IsomiR profile report

sRNA length distribution

Length distribution of diseased group (redundant reads) — Length distribution of control group (redundant reads)
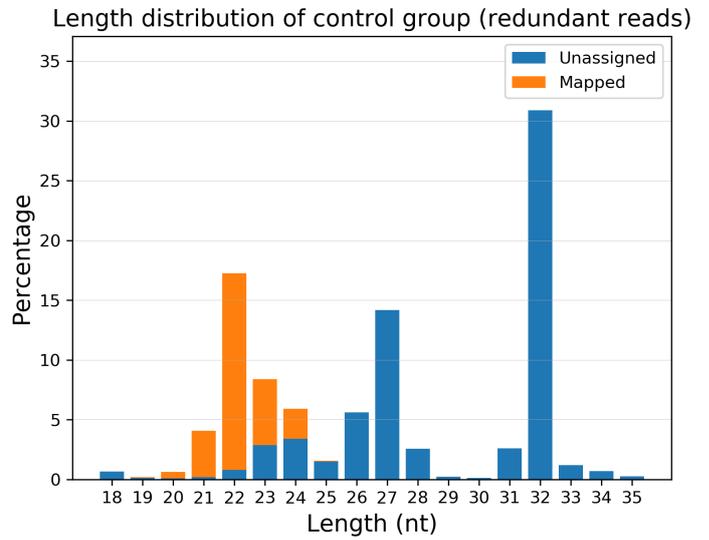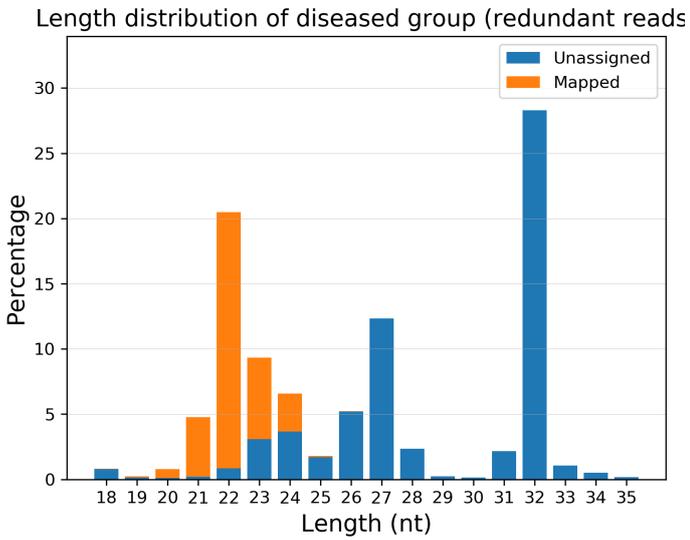
Mapped and unmapped reads to custom precursor arm reference DB (5p and 3p arms) in diseased (left) and control (right) groups

## Templated and non-templated isomiRs

Diseased group (reads)

- non-templated 8.4%
- miRNA RefSeq 22.3%
- templated 10.9%
- unassigned 58.4%

Control group (reads)

- non-templated 7.8%
- miRNA RefSeq 18.9%
- templated 9.4%
- unassigned 63.9%
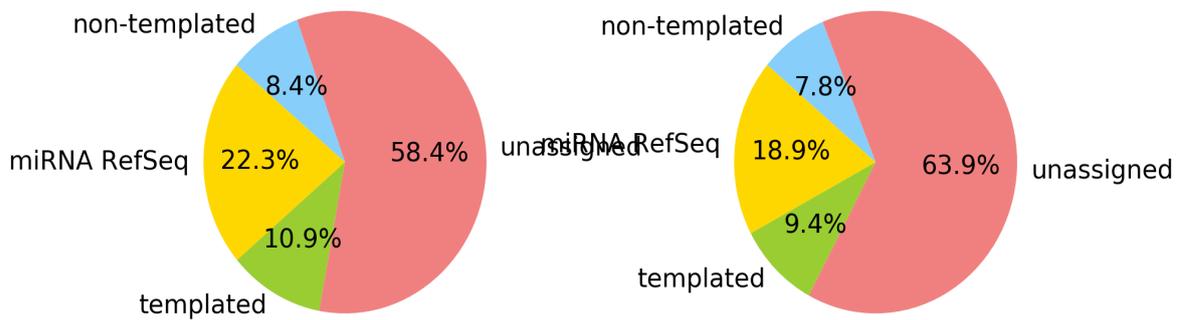
RefSeq miRNAs, templated isomiRs, non-templated isomiRs and unassigned sequences as percentage of total sRNA reads in diseased (left) and control (right) groups

