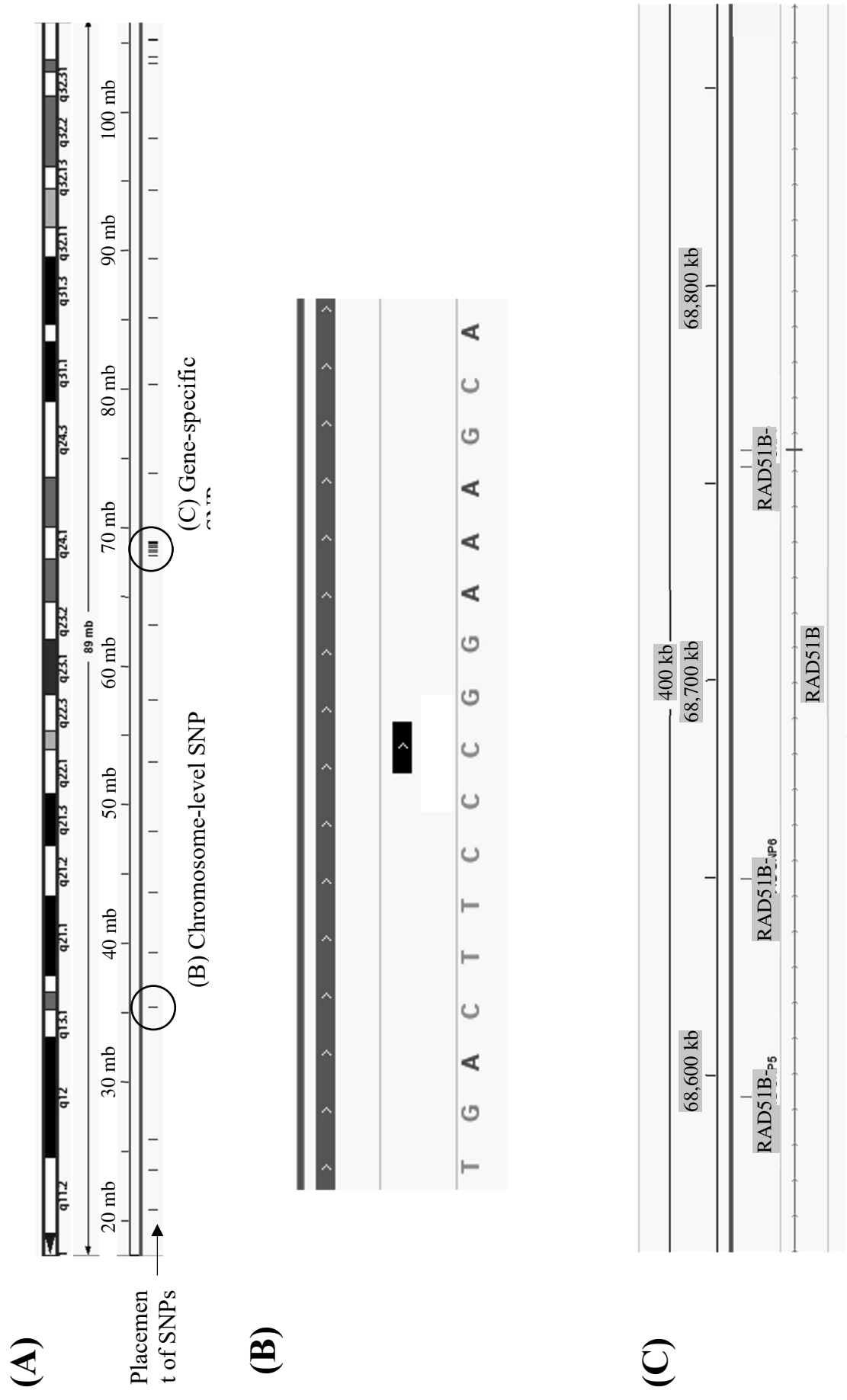

(A)
20 mb
30 mb
40 mb
50 mb
60 mb
70 mb
80 mb
90 mb
100 mb
89 mb
Placement of SNPs
(B) Chromosome-level SNP
(C) Gene-specific
(B)
T G A C T T C C C C G G A A A G C A
(C)
400 kb
68,600 kb
68,700 kb
68,800 kb
RAD51B-P5
RAD51B-
RAD51B

