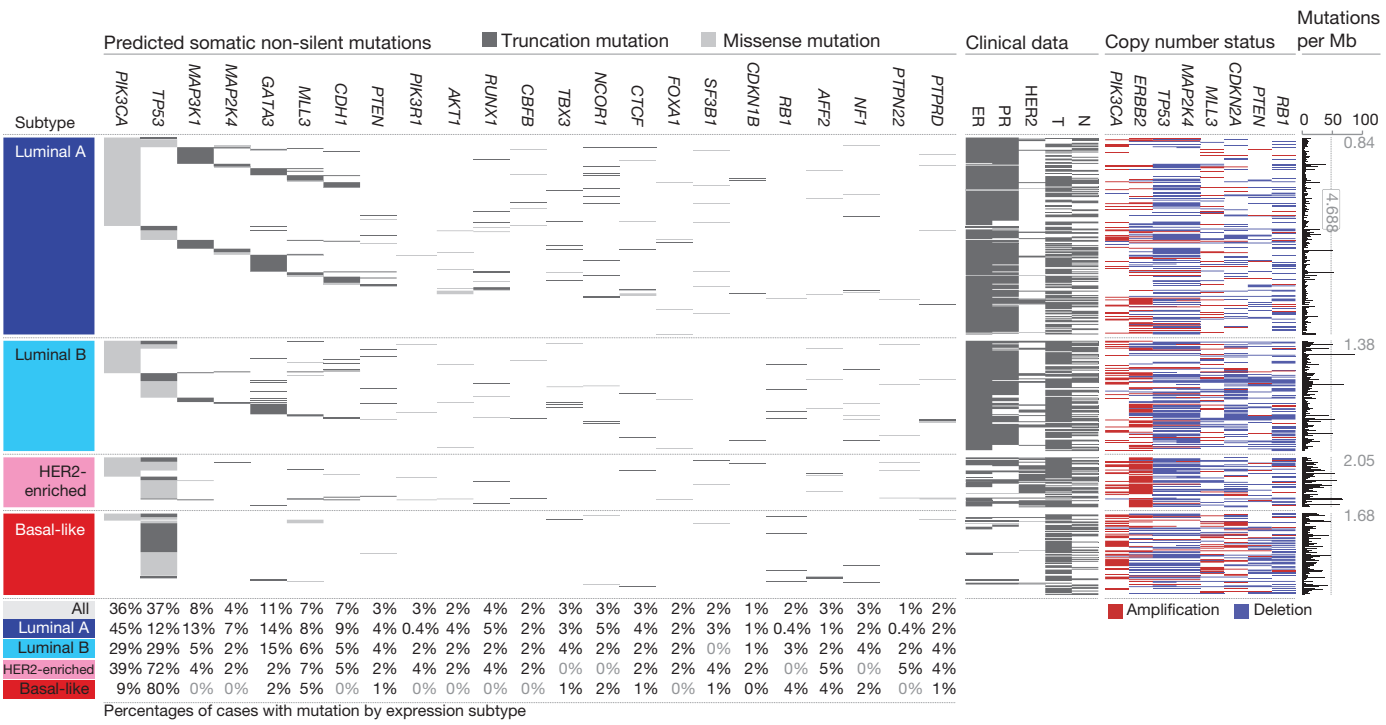

Figure 1 | Significantly mutated genes and correlations with genomic and clinical features. Tumour samples are grouped by mRNA subtype: luminal A ($n = 225$), luminal B ($n = 126$), HER2E ($n = 57$) and basal-like ($n = 93$). The left panel shows non-silent somatic mutation patterns and frequencies for significantly mutated genes. The middle panel shows clinical features: dark grey, positive or T2–4; white, negative or T1; light grey, N/A or equivocal. N, node status; T, tumour size. The right panel shows significantly mutated genes with frequent copy number amplifications (red) or deletions (blue). The far-right panel shows non-silent mutation rate per tumour (mutations per megabase, adjusted for coverage). The average mutation rate for each expression subtype is indicated. Hypermutated: mutation rates >3 s.d. above the mean (>4.688, indicated by grey line).