

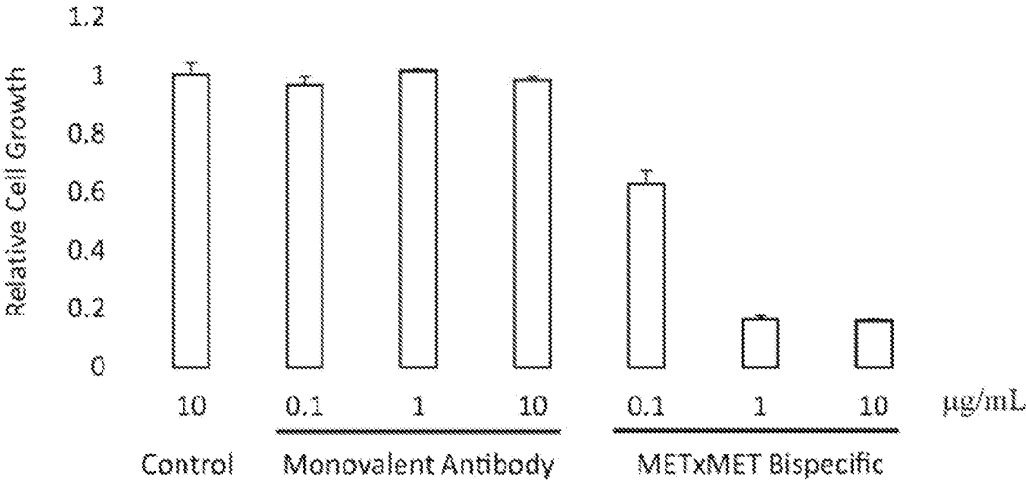


FIG. 1A

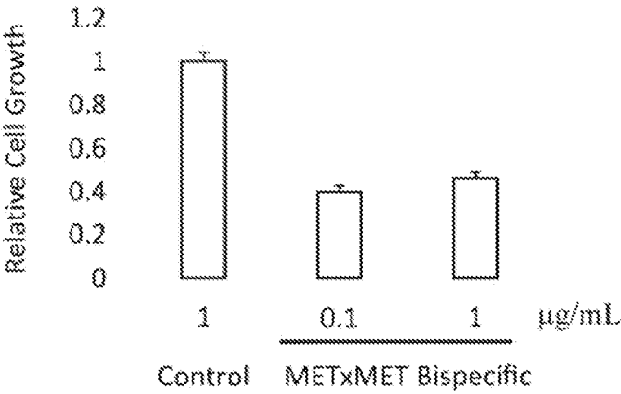


FIG. 1B

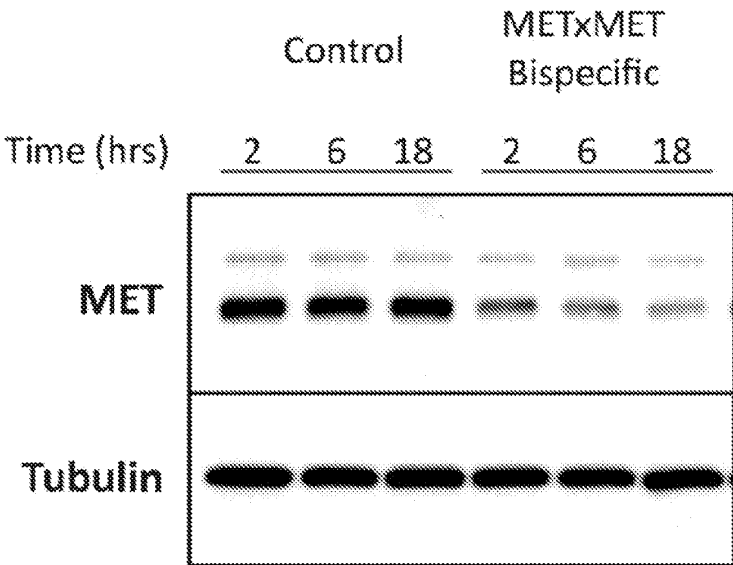


FIG. 2

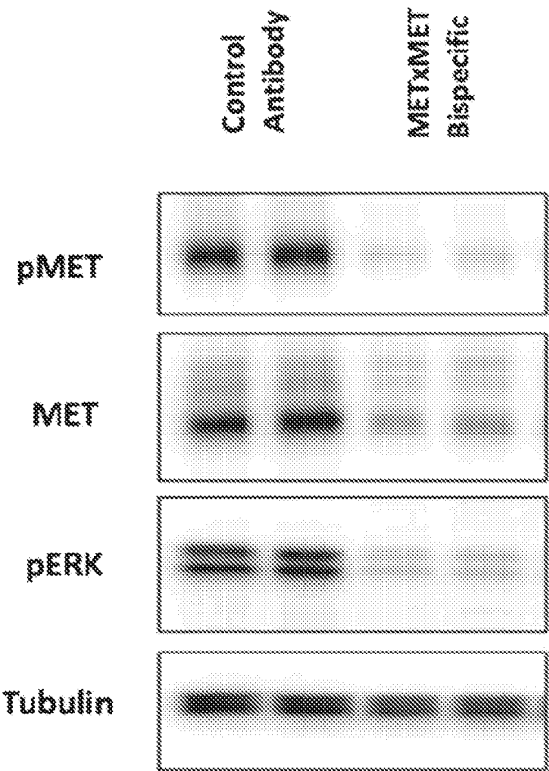


FIG. 3

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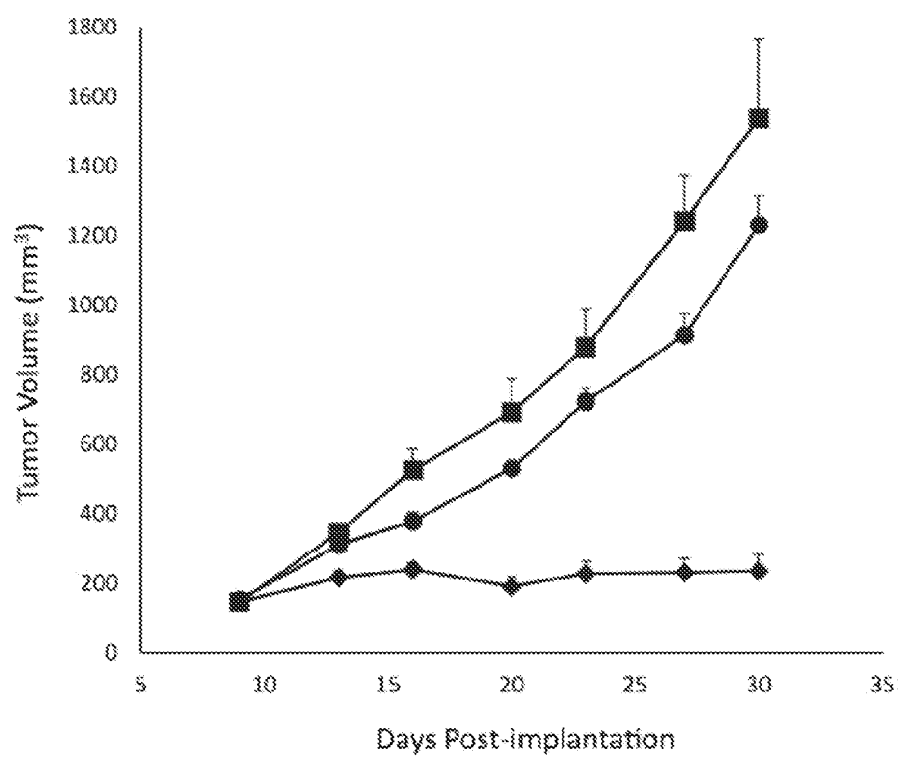