Fig. 1

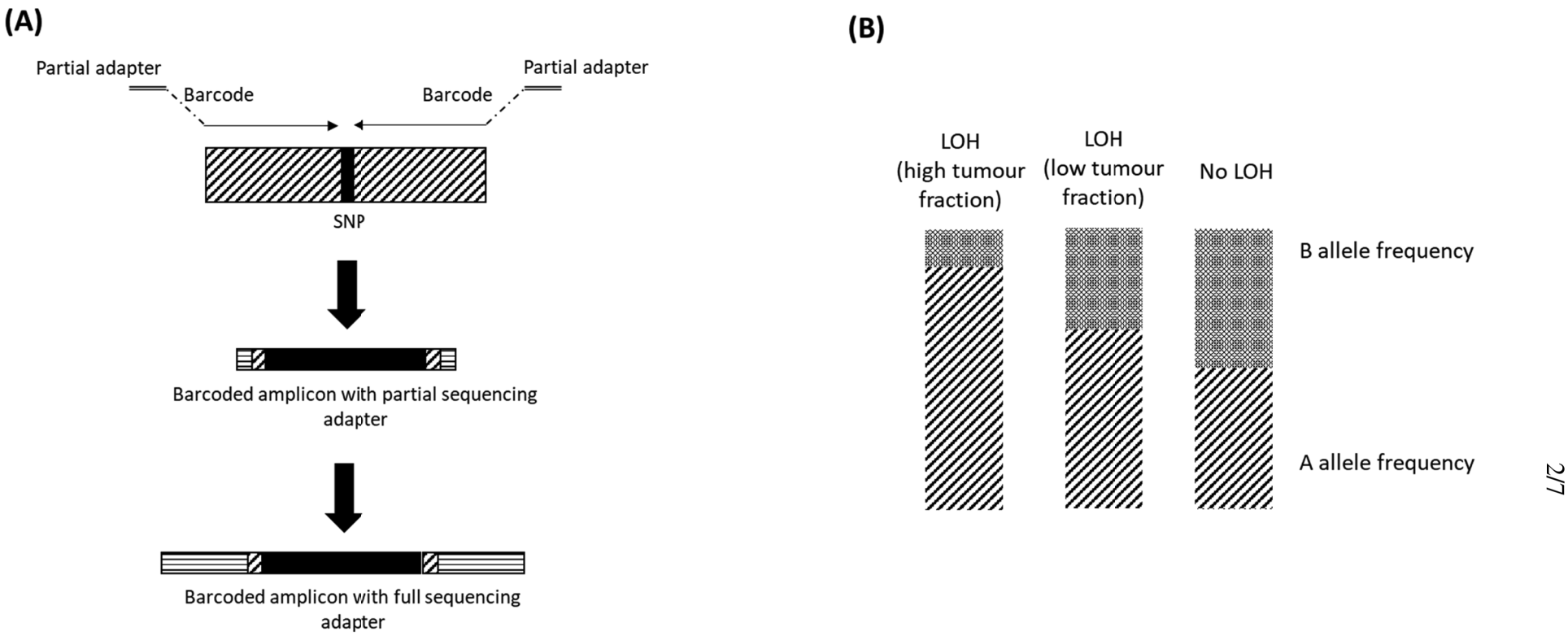

(A)
Partial adapter
Barcode
Barcode
Partial adapter
SNP
Barcoded amplicon with partial sequencing adapter
Barcoded amplicon with full sequencing adapter
(B)
LOH (high tumour fraction)
LOH (low tumour fraction)
No LOH
B allele frequency
A allele frequency

Fig. 2


(A)
VAF (%)
100
80
60
40
20
0
54.1
45.7
0
10
20
30
40
50
60
70
80
90
% of SNPs
(B)
Frequency
95th percentile = 4.9
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
6.5
7.0
7.5
8.0
8.5
9.0
9.5
Standard Deviation

