ABSTRACT
Our findings indicate that mouse cells have different interpretations of readthrough, influenced by both upstream and downstream stop codon contexts. This implies that there are intricate interactions between the mRNA and the translation termination machinery components. When comparing our results to those of plant cells and yeast, we conclude that the recognition of stop codesons in eukaryotes is conserved.

INTRODUCTION
A recent study by Hirsch et al. (2007a) has shown that UAG is a transcription factor that is expressed in many mammalian cells, including human cells, and that UAG is one of the factors involved in the regulation of many cell-cell interactions such as angiogenesis and migration. UAG is also known to regulate other cell-cell interactions including migration and cell survival.

The aim of this study was to investigate whether UAG is regulated in mammalian cells by the upstream or downstream codons of the MHC class I receptor. The upstream codon context is indicated by 'UAC', while the downstream context is indicated by 'UACA'. In the present study, we used the MHC class I receptor as an experiment.

Materials and Methods: The process of information decoding involves translation termination, which is a critical step. Its accuracy is approximately 10-4, meaning that only fewer abnormal products are produced during this process. In contrast, animal and plant viruses use translation terminating events to regulate expression by misreading stop codons as expressed by the translational apparatus, resulting in the synthesis of an extended polypeptide that carries novel activities. This stands out from the fact that it requires specialized partners within the genome, such as tRNA and elongation factor factors associated with silisilience, leading up to In mammalian cells, the termination context has been studied in vivo and "in silico" experiments. The results suggest that the nucleotide after the stop codon (defined as +4) is non random, with purines being the primary factor responsible for termination efficiency. This suggests that some programmed readthrough events are driven by a "four base signal", with modifications in these interactions likely occurring at different times. Understanding the mechanisms involved in translation may aid in understanding normal termination of translation. To this end, we have investigated the sequence CAA UAG CAUA, which is derived from the plant Tobbaco Mosaic Virus (TMV). This sequence has been shown to drive a high level readthrough both in vitro and in vivo in plant cells and yeast. We used luciferase reporters to analyze the 5' and 3' triplets at the stop codon.

CONCLUSION
Remarkable conclusions All in all, our findings show that there are multiple signals involved with the translational machinery related to the upstream and downstream stop codon contexts, which may also be present in eukaryotes.