	0.078	no	Bos taurus Deleted in lymphocytic leukemia 1 conserved region 2
URS0000759C73	2069	345	0.5704	0.12308877	0.132	no	0.5704	0.166592	0.234	no	Bos taurus H19, imprinted maternally expressed transcript (non-protein coding) (H19), long non-coding RNA.
URS0000759E04	539	348	1.0681	0.42958035	0.861	yes	1.0681	0.408492	0.675	yes	Bos taurus artiodactyl-specific transcript 1 (AST1), long non-coding RNA.
URS000075A1EC	978	177	0.9069	0.16822608	0.093	no	0.9069	0.171259	0.153	no	Bos taurus uncharacterized LOC100196901 (LOC100196901), transcript variant 1, long non-coding RNA.
URS000075A42C	801	282	0.6385	-0.0187509	0.039	no	0.6385	0.026889	0.119	no	Bos taurus uncharacterized LOC100847825 (LOC100847825), long non-coding RNA.
URS000075B4CA	1135	180	0.6608	-0.0817498	0.009	no	0.6608	-0.08575	0.042	no	Bos taurus chromosome 23 open reading frame, human C6orf52 (C23H6orf52), transcript variant 1, long non-coding RNA.
URS000075B604	1008	228	0.3596	-0.2278236	0.002	no	0.3596	-0.26194	0.018	no	Bos taurus uncharacterized LOC100847946 (LOC100847946), long non-coding RNA.
URS000075B9FD	955	144	0.6445	-0.1496252	0.004	no	0.6445	-0.17596	0.023	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 6, long non-coding RNA.
URS000075BC30	1638	381	0.7	0.06400548	0.189	no	0.7	0.097322	0.286	no	Bos taurus uncharacterized LOC100140121 (LOC100140121), long non-coding RNA.
URS000075C0CE	1954	555	0.7853	0.19222819	0.821	yes	0.7853	0.22794	0.731	yes	Bos taurus maternally expressed 3 (non-protein coding) (MEG3), long non-coding RNA.
URS000075C544	806	180	0.6608	-0.0817498	0.009	no	0.6608	-0.08575	0.042	no	Bos taurus chromosome 23 open reading frame, human C6orf52 (C23H6orf52), transcript variant 3, long non-coding RNA.
URS000075CDC9	446	78	0.8326	-0.1762391	0.003	no	0.8326	-0.21904	0.018	no	Bos taurus small nucleolar RNA host gene 4 (non-protein coding) (SNHG4), long non-coding RNA.
URS000075CF6E	888	165	0.6564	-0.1177284	0.006	no	0.6564	-0.14663	0.030	no	Bos taurus uncharacterized LOC788201 (LOC788201), long non-coding RNA.
URS000075D01A	1078	372	0.5896	0.07532513	0.143	no	0.5896	0.099628	0.235	no	Bos taurus small nucleolar RNA host gene 12 (non-protein coding) (SNHG12), transcript variant 2, long non-coding RNA.
URS000075D08D	546	144	0.8749	0.07291865	0.034	no	0.8749	0.058342	0.081	no	Bos taurus uncharacterized LOC100616526 (LOC100616526), transcript variant 3, long non-coding RNA.
URS000075D922	911	144	0.6445	-0.1496252	0.004	no	0.6445	-0.17596	0.023	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 4, long non-coding RNA.
URS000075DA73	3345	186	0.6977	0.2334901	0.072	no	0.6977	0.296428	0.162	no	Bos taurus uncharacterized LOC782788 (MGC148318), long non-coding RNA.
URS000075DAE4	413	168	0.9531	0.16216371	0.096	no	0.9531	0.159035	0.151	no	Bos taurus uncharacterized LOC100616098 (LOC100616098), long non-coding RNA.
URS000075DCA1	3462	342	0.7099	0.08846014	0.142	no	0.7099	0.070938	0.213	no	Bos taurus uncharacterized LOC100616526 (LOC100616526), transcript variant 1, long non-coding RNA.