Fig. 3

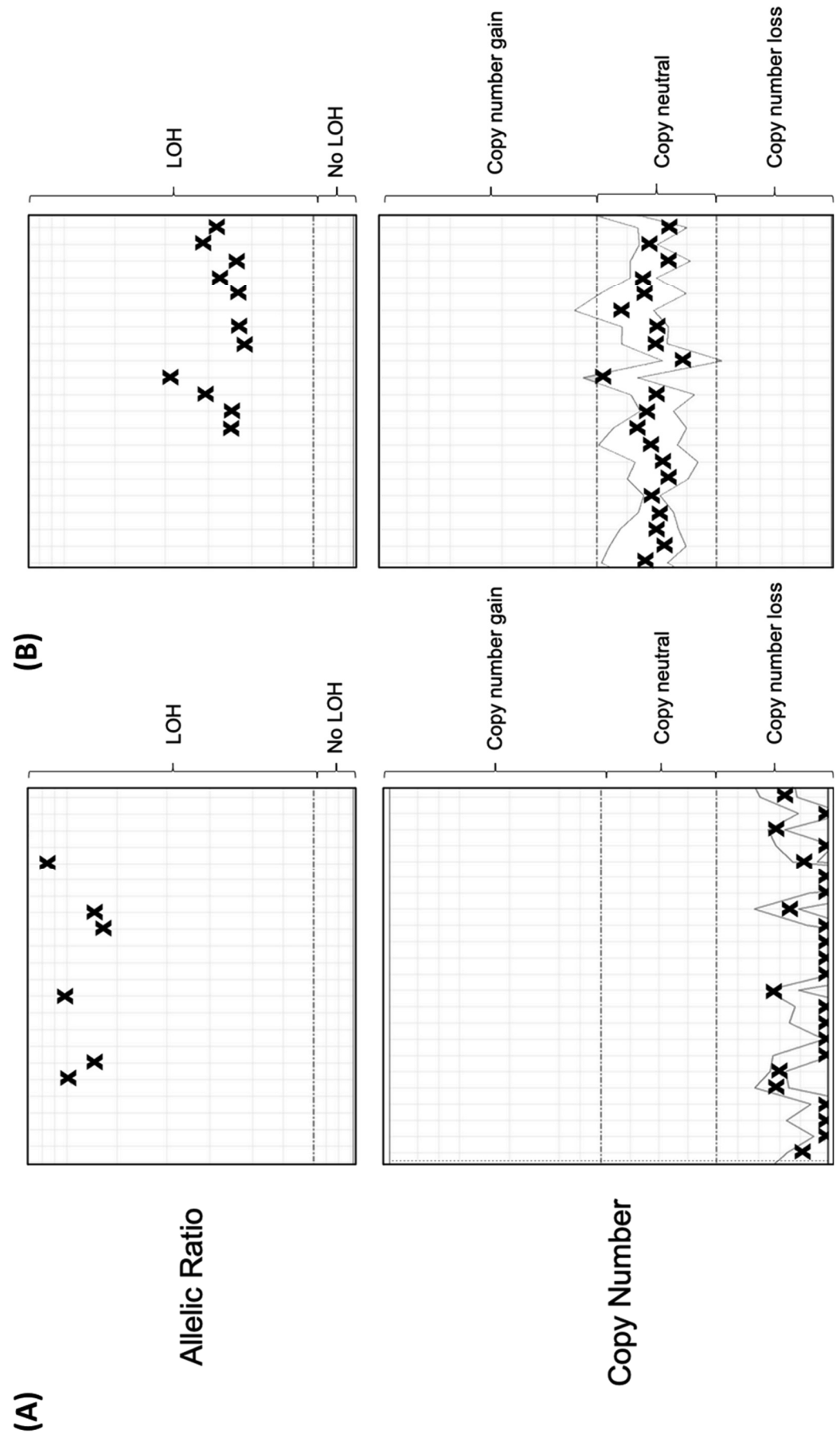

(A)
Allelic Ratio
LOH
No LOH
Copy Number
Copy number gain
Copy neutral
Copy number loss
(B)
LOH
No LOH
Copy number gain
Copy neutral
Copy number loss

