Risk profiling of patients with relapsed/refractory diffuse large B-cell lymphoma by measuring circulating tumor DNA. *Herrera et al.*

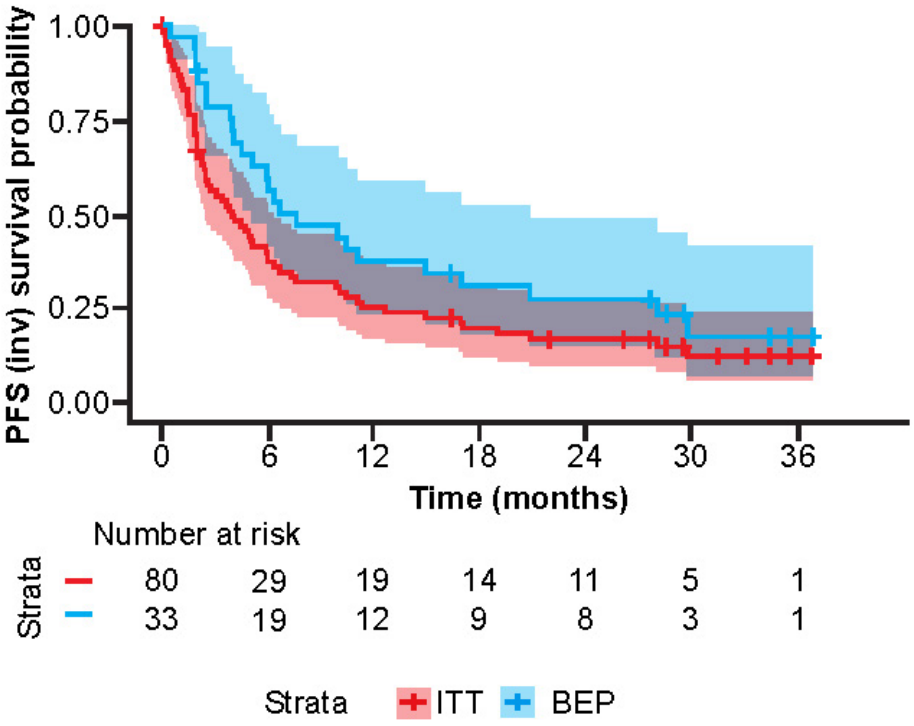
Supplementary Table 1. Distribution of most frequently mutated genes, in patients with and without ctDNA clearance at EOT

Genes	BEP* (*n* = 23)	ctDNA cleared (*n*=11)		ctDNA not cleared (*n*=12)	
		Baseline	EOT	Baseline	EOT
Linker histones	10	5	0	5	5
TP53	9	2	0	7	6
CREBBP	6	2	0	4	3
CARD11	6	2	0	4	2
LRRN3	6	4	0	2	2
PIM1	6	2	0	4	4
BCL2	4	0	0	4	3
BTG2	4	3	0	1	0
BCL10	3	2	0	1	0
NOTCH2	3	2	0	1	0

*Patients with paired baseline and EOT samples.

BEP, biomarker-evaluable population; ctDNA, circulating tumor DNA; EOT, end-of-treatment.

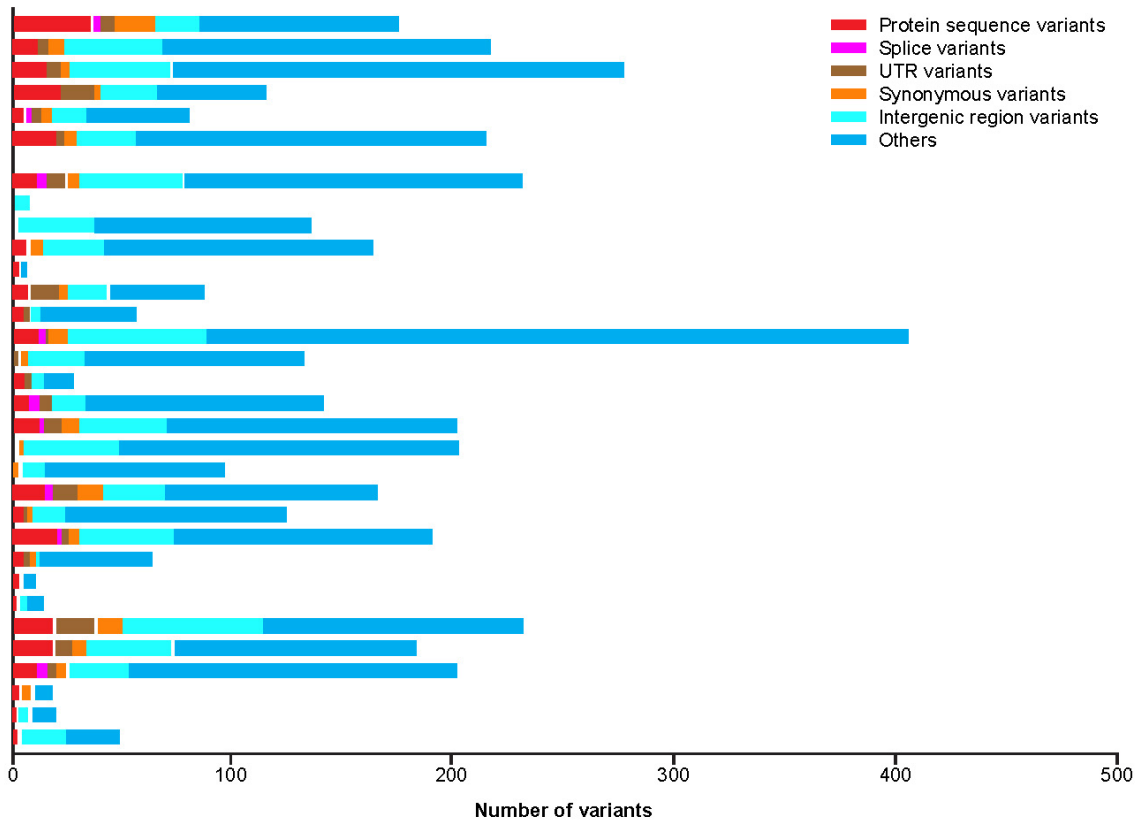
Supplementary Figure 1. Investigator-assessed PFS in the ITT population and BEP



