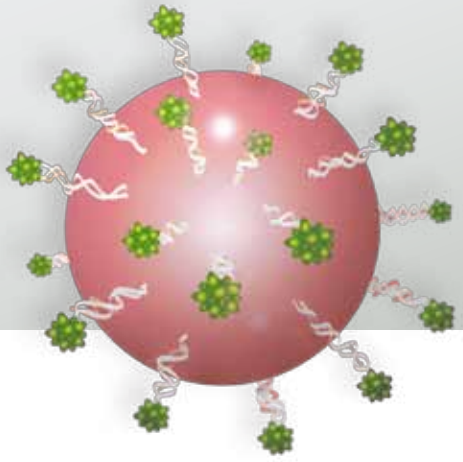
TECHNICAL NOTE

BACs-on-Beads™

Molecular karyotyping



Available in EU countries and Australia. Unavailable in non-listed countries.

Fast and targeted molecular karyotyping with new, revolutionary PerkinElmer technology BACs-on-Beads™

From arrays to assays

With nearly 100 PCR-amplified BAC clones attached to color-coded Luminex® beads, PerkinElmer's proprietary BACs-on-Beads technology enables molecular karyotyping in a well.

Results in less than 24 hours from minute DNA amounts

Replacing the standard microarray solid phase with beads enables fast results from minute DNA amounts.

No dye swaps or mismatched references

Both sample and references are labeled with biotin which in turn binds a phycoerythrin reporter for signal generation. With both male and female references included in every analysis no prior knowledge of the sex of the sample is needed.

THE POWER INSIDE xMAP TECHNOLOGY

PerkinElmer® For the Better

BACs-on-Beads™ Basics

BACs and Beads in BACs-on-Beads

BACs are Bacterial Artificial Chromosomes, large cloned sequences of human DNA, typically 170,000 bases long. BACs have long been used for fluorescent in situ hybridization (FISH). BACs-on-Beads is a technology where DNA probes generated from selected BACs are immobilized onto Luminex® encoded beads. The resulting bead sets are used to assay for chromosomal gains and losses from minute sample amounts with high throughput.

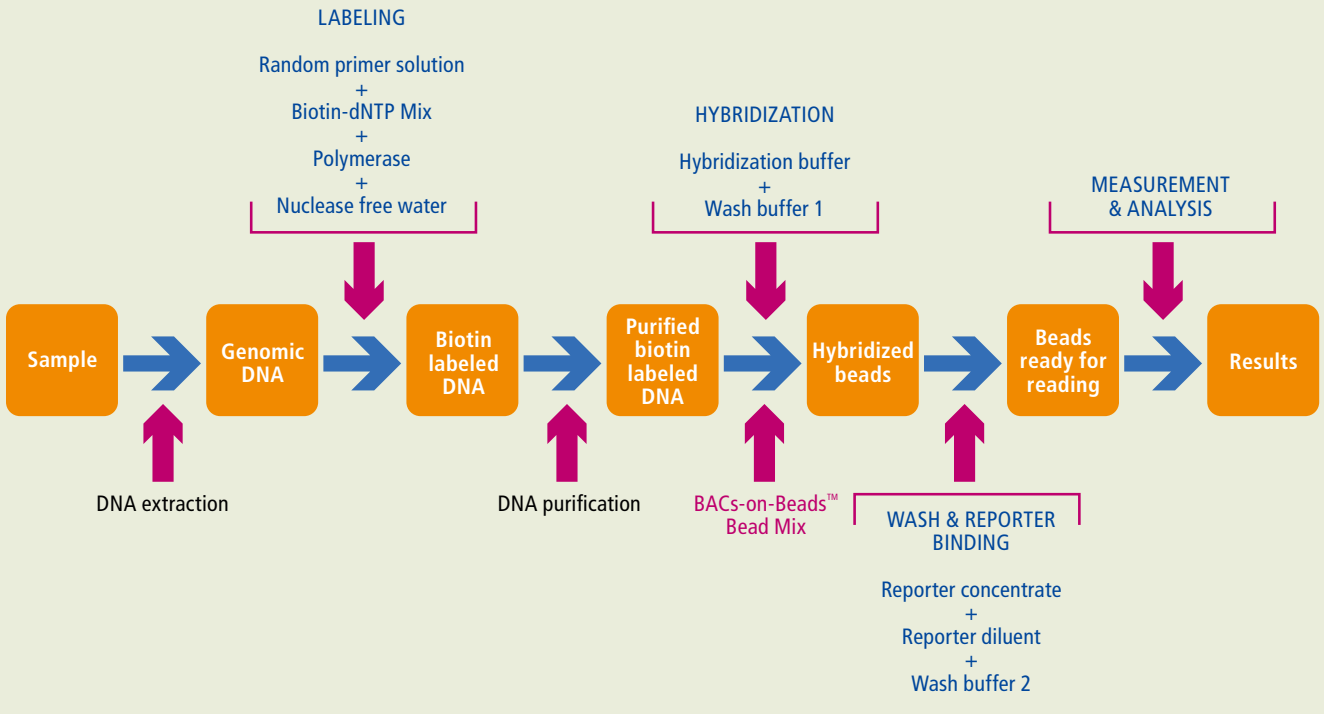
A BACs-on-Beads bead set can contain up to 98 different BACs-on-Beads probes targeted to various regions of the human genome. In addition 2 non-homologous oligonucleotide beads are used for background subtraction.

