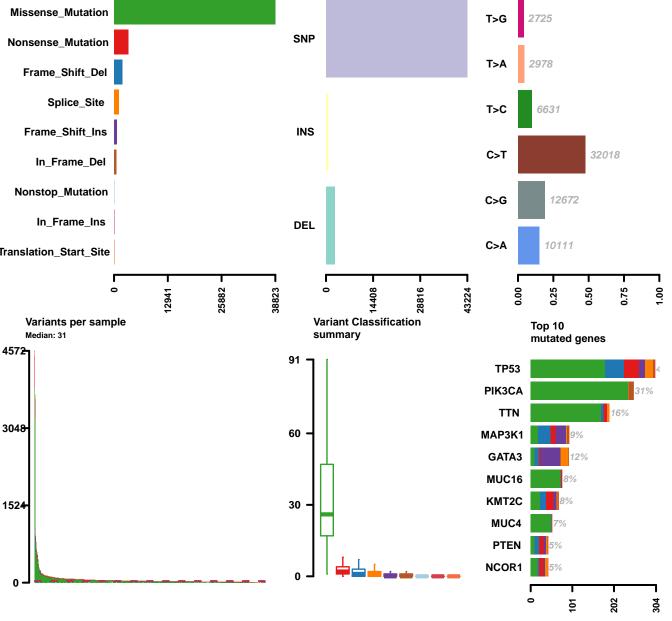
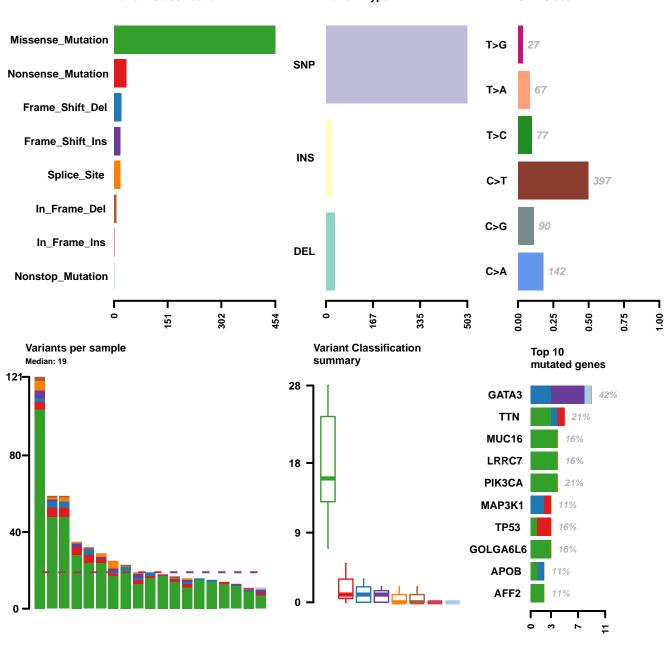
Mutation summary by Lobular carcinoma, NOS SNV Class Missense_Mutation **SNP** Nonsense_Mutation Frame_Shift_Del Splice_Site Frame_Shift_Ins INS C>T 7989 In_Frame_Del Translation_Start_Site C>G 3197 Nonstop_Mutation DEL C>A 1523 In_Frame_Ins 0 5159 5735 0.25 0.50 00. Variants per sample **Variant Classification** Top 10 Median: 24 summary mutated genes 1036-74 CDH₁ 62 PIK3CA 42% 20% TTN 690-49 MUC₄ **MUC16 PTEN TP53** 345-24 **TBX3 RUNX1** MYH9 34

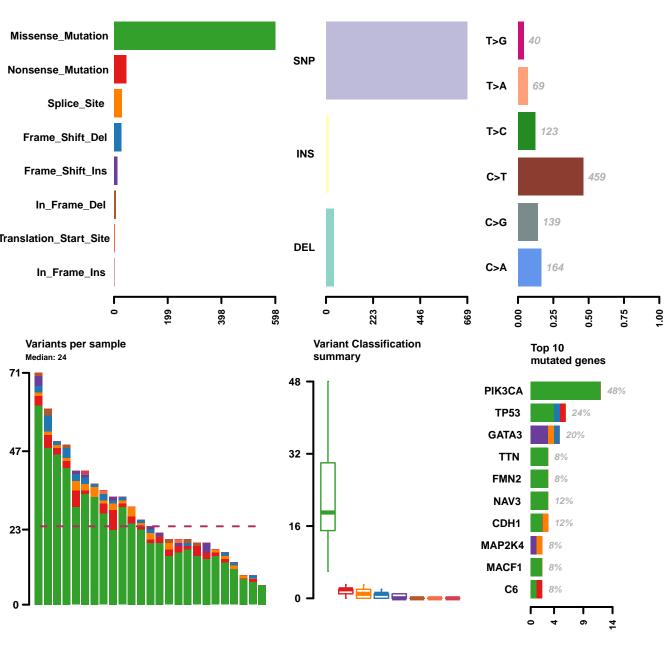
Mutation summary by Infiltrating duct carcinoma, NOS Variant Classification



