Title of the Invention: Massively parallel single cell analysis

Abstract Title: Massively parallel single cell analysis

The disclosure provides for methods, compositions, and kits for multiplex nucleic acid analysis of single cells. The methods, compositions and systems may be used for massively parallel single cell sequencing. The methods, compositions and systems may be used to analyze thousands of cells concurrently. The thousands of cells may comprise a mixed population of cells (e.g., cells of different types or subtypes, different sizes).
(56) Documents Cited:
G. MIKE MAKRIGIORGOS ET AL: “A PCR-based amplification method retaining the quantitative difference between two complex genomes” NATURE BIOTECHNOLOGY, vol. 20, no. 9, 1 September 2002 (2002-09-01), pages 836-839, XP055023044, ISSN: 1087-0156, DOI: 10.1038/nbt24the whole document
TANG FUCHOU ET AL: “RNA-Seq analysis to capture the transcriptome landscape of a single cell” NATURE PROTOCOLS, NATURE PUBLISHING GROUP, GB, vol. 5, no. 3, 1 March 2010 (2010-03-01), pages 516-535, XP009162232, ISSN: 1750-2799 the whole document
Genomics 98 (2011) 266-271 Fox-Walsh et al “A multiplex RNA-seq strategy to profile poly(A+) RNA: Application to analysis of transcription response and 3’ end formation”

(58) Field of Search:
INT CL C12Q
Other: EPO-Internal, BIOSIS, MEDLINE, EMBASE, WPI
Data