RNA Seq MagIC Beads

Targeted RNA enrichment: let us know the RNA sequence of interest and receive a custom ready-to-use kit

RNA Seq
MagIC Beads

Capture any transcripts:

The targeted capture of specific transcripts of interest from samples of total RNA can be utilized to bring a single transcript resolution to the downstream analysis. The ability to enrich the target RNA may be beneficial when the transcripts of interest are present in the samples in levels too low in relation to other transcripts to allow their successful study. In cases of some RNA sequencing experiments, enrichment setups also offer an attractive perspective of reducing overall sequencing costs, saving sequencing depth from being spent on inherently uninteresting portions of the transcriptome in a given experiment.

Directly from unprocessed RNA:

MagIC Beads for RNA enrichment provide the first standardized solution for the capture of any RNA of interest from complex samples of unprocessed RNA. Whether for targeted sequencing or for any other downstream application the unique properties of MagIC Beads RNA enrichment kits offer exceptional value.

MagIC Beads for RNA enrichment are particularly useful for those experiments that can be benefited by bringing the resolution of the sequencing to a group of transcripts or a single transcript. This can be especially valuable in the studies of:

- RNA-RNA interactions
- RNA modifications
- Alternative polyadenylation
- Alternative splicing
- Alternative transcription start sites
- Native elongating transcript sequencing (NET-seq)
- … and more

The ability of MagIC Beads to capture full length RNA targets makes them especially attractive when used in combination with sequencing technologies capable of producing long reads. This is particularly pronounced in the case of direct RNA sequencing with Oxford Nanopore sequencing, where the relatively low number of reads produced by the platform makes the transcriptome wide applications challenging.

Capture up to 99% of the target sequence from the input sample:

The kits consist of the target-specific MagIC Beads and sets of optimized buffers. They feature standardized capture conditions and capture probes properties, which ensure uniformly high efficiency of the system on varying RNA targets, independent of their length or secondary structures. The beads provide very high target enrichment levels, at the same time being able to capture up to 99% of the target sequence from a sample.

Efficiency guaranteed by design – we design the probes for you:

For any custom target transcript the optimal number of probes is established based on the target length and nucleotide composition. Experimentally validated design approach is used to provide uniformly highly efficient capture probe arrays for any target. Every probe is screened against potential binding to any off-targets in the transcriptome of interest to ensure superb probe specificity.

Compared to classic biotinylated probe-based approaches, MagIC Beads provide multiple benefits:

No probe design burden:	Reliable arrays of capture probes are designed by ElementZero Biolabs for any target
Reliable performance: **No need for RNA fragmentation**	Efficient capture regardless of the target length or the presence of secondary structures
Preserved target integrity:	During the enrichment, nucleases are inactivated by the buffers with no need for RNase inhibitors
Fast and simple protocol:	The enrichment procedure can be completed in 1-2h with a reduced number of hands-on steps
No need for additional key components of the experimental setup:	MagIC Beads enrichment kits are provided as complete, out of the box solution
Expert support:	Count on active support regarding the use of the kit as well as analysis planned downstream applications

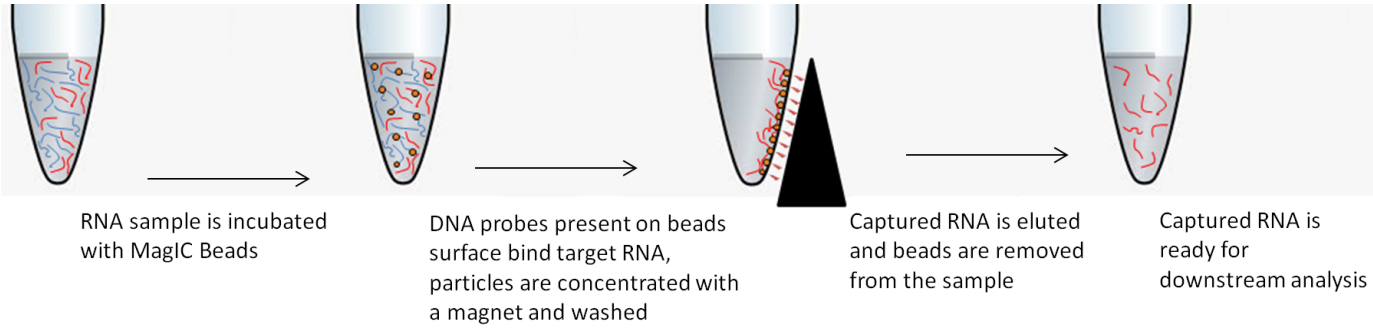
Advantages of MagIC Beads:

