MSBiosuite™

Bioinformatic Platform for MSB workflows

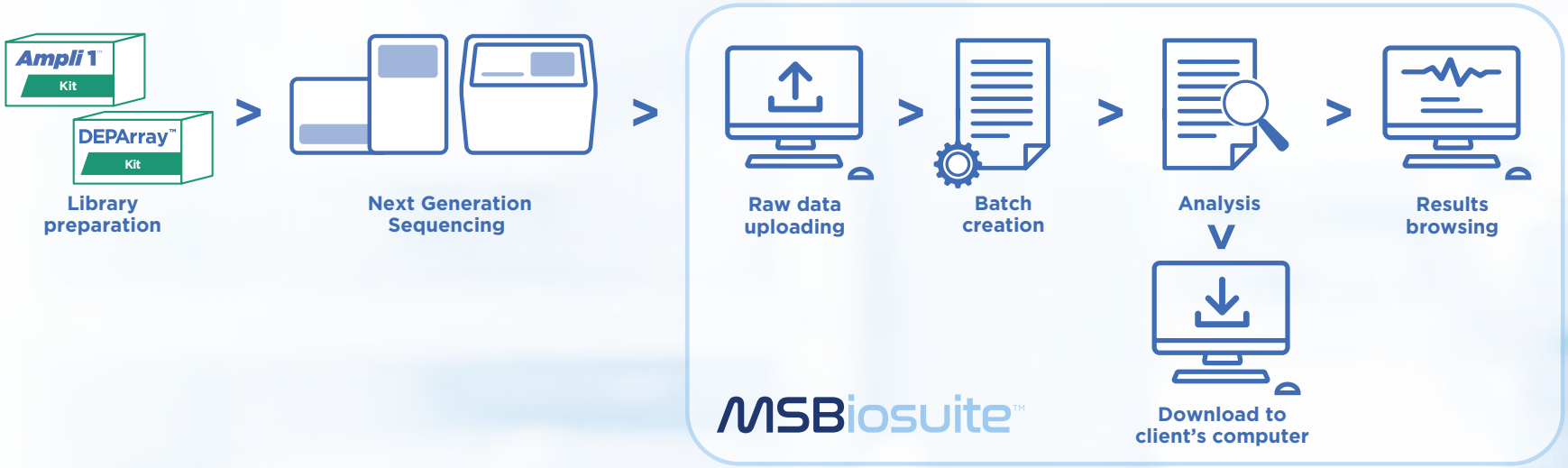
MENARINI
silicon biosystems

Completing our sample to results solution

MSBiosuite is a cloud based platform which automates processing of sequencing data generated from ***Ampli*1™** and **DEPArray™** NGS kits.

MSBiosuite manages your entire workflow from uploading of raw data, data processing, to the downloading of results directly onto your computer. The tailored proprietary analysis pipeline guarantees highly confident variant calling and generation of copy number aberration profiles.

MSBiosuite worfklow



Two level of reporting available

Analytical report with basic annotation of variant calling

Clinical interpretation report with advance annotation
(available for OncoSeek pipelines only)

Bridge the gap between your raw NGS data and consolidated results

Key Features

EASY DATA PROCESSING

- Automated analysis of sequencing data generated from *Ampli*™ and DEPArray™ NGS kits
- No bioinformatic skills required

USER FRIENDLY

- Custom graphical views of browsing results
- Remote support always available
- Easily share results of specific analysis runs with colleagues and collaborators

SECURE

- Data are encrypted both “in transit” and “at rest”
- Strong authentication mechanisms

DATA RESIDENCY

- Global data center deployment
- Processing and storage of genomics data are guaranteed to be in the users’ region of choice

AFFORDABLE

- Pre-paid analysis packages and monitoring of remaining analysis
- No hardware costs or license fees

MSBiosuite pipelines for single cell application

*Ampli*1™ LowPass pipeline

Sample of interest can be easily selected for a visual comparison of multiple copy number profiles (Fig 1). An interactive searchable and zoomable display allows browsing specific genomic regions. A hierarchical clustering of the samples included in the batch is provided to help in investigating the relationships between samples and to study tumor heterogeneity (Fig 2). Data and publication quality figures can be downloaded to your computer.

