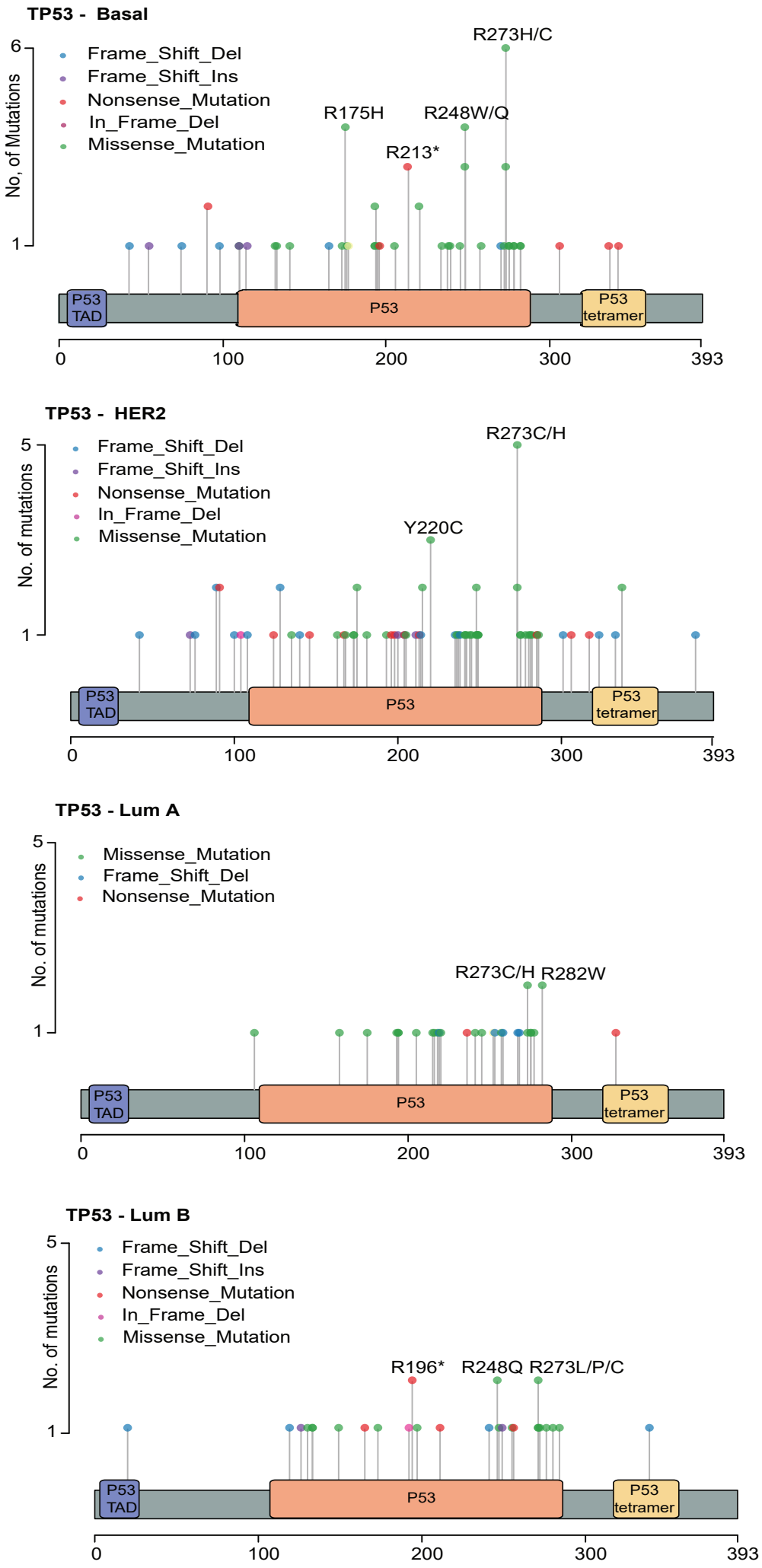
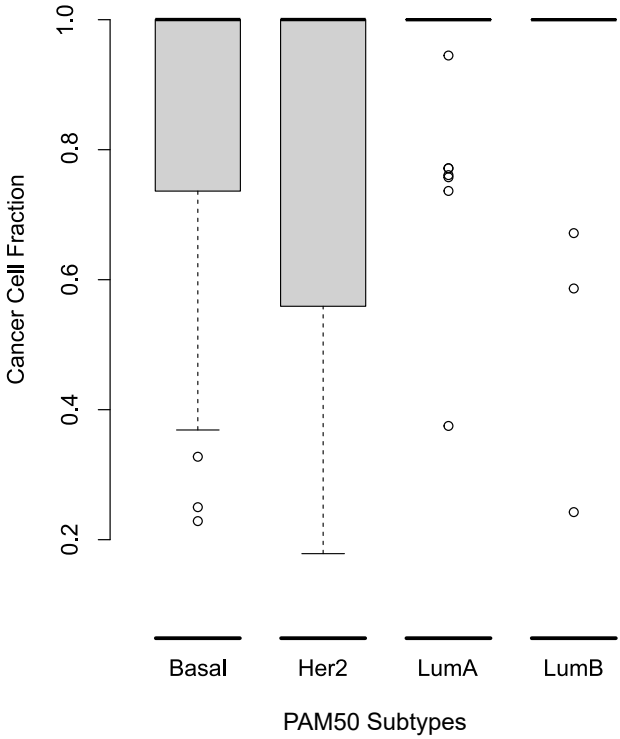
Supplemental Figures & Table



