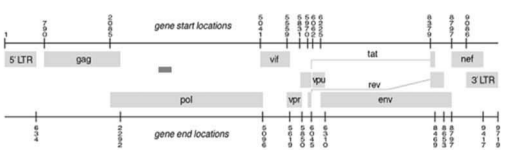
A

QuickAlign analysis of PCR product of Φ PS5 genome raised by single primer (Sc2)

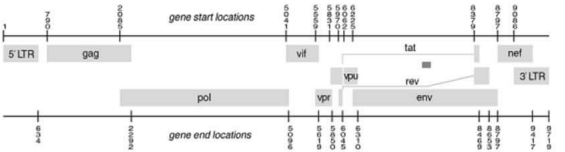
Query location shown as colored bar in map between reading frames 1 and 2.



Query: 081201-22_E07_20-Sc2..ab1230	GACCNCNNCGGTTTAATAGTTTTTTTTACTTTCTATACCCTGGTAAGAAA GTNTTTGGTCAAANATTTTAATCTTCTTTTTCTTACCCCCTTCCACTAGT GGNTCTGCCCCCCTAATNGGGTTTTGGATAGTGCCCAACGATTTCCCCGT CCAGANCCTTATTAACTAACAGGTCATCAGGGGCTAGATACATCTGTTAT TTTGATGTCGCGGAAAGATGACTANTCTTN
Query Length:	234
HXB2 Location:	genome: 3046? 3273reverse complement
Alignment used:	HIV1 Complete DNA, 1240 sequences*

* Matched with different sequences from all over the world HIV genotype

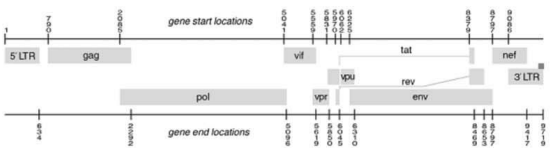
Query location shown as colored bar in map between reading frames 1 and 2.



Query: 081201-22_K05_17-Ac2.ab1126	ACNNCGANGNTNCNTNNGNNGNCAGATAAAAAGAGGGCGAAAGGAGGGGA GTTCTGAGACCCATCAAGAGCACAAAATAGAAGTTCTTAACNNATTTNTA CCTTNCAGTAAAGCANCCNGTGATCN
Query Length:	128
HXB2 Location:	genome: 7469? 7600
Alignment used:	HIV1 Complete DNA, 1241 sequences*

* Matched with different sequences from all over the world HIV genotype

B



Query: 071002-R4_G07_31-C3.ab1____640_____0____640__ABI	NAATGCGCATAATAGTGGTGGGGCGTCTGTCTCGGAGGGAGACGCCACC CGCGAGCCCTGGAGGGGGAGCCGTAGTTCTCTCCCCGGGGGAGAGAAATT CCCCCCGGGGGGGAAGGATGTTCCCCCCGAGGCTCTTGAATGTGGCATGG CATTGTCGGTGGTGGCGATCCCCTATTTATCCATCGAAACACCTCTATTT TTCCCTATAAATCATGCAATCCAGACAGGCACCTTCTGTAGCGACTCTAA AGCCTATTTCTTACAGGGGTGAACGACTCGATTCTTCCCCGGTGATGCTA CATAGTATCCGTGCGCTGCTTAATCCAGAATCTGCATCTACAGTCTGACT CTAGACAAGCTCCAGTAGGCCACTACGTAGAAATTTCTACAAGTACAGGGG ATAAAACCTAACCCACCCCACACCATATCACCGTGTTGATTACAACTAGC CCCCCCATTCTTGACTAAATCAACGTCTGAGATGCGACTTAAGCTGCGAG GAGCCTTAACTACCGCCAGAATCGATATAACCCACGCTGTGGGTCAAATC CCCTTAGCCTTGATTCCACAGCGAAACACCCAGTCAAAAATCCTCCGCCA GTACTGTTGTCCAGTAGTTCCGTCGCATCCCTATGAATCG
Query Length:	872
HXB2 Location:	genome: 9627? 9719
Alignment used:	HIV1 Complete DNA, 698 sequences*

* Matched with different sequences from all over the world HCV genotype