

1 **Article type: Research Article (Clinical Trials: Targeted Therapy)**

2

3 **Capivasertib, an AKT Kinase Inhibitor, as Monotherapy or in Combination With**

4 **Fulvestrant in Patients With *AKT1*^{E17K}-Mutant, ER-Positive Metastatic Breast Cancer**

5

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33 Data from this manuscript were partially reported at the San Antonio Breast Cancer Symposium
34 (SABCS), December 5–9, 2017, San Antonio, TX, USA.

35

36 **Running title:** Capivasertib in *AKT1*-mutant, ER+ metastatic breast cancer

37

38 **Keywords:** Capivasertib, fulvestrant, AKT, ER-positive, breast cancer

39

40 **Conflicts of interest**

41 **LMS** has acted in a consultancy or advisory role for AstraZeneca and Roche Genentech and
42 has received research funding from AstraZeneca, Puma Biotechnology, and Roche Genentech,
43 travel or accommodation expenses from AstraZeneca, Pfizer, Puma Biotechnology, and Roche
44 Genentech, and honoraria from Pfizer. **KT** has received research funding from Daiichi Sankyo,
45 Pfizer, and Lilly. **MO** has received research funding from AstraZeneca, Boehringer Ingelheim,
46 GSK, Immunomedics, Novartis, Puma Biotechnology, Roche Genentech, and Seattle Genetics
47 and consultancy fees from AstraZeneca, Eisai, GP Pharma, Grünenthal, GSK, Novartis, Pierre-
48 Fabre, Puma Biotechnology, Roche Genentech, and Seattle Genetics. **EC** has received
49 consultancy fees from Lilly, Novartis, Pfizer, and Roche. **IAM** has participated in advisory
50 boards (compensated) for Abbvie, AstraZeneca, Genentech, GSK, Lilly, MacroGenics, Novartis,
51 Immunogenics, Pfizer, Puma Biotechnology, and Seattle Genetics and has received institutional

52 research funding from Genentech, Novartis, and Pfizer. **LB** has acted in a consultancy or
53 advisory role for AstraZeneca, Celgene, Eisai, Genomic Health, Ipsen, Lilly, Novartis, Pfizer,
54 Pierre Fabre, and Roche and received research funding from Celgene, Genomic Health, and
55 Novartis, honoraria from Lilly, Novartis, and Pfizer, and travel or accommodation expenses from
56 Celgene, Pfizer, Ipsen, and Roche. **UB** has received research grants from AstraZeneca,
57 Chugai, and Onyx Pharmaceuticals and consultancy fees from Astex and Novartis. **MS** has
58 received research funds from Daiichi Sankyo, Immunomedics, Menarini Ricerche, Puma
59 Biotechnology, and Targimmune, has participated in scientific advisory boards for Menarini
60 Ricerche and Bioscience Institute, and is a cofounder of Medendi. **BST** has received honoraria
61 and research funding from Genentech and participated in advisory boards for Boehringer
62 Ingelheim and Loxo Oncology, a wholly owned subsidiary of Eli Lilly. **SC** has received a
63 research grant from Daiichi Sankyo and consultancy fees from BMS, Context Therapeutics, Eli
64 Lilly, Novartis, Revolution Medicines, and Sermonix Pharmaceutical. **DMH** reports stock
65 ownership in Fount Therapeutics, has acted in a consultancy or advisory role for AstraZeneca,
66 Bayer, Boehringer Ingelheim, Chugai Pharma, Eli Lilly, Genentech, and Pfizer, and has received
67 research funding from AstraZeneca, Bayer, Loxo Oncology, and Puma Biotechnology and travel
68 or accommodation expenses from Chugai Pharma and Genentech. **HA, JA, AB, DC, CC,**
69 **ECdB, AF, JH, JPOL, RM, RMc, MM, MP, VR, GS,** and **JB** are employees of AstraZeneca.
70 **M-PS** declared no competing interests.

71

72 **Statement of translational relevance** (119/150 words)

73 Early identification of the *AKT1*^{E17K} genomic biomarker, coupled with a novel targeted and
74 non-myeloablative agent, could enhance treatment options in *AKT1*^{E17K}-mutant ER+
75 metastatic breast cancer. In this first-in-human, multipart, Phase I expansion study,
76 capivasertib alone or in combination with fulvestrant was well tolerated and showed
77 promising anticancer activity in such a patient population, including those with prior disease
78 progression on fulvestrant. Tolerability and efficacy appeared marginally better with
79 combination therapy, suggesting that combination AKT and ER inhibition is an effective
80 targeted therapy approach for *AKT1*^{E17K}-mutant ER+ metastatic breast cancer. Furthermore,
81 our data provide a rationale for incorporating potentially actionable alterations in breast
82 cancer into diagnostic testing algorithms for the early identification of these alterations in the
83 metastatic disease course.

84 **Abstract** (250/250 words)

85 **Purpose:** The activating mutation *AKT1*^{E17K} occurs in ~7% of ER+ metastatic breast cancer
86 (MBC). We report, from a multipart, first-in-human, Phase I study (NCT01226316), tolerability
87 and activity of capivasertib, an oral AKT inhibitor, as monotherapy or combined with fulvestrant
88 in expansion cohorts of *AKT1*^{E17K}-mutant ER+ MBC patients.

89

90 **Patients and Methods:** Patients with an *AKT1*^{E17K} mutation, detected by local (NGS) or central
91 (plasma-based BEAMing) testing, received capivasertib 480 mg bid, 4 days on, 3 days off,
92 weekly or 400 mg bid combined with fulvestrant at the labeled dose. Study endpoints included
93 safety, objective response rate (ORR; RECIST v1.1), progression-free survival (PFS) and
94 clinical benefit rate at 24 weeks (CBR₂₄). Biomarker analyses were conducted in the
95 combination cohort.

96

97 **Results:** From October 2013 to August 2018, 63 heavily pretreated patients received
98 capivasertib (20 monotherapy, 43 combination). ORR was 20% with monotherapy, and within
99 the combination cohort was 36% in fulvestrant-pretreated and 20% in fulvestrant-naïve patients,
100 although this latter group may have had more aggressive disease at baseline. *AKT1*^{E17K}
101 mutations were detectable in plasma by BEAMing (95%, 41/43), ddPCR (80%, 33/41) and NGS
102 (76%, 31/41). A ≥50% decrease in *AKT1*^{E17K} at cycle 2 day 1 was associated with improved
103 PFS. Combination therapy appeared more tolerable than monotherapy (most frequent grade ≥3
104 adverse events: rash [9% vs 20%], hyperglycemia [5% vs 30%], diarrhea [5% vs 10%]).

105

106 **Conclusions:** Capivasertib demonstrated clinically meaningful activity in heavily pretreated
107 *AKT1*^{E17K}-mutant ER+ MBC patients, including those with prior disease progression on
108 fulvestrant. Tolerability and activity appeared improved by the combination.

109 **Introduction**

110 Estrogen-receptor-positive (ER+), HER2-negative (HER2-) breast cancer is the most common
111 subtype of metastatic breast cancer (MBC), accounting for >400,000 deaths worldwide every
112 year (1, 2). The incorporation of inhibitors of mTOR and CDK4/6 into endocrine therapy has led
113 to substantial improvements in patient outcomes (3-8). However, once endocrine-therapy-
114 refractory disease inevitably develops, chemotherapy remains the only approved option, and
115 little progress has been made for this phase of illness. Given the successes of genomically
116 selected therapy in other solid tumors harboring driver alterations (9, 10), widescale efforts to
117 identify therapeutically actionable genomic subsets of breast cancer have been undertaken (11-
118 15).

119

120 The PI3K pathway is one of the most commonly activated signaling pathways in ER+ breast
121 cancer (16). The efficacy of an isoform-selective PI3K inhibitor in *PIK3CA*-mutant ER+ HER2-
122 MBC was recently demonstrated in a Phase III study (17), providing proof of concept that this
123 pathway is therapeutically targetable in this clinical context. While *PIK3CA* mutations represent
124 the most common mechanism of PI3K pathway activation, in an estimated 7% of ER+ breast
125 cancers, pathway activation can occur through mutation in *AKT1* (15), predominantly *AKT1*^{E17K}
126 (~80%). In such cases, signaling is constitutively activated through pathologic localization of
127 *AKT1* to the plasma membrane (18-20). Although, in the largest comparative analysis of
128 matched *AKT1*-mutant and wild-type ER+ MBC patients, there did not appear to be significant
129 differences in terms of overall survival or duration on endocrine- and CDK4/6 inhibitor therapy,
130 patients with *AKT1*-mutant disease were, however, noted to have significantly longer durations
131 on MTOR inhibitor therapy (21), indicative of the potential therapeutic relevance of this alteration
132 in breast cancer. Moreover, *AKT1*^{E17K}-mutant tumors may not be amenable to PI3K inhibitors
133 owing to their PI3K-independent mechanism of AKT activation (15, 22-27). As such, patients

134 harboring *AKT1*^{E17K} mutations represent a genomic subset of ER+ MBC in need of unique
135 therapeutic approaches.