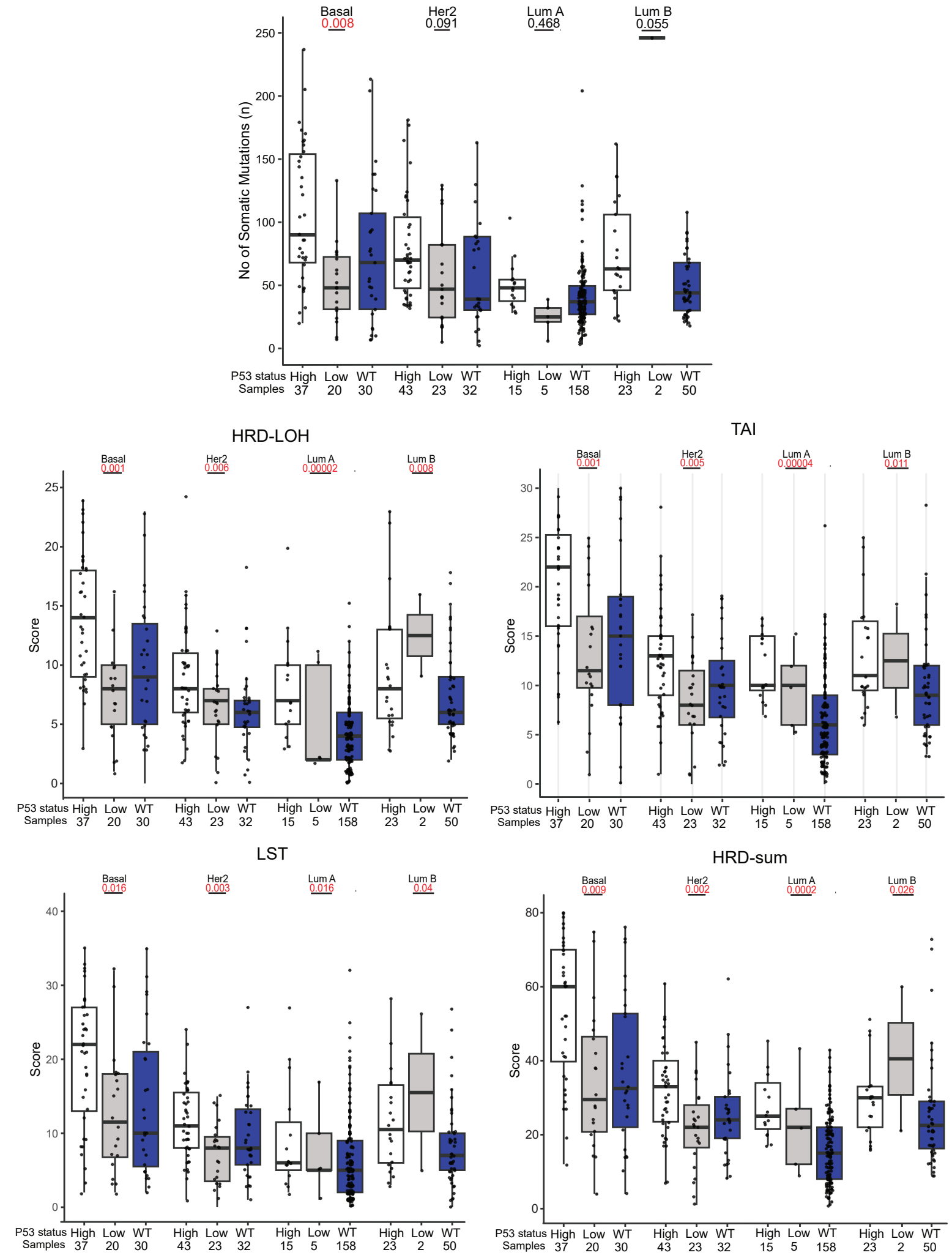
Supp. Figure 1. Distribution of somatic *TP53* mutations identified in MyBrCa. The lollipop plots compare the positions of somatic *TP53* mutations across PAM50 subtypes, with prominent positions indicated.



Supp. Figure 2. Cancer Cell Fraction (CCF) of *TP53* across somatic mutations. The proportion of cancer cells carrying somatic mutations in *TP53* across PAM50 subtypes in the MyBrCa cohort

cDNA_Change	Protein_Change	Prevalence (%)				Statistical Significance
		Basal (n=65)	Her2 (n=72)	LumA (n=26)	LumB (n=28)	
c.524G>A	p.R175H	6.20	2.80	3.85	3.57	0.797
c.586C>T	p.R196*	1.50	1.39	0.00	7.69	0.230
c.614A>G	p.Y205C	1.50	1.39	3.85	0.00	0.721
c.637C>T	p.R213*	4.62	1.39	0.00	3.57	0.524
c.659A>G	p.Y220C	3.07	4.17	3.85	0.00	0.753
c.743G>A	p.R248Q	6.15	2.78	0.00	7.14	0.435
c.817C>T	p.R273C	4.62	6.95	7.69	3.57	0.857
c.818G>A	p.R273H	9.23	2.78	3.85	0.00	0.173

Supp. Table 1. Common *TP53* somatic mutations in the MyBrCa cohort. The table indicates the top ten most common somatic mutations in *TP53* across PAM50 subtypes. The 273C and R175H mutations are common hotspot mutations that can be observed across all subtypes



Supp.Figure 3 : Comparison of TP53 mutations carriers with a high TP53 CCF to samples with low TP53 CCF of Tumour Mutational Burden and HRD scores.