

# Chapter 20

## KSHV Latent Genes and Their Regulation

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*“Herpesviridae omnia divisa est in partes tres.”*

Herpesviridae are divided into three groups: alpha herpesviruses, beta herpesviruses and gamma herpesviruses. Only the two gamma herpesviruses, Kaposi sarcoma-associated herpesvirus (KSHV, or human herpesvirus 8) and Epstein–Barr virus (EBV, or human herpesvirus 4) are associated with human cancer. Herpesvirus lytic replication is also customarily divided into three phases: alpha or immediate early (IE), beta or early (E) and gamma or late (L). We base this classification on the temporal order of viral gene expression. Here, I propose that KSHV latent genes likewise may be divided into three categories based upon their pattern of transcription in KSHV-associated diseases (Table 20.1).

KSHV is associated with three proliferative malignancies in immune-compromised patients: Kaposi sarcoma (KS), primary effusion lymphoma (PEL) and the plasmablastic variant of multicentric Castleman disease (MCD) (reviewed in (Antman and Chang 2000; Ablashi et al. 2002; Dourmishev et al. 2003)). Overwhelming epidemiological evidence shows that KSHV infection is required for the disease phenotypes. Every tumor cell carries the viral genome and expresses KSHV latent proteins. Every cell that stably maintains the KSHV genome must express the latency-associated nuclear antigen (LANA), as this protein is required for latent episome maintenance (see Chapter 19). LANA is expressed in KS as well as in PEL and MCD (Kedes et al. 1997a; Kellam et al. 1997a; Dittmer et al. 1998; Dupin et al. 1999a). LANA transcription is regulated by the LANA promoter, which is constitutively active in all cell types. LANA-2/vIRF-3/K10.2 is only expressed in PEL, a tumor of B cell origin. By contrast K9/vIRF-1 is seen more prominently in KS, a tumor of endothelial origin. Another KSHV latent gene *Kaposin/k12/t0.7* is also constitutively transcribed in all

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**Table 20.1** The three categories of KSHV latency

	KS (in situ)	PEL, MCD (in situ)	TPA inducible	Genes
Type I	100%	100%	Minimal	LANA*, vFLIP*, vCYC*
Type II	0%	100%	Not inducible	LANA-2/vIRF-3
Type III	100%	100%	Maximal	<i>Kaposin</i> *, K9/vIRF-1*

\*A second, proximal promoter drives transcription in response to Rta/orf50.

KSHV-associated tumors. K9/vIRF-1 and *Kaposin* are greatly induced by phorbol ester (TPA) stimulation of PEL. The transcriptional response to TPA of LANA/orf73, vCYC/orf72 and vFLIP/orf71/K13, which are derived from differentially spliced, overlapping transcripts, is complex and LANA-2/vIRF-3/K10.5-10.6/K10.7 mRNA levels are impervious to TPA.

In sum, KSHV latent transcription seems divinely designed, or rather evolutionarily tuned, to respond to different host environments. This ensures commensal coexistence of virus and host under normal circumstances, but can lead to tumorigenesis in the setting of immune deficiency.

## 20.1 Profiling KSHV Transcription in Experimental Models and Primary Tumors

Herpesvirus transcription is divided into four stages: the three lytic stages (alpha, beta and gamma) and the latent stage. In KSHV, and in the related EBV, latency can be further divided into additional types, based on gene expression and host cell origin. Many excellent studies have profiled KSHV transcription genome-wide (Table 20.2). Although the KSHV transcript map is of yet incomplete (see Chapter 19 for the current transcript map), all gene expression profiling studies concur as to the identity of the KSHV latent genes (Fig. 20.1). These are LANA (orf73), vCYC (orf72), vFLIP (orf71), the viral miR cluster, *Kaposin* (orf K12) and LANA-2/vIRF-3. Except for LANA-2/vIRF-3, all other latent genes are clustered in the far right region of the viral genome. Except for LANA-2/vIRF-3, which is B-cell specific, all other latent genes are expressed in all KSHV-associated cancers and all experimental models of KSHV latency.

The kinetics of KSHV latent transcripts outside of long-term latency forms a focus of recent research. Chandran and colleagues found that LANA is expressed as an early gene upon primary infection of a HUVEC and BJAB cells and that there exists a reciprocal relationship between IE transactivator Rta/orf50 message and LANA message (Krishnan et al. 2004). Rta/orf50 mRNA peaks within minutes of infection, but then declines as LANA mRNA increases. The relative ratios depend on the host propensity to establish latent or lytic infection. In cells that support high-level KSHV lytic replication (HUVEC, HEK293), Rta/orf50 levels stay high as a significant proportion of

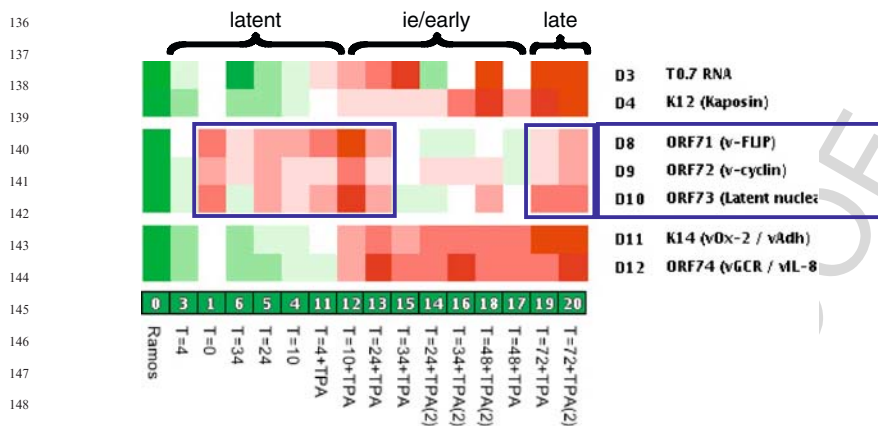
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**Table 2.2** Genome-wide profiling studies for KSHV viral gene transcription

Tissue	Platform	Citation
PEL		
BCBL-1	Reverse Northern Blot	(Zhong et al. 1996)
BCBL-1	70-mer array	(Wang et al. 2002)
BCBL-1	real-time QPCR	(Fakhari and Dittmer 2002)
BCBL-1	cDNA array	(Paulose-Murphy et al. 2001a)
BCBL-1/rapamycin	real-time QPCR	(Sin et al. 2007)
BCBL-1/cidofovir	cDNA array	(Lu et al. 2004)
BCBL-1/ganciclovir	real-time QPCR	(Staudt et al. 2004)
BC-1	Northern Blot	(Sarid et al. 1998)
BC-1	Real-time QPCR	(Whitby et al. 2007)
BC-3	cDNA array	(Jenner et al. 2001a)
JSC-1	real-time QPCR	Bagni et al. (submitted)
JSC-1	cDNA array	(Suscovich et al. 2004)
BCBL-1/K1	cDNA array	(Lee et al. 2002)
BCBL-1/Rta/orf50	cDNA array	(Nakamura et al. 2003)
BCBL-1/NotchIC	Real-time QPCR	(Chang et al. 2005)
Endothelial		
TIVE	Real-time QPCR	(An et al. 2006)
KS	Real-time QPCR	(Dittmer 2003)
Murine endothelial cells	Real-time QPCR	(Mutlu et al. 2007)
HMVEC-d	cDNA array	(Krishnan et al. 2004)
HMVEC-d	cDNA array	(Moses et al. 1999)
HUVEC	Real-time QPCR	(Yoo et al. 2005)

the culture enter complete lytic replication as characterized by subsequent E and L gene transcription. In cells that do not support KSHV lytic replication in the absence of external stimuli such as phorbol ester (BJAB, fibroblasts), Rta/orf50 levels rapidly decline as infected cells enter latency or lose the viral genome.