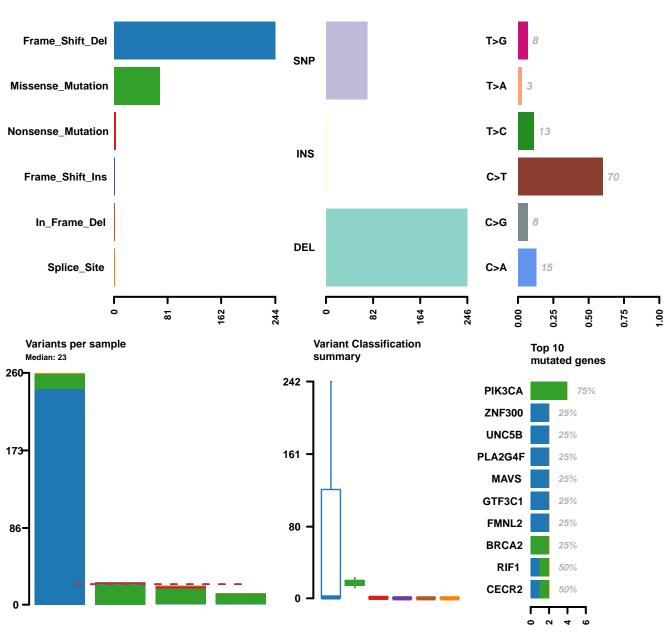
Mutation summary by Infiltrating duct mixed with other types of carcinoma



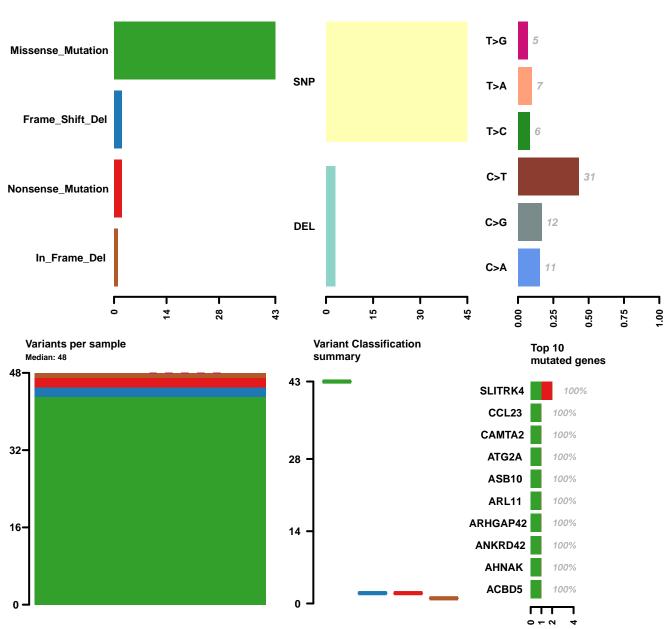
Mutation summary by Infiltrating duct and lobular carcinoma Variant Classification



