We sequenced the complete genome of *Felis catus* gammaherpesvirus 1 (FcaGHV1) from lymph node DNA of an infected cat. The genome includes a 121,556-nucleotide unique region with 87 predicted open reading frames (61 gammaherpesvirus conserved and 26 unique) flanked by multiple copies of a 966-nucleotide terminal repeat.

**REFERENCES**