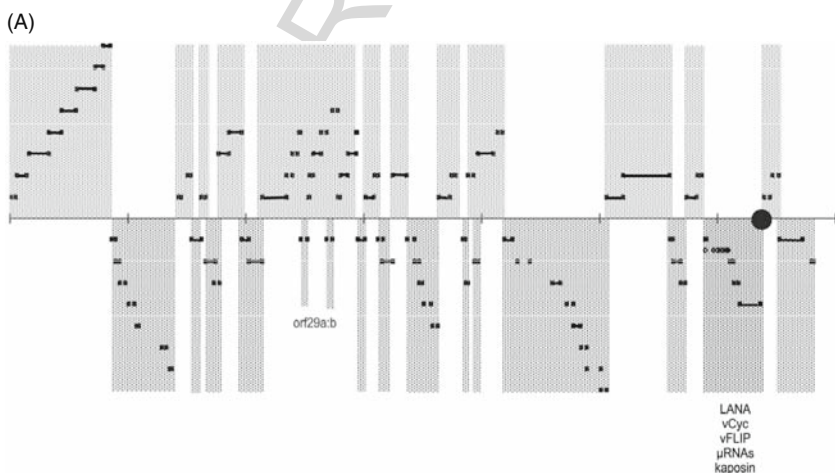
At times profiling studies also showed an increase of latent (LANA, vCYC, vFLIP) mRNA at late times after lytic reactivation (Jenner et al. 2001a), which would classify LANA as a gamma2 class mRNA (Fig. 20.1). A similar observation has recently been made in EBV (Yuan et al. 2006). We did not find evidence for significant latent mRNA induction at late times in BCBL-1 cells (Fakhari and Dittmer 2002); significant in as much, as it could not be explained by genome copy number amplification or changes in PEL culture composition. Unlike EBV-infected BL cell lines, in which the majority of cells reactivate from latency upon IgM cross-linking, in any PEL cell line never more than 50% (often less than 20%) of cells reactivate the virus in response to phorbol ester. This poses no problem for the study of lytic transcription, as lytic transcripts are virtually undetectable in latent cells and only cells that do reactivate contribute to the signal. However, it makes studies of latent gene transcription in response to stimuli difficult to interpret, since these are conducted in a background of uninduced cells.



**Fig. 20.1** Transcription profile of the KSHV latency locus (*See Color Insert*)  
 \*Primary data from (Jenner et al. 2001a) were re-analyzed using ArrayMiner™

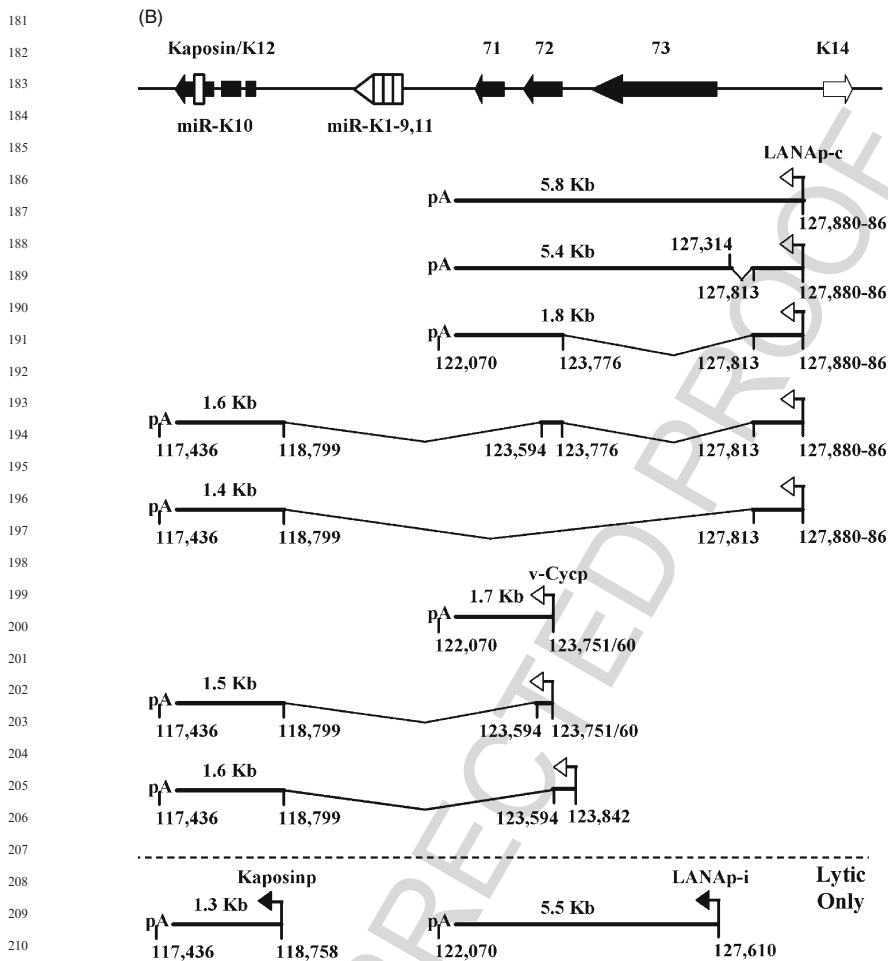
## 20.2 The KSHV Latency Locus

The KSHV latent genes LANA, vCYC and vFLIP (and miRs) all cluster together within one transcription unit (Fig. 20.2). At least one nascent transcript exists that traverses the entire locus (Pearce et al. 2005; Samols et al. 2005; Cai and Cullen 2006). It initiates at the constitutive LANA promoter start site at nt 127,880 and terminates at the *Kaposin*-distal poly-A site at nt 117,432. Transcription across this locus proceeds only in one direction: from right to left. To date no evidence for mRNAs originating at the opposite strand has been found. Furthermore, latent transcription was polymerase-II dependent.