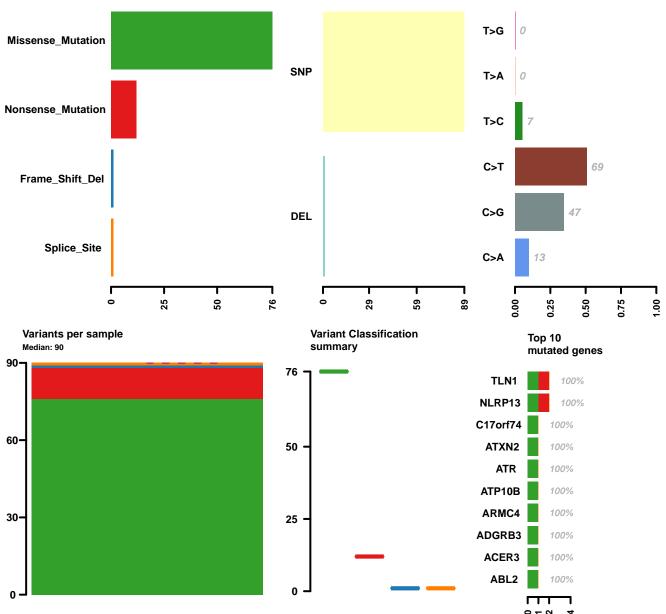
Mutation summary by Intraductal micropapillary carcinoma variant Classification



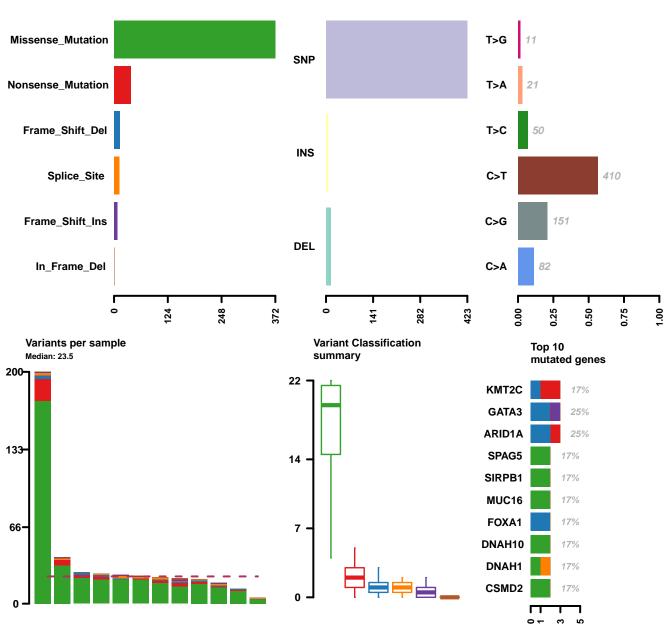
Mutation summary by Large cell neuroendocrine carcinoma variant Classification



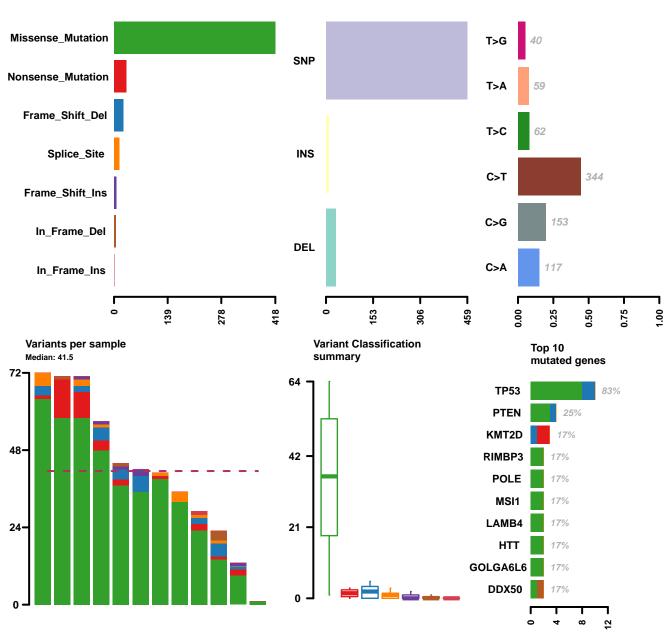
Mutation summary by Apocrine adenocarcinoma SNV Class