- **High efficiency and specificity:**
  - Isolate the target of interest instead of creating a generic RNA pool.
  - Enrich the target RNA up to 100 000 times.
  - Capture up to 99% of the target molecule.
  - No molecular tag related biases.
  - Reproducible and consistent levels of enrichment.
  - Purification can take place under very stringent conditions, unlike biotin based approaches.
- **Simple and time saving protocol:.**
  - Below 10 minutes of hands on time.
  - The whole procedure takes less than 2 hours.
  - No additional components needed.
- **Custom design for any RNA molecule:**
  - Target any transcript or pool of transcripts.

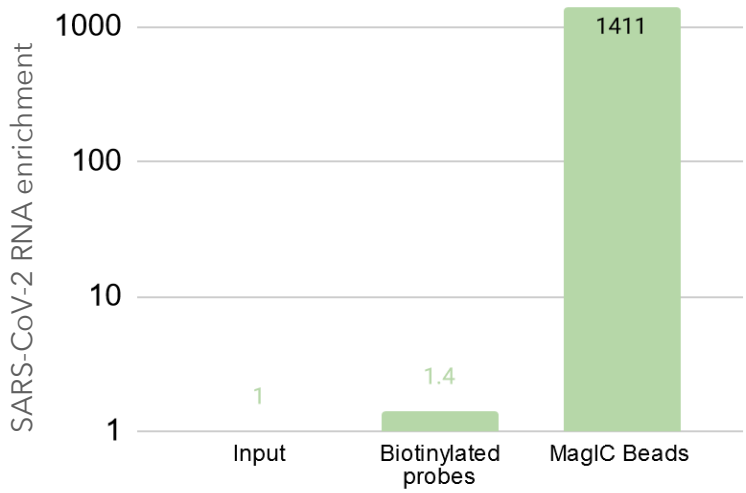
Additional Information:

- Supplied with beads, and hybridization and wash buffers.
- Shipping condition: room temperature.
- Storage temperature: 4°C.
- Durability: 36 months from date of manufacture.

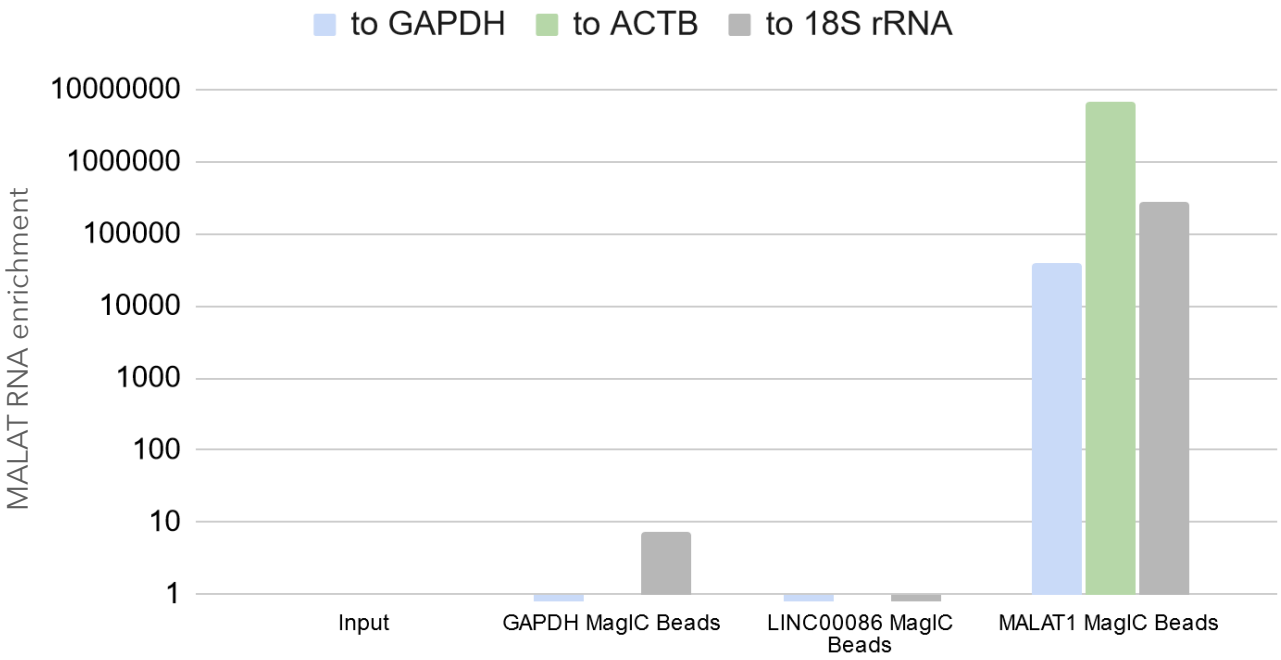
A simple and fast workflow for RNA enrichment