BEP, biomarker-evaluable population; INV, investigator-assessed; ITT, intention-to-treat;

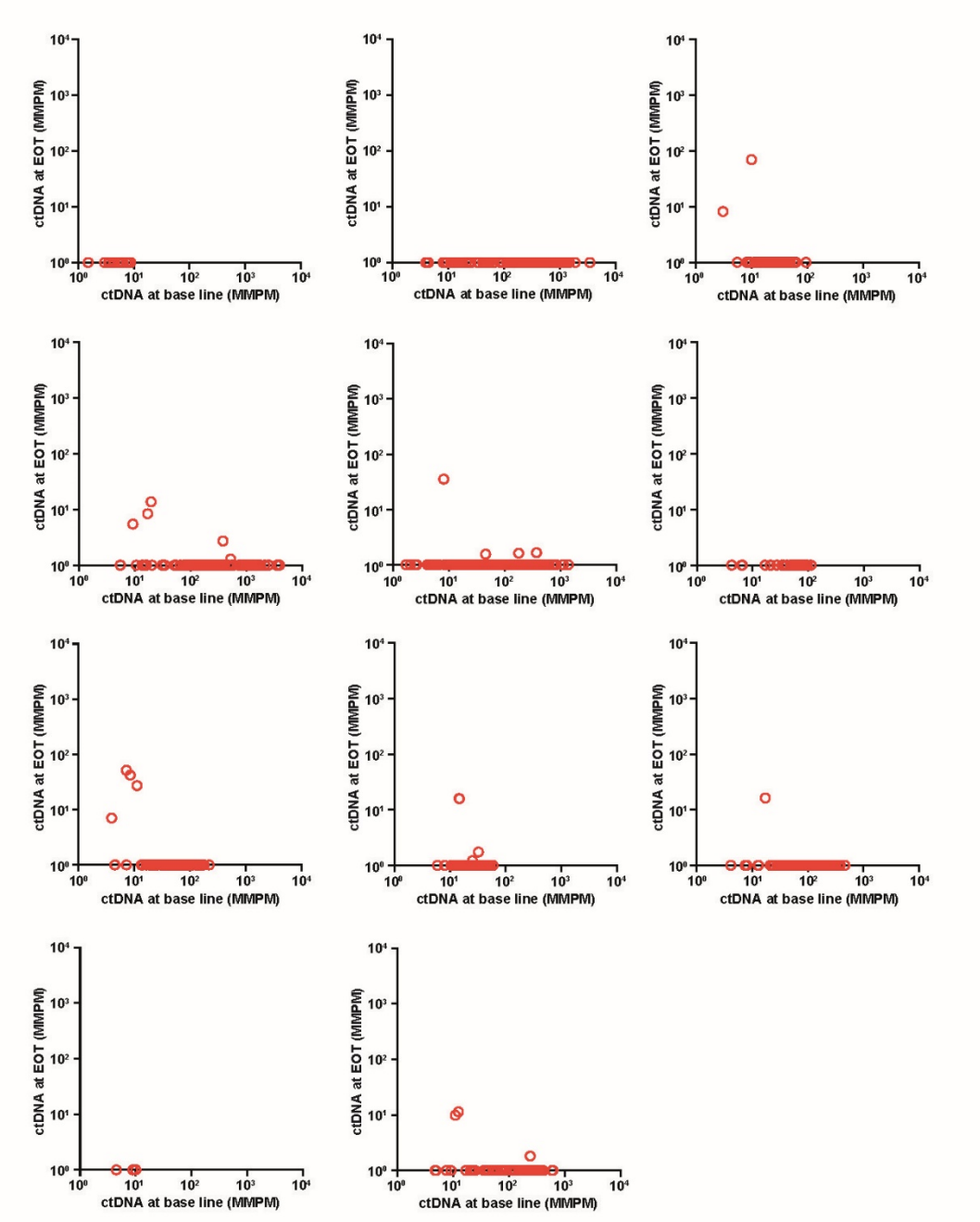
PFS, progression-free survival.