FIG. 4

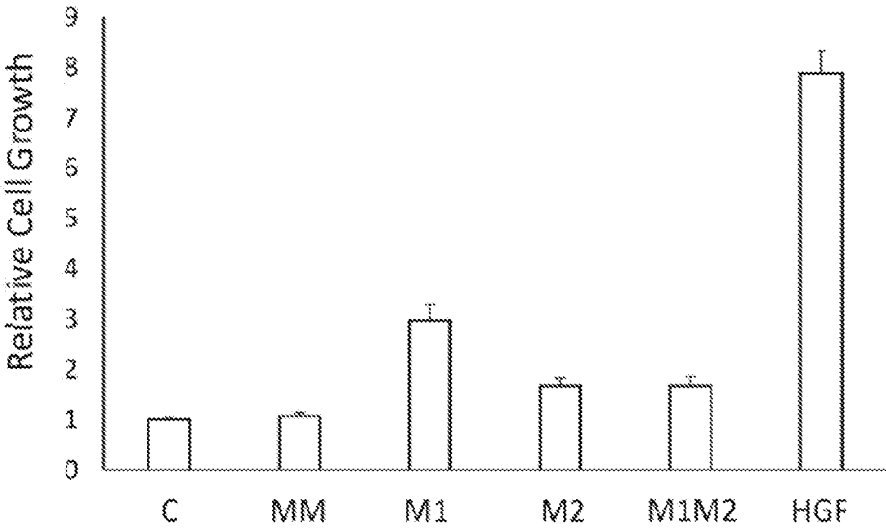


FIG. 5

Study Flow Diagram

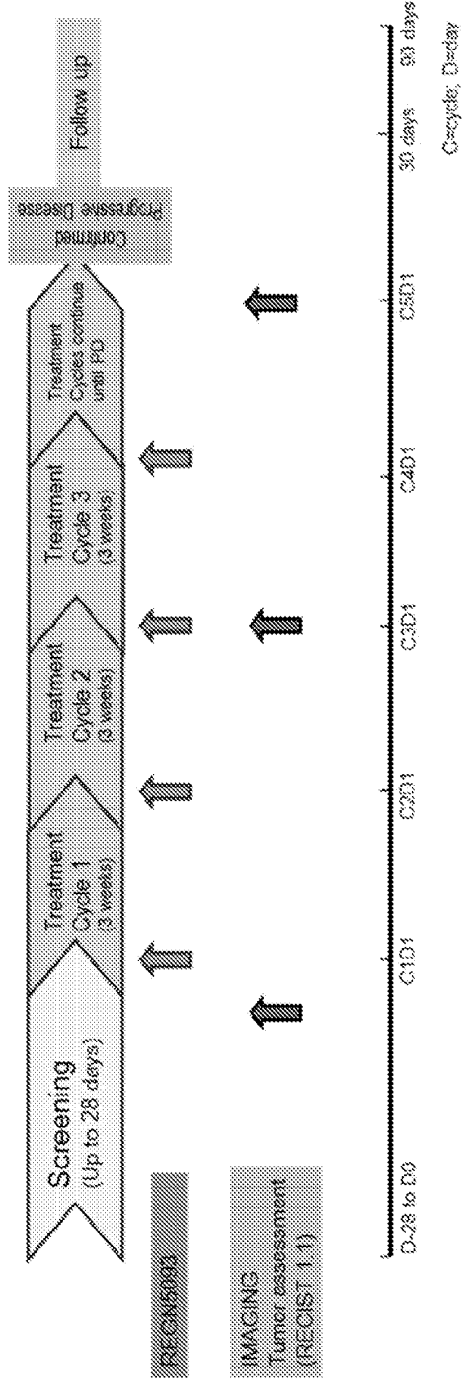


FIG. 6

Dose Escalation and Expansion Cohorts

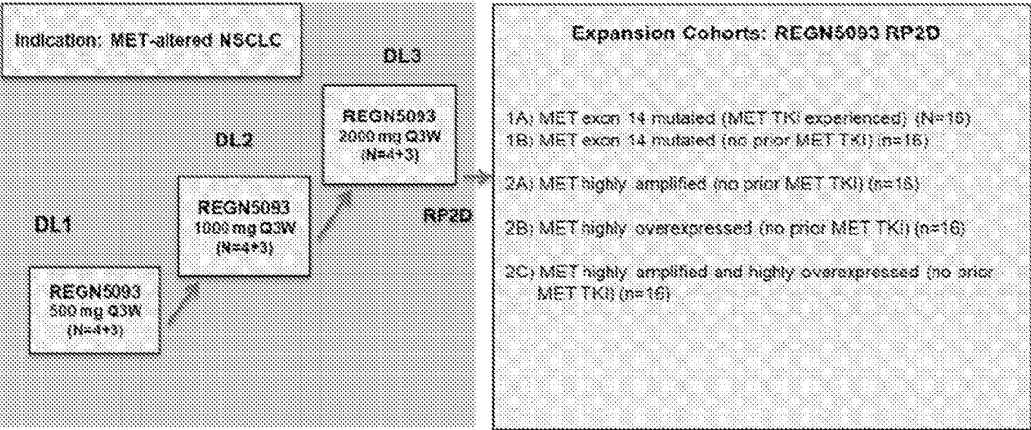
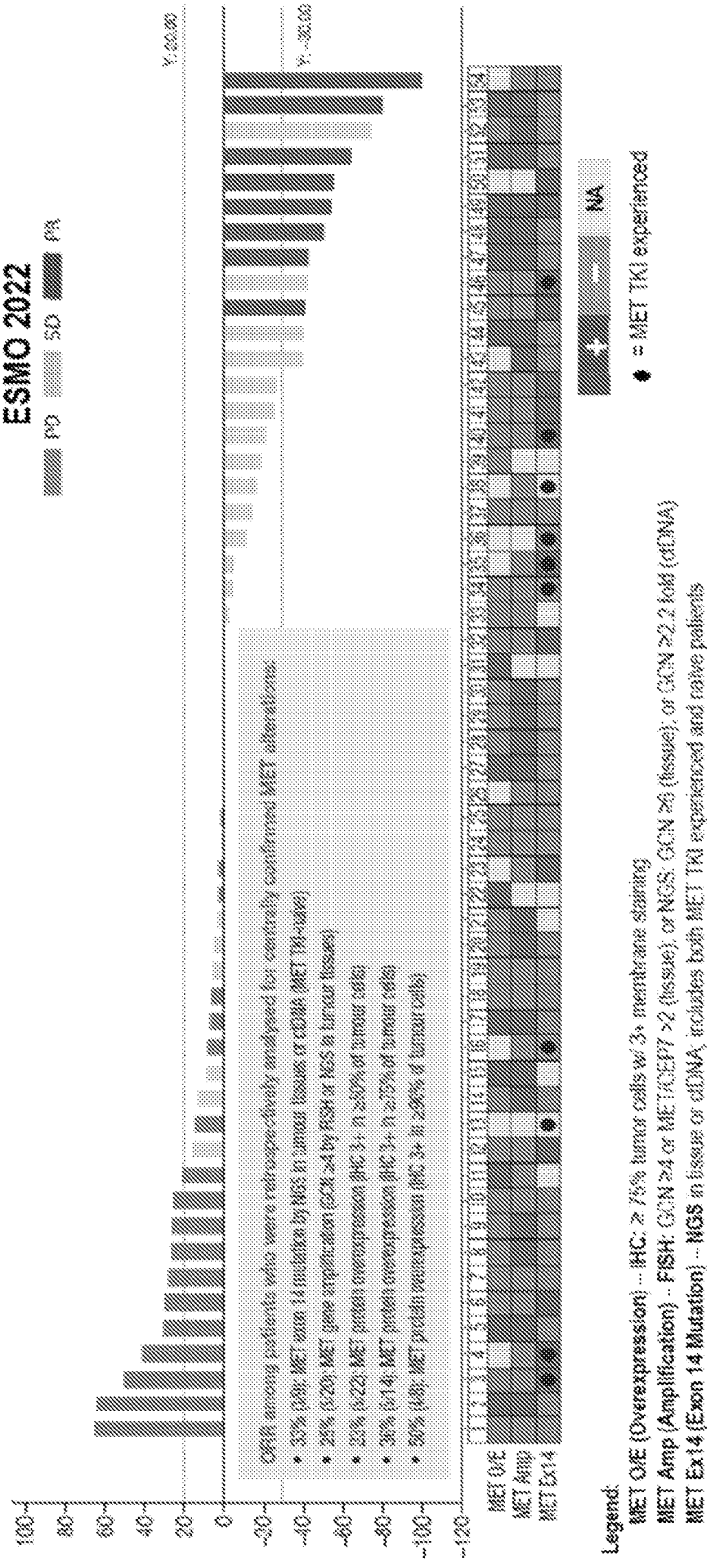