URS000075E3D6	3025	1380	0.9853	0.32875034	1.000	yes	0.9853	0.32318	1.000	yes	Bos taurus PPARG-TSEN2 (PPARG-TSEN2), transcript variant 1, long non-coding RNA.
URS000075EAE1	1030	180	0.6608	-0.0817498	0.009	no	0.6608	-0.08575	0.042	no	Bos taurus chromosome 23 open reading frame, human C6orf52 (C23H6orf52), transcript variant 2, long non-coding RNA.
URS000075EB28	1123	372	0.5896	0.07532513	0.143	no	0.5896	0.099628	0.235	no	Bos taurus small nucleolar RNA host gene 12 (non-protein coding) (SNHG12), transcript variant 1, long non-coding RNA.
URS000075EC71	1875	1107	0.9629	0.40041855	1.000	yes	0.9629	0.410277	0.998	yes	Bos taurus LOC100271850-MEF2B readthrough transcript (LOC100271850-MEF2B), long non-coding RNA.
URS000075EDB2	1014	147	0.894	0.0876376	0.040	no	0.894	0.048664	0.082	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 2, long non-coding RNA.
URS0000623174	121	72	1.0222	0.23927818	0.073	no	1.0222	0.241506	0.121	no	Bos taurus Nuclear enriched abundant transcript 1 conserved region 1
URS0000625647	155	42	0.6501	-0.1411949	0.001	no	0.6501	-0.13515	0.013	no	Bos taurus Pregnancy induced noncoding RNA
URS0000627F0B	157	45	0.8968	-0.0799771	0.005	no	0.8968	-0.12273	0.023	no	Bos taurus TP53 target 1 conserved region 1
URS0000627F39	113	6	0.3299	-2.901853	0.000	no	0.3299	-3.08032	0.000	no	Bos taurus Pvt1 oncogene conserved region 6
URS000062B719	131	24	0.7015	-0.1406256	0.001	no	0.7015	-0.11695	0.014	no	Bos taurus Prostate-specific transcript 1
URS000062B8A2	204	24	0.4446	0.45463191	0.031	no	0.4446	0.468966	0.067	no	Bos taurus Maternal intergenic circadian oscillating RNA 1
URS000062CBF8	135	15	1.0095	0.08828311	0.015	no	1.0095	0.066005	0.044	no	Bos taurus Deleted in lymphocytic leukemia 2 conserved region 6
URS000062EA6D	102	12	0.3194	-1.5470274	0.000	no	0.3194	-1.53147	0.000	no	Bos taurus HOX antisense intergenic RNA myeloid 1 conserved region 4
URS000062F99B	124	51	0.7689	0.02880937	0.007	no	0.7689	0.007589	0.029	no	Bos taurus Pvt1 oncogene conserved region 3
URS000063B8D5	85	0	0	0	0.000	no	0	0	0.004	no	Bos taurus X-chromosome inactivation gene exon 1
URS000063C398	76	0	0	0	0.000	no	0	0	0.004	no	Bos taurus ZNRD1 antisense RNA 1 conserved region 2
URS000063DD01	129	96	0.8591	-0.2202319	0.003	no	0.8591	-0.2425	0.020	no	Bos taurus CDKN2B antisense RNA 1 conserved region 3
URS000063E095	80	75	0.9386	-0.23211	0.003	no	0.9386	-0.23885	0.020	no	Bos taurus Deleted in lymphocytic leukemia 2 conserved region 5
URS000063F98F	146	21	0.7892	-0.4194346	0.000	no	0.7892	-0.41721	0.005	no	Bos taurus Myocardial infarction associated transcript exon 5 conserved region 1
URS0000641959	179	9	0.6695	-1.1386872	0.000	no	0.6695	-1.15941	0.000	no	Bos taurus Pvt1 oncogene conserved region 4
URS0000643C57	50	0	0	0	0.000	no	0	0	0.004	no	Bos taurus H19 conserved region 1
URS000064A264	176	105	0.9142	-0.244312	0.003	no	0.9142	-0.23639	0.024	no	Bos taurus NPPA antisense RNA 1 conserved region 1
URS000064D7DB	115	39	0.7422	-0.4039124	0.000	no	0.7422	-0.36695	0.007	no	Bos taurus KCNQ1 overlapping transcript 1 conserved region 3
URS0000660D10	85	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Myocardial infarction associated transcript exon 5 conserved region 2
URS0000662396	89	60	1.1772	-0.651044	0.000	no	1.1772	-0.70488	0.005	no	Bos taurus Taurine upregulated gene 1 conserved region 2
URS000066403E	107	69	0.5719	-0.3791522	0.000	no	0.5719	-0.35714	0.006	no	Bos taurus Polled intersex syndrome regulated transcript 1
URS00006643D0	215	186	0.5145	0.08017167	0.019	no	0.5145	0.097536	0.064	no	Bos taurus Six3os1 conserved region 2
URS0000665133	237	9	0.6218	-1.8230951	0.000	no	0.6218	-1.55709	0.000	no	Bos taurus Hydatidiform mole associated and imprinted conserved region
URS0000666A1B	92	78	0.9769	0.01201435	0.016	no	0.9769	0.037318	0.059	no	Bos taurus ZNFX1 antisense RNA 1 conserved region 2
URS00006678DE	168	9	0.876	-1.8762211	0.000	no	0.876	-1.53144	0.000	no	Bos taurus FAS antisense RNA 1 conserved region
URS0000668B27	210	39	0.8128	-0.3463585	0.001	no	0.8128	-0.4175	0.006	no	Bos taurus HOXA11 antisense RNA 1 conserved region 5
URS0000669E60	118	57	0.8845	-0.3215334	0.001	no	0.8845	-0.38115	0.010	no	Bos taurus Highly accelerated region 1A/1B
URS0000669F75	150	36	0.7222	-0.1034753	0.002	no	0.7222	-0.11845	0.015	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 10
URS000066A9DA	206	81	0.8972	-0.3519839	0.001	no	0.8972	-0.39404	0.011	no	Bos taurus ST7 overlapping transcript 4 conserved region 4
URS000066CA78	70	24	0.8507	-0.5007781	0.000	no	0.8507	-0.37277	0.007	no	Bos taurus JPX transcript, XIST activator conserved region 2
URS000066DB40	239	66	1.2803	0.22602503	0.132	no	1.2803	0.221907	0.169	no	Bos taurus Taurine upregulated gene 1 conserved region 3

