

982P Final results and biomarker analysis of a randomized phase II study of osimertinib plus bevacizumab versus osimertinib monotherapy for untreated patients with non-squamous non-small-cell lung cancer harboring EGFR mutations; WJOG9717L study



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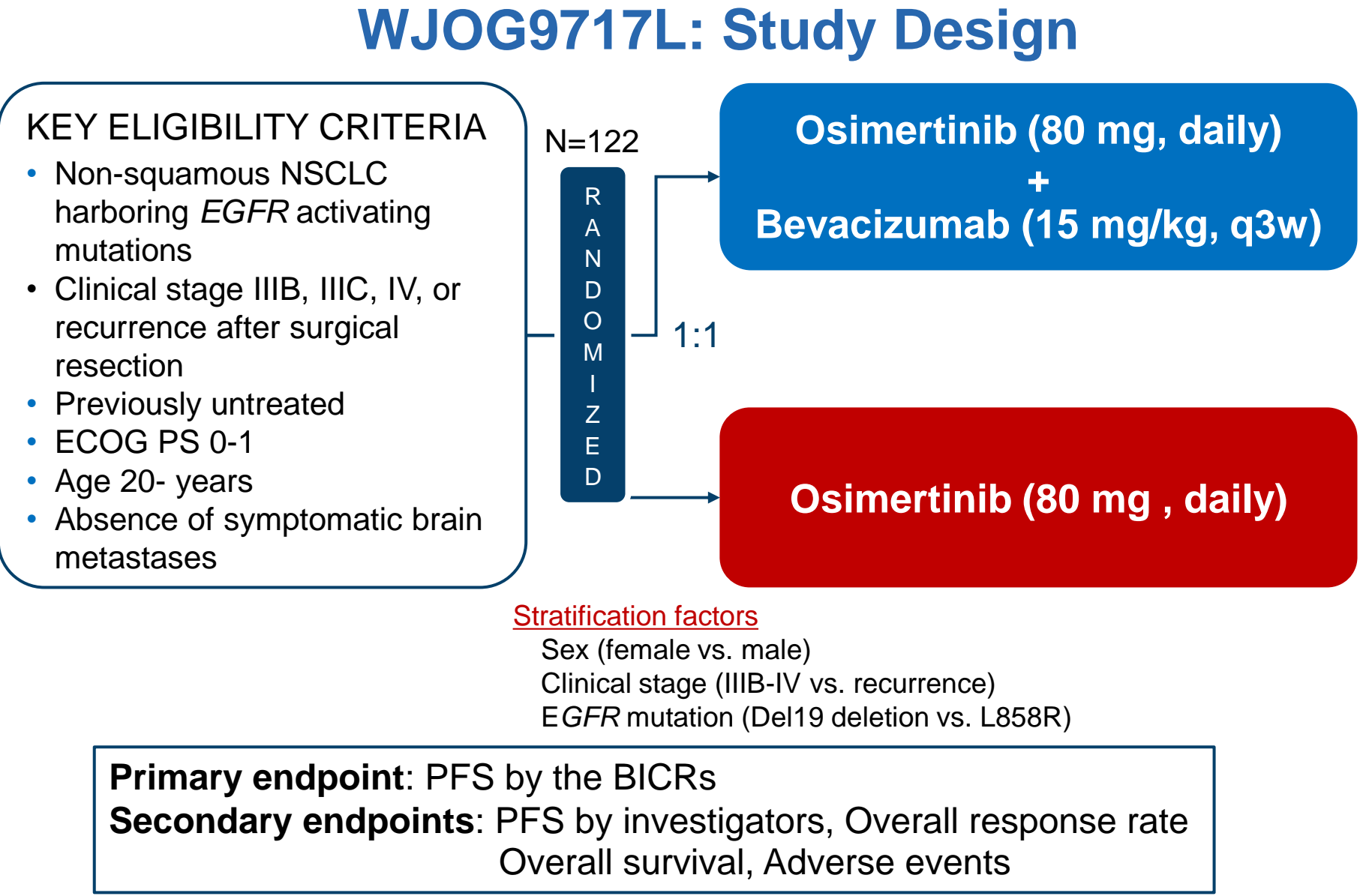
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Background

- Previous studies showed that the addition of anti-VEGF inhibitors to erlotinib prolonged progression-free survival in EGFR mutated non-squamous non-small-cell lung cancer (Ns-NSCLC) patients.
- The primary results of WJOG9717L study, open-label, randomized phase II trial comparing osimertinib plus bevacizumab with osimertinib monotherapy for untreated patients with advanced EGFR mutated Ns-NSCLC, were reported at ESMO2021.