FIG. 7

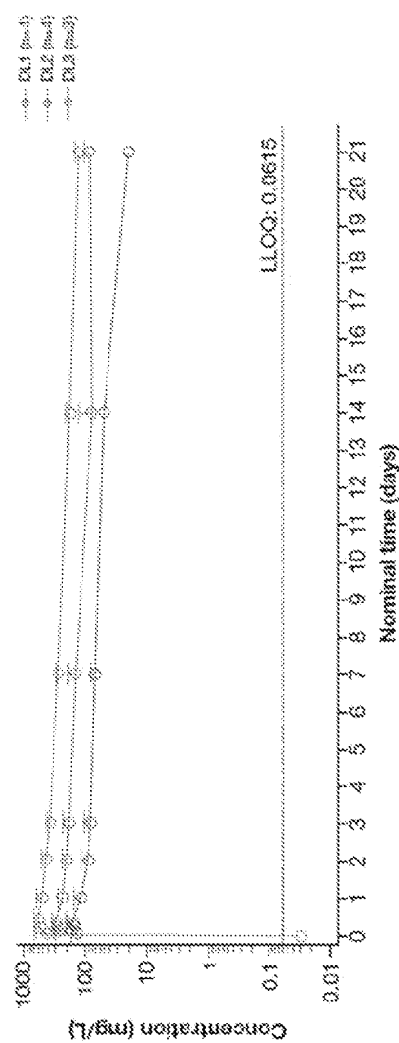
TUMOUR RESPONSE CONFIRMED BY CENTRAL LABORATORY IS ENRICHED BY MET ALTERATIONS
Tumour response is enriched by increasing MET IHC



Data are based on central laboratory testing. NA: sample unavailable or to be determined.
FISH: fluorescence in situ hybridisation; IHC: immunohistochemistry; MET: mesenchymal epithelial transition; NA: not available; NGS: next-generation sequencing; TBL: to be determined

FIG. 8

PK Profile After The First Dose (Log Scale)



DL, dose level; EXP, expansion cohort; LLOQ, lower limit of quantification; PK, pharmacokinetic.