URS000066F704	277	174	0.7893	0.03494329	0.029	no	0.7893	0.004977	0.071	no	Bos taurus SOX2 overlapping transcript exon 3
URS000066F725	208	63	1.2486	-0.5533622	0.001	no	1.2486	-0.56091	0.011	no	Bos taurus Six3os1 conserved region 7
URS00006703D9	127	12	0.9238	-0.5402292	0.000	no	0.9238	-0.50023	0.005	no	Bos taurus T-cell leukemia/lymphoma 6 conserved region 2
URS0000671CC7	151	60	1.0555	-0.0020796	0.015	no	1.0555	0.017072	0.056	no	Bos taurus FTX transcript, XIST regulator conserved region 3
URS0000673933	177	6	0.3194	-3.3444442	0.000	no	0.3194	-3.14823	0.000	no	Bos taurus Taurine upregulated gene 1 conserved region 4
URS000067E11A	215	72	1.104	0.12378344	0.045	no	1.104	0.144991	0.102	no	Bos taurus DLG2 antisense RNA 1 conserved region 1
URS0000680E2C	185	177	1.0005	0.12838402	0.099	no	1.0005	0.174034	0.182	no	Bos taurus Pvt1 oncogene conserved region 1
URS0000682766	223	6	0.3194	-3.3444442	0.000	no	0.3194	-3.14823	0.000	no	Bos taurus Prostate androgen-regulated transcript 1 conserved region 1
URS00006867A3	69	24	0.8507	-0.5007781	0.000	no	0.8507	-0.37277	0.007	no	Bos taurus JPX transcript, XIST activator conserved region 2
URS000068C47E	123	21	0.6706	-0.9344654	0.000	no	0.6706	-0.9314	0.001	no	Bos taurus SPRY4-IT1 conserved region 2
URS0000691107	97	15	0.3752	-0.5360566	0.000	no	0.3752	-0.64961	0.001	no	Bos taurus Maternally expressed 8 exon 1
URS0000693A09	374	69	0.8801	0.12245743	0.022	no	0.8801	0.177823	0.074	no	Bos taurus HOXA transcript at the distal tip, conserved region 2
URS0000696C1D	135	90	0.7435	-0.0272282	0.007	no	0.7435	-0.01036	0.035	no	Bos taurus HOXB13 antisense RNA 1 conserved region 1
URS0000697ADE	122	0	0	0	0.000	no	0	0	0.004	no	Bos taurus WT1 antisense RNA conserved region 4
URS000069BEA8	98	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Maternally expressed 8 exon 2
URS00006A3960	201	189	0.8598	-0.018075	0.030	no	0.8598	-0.01015	0.085	no	Bos taurus DAOA antisense RNA 1 conserved region 2
URS00006A711E	271	57	0.627	-0.289817	0.001	no	0.627	-0.2342	0.010	no	Bos taurus Six3os1 conserved region 5
URS00006A7D6B	198	0	0	0	0.000	no	0	0	0.004	no	Bos taurus ST7 overlapping transcript 4 conserved region 1
URS00006A961C	61	39	1.0075	0.13282328	0.026	no	1.0075	0.116644	0.062	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 1
URS00006AAE04	85	36	0.8983	0.35988544	0.075	no	0.8983	0.35483	0.112	no	Bos taurus NPPA antisense RNA 1 conserved region 3
URS00006AD16C	129	87	0.4435	-0.0253377	0.003	no	0.4435	-0.00984	0.019	no	Bos taurus WT1 antisense RNA conserved region 2
URS00006AD459	105	9	0.6632	-0.9039742	0.000	no	0.6632	-0.98346	0.000	no	Bos taurus Maternally expressed 3 conserved region 2
URS00006AE16B	272	21	0.7803	-1.0359179	0.000	no	0.7803	-0.85649	0.001	no	Bos taurus WT1 antisense RNA conserved region 8
URS00006AEBC0	98	0	0	0	0.000	no	0	0	0.004	no	Bos taurus HOTAIR conserved region 3
URS00006B25E5	109	18	0.4709	-0.3128058	0.000	no	0.4709	-0.34822	0.004	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 3
URS00006B2E3C	166	84	0.7209	0.15808265	0.020	no	0.7209	0.129369	0.052	no	Bos taurus HOXA transcript at the distal tip, conserved region 4
URS00006B6641	202	84	0.8651	-0.0218437	0.010	no	0.8651	-0.04986	0.036	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 6
URS00006BB24D	217	138	0.9914	0.02906229	0.035	no	0.9914	0.011574	0.083	no	Bos taurus HOX antisense intergenic RNA myeloid 1 conserved region 2
URS00006BE6E9	113	54	0.5573	-0.5017926	0.000	no	0.5573	-0.52344	0.003	no	Bos taurus ST7 overlapping transcript 3 conserved region 3
URS00006C52CB	173	0	0	0	0.000	no	0	0	0.004	no	Bos taurus TTC28 antisense RNA 1 conserved region 3
URS00006C91FB	196	33	0.6767	0.20344683	0.014	no	0.6767	0.271954	0.055	no	Bos taurus Vax2os1 conserved region 3
URS00006CB091	133	30	0.8607	-0.0340372	0.005	no	0.8607	-0.05183	0.025	no	Bos taurus JPX transcript, XIST activator conserved region 1
URS00006CCFE8	99	69	1.0945	0.11334694	0.040	no	1.0945	0.102862	0.086	no	Bos taurus MEST intronic transcript 1, antisense RNA conserved region
URS00006CF2CE	193	90	1.101	0.3749089	0.231	no	1.101	0.311005	0.191	no	Bos taurus Rhabdomyosarcoma 2 associated transcript conserved region 9
URS00006D0C82	383	18	0.9971	-0.6064877	0.000	no	0.9971	-0.46047	0.007	no	Bos taurus Myocardial infarction associated transcript exon 5 conserved region 3
URS00006D2A59	83	36	0.9707	-0.129272	0.004	no	0.9707	-0.1004	0.027	no	Bos taurus NPPA antisense RNA 1 conserved region 3
URS00006D6D45	159	120	0.7575	0.18214124	0.038	no	0.7575	0.191946	0.088	no	Bos taurus Nuclear enriched abundant transcript 1 conserved region 3
URS00006D8830	56	36	0.9322	0.21146634	0.033	no	0.9322	0.255745	0.085	no	Bos taurus HOXA transcript at the distal tip, conserved region 1
URS00006DCB57	191	54	0.6521	-0.3547823	0.000	no	0.6521	-0.35512	0.006	no	Bos taurus Deleted in lymphocytic leukemia 1 conserved region 1
URS00006E0845	38	0	0	0	0.000	no	0	0	0.004	no	Bos taurus GNAS antisense RNA 1 conserved region 3



