

Supplementary figure legends

| | | |
|---------|---|-----|
| C-Myc67 | MDFFRVVENQPPATMPLNVSFTRNRYDLDYDSVQPYFYCDEEENFYQQQQQSELQPPAPS | 60 |
| C-Myc64 | -----MPLNVSFTRNRYDLDYDSVQPYFYCDEEENFYQQQQQSELQPPAPS | 46 |
| C-MycS | ----- | 0 |
| C-MycS1 | ----- | 0 |
| C-MycS2 | ----- | 0 |
| C-Myc67 | EDIWKKFELLPTPPLSPRRSGLCSPSYAVTTPFSLRGDNDGGGGSFSTADQLEMVTELL | 120 |
| C-Myc64 | EDIWKKFELLPTPPLSPRRSGLCSPSYAVTTPFSLRGDNDGGGGSFSTADQLEMVTELL | 106 |
| C-MycS | -----MVTELL | 6 |
| C-MycS1 | ----- | 0 |
| C-MycS2 | ----- | 0 |
| C-Myc67 | GGDMVNQSFICDPDDETFIKNIIQDCMWSGFSAAAKLVSEKLASYQAARKDSGSPNPAR | 180 |
| C-Myc64 | GGDMVNQSFICDPDDETFIKNIIQDCMWSGFSAAAKLVSEKLASYQAARKDSGSPNPAR | 166 |
| C-MycS | GGDMVNQSFICDPDDETFIKNIIQDCMWSGFSAAAKLVSEKLASYQAARKDSGSPNPAR | 66 |
| C-MycS1 | ---MVNQSFICDPDDETFIKNIIQDCMWSGFSAAAKLVSEKLASYQAARKDSGSPNPAR | 57 |
| C-MycS2 | -----MWSGFSAAAKLVSEKLASYQAARKDSGSPNPAR | 33 |
| | ***** | |
| C-Myc67 | GHSVCSTSSLYLQDLASAAASECIDPSVVFYPYPLNDSSSPKSCASQDSSAFSPSSDSLSS | 240 |
| C-Myc64 | GHSVCSTSSLYLQDLASAAASECIDPSVVFYPYPLNDSSSPKSCASQDSSAFSPSSDSLSS | 226 |
| C-MycS | GHSVCSTSSLYLQDLASAAASECIDPSVVFYPYPLNDSSSPKSCASQDSSAFSPSSDSLSS | 126 |
| C-MycS1 | GHSVCSTSSLYLQDLASAAASECIDPSVVFYPYPLNDSSSPKSCASQDSSAFSPSSDSLSS | 117 |
| C-MycS2 | GHSVCSTSSLYLQDLASAAASECIDPSVVFYPYPLNDSSSPKSCASQDSSAFSPSSDSLSS | 93 |
| | ***** | |
| C-Myc67 | TESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGG | 300 |
| C-Myc64 | TESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGG | 286 |
| C-MycS | TESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGG | 186 |
| C-MycS1 | TESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGG | 177 |
| C-MycS2 | TESSPQGSPEPLVLHEETPPTTSSDSEEEQEDEEIDVVSVEKRQAPGKRSESGSPSAGG | 153 |
| | ***** | |
| C-Myc67 | HSKPPHSPVLKRVCHVSTHQHNYAAPSTRKDYPAARVKLDSVRVLRQISNNRKCTSPR | 360 |
| C-Myc64 | HSKPPHSPVLKRVCHVSTHQHNYAAPSTRKDYPAARVKLDSVRVLRQISNNRKCTSPR | 346 |
| C-MycS | HSKPPHSPVLKRVCHVSTHQHNYAAPSTRKDYPAARVKLDSVRVLRQISNNRKCTSPR | 246 |
| C-MycS1 | HSKPPHSPVLKRVCHVSTHQHNYAAPSTRKDYPAARVKLDSVRVLRQISNNRKCTSPR | 237 |
| C-MycS2 | HSKPPHSPVLKRVCHVSTHQHNYAAPSTRKDYPAARVKLDSVRVLRQISNNRKCTSPR | 213 |
| | ***** | |
| C-Myc67 | SSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVLKKATAYILSV | 420 |
| C-Myc64 | SSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVLKKATAYILSV | 406 |
| C-MycS | SSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVLKKATAYILSV | 306 |
| C-MycS1 | SSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVLKKATAYILSV | 297 |
| C-MycS2 | SSDTEENVKRRTHNVLERQRRNELKRSFFALRDQIPELENNEKAPKVVLKKATAYILSV | 273 |
| | ***** | |
| C-Myc67 | QAEEQKLISEEDLLRKRREQLKHKLEQLRNCA | 453 |
| C-Myc64 | QAEEQKLISEEDLLRKRREQLKHKLEQLRNCA | 439 |
| C-MycS | QAEEQKLISEEDLLRKRREQLKHKLEQLRNCA | 339 |
| C-MycS1 | QAEEQKLISEEDLLRKRREQLKHKLEQLRNCA | 330 |
| C-MycS2 | QAEEQKLISEEDLLRKRREQLKHKLEQLRNCA | 306 |
| | ***** | |

