Technology Offer

Methods of analysis of composition of nucleic acid mixture

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A novel NGS library preparation techniques allowing cheap and reproducible transcriptome analysis of samples with both abundant and rare components, making these techniques very useful in clinical diagnostics as well as biodiversity analysis.

Background

Next-Generation Sequencing (NGS) is a powerful technology used in a wide variety of applications. When NGS is used for the analysis of composition of nucleic acid mixtures with a large dynamic range of concentrations of individual components, the reliability of results significantly differs for abundant and rare components. This is a common problem for example for studying transcriptomes and for analysis of biodiversity.
In expression profiling studies, in order to characterize low-expressed genes it is necessary to over- sequence highly expressed ones, while the more sequencing reads correspond to a particular transcript, the more reliably its expression level is determined. But this increases the cost of the analysis. It would be more attractive to reduce the number of sequencing reads corresponding to abundant transcripts. In this case the reliability of the analysis of rare transcripts would increase without altering the price of the analysis. Although several methods have been proposed to prepare normalised libraries, they have certain restrictions: mainly, normalization effect is not controllable and has limited reproducibility.

Technology

In this invention, the researchers from the Max-Planck-Institute for Molecular Genetics suggest an approach, called Controllable Oligonucleotide-Based Ratio Adjustment (COBRA), which allows adjusting the reliability of results individually for each component of the nucleic acid mixture in a predictable and reproducible manner. The strategy uses locus-specific oligonucleotides to change the relative abundance of individual components of nucleic acid mixture before sequencing.

The inventors suggest three methods for reproducible and predictable regulation of abundance of sequencing library molecules correspondent to different components of nucleic acid mixture:

1. Selection of different number of detectable loci for different components of nucleic acid mixture;
2. Combining of loci in several groups according to a desirable “abundance change factor” and using of different library-preparation protocols for different groups;
3. Using a mixture of “functional” / “blocked” oligonucleotides to adjust “abundance change factor” individually for each detectable locus.

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The COBRA methods are especially useful for routine analysis of biodiversity and routine expression profiling, like for clinical studies.

We are now looking for a licensing partner for this promising technology.

Patent Information

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