**Fig. 20.2** (continued)

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212 **Fig. 20.2** The KSHV latency locus (A) KSHV genome to scale. Upper half, rightward orfs;  
 213 lower half, leftward orfs, (B) Transcript architecture of the major latency locus of KSHV  
 214 (modified from Cai and Cullen (2006)). The relative genomic position of KSHV open reading  
 215 frames (ORFs) are shown along the top line as filled arrows to denote ORF directionality  
 216 (*Kaposin/K12*; *ORF71/v-FLIP*; *ORF72/v-cyclin*; *ORF73/LANA*; *K14/v-Ox2*). The KSHV  
 217 microRNAs (miR) are denoted as white boxes and are designated with the *K*-prefix (miR-  
 218 K1-11). Transcripts expressed during latency in the absence of viral transactivators are  
 219 denoted with white arrowheads; these originate at either the predominant LANAp-c or the  
 220 weak v-Cycp. Transcripts dependent on the KSHV lytic-switch transactivator, Rta/ORF50,  
 221 are denoted with black arrowheads and are shown below the dotted line for clarity. Lytic  
 222 transcripts originate at either the LANAp-i or the *Kaposinp*. Genomic coordinates of transcript  
 223 start sites and splice donors/acceptors are shown below the transcript diagram according  
 224 to Russo et al. (1996a, b)

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224  
225

226 We are very confident in our assignment of the type I and type II latent genes,  
227 which show a dramatically different transcription profile than any of the other  
228 KSHV mRNAs regardless of experimental platform, PEL line or study  
229 (Fig. 20.1), and for which we have independent verification by in situ analysis  
230 (Dittmer et al. 1998; Dupin et al. 1999a; Katano et al. 1999, 2000; Parravicini  
231 et al. 2000; Rivas et al. 2001a). However, the PEL experimental system is far  
232 from perfect. At any given time 2–5% of PEL cells reactivate KSHV, such that  
233 highly expressed lytic mRNAs are detectable in uninduced cultures. The best  
234 example is early *nut-1* RNA, which can be detected by Northern blot analysis of  
235 induced PEL (Zhong et al. 1996), since the few cells that express *nut-1* make  
236 large amounts of RNA. *Kaposin* lytic transcripts, which originate from the gene  
237 proximal lytic promoter, likewise can be detected in latent PEL (Sadler et al.  
238 1999), as can be those for K9/*vIRF-1* (Chen et al. 2000). Yet, different latent  
239 mRNAs have been identified for K9/*vIRF-1* and *Kaposin*, which map to a more  
240 distal constitutive start site. In addition, the latent genes respond to changes in  
241 the host cell. The spliced *vCYC* mRNA may be subjected to cell cycle regulation  
242 (Sarid et al. 1999a), or the cell cycle stage may influence the rate of spontaneous  
243 lytic reactivation (McAllister et al. 2005) thus changing the *vCYC* transcription  
244 pattern. In MCD, the *vIL-6/K2* protein is expressed in a large percentage of  
245 cells, far more than any structural lytic protein (Staskus et al. 1999; Deng et al.  
246 2002), suggesting that the *vIL-6/K2* promoter can respond to MCD-specific  
247 transcription factors irrespective of the status of all other KSHV genes  
248 (Chatterjee et al. 2002).

249 Understanding KSHV transcription is a work in progress that requires  
250 careful molecular characterization of the viral regulatory elements. As we are  
251 starting to map the virus–host interactions at the transcriptional level, we gain  
252 fascinating insights into the pathogenesis of KSHV, which ultimately will lead  
253 to novel intervention targets.

## 254 255 256 **20.2.1 LANA, *vCYC*, *vFLIP***

### 257 258 **20.2.1.1 Latency-Associated Nuclear Antigen (LANA)**

259 During latency, all KSHV-infected cells express the viral latency-associated  
260 nuclear antigen (LANA/ORF73) (Dittmer et al.; Dupin et al. 1999b). LANA  
261 is the predominant target of anti-KSHV antibodies in infected individuals.  
262 LANA is necessary and sufficient for latent viral episome persistence (Ballestas  
263 et al. 1999; Cotter and Robertson 1999; Hu et al.; Ye et al. 2004). Although  
264 LANA shows no homology at the DNA sequence level, its function and  
265 structural features are reminiscent of the Epstein–Barr virus EBNA-1 and  
266 EBNA-2 proteins. LANA contains a central region of acidic repeats, a leucine  
267 zipper, an N-terminal proline-rich domain and two nuclear localization  
268 sequences – one located at each terminus of the polypeptide (diagrammed in  
269 Fig. 20.4). The acidic repeat regions and leucine zipper (EEDD, DE[E,Q]QQ  
270

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271 and LEEQEQL between amino acids (aa) 338 . .840) and (LEEQEQL at aa  
272 840) are highly immunogenic and the target for the widely used commercial  
273 anti-LANA monoclonal antibody LN53 (Kellam et al. 1999).

274 The first function of LANA is to tether the viral episome to cellular chromatin  
275 and thus facilitate proper inheritance during cell division. The details of  
276 how LANA maintains the latent viral episome have been carefully studied. The  
277 C-terminus of LANA binds directly to two adjacent 16-bp motifs within the  
278 KSHV terminal repeats (TR), termed the LANAbinding sites 1 and 2 (LBS1  
279 and LBS2). Both LBS share the conservation of 13 nucleotides, though nucleotides  
280 flanking this 13 nt. core are different between the two (Garber et al. 2001,  
281 2002). LANA binds with higher affinity to LBS1 than to LBS2, suggesting the  
282 nucleotide sequence flanking the conserved 13 bp. LBS motif influences the  
283 binding affinity of LANA. This hypothesis has been directly investigated: Kaye  
284 and colleagues have found that nucleotides within and surrounding the LBS1  
285 do affect LANA's-binding affinity for that site (Srinivasan et al. 2004).

286 LANA has been shown to bind cellular chromatin and mitotic chromosomes  
287 through its N-terminus (Shinohara et al. 2002). In this manner, LANA  
288 tethers the KSHV episome to cellular chromatin and chromosomes – thereby  
289 ensuring proper segregation of the viral genome during host cell division  
290 (Kedes et al. 1997b; Kellam et al. 1997b; Rainbow et al. 1997; Ballestas et al.  
291 1999; Cotter and Robertson 1999; Szekely et al. 1999) (Kelley-Clarke et al.  
292 2007a). Experimental abrogation of LANA expression through siRNA or  
293 genomic knockout leads to loss of KSHV episomes from latently infected  
294 cells, genetically demonstrating that LANA is necessary for maintenance of  
295 latency (Ye et al. 2004; Godfrey et al. 2005). Barbera et al. (2006) demon-  
296 strated that the N-terminus of LANA docks onto cellular chromosomes by  
297 directly binding to the folded regions of histones H2A and H2B to mediate  
298 nucleosome attachment (Barbera et al. 2006). Both histones H2A and H2B  
299 were necessary for LANA to bind nucleosomes. In contrast, Robertson and  
300 colleagues have found that LANA binds histone H1 (Barbera et al. 2006) as  
301 well as a host of other proteins involved in DNA structure remodeling (Verma  
302 et al. 2006a). Cellular replication and replication-licensing factors can also  
303 bind to LANA (Stedman et al. 2004; Lu et al. 2006; Verma et al. 2006b),  
304 suggesting that the KSHV episome– host chromatin interaction is not static  
305 but responds to viral latent replication (via the latent ori in the KSHV TRs) as  
306 well as host replication.