URS00006E2E2E	92	78	1.1063	0.0950567	0.041	no	1.1063	0.056084	0.079	no	Bos taurus ZNFX1 antisense RNA 1 conserved region 2
URS00006E4C4E	118	0	0	0	0.000	no	0	0	0.004	no	Bos taurus ST7 antisense RNA 1 conserved region 1
URS00006E63B7	107	0	0	0	0.000	no	0	0	0.004	no	Bos taurus Maternally expressed 8 exon 2
URS00006E88AE	71	51	0.6392	-0.2225712	0.001	no	0.6392	-0.27969	0.008	no	Bos taurus FTX transcript, XIST regulator conserved region 1
URS00006FBAD6	179	126	0.9038	-0.2132939	0.005	no	0.9038	-0.16021	0.036	no	Bos taurus HOXA11 antisense RNA 1 conserved region 6
URS00006FEDB4	112	75	0.3852	-0.1964278	0.001	no	0.3852	-0.2353	0.007	no	Bos taurus Non-protein coding RNA, upstream of F2R/PAR1 conserved region 1
URS0000703281	211	39	0.9198	-0.2777535	0.001	no	0.9198	-0.44458	0.007	no	Bos taurus HOXA11 antisense RNA 1 conserved region 5
URS0000703385	76	6	0.3299	-2.901853	0.000	no	0.3299	-3.08032	0.000	no	Bos taurus CLRN1 antisense RNA 1 conserved region
URS0000705FA5	122	18	0.8956	-0.6394999	0.000	no	0.8956	-0.64138	0.003	no	Bos taurus Deleted in lymphocytic leukemia 2 conserved region 1
URS000071003F	98	63	0.8698	0.48692793	0.186	no	0.8698	0.520013	0.210	no	Bos taurus HOXA11 antisense RNA 1 conserved region 3
URS0000710D82	223	60	0.8505	-0.4381931	0.000	no	0.8505	-0.39521	0.009	no	Bos taurus Prostate androgen-regulated transcript 1 conserved region 1
URS00007164B5	194	54	0.7073	-0.1455383	0.002	no	0.7073	-0.24467	0.011	no	Bos taurus KCNQ1 overlapping transcript 1 conserved region 2
URS0000719068	232	78	0.7878	-0.1269287	0.004	no	0.7878	-0.11622	0.024	no	Bos taurus WT1 antisense RNA conserved region 3
URS0000720259	105	0	0	0	0.000	no	0	0	0.004	no	Bos taurus GNAS antisense RNA 1 conserved region 1
URS000072B58A	126	0	0	0	0.000	no	0	0	0.004	no	Bos taurus GNAS antisense RNA 1 conserved region 4
URS000072C9A4	105	9	0.6632	-0.9039742	0.000	no	0.6632	-0.98346	0.000	no	Bos taurus Maternally expressed 3 conserved region 2
URS000072DC14	201	81	0.8558	-0.0937773	0.006	no	0.8558	-0.11216	0.028	no	Bos taurus DAOA antisense RNA 1 conserved region 1
URS0000751D1A	820	324	0.8015	0.07230413	0.161	no	0.8015	0.11947	0.262	no	Bos taurus (cattle) X5
URS0000759E9B	22812	567	0.48	-0.058008	0.097	no	0.48	-0.06463	0.277	no	Bos taurus X (inactive)-specific transcript (XIST), long non-coding RNA.
URS000075A02E	1894	306	0.6476	-0.0680364	0.035	no	0.6476	-0.03546	0.113	no	Bos taurus uncharacterized LOC100848703 (LOC100848703), long non-coding RNA.
URS000075AAC6	930	177	0.9069	0.16822608	0.093	no	0.9069	0.171259	0.153	no	Bos taurus uncharacterized LOC100196901 (LOC100196901), transcript variant 2, long non-coding RNA.
URS000075AD92	751	144	0.6445	-0.1496252	0.004	no	0.6445	-0.17596	0.023	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 7, long non-coding RNA.
URS000075B437	926	177	0.9069	0.16822608	0.093	no	0.9069	0.171259	0.153	no	Bos taurus uncharacterized LOC100196901 (LOC100196901), transcript variant 3, long non-coding RNA.
URS000075B61B	886	144	0.6445	-0.1496252	0.004	no	0.6445	-0.17596	0.023	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 5, long non-coding RNA.
URS000075B744	2851	2676	1.1013	0.33495888	1.000	yes	1.1013	0.329076	1.000	yes	Bos taurus PPARG-TSEN2 (PPARG-TSEN2), transcript variant 2, long non-coding RNA.
URS000075BB85	892	114	0.6841	0.02240328	0.010	no	0.6841	0.042168	0.044	no	Bos taurus antisense IGF2R RNA noncoding (AIRN), long non-coding RNA.
URS000075C9BA	795	111	0.9282	0.05455613	0.025	no	0.9282	0.07886	0.076	no	Bos taurus uncharacterized LOC100616526 (LOC100616526), transcript variant 2, long non-coding RNA.
URS000075CB6C	1120	147	0.894	0.0876376	0.040	no	0.894	0.048664	0.082	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 1, long non-coding RNA.
URS000075DFAF	777	135	0.7837	-0.1091227	0.007	no	0.7837	-0.11944	0.035	no	Bos taurus small nucleolar RNA host gene 3 (non-protein coding) (SNHG3), long non-coding RNA.
URS00001A8549	918	543	1.1996	0.36515742	0.980	yes	1.1996	0.376433	0.908	yes	Bos taurus (cattle) partial PEG11 antisense RNA
URS000061E61B	644	189	0.7462	-0.1219713	0.010	no	0.7462	-0.14049	0.044	no	Bos taurus (cattle) noncoding RNA
URS0000626285	61	6	0.3621	1.18215914	0.712	yes	0.3621	1.040412	0.302	no	Bos taurus ZEB2 antisense RNA 1 conserved region 2
URS000062C8E7	67	15	0.6556	0.07351687	0.005	no	0.6556	0.056913	0.022	no	Bos grunniens H19 conserved region 2
URS000063BDFC	58	3	0.3299	0	0.001	no	0.3299	0	0.009	no	Ovis aries HOX antisense intergenic RNA myeloid 1 conserved region 3
URS00006515F5	126	54	0.9473	0.13648592	0.026	no	0.9473	0.149701	0.069	no	Ovis aries X-chromosome inactivation gene exon 4