Methods



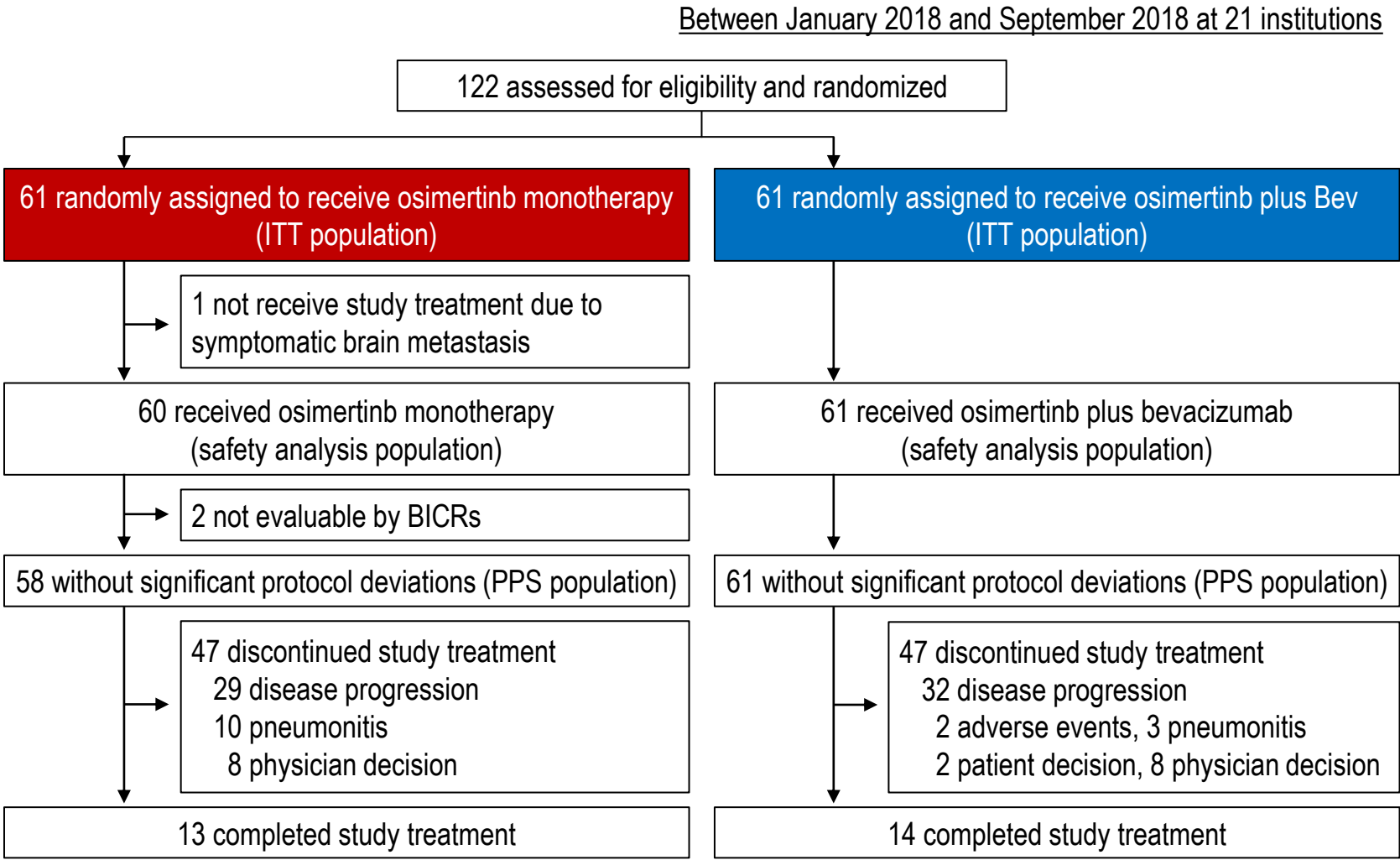
Clinical trial information: UMIN000030206

