Supplemental figure legends

Fig S1 Coding potential analysis of rightward (aquamarine rightward arrow) and leftward (Red leftward arrow) transcripts. Analysis was performed using the “Coding Potential Calculator” which incorporates reading frame length as well as analysis of candidate ORF coding sequence homologues. Candidate ORFs are indicated by blue bars/arrows and Blast homologies are indicated by orange bars.

Fig S2 Sense and antisense read coverage across the *oriP* region extending from upstream from the EBER2 gene to just downstream from the BCRF1 gene. Number of reads covering each genomic position is indicated by positive values (in turquois) for sense reads and negative values (red) for antisense reads.

Fig S3 Expandable view of Fig. 3 showing hairpin calculations for oriPts. (A) Covariance hairpin structures were predicted in the FR region of *oriP* across 5 EBV strains (Akata, EBV1, EBV2, Mutu and GD1) and Macacine herpesvirus 4 (MHV4). The average pairwise sequence identity (APSI) was calculated for the regions where the hairpin structures were identified in the 6 virus strains. The Z-scores were calculated for the hairpin structures in sense (Fwd) and antisense (Rev) transcripts in each virus. (B) Predicted hairpin structures for oriPtR (left) and oriPtL (right) with associated folding free energy values. Editing frequencies for each adenosine through each hairpin are shown. Heat maps show relative average editing for As, Us, Gs, and Cs located at positions -2, -1, 0 and +1 relative to the edited adenosine residue (0 position). (C) Stem annealing of OriP repeats.

Fig S4 Genomic locations of previously discovered NONO and SFPQ binding sequences across the Akata EBV genome (upper panel) with an expanded view of these sites in the *oriP* region (lower panel).

Supplemental Tables

Table S1 RNA editing statistics for sense and antisense FR region.

Table S2 RNA editing statistics for EBV microRNAs.

Table S3 Gene expression values for core paraspeckle components and the RNA editing enzyme, ADAR, as determined by RNA-seq in the Akata induction/oriPtL-GapmeR experiment and in the Mutu control and oriPtL retroviral expression vector transductants.

Table S4 Gene expression values for EBV genes as determined by RNA-seq in the Akata induction/oriPtL-GapmeR experiment and in the Mutu control and oriPtL retroviral expression vector transductants.

Table S5 Gene expression patterns observed in EBseq analysis and numbers of statistically significant viral genes attributed to each pattern.

