Recent patent applications in differential gene expression

Patent number	Description	Assignee	Inventor	Priority application date	Publication date
US20140128291A1	An oligonucleotide comprising a first segment at a 5′ end and a second segment at a 3′ end, where the first segment hybridizes with a first nucleotide adaptor molecule, and the second segment hybridizes with a second nucleotide adaptor molecule. Useful for simplifying the process of library preparation for RNA sequencing, gene expression profiling, microarray and other applications.	Life Technologies (Carlsbad, CA, USA)	Gu J, Bramlett K, Burnett C	4/16/2012	5/8/2014
JP05466237B2	Systems and methods for analyzing data generated by expression arrays. The method involves receiving microarray data representing probe pairs for a single microarray, determining differences between intensities of perfect match probes and intensities of mismatched probes for each probe pair, determining a difference signal based on the determined differences, scaling the difference signal to produce an expression signal, and normalizing the expression signal based on a theoretical distribution at the unit level to produce a normalized expression signal for single microarray that is independent of other microarrays.	Hoffmann La Roche (Basel)	–	10/13/2008	4/9/2014
US20140024547A1	Evaluating the presence of colon cancer in a subject based on a subject's sample that provides a source of RNAs comprises: (i) determining a quantitative measure of the amount of at least one constituent of the constituents in Tables 1–5 of the specification as a distinct RNA constituent in the subject sample; and (ii) comparing the quantitative measure of the constituent in the subject's sample to a reference value.	GeneNews (Richmond Hill, CA, USA)	Bankaitis-Davis DM, Siconolfi L, Storm K, Wassmann K	11/13/2006	1/23/2014
US20130338025A1	Searching a pathway database using genes in the genome-wide gene expression profiling as an index to find pathways. Screened pathways are identified for have statistical significance. The pathway sets are established according to the genes associated with the identified screened pathways. The biological information of the genes that are common to the screened pathways is determined in the pathway set for each of the pathway sets, and a network relationship among the screened pathways is determined.	National Chung Cheng University (Minxiong, Taiwan)	–	5/24/2012	12/1/2013
AU2007317753B2	Inhibiting pathological angiogenesis in a subject comprises administering to the subject a therapeutic amount of a composition, where the composition comprises a specific binding agent that preferentially binds to one or more pathological angiogenesis marker proteins comprising Vscp, CD276, ETSvg4 (Pea3), CD137(4-1BB), MiRP2, Ubiquitin D (Fat10), Doppel (prion-PLP), Apelin, Plgf, Ptprn (IA-2), CD109, Ankylosis, and collagen VIII 1, thus inhibiting pathological angiogenesis in the subject.	US Department of Health and Human Services (Washington, DC, USA)	St. Croix B, Seaman S	11/9/2006	11/7/2013
US20130244900A1	Use of gene expression profiling in primary ovarian serous papillary tumors and normal ovarian epithelium for detecting and treating ovarian serous papillary carcinoma.	Santin AD	Santin AD	6/9/2003	9/19/2013
US20130210013A1	Contacting a nucleic acid sample in a reaction vessel with a set of pairs of oligonucleotide primers and subjecting the mixture resulting from the contacting step to an amplification regimen comprising iterative cycles of nucleic acid strand separation, oligonucleotide primer annealing and polymerase extension of annealed primers in the presence of a fluorescent label, which is incorporated into products generated in the amplification regimen. Each pair of oligonucleotide primers comprises a first oligonucleotide primer.	PrimeraDx (Mansfield, MA, USA), Slepnev VI	Slepnev VI	4/12/2002	8/15/2013
US20130165369A1	Identifying genes that are overexpressed in adipose tissue as compared to nonadipose tissue, comprising performing differential gene expression analysis between the white adipose tissue or stromal vascular tissue from any two different mice, such as wild-type, HMGI-C –/–, ob/ob or HMGI-C –/– ob/ob genotype mice.	HMGene (New York), Chada KK, Chouinard R, Ashar H, Sayed A	Chada KK, Chouinard R, Ashar H, Sayed A	7/29/2002	6/27/2013
US8435739B2	A method for analyzing expressed RNA from cells of a deparaffinized, formalin-fixed, paraffin embedded (FFPE) sample, involving synthesizing first cDNA strands using a primer comprising a sequence complementary to RNA extracted from the cells of the deparaffinized FFPE sample, amplifying the cDNA strands to produce amplified molecules, binding the amplified molecules to a solid support, and producing signals from the bound molecules, where the signals reflect expressed RNA in the cells.	Life Technologies (Carlsbad, CA, USA), Erlander MG, Salunga RC	Erlander MG, Salunga RC	10/11/2002	5/7/2013

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