Statistical Considerations

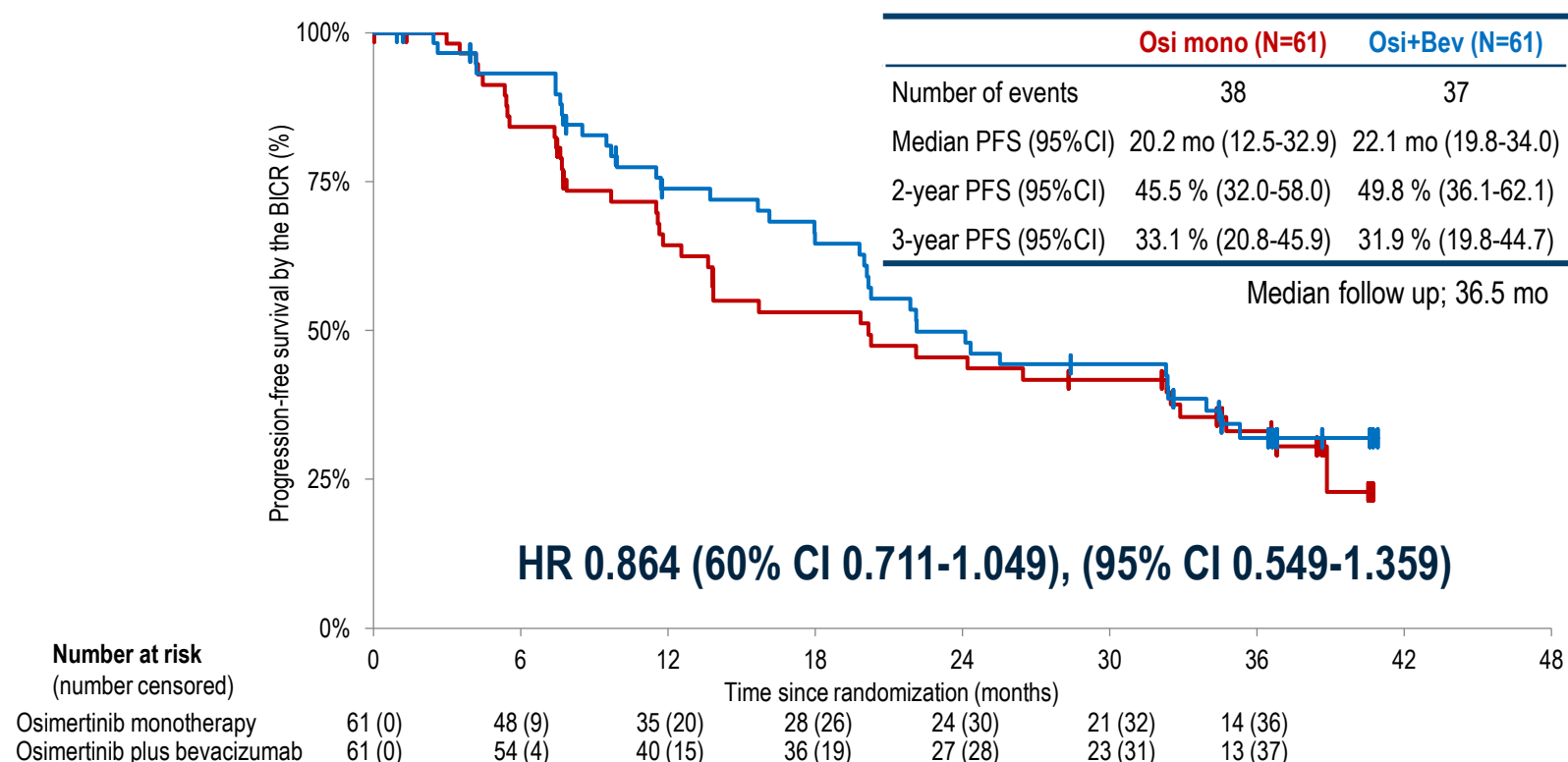
- The planned total sample size was 120 patients.
- We assumed the median PFS with osimertinib monotherapy as 18 months and expected as 27 months for osimertinib plus bevacizumab, with HR 0.67.
- One-sided  $\alpha = 0.20$ , a power of 80%, an expected accrual period of 1.5 years, and a follow-up period of 2 years.
- This final analysis were performed at the data cut-off, 31th July 2021.