136

137 Capivasertib (AZD5363) is an oral, potent, selective ATP-competitive pan-AKT kinase inhibitor
138 (28). We previously explored the efficacy of capivasertib monotherapy in patients with advanced
139 solid tumors harboring an *AKT1*^{E17K} mutation, including 20 patients with ER+ MBC, whereby the
140 objective response rate (ORR) was 20% and median progression-free survival (PFS) was 5.5
141 months (29). Consistent with this observation, similar capivasertib monotherapy efficacy was
142 recently reported in the *AKT1*-mutant arm of the NCI-MATCH study in multiple solid tumors,
143 including ER+ MBC (30).

144

145 As observed with isoform-selective PI3K inhibitors, preclinical data with capivasertib suggests
146 that efficacy in ER+ breast cancer may be limited in part by a compensatory increase in ER-
147 dependent gene transcription, suggesting that combination strategies may be required to
148 maximize therapeutic efficacy in this subtype (31-33). Accordingly, preclinical models suggest
149 synergistic efficacy when capivasertib is combined with fulvestrant, an ER antagonist and
150 degrader approved for the treatment of ER+ MBC (32). Therefore, to clinically explore the
151 hypothesis that simultaneous inhibition of AKT and ER would enhance antitumor efficacy in
152 *AKT1*^{E17K}-mutant ER+ breast cancer, we amended the prior Phase I study to include a
153 multicohort expansion of the combination of capivasertib and fulvestrant.

154

155 Here we present the safety, efficacy and biomarker analysis for the combination of capivasertib
156 and fulvestrant in ER+, *AKT1*^{E17K}-mutant MBC. To provide additional clinical context, final
157 results for capivasertib monotherapy in ER+, *AKT1*^{E17K}-mutant MBC are also presented.

158 **Methods**

159 ***Study Design and Participants***

160 The protocol started as the first-in-human, multipart, Phase I, dose- and schedule-finding study
161 of capivasertib. Following identification of a recommended Phase II dose, the safety and
162 efficacy of capivasertib was further explored in multiple molecularly and histologically defined
163 Phase I expansion cohorts recruited at study centers worldwide. Results of the initial dose
164 escalation, pharmacodynamic cohort, and monotherapy efficacy in patients with advanced solid
165 tumors, as well as those with activating *PIK3CA* or *AKT1* mutations, have previously been
166 reported (29, 34). The study start date was December 2010 and the estimated completion date
167 is December 2019 (ClinicalTrials.gov, NCT01226316).

168

169 Here we report the results of capivasertib plus fulvestrant in patients with advanced ER+ breast
170 cancer with *AKT1*^{E17K} mutations, including patients without prior fulvestrant therapy (fulvestrant-
171 naïve cohort) and those who received prior fulvestrant (fulvestrant-pretreated cohort; Figure 1).
172 Updated and final efficacy data of capivasertib monotherapy in ER+ *AKT1*^{E17K}-mutant breast
173 cancer are also included.

174

175 Eligible patients had histologically confirmed ER+, HER2– MBC with progressive measurable
176 disease (according to Response Evaluation Criteria in Solid Tumors [RECIST] v1.1) that was
177 refractory to standard therapies or for which no standard therapies exist, and they harbored an
178 *AKT1*^{E17K} tumor mutation. Qualifying *AKT1*^{E17K} mutations were identified either through local
179 testing, as routinely obtained at participating sites, or via a central plasma-based analysis using
180 the OncoBEAM™ BEAMing (beads, emulsification, amplification, and magnetics) assay with
181 previously described methods (11). Specifically, local testing employed various next-generation
182 sequencing (NGS)-based assays, in accordance with local standard practice without any
183 threshold for positivity mandated by AstraZeneca for enrollment. Central plasma-based

184 BEAMing analysis with the OncoBEAM™ assay used a 0.02% threshold of analyzed *AKT1*
185 copies containing the E17K mutation for positivity (35). Further inclusion criteria included age 18
186 years or older and an Eastern Cooperative Oncology Group (ECOG) performance status of 0 or
187 1. Key exclusion criteria included active central nervous system metastases, prior treatment with
188 catalytic AKT inhibitors (prior exposure to all other agents in the PI3K/AKT/mTOR pathway,
189 including allosteric AKT inhibitors, was allowed), and clinically significant abnormalities of
190 glucose metabolism, defined by any of the following criteria: i) diagnosis of diabetes mellitus
191 type 1 or 2 (irrespective of management); ii) baseline fasting glucose value of ≥ 7 mmol/L
192 (fasting is defined as no calorific intake for at least 8 hours); and iii) glycated hemoglobin
193 (HbA_{1c}) $> 8\%$ (> 64 mmol/mol).

194

195 All patients provided written informed consent, and the study was performed in accordance with
196 the Declaration of Helsinki, Good Clinical Practice, and the AstraZeneca policy on bioethics
197 (36).

198

199 ***Procedures***

200 Monotherapy patients were treated with capivasertib at the previously determined
201 recommended Phase II monotherapy dose of 480 mg (34), administered orally, twice daily (bid)
202 for 4 days on followed by 3 days off, repeated weekly. A treatment cycle was defined as 3
203 weeks. In the combination cohorts, capivasertib was administered at the previously determined
204 recommended Phase II combination therapy dose of 400 mg bid, 4 days on, 3 days off,
205 repeated weekly, in addition to fulvestrant at the labeled dose (37).

206

207 Response assessments were performed by computed tomography (CT) or magnetic resonance
208 imaging (MRI) every two cycles for 24 weeks, then every 12 weeks until disease progression,
209 death, or withdrawal. Safety was assessed throughout the study period and until day 28 after

210 discontinuation of study treatment according to the National Cancer Institute's Common
211 Terminology Criteria for Adverse Events (CTCAE) v4.0. Adverse events were coded with the
212 Medical Dictionary for Regulatory Activities (MedDRA) v19.1.

213

214 Blood was collected at every study visit for analysis of tumor-derived, cell-free DNA (cfDNA).
215 *AKT1*^{E17K} mutation status was assessed in tumor tissue by local testing and/or in cfDNA by
216 central testing using BEAMing (OncoBEAM™, Sysmex Inostics, Baltimore, MD, USA) (38) and
217 droplet digital polymerase chain reaction technology (ddPCR) with an allele-specific assay for
218 both the mutant and the wild-type allele (39). Central NGS was performed retrospectively on
219 tumor tissue when available, by FoundationOne (40), and on cfDNA using a hybrid capture-
220 based panel covering 300 genes (AZ300).

221

222 **Outcomes**

223 The primary study endpoint was safety and tolerability of capivasertib in combination with
224 fulvestrant. Secondary endpoints included: ORR, defined as a confirmed partial response (PR)
225 or complete response (CR); duration of response (DOR), defined as the time from confirmed
226 objective response to disease progression or death; PFS, defined as the time from the first day
227 of treatment to disease progression or death; and clinical benefit rate at 24 weeks (CBR₂₄),
228 defined as disease response (PR or CR) or stabilization for ≥24 weeks. Responses were
229 investigator assessed according to RECIST v1.1 and required confirmation. Patients who
230 discontinued prior to their first response assessment were considered non-evaluable for best
231 overall response and non-responders by intent-to-treat analysis.

232

233 **Statistical Analysis**

234 All analyses were conducted according to the protocol and statistical analysis plan (and were as
235 previously reported for the monotherapy cohort) (29). Although the primary endpoint throughout

236 this multipart Phase I study remained safety and tolerability, the sample size of the expansion
237 cohort reported here was determined with the aim of detecting a signal of efficacy, should one
238 exist, using CBR₂₄. The capivasertib and fulvestrant combination cohorts underwent protocol-
239 specified analyses, conducted independently for each (fulvestrant-naïve and fulvestrant-
240 pretreated) cohort, when 12 patients (at interim analysis) and 24 (at final analysis) per cohort
241 were evaluable for CBR₂₄ (Figure 1). The sample size was determined based on pre-specified
242 target values for CBR₂₄ of 65% and 40% for fulvestrant-naïve and fulvestrant-pretreated
243 patients, respectively (with 24 patients per cohort, there would be a 90% chance of at least 13
244 and 7 clinical benefit responses, respectively). At interim analysis, enrollment to the fulvestrant-
245 naïve cohort halted, while the fulvestrant-pretreated cohort continued and completed accrual.
246 Eight subsequent patients who were being screened at the time of closing each cohort were
247 permitted to enroll, leading to a total of 16 and 28 patients in the fulvestrant-naïve and
248 fulvestrant-pretreated cohorts, respectively. Final analysis occurred on August 7, 2018, when all
249 44 patients had had the opportunity to reach 24 weeks of treatment. All patients who received at
250 least one dose of capivasertib (n=44) were evaluable for safety. Efficacy data are reported for
251 43 *AKT1*^{E17K}-mutant patients and exclude one patient enrolled with a non-E17K mutation
252 (*AKT1*^{E40K}).

253
254 DOR and PFS were estimated using the Kaplan–Meier method. Patients without a progression
255 event as of the analysis date were censored at the last known assessment. *Post hoc* analyses
256 of endocrine-sensitive and -pretreated subpopulations and of patients treated with ≤2 or ≥3 prior
257 lines of chemotherapy for MBC were performed. Patients were defined as sensitive to prior
258 endocrine therapy if they had ≥24 months of endocrine therapy before recurrence in the
259 adjuvant setting and/or a response or stabilization for ≥6 months of endocrine therapy for
260 advanced disease. Exploratory biomarker analyses investigated the association between cfDNA

261 response, defined as >50% decrease in *AKT1*^{E17K}-mutant copies/mL plasma from baseline to
262 cycle 2 day 1, and radiographic response. All analyses were done with SAS v9.04.