URS0000667B4F	76	0	0	0	0.000	no	0	0	0.004	no	Ovis aries Deleted in lymphocytic leukemia 2 conserved region 3
URS000067C63C	125	123	1.1507	0.04518516	0.054	no	1.1507	0.049557	0.113	no	Bos taurus H19 conserved region 3
URS000068C069	46	0	0	0	0.000	no	0	0	0.004	no	Ovis aries CDKN2B antisense RNA 1 conserved region 2
URS000069115D	96	48	0.8041	-0.1356044	0.003	no	0.8041	-0.10815	0.020	no	Bos taurus HOXA11 antisense RNA 1 conserved region 1
URS000069C46C	71	33	1.0113	-0.0135459	0.009	no	1.0113	-0.08887	0.029	no	Bos taurus Ghrelin opposite strand RNA conserved region
URS00006A38EC	125	111	0.9834	0.221769	0.087	no	0.9834	0.212901	0.133	no	Bos taurus SMAD5 antisense RNA 1 conserved region 3
URS00006BA301	186	24	0.7776	-0.4064206	0.000	no	0.7776	-0.2448	0.010	no	Ovis aries HOXA11 antisense RNA 1 conserved region 2
URS00006BB01F	140	27	0.5365	-0.3212849	0.000	no	0.5365	-0.44433	0.003	no	Ovis aries FTX transcript, XIST regulator conserved region 4
URS00006D6533	105	54	1.0745	0.32541807	0.120	no	1.0745	0.334339	0.158	no	Bos taurus ST7 antisense RNA 1 conserved region 2
URS00006DD98B	78	51	0.8067	-0.8603869	0.000	no	0.8067	-0.83543	0.001	no	Ovis aries ZEB2 antisense RNA 1 conserved region 4
URS00006FC8F0	99	51	0.8301	-0.1825912	0.002	no	0.8301	-0.20831	0.015	no	Bos taurus MEST intronic transcript 1, antisense RNA conserved region
URS00006FECED	151	84	0.7746	-0.0439212	0.006	no	0.7746	-0.06789	0.029	no	Bos taurus Non-coding RNA BC040587
URS0000709DD8	124	0	0	0	0.000	no	0	0	0.004	no	Bos taurus GNAS antisense RNA 1 conserved region 5
URS000070AAE0	109	0	0	0	0.000	no	0	0	0.004	no	Bos taurus SOX2 overlapping transcript exon 4
URS00007294CE	76	57	0.5418	-0.2044881	0.001	no	0.5418	-0.15935	0.011	no	Ovis aries ZNRD1 antisense RNA 1 conserved region 2
URS000075E02A	947	84	0.5671	-0.2743852	0.001	no	0.5671	-0.26996	0.009	no	Bos taurus uncharacterized LOC100848574 (LOC100848574), transcript variant 3, long non-coding RNA.