Fig S1

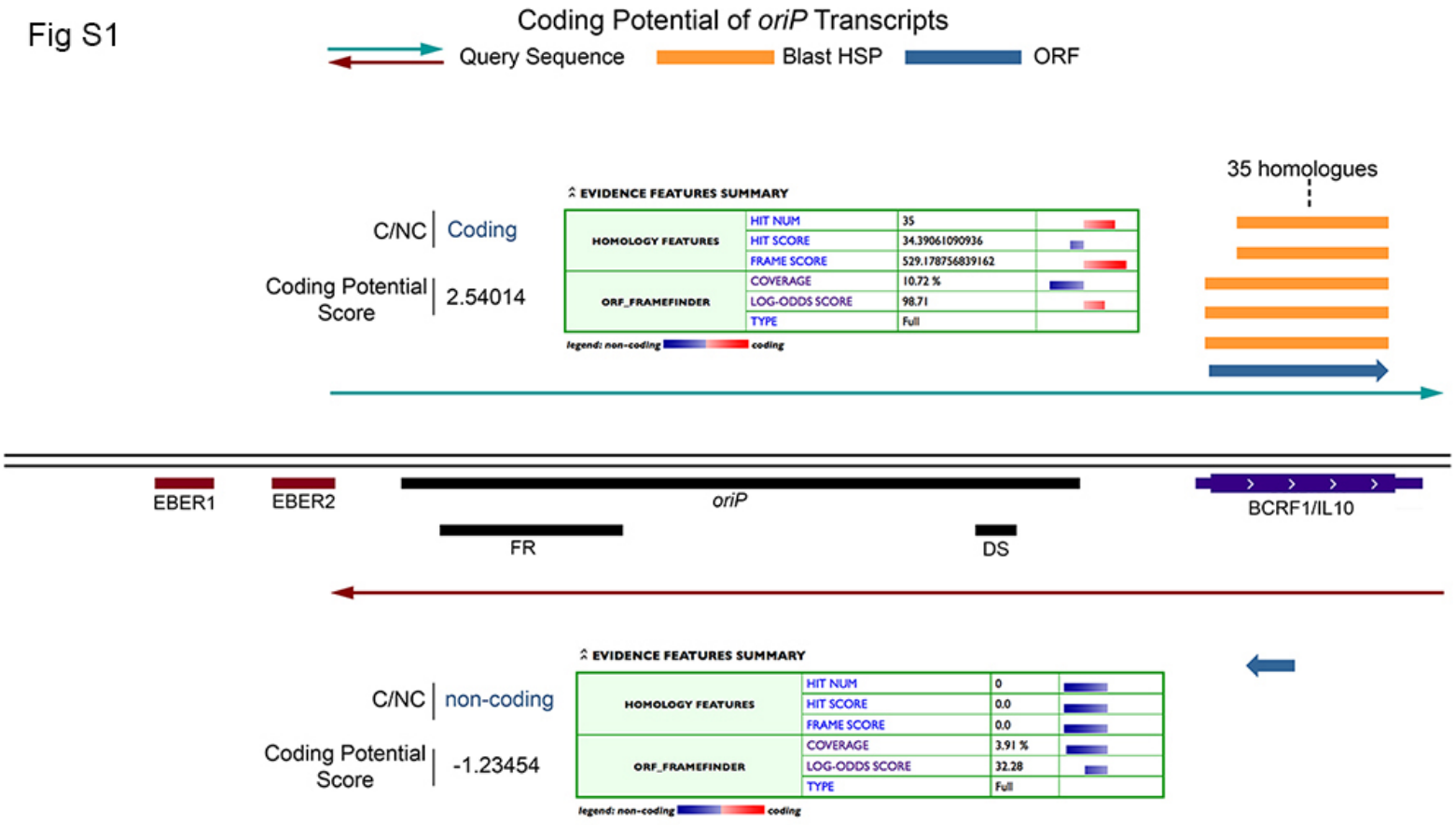