FIG. 9A

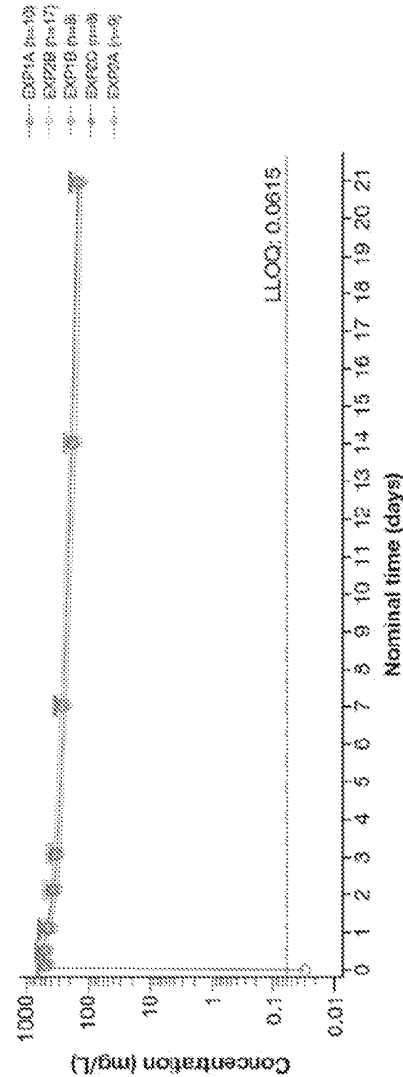


FIG. 9B

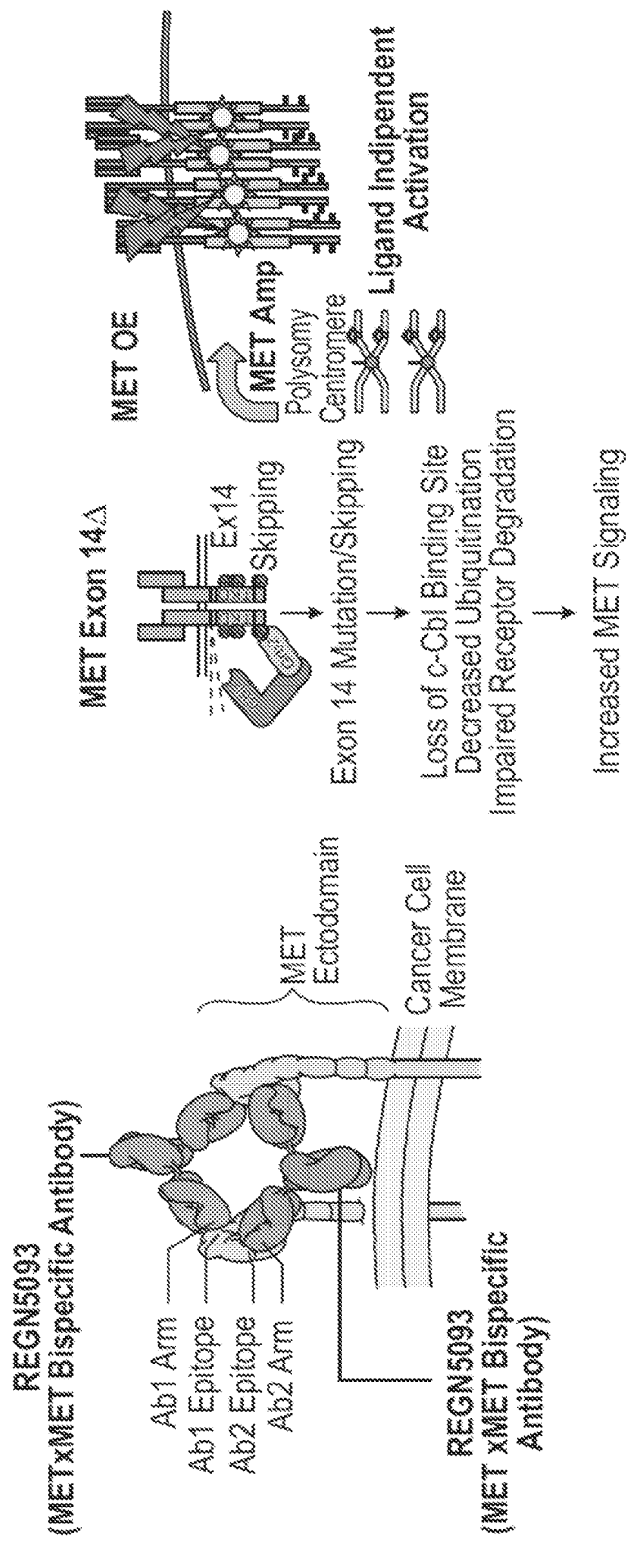
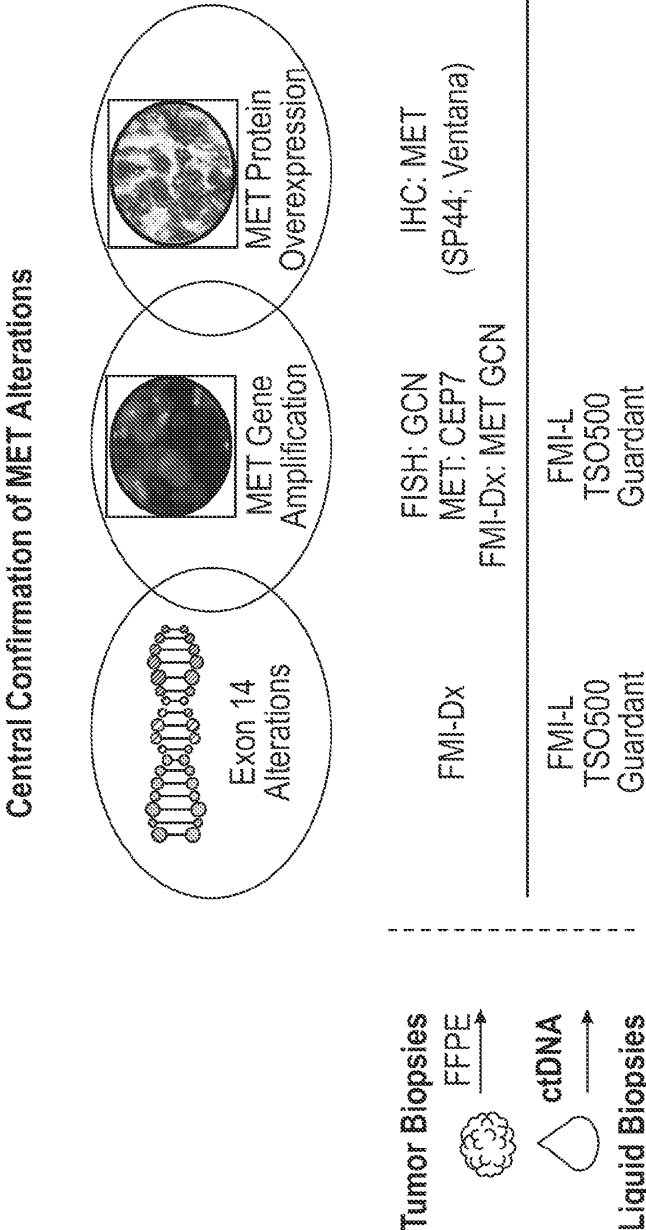
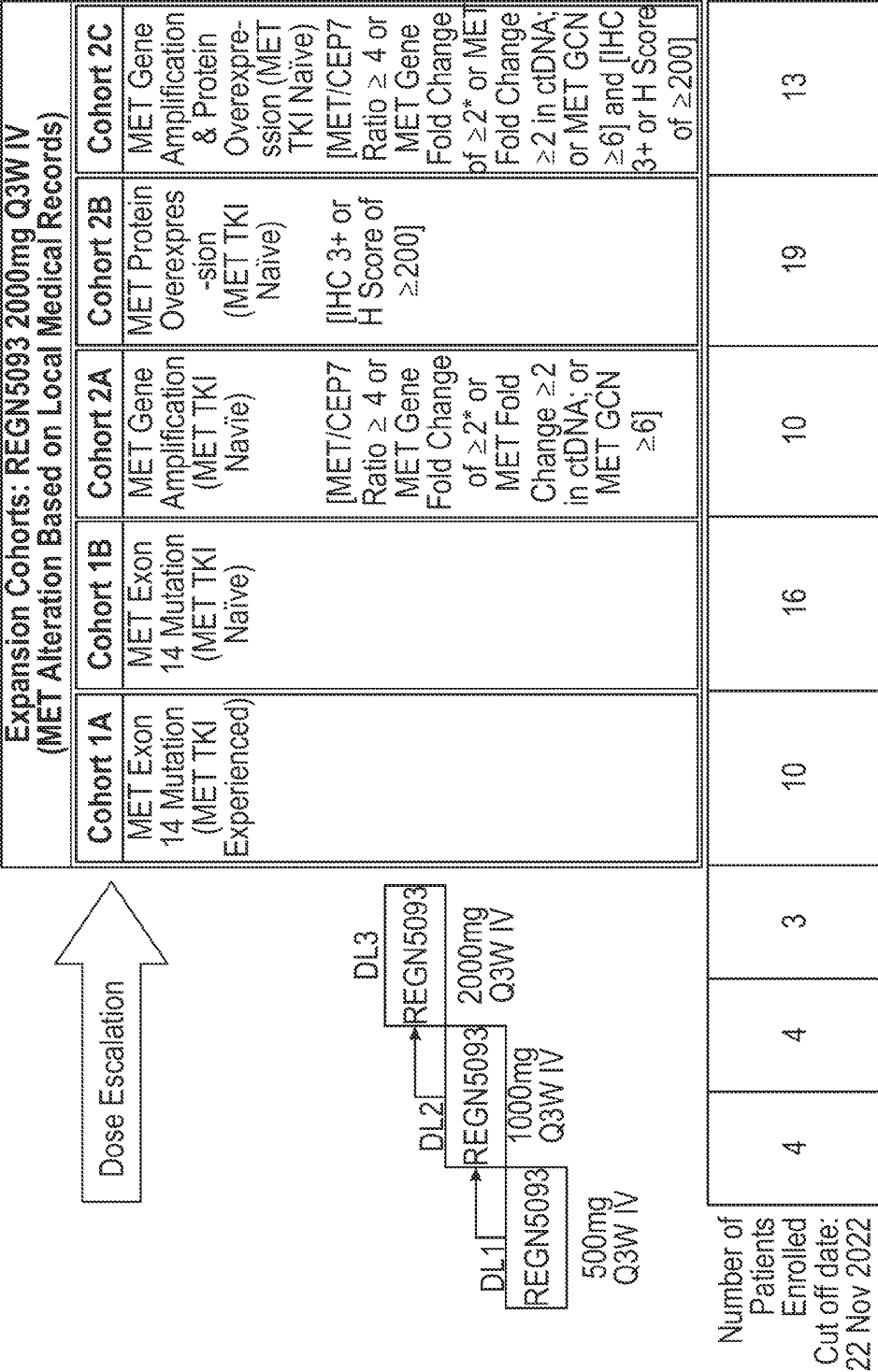