Supplementary Figure 2. Distribution of all variants in ctDNA at baseline in 33 individual patients



ctDNA, circulating tumor DNA; UTR, untranslated region.

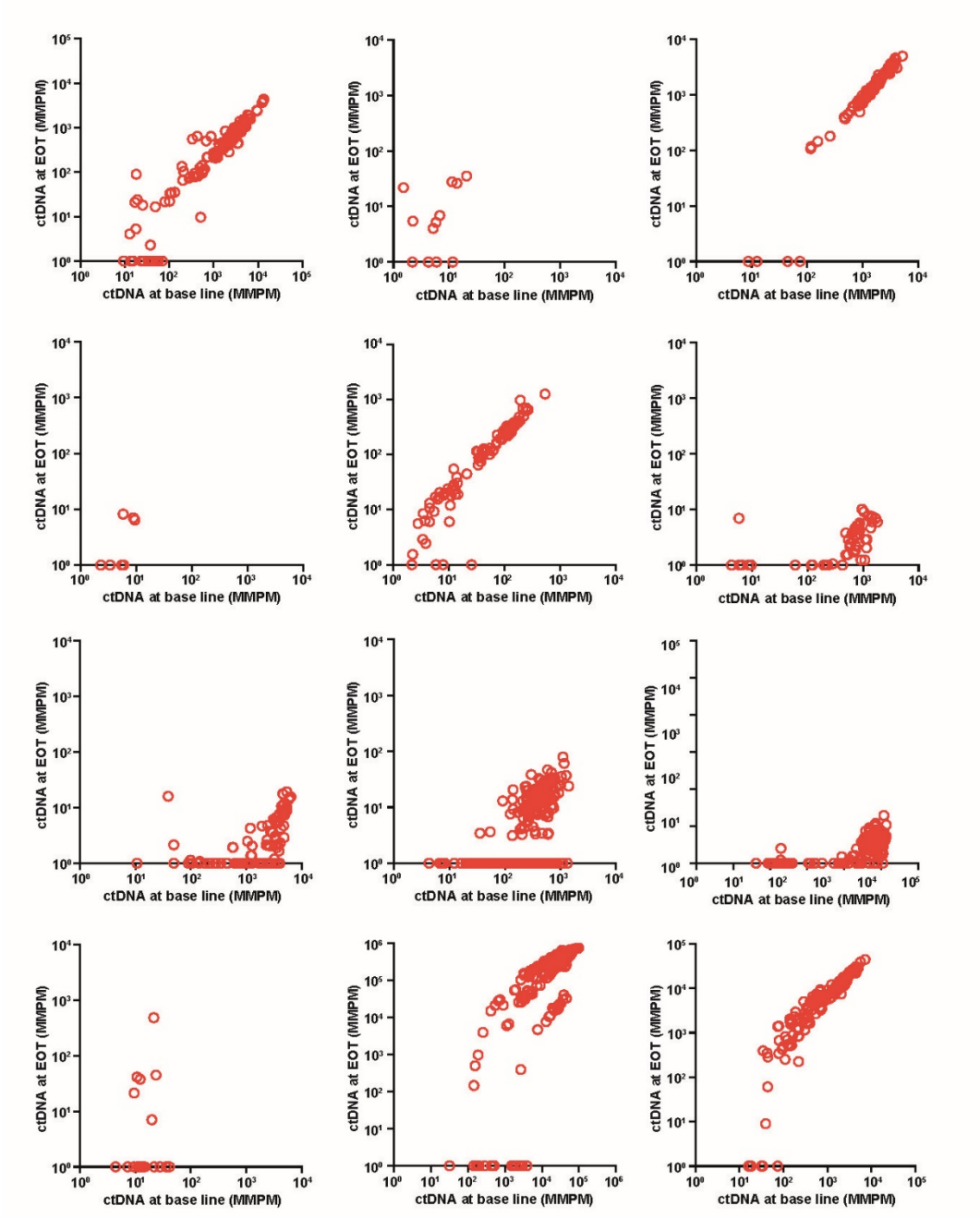
Supplementary Figure 3. ctDNA levels in 11 individual patients with ctDNA* clearance at EOT



*All variants of ctDNA are shown.

ctDNA, circulating tumor DNA; EOT, end of treatment; MMPM, mutant molecules per mL.

Supplementary Figure 4. ctDNA levels in 12 individual patients with ctDNA* not cleared at EOT



*All variants of ctDNA are shown.

ctDNA, circulating tumor DNA; EOT, end of treatment; MMPM, mutant molecules per mL.