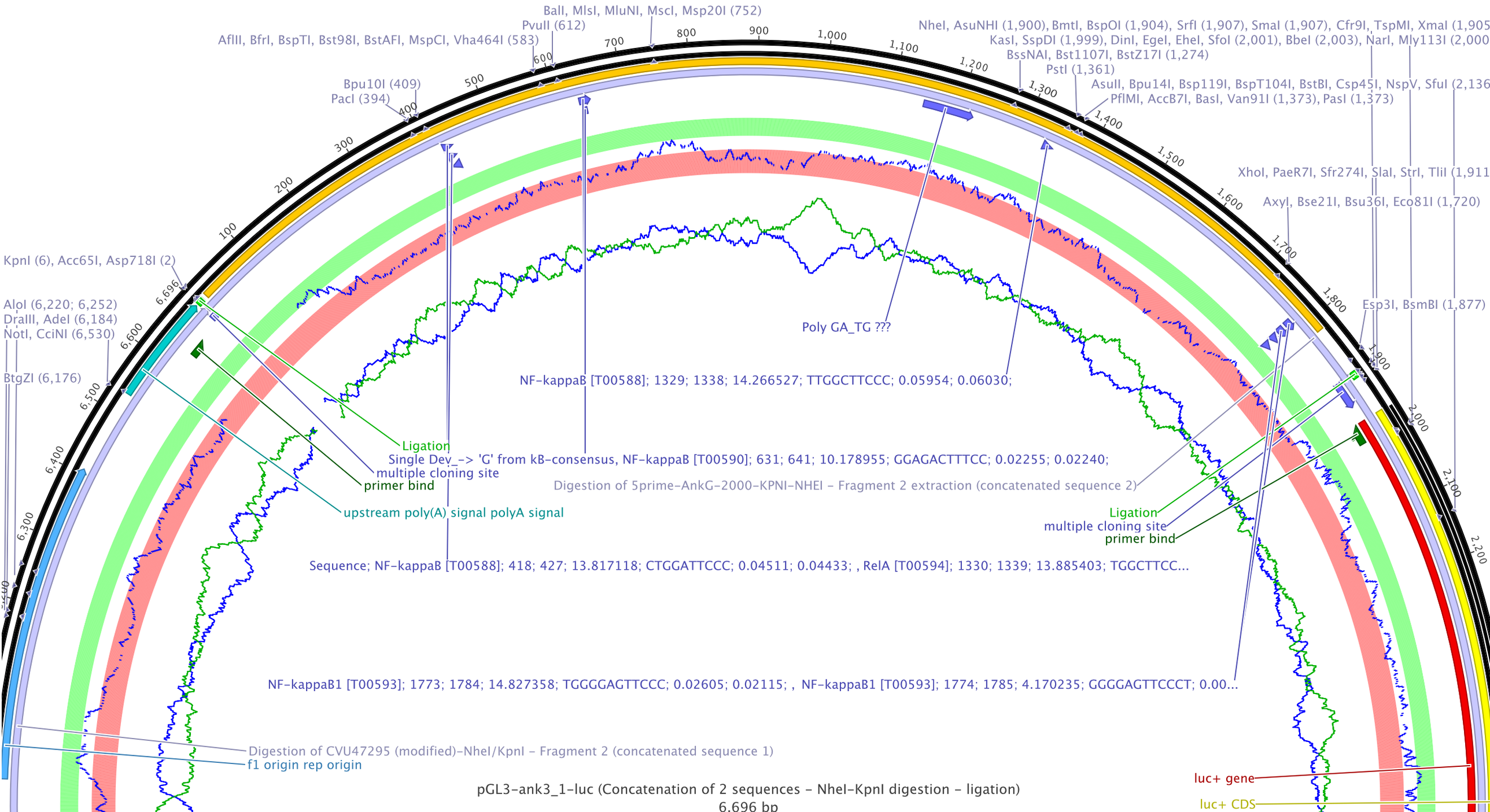
BalI, MlsI, MluNI, MscI, Msp20I (752)
PvuII (612)
AflII, BfrI, BspTI, Bst98I, BstAFI, MspCI, Vha464I (583)
Bpu10I (409)
PacI (394)
NheI, AsuNHI (1,900), BmtI, BspOI (1,904), SrfI (1,907), SmaI (1,907), Cfr9I, TspMI, XmaI (1,905
KasI, SspDI (1,999), DinI, EgeI, EheI, SfoI (2,001), BbeI (2,003), NarI, Mly113I (2,000
BssNAI, Bst1107I, BstZ17I (1,274)
PstI (1,361)
AsuII, Bpu14I, Bsp119I, BspT104I, BstBI, Csp45I, NspV, SfuI (2,136
PflMI, AccB7I, BasI, Van91I (1,373), PasI (1,373)
XhoI, PaeR7I, Sfr274I, SlaI, StrI, TliI (1,911
AxyI, Bse21I, Bsu36I, Eco81I (1,720)
Esp3I, BsmBI (1,877)
KpnI (6), Acc65I, Asp718I (2)
AlwI (6,220; 6,252)
DraIII, AdeI (6,184)
NotI, CciNI (6,530)
BtgZI (6,176)
Poly GA_TG ???
NF-kappaB [T00588]; 1329; 1338; 14.266527; TTGGCTTCCC; 0.05954; 0.06030;
Ligation
Single Dev_-> 'G' from kB-consensus, NF-kappaB [T00590]; 631; 641; 10.178955; GGAGACTTTCC; 0.02255; 0.02240;
multiple cloning site
primer bind
Digestion of 5prime-AnkG-2000-KPNI-NHEI - Fragment 2 extraction (concatenated sequence 2)
upstream poly(A) signal polyA signal
Ligation
multiple cloning site
primer bind
Sequence; NF-kappaB [T00588]; 418; 427; 13.817118; CTGGATTCCC; 0.04511; 0.04433; , RelA [T00594]; 1330; 1339; 13.885403; TGGCTTCC...
NF-kappaB1 [T00593]; 1773; 1784; 14.827358; TGGGGAGTTCCC; 0.02605; 0.02115; , NF-kappaB1 [T00593]; 1774; 1785; 4.170235; GGGGAGTTCCCT; 0.00...
Digestion of CVU47295 (modified)-NheI/KpnI - Fragment 2 (concatenated sequence 1)
f1 origin rep origin
luc+ gene
luc+ CDS
pGL3-ank3_1-luc (Concatenation of 2 sequences - NheI-KpnI digestion - ligation)
6,696 bp