263 **Results**

264 ***Patient Characteristics***

265 Sixty-three *AKT1*^{E17K}-mutant ER+ MBC patients received capivasertib either as monotherapy
266 (n=20) or in combination with fulvestrant (n=43; Table 1). The majority of combination therapy
267 patients were enrolled based on *AKT1*^{E17K} mutation detection by local laboratory testing of tumor
268 tissue (77%, 33/43), with the remaining (n=10) patients enrolled through central laboratory
269 plasma testing. Among patients who received the combination, 28 were previously fulvestrant
270 pretreated and 15 were fulvestrant naïve. Median age was 57 years (range: 38–76). Most
271 patients had visceral disease at enrollment (87%) and were heavily pretreated. Overall, 91% of
272 patients had received prior chemotherapy, 35% mTOR inhibitors, and 24% CDK4/6 inhibitors for
273 metastatic disease. Only 54% of patients exhibited sensitivity to prior endocrine therapy, defined
274 by at least 24 months of endocrine therapy before recurrence in the adjuvant setting and/or a
275 response or stabilization for at least 6 months of endocrine therapy for advanced disease.
276 However, caution should be exercised in interpreting this seemingly low rate of endocrine
277 therapy sensitivity compared with rates of ~80% reported in pivotal Phase III trials conducted in
278 ER+ MBC patients (5, 41), given the retrospective and exploratory nature of this analysis. In
279 combining both monotherapy and combination therapy cohorts, certain differentiating baseline
280 characteristics were apparent between the fulvestrant-naïve (n=21) and fulvestrant-pretreated
281 (n=42) patients. Specifically, a high proportion of fulvestrant-naïve patients were treated with
282 first-line chemotherapy in the metastatic setting (38% vs 12%, respectively) and had received
283 fewer total lines of endocrine therapy (median 2 vs 4, respectively).

284

285 ***Safety***

286 Adverse events (AEs) causally linked to study treatment by the investigator are shown in
287 Table 2. The most common all-grade AEs for the monotherapy cohort were diarrhea (65%),
288 nausea (50%), hyperglycemia (45%), and vomiting (45%). Similarly, for the combination cohort,

289 the most common AEs were diarrhea (59%), nausea (30%), maculopapular rash (21%), fatigue
290 (18%), and hyperglycemia (18%). Grade ≥ 3 AEs attributed to study treatments were observed in
291 50% of patients in the monotherapy cohort, most commonly hyperglycemia (30%) and
292 maculopapular rash (20%), and 21% of patients in the combination cohort, most commonly
293 maculopapular rash (9%). AEs irrespective of causality are shown in Supplementary Table 1.
294 No new safety signals were identified with the combination of fulvestrant.

295
296 Median duration of capivasertib exposure in the monotherapy cohort and combination cohort
297 was 166 days (mean daily dose 870 mg) and 123 days (775 mg), respectively. In the
298 monotherapy cohort, 13 (65%) patients required dose interruption, 7 (35%) dose reduction, and
299 1 (5%) discontinuation as a result of a treatment-related AE (confusion). In the combination
300 cohort, 19 (43%) patients required dose interruption, 4 (9%) dose reduction, and 5 (11%)
301 discontinuation because of an AE (Supplementary Table 2), three of which were treatment
302 related (eosinophilic pneumonia, fatigue, and rash). There were no treatment-related or AE-
303 attributable deaths in either cohort.

304

305 ***Efficacy Analyses***

306 At the time of data cut-off, seven patients remained on therapy, the majority having discontinued
307 because of disease progression (Supplementary Figure 1). Median follow-up (time to event) for
308 all capivasertib-treated patients who were censored at the time of primary analysis was 8.1
309 months (range: 0–27.5). Efficacy in the monotherapy cohort and combination cohorts (overall
310 and by prior fulvestrant therapy exposure) is shown in Table 3 and Figures 2 and 3. Among
311 patients receiving combination therapy, ORR was 36% (95% CI: 19–56) in fulvestrant-
312 pretreated patients and 20% (95% CI: 4–48) in fulvestrant-naïve patients. ORR in the
313 monotherapy cohort was 20% (95% CI: 8–58). Across both monotherapy and combination

314 cohorts (n=63), ORR was 33% (95% CI: 20–50) in fulvestrant-pretreated patients and 14%
315 (95% CI: 3–36) in fulvestrant-naïve patients. Despite the numerically higher ORRs observed in
316 the fulvestrant-pretreated patients, CBR₂₄ was broadly similar across groups. Specifically, in the
317 combination cohort, CBR₂₄ was 50% (95% CI: 31–69) in fulvestrant-pretreated and 47% (95%
318 CI: 21–73) in fulvestrant-naïve patients. Across both monotherapy and combination cohorts,
319 CBR₂₄ was 50% (95% CI: 34–66) in fulvestrant-pretreated and 43% (95% CI: 22–66) in
320 fulvestrant-naïve patients.

321
322 To determine whether additional patient and treatment characteristics could further enrich for
323 patients who experienced benefit from capivasertib, several exploratory *post hoc* subgroup
324 analyses were conducted. Across monotherapy and combination therapy patients, ORR and
325 CBR₂₄ were numerically higher in patients who had received ≤2 prior lines of chemotherapy
326 (35% and 62%, respectively) compared with those who had received ≥3 prior lines (22% and
327 38%, respectively; Supplementary Table 3). Analyses classifying patients based on prior
328 endocrine therapy sensitivity were also conducted but did not clearly predict benefit of
329 capivasertib-based therapy.

330

331 ***Exploratory Biomarker Analyses***

332 Central biomarker assessments in the combination cohort utilized a variety of assays. Central
333 tissue NGS was performed in 42% (18/43) of patients. BEAMing was used for mutation
334 detection in plasma cfDNA collected at screening and detected the *AKT1*^{E17K} mutation in 95%
335 (41/43) of patients. ddPCR and broader NGS profiling were performed on plasma cfDNA
336 collected on the first day of treatment (cycle 1 day 1), detecting the *AKT1*^{E17K} mutation in 80%
337 (33/41) and 76% (31/41) of patients tested, respectively (Figure 3). These data demonstrate that
338 plasma-based analyses offer an additional diagnostic opportunity for *AKT1*^{E17K} mutation testing

339 (35). In this cohort, a $\geq 50\%$ decrease from baseline at cycle 2 day 1 was associated with
340 improved PFS (Supplementary Figure 2), similar to that previously demonstrated in the
341 monotherapy cohort (29).

342

343 In 41 patients tested, the broader genetic profiling of plasma samples by NGS identified co-
344 occurring alterations in *ESR1* (n=10, almost all in fulvestrant-pretreated patients and all in those
345 with a detectable *AKT1*^{E17K} mutation by plasma NGS), *TP53* (n=8, predominantly in fulvestrant-
346 naïve patients), *MAP3K1* (n=4), *PIK3CA* (n=4) and *FGFR1* (n=2) (Figure 3). In one of the
347 *PIK3CA*-mutant cases, despite an *AKT1*^{E17K} mutation being detected by BEAMing at a very low
348 mutant allele fraction (MAF), the *AKT1*^{E17K} mutation was not in fact detectable by NGS,
349 indicative of the subclonality of the alteration in this patient (Supplementary Figure 3). Evidence
350 of a subclonal *AKT1*^{E17K} mutation could also be found in another patient, in whom the *AKT1*^{E17K}
351 mutation was detected by BEAMing and ddPCR but not by the NGS analysis that detected other
352 somatic mutations in this patient. While 8 (20%) patients did not shed sufficient circulating tumor
353 DNA for mutation detection by NGS (ie low shedders), in all other (31; 94%) patients, the
354 *AKT1*^{E17K} mutation was detected at a level around or above the median MAF indicative of the
355 predominantly clonal nature of this alteration (Figure 3 and Supplementary Figure 3). In this
356 limited sample set, no obvious pattern in *AKT1*^{E17K} clonality or co-incident tumor mutations was
357 associated with clinical outcome, although, potentially of interest, 6 of the 8 (75%) cases
358 identified as low shedders by NGS had an objective response, and none of the patients whose
359 tumors harbored a *TP53* mutation achieved an objective response. While the sample size was
360 small, the observed higher frequency of *TP53* mutations in the fulvestrant-naïve compared with
361 the fulvestrant-pretreated cohort (33% vs 12%, respectively) potentially supports the
362 observation that this group had more aggressive disease biology (42). Equally, the identified
363 *TP53* mutations could be related to the greater degree of cytotoxic chemotherapy exposure in
364 this cohort (43, 44). An integrated analysis of efficacy and genomic data is shown in Figure 3.