307 Second to facilitating episomal attachment, LANA can mediate transcrip-  
308 tional suppression. In the presence of LANA, LBS1 and LBS2 repress tran-  
309 scription of an artificial minimal promoter when placed upstream (Garber et al.  
310 2001, 2002). The ability of LANA to carry out these functions is directly  
311 proportional to LANA's-binding affinity for these two sites. In the context of  
312 the viral genome, LANA can repress transcription of the K1 promoter via the  
313 LBS1 and LBS2 of the TRs (Verma et al.).

314 Other than by direct DNA binding, the transcriptional repressor function of  
315 LANA can also be mediated by cellular methyl transferases (Shamay et al.

316 2006). Currently there exists no evidence that this mechanism is used to mod-  
317 ulate viral transcription. More likely, DNA-independent transcriptional silen-  
318 cing provides one avenue by which LANA reprograms the latently infected host  
319 cell. Ectopic expression of LANA leads to both up- and down-modulation over  
320 147 cellular genes (Renne et al. 2001; An et al.) and this global reprogramming  
321 may provide one mechanism that mediates LANA's *in vivo* transforming  
322 function (Fakhari et al. 2006).

323 Third, LANA positively modulates the transcriptional activity of its own  
324 promoter (Jeonget al.; Renne et al. 2001; Jeong et al.). Although the LANA  
325 promoter (LANAp) is constitutively active in the absence of viral proteins,  
326 expression of LANA leads to auto-activation of its own promoter to maintain  
327 a positive-feedback loop. The C-terminus of LANA protein is required for  
328 auto-activation of the LANAp since deletions of amino acids (aa) 1002–1062  
329 or 1113–1162 reduced LANAp auto-activation (Jeong et al.). This comprises  
330 the DNA-binding region of LANA (Kelley-Clarke et al. 2007b) and is also  
331 required for binding to KSHV TR sequences LBS1 and LBS2 (Garber et al.  
332 2001, 2002). The central repeat domains of LANA that span aa 214–750  
333 (including a proline-rich, a DE acidic repeat, and a Q-rich domain) are  
334 dispensable for auto-activation of the LANAp since expression of these dele-  
335 tion mutants still transactivated the LANAp to wild-type/full-length levels  
336 (Jeong et al.). This is not surprising since the central acidic repeat region of  
337 LANA is highly variable among KSHV isolates and is missing entirely from  
338 the rhesus rhadinovirus (RRV) LANA (Zhang et al. 2000; DeWire and  
339 Damania 2005).

340 LANA protein binds to nt. 127,903–127,923 of the core LANAp as demon-  
341 strated by EMSA (Jeong et al.). Sequence analysis of nt. 127,908–127,915  
342 revealed the presence of an 8 bp motif that is centrally present with LBS1 within  
343 the KSHV terminal repeats (TRs). In contrast to each TR where two 16 nt. LBS  
344 exist in tandem, the LANA promoter contains only a single core LANA-  
345 binding site motif upstream of the latent 127,880 start site.

346 A detailed investigation has reported on LANA's transactivation of the  
347 cellular human telomerase reverse transcriptase (hTERT) promoter through  
348 interaction with cellular Sp1 protein (Verma et al.). Verma et al. showed that the  
349 C-terminus of LANA is necessary and sufficient to bind Sp1 protein. LANA  
350 was shown to bind to Sp1 via Sp1's glutamine-rich "B" domain, which is one of  
351 two (A and B) domains required for transcriptional activation (Courey et al.  
352 1989; Verma et al.) but not DNA binding (Kardassis et al. 1999). This report  
353 implicates synergism between LANA and Sp1 to activate transcription on the  
354 cellular hTERT promoter. Of interest to this idea is the location of the core  
355 LANA-binding site within the core LANAp (127,908–920), which is adjacent to  
356 the Sp1-binding site (127,928–933) (Jeong et al. 2004). Based on these observa-  
357 tions, it is likely that LANA and Sp1 synergize to activate LANAp transcription.

358 In addition to specific DNA binding, LANA can act as a promiscuous  
359 transcription co-factor on other promoters independent of its own DNA-bind-  
360 ing recognition element through interaction with cellular proteins including:

AQ4



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361 Sp-1 (Verma et al.), RBP-jkappa (also known as CSL) (Lan et al. 2005a), p53  
362 (Friborg et al. 1999), Rb (Radkov et al. 2000a, b), GSK-3beta (Fujimuro et al.  
363 2003), CBP (Lim et al. 2000, 2001), ATF4/CREB2 (Lim et al. 2000, 2001),  
364 Ring3 (Platt et al. 1999) (Mattsson et al. 2002) (Viejo-Borbolla et al. 2005;  
365 Ottinger et al. 2006) and KSHV Rta/orf50 (Lan et al. 2005b). Chromatin-  
366 modifying factors SAP30, mSin3A and CIR (Krithivas et al. 2000, 2002),  
367 meCP2, DEK (Krithivas et al. 2000, 2002), Histone H1 (Cotter and Robertson  
368 1999) and Histones H2A and H2B (Barbera et al. 2006) also can mediate these  
369 effects.

370 Finally, LANA binds to and inhibits Rb (Radkov et al. 2000b) as well p53  
371 function in reporter assays (Friborg et al. 1999; Wong et al. 2004). Conversely,  
372 p53 can inhibit the LANA promoter (Jeong et al. 2001). This initially led to a  
373 model, in which LANA behaved very much like the small DNA tumor virus  
374 transforming proteins. In fact, because of its ability to decorate host chromo-  
375 somes LANA can induce chromosome instability phenotypes that are akin to  
376 p53 inactivation (Pan et al. 2004; Si and Robertson 2006). However, the situa-  
377 tion is more complex. At least one PEL cell line (BC-3) has lost Rb protein  
378 expression (Platt et al. 2002), which seems unnecessary if LANA efficiently  
379 counteracted all Rb functions, but it leaves open the possibility that LANA may  
380 interact with and inactivate other RB family members. LANA, of course, has  
381 multiple binding partners ( $\geq 10$ ) and functions (Si et al. 2006; Cai et al. 2006).  
382 These include Ku70, Ku80 and PARP-1, which can also be in complexes  
383 containing p53. Hence, it is easy to rationalize how some LANA can be  
384 found in complex with p53. Despite being in complex with LANA, p53 is  
385 fully functional in PEL (Petre et al. 2007) and can be activated by doxorubicin.  
386 Moreover, the LANA-p53 complex can be destroyed by the mdm-2/p53 inter-  
387 action inhibitor nutlin (Petre et al. 2007; Sarek et al. 2007), which leads to p53-  
388 dependent apoptosis in PEL.