Templated isomiR subtypes

Templated isomiR profile (redundant reads)
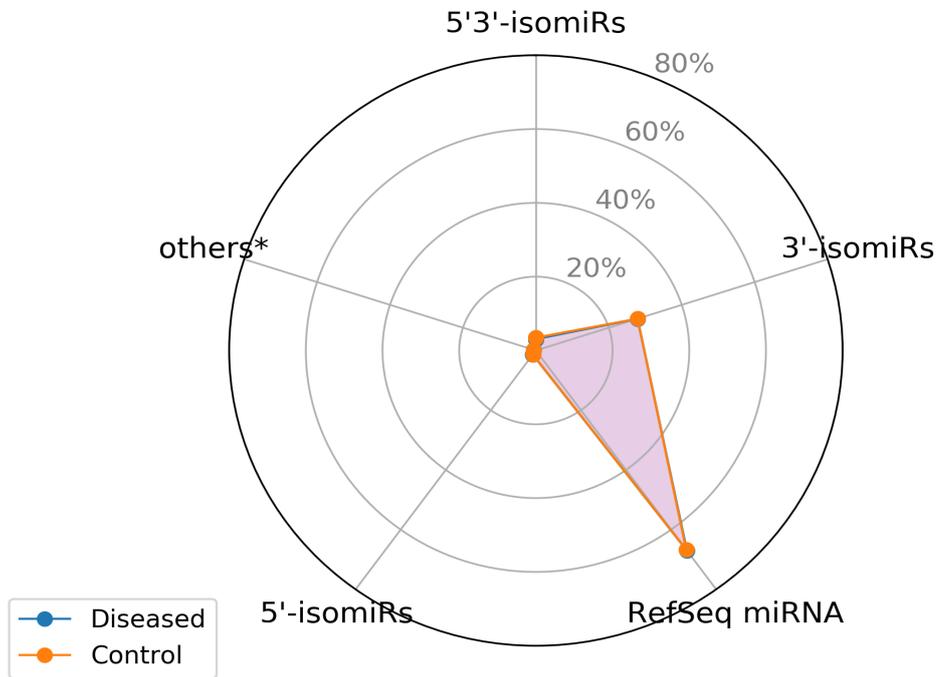
Templated isomiR profile (non-redundant reads)
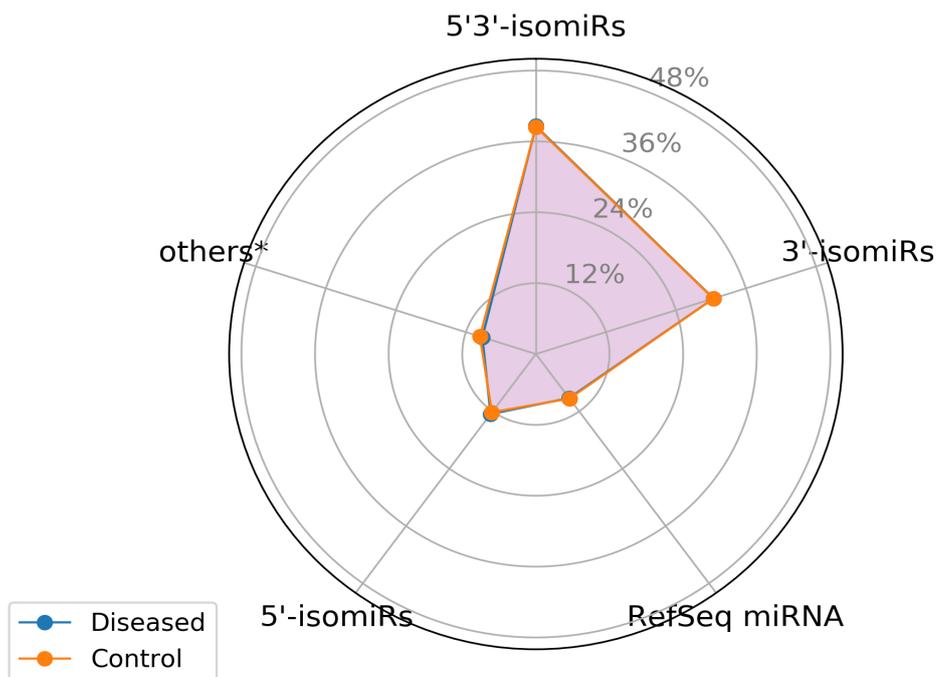
* IsomiRs potentially generated from multiple loci

Non-templated isomiRs

3'-end additions to RefSeq miRNAs and templated isomiRs