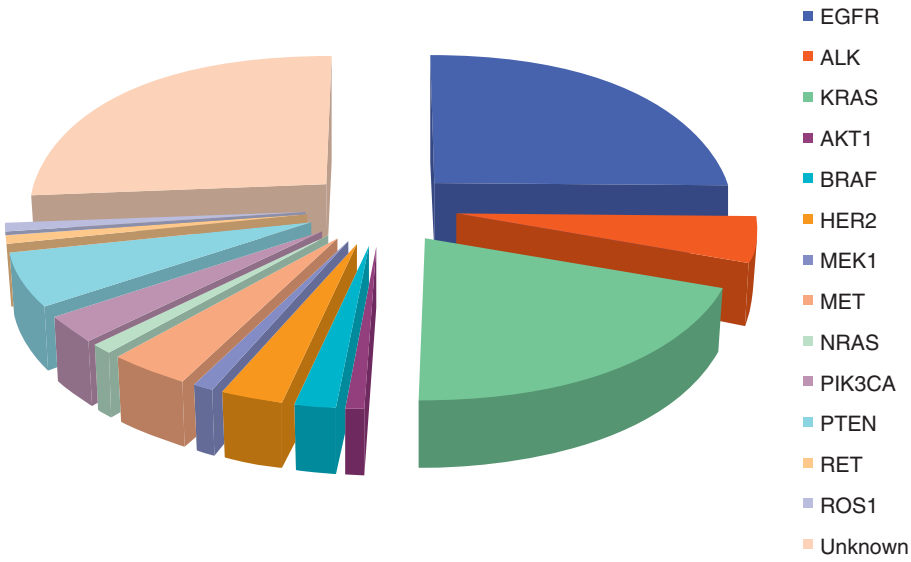

E-FIGURE 56-14 Molecular-genomic classification in lung adenocarcinoma. Various molecular and genomic driver oncogenic alterations have been identified within non–small cell lung cancer, especially adenocarcinoma, through molecular and genomic tumor profiling. Many of these alterations represent "actionable" or "druggable" therapeutic targets. The pie chart presents the affected genes and the proportions of lung adenocarcinomas containing alterations in them. ALK, Anaplastic lymphoma kinase; AKT1, v-akt murine thymoma viral oncogene homolog 1; BRAF, B-Raf proto-oncogene, serine/threonine kinase; EGFR, epithelial growth factor receptor; HER2, v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2; KRAS, Kirsten rat sarcoma viral oncogene homolog; MEK1, mitogen-activated protein kinase kinase 1; MET, MET proto-oncogene, receptor tyrosine kinase; NRAS, neuroblastoma RAS viral (v-ras) oncogene homolog; PIK3CA, phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha; PTEN, phosphatase and tensin homolog; RET, ret proto-oncogene; ROS1, ROS proto-oncogene 1, receptor tyrosine kinase.