**iScan System**

**Equipment:** iScan System Illumina

**No. of Equipment: IEM5**

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**Equipment Description**

**Description of equipment:**

The iScan System is a laser-based, high-resolution optical imaging system that can rapidly scan and collect large volumes of data from Illumina DNA analysis and RNA analysis high‐density BeadChips.

Specifications and technical features:

iScan Reader

Instrument computer workstation installed with iScan Control Software (ICS) BeadChip carrier

*iScan Reader* placed on air table is loaded by one BeadChip carrier with up to four BeadChips with specific barcode for automatic identification.

Average scan time per sample (HumanOmni2.5-8 BeadChip) is 11.4 minutes

Pixel resolution: 0.53 m

Laser excitation: 532 nm and 658 nm dual-laser excitation

*Instrument control computer* with installed iScan Control Software (ICS) allows controlling the iScan Reader during BeadChip scanning.

Instrument control computer hardware specifications:

2 permanent separated drives (C: and D:) on the computer

Removable drive (H:)

*iScan Control Software (ICS)* provides:

Loading BeadChips

Acquiring images

Automatically registering and extracting images

Organizing and viewing the acquired images

**Specification of expertise relevant to NanoEnviCz workpackages:**

**WP3**a,d,f,g,h, **WP4**a,b, **WP6**a,d, **WP7**a,c,e,h,i, **WP9**a,b,c,d

**Detailed description of expertise**

**Please, specify the main research topics connected with equipment**:

**Gene expression analysis**

Gene expression arrays provide insight into gene activity within cells. HumanHT-12 v4 Expression BeadChip Arrays provide a coverage for more than 47,000 transcripts and known splice variants across the human transcriptome. Overall, gene expression analysis makes accurate measurements of cellular response to nanoparticle exposure.

**Methylation analysis**

DNA methylation is important in regulating gene expression. Specialized MethylationEPIC BeadChips are used to identify more than 850,000 methylation sites in genome and by this array it is possible to identify changes in gene regulation.

**Please, specify the secondary research topics connected with equipment**:

**Genotyping**

Genotyping enables researchers to explore the underlying genetic variants, including single nucleotide polymorphisms (SNPs) and large structural changes in DNA induced by nanoparticles.

Genomic microarrays enable to identify genetic variants including single nucleotide polymorphism (SNPs) induced by nanoparticles. It provides deeper understanding of molecular effect of nanoparticles.

**Keywords describing research area:**

Biological effects of nanomaterials, genotoxicity of nanomaterials, gene expression analysis, methylation analysis

**Competence**

**Relevance for applied and industrial research:**

Systems toxicology using functional genomic strategies is required for the risk assessment of health and environmental impacts of existing and newly synthesized engineered nanomaterials. The integrated and systemic approach involving toxico-genomics, toxico-proteomics and toxico-metabolomics is valuable in the identification and characterization of the mode of action of nanomaterials as well as for the development of predictive structure-activity relationships. The iScan system enables to carry out a broad portfolio of innovative genetic analysis assays for genotyping, CNV analysis, DNA methylation, and gene expression profiling thus providing a robust and cost-effective tool to evaluate nanomaterial toxicity.

The data driven from systems toxicology are valuable in the identification and characterization of the mode of action of nanomaterials

**Relevance for fundamental studies:**

The molecular mechanism of in vivo and in vitro system exposed to nanomaterials Parallel toxico-genomic technologies promote a platform for the development of biomarkers, in order to predict possible nanomaterial’s toxicity.

Toxico-genomic tools include following assays:

The measurement of gene-expression levels to reveal a “genetic fingerprinting”, a unique pattern of gene expression changes

DNA methylation to reflect epigenetic changes upon exposure to nanomaterials can not only provide information about the mechanism of action of nanomaterials, but also from the pattern of gene expression changes it elicits in vitro and in vivo