

# Genome Wide Analysis of Porcine miRNA Editing

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## Background

MicroRNAs (miRNAs) are small RNAs, usually ~23nt long, that play a prominent role in the post-transcriptional regulation of gene expression. RNA molecules can be altered by nucleotide modifications through RNA editing, one of the post-transcription modifications of RNA. The most frequent and well characterized RNA editing event is conversion of adenosine (A) to inosine (I) in double stranded RNAs by ADARs enzymes. This modification can lead to alteration in the splicing and translation process [1]. In case of RNA editing in the miRNA seed region or miRNA target site in mRNA this may affect miRNA-mRNA target interaction [2].

The "WUR-pigENCODE" is a Dutch pilot project aiming at increasing the functional annotation of the pig genome and developing of the analytic framework needed for the FAANG (Functional Annotation of Animal Genomes) community.

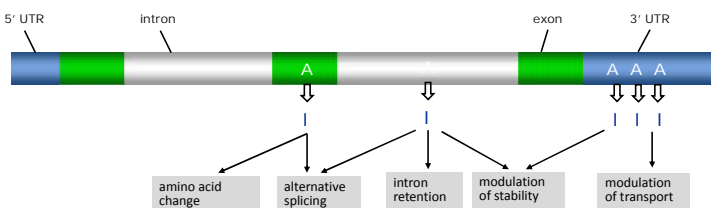


Figure 1. Ways that A-I editing can change the transcriptome

Adapted from: <http://www.su.se/mbl/research/research-groups/molecular-cell-biology/group-%C3%B6hman/research-projects/rna-editing-in-the-mammalian-brain-1.131690>

## Objective

To assess the interplay between RNA-editing events (A -> I) in seed regions of miRNAs and target sites in mRNA - to understand how RNA-editing may change the target profile of the edited miRNAs and regulate gene expression

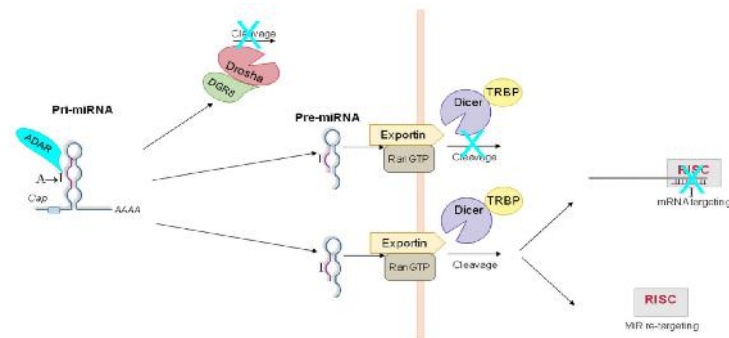
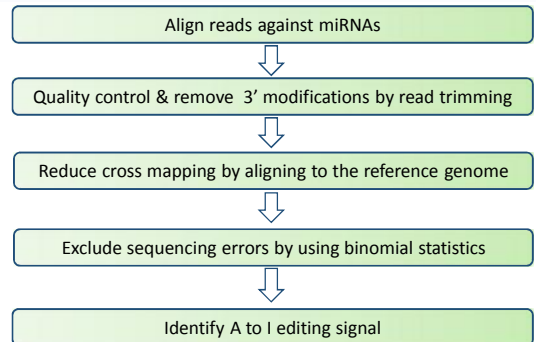


Figure 2. Editing-dependent effects of ADARs on miRNA pathway  
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## Materials

Breed	PigWUR_NRs	sample type	acronym
Duroc	PigWUR_136	liver	dul
	PigWUR_139	spleen	dus
	PigWUR_142	testis	dut
	PigWUR_145	Brain: frontal lobe	dub
	PigWUR_148	muscle	dum
Pietrain	PigWUR_152	liver	ptl
	PigWUR_155	spleen	pts
	PigWUR_158	testis	ptt
	PigWUR_161	Brain: frontal lobe	ptb
	PigWUR_164	muscle	ptm
LargeWhite	PigWUR_168	liver	lwl
	PigWUR_171	spleen	lws
	PigWUR_174	testis	lwt
	PigWUR_177	Brain: frontal lobe	lwb
	PigWUR_180	muscle	lwm
	PigWUR_188	olfactory bulb	lwo

## Method



## Results

### Trimming and Mapping

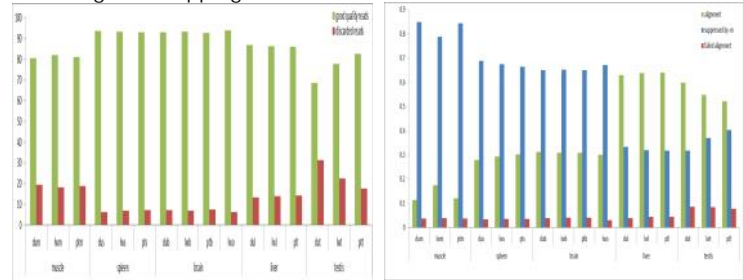


Figure 3. Quality Control and trimming results: Adaptors are removed and the reads are selected on the bases of read quality and read length.

Figure 4. The mapping results: The number of percent of reads that map to the reference genome per sample

### Mismatch and Editing Event

	muscle			spleen			brain			liver			testis			
	dum	lwm	ptm	dus	lws	pts	dub	lwb	lwo	ptb	dul	lwl	ptl	dut	lwt	ptt
total mismatch	42504	64692	36478	603606	579184	604288	589536	481817	713849	543262	376705	300252	283004	181572	265294	239397
significant mismatch	40	52	43	91	100	94	93	78	77	100	66	65	63	60	69	62
after removing SNP	40	52	43	91	100	94	93	78	77	100	66	65	63	60	69	62

Table 2. Number of significant editing events per sample. The total number of mismatch is calculated, subsequently the significant editing events are analysed by removing the sequencing errors and applying binomial statistics. From the significant editing results the SNPs are removed to get actual editing events, in this case no SNP was found in any sample.

## Conclusions and future work

- RNA editing of miRNAs is common in all tissues (at-least 40 RNA editing events seen in each sample)
- Future analysis are aimed to:
  - Identify the A to I editing events and the position of editing site in miRNA
  - Establish if editing may create new miRNA in the given samples
  - Compare differential expression of non-edited and edited miRNA

## References

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- Tomaselli S, Bonamassa B, Alisi A, Nobili V, Locatelli F, Gallo A. ADAR Enzyme and miRNA Story: A Nucleotide that Can Make the Difference. *International Journal of Molecular Sciences* 2013; 14(11): 22796-22816. doi: 10.3390/ijms141122796.



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