FIG. 10

1L, First-line; 2L, Second-line; MET, Mesenchymal Epithelial Transition; NSCLC, Non-small Cell Lung Cancer; TKI, Tyrosine Kinase Inhibitor.





R5093-ONC-1863 Response Data at 2000mg Dose

Cohort	# Treated	Confirmed PR	ORR (CR+PR) 95% CI	DCR (CR+PR+SD) 95% CI
Dose Level 3 MET Altered	3	1	33.3% 0.8, 90.6%	66.7% 9.4, 99.2%
Cohort 1A Exon14 Skip Mutation, MET TKI Experienced	10	0	0% 0, 30.8%	50% 18.7, 81.3%
Cohort 1B Exon14 Skip Mutation, MET TKI Naïve	16	4	25% 7.3, 52.4%	75% 47.6, 92.7%
Cohort 2A MET Gene Amplified, MET TKI Naïve	10	0	0% 0, 30.8%	30% 6.7, 65.2%
Cohort 2B MET Protein Overexpressed, MET TKI Naïve	19	1	5.3% 0.1, 26%	57.9% 33.5, 79.7%
Cohort 2C MET Gene Amplified AND MET Protein Overexpressed, MET TKI Naïve	12	3	25% 5.5, 57.2%	66.7% 34.9, 90.1%

FIG. 13

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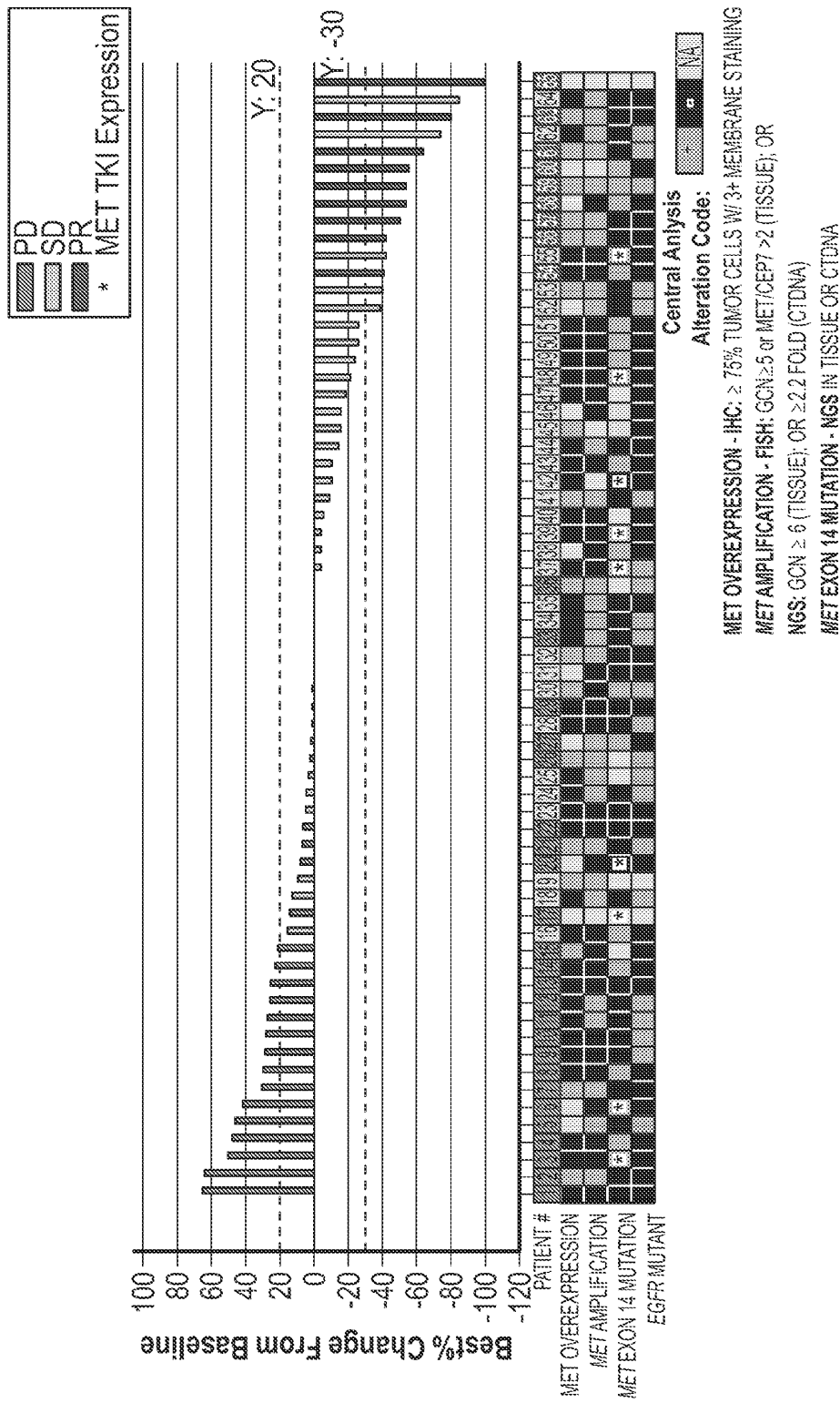