**Table S4 Sequence conservation of BLV AS1 and Tax sequences**

	AS1	AS1 3rd	AS1 no overlap	AS1 no overlap 3rd	Tax	Tax 3rd
AS1	<b>0.01485 (264)</b>	0.0286	0.3265	0.0198	0.2995	0.1298
AS1 3rd		<b>0.034 (88)</b>	0.4859	0.4595	0.0011	0.4105
AS1 no overlap			<b>0.0236 (72)</b>	0.2278	0.0382	0.9165
AS1 no overlap 3rd				<b>0.0521 (24)</b>	0.0035	0.1246
Tax					<b>0.0106 (930)</b>	0.0031
Tax 3rd						<b>0.0247 (170)</b>

Sequence conservation of BLV AS1 and Tax sequences using sequence data from 12 bovine and 28 ovine tumors supplemented with six publicly available whole genome BLV sequences from NCBI

AS1: sequence segment corresponding to the putative protein coding sequence of AS1

AS1 3rd: 3rd codon positions of the putative protein coding sequence of AS1

AS1 no overlap: segment corresponding to the putative protein coding sequence of AS1 that does not overlap with R3 or G4

AS1 no overlap 3rd: 3rd codon positions of the putative protein coding sequence of AS1 that does not overlap with R3 or G4

Tax: full length Tax coding sequence, Tax 3rd: 3rd codon positions of the segment of Tax that does not overlap with Rex

Diagonal: nucleotide diversity (= average difference per nucleotide site across all pairs of isolates) for the corresponding sequence segment, and – between brackets – number of corresponding nucleotide positions. Off-diagonal: p-value of the differences between corresponding nucleotide diversities.

## Table S5 Oligos used

BLV genome coordinates correspond to the provirus found in the YR2 cell line (NCBI Accession: KT122858)

### End point PCR oligos

Name	Forward 5'-3'	Reverse 5'-3'	Region
AS1-S/L	TCCCTTCTGTTTCCACAACG	CAGAGGACCGGAGATAGAGC	BLV:7121-8564
AS1-L	CCCCTAAACCCGATTCTGAT	CAGAGGACCGGAGATAGAGC	BLV:6263-8564
AS2	CCCAGTCTCTTCTGGTGTCC	CAGAGGACCGGAGATAGAGC	BLV:2782-8564
ACTB	GACAAATGGTTCGGCATGTG	TCCCTGATGTCACGCAAT	chr11:50421140-50422030 (oviAri3)

### Real Time PCR oligos for use with sybr green

Name	Forward 5'-3'	Reverse 5'-3'	Region
Tax	GCCTTCAAATGCCAAAGAAC	CAACCAACAACACTTGCCATC	BLV:4818-7267
Env-Tax-Rex-R3	TCCTTCTCCCGAGACCTT	CTAGCCACCGAGCATTTGTTT	BLV:262-4712
AS1	TCCCTTCTGTTTCCACAACG	CTTCTGGTCCGCCAACTC	BLV:7121-8404
AS2	TTTCGAACGGGCACTACAG	CTTCTGGTCCGCCAACTC	BLV:2732-8404
TBP	CTTGACCTAAAGACCATTGCAC	CCATCTTCCCAGAGTGAATATC	chr8:90670093-90671593 (oviAri3)
HPRT1	GACCAGTCAACAGCGGACAT	CTTGACCAAGGCAAGCAAAG	chrX:95382926-95389315 (oviAri3)
U6	CTCGCTTCGGCAGCACATATAC	GGAACGCTTACGAAATTTGCGTG	U6 Small nuclear RNA
Tyr-tRNA	CCTTCGATAGCTCAGTTGGT	GTCCTTCGAGCCGGAATC	Tyrosine transfer RNA