Fig. 4

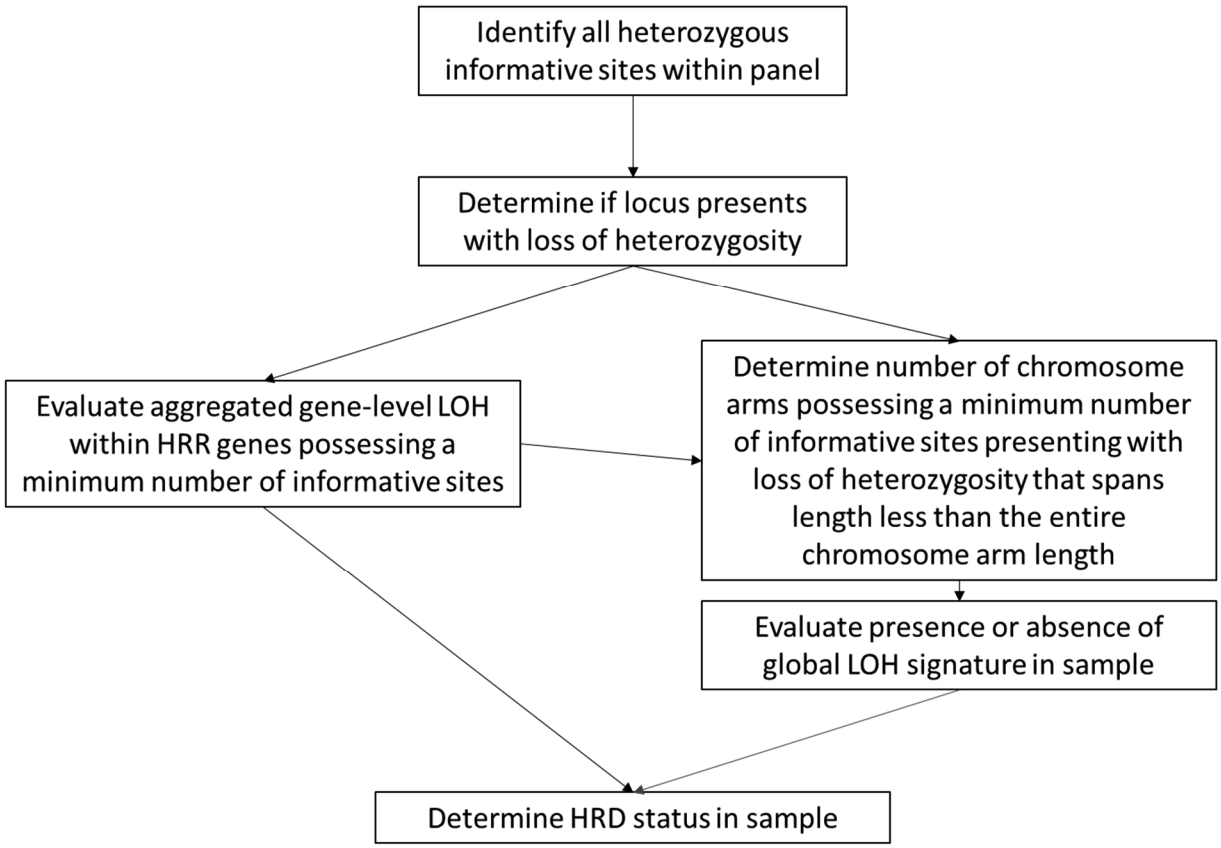

Identify all heterozygous informative sites within panel
Determine if locus presents with loss of heterozygosity
Evaluate aggregated gene-level LOH within HRR genes possessing a minimum number of informative sites
Determine number of chromosome arms possessing a minimum number of informative sites presenting with loss of heterozygosity that spans length less than the entire chromosome arm length
Evaluate presence or absence of global LOH signature in sample
Determine HRD status in sample