Unmatched enrichment levels



Samples of total, unfragmented RNA from cultured, SARS-CoV-2 infected cells were subjected to the capture with a pool of biotinylated DNA probes and streptavidin beads or MagIC Beads targeting SARS-CoV-2 RNA. RNA attached to the beads was washed, eluted and subjected to cDNA synthesis. Levels of GAPDH transcript and SARS-CoV-2 were measured in the input and enriched samples with RT-qPCR. The target RNA was not enriched successfully with biotinylated probes, but successfully enriched with MagIC Beads at the level of over 1.400 fold over the non-target transcript.



Samples of total, unfragmented RNA from HEK293 cells were incubated with MagIC Beads targeting human GAPDH, LINC00086 or MALAT1 transcripts. RNA attached to the beads was washed, eluted and subjected to cDNA synthesis. Levels of MALAT1, GAPDH, ACTB and 18S rRNA were measured in the input and enriched samples with RT-qPCR. The target RNA was enriched from over 10.000 to over 1.000.000 fold over non-target transcripts by MALAT1 targeting MagIC Beads, but not by beads targeting other transcripts.

RNA Interactome MagIC Beads

RNA-protein interactome: let us know the RNA sequence of interest and receive a custom ready-to-use kit

Identify ribonucleoprotein complexes:

RNA Interactome
MagIC Beads

The identification of the compositions of ribonucleoprotein complexes (RNPs) formed by a specific transcript is of great value in RNA studies. It is, however, a challenging task, and is difficult to accomplish with a classic toolbox of biochemical methods. Such studies can be performed on lysates of UV cross-linked cells with sequence-specific target capture utilizing antisense oligonucleotides. Typically systems based on biotinylated oligonucleotides complementary to the sequence of the transcript of interest in combination with streptavidin beads are employed. Proteins co-captured in such procedures can be identified by mass spectrometry.

Directly from cellular or tissue lysates:

MagIC Beads based systems for the study of RNA-protein interactome feature exceptionally efficient hybridization based approach of sequence specific RNP captures free of the weaknesses and shortcomings of biotin-streptavidin based workflows.

The kits consist of the target-specific MagIC Beads and sets of optimized buffers. They feature standardized cell lysis and capture conditions as well as capture probes properties, which ensure uniformly high efficiency of the system on varying RNA targets, independently of their length or secondary structures. The beads provide very high target capture efficiency and enrichment levels.

For any custom target transcript the optimal number of probes is established based on the target length and nucleotide composition. Experimentally validated design approach is used to provide uniformly highly efficient capture probe arrays for any target. Every probe is extensively screened against potential binding to any off-targets in the transcriptome of interest to ensure superb probe specificity.

Downstream application agnostic:

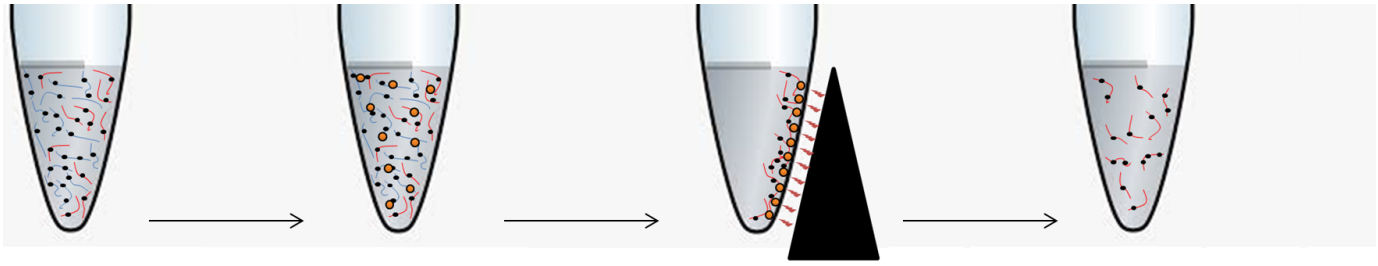
The enrichment method is downstream application agnostic and the proteins co-captured with the target RNA can be subjected to analysis with various methods, including:

- Mass spectrometry
- Western blotting
- Silver staining on a protein gel

Compared to classic biotinylated probe-based approaches, MagIC Beads provide multiple benefits:

No probe design burden:	Reliable arrays of capture probes are designed by ElementZero Biolabs for any target
Reliable performance: **No need for RNA fragmentation**	Efficient capture regardless of the target length or the presence of secondary structures
No sequence capture biases:	Full length target transcripts are captured, including fragments of the target not covered by probes
No chromatin fragmentation needed: sonication or DNases not necessary	Full length genomic DNA is not co-captured by the beads
Reduced experimental background due to stringent capture conditions:	Reduced capture of non-target transcripts and molecules not cross-linked to the target transcript
No background from naturally biotinylated molecules:	MagIC Beads do not capture non-target biotinylated molecules from the sample
Significantly lower costs:	RNase inhibitors, DNases, streptavidin beads or additional buffers are not required
Preserved target integrity:	During the enrichment, nucleases are inactivated by the buffers (no need for RNase inhibitors)
Fast and simple workflow:	The enrichment procedure can be completed in about 2h with a reduced number of hands-on steps
No need for additional key components of the experimental setup:	MagIC Beads enrichment kits are provided as complete, out of the box solution
Expert support:	Count on active support regarding the use of the kit as well as analysis planned downstream applications

A simple and fast workflow for RNA enrichment



Lysate of cross-linked cells is incubated with MagIC Beads

DNA probes present on beads surface bind target RNA-protein complexes, particles are concentrated with a magnet and washed

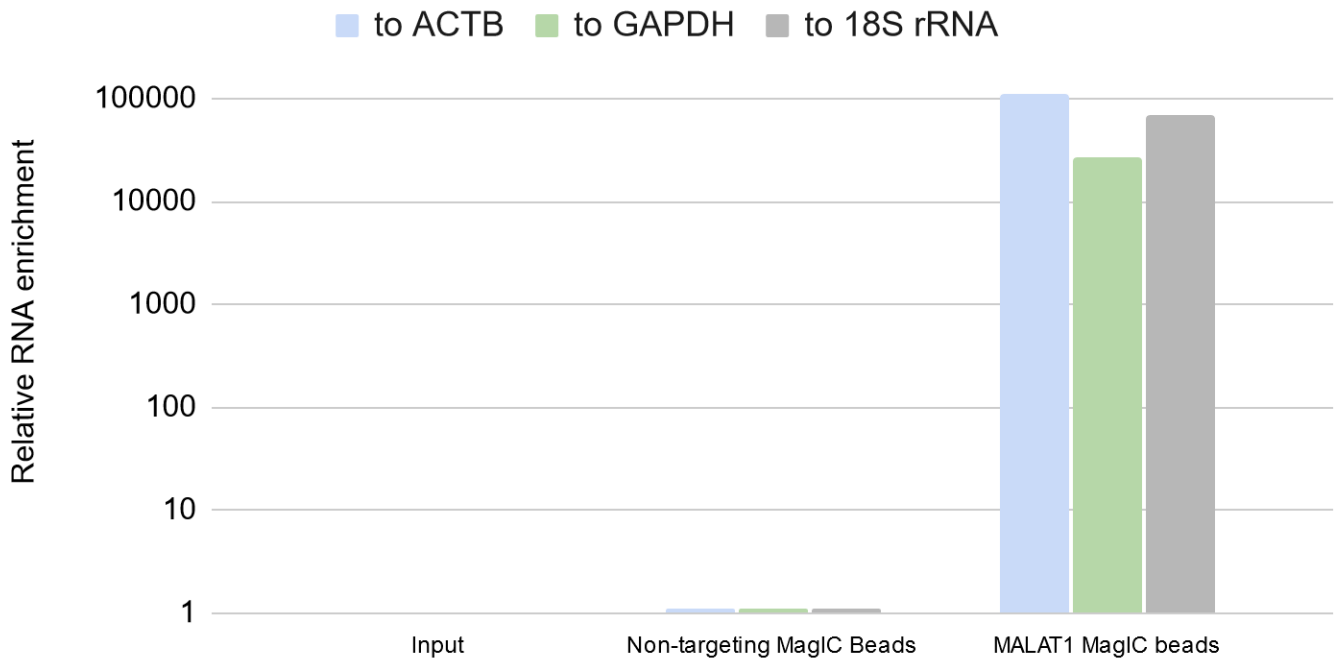
Captured RNA-protein complexes are eluted and beads are removed from the sample