Results

Disposition of Study Treatment



Primary Endpoint: PFS (ITT), assessed by BICRs



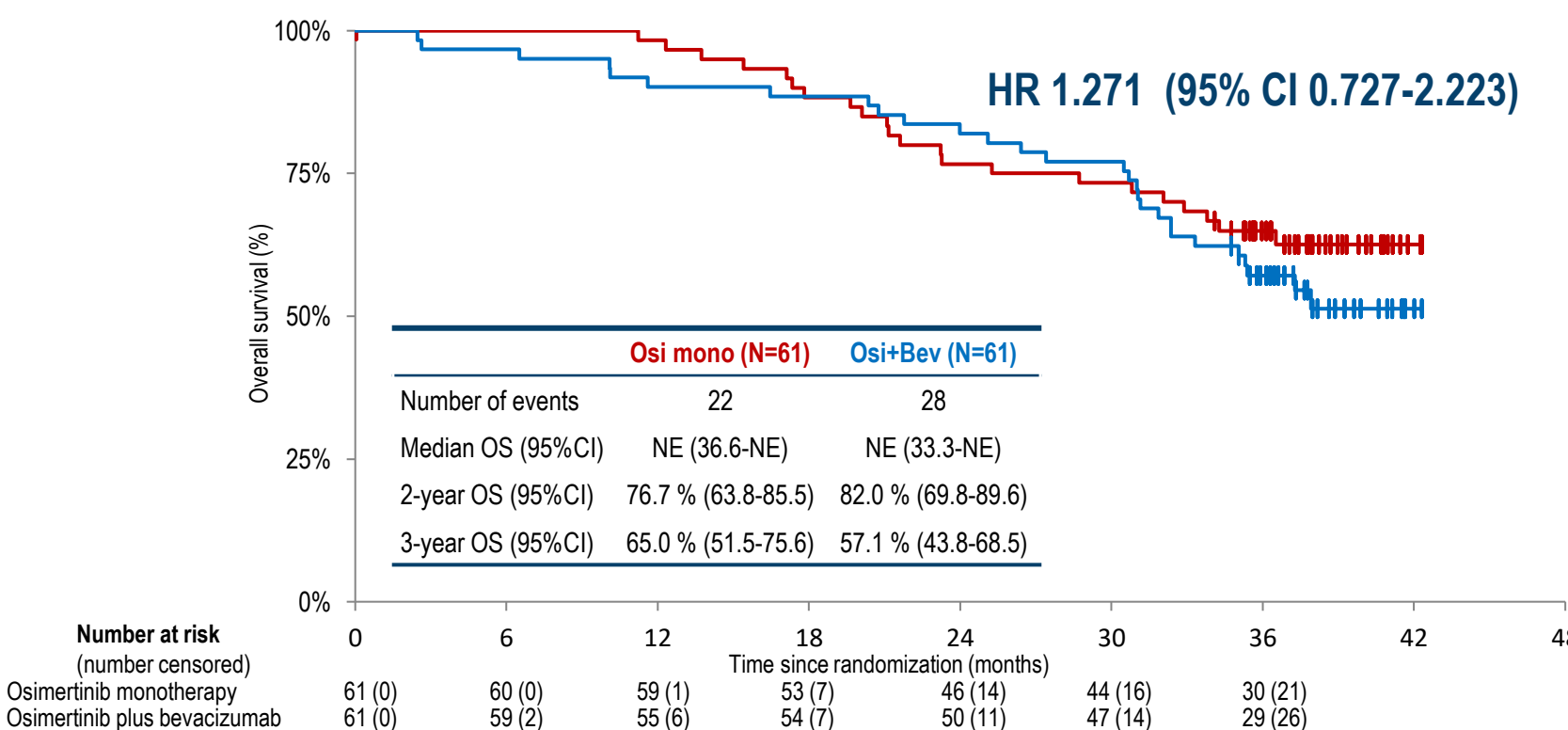
Safety summary

	Osimertinib monotherapy (N=60)	Osimertinib plus bevacizumab (N=61)
Median duration of osimertinib (weeks)(range)	57.6 (1.4 – 183.6)	94.0 (1.6 – 183.6)
Median duration of bevacizumab (weeks)(range)	-	33.4 (3.0 – 159.0)
Grade 3-5 adverse events (AEs)	29 (48.3 %)	35 (57.4 %)
Serious adverse events (SAEs)	13 (21.7 %)	21 (34.4 %)
AEs leading to treatment discontinuation	16 (26.7 %)	37 (60.7 %)
SAEs leading to treatment discontinuation	4 (6.7 %)	8 (13.1 %)
AEs leading to dose modification	24 (40.0 %)	39 (63.9 %)
AEs leading to dose reduction	0 -	3 (4.9 %)
AEs leading to treatment-related death	0 -	1 (1.6 %)