Figure S1: Alignment of the predicted primary translational structures of the five open reading frames corresponding to c-Myc1, c-Myc2 c-MycS previously described plus two additional potential open reading frames c-MycS1 and cMycS2 suggested by the present work. Note that all these isoforms differ only in the N-terminal part.

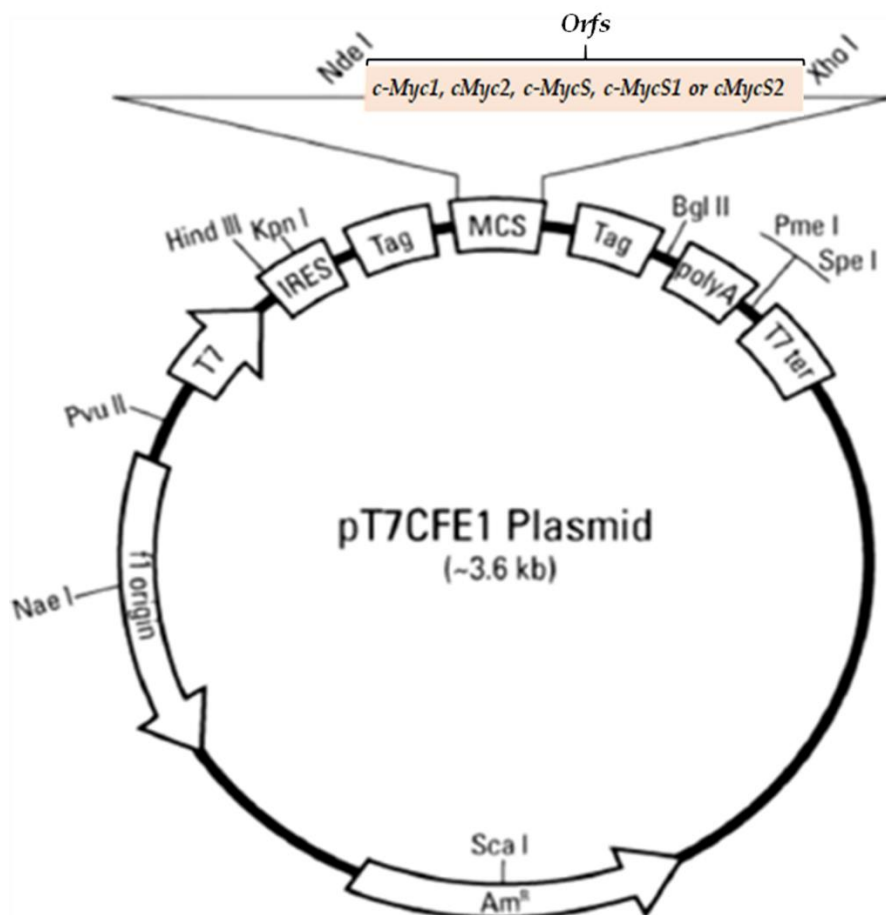


Figure S2: Full-length open reading frames (Orf) encoding c-Myc1, c-Myc2 or c-MycS, c-MycS1 and c-MycS2 cloned into the pT7CFE1 vector subjected to transcription (T7 promoter) and translation using a mammalian in vitro translation system based on HeLa cell lysates

Genomic TAAGGAAAACGATTCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAACCTGTTTCAAATGCATGATCAAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTAGC 120
 3'UTR1 TAAGGAAAACGATTCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAACCTGTTTCAAATGCATGATCAAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTAGC
 3'UTR2 TAAGGAAAACGATTCTTCTAACAGAAATGTCCTGAGCAATCACCTATGAACCTGTTTCAAATGCATGATCAAAATGCAACCTCACAACCTTGGCTGAGTCTTGAGACTGAAAGATTAGC

-----/continuation of 3'UTR/-----

Genomic TACACAATGTTTCTCTGTAATAATGCCATTAAATGTAATAACTTTAATAAAAACGTTTATAGCAGTTACACAGAATTTCATCTCTAGTATATAGTACCTAGTATTATAGTACTATAAA 360
 3'UTR1 TACACAATGTTTCTCTGTAATAATGCCATTAAATGTAATAACTTTAATAAAAACGTTTATAGCAGTTAAAAA
 3'UTR2 TACACAATGTTTCTCTGTAATAATGCCATTAAATGTAATAACTTTAATAAAAACGTTTATAGCAGTTACACAGAATTTCATCTCTAGTATATAGTACCTAGTATTATAGTACTATAAA

Genomic CCCTAATTTTTTTTATTAAAGTACATTTTGCTTTTAAAGTTGATTTTTTCTATGTTTTAGAAAAATAAAAATACTGGCAATATATCATTGAGCCAAATCTTAAGTTGTGAATGT 480
 3'UTR2 CCCTAATTTTTTTTATTAAAGTACATTTTGCTTTTAAAGTTGATTTTTTCTATGTTTTAGAAAAATAAAAATACTGGCAATATATCATTGAGCCAAATCTTAAAAA → Poly A tail

Figure S3: Nucleotide sequences of the identified 3'UTR types. The translational TAA stop codon is indicated. Alternative AATAAA polyadenylation sites are underlined.



Figure S4: Nucleotide sequences of Trans1 and Trans2 transcripts compared to the corresponding genomic structure. Underlined splice donor (GT), acceptor (AG) sites, and initiation codons (CTG, ATG) are indicated. The first amino acids of c- Myc2 and c-MycS are shown. Translation from CTG of Trans1 is prevented by the PvuII mutation. P1:+1: Transcription initiation site from the P1 promoter. PFull1: Primer (Table1); M: The first amino acid, methionine. The rest of *c-MYC* sequence until the translation stop codon (TAA) is not shown.