Captured RNA-protein complexes are ready for downstream processing and analysis

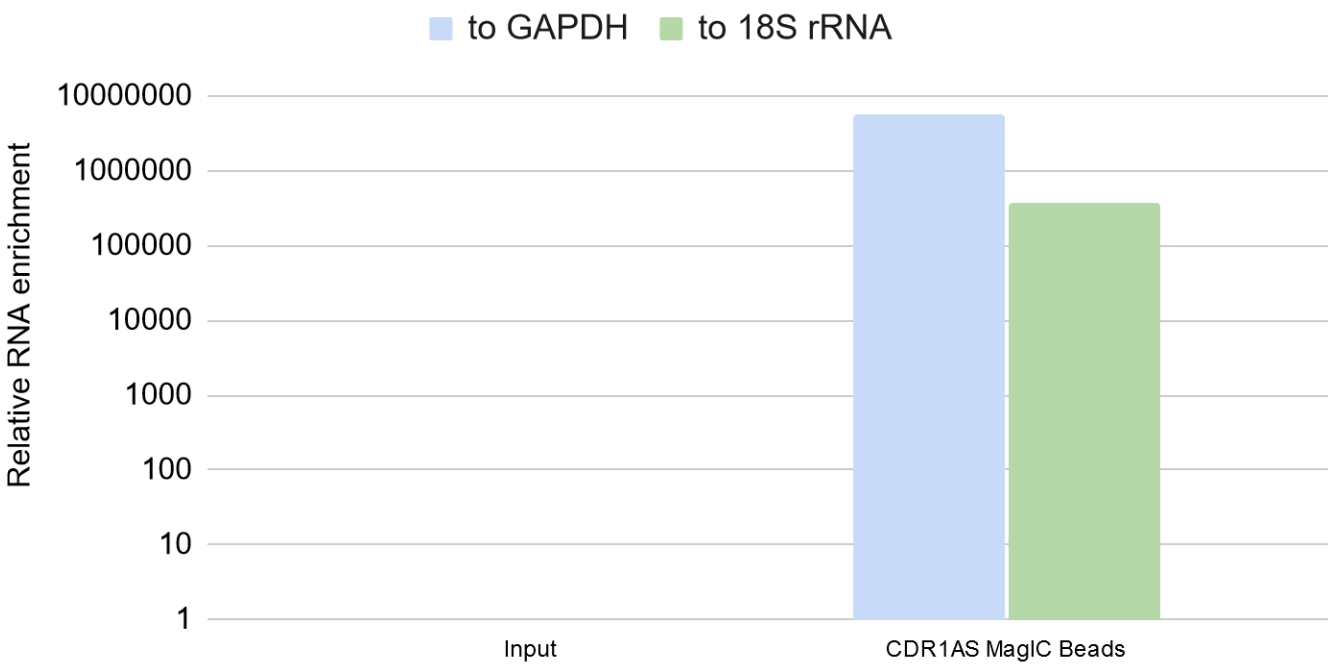
Additional information:

- Supplied with beads, lysis, hybridization and wash buffers.
- Shipping condition: room temperature.
- Storage temperature: 4°C.
- Durability: 36 months from date of manufacture.

Unique performance



Lysates of UV cross-lined HEK293 cells were incubated with non-targeting or MALAT1 targeting MagIC Beads. RNA-protein complexes attached to the beads were washed and eluted. RNA was isolated and subjected to cDNA synthesis. Levels of MALAT1, ACTB, GAPDH and 18S rRNA were measured in the input and enriched samples with RT-qPCR. The target RNA was enriched from over 10.000 to over 100.000 fold over non-target transcripts by MALAT1 targeting MagIC Beads, but not by the non-targeting beads.



Lysates of UV cross-linked mouse brains were incubated with CDR1AS targeting MagIC Beads. RNA-protein complexes attached to the beads were washed and eluted. RNA was isolated and subjected to cDNA synthesis. Levels of CDR1AS, GAPDH and 18S rRNA were measured in the input and enriched samples with RT-qPCR. The target RNA was enriched from over 100.000 to over 1.000.000 fold over non-target transcripts by CDR1AS targeting MagIC Beads.

DNA Seq MagIC Beads

Targeted DNA enrichment

DNA
MagIC Beads

Save on sequencing costs:

The targeted capture of specific DNA segments of interest can be used to bring a better resolution on them in the downstream analysis by sequencing. The ability to enrich specific DNA segments can simplify the sequencing experiments and reduce their overall costs, saving sequencing depth from being spent on inherently uninteresting portions of the genome.