### 391 20.2.1.2 v-CYC/orf72

392 v-cyclin (orf72) represents another candidate KSHV oncogene because of its  
393 homology to the human cyclin-D/Prad oncogene. In general, cyclin-D proteins  
394 ( $D_1$ ,  $D_2$ ,  $D_3$ ) associate with specific cyclin-dependent kinases (CDKs) and these  
395 complexes phosphorylate Rb family members (reviewed in Sherr (1996)). This  
396 in turn liberates E2F/DP-1 transactivation functions that are necessary and  
397 sufficient for S-phase entry. Importantly, the human cyclin-D<sub>1</sub> gene is amplified  
398 in parathyroid tumors, a subset of prostate and breast cancers as well as human  
399 mantle cell lymphomas. It can complement *ras* in transforming low passage  
400 rodent cells in culture (Hinds et al. 1994; Lovec et al. 1994) as well as *c-myc* in  
401 transgenic mice (Bodrug et al. 1994). An oncogenic cyclin-D homolog is also  
402 present in other gamma herpesviruses (reviewed in Neipel et al. (1997)). Ectopic  
403 expression of the murine herpesvirus 68 (MHV68) cyclin in T cells causes T-cell  
404 lymphomas in transgenic mice (van Dyk et al. 1999).

406 The mechanism of transformation by KSHV v-cyclin is most likely novel and  
407 unique, since it phosphorylates pRb but, unexpectedly, also histone H1,  
408 p27<sup>KIP1</sup> and bcl-2 (Chang et al. 1996; GoddenKent et al. 1997; Li et al. 1997;  
409 Ojala et al. 2000; Laman et al. 2001). Unlike human cyclin-D, v-cyclin/cdk6-  
410 mediated phosphorylation of Rb is resistant to inhibition by the cyclin-depend-  
411 ent-kinase-inhibitors (CDKIs) p16<sup>INK4</sup>, p21<sup>CIP1</sup> and p27<sup>KIP1</sup> (Swanton et al.  
412 1997). Moreover, v-cyclin/cdk6 induces the degradation of p27<sup>KIP1</sup> (Ellis et al.  
413 1999; Mann et al. 1999). Yet, the results of these transient expression studies  
414 remain controversial: v-cyclin can overcome a p16<sup>INK4</sup> G<sub>1</sub> arrest (Swanton et al.  
415 1997), but its activation of the E2F-responsive cyclin A promoter is inhibited by  
416 p16<sup>INK4</sup> (Duro et al. 1999). Depending on the cell line used, v-cyclin binds  
417 exclusively to cdk6 (GoddenKent et al. 1997), to cdk4 and cdk6 (Li et al.  
418 1997) or to cdk4, cdk6 and cdk2 (Mann et al. 1999).

419 Despite significant overall sequence identity, key residues required for cyclin  
420 D1 nuclear export and degradation are lacking in the K-cyclin C-terminus. As a  
421 result, K-cyclin possesses a longer half life than cyclin D1 and displays more  
422 pronounced nuclear accumulation. In the case of human cyclin D, a mutant  
423 allele (K112E or K114E) has been generated, which is incapable of activating  
424 CDKs. Mutation of the homologous K-cyclin residue (K106 to E) significantly  
425 (~50%) reduced CDK6 interaction as well as RB phosphorylation. Recent  
426 evidence (Upton and Speck 2006) suggests that the homologous, cdk-binding  
427 deficient mutant in the murid herpesvirus 68 (MHV-68) viral cyclin D homolog  
428 was able to replicate in culture, but was attenuated for replication in vivo.

429 V-cyclin over-expression induces transient proliferation (Swanton et al. 1997), as  
430 well as apoptosis (Ojala et al. 1999; Hardwick 2000; Ojala et al. 2000). To date, no  
431 stable cell lines that express v-cyclin have been reported, suggesting that high-level  
432 expression of v-cyclin is not compatible with continued cell growth. However, loss  
433 of p53 uncovered the transforming potential of vCYC in vivo. While KSHV vCYC  
434 single transgenic mice did not develop tumors, lymphomas developed rapidly in a  
435 p53null background (Verschuren et al. 2002, 2004). An analogous phenotype has  
436 been observed in at least one transgenic model for human cyclin D1, where either  
437 deletion or targeted overexpression of wild-type cyclin D1 in photoreceptor cells  
438 was associated with apoptosis (Fantl et al. 1995; Ma et al. 1998; Skapek et al. 2001).  
439 Presumably, loss of p53 counteracted the pro-apoptotic signals that were associated  
440 with forced KSHV vCYC expression. In contrast to KSHV, 60% of transgenic mice  
441 expressing the MHV-68 cyclin D homolog in T cell developed lymphoma within  
442 12 months (van Dyk et al. 1999). This suggests that cell lineage and the differentia-  
443 tion state of the host cell and cyclin needed to be in the right balance. This data  
444 suggest a model that requires multiple events initiated by the concerted action of all  
445 KSHV latent proteins for KSHV-dependent lymphomagenesis.

### 447 20.2.1.3 vFLIP/orf71

448 v-FLIP/orf71 is transcribed from the LANA promoter and translated from an  
449 internal ribosome entry site located within the vCYC coding region (Grundhoff  
450

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451 and Ganem 2001) (Low et al. 2001). The vFLIP protein has sequence homology  
452 to equine herpesvirus-2 E8 and herpesvirus Saimiri (HVS) orf71 (Hu et al.  
453 1997). It inhibits CD95/FAS-induced apoptosis in vitro by blocking caspase-  
454 3, -8 and -9 (Djerbi et al. 1999). Both CD95/Fas-L and TRAIL/TNF-alpha  
455 induce apoptosis through a similar mechanism (Muzio et al. 1996; Medema  
456 et al. 1997). Clustering of the receptor upon binding of the ligand recruits an  
457 adapter molecule (FADD and TRADD, respectively) with a binding domain  
458 (DD) for the receptor and a conserved “death-effector-domain” (DED) that  
459 binds and triggers the activation of caspase-8. The death signal is then trans-  
460 duced through a number of cellular caspases resulting in the commencement of  
461 cellular apoptosis (for review see Hu et al. 1997). A possible mechanism for viral  
462 FLIPs postulates competition with the adapter molecule for binding to caspase  
463 8 via its DED domain.