Fig. 5

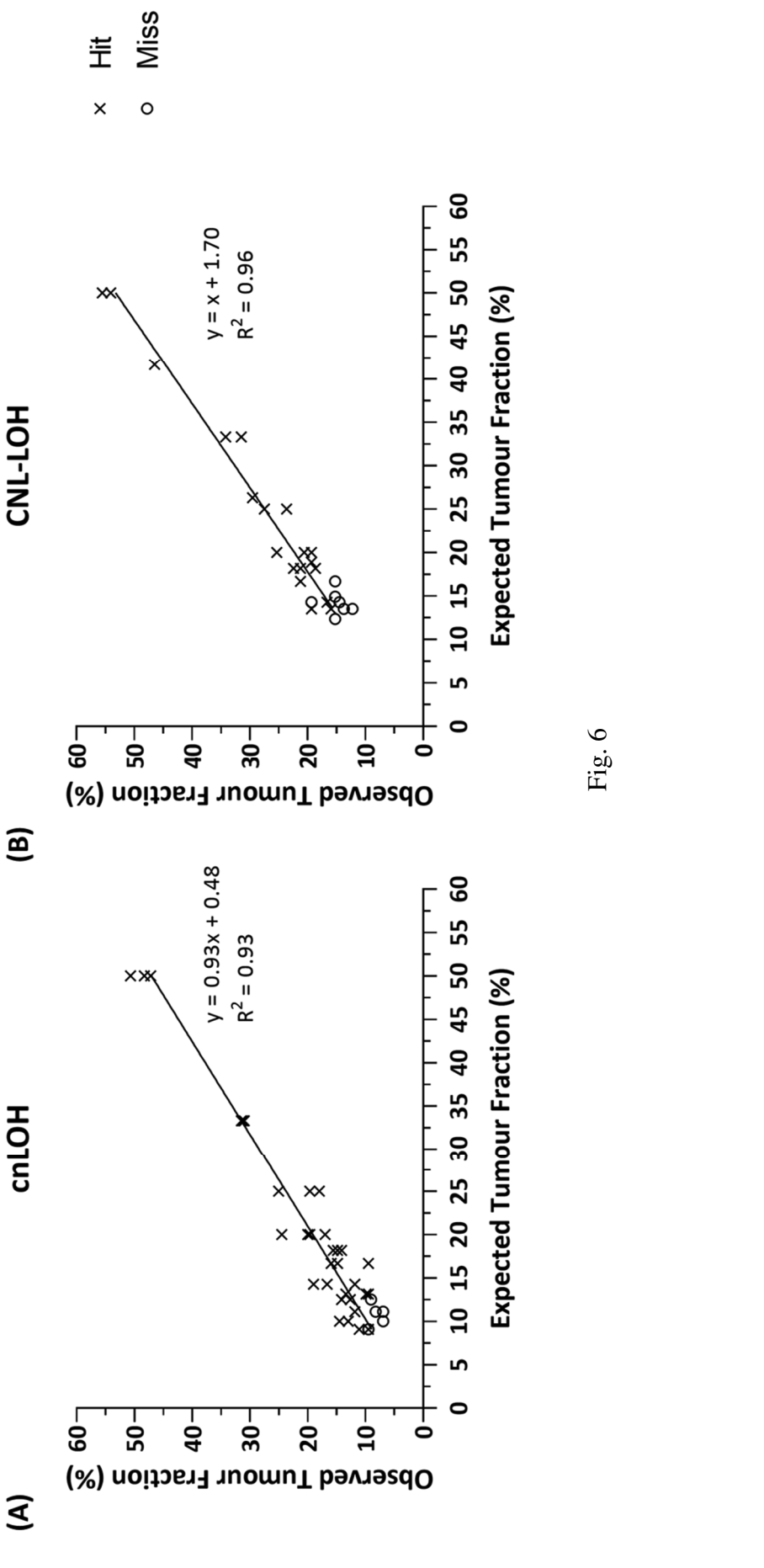

(A)
cnLOH
y = 0.93x + 0.48
R2 = 0.93
Observed Tumour Fraction (%)
Expected Tumour Fraction (%)
(B)
CNL-LOH
y = x + 1.70
R2 = 0.96
Observed Tumour Fraction (%)
Expected Tumour Fraction (%)
Hit
Miss

Fig. 6

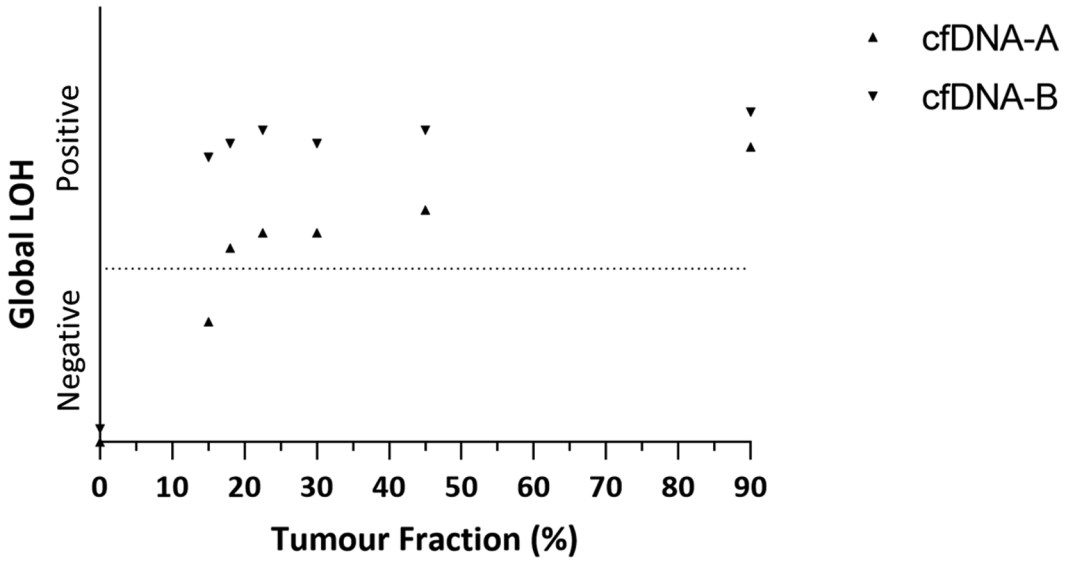

Global LOH
Positive
Negative
0
10
20
30
40
50
60
70
80
90
Tumour Fraction (%)
cfDNA-A
cfDNA-B

Fig. 7