365 **Discussion**

366 In this multicohort Phase I study, we sequentially explored the safety and efficacy of the pan-
367 AKT inhibitor capivasertib, initially alone and later in combination with fulvestrant, in ER+
368 *AKT1*^{E17K}-mutant MBC patients. The safety profile was similar to that in prior reports (29, 34, 45),
369 although combination therapy appeared better tolerated, likely because of the lower dose of
370 capivasertib (400 mg bid 4 days on, 3 days off) administered with fulvestrant compared with the
371 monotherapy dose of capivasertib (480 mg bid 4 days on, 3 days off), as suggested by the
372 dose–response relationship observed for key capivasertib-related toxicities such as
373 hyperglycemia (46).

374

375 Although the study was not designed to directly compare activity across groups, and noting that
376 the fulvestrant-naïve (n=21) patients treated in this study may have had a more aggressive
377 disease profile at baseline than those who were fulvestrant pretreated (n=42), optimal efficacy
378 was nonetheless observed with combination therapy, specifically in fulvestrant-pretreated
379 patients (ORR 36%; CBR₂₄ 50%). Taken together, these findings are encouraging, particularly
380 given the heavily pretreated nature of the study population. There is also reason to believe that
381 our data compare favorably with prior reports on molecular therapy in the clinic. For example,
382 BELLE-3 evaluated fulvestrant, with or without the pan-PI3K inhibitor buparlisib, in mTOR-
383 inhibitor-exposed patients, reporting, respectively, an ORR of 8% versus 2% and CBR₂₄ of 25%
384 versus 15% (47). This provides a useful benchmark for fulvestrant monotherapy following
385 mTOR inhibitor exposure in a notably less pretreated (no more than one line of chemotherapy
386 and no prior fulvestrant were permitted) population. Similarly, our data compare favorably with
387 expected chemotherapy outcomes in endocrine-resistant patients (48).

388

389 The benefit of adding capivasertib to hormone therapy in *AKT1*^{E17K}-mutant patients is consistent
390 with preclinical data (32). More broadly, the role for co-targeting ER and PI3K pathway

391 alterations has been demonstrated in multiple randomized, Phase III studies of PI3K inhibitors
392 (17, 49). Furthermore, in the recently reported randomized Phase II FAKTION study, the
393 addition of capivasertib to fulvestrant showed a significant improvement in PFS in a molecularly
394 unselected, aromatase-inhibitor-pretreated but fulvestrant-naïve ER+ MBC population (50).
395 Given the increasing genomic complexity of breast cancer as it advances through multiple lines
396 of therapy, this recent trial report supports our observation and hypothesis, and others', that
397 earlier introduction of targeted therapies to a less clonally diverse disease is likely to be
398 necessary to garner significant improvements in outcome in patients harboring these driver
399 oncogenic alterations (14).

400

401 Acknowledging that only 24% of enrolled patients in this study received prior CDK4/6 inhibitors,
402 agents that are now standard of care in combination with an aromatase inhibitor or fulvestrant in
403 the first- or second-line setting, these data remain of interest. Outcomes of targeted therapy
404 following CDK4/6 inhibitor exposure in ER+ MBC are largely unknown. However, preclinical
405 models with acquired resistance to CDK4/6 inhibitors do indicate retained sensitivity to PI3K
406 pathway inhibition combined with endocrine therapy (51, 52). Indeed, in SOLAR-1, the small
407 subset of patients with prior CDK4/6 inhibitor exposure did still appear to derive benefit from the
408 addition of apelisib to fulvestrant (17). Additionally, of interest, recent preclinical data have
409 implicated PTEN loss, as a potential mechanism of resistance to CDK4/6 inhibitors, via
410 increased AKT activation *in vitro* and *in vivo* (53), a hypothesis since observed in the clinic
411 where enrichment of *PTEN* loss-of-function alterations has been described in tumor samples
412 obtained after CDK4/6 inhibitor therapy (54). Intriguingly, in this context (PTEN-null models
413 resistant to CDK4/6 inhibitors), AKT inhibition may in fact be superior to PI3K inhibition (53). It is
414 also clear from preclinical work that constitutively active AKT induces resistance to PI3K
415 inhibition in breast cancer cell lines, and, interestingly, increased *AKT1* expression was
416 identified in a very small cohort of biopsies collected post-treatment with alpelisib (55). Clinical

417 data demonstrating a role for *AKT1* mutations mediating resistance to anti-estrogens or CDK4/6
418 inhibitors are limited. A recent clinical series (n=57) noted an over-representation of PI3K
419 pathway mutations (*PIK3CA*, *AKT1*, *TSC2*, and/or loss or truncation mutations of *PTEN*) among
420 patients with a poor response to neoadjuvant letrozole (Pre-operative Endocrine Prognostic
421 Index [PEPI] >4 and/or recurrence), although this was unlikely to be driven by *AKT1*, as none of
422 the three *AKT1*-mutant cases in this report experienced a recurrence and two of the three were
423 actually categorized in the responder group (PEPI <4 and no recurrence) (56). Additionally, an
424 endocrine-therapy-exposed ER+ breast cancer dataset did not identify *AKT1* mutations in
425 tumors intrinsically resistant to letrozole; rather, *AKT1* mutations were detected in those
426 sensitive to the therapy (57, 58). In agreement with this, genomic profiling of a large (n=1501)
427 cohort of endocrine-therapy-naïve versus endocrine-therapy-exposed ER+ breast cancers did
428 not show any evidence of *AKT1* mutations being associated with resistance to hormonal therapy
429 (15). Finally, findings from a recent institutional dataset (n=58) have proposed activating events
430 in *AKT1* as a possible mechanism of resistance to therapy containing CDK4/6 inhibitors, along
431 with *in vitro* data showing overexpression of *AKT1* as conferring resistance to CDK4/6 inhibitors
432 (50), although, thus far, this has not been observed in genomic analysis from the registration
433 studies of these agents (59, 60). Moreover, genomic analysis of 348 ER+ breast cancers
434 treated with CDK4/6 inhibitors, as well as comparative analysis of tumors before (n=838) versus
435 after (n=221) CDK4/6 inhibitor therapy, along with paired analysis of tumors before versus after
436 CDK4/6 inhibitor therapy (n=210), has not identified an association between *AKT1* mutations
437 and therapeutic resistance to CDK4/6 inhibitors (54, 61).

438

439 Our study has several important limitations. Firstly, this trial was not formally powered to
440 compare efficacy across treatment groups. Secondly, although efficacy appeared most robust in
441 fulvestrant-pretreated patients, it is noteworthy that the fulvestrant-naïve patients enrolled here
442 appeared to be a subgroup with poorer prognosis. Given this, we cannot rule out the role that

443 demographic imbalance between the groups driven by adverse patient selection factors may
444 have played in the apparent difference in treatment outcomes. Thirdly, we do not know the
445 extent to which the presence of an *AKT1*^{E17K} mutation may influence the natural history or
446 response to standard therapy for MBC. Despite this, recent analyses suggest that prognoses of
447 *AKT1*^{E17K}-mutant and wild-type MBC patients appear largely comparable, somewhat mitigating
448 this concern (21). Finally, despite opening this study at 16 sites internationally, the rarity of this
449 biomarker led to slow accrual (22 months to enroll 44 patients in the combination cohort),
450 despite having central screening by BEAMing in plasma implemented, in addition to local
451 testing.

452

453 In conclusion, this study demonstrates that *AKT1*^{E17K} is a clinically relevant, valid target in ER+
454 breast cancer and that the AKT inhibitor capivasertib is tolerable and active as both
455 monotherapy and in combination with fulvestrant, including in patients with prior fulvestrant
456 resistance. We confirm that the majority of enrolled patients had detectable *AKT1*^{E17K} in plasma
457 at baseline and demonstrate the feasibility of enrollment based on centralized plasma screening
458 for this rare genomic biomarker (35). With other genomic biomarkers such as *PIK3CA* mutations
459 expected to become part of routine management paradigms over the coming years in breast
460 cancer, these data have the prospect of becoming part of a rationale to incorporate other
461 potentially actionable alterations in breast cancer, including *ERBB2* and *AKT1*, into diagnostic
462 testing algorithms and for the early identification of these alterations in the metastatic disease
463 course (62, 63). Finally, data from this study, along with the FAKTION study, have provided the
464 basis for a confirmatory Phase III study that will take into account populations with and without
465 prior use of CDK4/6 inhibitors.

466

467

468 **Acknowledgments**

469 This study was sponsored by AstraZeneca. Capivasertib was discovered by AstraZeneca
470 subsequent to a collaboration with Astex Therapeutics (and its collaboration with the Institute of
471 Cancer Research and Cancer Research Technology Limited). U. Banerji acknowledges
472 infrastructural funding from Cancer Research UK, Experimental Cancer Medicine Centre and
473 Biomedical Research Centre grants, in addition to a National Institutes of Health Research
474 Professorship award (RP-2016-07-028). All investigators at Memorial Sloan Kettering Cancer
475 Center (L.M. Smyth, M. Scaltriti, B.S. Taylor, S. Chandarlapaty, J. Baselga, D.M. Hyman) wish
476 to acknowledge the support of the NCI Cancer Center Support Grant (CCSG P30 CA08748). S.
477 Chandarlapaty acknowledges support of the BCRF. We are grateful for the assistance of Neville
478 Cope, Lucy Keeling, Jayantha Ratnayake and Carolina Salinas-de Souza for contributing to
479 the preparation of this manuscript. We thank the patients and their carers who participated in
480 this study. Medical writing assistance was provided by Martin Goulding, DPhil and Kristin
481 Almond, PhD from Mudskipper Business Ltd, funded by AstraZeneca. Capivasertib (AZD5363)
482 is an investigational medical product with no approved indication.

