

DHFR-C11-Pk

ATGATCAGTCTGATTGCGGCGTTAGCGGTAGATCGCGTTATCGGCATGGAAAACGCCATGCCGTGGAACCTGCCTGC
CGATCTCGCCTGGTTTAAACGCAACACCTTAAATAAACCCGTGATTATGGGCCGCCATACCTGGGAATCAATCGGTTCG
TCCGTTGCCAGGACGCAAAAAATATTATCCTCAGCAGTCAACCGGGTACGGACGATCGCGTAACGTGGGTGAAGTCGG
TGGATGAAGCCATCGCGGCGTGTGGTGACGTACCAGAAATCATGGTGATTGGCGGCGGTTCGCGTTTATGAACAGTTC
TTGCCAAAAGCGCAAAAACTGTATCTGACGCATATCGACGCAGAAAGTGAAGGCGACACCCATTTCCCGGATTACGA
GCCGGATGACTGGGAATCGGTATTACGCGAATTCCACGATGCTGATGCGCAGAACTCTCACAGCTATTGCTTTGAGAT
TCTGGAGCGGCGGGAGCCCAGCGCCCCCCCCCATCGTGCAGAACATCCCAACCCCCTGCTGGGCTGGACGTAC
CCATACGATGTTCCAGATTACGCTGGAACAAAACTCATCTCAGAAGAGGATCTGTAA

DHFR-C12-Myc

ATGATCAGTCTGATTGCGGCGTTAGCGGTAGATCGCGTTATCGGCATGGAAAACGCCATGCCGTGGAACCTGCCTGC
CGATCTCGCCTGGTTTAAACGCAACACCTTAAATAAACCCGTGATTATGGGCCGCCATACCTGGGAATCAATCGGTTCG
TCCGTTGCCAGGACGCAAAAAATATTATCCTCAGCAGTCAACCGGGTACGGACGATCGCGTAACGTGGGTGAAGTCGG
TGGATGAAGCCATCGCGGCGTGTGGTGACGTACCAGAAATCATGGTGATTGGCGGCGGTTCGCGTTTATGAACAGTTC
TTGCCAAAAGCGCAAAAACTGTATCTGACGCATATCGACGCAGAAAGTGAAGGCGACACCCATTTCCCGGATTACGA
GCCGGATGACTGGGAATCGGTATTACGCGAATTCCACGATGCTGATGCGCAGAACTCTCACAGCTATTGCTTTGAGAT
TCTGGAGCGGCGGGAGCCCAGCGCCCCCCCCCATCGTGCAGAACATCCCAACCCCCTGCTGGGCCTGGACGTAC
CCATACGATGTTCCAGATTACGCTGGAACAAAACTCATCTCAGAAGAGGATCTGTAA

DHFR-C13-HA

ATGATCAGTCTGATTGCGGCGTTAGCGGTAGATCGCGTTATCGGCATGGAAAACGCCATGCCGTGGAACCTGCCTGC
CGATCTCGCCTGGTTTAAACGCAACACCTTAAATAAACCCGTGATTATGGGCCGCCATACCTGGGAATCAATCGGTTCG
TCCGTTGCCAGGACGCAAAAAATATTATCCTCAGCAGTCAACCGGGTACGGACGATCGCGTAACGTGGGTGAAGTCGG
TGGATGAAGCCATCGCGGCGTGTGGTGACGTACCAGAAATCATGGTGATTGGCGGCGGTTCGCGTTTATGAACAGTTC
TTGCCAAAAGCGCAAAAACTGTATCTGACGCATATCGACGCAGAAAGTGAAGGCGACACCCATTTCCCGGATTACGA
GCCGGATGACTGGGAATCGGTATTACGCGAATTCCACGATGCTGATGCGCAGAACTCTCACAGCTATTGCTTTGAGAT
TCTGGAGCGGCGGGAGCCCAGCGCCCCCCCCCATCGTGCAGAACATCCCAACCCCCTGCTGGGCCTGGACGTAC
CCATACGATGTTCCAGATTACGCTGGAACAAAACTCATCTCAGAAGAGGATCTGTAA

(a)

INPUT	DHFR-C11-Pk	DHFR-C12-Myc	DHFR-C13-HA
No addition	11 C's 198 aa 22.39 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP IVQNI PNPLLGLD VPIRCS RLRWKNKSSQKRI	12 C's 199 aa 22.43 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP HRAEHPQPPAGPGRTH MFQITL EQKLISEEDL	13 C's 199 aa 22.43 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP PSCRTSPTPCWAWT TPY DVPDYA GTKTHLRGS
One C added	12 C's 207 aa 23.34 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP HRAEHPQPPAGPGRTH MFQITL EQKLISEEDL MRIPG LE	13 C's 208 aa 23.44 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP PSCRTSPTPCWAWT TPY DVPDYA GTKTHLRGSVMRI PGILE	14 C's 208 aa 23.51 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP PIVQNI PNPLLGLD VPIRC SRLRWKNKSSQKRILMRIPG LE
Two C's added	13 C's 223 aa 25.24 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP PSCRTSPTPCWAWT TPY DVPDYA GTKTHLRGSNEDP GNSRVRLTCRRPLIKVVRPR	14 C's 224 aa 25.40 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP PIVQNI PNPLLGLD VPIRC SRLRWKNKSSQKRICNEDPG NSRVRLTCRRPLIKVVRPR	15 C's 224 aa 25.34 kDa MISLIAALAVDRVIGMENAM PWNLPADLAWFKRNTLNKP VIMGRHTWESIGRPLPGRKN IILSSQPGTDDRVTWVKSVD AIAACGDVPEIMVIGGGRVYE QFLPKAQKLYLTHIDAEVEGD THFPDYEPDDWESVFSEFHD ADAQNSHSYCFEILERREPSA PPP HRAEHPQPPAGPGRTH TMFQITL EQKLISEEDL NEDP GNSRVRLTCRRPLIKVVRPR

(b)

Supplementary Figure S1. Open reading frames and their predicted protein products used in the *in vitro* transcription/translation assay. Homocytidine runs are shown in bold. (a) Open reading frames of the input plasmids containing 11-, 12- and 13- cytidine runs. (b) The predicted translated products of the three input plasmids and their derivatives with one or two additional cytidines in the homocytidine run. DHFR - dihydrofolate reductase. Amino acids of the Pk (also known as SV5 – IPNPLLGLD), Myc (EQKLISEEDL) and HA (YDVPDYA) tags are colour coded. The homocytidine stretch is highlighted (yellow box).