### PrimeTime qPCR Assays (Integrated DNA Technologies)

	Forward 5'-3'	Probe	Reverse 5'-3'	Region
AS1 cDNA	TCCCTTCTGTTTCCACAACG	/56-FAM/AAGCTCTTC/zen/GGATCCATTACCTGC/3IAbkFQ/	CTTCTGGTCCCGCTAACTC	BLV:7121-8404
AS2 cDNA	TTTCGAACGGGCACTACAG	/56-FAM/CCGCTTCT/zen/CCCAGTCTCTCT/3IAbkFQ/	CTTCTGGTCCCGCTAACTC	BLV:2732-8404
TAX cDNA	GCCTTCAAATGCCAAAGAAC	/56-FAM/TGATGATCG/zen/GTTGTGGCGTCTTC/3IAbkFQ/	CAACCAACAACACTTGCCATC	BLV:4818-7267
RPS9 cDNA	TGACGCTGGATGAGAAAGAC	/56-FAM/CTGTTCGAA/zen/GGTAATGCCCTG/3IAbkFQ/	CTTCAGGCCAGGATGTAATC	chr14:60,263,509-60,268,300 (oviAri3)
TBP cDNA	CTTGACCTAAAGACCATTGCAC	/56-FAM/TGCCCGAAA/zen/TGCTGAGTATAATCCCAA/3IAbkFQ/	CCATCTTCCCAGAGTGAATATC	chr8:90670093-90671593 (oviAri3)
BLV DNA	CTTACAACGCTTCCTCCATGAC	/56-FAM/ACGCTCAC/zen/TGGTCAGAATTGGTT/3IAbkFQ/	GGCGGGAGAGCCATTTATTT	BLV:5806-5916
RPS9 DNA	TGGATGTTGGTATTGGGTGG	/56-FAM/TTCTGGTCT/zen/CAGGGAACTTGTGG/3IAbkFQ/	CCCTGTGCATCTCTTTGTC	chr18:63386124-63386267 (BosTau6)

### Oligos for Luciferase assays

Name	Forward 5'-3'	Reverse 5'-3'	Region
5'LTR	TGACGCTAGCTGTATGAAAGATCATGCCGACCT	TGACAAGCTTACGAGCCCCAATTGTTT	BLV:1-544
3'LTR	TGACAAGCTTTGAGGGGAGTCAATTTGTATG	TGACGCTAGCTGTTTGGCGGTCTCTCT	BLV:8175-8720
3'LTRA	TGACAAGCTTTGCTGACCTCACCTGCTGATA	TGACGCTAGCTGTTTGGCGGTCTCTCT	BLV:8342-8720
mut DAS	CCTCTGACCGTCTCCATCAGGACTCTCTCTCTTG	CAAGAGAGAGAGTCTGATGGAGACGGTCAGAGG	BLV:370-403/8559-8592
mut IRF	GTTTCCGTCTTACAGTCTGTGTCTCGCGGCCCG	GCGGGCCGAGACACAGACTGTAAGACAGGAAAC	BLV:450-484/8639-8673

### Oligos for producing altered pBLV344

Name	Forward 5'-3'	Reverse 5'-3'	Region	Additional info
up_miR	CCACCTGGTACTCTTCCAA	TGACAGCGCTGTGAACATGGGGGTGTC	BLV:3268-6388	Region upstream of miRs
down_miR	TGACAGCGCTTAGACCCCTAACGGAGGTT	AAGCAGAAAGAACGCTCGAA	BLV:6943--6962 & *chr12:59,152,995-59,153,014 (oviAri3)	Region downstream of miRs
amp_lig	CCACCTGGTACTCTTCCAA	GCGGGAGAGCCATTTATTTT	BLV:3268-8168	Amplifies ligated DNA
amp_miR	TGACAGCGCTGACCCCTCAGGCTGTGG	TGACAGCGCTGAAACCCGGGCTTG	BLV:6389-6942	Amplifies miR region

Red bases = restriction recognition site, \*pBLV344 contains flanking DNA derived from the host

**Oligos for 5'RACE**

Description	Oligo 5'-3'
GeneRacer 5' Nested With Nextera Forward	<b>TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGACACTGACATGGACTGAAGGAGTA</b>
5'RACE AS1 + Nextera Reverse	<b>GTCTCTGGGGCTCGGAGATGTGTATAAGAGACAGGGCTGCCCTGCATCTTCTA</b>
5'RACE AS2 + Nextera Reverse	<b>GTCTCTGGGGCTCGGAGATGTGTATAAGAGACAGCCAGTCTTCTTCTGGTGTC</b>

Bold = region corresponding to either the nextera reverse or forward

**Oligos for 3'RACE with GeneRacer oligo**

Description	Oligo 5'-3'
GeneRace3	GCTGTCAACGATACGCTACGTAACGGCATGACAGTGTTTTTTTTTTTTTTTTTT
PCR1 GeneRacer3	GCTGTCAACGATACGCTACGTAACG
PCR1 BLV LTR (8489-8508)	GTGGTTTGCCTTACCTGACC
PCR2 GeneRacer3 nest with Nextera Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGCTACGTAACGGCATGACAGTG
PCR2 BLV LTR (8405-8424)	AGGGTCTCAGGAGGAGAAGC