FIG. 14

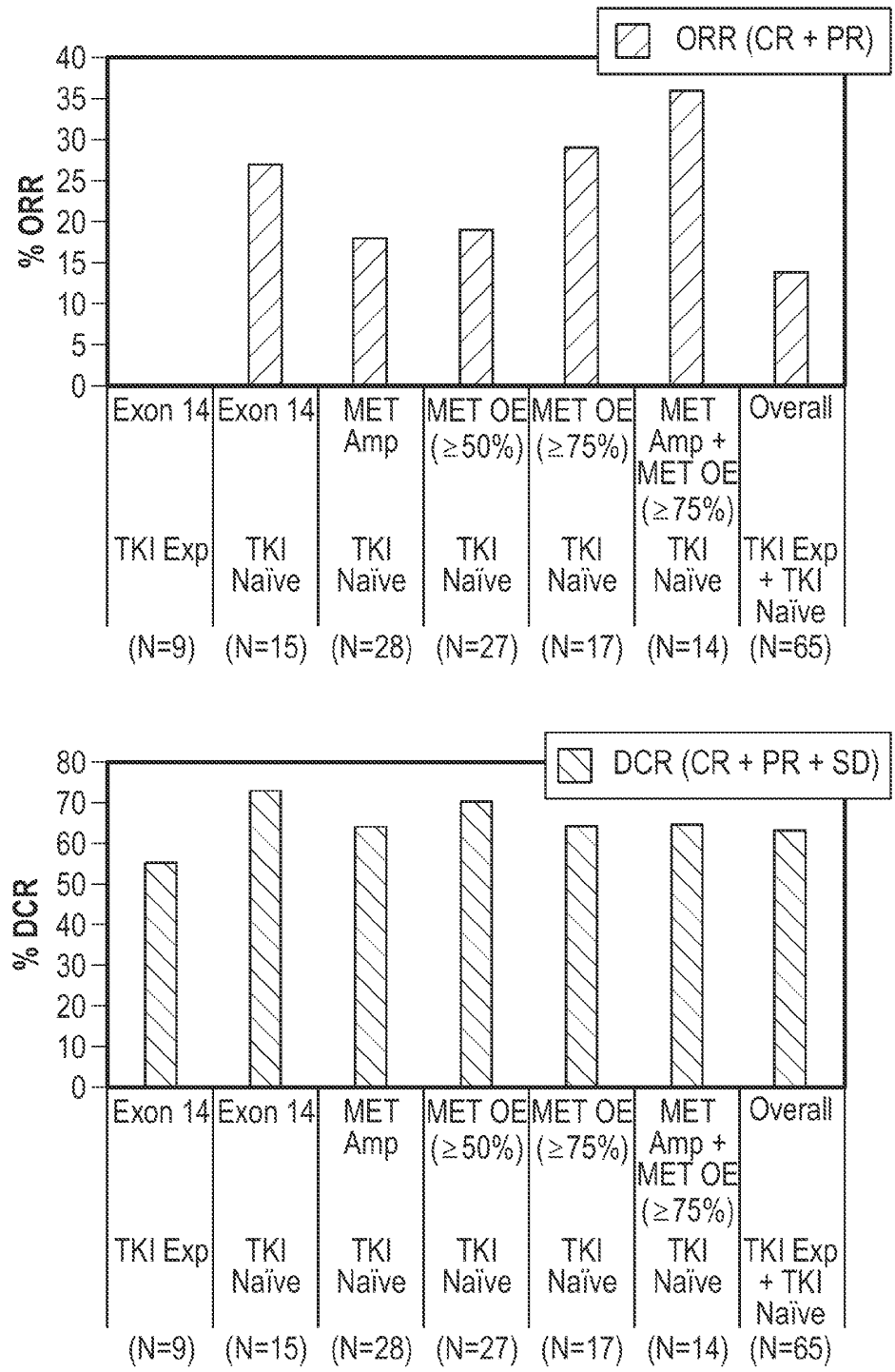


FIG. 15

Characteristic	Total (N=78)	
Age	Median (range), years	66 (30-85)
	≥65 year, n(%)	46 (59.0)
Sex, n(%)	Male	42 (53.8)
	Female	36(46.2)
Race, n(%)	Asian	55 (70.5)
	White	11 (14.1)
	Black	1 (1.3)
	Not reported/missing	11 (14.1)
ECOG PS, n (%)	0	15 (19.2)
	1	63 (80.8)
Histology, n (%)	Non-squamous	73 (93.6)
	Squamous	5 (6.4)
Metastases, n (%)	Liver	22 (28.2)
	Brain	22 (28.2)
EGFR status, n (%)	Wild type	36 (46.2)
	Mutant	29 (37.2)
Number of prior lines of therapy	Unknown	13 (16.7)
	Median, (range)	2.5 (1-8)

FIG. 16

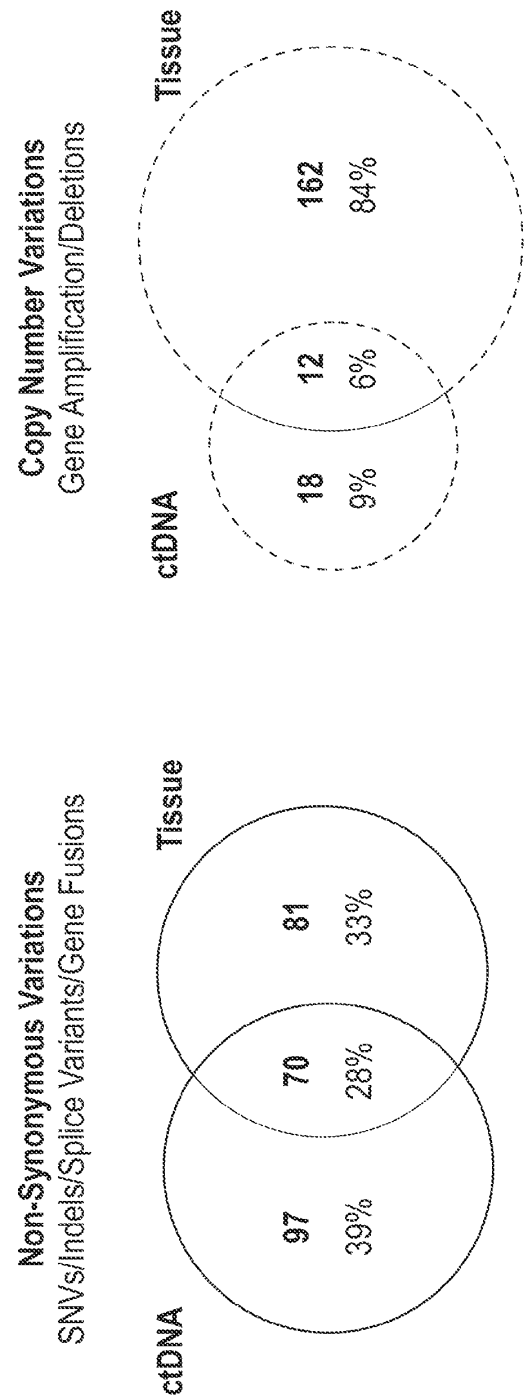


FIG. 17

Unbiased clustering of baseline somatic variants with MET alterations and Clinical Response

