Supplementary Table 1:

Biomarker Eligibility for AZD4547 FGFR Inhibitor Sub-study D

Gene	Alteration type	Eligible alteration
FGFR1	Substitution	T141R, R445W, N546K, K656E, G818R
	Fusion*	FGFR1-TACC1
	Amplification	FM standard thresholds: ≥6 estimated copies (or ≥ 7 in triploid, ≥ 8 in tetraploid+ samples)
FGFR2	Substitution	A97T, W156*, N211I, S252L, S252W, P253R, D283N, W290C, A315T, S320C, D336N, Y375C, C382R, V395D, E470Q, D471N, H544Q , I547V, N549D, N549K, N549S, N549Y, G613V, K659E, K659N, R678G, P708S, E777K, T786K
	Fusion	FGFR2-TACC2, FGFR2-BICC1, FGFR2-PPAPDC1A, FGFR2-SLC45A3, FGFR2-AFF3, FGFR2-CASP7, FGFR2-CCDC6, FGFR2-AHCYL1, FGFR2-KIAA1967, FGFR2-OFD1
	Amplification	FM standard thresholds: ≥6 estimated copies (or ≥ 7 in triploid, ≥ 8 in tetraploid+ samples)
FGFR3	Substitution	S131L, R248C, S249C, G370C, Y373C, R399C, S433C, D641N, K650E, K650M, V677I, K715M
	Fusion	FGFR3-TACC3, FGFR3-WHSC1, FGFR3-LETM1, FGFR3-BAIAP2L1
	Amplification	FM standard thresholds: ≥ 6 estimated copies (or ≥ 7 in triploid, ≥ 8 in tetraploid+ samples)

*Note: FGFR gene introns are not targeted on current version of FM platform (T5) and therefore FGFR gene fusions are only detected when breakpoints occur in proximity to FGFR exons (reduced sensitivity)