Baseline Characteristics

		Osimertinib monotherapy (N=61)	Osimertinib plus bevacizumab (N=61)
Age (years)	median (range)	66 (29 - 85)	67 (41 - 86)
Sex	Male	23 (37.7 %)	24 (39.3 %)
	Female	38 (62.3 %)	37 (60.7 %)
Smoking	Never	30 (49.2 %)	38 (62.3 %)
	Ever	31 (50.8 %)	23 (37.7 %)
ECOG performance status	0	34 (55.7 %)	32 (52.5 %)
	1	27 (44.3 %)	29 (47.5 %)
Histopathological diagnosis	Adenocarcinoma	60 (98.4 %)	61 (100 %)
	Others	1 (1.6 %)	-
Clinical stage	IIIB	2 (3.3 %)	1 (1.6 %)
	IV	46 (75.4 %)	48 (78.7 %)
	Recurrence after surgical resection	13 (21.3 %)	12 (19.7 %)
EGFR mutation type	Deletion in exon 19	36 (59.0 %)	35 (57.4 %)
	Leu858Arg	25 (41.0 %)	26 (42.6 %)

Secondary Endpoint: Overall survival (ITT)



Summary

- This study did not show the efficacy of osimertinib plus bevacizumab against osimertinib monotherapy with respect to improving PFS in patients with non-squamous NSCLC harboring EGFR mutation.
- Regardless of TP53 mutation at baseline, there was also no significant difference in updated PFS between two arms.

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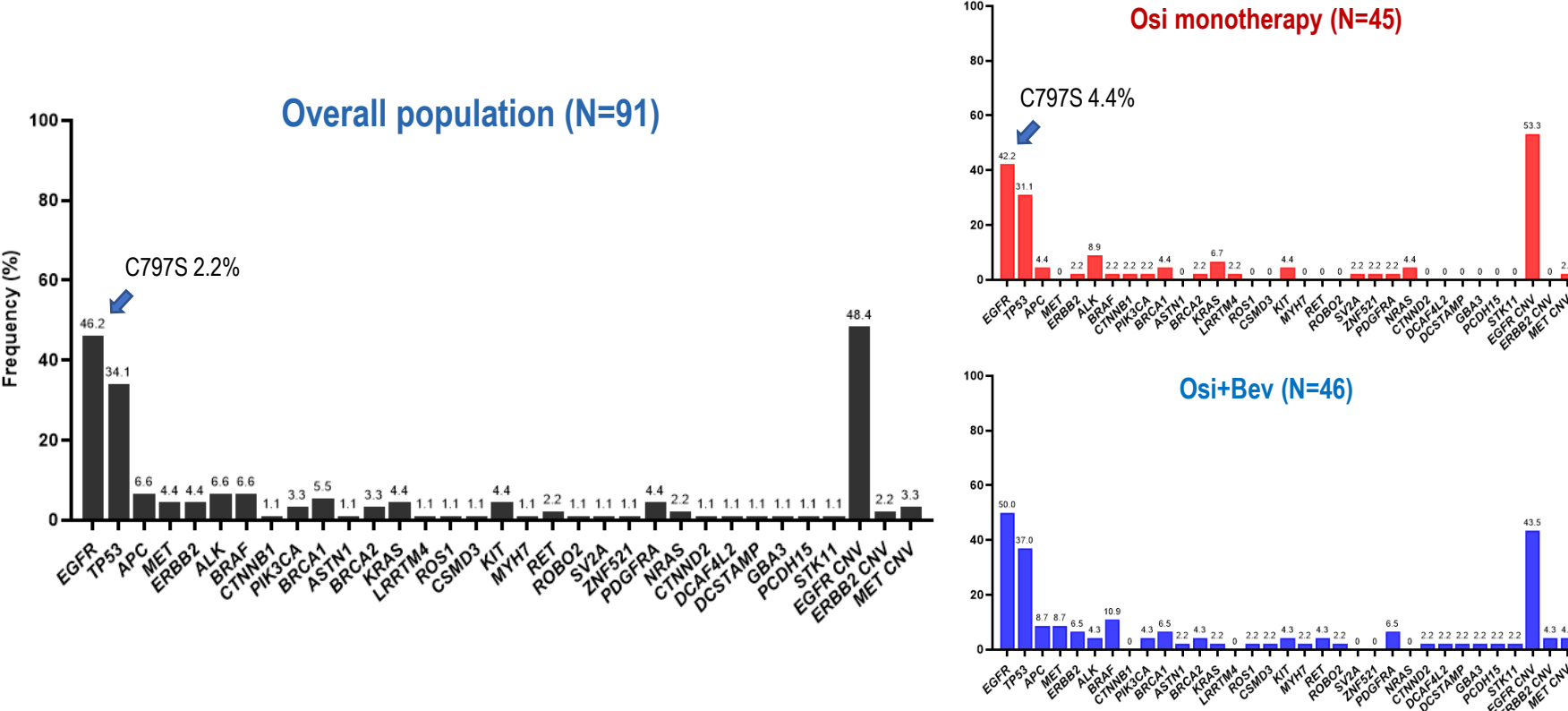
Biomarker study