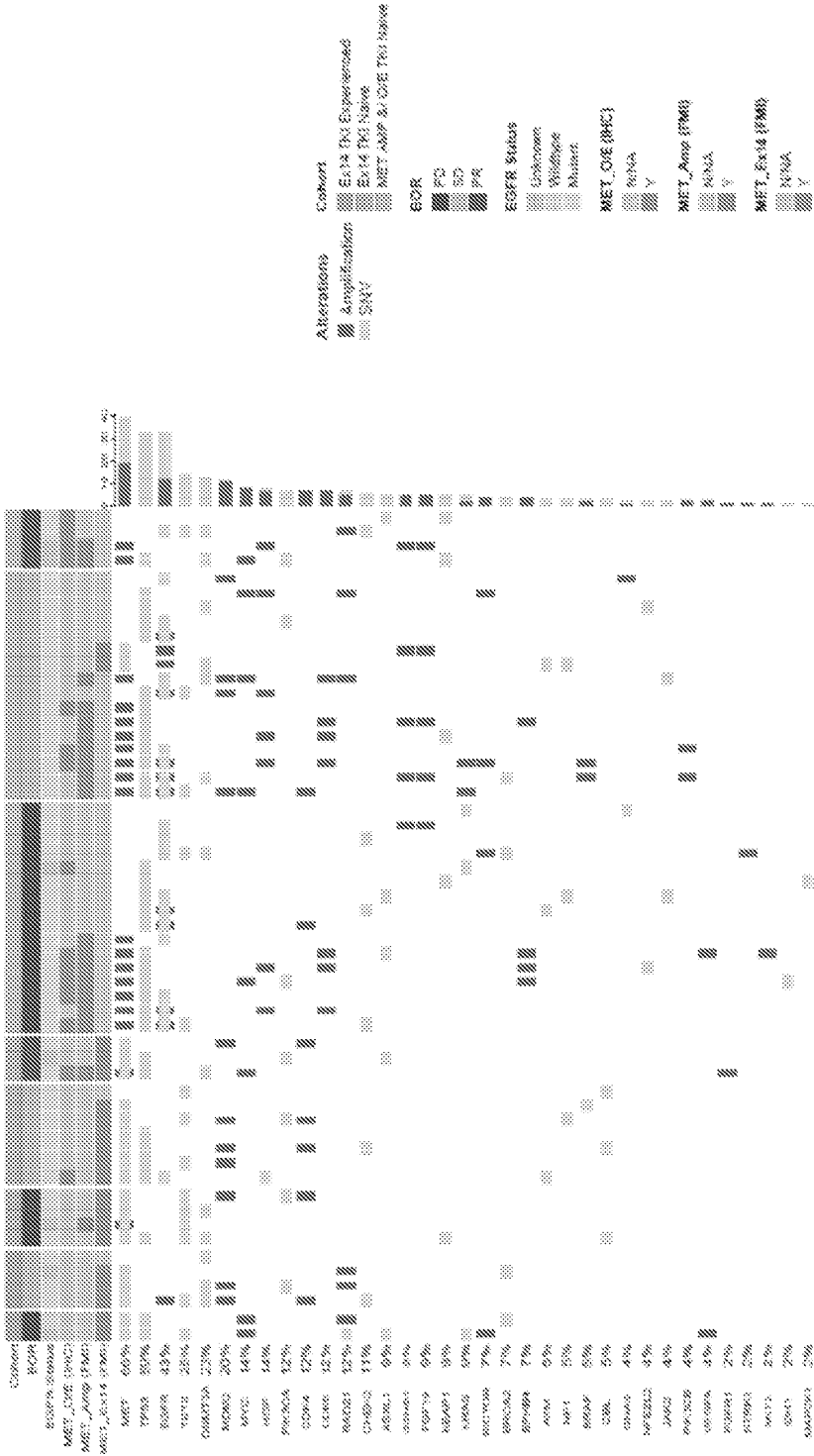


FIG. 19

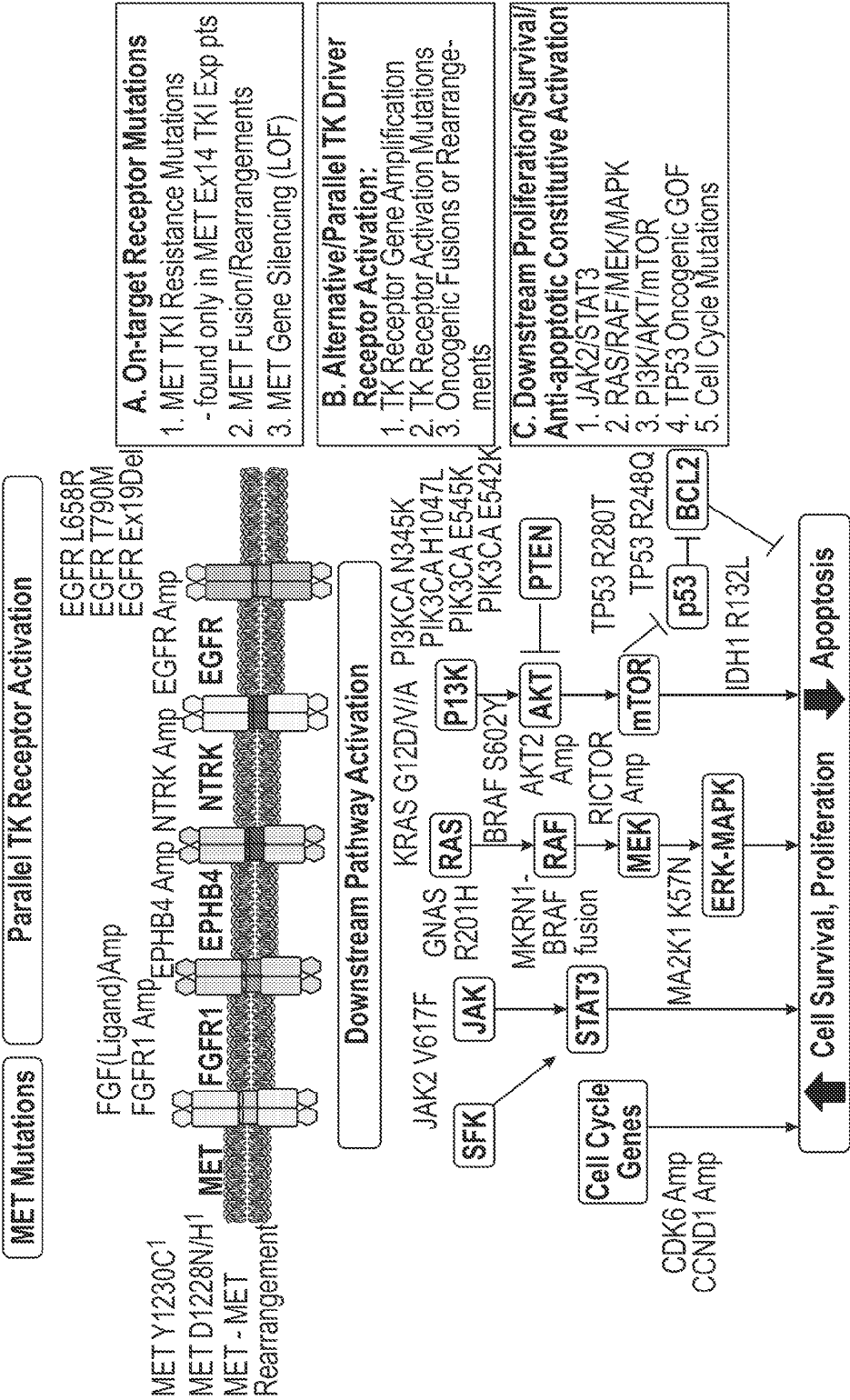


FIG. 20

