

**Supplementary Table 1 – Statistical analysis of the frequency of co-occurring mutations detectable in plasma at acquired resistance (FLAURA resistance analysis subset)**

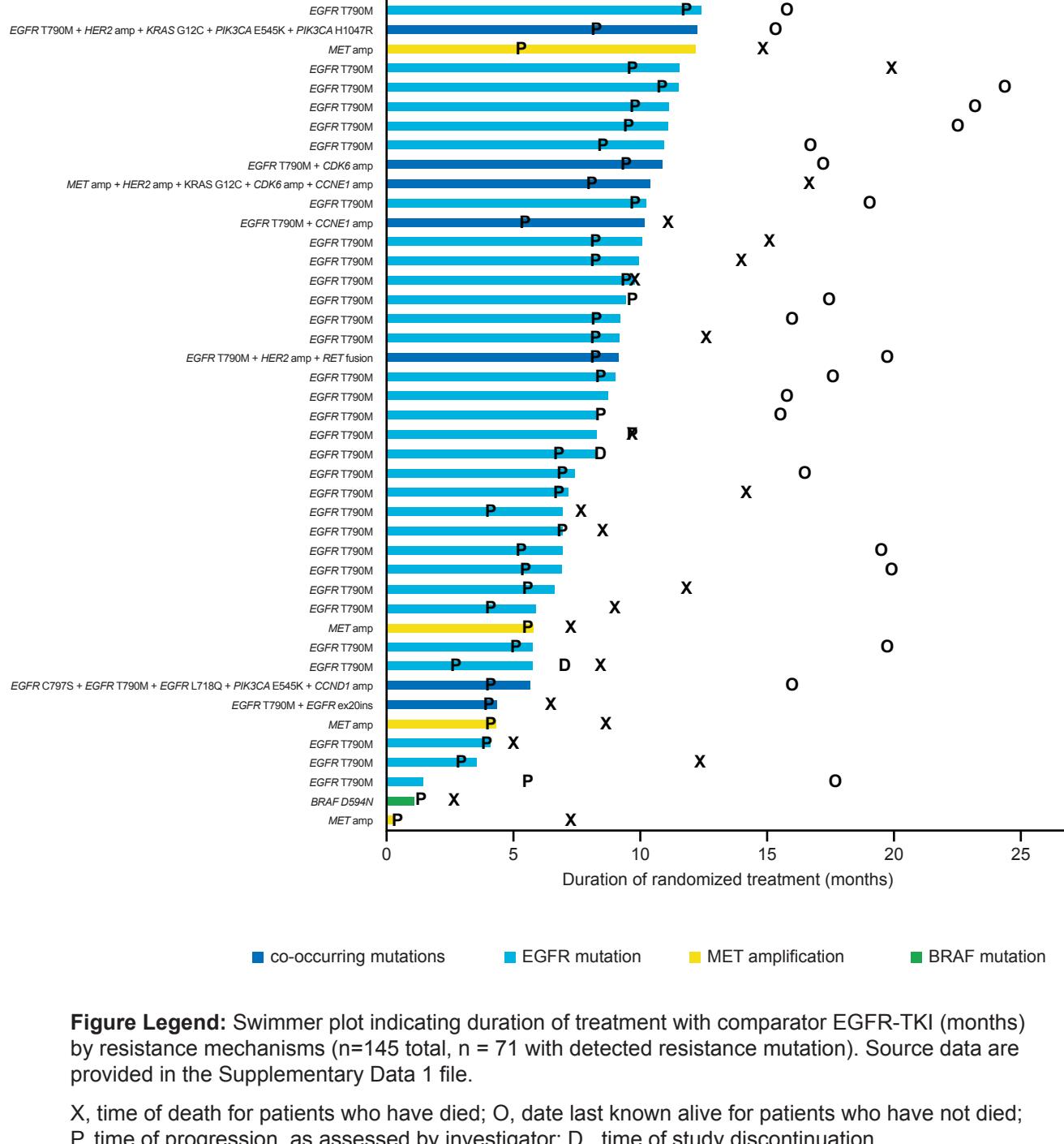
n	(n=109)		(n=145)		p-value (Fisher)	p-value (Bonferroni)	Fisher Odds*
	Mutation detected	Mutation not detected	Osimertinib	Comparator EGFR-TKI			
T790M	0	109	64	81	0	0	0
EGFR mutations	11	98	2	143	0.0026	0.026	7.97
MET amplification	17	92	9	136	0.0204	0.204	2.78
HER2 amplification	2	107	3	142	1	1	0.89
RET	0	109	2	143	0.5081	1	0
ALK	1	108	0	145	0.4291	1	Inf
MAPK	6	103	4	141	0.3345	1	2.05
PIK3CA	6	103	3	142	0.1782	1	2.75
Cell cycle	12	97	8	137	0.1565	1	2.11

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The diagram illustrates the EGFR gene structure. The top row shows the wild-type EGFR with a single 'P' at position 790. The middle row shows the EGFR T790M mutation, where the wild-type 'P' is replaced by a 'T' (represented by an 'O'). The bottom row shows another EGFR T790M mutation, where both the wild-type 'P' and the mutated 'T' are present at position 790.

Treatment Regimen	Percentage (%)	Status
<i>EGFR T790M</i>	~95	O
<i>EGFR T790M</i>	~95	O
<i>EGFR T790M + CDK6 amp + CCND2 amp</i>	~95	PO
<i>EGFR T790M + MET amp + CDK6 amp</i>	~95	PO
<i>EGFR T790M</i>	~95	P
<i>EGFR T790M + MET amp</i>	~95	P
<i>EGFR T790M</i>	~95	P

Sample	EGFR T790M Status
EGFR T790M + RET fusion	P
EGFR T790M	X
EGFR T790M	P
EGFR T790M	X



**Figure Legend:** Swimmer plot indicating duration of treatment with comparator EGFR-TKI (months) by resistance mechanisms (n=145 total, n = 71 with detected resistance mutation). Source data are provided in the Supplementary Data 1 file.

X, time of death for patients who have died; O, date last known alive for patients who have not died  
 P, time of progression, as assessed by investigator; D, time of study discontinuation.