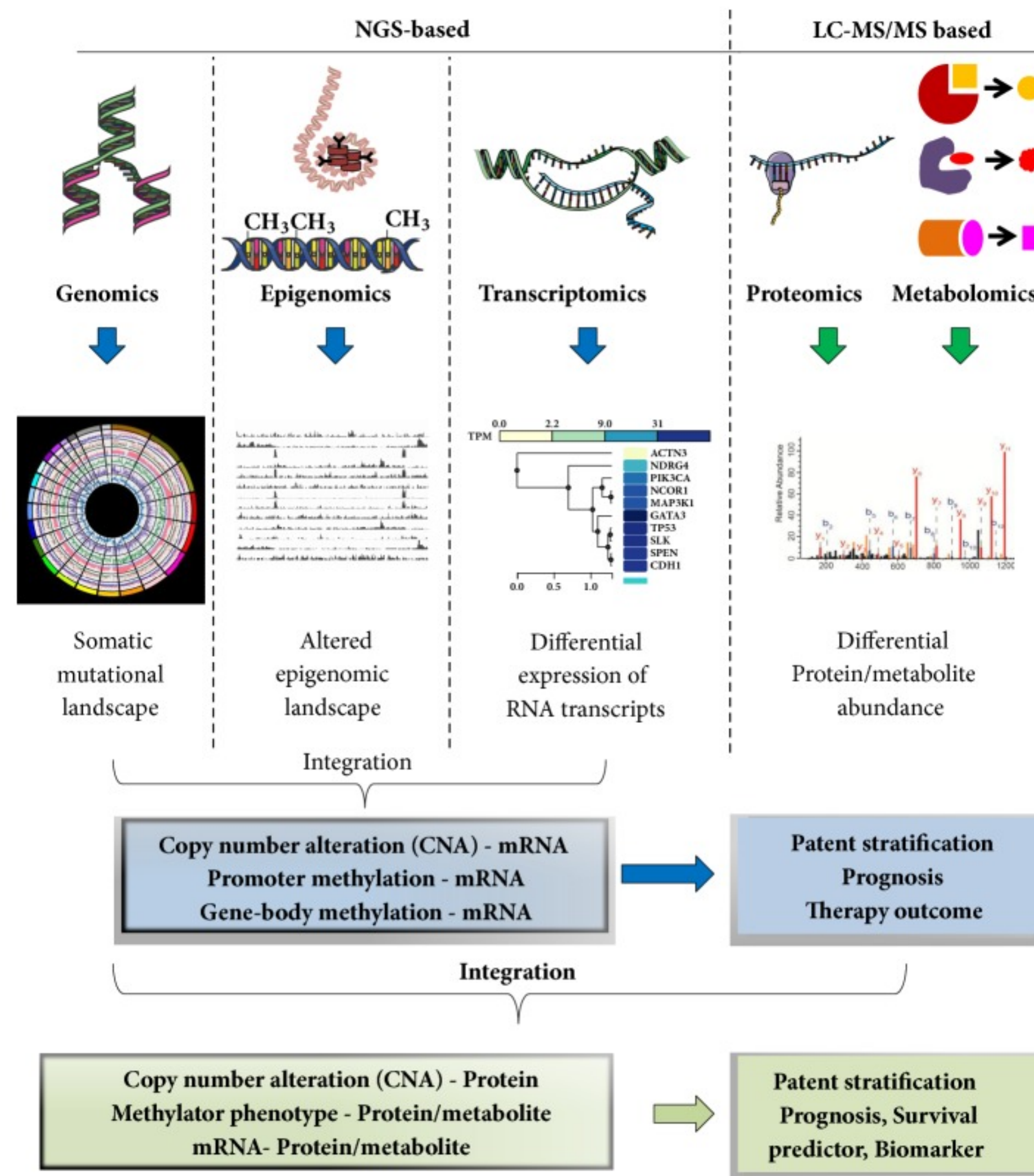


Figure 4



Application of NGS and mass-spectrometry (LC-MS/MS) based OMICS techniques in cancer research. Genomics, epigenomics, and transcriptomics are based on NGS techniques; whereas proteomics and metabolomics are driven by mass-spectrometric (LC-MS/MS) technique. The principal application of genomics, epigenomics, and transcriptomics is screening of genome-wide somatic mutations, identification of altered epigenomic landscape, and exploring differential RNA expression, respectively. The major application of proteomics/metabolomics is identification of differentially regulated proteins/phosphoproteins/metabolites. The integration of NGS-based techniques can identify the concordance or discordance between copy number alterations (CNAs), promoter/gene-body methylation, and RNA levels. Integration of NGS and LC-MS/MS based techniques may result in the correlation analysis between CNAs, promoter/gene-body methylation, and mRNA levels with protein/metabolite levels.