483

484 The study sponsor, AstraZeneca, provided organizational support, obtained data, performed the
485 analyses, and had a role in data interpretation and writing of the manuscript. All authors had
486 access to study data, and the corresponding author had final responsibility for the decision to
487 submit the manuscript for publication.

488

489

490 **Data-Sharing Statement**

491 Data underlying the findings described in this manuscript may be obtained in accordance with
492 AstraZeneca's data sharing policy described at:

493 <https://astrazenecagrouptrials.pharmacm.com/ST/Submission/Disclosure>.

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683

Table 1. Baseline Characteristics in Patients With ER+ HER2– *AKT1*^{E17K}-Mutant Metastatic Breast Cancer

	Capivasertib	Capivasertib + Fulvestrant		All Capivasertib-Treated Patients		
	Monotherapy	(N=43) ^a		(N=63) ^a		
	Breast-Specific Cohort (N=20)	Fulvestrant Naïve (n=15)	Fulvestrant Pretreated (n=28)	Fulvestrant Naïve (n=21)	Fulvestrant Pretreated (n=42)	Total (n=63) ^a
Median age, years (range)	57 (38–71)	58 (42–76)	56 (40–73)	57 (39–76)	57 (38–73)	57 (38–76)
Female gender, n (%)	20 (100)	15 (100)	28 (100)	21 (100)	42 (100)	63 (100)
Race, n (%)						
White	16 (80)	9 (60)	18 (64)	12 (57%)	31 (74)	43 (68)
Asian	1 (5)	6 (40)	5 (18)	7 (33%)	5 (12)	12 (19)
Black	2 (10)	0	1 (4)	1 (5%)	2 (5)	3 (5)
Other/missing	1 (5)	0	4 (14)	1 (5%)	4 (10)	5 (8)
WHO/ECOG performance status, n (%)						
0	10 (50)	4 (27)	10 (36)	8 (38)	16 (38)	24 (38)
1	10 (50)	11 (73)	18 (64)	13 (62)	26 (62)	39 (62)
Hormone receptor status ^b						
ER+ and PR+, n (%)	14 (70)	11 (73)	23 (82)	15 (71)	33 (79)	48 (76)
ER+ and PR–, n (%)	5 (25)	4 (27)	5 (18)	5 (24)	9 (21)	14 (22)
HER2–, n (%)	20 (100)	15 (100)	28 (100)	21 (100)	42 (100)	63 (100)
Visceral disease, n (%)	20 (100)	12 (80)	23 (82)	18 (86)	37 (88)	55 (87)

Median number of prior anticancer regimens,						
n (range) ^c						
Total	7 (3–14)	4 (1–7)	6 (2–12)	5 (1–7)	7 (2–14)	6 (1–14)
Chemotherapy	4 (0–6)	2 (0–5)	2 (0–6)	3 (0–5)	3 (0–6)	3 (0–6)
Endocrine therapy	4 (0–7)	1 (0–4)	4 (2–6)	2 (0–4)	4 (1–7)	3 (0–7)
Number of prior endocrine therapies, n (%) ^c						
1	1 (5)	6 (40)	0	6 (29)	1 (2)	7 (11)
2	4 (20)	5 (33)	5 (18)	8 (38)	6 (14)	14 (22)
≥3	14 (70)	2 (13)	23 (82)	4 (19)	35 (83)	39 (62)
Prior endocrine therapy ^c						
Aromatase inhibitor	0	6 (40)	8 (29)	6 (29)	8 (19)	14 (22)
Tamoxifen	0	3 (20)	0	3 (14)	0	3 (5)
Aromatase inhibitor and tamoxifen	18 (90)	4 (27)	20 (71)	9 (43)	33 (79)	42 (67)
Prior sensitivity to endocrine therapy, n (%) ^d						
Prior chemotherapy for metastatic disease,	11 (55)	7 (47)	16 (57)	10 (48)	24 (57)	34 (54)
n (%)	19 (95)	12 (80)	26 (93)	17 (81)	40 (95)	57 (91)
Chemotherapy as first-line therapy in the metastatic setting, n (%)						
Prior CDK4/6 inhibitor, n (%)	5 (25)	6 (40)	2 (7)	8 (38)	5 (12)	13 (21)
Prior mTOR inhibitor, n (%)	3 (15)	1 (7)	11 (39)	2 (10)	13 (31)	15 (24)
Prior P13K inhibitor, n (%)	11 (55)	2 (13)	9 (32)	4 (19)	18 (43)	22 (35)
Prior P13K inhibitor, n (%)	1 (5)	1 (7)	4 (14)	1 (5)	5 (12)	6 (10)

Percentage calculated based on total N in each treatment group. In the monotherapy group, 6 patients were fulvestrant naïve and 14 fulvestrant pretreated. ^aExcludes one non-*AKT1*^{E17K} patient, who was enrolled based on an *AKT1*^{E40K} mutation detected by local NGS; ^bIncludes both primary and metastatic biopsy; ^cInclusive of adjuvant or metastatic therapies; ^dDefined by at least 24 months of endocrine therapy before recurrence in the adjuvant setting and/or a response or stabilization for at least 6 months of endocrine therapy for advanced disease. ECOG, Eastern Cooperative Oncology Group; ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; PR, progesterone receptor; WHO, World Health Organization.

Table 2. AEs Causally Linked to Study Treatment (>10% of Patients) and Grade ≥3 AEs (>2 Patients)

AE by Preferred Term	Capivasertib		Capivasertib + Fulvestrant		Total (N=64) ^a	
	Breast-Specific Cohort (N=20)		Combination (N=44) ^a		All grades	Grade ≥3
	All grades	Grade ≥3	All grades	Grade ≥3	All grades	Grade ≥3
Any AE (causally related to capivasertib), n (%)	19 (95)	10 (50)	38 (86)	9 (21)	57 (89)	19 (30)
Diarrhea	13 (65)	2 (10)	26 (59)	2 (5)	39 (61)	4 (6)
Nausea	10 (50)	0	13 (30)	1 (2)	23 (36)	1 (2)
Hyperglycemia	9 (45)	6 (30)	8 (18)	2 (5)	17 (27)	8 (13)
Vomiting	9 (45)	0	7 (16)	0	16 (25)	0
Fatigue	8 (40)	0	8 (18)	1 (2)	16 (25)	1 (2)
Rash maculopapular	6 (30)	4 (20)	9 (21)	4 (9)	15 (23)	8 (13)
Decreased appetite	3 (15)	0	7 (16)	1 (2)	10 (16)	1 (2)
Stomatitis	4 (20)	0	6 (14)	0	10 (16)	0
Dry skin	4 (20)	0	3 (7)	0	7 (11)	0
Abdominal pain	4 (20)	0	2 (5)	0	6 (9)	0
Dizziness	4 (20)	0	2 (5)	0	6 (9)	0
Pruritus	3 (15)	0	3 (7)	0	6 (9)	0
Dry mouth	4 (20)	0	0	0	4 (6)	0

Includes AEs with an onset date on or after the date of first dose and up to and including 28 days following the date of last dose of study. A patient is only counted once for each preferred term. ^aIncludes one non-*AKT1*^{E17K} patient excluded from the efficacy analyses, who was enrolled based on an *AKT1*^{E40K} mutation detected by local NGS. AE, adverse event; NGS, next-generation sequencing.

Table 3. Treatment Efficacy for Patients With ER+ HER2– AKT1^{E17K}-Mutant Metastatic Breast Cancer

	Capivasertib Monotherapy	Capivasertib + Fulvestrant Combination (N=43)		All Capivasertib-Treated Patients (N=63)		
Breast-Specific Cohort	Fulvestrant Naïve	Fulvestrant Pretreated	Fulvestrant Naïve	Fulvestrant Pretreated	Total (n=63)	
(N=20)	(n=15)	(n=28)	(n=21)	(n=42)		
Objective response ^a						
ORR, % (95% CI)	20 (8–58)	20 (4–48)	36 (19–56)	14 (3–36)	33 (20–50)	27 (17–40)
Complete response, n (%)	0	0	0	0	0	0
Partial response, n (%)	4 (20)	3 (20)	10 (36)	3 (14)	14 (33)	17 (27)
DOR ≥6 months, n (%)	2 (10)	3 (20)	8 (29)	3 (14)	10 (24)	13 (21)
Stable disease 24 weeks, n (%)	5 (25)	4 (27)	4 (14)	6 (29)	7 (17)	13 (21)
Clinical benefit rate at 24 weeks, % (95% CI) ^b	45 (23–69)	47 (21–73)	50 (31–69)	43 (22–66)	50 (34–66)	48 (35–61)
Median PFS, months (95% CI)	5.4 (3–7)	5.6 (2–14)	5.0 (3–8)	5.4 (3–10)	5.0 (4–7)	5.4 (4–7)

Response is based on investigator tumor assessments in accordance with RECIST v1.1 in patients with measurable disease. ^aConfirmed no fewer than 4 weeks after the criteria for response were initially met; ^bClinical benefit defined as confirmed best overall response of complete response, partial response, or stable disease for at least 24 weeks. CI, confidence interval; DOR, duration of response; ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; ORR, objective response ratio; PFS, progression-free survival; RECIST, Response Evaluation Criteria in Solid Tumors.