Standardized capture of long DNA fragments - tens of kilobases:

MagIC Beads for DNA enrichment provide the first standardized solution for the capture of any sequence of interest from samples of long DNA fragments. Whether for targeted sequencing or for any other downstream application the unique properties of MagIC Beads DNA enrichment kits offer exceptional value.

MagIC Beads for DNA enrichment are particularly useful for those experiments that can be benefited by bringing the resolution of the sequencing to specific, long segments of the genome. This can be especially valuable in the studies of:

- DNA epigenetic modifications
- Chromosomal rearrangements
- Genome integration sites (viruses, transposons, genetic engineering etc.)
- Detection of mutations
- … and more

The ability of MagIC Beads to capture DNA segments up to tens of kilobases in length makes them especially attractive when used in combination with sequencing technologies capable of producing long reads. This is particularly pronounced in the case of amplification free sequencing with Oxford Nanopore sequencing, where the relatively low number of reads produced by the platform makes the genome wide applications challenging.

Capture up to 60% of target sequences from the input sample:

The kits consist of the target-specific MagIC Beads and sets of optimized buffers. They feature standardized capture conditions and capture probes properties, which ensure uniformly high efficiency of the system on varying DNA targets, independently of their length. The beads provide very high target enrichment levels, at the same time being able to capture up to 60% of the double stranded target sequences from the input sample.