464 A more recent line of inquiry found vFLIP to be involved in NFkappaB  
465 signaling. Here, vFLIP uses its TRAF-binding domain to activate NFkappaB  
466 signaling (Guasparri et al. 2006). vFLIP activated IkkappaB-kinase (An et al.  
467 2003; Field et al. 2003) and thereby increases NF-kappaB activity, which is anti-  
468 apoptotic in PEL cell. In addition, vFLIP induced MHC-I expression through  
469 NF-kappaB in KSHV-infected lymphatic endothelial cells (Lagos et al. 2007),  
470 which underscores the physiological importance of the vFLIP-NF-kappaB  
471 interaction. Moreover, vFLIP transgenic mice develop lymphoma (Chugh  
472 et al. 2005). Eliminating either vFLIP or NF-kappaB activity from PEL induces  
473 apoptosis (Keller et al. 2000; Guasparri et al. 2004; Godfrey et al. 2005),  
474 demonstrating that this pathway is essential for lymphomagenesis.

### 477 **20.2.2 KSHV miRNAs**

478  
479 Micro RNAs (miRNAs) are a novel class of mammalian genes. They regulate  
480 the transcription and translation of many target proteins and have been  
481 implicated in normal development as well as carcinogenesis. Viruses also  
482 encode miRNAs. In KSHV, the miRNAs are conserved among different  
483 isolates (Marshall et al. 2007) and grouped together in the viral latency region  
484 (nucleotide 119305–121911) (Cai et al. 2005; Pfeffer et al. 2005; Samols et al.  
485 2005). This organization is similar to mammalian miRNA gene organization  
486 where clustering has been observed for 50–70% of miRNA genes (Altuvia  
487 et al. 2005). The maturation of miRNAs is the subject of active research  
488 (reviewed in (Cullen 2004)). First, a primary miRNA, or pri-miRNA, is  
489 transcribed by RNA polymerase II. It is capped and polyadenylated in the  
490 nucleus (Cai et al. 2004). The pri-miRNA can be of any length and contain any  
491 number of clustered miRNAs. The KSHV miRNAs are derived from a com-  
492 mon precursor molecule (Pearce et al. 2005; Cai and Cullen 2006), comparable  
493 to the stable HSV-1 lat intron (Cui et al. 2006). They share a common  
494 leftward-orientation and are regulated by multiple splicing events, multiple  
495

496 termination sites and multiple transcription initiation sites (at nt 127,880,  
497 123,848, 118,758) (Dittmer et al. 1998; Sadler et al. 1999; Sarid et al. 1999a;  
498 Talbot et al. 1999; Li et al. 2002; Marshall et al. 2007). Promoter–reporter  
499 constructs encompassing these three latent start sites all exhibited activity  
500 after transient transfection, but by comparison the constitutive LANA pro-  
501 moter at nt 127,880 exhibited 20-fold higher basal activity than the vCYC  
502 promoter (O’Hara and Dittmer, unpublished observation). This pattern of  
503 promoter activity is consistent with a model whereby the common LANA  
504 promoter regulates all KSHV latent RNA species, giving rise to mRNAs as  
505 well as all miRNAs in KSHV-associated cancers.

506 The pri-miRNA serves as substrate for the Drosha nuclease complex (Zeng  
507 et al. 2005). Through Drosha the precursor miRNAs, or pre-miRNAs, are  
508 generated, each serving as the precursor of one or two mature miRNAs.  
509 The pre-miRNAs reside in the nucleus and are ~70 nucleotides in length.  
510 The stability of the pre-miRNAs can vary (Schmittgen et al. 2004; Pfeffer et al.  
511 2005). In KSHV, the pre-miRNAs are stable as they can be detected by  
512 Northern hybridization. Overall their levels correlate with the level of the  
513 mature KSHV miRNAs (Cai et al. 2005; Pfeffer et al. 2005); Samols et al.  
514 2005) (see reference (Gottwein et al. 2006) for an exception) and can be  
515 detected in all PEL cell lines as well as in primary KS biopsies (O’Hara and  
516 Dittmer, submitted). The pre-miRNAs are subsequently exported out of the  
517 nucleus with the help of Exportin 5 and serve as a substrate for Dicer in the  
518 cytoplasm. Mature miRNA levels can be regulated by modulating exportin-5  
519 expression (Yi et al. 2005). In the cytoplasm, Dicer processes the pre-miRNA  
520 into the mature miRNA and complementary strand, each comprising ~22 nt  
521 in length. For some miRNAs, both the sense and the anti-sense pre-miRNA  
522 strands serve as template for mature miRNAs. For KSHV, this has been  
523 demonstrated for miR-K4, miR-K6 and miR-K9. The mature miRNAs are  
524 then incorporated into the RISC complex, which carries out the enzymatic  
525 function.

526 The elucidation of miRNA targets and the function that the KSHV miRNAs  
527 play in the viral life cycle is the subject of active research and covered in detail in  
528 Chapter 25.

### 530 20.2.3 *Kaposin/K12*

533 *Kaposin* is located immediately downstream of LANA, vCYC and vFLIP and  
534 in addition to the common promoter can be regulated by a promoter located  
535 between LANA and cyclin (Li et al. 2002) and during lytic reactivation yet  
536 another, orf-proximal promoter (Sadler et al. 1999). Like LANA, *Kaposin* too is  
537 expressed in every tumor cell (Staskus et al. 1997). In fact, *Kaposin* mRNA is the  
538 most abundant mRNA in latently infected PEL. It gives rise to an interesting  
539 group of alternatively translated proteins (Sadler et al. 1999), at least some of  
540 which can transform NIH3T3 cells in culture (Muralidhar et al. 1998). *Kaposin*

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interacts with cytohesin-1 (Kliche et al. 2001). In addition, it has been shown to stabilize cellular cytokine mRNAs through the p38 mitogen-activated protein kinase (MAPK)/MK2 kinase pathway (McCormick and Ganem 2005; McCormick and Ganem 2006). Interestingly, and perhaps because of its high expression and protein repeats, *Kaposin* provides target peptides for the human CD8 cytotoxic T-cell response (Brander et al. 2001); Micheletti et al. 2002).

### 20.3 LANA-2/vIRF-3 and K9/vIRF-1

Profiling of KSHV mRNAs in PEL revealed one new lated orf that was not included within the LANA latency locus (Fakhari and Dittmer 2002). It belonged to a KSHV vIRF homolog, also called LANA-2/v-IRF-3, which is not expressed in KS, but is expressed in 100% of PEL and MCD in a pattern similar to LANA (Lubyova and Pitha 2000; Rivas et al. 2001a). LANA-2/vIRF-3 counteracts cellular IRFs, but also p53 function (Rivas et al. 2001a). LANA-2/vIRF-3 is a member of several KSHV IRF homologs. Their function in immune evasion is described in detail in elsewhere (see Chapter by J. Jung). The viral IRFs, just like the viral latent genes are clustered and oriented as repeats of leftward orfs (see Table 20.3). Their transcription is complex and not fully understood. LANA2/vIrf-3 is only expressed in B lineage cells, but here in every cell, whereas for K9/vIRF-1 has both latent and lytic transcriptional start sites (Chen et al. 2000) have been described in PEL. More important, by cluster analysis, K9/vIRF-1 clustered with the other latency genes in endothelial-cell lineage KS tumors (Dittmer 2003), as if at least one vIRF has to be expressed during viral latency.