Figure 1. Study Design of the ER+ AKT1-Mutant Breast Cancer Patient Cohorts

The breast cancer cohorts were part of a larger open-label, multipart, Phase I study of the first-in-human evaluation of oral capivasertib in patients with advanced solid malignancies. These Phase I expansion cohorts were non-randomized; the monotherapy cohort enrolled first, followed by the combination therapy cohort. Protocol-specified analyses planned for each study part: For monotherapy, analyses were planned after 20 patients were followed up for 12 weeks/withdrawn from the study. For combination therapy, interim analysis was planned after 12 patients in each cohort were followed up for 24 weeks/withdrawn from the study, and final analysis was planned after up to 24 patients in total in each cohort were followed up for 24 weeks/withdrawn from the study. ^aUp to 120. CBR₂₄, clinical benefit rate at 24 weeks; ER, estrogen receptor; ORR, objective response rate; PFS, progression-free survival.

Figure 2. Efficacy of Capivasertib Monotherapy in ER+ AKT1^{E17K}-Mutant MBC (n=20)

Plot based on patients with available RECIST data at baseline and at least one follow-up assessment. Investigator-assessed best percentage change from baseline was the change in the sum of longest diameters of target lesions. BoR, best objective response; ER, estrogen receptor; MBC, metastatic breast cancer; PFS, progression-free survival; RECIST, Response Evaluation Criteria in Solid Tumors.

Figure 3. Combined Efficacy and Biomarker Data From the Combination Therapy (Capivasertib + Fulvestrant) Cohort in ER+ AKT1^{E17K}-Mutant MBC (n=43)

Best RECIST response and associated PFS integrated with genomic analyses for all 43 patients enrolled in the combination cohorts. Top to bottom: prior exposure to a CDK4/6 inhibitor; best objective response; best change from baseline in target lesion diameter according to RECIST v1.1; PFS in months; AKT1^{E17K} mutation detection at baseline by various testing platforms (BEAMing, ddPCR, NGS) in tissue and/or ctDNA, and at C2D1 by ddPCR in ctDNA; and percentage change (≥50% decrease) in AKT1^{E17K}-mutant copies in ctDNA by ddPCR measured on C2D1 of study treatment compared with baseline (C1D1). For 33 patients with somatic mutations detected in ctDNA by NGS, the AKT1^{E17K} MAF, as well as the MAF from other key alterations, is presented together with the median MAF of all somatic mutations detected in each sample. Two patients lacked genomic data (not tested), and eight patients had no somatic

mutations detected in their ctDNA samples by NGS, although they did by the more sensitive OncoBEAM™ and/or ddPCR assays and were deemed low shedders. Key co-occurring gene mutations detected by NGS analysis in ctDNA samples are indicated in the genomic heat map at the bottom of the figure. AF, allele frequency; C1D1, cycle 1 day 1; C2D1, cycle 2 day 1; ctDNA, circulating tumor DNA; ddPCR, droplet digital polymerase chain reaction; ER, estrogen receptor; FMI, Foundation Medicine, Inc; MAF, mutant allele fraction; MBC, metastatic breast cancer; NGS, next-generation sequencing; PFS, progression-free survival; RECIST, Response Evaluation Criteria in Solid Tumors.