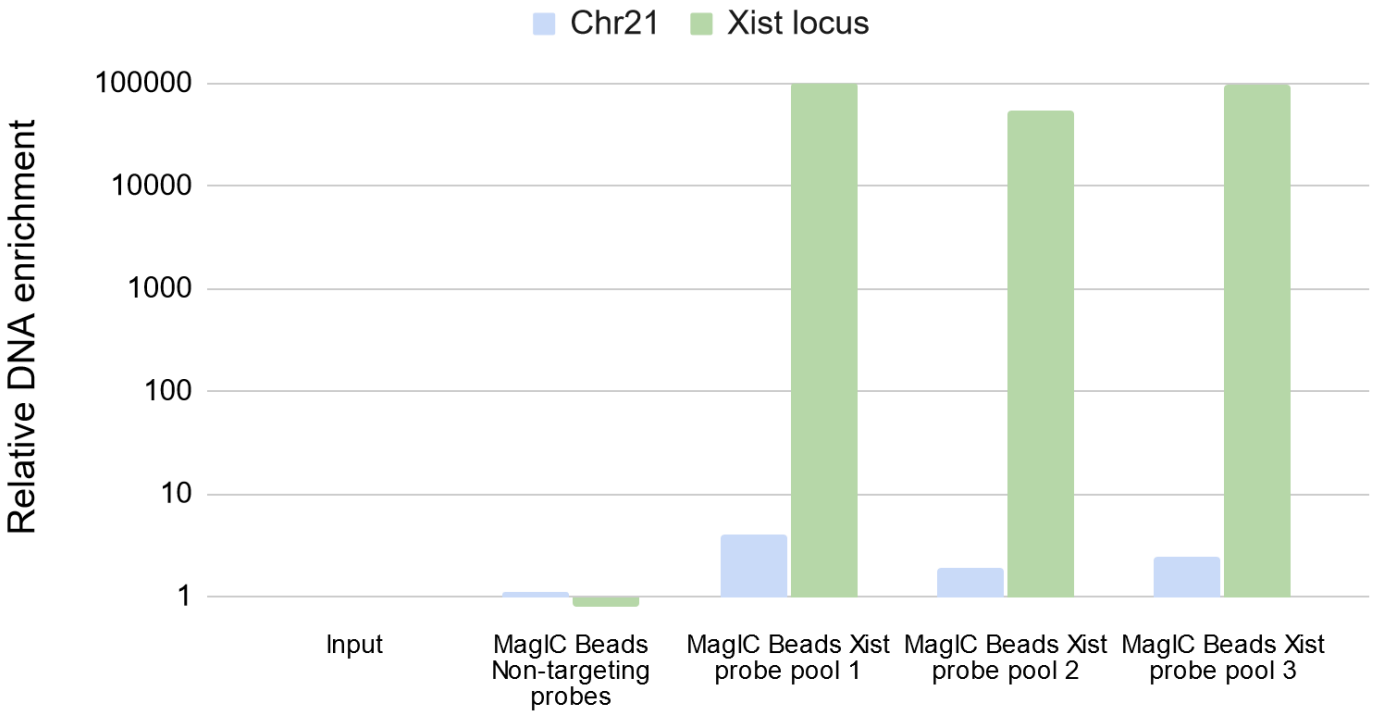
Efficiency guaranteed by design

For any custom DNA target only the information on 1-2kb of the sequence is necessary for efficient capture of tens kb long genomic segments. The optimal number of probes is established based on the target length and nucleotide composition. Experimentally validated design approach is used to provide uniformly highly efficient capture probe arrays for any target sequence. Every probe is extensively screened against potential binding to any off-targets in the genome of interest to ensure superb probe specificity.

Compared to classic targeted DNA sequencing approaches, MagIC Beads provide multiple benefits:

No comprehensive knowledge of the target sequence required:	Targeting a 1-2kb long sequence of a large DNA target (10kb+) for the capture results in efficient capture of the full length target
Reliable capture of long sequences, prior to preparation of the seq library:	Efficient capture regardless of the target length or the presence of secondary structures
Fast and simple protocol:	The enrichment procedure can be completed in 1-2h with a reduced number of hands-on steps
No need for additional key components of the experimental setup:	MagIC Beads enrichment kits are provided as complete, out of the box solution
Expert support:	Count on active support regarding the use of the kit as well as analysis planned downstream applications

Unmatched enrichment levels



Samples of genomic DNA from HEK293 cells fragmented by sonication to the size fraction of ~10-30kb were incubated with MagIC Beads carrying non-targeting probes or different pools of capture probes designed to target Xist locus (pre-incubation at 94°C, followed by incubation at the hybridization temperature). DNA attached to the beads was washed, eluted and subjected to qPCR analysis. Levels of chromosomes 11, 12, 21, 22 and X were measured using multiple primer pairs per chromosome with qPCR. All of the targeting MagIC Beads enriched the Xist locus close to 100 000 fold over the non-target DNA segments, but not the assayed region of the chromosome 21.

MagIC Beads

The technology behind our Targeted Nucleic Acids Capture

RNA
MagIC Beads

DNA
MagIC Beads

Magnetic **I**nstant **C**apture **Beads** (MagIC Beads) based systems offer unmatched effi ciency in hybridization-based, sequence-specifi c capture of nucleic acids for various research use cases.

MagIC Beads are an interesting alternative to classic approaches that utilize a combination of biotinylated oligonucleotide probes and streptavidin-coated beads for the enrichment of nucleic acids.

One technology – multiple use cases

RNA-protein interactions

- Mass-spectrometry
- Western blotting
- Silver staining on a protein gel

RNA enrichment

- RNA-RNA interactions
- RNA modifications
- Alternative polydenylation
- Alternative splicing
- Alternative transcription start sites
- Native elongating transcript sequencing (NET-seq)

DNA enrichment

- DNA epigenetic modifications
- Chromosomal rearrangements
- Genome integration sites (viruses, transposons, genetic engineering etc.)
- Detection of mutations

The Beads

DNA probes covalently attached to the beads:

The beads are produced through a novel approach of direct synthesis of DNA capture probes on the surface of functionalized magnetic nanoparticles. The synthesis reaction produces a high number of oligonucleotide chains, which are covalently attached to the surface of the particles through their 5′ ends.

Arrays of probes with different sequences on a single population of the particles:

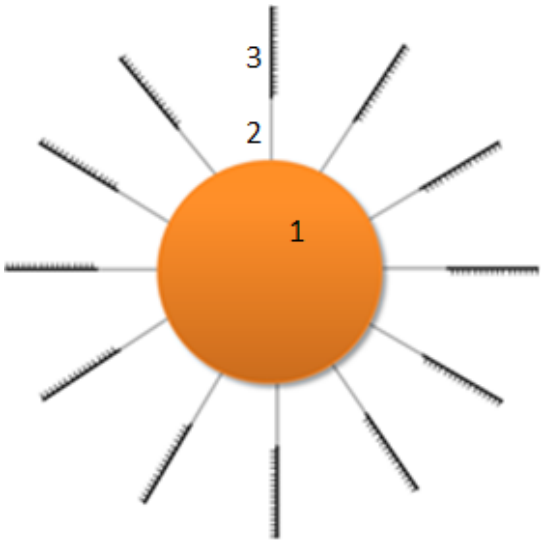
The process allows for the simultaneous, unbiased synthesis of complex arrays of capture probes with different sequences on a single population of the particles. All of the probes from the array are present on the surface of each particle in a 1:1 ratio.