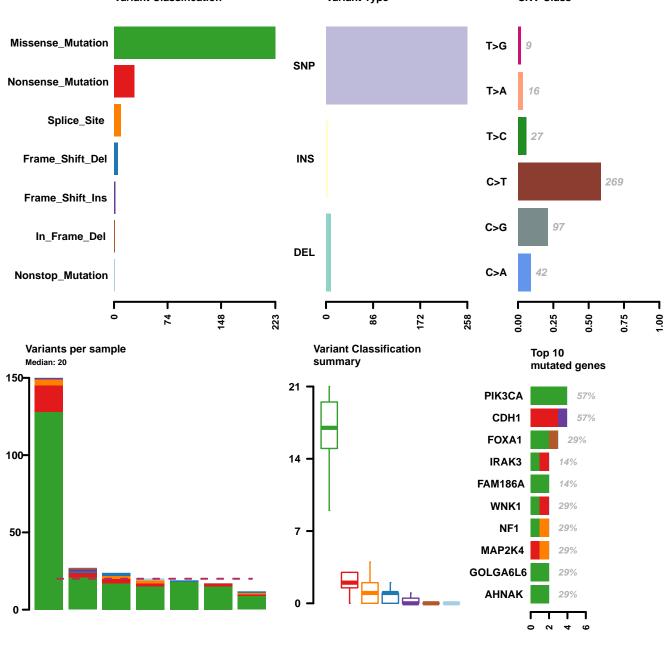
Mutation summary by Mucinous adenocarcinoma Nariant Classification SNV Class



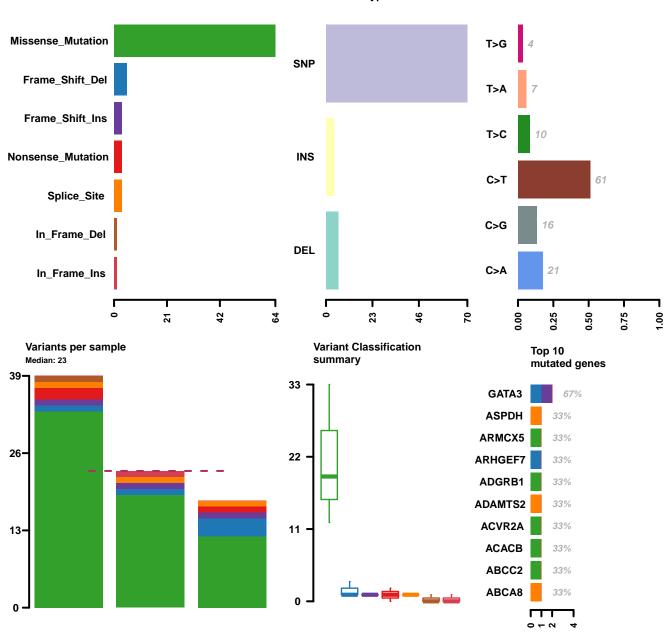
Mutation summary by Metaplastic carcinoma, NOS NV Class

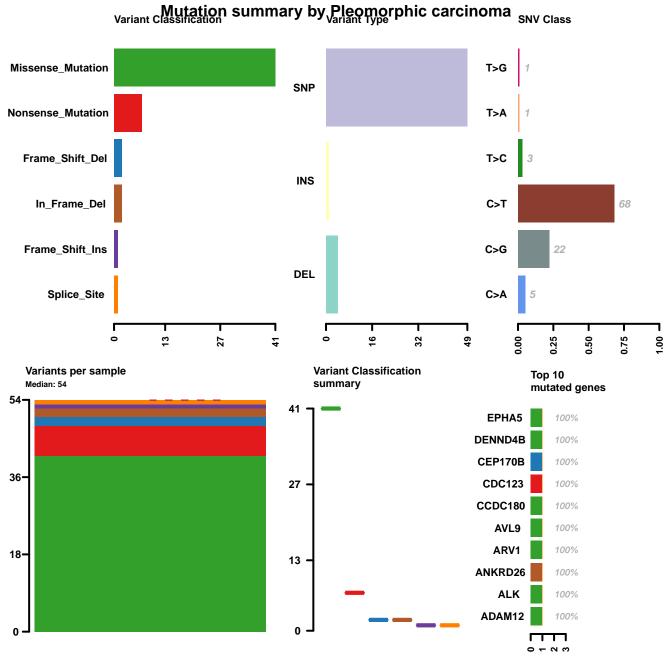


Mutation summary by Infiltrating lobular mixed with other types of carcinoma Variant Classification