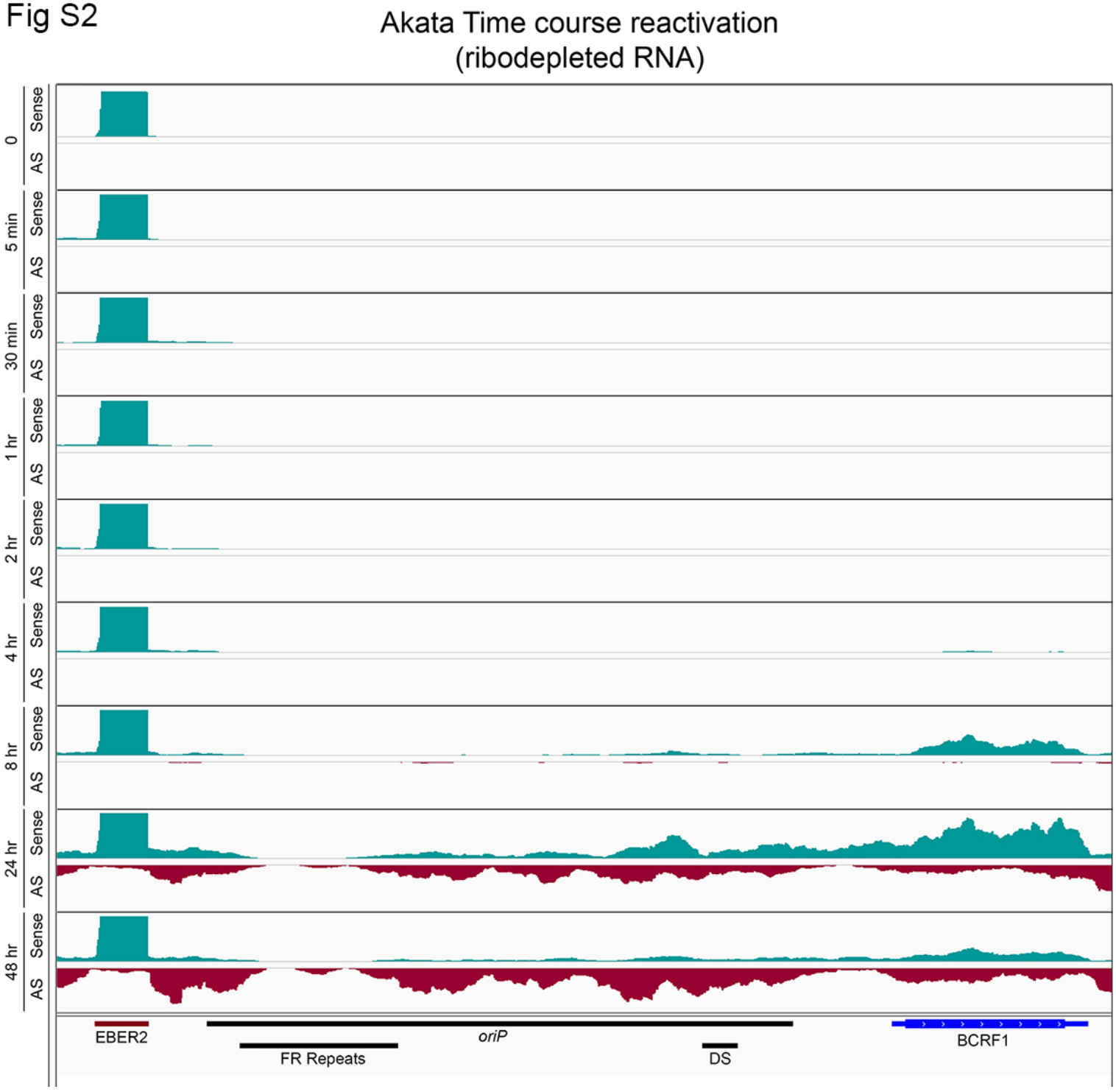

