complementary to that of a target region of a nucleic acid molecule of interest (e.g., target nucleic acid molecule). A method may comprise hybridizing a first probe and a second probe to first and second target regions of the nucleic acid molecule, linking the first and second probes to provide a probe-linked nucleic acid molecule, and barcoding the probe-linked nucleic acid molecule. A method may comprise hybridizing a first probe to a first target region of a nucleic acid molecule, barcoding the probe, and hybridizing a second probe to a second target region of the nucleic acid molecule to generate a barcoded, probe-linked nucleic acid molecule. In some aspects, the method may comprise hybridizing a probe to a nucleic acid molecule attached to a feature-binding moiety to provide a probe-binding moiety complex and barcoding the probe. One or more processes of the methods provided herein may be performed within a partition such as a droplet or well. The methods of the present disclosure be useful, for example, in controlled analysis and processing of analytes such as biological particles, nucleic acids, and proteins. One or more of the methods described herein may allow for genomic, transcriptomic, or exomic profiling with higher sensitivity. The methods of the present disclosure may be useful in detecting variants and characterizing nucleic acid molecules, e.g., for assessment of single nucleotide polymorphisms (SNPs), alternative splice junctions, insertions, deletions, V(D)J rearrangements, etc. The methods of the present disclosure may be useful for multiplexed analysis of nucleic acids and proteins while minimizing reagent usage, e.g., by decreasing the number of unoccupied partitions for analysis.

[0006a] In one aspect, disclosed herein is a method of analyzing a cell, comprising: (a) providing a sample comprising a cell, wherein the cell comprises: (i) a feature, wherein the feature comprises a protein, a peptide, a lipid, or a carbohydrate; and (ii) a nucleic acid molecule; and (b) contacting the cell with a feature binding group and coupling the feature binding group to the feature, wherein the feature binding group comprises an oligonucleotide comprising a feature nucleic acid sequence that identifies the feature binding group; (c) hybridizing a first nucleic acid probe to the nucleic acid molecule; wherein the first nucleic acid probe comprises (i) a hybridizing sequence that hybridizes to a first target sequence of the nucleic acid molecule and (ii) a non-hybridizing sequence; (d) using the feature nucleic acid sequence and a first barcode molecule comprising a first barcode sequence to generate a first barcoded nucleic acid molecule comprising (i) the feature nucleic acid sequence or reverse complement thereof, and (ii) the first barcode sequence or reverse complement thereof; and (e) using the non-hybridizing sequence and a second barcode molecule comprising a second barcode sequence to generate a second barcoded nucleic acid molecule comprising (i) the first target sequence or reverse complement thereof and (ii) the second barcode sequence or reverse complement thereof.

[0007] In an aspect, disclosed herein is a method for multiplexed nucleic acid assays, comprising: (a) contacting a cell, nucleus, or cell bead with a first probe, a second probe, and a third probe under conditions sufficient to generate a first probe-associated molecule and a second probe-associated molecule, wherein the cell, nucleus, or cell bead comprises (i) a nucleic acid molecule comprising a first target region and a second target region and (ii) a feature coupled to a feature binding group, wherein the feature binding group comprises (i) a reporter oligonucleotide associated with the feature and (ii) a feature probe binding sequence, wherein the first probe comprises (i) a first probe sequence complementary to the first target region and (ii) a probe capture sequence, wherein the second probe comprises a second probe sequence complementary to the second target region, wherein the third probe comprises a (i) third probe sequence complementary to the feature probe binding sequence and (ii) the probe capture sequence; (b) in a first partition of a first set of partitions, contacting the first probe-associated molecule and the second probe-associated molecule to probe binding molecules and barcode molecules under conditions sufficient to generate a first barcoded nucleic acid molecule and a second barcoded nucleic acid molecule, wherein the barcode molecules comprise (i) a common sequence common to a plurality of barcode molecules comprising the barcode molecules and (ii)