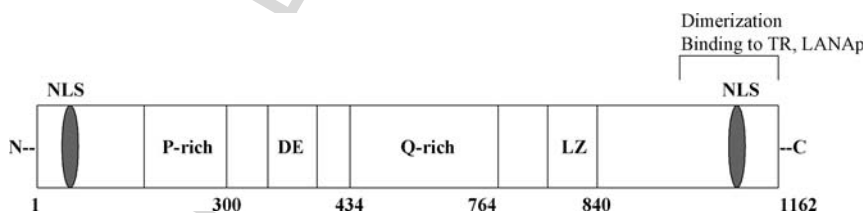
**Table 20.3** KSHV encodes multiple viral interferon regulatory genes as clustered leftward orfs

Name	Location based on (Russo et al. 1996b)	Transcriptional class
orf57/Mta/Sm (right)		IE
K9/vIRF-1	polyA-termination: 83637	
	83860–85209	E
	Upstream start (-84)	LATENT
K10 s	polyA-termination: 86006	
	88085–86074	LATENT
K10:	88164–86074	LYTIC
K10-K10.1/vIR-4	88910–86076 (intron: 88443–88343)	LYTIC
K10-K10.1	88910–86076 (intron: 88443–88343 intron: 89034–88799)	LATENT
K10.5-K10.6 (or 10.7)/ LANA-2/ vIRF-3	91393–89599 (intron: 90938–90847)	LATENT
K11:	91964–93367	LYTIC
K11-K11.2:	94123–91964 (intron: undefined)	LYTIC
K11.2/ vIRF-2	94123–93623	LYTIC

## 20.4 Architecture of the KSHV Latency Locus Promoter (LANAp)

LANA transcription is regulated by the LANA promoter (LANAp), depicted in Fig. 20.3 (Dittmer et al.; Sarid et al.; Talbot et al.). In its initial characterizations, the LANAp was found to direct transcription of poly-cistronic mRNAs encoding either LANA/ORF73, v-cyclin/ORF72, and v-FLIP/ORF71 or only v-cyclin/ORF72 and v-FLIP/ORF71 through alternative splicing out of LANA/ORF73 (Dittmer et al.; Sarid et al.) (diagrammed in Fig. 20.2, *top three transcripts*). Transcriptional profiling of viral gene expression showed that during viral latency in PEL and in primary KS biopsies, LANA, v-cyclin, v-FLIP and *Kaposin* were constitutively expressed (Jenner et al.; Paulose-Murphy et al.; Fakhari and Dittmer; Dittmer). Therefore, under conditions where other KSHV promoters were silenced, the LANA promoter remained constitutively active. GpC islands within the LANAp are constitutively unmethylated in both PEL and KS (Chen et al. 2001) and are associated with an “open” chromatin environment. This is in contrast to, for instance, the promoter for the KSHV lytic-switch protein Rta/ORF50. Treatment with sodium butyrate, an inhibitor of histone deacetylases (HDACs), did not change the acetylation status of histones H3 and H4 on the LANAp since the promoter was already de-repressed, contrasting the response observed on the Rta/ORF50 promoter (Lu et al. 2003).

Left of the LANA/v-cyclin/v-FLIP locus is another latently expressed gene, *Kaposin/K12*. While *Kaposin/K12* has its own promoter that is highly responsive to the lytic-switch protein, Rta/ORF50. Recent work has discovered transcripts containing *Kaposin/K12* message originating from a weak promoter located in front of v-cyclin/ORF72 (Pearce et al.; Cai and Cullen) and also originating from the latent LANAp (Cai and Cullen). Importantly, the newly discovered KSHV microRNAs (miRNAs) are located within the intergenic region between the v-FLIP/ORF71 and the *Kaposin/K12* open reading frames (Cai et al.; Pfeffer et al.; Samols et al.). Therefore, transcripts that originate from the latent



**Fig. 20.3 Domain structure of LANA** Diagram of the KSHV Latency-Associated Nuclear Antigen, LANA (with permission from M. Staudt, 2006). The gene product of *ORF73* is the KSHV latency-associated nuclear antigen (LANA). LANA is an 1162 amino acid (aa) protein that contains a nuclear localization sequence (NLS) at both the N- and C-termini, a proline-rich domain (P-rich), an acidic repeat domain of aspartic and glutamic acid (DE), a glutamine-rich domain (Q) and a leucine zipper domain (LZ). The C-terminal 231 aa facilitates binding to genomic terminal repeat (TR) DNA and to LANA promoter DNA

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LANAp and encode the *Kaposin/K12* ORF also encode the miRNAs, and as such can explain the constitutive expression of the KSHV miRNAs during latency (Cai and Cullen 2006) (see Fig. 20.2 for diagram of transcripts). These novel reports demonstrate that despite its name, the LANAp can also direct expression of every viral gene expressed during latency. An exception to this is the latent PEL-specific LANA-2/*vIRF3*, which is located in a distant genomic location outside of the LANA latency locus (Rivas et al. 2001a, b). Spatial clustering and 5'-co-terminal regulation underscores the importance of this region and sets the latency-associated locus and the LANAp apart from all other viral transcription regions.

The LANAp is constitutively active in the absence of viral proteins in all cell lines tested, including KSHV-positive and -negative B cells, HEK293 epithelial cells and SLK endothelial cells (Jeong et al.; Jeong et al.). Moreover, a 1,861 bp DNA fragment originating at the LANA AUG at position 127,300 and extending to position 129,161 (-1299 bp relative to the latent transcription start site) was able to direct B cell-specific reporter gene expression in transgenic mice (Jeong et al.). This demonstrated that host cell transcription factors in the absence of any viral transactivators suffice to direct LANAp activity and, by inference, LANA, *v*-cyclin, *v*-FLIP, *Kaposin/K12* and miRNA transcription during viral latency.

Previous reports on LANAp deletion analyses mapped the core promoter region from +10 to -88 (nt. 127,870-127,968) relative to the latent transcription start site at 127,880 (Dittmer et al.; Jeong et al.). While the core promoter mediates minimal LANAp activity, the presence of additional promoter sequence both up- and downstream of the core promoter significantly contributed to LANAp activity (Jeong et al.). The presence of distal sequences from -88 up to -279 (nt. 127,968-128,159) as well as sequences within the 5'UTR from +10 down to +271 (nt. 127,870-127,609) enhanced reporter activity more than 10-fold relative to the minimal core promoter (Jeong et al.).