Coding Potential of oriP Transcripts
Query Sequence
Blast HSP
ORF
35 homologues
EVIDENCE FEATURES SUMMARY
C/NC
Coding
Coding Potential Score
2.54014
HOMOLOGY FEATURES
HIT NUM
35
HIT SCORE
34.39061090936
FRAME SCORE
529.178756839162
ORF_FRAMEFINDER
COVERAGE
10.72 %
LOG-ODDS SCORE
98.71
TYPE
Full
legend: non-coding
coding
EBER1
EBER2
oriP
FR
DS
BCRF1/IL10
EVIDENCE FEATURES SUMMARY
C/NC
non-coding
Coding Potential Score
-1.23454
HOMOLOGY FEATURES
HIT NUM
0
HIT SCORE
0.0
FRAME SCORE
0.0
ORF_FRAMEFINDER
COVERAGE
3.91 %
LOG-ODDS SCORE
32.28
TYPE
Full
legend: non-coding
coding

Fig S2

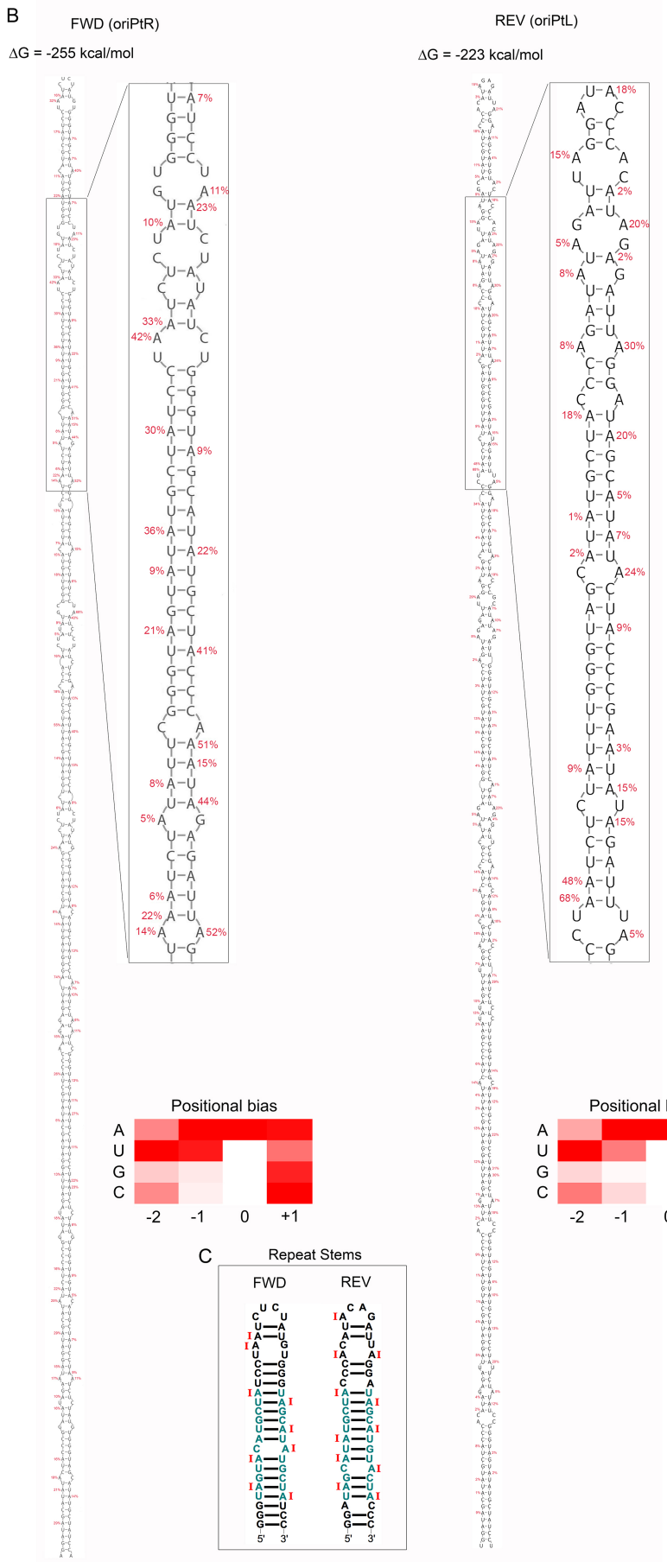

Akata Time course reactivation
(ribodepleted RNA)
0
5 min
30 min
1 hr
2 hr
4 hr
8 hr
24 hr
48 hr
Sense
AS
EBER2
FR Repeats
oriP
DS
BCRF1

