Supplementary Table 1. Clinically relevant or potentially clinically relevant somatic mutations of by subtype

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

Above table shows the top ten most common mutations across pam50 subtypes. The 273C and R175H mutations can be observed across all the subtypes and known to be common hotspot mutation in TP53.