From Sample to Result with BACs-on-Beads

Sample and reference DNAs are enzymatically labeled with biotin. The enzymatic labeling step provides significant amplification of the sample and therefore small DNA amounts can be used as input.

BACs-on-Beads analysis comprises hybridization of the purified biotin labeled DNA to BACs-on-Beads probes representing the specific targeted sequences. Post hybridization a fluorescent streptavidin-phycoerythrin reporter is added and bound to the biotin labels. The relative amount of fluorescent DNA bound to the beads is determined using a Luminex instrument system and BoBsoft™ analysis software.

BoBsoft performs normalization of data measured from each sample with respect to data from the male and female references. All samples are compared to both male and female references, so the sex of the sample does not need to be known prior to the assay. Normal diploid loci generate ratios of 1.0. Single copy gains generate ratios of 1.3 to 1.4, and single-allele deletions generate ratios of 0.6 to 0.8. Reliability in the result is achieved by having carefully selected the probes used as well as by having several probes covering a chromosomal region generally deflecting together if a gain or loss has occurred in this region.



BACs-on-Beads workflow

For fast, precise and cost-effective molecular karyotyping

- **Results in less than 24 hours**

  Complete procedure from sample to result takes less than 24 hours, allowing your laboratory to provide results the following day.

- **Quick and easy implementation**

  All main reagents needed to perform BACs-on-Beads are provided in a single kit with easy to learn protocols. Both male and female references are included in every run to enable both sex-mismatch and sex-match interpretation of the results.

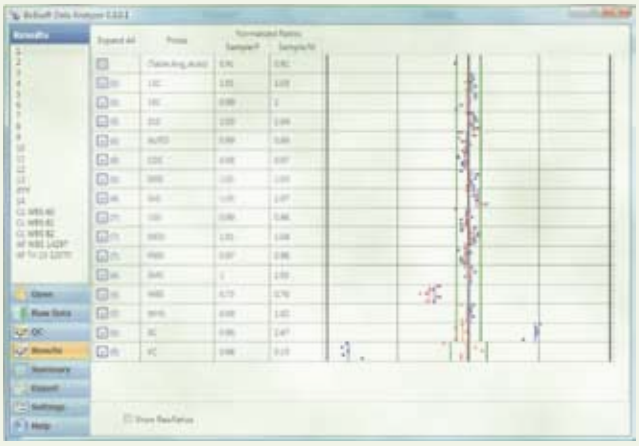
- **Cost-efficiency**

  Tens of samples can be run simultaneously and this very simple procedure really reduces the hands-on time required.

- **Easy interpretation**

  With excellent coverage of each target region, both male and female references and the intuitive BoBsoft* analysis software results are always clear and easy to interpret.

Work-module	Hands-on time	Total time
Labeling	45 min	1 hr 40 min
Purification	35 min	35 min
Hybridization setup	25 min	25 min
Hybridization incubation	–	16 hrs (o/n)
Wash + Reporter addition	30 min	50 min
Result generation	15 min	30 min
Total procedure	2 hrs 30 min	20 hrs



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