**Category and Function** Description **Returned class** Constructors MultiAssayExperiment Create a MultiAssayExperiment object MultiAssayExperiment ExperimentList Create an ExperimentList from a List or list ExperimentList Accessors colData Get or set data that describe patients / biological units DataFrame Get or set the list of experimental data objects as original classes experiments ExperimentList Get the list of experimental data numeric matrices assays SimpleList Get the first experimental data numeric matrix matrix, matrix-like assay sampleMap Get or set the map relating observations to subjects DataFrame metadata Get or set additional data descriptions list rownames Get row names for all experiments CharacterList colnames Get column names for all experiments CharacterList Subsetting mae[ i, j, k ] Get rows, columns, and/or experiments MultiAssayExperiment mae[ i, , ] i: GRanges, character, integer, logical, List, list MultiAssayExperiment MultiAssayExperiment mae[, j, ] j: character, integer, logical, List, list mae[,,k] k: character, integer, logical **MultiAssayExperiment** Get or set object of arbitrary class from experiments mae[[ n ]] (varies) mae[[ n ]] n: character, integer, logical mae\$column Get or set colData column vector (varies) Management complete.cases Identify subjects with complete data in all experiments vector (logical) duplicated replicated\* Identify subjects with replicate observations per experiment list of LogicalLists anyReplicated Displays whether there are any replicate observations in each assay vector (logical) Merge replicate observations within each experiment, using function MultiAssayExperiment mergeReplicates intersectRows Return features that are present for all experiments **MultiAssayExperiment** Return subjects with data available for all experiments MultiAssayExperiment intersectColumns prepMultiAssay Troubleshoot common problems when constructing main class list Reshaping Return a long and tidy DataFrame with optional colData columns DataFrame longFormat wideFormat Create a wide DataFrame, 1 row per subject DataFrame Combining С Concatenate an experiment to an existing MultiAssayExperiment MultiAssayExperiment

Table 1. Summary of the MultiAssayExperiment API (Ramos et al. Can. Res. 2017; DOI: 10.1158/0008-5472.CAN-17-0344)

*Note. assay* refers to a procedure for measuring the biochemical or immunological activity of a sample, e.g. RNA-seq, segmented copy number, and somatic mutation calls would be considered three different assays. *experiment* refers to the application of an assay to a set of samples. In general it is assumed that each experiment uses a different assay type, although an assay type may of course be repeated in different experiments. *mae* refers to a MultiAssayExperiment object. *subject* refers to patient, cell line, or other biological unit. *observation* refers to results of an assay, e.g. gene expression, somatic mutations, etc. *features* refer to measurements returned by the assays, labeled by row names or genomic ranges.

\* "duplicated" was deprecated in Bioconductor 3.7 and replaced by "replicated"