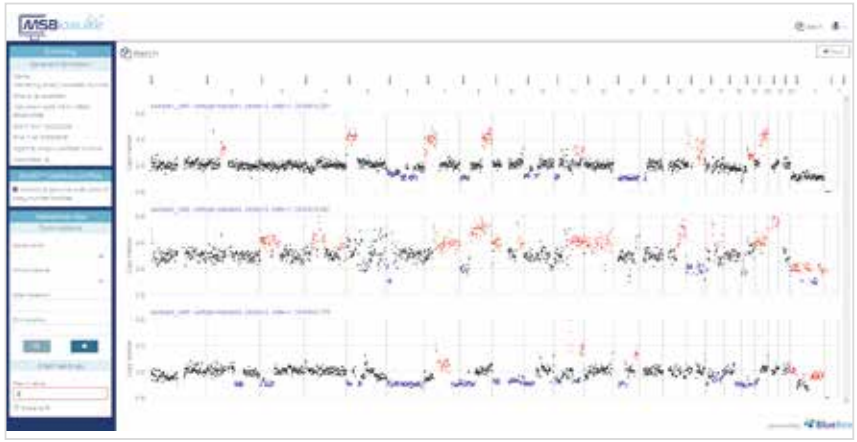


Fig 1 Each track corresponds to the copy number profile of the selected single cell. The track header includes sample name, cell type, ploidy, cell number and DLRS information. In the plot, absolute copy numbers (y-axis) are displayed along the genome chromosomes (x-axis).

Fig 2 Hierarchical clustering is displayed as a dendrogram on the left side of an heatmap showing the copy number profiles arranged in rows, where copy-gains and losses are highlighted using a red and blue gradient respectively.

MSBiosuite pipelines for single cell application

LEVEL 1

*Ampli*1™ OncoSeek pipeline

Putative somatic variants are listed and grouped by sample.

The allelic frequencies of each variant and basic annotation are also listed (Fig 3).

A more comprehensive list of all variants, both somatic and germline, listing also putative LOH events is available as download in Excel format.

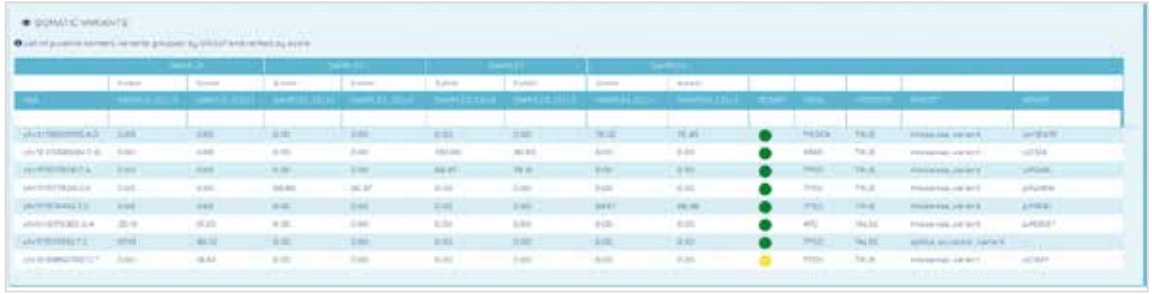


Figure 3. Somatic variants list

The copy number amplifications section shows, both in text form and as a barchart (Fig. 4), the copy number amplifications detected in 19 target genes, grouped by group/patient.

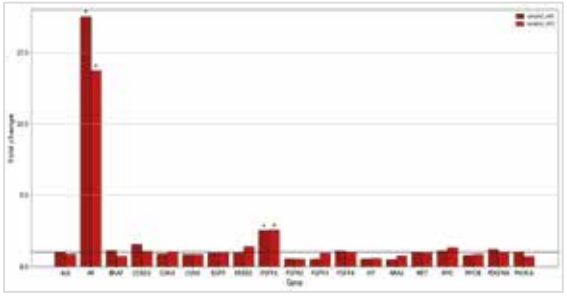


Figure 4. Barchart of copy number amplifications. Copy number gains whose fold change value is >2 and >5 Z-score calculated on reference samples are highlighted with an asterisk.

