

**Table S3: 3'UTR variants**

GENE	SNPID	Transcript	MIRNA	DiffSc_SVM	Sc1_SVM	Sc2_SVM	DiffSc_TS	Sc1_TS	Sc2_TS	A1	SITE_A1	A2	SITE_A2	MiRExp	CANDIDATE
EXO1	chr1:242052986_T/G	NM_130398	miR-370-3p	0.9183	0	0.9183	0.477	0	-0.477	T	[ ]	G	[(CAGCA[G]GA 8m)]	medRpm	TRUE
			miR-93-3p	0.7675	0	0.7675	0.24	0	-0.24	T	[ ]	G	[(UCAGCA[G]G m8)]	medRpm	TRUE

## \*Table Description:

- SNPID: SNP ID with chromosome, position, ref allele, and alt allele
  - DiffSc\_SVM: Difference of SVM prediction scores between each allele:  $\text{abs}(\text{Sc1\_SVM} - \text{Sc2\_SVM})$
  - Sc1\_SVM: SVM prediction score of allele A1
  - Sc2\_SVM: SVM prediction score of allele A2
  - DiffSc\_TS: Difference of TargetScan prediction scores between each allele:  $\text{abs}(\text{Sc1\_TS} - \text{Sc2\_TS})$
  - Sc1\_TS: TargetScan prediction score of allele A1
  - Sc2\_TS: TargetScan prediction score of allele A2
  - A1: Allele 1 (Ref Allele)
  - SITE\_A1: miRNA target site at allele A1
  - A2: Allele 2 (Alt Allele)
  - SITE\_A2: miRNA target site at allele A2
  - MiRExp: maximum miRNA expression level in FANTOM5 cell lines
  - CANDIDATE: Possible filtering (MiRExp is highRpm or medRpm, MirSNP detected by both tools, and  $\text{DiffSc\_SVM} \geq 0.4$ )
- Target sites:**
- - [ ] means no site at the allele
  - - Each site is listed between parentheses: "(" and ")"
  - - The 8mer sequence is the sequence of the 3'UTR mRNA which is reversed complement of the miRNA seed region (nucleotides 1-8 at the 5' end of the miRNA)
  - - Within the sequence, the allele with the site is denoted within brackets (for instance [G])
  - - After the space character, the seed type is denoted by:
    - - "8m" for 8mer (sequence matching from miR nucleotides 1-8),
    - - "m8" for 7merM8 (sequence matching from miR nucleotides 2-8)
- Scores:**
- - DiffSc\_SVM and DiffSc\_TS: the higher the better is the prediction of functional SNP
  - - Sc1\_SVM and Sc2\_SVM: the higher the better is the prediction of miRNA target
  - - Sc1\_TS and Sc2\_TS: the lower the better is the prediction of miRNA target