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Press Release:

Global Genomics announces improved version of tangerine[®] gene expression profiling database covering 168 000 human transcripts

Global GenomicsSM AB (Stockholm, Sweden) announced today the availability of an improved version of its tangerine[®] whole-genome expression profiling technology, substantially increasing coverage of the human, mouse and rat transcriptomes.

By assembling transcriptomes much like genomes are assembled from individual sequence reads, researchers at Global Genomics were able to discover novel splice variants and alternative polyadenylation sites, as well as to correct sequencing errors in publically available mRNA sequences.

- Although the number of genes has been revised downwards several times, most recently to about 22 000, much of the complexity of mammalian genomes is produced by alternative splicing and alternative polyadenylation, said CTO Sten Linnarsson. Our latest assembly of the human transcriptome contains well over 168 000 different transcripts, all derived from experimental data.

- The new transcriptome assemblies represent a significant step forward for tangerine gene expression profiling. We believe that microarray manufacturers seeking to improve the scope and accuracy of their probe sets would benefit from these same features – sequence error correction, splice variant assembly and the mapping of alternative polyadenylation, said CEO Ulf Boberg.

The mouse transcriptome (103 000 transcripts) is available immediately for expression profiling using Global Genomics' tangerine technology. The human (168 000) and rat (43 000) transcriptomes will be commercially available soon.

About Global Genomics

Global Genomics develops and out-licenses innovative tools in functional genomics that provide unique insight into healthy, diseased or drug-treated cells. The company's expertise in advanced molecular biology techniques and computational analysis has resulted in the recent launch of tangerine[®] gene expression profiling, a proprietary solution that reveals a whole genome expression profile in a single experiment.

High coverage and sensitivity ensure complete profiles of expressed genes, giving researchers the ability to study gene regulation in any disease or eukaryotic model, since there is no prerequisite for sequence data. The tangerine technology is based on PCR, capillary electrophoresis, proprietary databases and algorithms that generate gene expression profiles. Incorporating such comprehensive gene expression profiling at key stages in drug discovery significantly improves selection of targets and lead compounds, leading to well-validated drug candidates and expediting development of a strong pharmaceuticals portfolio.

Questions regarding this press release or other issues should be directed to Dr. Sten Linnarsson, Chief Technology Officer, +46 8 50 88 47 18 or Ms. Erika Johnson, Chief Financial Officer, +46 8 50 88 47 03 or Mr. Martin Vidaeus, Manager Market Development, +46 8 50 88 47 29.

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