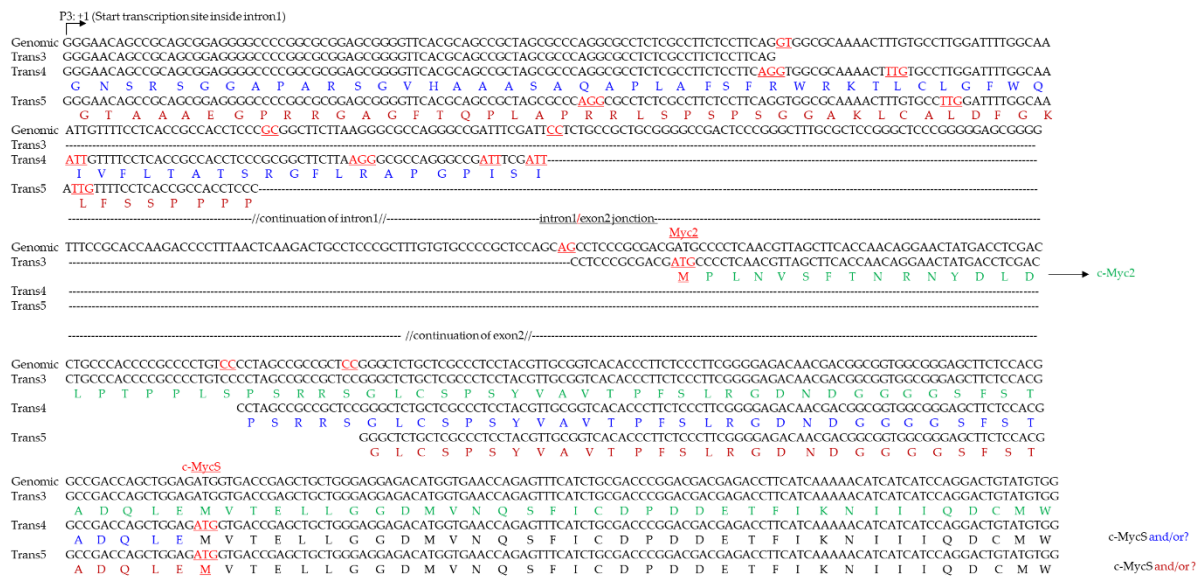


Figure S5: Nucleotide sequences of Trans3, Trans4, and Trans5 transcripts compared to the corresponding genomic structure. Underlined dinucleotides represent the splice sites found. The ATG initiation codons for c-Myc2 and c-MycS are indicated. Trans3 translation predicts c-Myc2 protein. Curiously and despite different splicings, Trans4 and Trans5 transcripts do not have a stop codon in their 5'UTR region. Potential non-ATG initiation sites are underlined. P3:+1: transcription initiation site from the P3 promoter. PFull3: Primer; M: The first amino acid, methionine. The rest of *c-MYC* sequence until the translation stop codon (TAA) is not shown.

BL41 P?:+1
 Genomic GGAGATAGTGGGCTCAGAGCATGTCAGAAATGTCCTCGGGGAGATCTGTGATATTGAAAGCAT IGH sequence GGTTCAC TAAGTGC GTCTCC GAGATAG CAGGGG ACTGTCC AAAGGG GTGAA AGGG 120
 -----GGTTCAC TAAGTGC GTCTCC GAGATAG CAGGGG ACTGTCC AAAGGG GTGAA AGGG 56 remaining c-Myc intron1 sequence
 BL41 TGCTCCCTTTATTCCCCACCAAGACCACCCAGCCGCTTTAGGGGATAGCTCTGCAAGGGGAGAGGTTCTGGGACTGTGGCGCGCACTGCGCGCTGCGCCAGGTTTCCGCACCAAGACCCC 240
 Genomic TGCTCCCTTTATTCCCCACCAAGACCACCCAGCCGCTTTAGGGGATAGCTCTGCAAGGGGAGAGGTTCTGGGACTGTGGCGCGCACTGCGCGCTGCGCCAGGTTTCCGCACCAAGACCCC 176
 BL41 TTTAACTCAAGACTGCCTCCCGCTTTGTGTGCCCCGCTCCAGCAGCCTCCCGCGACGATGCCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACCTCGACTACGACTCGGTGCAGCCG c-Myc2 360
 Genomic TTTAACTCAAGACTGCCTCCCGCTTTGTGTGCCCCGCTCCAGCAGCCTCCCGCGACGATGCCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACCTCGACTACGACTCGGTGCAGCCG M 296 P L N V S F T N R N Y D L D Y D S V Q P → c-Myc2

Figure S6: Nucleotide sequences of the only transcript expressed from a yet to be determined promoter (P?). The transcript exhibits an IGH sequence. This transcript encodes c-Myc2. PFull4: Primer; M: Methionine. The rest of *c-MYC* sequence until the translation stop codon (TAA) is not shown.