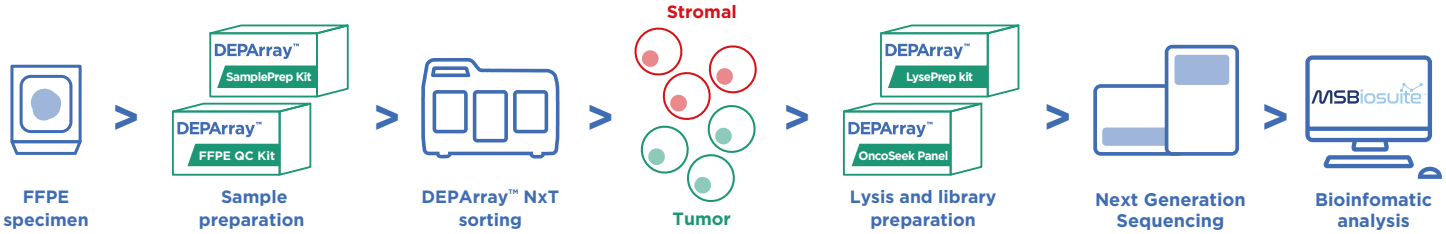
Optional advanced annotation is available on demand for OncoSeek pipeline. (Powered by N-Of-One)

LEVEL 2

MSBiosuite Pipeline for FFPE Application

LEVEL 1

DEPArray™ OncoSeek pipeline

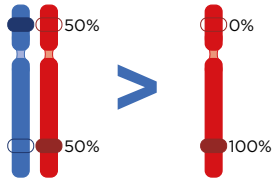


Visualize putative somatic variants with basic annotation and a table/barchart view of focal copy-number amplifications (see Fig.3 and 4 as an example). Result files can be downloaded to your computer and provide more comprehensive insight, including information on germline and LOH variants, target coverage and additional annotation.
A variant report table can be derived providing unambiguous identification of genetics event in each cell population (Fig. 5).

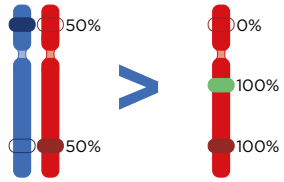
					stromal		tumor		unsorted	
gene	**chromosome**	**position**	**reference**	**alternative**	**lib1**	**lib2**	**lib3**	**lib4**	**lib5**	**event**
PDGFRA	chr4	55.149.258	G	A	55,22	43,54	0,00	0,00	15,29	**LOH**
KIT	chr4	55.563.683	T	G	40,42	71,27	100,00	100,00	91,34	**LOH**
CDK6	chr7	92.313.733	A	G	82,94	56,58	0,00	0,00	17,78	**LOH**
CDK6	chr7	92.333.408	A	G	50,93	32,86	0,00	5,26	19,05	**LOH**
TP53	chr17	7.577.094	G	A	0,00	0,00	100,00	100,00	56,01	**SOM + LOH**

Fig. 5. Pure tumor and stromal populations from primary adenocarcinoma were sorted and analysed with the DEPArray FFPE workflow. Relevant variants in the sorted pure populations of tumor (orange), stromal (blue) cells and unsorted fractions (green) are shown in the table. Loss Of Heterozygosity (LOH), somatic variant (SOM) and dual events (SOM + LOH) are easily detected in the sorted cell populations. Adapted from a case report, Isidori F et al., BMC Cancer, 2018.

