



The Genome Informatics Specialist

InteRNA Genomics offers services for processing,
analyzing and presenting massively parallel
sequencing data generated by various platforms

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Corporate Facts

Founded:

November 2007

Status:

Private

Subsidiary of:

InterNA Technologies B.V.

Who are we?

InterNA Genomics was incorporated in 2007 by Aglaia Oncology Fund as a subsidiary of InterNA Technologies. We have close relationships with the research groups of our founders Edwin Cuppen and Eugene Berezikov of the Hubrecht Institute

What do we stand for?

InterNA Genomics offers services for processing, analyzing and presenting massively parallel sequencing data generated by various platforms.

InterNA Genomics is dedicated to facilitate your small RNA and massively parallel sequencing research by taking care of all bioinformatic aspects so that you can focus on the biology behind it!

Intess™ – InterNA Genomics Software and Services

While the generation of massively parallel sequencing (MPS) data can be outsourced to a number of sequencing service providers, data processing and interpretation requires highly skilled bioinformaticians and a dedicated computational infrastructure – a challenge for many organizations. The software and services that are developed by InterNA Genomics are built on many years of experience analyzing DNA sequencing data as well as pioneering work in the generation and analysis of small RNA data generated by massively parallel sequencing (see Publications, p.4).

The Intess™ solutions deliver complete, up-to-date and ready-to-interpret analyses of raw sequencing data, allowing the researcher to focus on the biological problem at hand. The informatics solutions are modular and easily customized, enabling development of data analysis pipelines that take into account specifics of every individual project.

The Intess™ solutions are platform-independent and have been validated with experimental data obtained on Roche/454 (GS-20 and GS-FLX), Illumina (Genome Analyzer) and Applied Biosystems (SOLiD) platforms. InterNA Genomics provides solutions for all MPS application areas, including:

- Small RNA analysis (miR-Intess™)
- Gene expression profiling (Gene-Intess™)
- ChIP sequencing (ChIP-Intess™)
- Genome variation (Genome-Intess™)

InterNA Genomics also provides a complete next-generation sequencing service, which includes consultancy for the experimental design, preparation and sequencing of customer samples on various sequencing platforms and data analysis. The state of the art facilities and extensive know-how and experience guarantee high quality results. InterNA Genomics provides its customized services to academic institutions as well as commercial organizations.

DISCLAIMER

This document is not an offer to sell any securities. Additional information is available upon request. This document contains forward-looking statements about potential therapeutic uses and effects of our products. Actual results may differ materially depending on the actual therapeutic effect of the products, whether trials are initiated, the actual timing and results of the (pre)clinical trials, the actual timing and content of regulatory submissions and decisions of the FDA, EMEA and other regulatory bodies. We expect that our sources of income, if any, for the next years will continue to primarily consist of payments under collaborative agreements. In addition, we may not successfully develop, commercialize, manufacture or market any products or generate sufficient revenues to ever achieve or sustain profitability.

miR-Intess™ small RNA analysis pipeline

The miR-Intess™ analysis platform utilizes proprietary miRNA discovery and small RNA classification tools based on the latest insights and standards in the field. Versatile summaries, both graphically and tabular, are provided to obtain insight into the small RNA component of any sample that was analyzed on any of the next-generation sequencing platforms.

Examples of miR-Intess™ outputs

Small RNAs from various rat tissues

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

Table | Graph | Length | Chromosome view

InterNA Genomics small RNA analysis pipeline miR-Intess™. Jan 23, 2009.

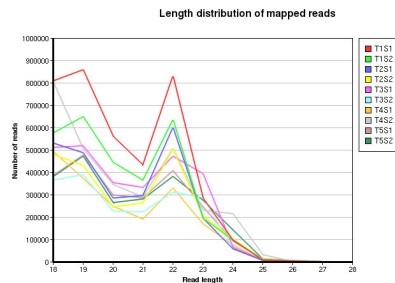
- Total number of analysed libraries: 10
- Total number of raw reads: 98,614,116
- Total number of accepted reads: 60,757,867
- Total number of mapped reads: 25,314,950
- Total number of cloned miRBase miRNAs: 278
- Total number of homolog miRBase miRNAs: 33
- Total number of novel identified miRNAs: 50

Length distribution of mapped reads

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

Table | Graph | Length | Chromosome view

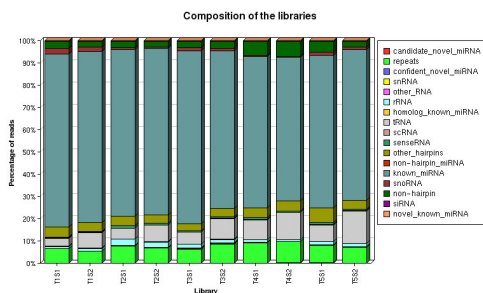


Composition of the libraries

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

Table | Graph | Length



Analysis of miRNA families and clusters

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

Table | Thresholds | Families | Clusters

Families of known and novel miRNAs

Family	Size	Seed	Members
let-7a/7b/7c/7d/7a/7f/7g/miR-98	13 miRNAs	GAGGUAG	miR-let-7a-2 miR-let-7f-2 miR-let-7a miR-let-7a-1 miR-let-7f-1 miR-let-7d miR-let-7c-2 miR-let-7b miR-mir-98 miR-let-7c-1 miR-let-7 block113823_cand block2624833_cand
miR-30a/30b/30c/30d/30e/384	9 miRNAs	GUAAACA	miR-mir-30a miR-mir-30c-2

Discovery of novel miRNA genes

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

List | Heatmaps | Tables

miRBase miRNAs | Novel miRNAs | Candidate miRNAs

List of novel miRNAs

no.	ID	Total reads	Total ligs	Locations	Cluster	Family	Mature	Star	Classification
1.	sblock12689_novel	14246	10	1		novel15	5'	3'	novel_dorningHIGH_multitarm_1
2.	sblock2023_novel	1487	10	1			3'		novel_dorningHIGH_multitarm_ra
3.	sblock652_novel	1175	5	7		novel15	3'	5'	MANUAL_level1
4.	sblock647_novel	1089	5	4		novel15	3'	5'	MANUAL_level1
5.	sblock651_novel	1087	5	4		novel15	3'	5'	MANUAL_level1
6.	sblock650_novel	886	5	7		novel15	3'	5'	MANUAL_level1
7.	sblock646_novel	477	4	7		miR-410	3'	5'	MANUAL_level1
8.	sblock12740_novel	206	9	1			5'	3'	novel_dorningHIGH_multitarm_1
9.	sblock508_novel	179	2	1		novel236	3'	5'	MANUAL_level1
10.	sblock2895936_novel	172	7	1			3'		novel_dorningHIGH_randfoldCI

Expression analysis of miRNAs

miR-Intess™

Summary | Preprocessing | Mapping | Composition | miR classification | miR expression | Downloads

List | Heatmaps | Tables

miRBase and Novel | Candidates