Bold = region corresponding to either the nextera reverse or forward

**Oligos for 3'RACE with oligo dT + Nextera**

Description	Oligo 5'-3'
Oligo dT tailed wtihi Nextera reverse	GTCTCTGGGGCTCGGAGATGTGTATAAGAGACAGTTTTTTTTTTTTTTTTT
PCR1 BLV LTR (8489-8508)	GTGGTTTGCCTTACCTGACC
PCR1 Nextera reverse	<b>GTCTCTGGGGCTCGGAGAT</b>
PCR2 BLV LTR (8405-8424)	AGGGTCTCAGGAGGAGAAGC
PCR2 Nextera reverse	<b>GTCTCTGGGGCTCGGAGAT</b>

Bold = region corresponding to either the nextera reverse or forward

**Nextera Based oligos annealed together and ligated to fragmented 3'RACE PCR**

Nextera Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGT
Nextera Reverse	/5Phos/ <b>CTGTCTCTTATACACATCTCCGAGCCACGAGAC</b>

Bold = region of complementarity in oligos

**Oligos for 3'RACE with GeneRacer oligo primer adjacent to end of AS1-L**

Description	Oligo 5'-3'
BLV (5393-5412) + Nextera Reverse	<b>GTCTCTGGGGCTCGGAGATGTGTATAAGAGACAGCTGACAGAGGGAACCCAGTC</b>
GeneRacer3 nest with Nextera Forward	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCGCTACGTAACGGCATGACAGTG

**Oligos for 3'RACE using GeneRacer oligo for MinION sequencing**

Description	Oligo 5'-3'
GeneRace3	GCTGTCAACGATACGCTACGTAACGGCATGACAGTGTTTTTTTTTTTTTTTTTT
PCR1 GeneRacer3	GCTGTCAACGATACGCTACGTAACG
PCR1 BLV LTR (8489-8508)	GTGGTTTGCCTTACCTGACC
PCR2 GeneRacer3	CGTACGTAACGGCATGACAGTG
PCR2 BLV LTR (8405-8424)	<b>GGTGCTGAAGAAGTTGTCGGTGTCTTTGTGTTAACCTAGGGTCTCAGGAGGAGAAGC</b>

Bold = MinION barcode 1

**Oligos for modified 5' RACE to detect RNA cleavage**

Description PCR1 oligos	Oligo 5'-3'
GeneRacer 5' Primer	CGACTGGAGCACGAGGACACTGA
miR1-RACE (BLV:6357-6376)	TCGACCCCTGCCCTTGACACC
miR2-RACE (BLV:6454-6473)	CTTGTGCCAGCGCCGAGTT
miR3-RACE (BLV:6584-6603)	GCCCTCCCGTTGCCGTGTGAC

miR4-RACE (BLV:6682-6703)	GGGCGATTTCTTGCAGCTGTGC
miR5-RACE (BLV:6803-6827)	TACGCCCTGTTCACACCCCTTCTA

Description PCR2 oligos	Oligo 5'-3'
GeneRacer 5' Nested Primer with Nextera Forward	<b>TCGTCGGCAGCCTCAGATGTGTATAAGAGACAG</b> GGACACTGACATGGACTGAAGGAGTA
miR1-Nest + Nextera Reverse	<b>GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG</b> CCATGTTTCACGCACCCCTCA
miR2-Nest + Nextera Reverse	<b>GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG</b> CCCTACCCTGACCCCTCTCTG
miR3-Nest + Nextera Reverse	<b>GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG</b> CCCTCTCACTTCTGCTTACCA
miR4-Nest + Nextera Reverse	<b>GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG</b> CAGCTGTGCTAAGCGAGAGG
miR5-Nest + Nextera Reverse	<b>GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG</b> ATCTCAGCTCGCACCCCAAG

Bold = region corresponding to either the nextera reverse or forward

#### Oligos for High-throughput sequencing of BLV integration sites

Description Oligos annealed to make adapter	Oligo 5'-3'
Linker-Long	TCATGATCAATGGGACGATCAGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGNNNNNNNGCTCTCCGATCT
Linker-Short	/5Phos/GATCGGAAGAGCGAAAAAAAAAAAAA

Description PCR1 oligos	Oligo 5'-3'
Link-PCR1	TCATGATCAATGGGACGATCAGTC
BLV-5' END	GCAGCTGACGTCTCTGTCTG
BLV-3' END	AGCTCTATCTCCGGTCTCT

Description PCR2 oligos	Oligo 5'-3'
Link-PCR2	GTCTCGTGGGCTCGGAGAT
BLV-5' END-2	TCGTCGGCAGCCTCAGATGTGTATAAGAGACAGNNNNNNNGGCTCCTAGGTCGGCATGAT
BLV-3' END-2	TCGTCGGCAGCCTCAGATGTGTATAAGAGACAGNNNNNNCTAGCGCCAGGAGAGACC

#### Locked nucleic acid antisense oligos for AS transcript knockdown

Name	Oligo 5'-3'	Region
BLV_AS_LNA1	CCAAGTGTGCACAATA	BLV:6994-7009
BLV_AS_LNA2	TACCTGCTGATAAAC	BLV:7215-7217 & 8353-8365 covers AS1 splice site
BLV_AS_LNA3	AGCGTTCTCTCTGAG	BLV:8403-8419 Common to AS1 & AS2