Figure 1

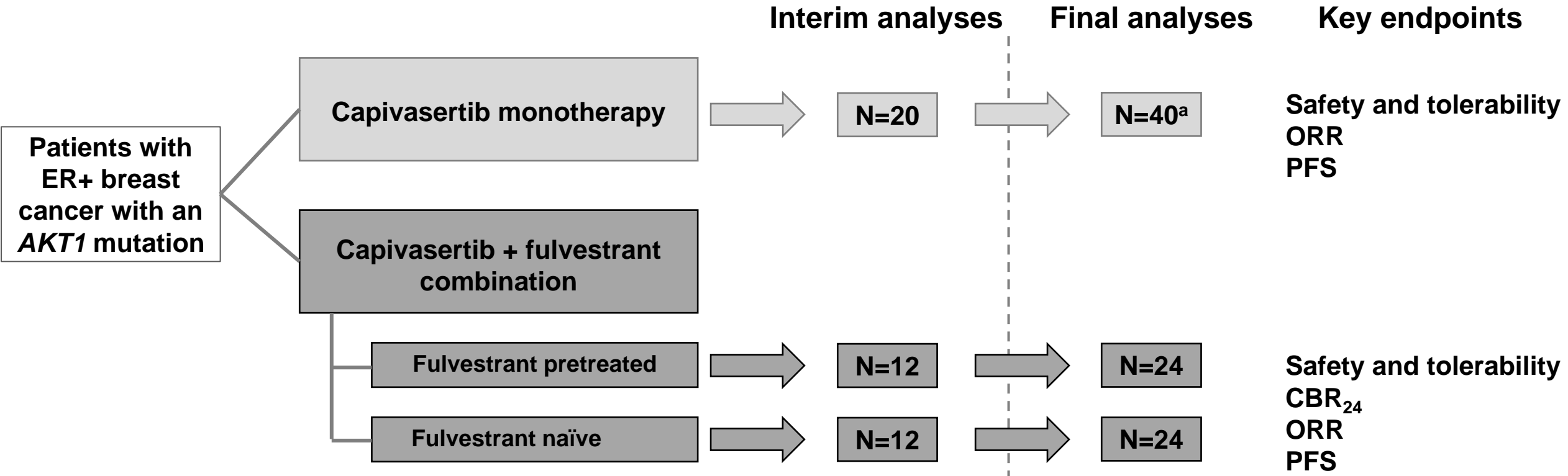
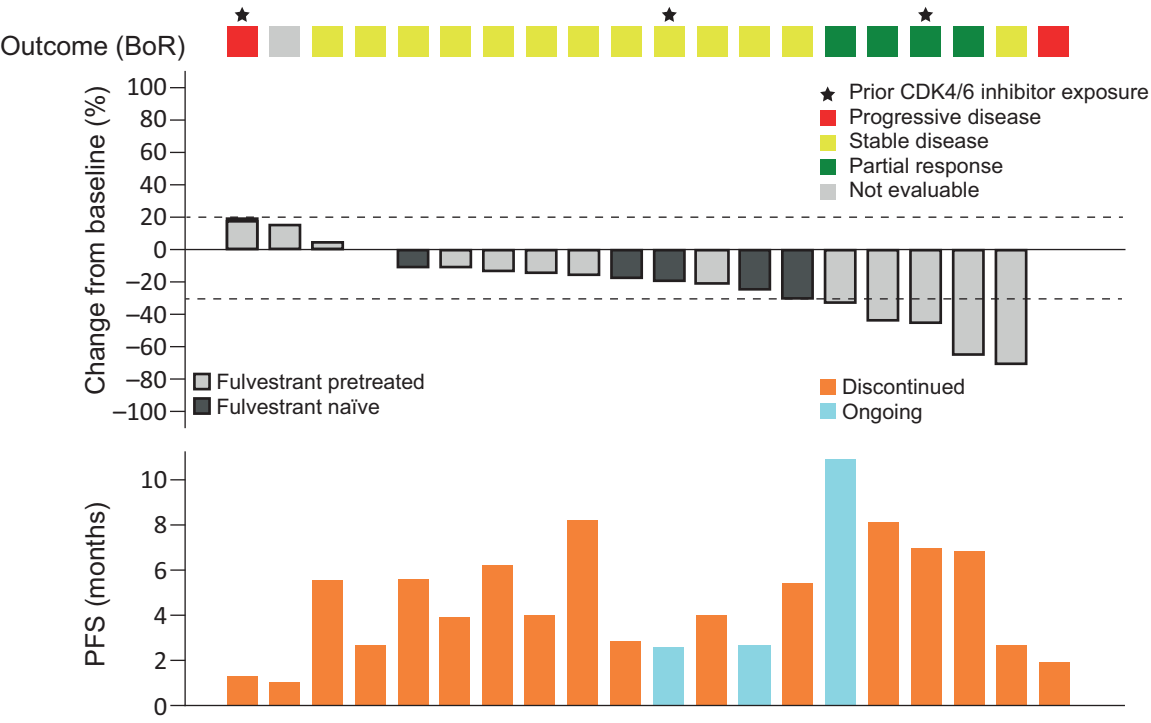
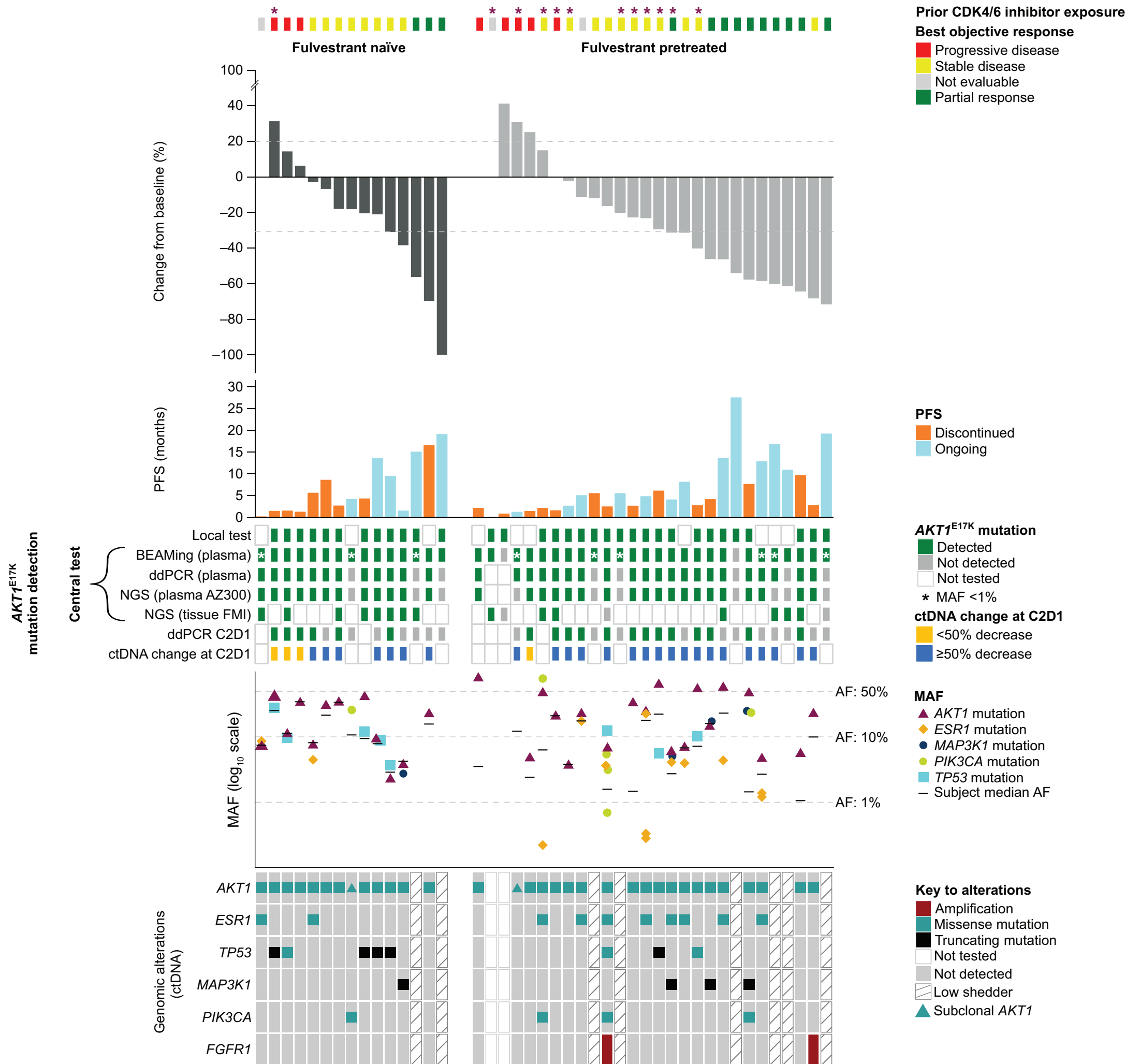
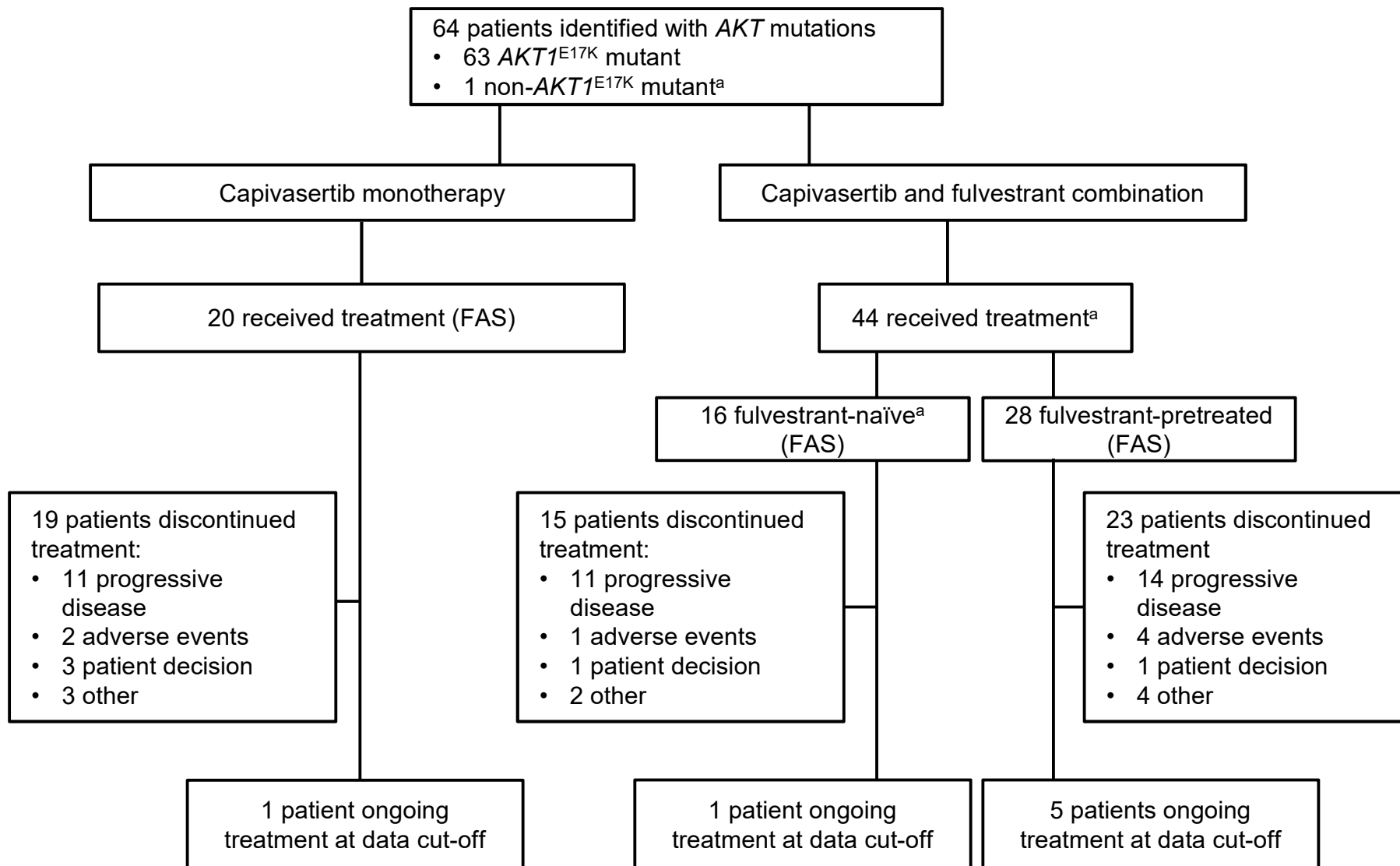