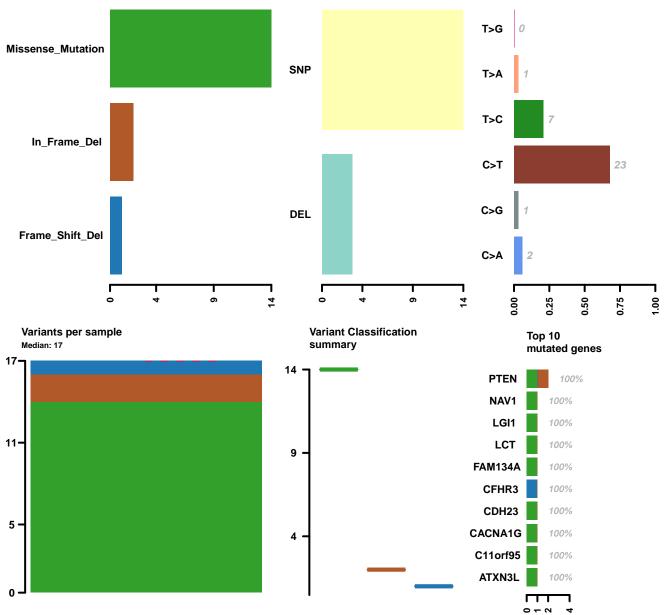


Mutation summary by Paget disease and infiltrating duct carcinoma of breast

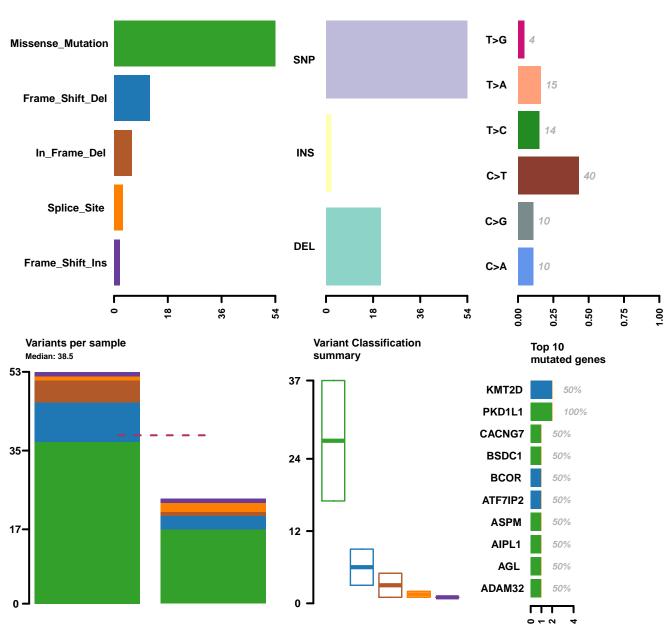




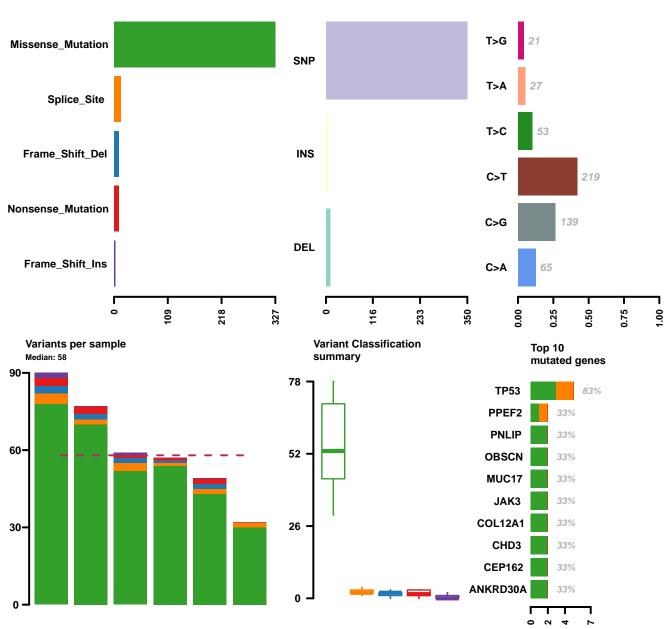
Variant Classification summary by Papillary carcinoma, NOS SNV Class