LOH



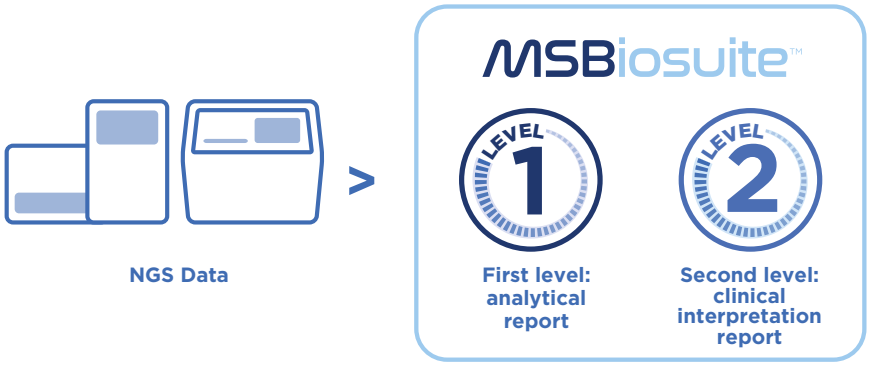
SOM + LOH



Optional advanced annotation is available on demand for OncoSeek pipeline. (Powered by N-Of-One)

LEVEL 2

Clinical interpretation report with advanced annotation for Oncoseek pipelines



The service takes advantage of RapidInsights™ by clinical interpreparation company N-of-One. The service includes also TrialMatch™, N-of-One proprietary process for incorporating deep scientific and clinical analysis of each patient's molecular data, to identify and prioritize the best clinical trial options for that patient.*

Information provided:

- Clinically relevant alterations divided in variants of strong, potential and uncertain clinical significance
- Predictive, prognostic and diagnostic level of evidence
- For each predictive variant listed the therapies approved in the specific indication and in other indications, and if the variant may indicate resistance to therapy
- Detailed biomarkers informations
- Matching clinical trial prioritized by clinical specificity and by region.


MSBiosuite

Summary

Clinically relevant alterations

Tier 1: Variants of strong clinical significance

Predictive Variants

Tier 2: Variants of potential clinical significance

Predictive Variants

Prognostic and Diagnostic Variants

*The content contained heren (Content) is a publication of Menarini Silicon Biosystems (MSB). MSB does not provide medical services, nor is any MSB employee engaged in the practice of medicine for or on behalf of MSB. Some tests, drugs and biomarkers identified in this report may not be approved for a particular use or validated for that use. The Content is compiled from sources believed to be reliable. Extensive efforts have been made to make the Content as accurate and as up-to-date as possible. Despite our best efforts, the Content may contain typographical errors and omissions. The Content is for professional medical and scientific use only.N-of-One, Inc. has provided to Menarini Silicon Biosystems the research, analysis and interpretation in this report. Additional information about N-of-One is available on its website at www.n-of-one.com

Ordering information

MSBiosuite products	Code
MSBiosuite *Ampli*1™ LowPass Analysis (Ion Torrent)	KI0129 (16 samples),KI0130 (48 samples), KI0131 (320 samples)
MSBiosuite *Ampli*1™ LowPass Analysis (Illumina)	KI0132 (16 samples), KI0133 (48 samples), KI0134 (320 samples)
MSBiosuite *Ampli*1™ Oncoseek Analysis	KI0138 (9 samples), KI0139 (24 samples), KI0140 (120 samples)
MSBiosuite DEPArray™ OncoSeek Analysis	KI0135 (9 samples), KI0136 (24 samples), KI0137 (120 samples)
Clinical Interpretation Report (available only for OncoSeek panels)	KI0141 (1 sample)

Valid only for EU Customers.

*Ampli*1™ Kits, DEPArray™ Kits and MSBiosuite™ are for research use only, not to use in diagnostic procedures.

MSBiosuite™ is powered by BlueBee

Menarini Silicon Biosystems S.p.A.
Via Giuseppe di Vittorio, 21 b/3
I-40013 Castel Maggiore (BO),
Italy t: +39 051 9944100
f: +39 051 9944199
e: info@siliconbiosystems.com

CMD_MKT_008 Rev. 2 - 2020 October

www.siliconbiosystems.com

MENARINI
silicon biosystems