Tissue samples (N=40) and plasma samples (N=94) at baseline were evaluable, and 197 genes were evaluated by targeted deep sequencing.

Tissue samples at baseline				Plasma samples at baseline			
	All cases N=40 (%)	Osi mono N=22 (%)	Osi+Bev N=18 (%)		All cases N=94 (%)	Osi mono N=46 (%)	Osi+Bev N=48 (%)
EGFR	38 (95.0)	21 (95.5)	17 (94.4)	EGFR	72 (76.6)	39 (84.8)	33 (68.8)
TP53	20 (50.0)	11 (50.0)	9 (50.0)	TP53	42 (44.7)	23 (50.0)	19 (39.6)
APC	11 (27.5)	6 (27.3)	5 (27.8)	APC	11 (11.7)	4 (8.7)	7 (14.6)
MET	9 (22.5)	5 (22.7)	4 (22.2)	MET	9 (9.6)	4 (8.7)	5 (10.4)
ERBB2	6 (15.0)	3 (13.6)	3 (16.7)	ERBB2	6 (6.4)	2 (4.3)	4 (8.3)
ALK	1 (2.5)	1 (4.5)	0 (0.0)	ALK	5 (5.3)	4 (8.7)	1 (2.1)
BRAF	1 (2.5)	0 (0.0)	1 (5.6)	BRAF	5 (5.3)	2 (4.3)	3 (6.3)
CTNNB1	1 (2.5)	1 (4.5)	0 (0.0)	CTNNB1	5 (5.3)	3 (6.5)	2 (4.2)
CTNNB1	2 (5.0)	1 (4.5)	1 (5.6)	PIK3CA	5 (5.3)	3 (6.5)	2 (4.2)
KRAS	1 (2.5)	0 (0.0)	1 (5.6)	BRCA1	4 (4.3)	2 (4.3)	2 (4.2)
SLITRK1	1 (2.5)	1 (4.5)	0 (0.0)	ASTN1	2 (2.1)	1 (2.2)	1 (2.1)
PDGFRA	1 (2.5)	1 (4.5)	0 (0.0)	BRCA2	2 (2.1)	1 (2.2)	1 (2.1)
NRAS	1 (2.5)	1 (4.5)	0 (0.0)	KRAS	2 (2.1)	1 (2.2)	1 (2.1)
LRRF5	1 (2.5)	1 (4.5)	0 (0.0)	LRRF5	2 (2.1)	1 (2.2)	1 (2.1)
LRRF5	1 (2.5)	1 (4.5)	0 (0.0)	LRRF5	2 (2.1)	2 (4.3)	0 (0.0)
ROS1	1 (2.5)	0 (0.0)	1 (5.6)	ROS1	2 (2.1)	2 (4.3)	0 (0.0)
TRPS1	1 (2.5)	0 (0.0)	1 (5.6)	TRPS1	2 (2.1)	2 (4.3)	0 (0.0)
EGFR CNV	8 (20.0)	4 (18.2)	4 (22.2)	EGFR CNV	51 (54.3)	28 (60.9)	23 (47.9)
ERBB2 CNV	3 (7.5)	2 (9.1)	1 (5.6)	ERBB2 CNV	2 (2.1)	2 (4.3)	0 (0.0)
MET CNV	18 (45.0)	10 (45.5)	8 (44.4)	MET CNV	18 (19.1)	10 (21.7)	8 (16.7)

Gene alterations of plasma samples at PD or last dose

Plasma samples (N=91) at PD or last dose were evaluable, and 197 genes were evaluated by targeted deep sequencing.



PFS assessed by BICRs, by TP53 mutation in plasma at baseline