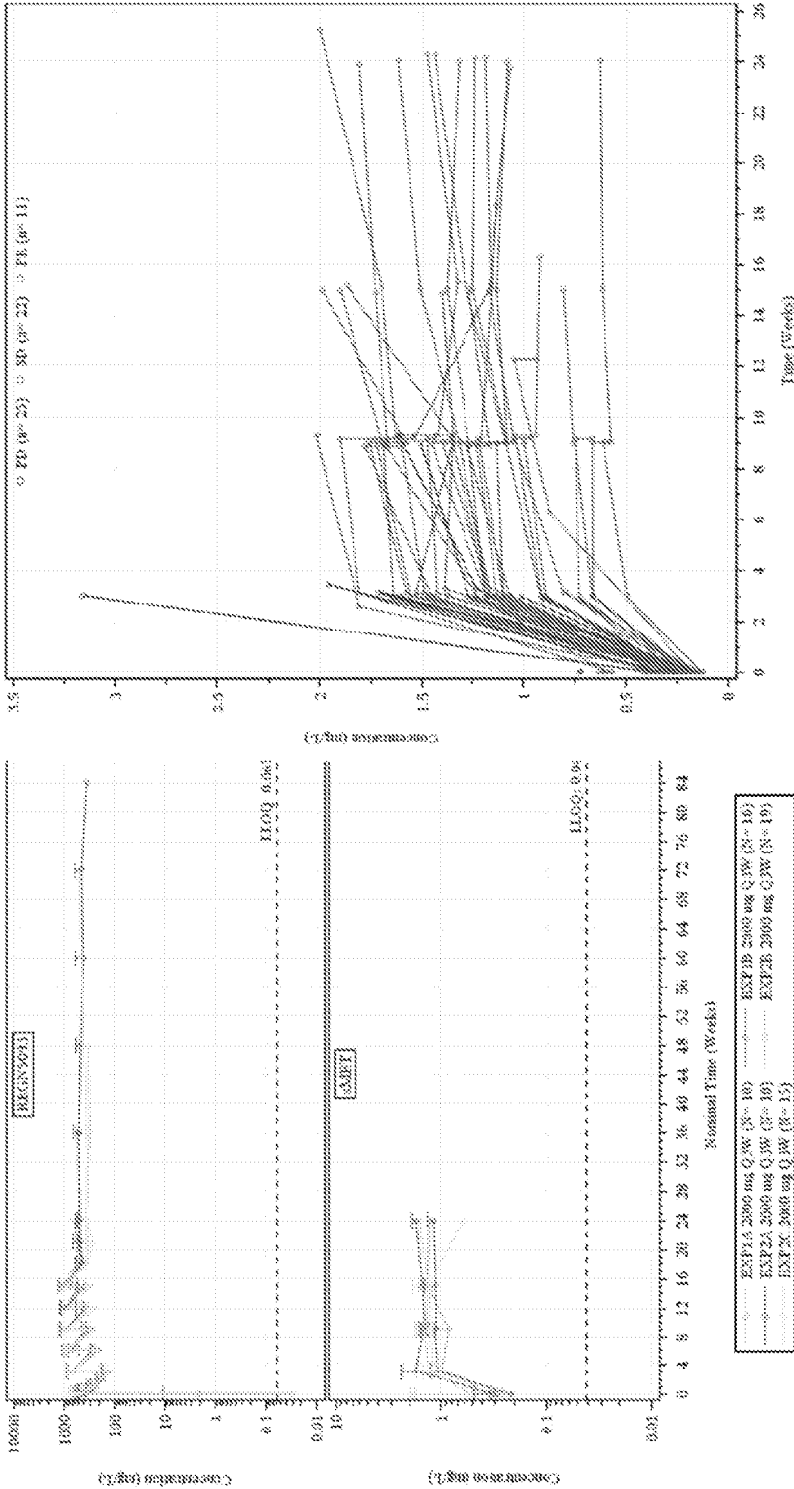


FIG. 21

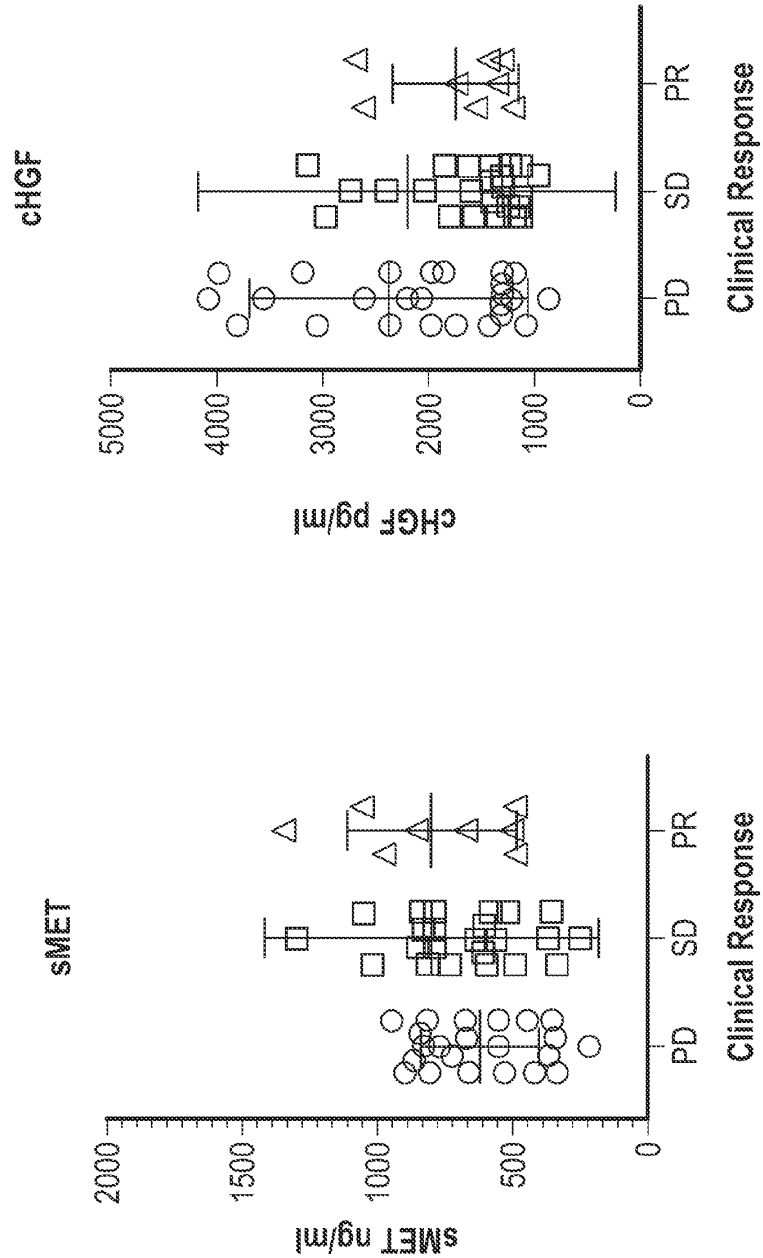


FIG. 22