Bind to multiple regions of a target:

The beads developed for the capture of a specific sequence carry an array of different probe sequences which target multiple regions of the same target DNA or RNA molecule. The fact that those unique probes are clustered together in close proximity to one another allows them to act in synergy in binding the target (hybridization of a single probe brings the target within close proximity to other capture probes). This effect leads to rapid and stable binding of the beads to the target molecules and provides a marked advantage over approaches using arrays of biotinylated capture probes in which no probe synergy is observed.

No steric hindrance effect – long molecular linker:

The proprietary functional modification of the particles also provides an exceptionally long molecular linker, which provides an appropriate distance between the surface of the particles and the sequence of the capture probes. This property eliminates the steric hindrance effect, which is known to have the potential of interfering with the ability of the capture probe to correctly hybridize with its complementary sequence.



Graphical representation of the MagIC Bead design:

1 - Magnetic particle.
2 - Long molecular linker.
3 - Capture probe sequences. The capture probes attached to the bead surface can represent any number of unique sequences, which are evenly spread and represented on the beads at equal ratios to one another.

The Probes

We design the probes for you:

MagIC Beads based systems are supplied with the capture probes designed by ElementZero Biolabs, relieving the researchers from the burden of having to design their own capture probes. The probe design strategy has been optimized for the unique properties of the system, it ensures full compatibility with the bead and buffer design provided by the company.

ElementZero Biolabs offers its wealth of experience providing arrays of efficient capture probes screened and selected against potential off-target binding in any organism with annotated genome and/or transcriptome for any sequence of interest.

High specificity, precise capture – 25-40nt probes:

The probes present in each array provided by ElementZero have varying lengths (typically 25-40nt) but have a strict, standardized GC content, hybridization temperature, and specificity towards the intended target for ensuring optimal performance in various experimental setups.

The Buffers

Optimized for each use case:

MagIC Beads based kits are provided with buffers specifically optimized for various use cases, ensuring optimal efficiency and specificity in different aims and environments of the capture.

In classic workflows utilizing biotinylated oligonucleotides in combination with streptavidin beads, the environment of the capture reaction has to allow for the stable binding of biotin to streptavidin. This limits the possibility of applying the conditions which would be particularly beneficial for the capture from the perspective of probe hybridization.

The best conditions for the capture of unfragmented nucleic acids

Traditional workflows:

- **Salt concentration impairs the hybridisation of the target sequences to capture probes:** Salt concentration has to be high enough to preserve the stability of biotin-streptavidin interactions in elevated temperatures. Buffers with high salt concentration are used (500 mM or more), leading to the stabilization of secondary structures formed by potential nucleic acid targets, in turn preventing the hybridization of the target sequences to the capture probes, rendering the system unreliable for the capture of highly structured or long, unfragmented transcripts and DNA segments.
- **Low concentration of chaotropic agents increases unspecific probe binding:** Chaotropic agents can disrupt the biotin-strepavidin interactions. High concentrations of chaotropic agents, however, have beneficial properties for the regulation of nucleic acids base pairing. Certain agents can regulate the temperature in which probes will hybridize to the complementary sequences and help disrupt the hybridization between sequences with imperfect complementarity, resulting in a reduction of the binding of the probes to the off-target sequences.
- **Low concentration of denaturing agents that preserve the integrity of target nucleic acid:** The high concentration of denaturing agents in the buffers in combination with other buffer components can ensure a deactivation of nucleases, thus ensuring the integrity of assayed nucleic acids throughout the process of the target capture. Denaturing agents also help ensure full disruption of protein-nucleic acid interactions, which are undesirable in some experimental setups.

With MagIC Beads:

- **Low salt concentration - capture unfragmented nucleic acids:** Employs buffers with relatively low salt concentration, to allow in combination with other buffer components for reliable capture of unfragmented nucleic acid targets independently of their length or secondary structure.
- **Optimized concentrations of chaotropic agents:** Buffers supplied with MagIC Beads contain well-optimized concentrations of chaotropic agents, utilizing their properties to provide superb probe hybridization specificity and efficiency.
- **Leverage the benefits of denaturing factors:** MagIC Buffers contain optimized concentrations of denaturing factors. As a result, MagIC Beads based kits do not require the use of nuclease inhibitors in capture reactions (DNase and RNase inhibition is provided by the composition of the buffers) and allow for the capture of target nucleic acids free from other types of molecules.