Although the LANAp exhibits constitutive activity in the absence of viral proteins, expression of LANA protein leads to an increase in promoter activity (Jeong et al.; Renne et al. 2001). Presumably central to this function, LANA has been shown to directly bind within its own promoter to a region that contains a small 8 bp consensus motif that is centrally located within the larger 16 bp. LANA-binding site 1 (LBS1) of the KSHV terminal repeats (TRs) (Garber et al. 2001, 2002). Enhancement of LANAp activity by LANA protein establishes a self-stabilizing feedback loop to maintain KSHV latency (Renne et al. 2001; Chiou et al.; Wong et al.).

The mammalian core promoter is generally defined as the minimal stretch of contiguous DNA sequence that is sufficient to direct accurate initiation of transcription by the RNA polymerase II machinery. They typically encompass DNA sequences between approximately +50 and -40 relative to a transcriptional start site (Weis and Reinberg; Javahery et al. 1994; Smale 1997; Smale 2001). Several sequence motifs are commonly found in mammalian core promoters: these include the TATA box, initiator (Inr), the TFIIB

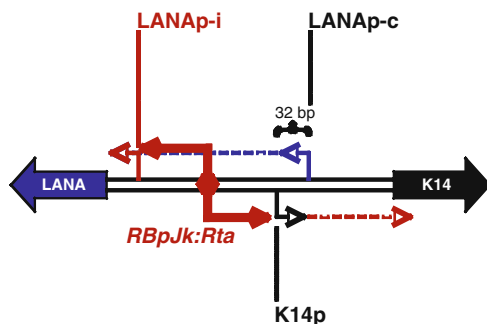
676 recognition element (BRE) and the downstream core promoter element (DPE).  
 677 Each core promoter element can be found in some but not all core promoters,  
 678 and it is a misconception that all promoters must contain each element. The  
 679 core LANAp has been defined as +10 to -88 (Jeong et al.; Jeong et al.) and it  
 680 contains the expected mammalian core promoter elements as well as an essen-  
 681 tial Sp1 site. These elements are independently required as shown by site-  
 682 directed mutagenesis (Staudt and Dittmer 2006).

683 Other than during asymptomatic latency in B cells (Mesri et al.; Dittmer et al.)  
 684 or in KSHV-associated tumors (Dittmer et al.; Dupin et al. 1999b), LANA  
 685 protein and LANAp originating mRNAs have also been detected immediately  
 686 after de novo infection of permissive endothelial cells and non-permissive fibro-  
 687 blasts (Krishnan et al. 2004; Yoo et al. 2005). In these experiments, KSHV rapidly  
 688 establishes latency but can be reactivated by TPA. LANA and Rta/ORF50  
 689 mRNAs were described as immediate early mRNAs upon de novo infection.  
 690 This prompted the discovery of a novel lytic-phase LANA promoter (Lan et al.  
 691 2005b; Matsumura et al. 2005, Staudt and Dittmer 2006).

692 The LANAp-c (127,880) is constitutively active during all forms of latency;  
 693 its activity is enhanced by LANA (Jeong et al.) and independent of Rta/ORF50.  
 694 A second, novel, downstream start site is only active in the presence of Rta/  
 695 ORF50. Nucleotides 127,607-127,675 are sufficient and required for Rta/  
 696 ORF50-responsiveness and encompass the core elements of the LANAp-i.

697 Interestingly, the LANAp-i was significantly more responsive to Rta/  
 698 ORF50 in isolation than when linked to the LANAp-c as in the LANA-FL  
 699 reporter. This effect could be a result of transcript elongation ensuing from the  
 700 LANAp-c through the *LANA/ORF73* 5' -UTR (containing the LANAp-i),  
 701 which might prevent initiation events on LANAp-i *cis* regions. Such a mechan-  
 702 ism was previously reported for the *GAL10* and *GAL7* promoters of *Saccharo-*  
 703 *myces cerevisiae* and for transcription through tandem HIV-1 promoters  
 704 (Greger et al. 1998; Greger and Proudfoot 1998). In support of this notion,  
 705 deletions of core LANAp-c regions that decreased basal promoter activity were  
 706 associated with increased Rta/ORF50-responsiveness.

707 In the opposite direction of LANA and the latent transcripts is K14 and the  
 708 vGPCR (see Fig. 20.4). The vGPCR promoter is absolutely dependent on Rta/  
 709



719 **Fig. 20.4** The LANA  
 720 promoter



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721 orf50 (Liang and Ganem 2004; Liang et al. 2002). Mutation of a shared consen-  
 722 sensus RBP- $\text{j}\kappa$  site at 127,736–127,740 reduced the ability of Rta/ORF50 to  
 723 transactivate both the LANAp-i and the K14 promoters (Staudt and Dittmer  
 724 2006). These data suggest a mechanism whereby LANA transcripts derived  
 725 from the LANAp-i can be transcribed during lytic reactivation without poly-  
 726 merase interference by K14/vGPCR transcripts that are simultaneously being  
 727 transcribed on the complementary strand in the opposite orientation as a result  
 728 of bi-directional transactivation from the KSHV lytic-switch protein, Rta/  
 729 ORF50.

730 During de novo infection, Rta/ORF50 is present within KSHV virions  
 731 (Bechtel et al.; Lan et al.) and as such is delivered into the host cell upon  
 732 infection in the absence of LANA protein expression. Therefore, based on the  
 733 data reported herein we speculate that Rta/ORF50 protein could initially  
 734 transactivate the LANAp-i and K14/vGPCR promoters through direct  
 735 DNA binding or via the shared consensus RBP- $\text{j}\kappa$  site during de novo infec-  
 736 tion. As LANA protein expression ensues and LANA accumulates within the  
 737 cell, expression of Rta/ORF50 protein is silenced as a result of LANA repres-  
 738 sion of the Rta/ORF50 promoter and LANA's inhibition of Rta/ORF50's  
 739 transactivation function (Lan et al.). As a result, the LANAp-i and K14/  
 740 vGPCR promoter activity would cease and LANA-coding mRNA could be  
 741 transcribed from the latent LANAp-c, which is auto-regulated by LANA  
 742 protein. This sequence of events can establish a positive-feedback loop that  
 743 is sufficient to initiate and maintain viral latency within a permissive cellular  
 744 environment.

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**Chapter 20**

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AQ1	261	Please specify the year for reference citation “Dittmer et al.”.
AQ2	264	Please specify the year for reference citation “Hu et al.”
AQ3	313	Please specify the year for the reference citation “Verma et al. through out the chapters.
AQ4	324	Please specify the exact year for the reference citation Jeong et al.
AQ5	557	Please provide the chapter number in the sentence “Their function ...”
AQ6	571	Please check the alignment of “Table 20.3”

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