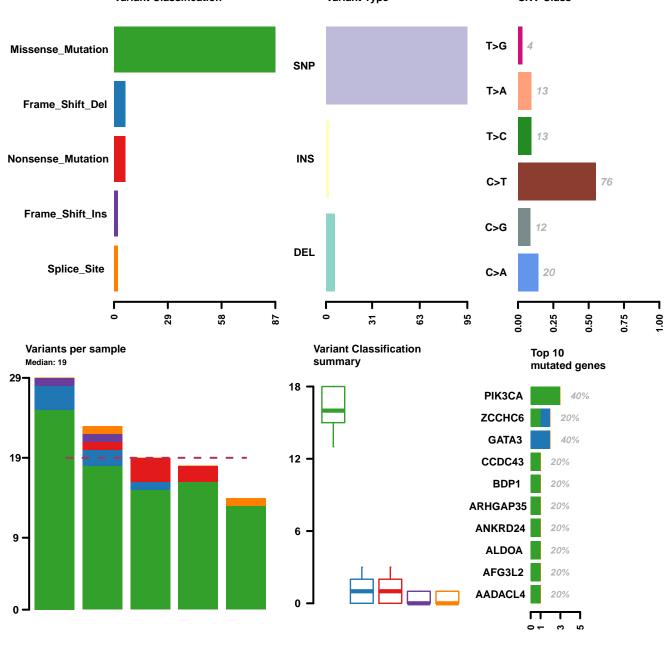
Mutation summary by Phyllodes tumor, malignant Class



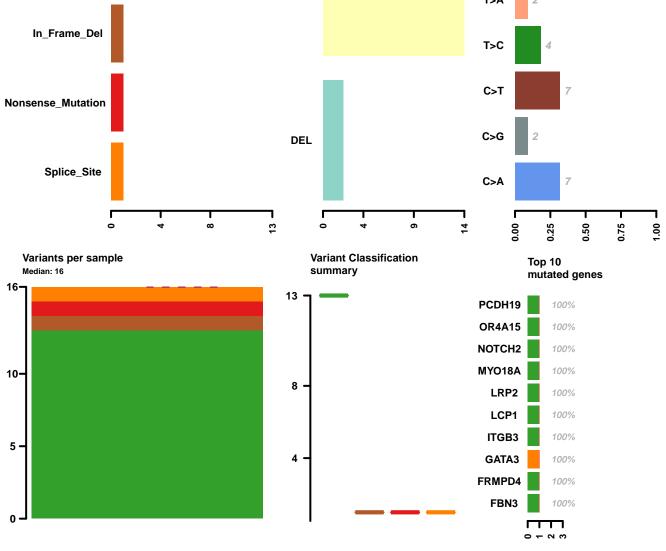
Mutation summary by Medullary carcinoma, NOS SNV Class

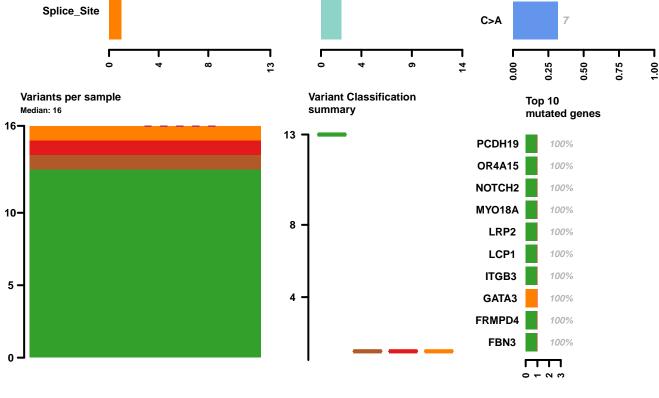


Mutation summary by Intraductal papillary adenocarcinoma with invasion Warlant Type



Mutation summary by Cribriform carcinoma, NOS NV Class T>G Missense_Mutation **SNP** T>A In_Frame_Del T>C C>T C>G DEL Splice_Site C>A





Mutation summary by Tubular adenocarcinoma SNV Class Missense_Mutation **SNP** T>A Frame_Shift_Del 10 T>C C>T 23 In_Frame_Del C>G DEL Nonsense_Mutation C>A 10 5 0.25 0.50 00. Variants per sample **Variant Classification** Top 10 Median: 25 summary mutated genes 25-22 MAP3K1 100% 100% **NEB** KLHDC7A 100% KIF5B 16-100% 14 **KIAA1279** 100% **FCGBP** 100% FBXO38 100% 8 -7 EIF3I 100% CX3CR1 100% CFAP46 100%