

Region	Start	End	Forward	Reverse
Per E1	-9095	-8994	CTA TAC ACA GAC ACG TGC ATA CAC CGA C	CGG CTT CTT TGC TCA TTA TCA TCA ACG AAT C
Per E2	-3066	-2889	CTC GCC AAT CTC AAA CGG AGC G	GGA ACA GTG CGA TCC GGA CAT G
Per E3 and E4	-1504	-1374	GGC AGG CGT CTG TGA CTT TGT G	CTC CAC ACG CAG CTC CTT TGT G
Per Up 1	-1274	-1079	GGC TGA TAA GGC ATA AAG ACA TCC TTG G	GTG CAT TGA ATT TGG CTT TTA GTC TTC GC
Per E5 (CRS)	-628	-352	CCA GTG CCA GTG CGA GTT C	GAT GCC AAG TGT CAA TCC AAG C
Per Up 3	-81	107	GAG AGC AGC GAG TGA GTG TGA G	GCG TGA TTC GAC AGG TCG TTG TTG
Per Up 3-2	-144	6	GTA TCT CAG CCG ACC AGC GAT TTC	GAA CAC TAG TGC TCG CAT CGC AAG
Per 56	452	608	GTT CAT AAC GTC CAA TGG CGC ACT TAC	GGA AGG AAG TGG TGG GGC ATT C
Per E6	826	946	GGG CAT TGC ACC TTG GTA TTT TCA GC	CTG CGA CTG CGG CTA TCC AAA TC
Per 67	1227	1392	GGT TAA CCA GCG AGT TAC ACA ATC CTT GG	GTT TCG ACG GCC CAG AAT TCA AGA AG
Per E7	1779	1933	GGA TGC ATT GCG ACT GCA TAA CGA C	CCT GCA ACG AGG CTT CAC TGT G
Per E8	2086	2236	CAA GCC ATG ATT CAT GAA CAT GAA TGG CAG	CTT CAC GTT GCT CGC CAA TAG TAT TGT G
Per Trans	2559	2708	CCA TTC AAG GTC CTA TCA AGG ATA ACT GAA GTG C	CCT TGG TGT TGT GTG TGG ACT CC
Per MT	5992	6133	CAA CGC TCT CCA GAT TCC CGA AC	GTG GTC TAT GGA CGA GTA TGG AGT TGA G
Tim Up 1	-1242	-1048	GCC TGC AAC CAA CTG TTG ATT CC	GAA CGA CTC TGC CGT AGG CTT C
Tim E1	-697	-535	GCG GCA CGT TGT GAT TAC AC	ACA CTG ACC GAA ACA CCC ACT C
Tim Up 3	-198	41	GCT ATT GAA GTT GCA TTT TAC ATA AGC CAA CAA CGA G	GAT CGT GTT ATA GTT TCA GTG CTG TTA TAT ACA CTG ATG
Tim Up 3-2	5	188	CAT CAG TGT ATA TAA CAG CAC TGA AAC TAT AAC ACG	CTT ACC AAT TAT TTA AAT TTT TTC TAT CGC AGA CAA TTT TAC TG
Tim E2	1726	1917	GGG AAC TTT CGG GGC TCG TCT G	CGC CAC CCA TGT GAC CAT CAA G
Tim Trans	2162	2307	GTT ACA GAT ACC GCG CAA ATG GCT AAG	CGG AGT TGC TAG TAA CCA GTC CAT AAC C
Tim LE	12152	12302	CCA GAA TGT ATG TGA GCG ATG AGG AC	CAA TTC TTT CCA GCT GGG TGG G

Supplemental Table 1. Primers used for quantitative PCR (qPCR) and semi-quantitative PCR analysis of ChIP samples. Sense (forward) and antisense (reverse) primer sequences are indicated for each amplified region. All primer sequences are shown in the 5' to 3' orientation. The start and end of each amplified region is indicated relative to the *per* and *tim* transcription start (+1).