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- (71) Applicant (for all designated States except US): **FOUNDATION MEDICINE, INC.** [US/US]; One Kendall Square, Suite B6501, Cambridge, MA 02139 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **DOWNING, Sean, R.** [US/US]; 236 Forest Street, Methuen, MA 01844 (US).

JAROSZ, Mirna [US/US]; 38 Kimball Road, Arlington, MA 02474 (US). **LIPSON, Doron** [IL/US]; 142 Middlesex Road, #1, Chestnut Hill, MA 02467 (US). **OTTO, Geoffrey, Alan** [US/US]; 114 Saint Paul Street, Apt.3, Brookline, MA 02446 (US). **PARKER, Alexander, N.** [US/US]; 35 Elgin Street, West Roxbury, MA 02132-3320 (US). **SHAPIRO, Mikhail, G.** [US/US]; 855 Folsom St., #916, San Francisco, CA 94107 (US). **STEPHENS, Philip, James** [GB/US]; 5112 Lexington Ridge Drive, Lexington, MA 02421 (US). **YELENSKY, Roman** [US/US]; 514 Lowell Avenue, Newton, MA 02460 (US).

(74) Agent: **COLLAZO, Diana, M.**; Lando & Anastasi LLP, Riverfront Office Park, One Main Street, Suite 1100, Cambridge, MA 02142 (US).

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(54) Title: OPTIMIZATION OF MULTIGENE ANALYSIS OF TUMOR SAMPLES

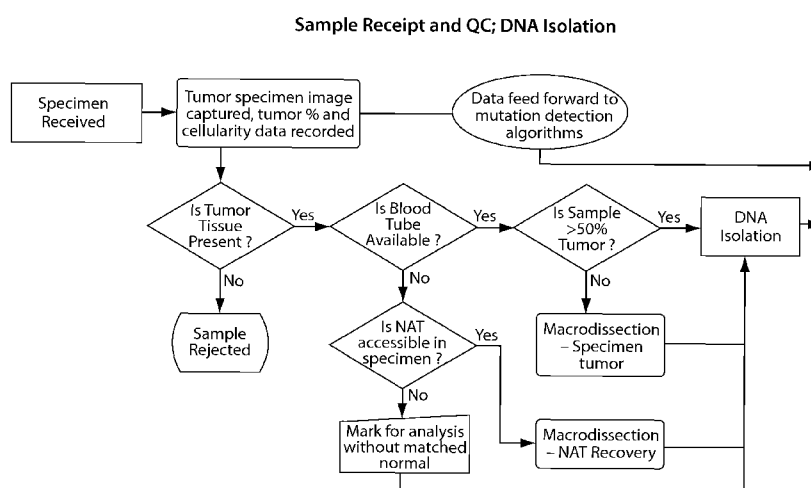


Fig. 1A

(57) Abstract: A method of analyzing a tumor sample includes acquiring a library comprising a plurality of tumor members from the sample, contacting the library with a bait set to isolate selected members, acquiring a read for a sub-genomic interval from a selected member, aligning said read and assigning a nucleotide value (e.g., calling a mutation) from said read for a preselected nucleotide position



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