A

Fig S3

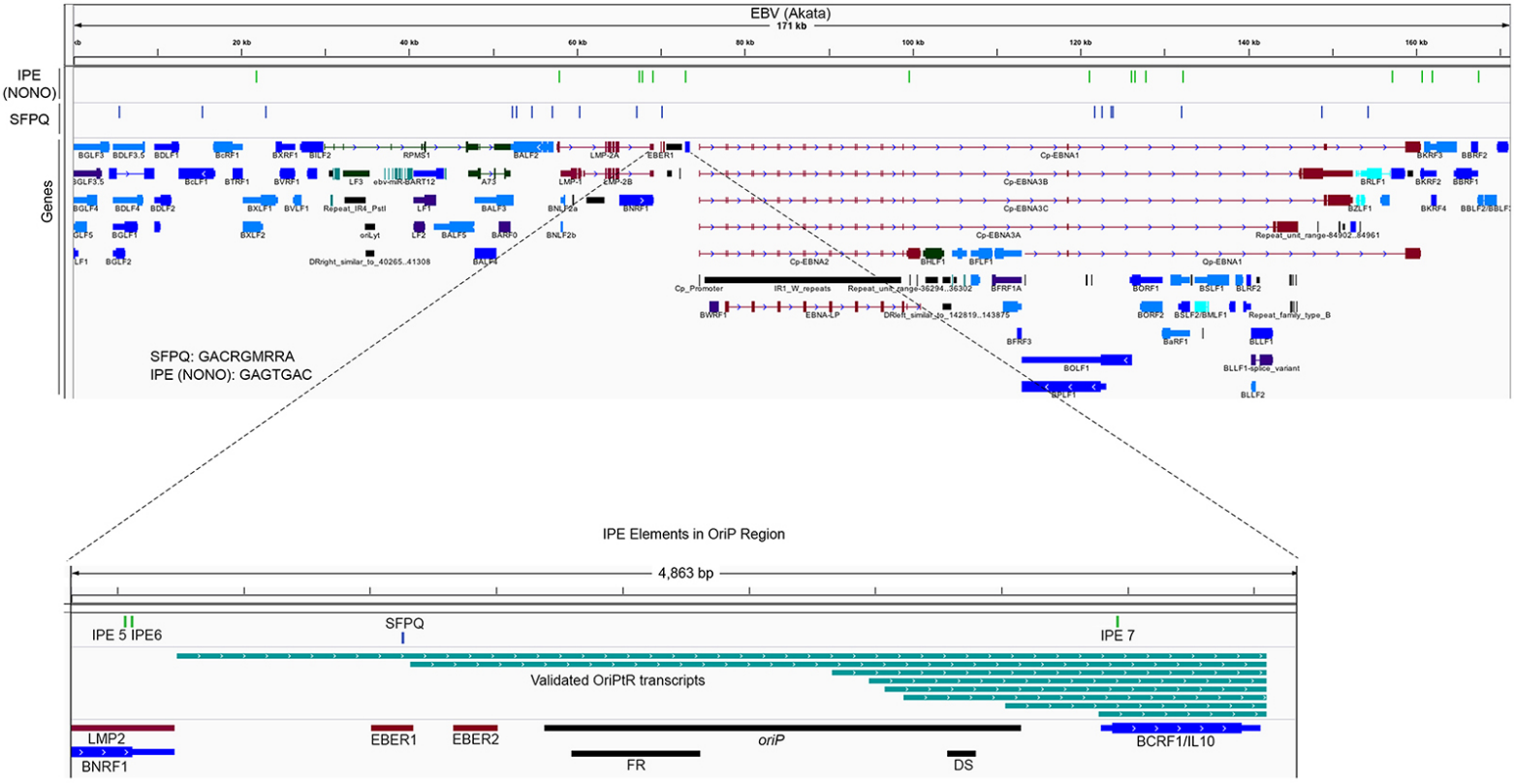
EBV genome	Coordinates	APSI						Z-score	
		Akata	B85-8	AG872	Mutu	GD1	MHV4	FWD	REV
Akata (KC207813.1)	7458-7927	1	0.75	0.82	0.76	0.74	0.66	-4.32	-4.31
B95-8 (NC_007605.1)	7492-8148	0.75	1	0.83	0.88	0.88	0.73	-4.22	-4.07
AG876 (NC_009334.1)	7450-7915	0.82	0.83	1	0.82	0.83	0.69	-4.25	-4.24
Mutu (KC207814.1)	7545-8014	0.76	0.88	0.82	1	0.9	0.71	-3.93	-3.8
GD1 (AY961628.3)	7363-8087	0.74	0.88	0.83	0.9	1	0.72	-4.18	-4.01
MHV4 (NC_006146.1)	7512-7936	0.66	0.73	0.69	0.71	0.72	1	-3.79	-4.13

B



C

Fig S4


EBV (Akata)
171 kb
IPE (NONO)
SFPQ
Genes
SFPQ: GACRGMRRA
IPE (NONO): GAGTGAC
IPE Elements in OriP Region
4,863 bp
IPE 5 IPE6
SFPQ
IPE 7
Validated OriPtR transcripts
LMP2
BNRF1
EBER1
EBER2
oriP
FR
DS
BCRF1/IL10