Figure 2



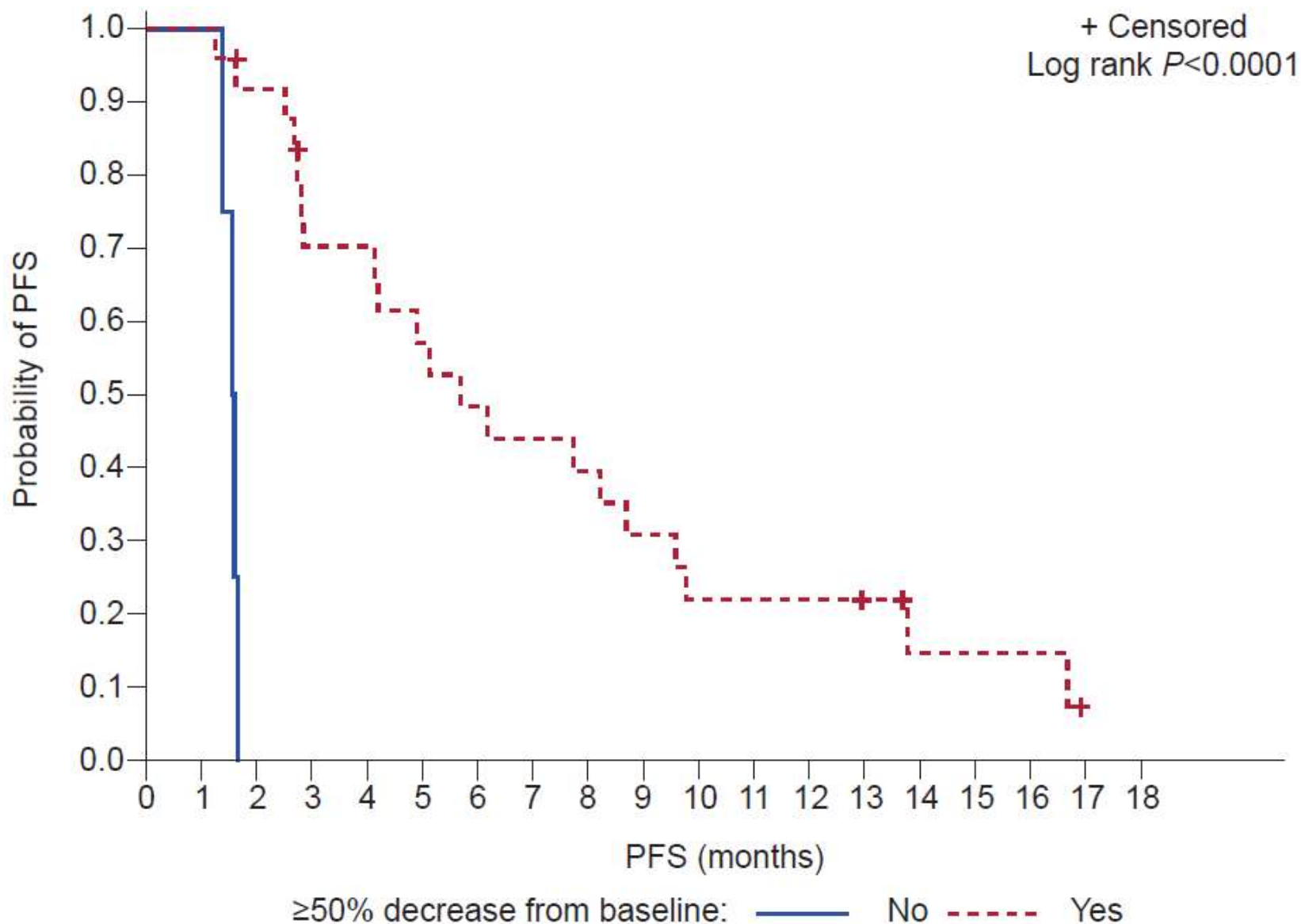


Supplementary Figure 1. Participant Flow Diagram



^aThe non-*AKT1*^{E17K}-mutant patient was enrolled based on an *AKT1*^{E40K} mutation detected by local NGS; this patient was excluded from the efficacy analyses. FAS, full analysis set; NGS, next-generation sequencing.

Supplementary Figure 2. PFS Association With $\geq 50\%$ Decrease from Baseline in $AKT1^{E17K}$ at Cycle 2 Day 1 in ctDNA



A $\geq 50\%$ decrease in circulating $AKT1^{E17K}$ at cycle 2 day 1 compared with baseline (cycle 1 day 1), as measured by ddPCR, was associated with improved PFS on treatment. ctDNA, circulating tumor DNA; ddPCR, droplet digital polymerase chain reaction; PFS, progression-free survival.

Capivasertib, an AKT Kinase Inhibitor, as Monotherapy or in Combination With Fulvestrant in Patients With *AKT1*^{E17K}-Mutant, ER-Positive Metastatic Breast Cancer

Data Supplement

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Supplementary Table 1. Adverse Events Irrespective of Causality Occurring in >10% of Patients

n (%)	Capivasertib Monotherapy Breast-Specific Cohort (N=20)		Capivasertib + Fulvestrant Combination (N=44)		All Capivasertib-Treated Patients (N=64)	
Any AE (irrespective of causality)	20 (100)		43 (97.7)		63 (98.4)	
AE by preferred term (irrespective of causality)	All grades	Grade ≥3	All grades	Grade ≥3	All grades	Grade ≥3
Diarrhea	13 (65)	2 (10)	28 (64)	2 (5)	41 (64)	4 (6)
Nausea	11 (55)	0	23 (52)	2 (5)	34 (53)	2 (3)
Vomiting	9 (45)	0	11 (25)	1 (2)	20 (31)	1 (2)
Hyperglycemia	10 (50)	7 (35)	9 (21)	3 (7)	19 (30)	11 (17)
Fatigue	8 (40)	0	10 (23)	1 (2)	19 (28)	1 (2)
Decreased appetite	4 (20)	0	14 (32)	1 (2)	18 (28)	1 (2)
Rash maculopapular	7 (35)	4 (20)	10 (23)	5 (11)	17 (27)	9 (14)
Back pain	6 (30)	0	9 (21)	2 (5)	15 (23)	2 (3)
Abdominal pain	7 (35)	1 (5)	7 (16)	0	14 (22)	1 (2)
Stomatitis	4 (20)	0	9 (21)	0	13 (20)	0

Aspartate aminotransferase increased	3 (15)	2 (10)	8 (18)	2 (5)	11 (17)	4 (6)
Dizziness	5 (25)	0	5 (11)	0	10 (16)	0
Anemia	2 (10)	0	7 (16)	1 (2)	9 (14)	2 (3)
Alanine aminotransferase increased	3 (15)	3 (15)	6 (14)	3 (7)	9 (14)	6 (9)
Pruritus	3 (15)	0	6 (14)	0	9 (14)	0
Pyrexia	3 (15)	0	6 (14)	0	9 (14)	0
Asthenia	1 (5)	0	7 (16)	0	8 (13)	0
Cough	3 (15)	0	5 (11)	0	8 (13)	0
Headache	4 (20)	1 (5)	4 (9)	1 (2)	8 (13)	2 (3)
Dry skin	4 (20)	0	4 (9)	0	8 (13)	0
Arthralgia	1 (5)	0	6 (14)	0	7 (11)	0
Nasal congestion	3 (15)	0	4 (9)	0	7 (11)	0
Blood alkaline phosphatase increased	1 (5)	1 (5)	5 (11)	0	6 (9)	1 (2)
Dry mouth	5 (25)	0	1 (2)	0	6 (9)	0
Constipation	3 (15)	0	3 (7)	0	6 (9)	0
Neutrophil count decreased	0	0	5 (11)	1 (2)	5 (8)	1 (2)
Weight decreased	0	0	5 (11)	0	5 (8)	0

Hypertension	2 (10)	0	3 (7)	1 (2)	5 (8)	1 (2)
Myalgia	4 (20)	0	1 (2)	0	5 (8)	0

Includes AEs with an onset date on or after the date of first dose and up to and including 28 days following the date of last dose of study. A patient is only counted once for each preferred term. AE, adverse event.

Supplementary Table 2. Treatment Exposure, Dose Modifications and Dose Discontinuation of Capivasertib for the Combination Therapy Cohort (Any Grade, Safety Analysis Set)^a

	Capivasertib	Capivasertib + Fulvestrant Combination		
	Monotherapy	(N=44)		
	Breast-Specific	Fulvestrant Naïve	Fulvestrant-Pretreated	All
	Cohort (N=20)	(n=16)	(n=28)	(N=44)
Mean capivasertib relative dose intensity (SD) ^b	93 (29)	92 (11)	96 (23)	94 (20)
Mean daily dose, mg ^c	870	762	783	775
Median daily capivasertib dose, mg (range)	945 (535–960)	791 (619–800)	800 (659–800)	799 (619–800)
Median total capivasertib treatment duration, days (range) ^d	166 (22–584)	116 (15–709)	123 (4–838)	123 (4–838)
Median actual capivasertib treatment duration, days (range) ^e	96 (13–332)	67 (4–401)	72 (4–476)	72 (4–476)
Patients with a dose interruption and/or modification, n (%)	13 (65)	11 (69)	11 (39)	22 (50)

Any AE leading to dose interruption of capivasertib (irrespective of causality), n (%)	11 (55)	9 (56)	10 (36)	19 (43)
Any AE leading to dose reduction of capivasertib (irrespective of causality), n (%)	7 (35)	2 (13)	2 (7)	4 (9)
Any AE leading to discontinuation of capivasertib (irrespective of causality), n (%)	1 (5)	1 (6)	4 (14)	5 (11)

^aAE data for Part D have been reported previously (1); ^bRelative dose intensity is actual dose intensity delivered relative to intended dose intensity up to progression or actual last dosing day; ^cMean daily dose = total dose/actual treatment duration; ^dTotal treatment duration = last dose date on which dose >0 mg – first dose date + 1; ^eActual treatment duration = total treatment duration, excluding dose interruptions and planned ‘no dose’ periods for intermittent dosing (‘4 days on, 3 days off’ schedule). SD, standard deviation.

Supplementary Table 3. Exploratory Subgroup Analysis of Treatment Efficacy for Patients With ER+ HER2- *AKT1*^{E17K}-Mutant Metastatic Breast Cancer by Number of Prior Lines of Chemotherapy for Metastatic Breast Cancer

	All Capivasertib-Treated Patients	
	(Monotherapy Breast-Specific Cohort + Combination Therapy Cohort)	
	≤2 Prior Lines	≥3 Prior Lines
	(n=26)	(n=37)
ORR, % (95% CI) ^a	35 (17–56)	22 (10–38)
CBR, % (95% CI) ^b	62 (41–80)	38 (23–55)
Median PFS, months (95% CI)	9 (4–15)	4 (3–6)

^aConfirmed no fewer than 4 weeks after the criteria for response were initially met; ^bClinical benefit defined as confirmed best overall response of complete response, partial response, or stable disease for at least 24 weeks. CBR, clinical benefit rate; CI, confidence interval; ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; ORR, objective response rate; PFS, progression-free survival.

Reference

1. Hyman DM, Smyth LM, Donoghue MTA, Westin SN, Bedard PL, Dean EJ, et al. AKT inhibition in solid tumors with *AKT1* mutations. *J Clin Oncol* 2017;35:2251-9.