

Supplementary Materials: Genomic Instability in Cerebrospinal Fluid Cell-Free DNA Predicts Poor Prognosis in Solid Tumor Patients with Meningeal Metastasis

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Table S1. Distribution of variation in the top 35 genes for different genomic status.

Characteristic	GI, N = 37 ¹	GS, N = 19 ¹	p-Value ²
TP53			<0.001
variant	29 (78%)	6 (32%)	
wildtype	8 (22%)	13 (68%)	
CDKN2A			0.077
variant	10 (27%)	1 (5.3%)	
wildtype	27 (73%)	18 (95%)	
APC			0.082
variant	7 (19%)	0 (0%)	
wildtype	30 (81%)	19 (100%)	
RICTOR			0.11
variant	18 (49%)	5 (26%)	
wildtype	19 (51%)	14 (74%)	
KMT2C			0.14
variant	9 (24%)	1 (5.3%)	
wildtype	28 (76%)	18 (95%)	
ERBB2			0.15
variant	8 (22%)	1 (5.3%)	
wildtype	29 (78%)	18 (95%)	
RB1			0.15
variant	8 (22%)	1 (5.3%)	
wildtype	29 (78%)	18 (95%)	
EGFR			0.2
variant	28 (76%)	11 (58%)	
wildtype	9 (24%)	8 (42%)	
SMAD4			0.2
variant	5 (14%)	0 (0%)	
wildtype	32 (86%)	19 (100%)	
FGFR4			0.3
variant	4 (11%)	0 (0%)	
wildtype	33 (89%)	19 (100%)	
SETD2			0.3
variant	4 (11%)	0 (0%)	
wildtype	33 (89%)	19 (100%)	
STAG2			0.3
variant	2 (5.4%)	3 (16%)	
wildtype	35 (95%)	16 (84%)	
STK11			0.3
variant	4 (11%)	0 (0%)	
wildtype	33 (89%)	19 (100%)	

RBM10			0.4
variant	6 (16%)	1 (5.3%)	
wildtype	31 (84%)	18 (95%)	
CDH1			0.4
variant	3 (8.1%)	3 (16%)	
wildtype	34 (92%)	16 (84%)	
KMT2D			0.4
variant	3 (8.1%)	3 (16%)	
wildtype	34 (92%)	16 (84%)	
MYC			0.4
variant	6 (16%)	1 (5.3%)	
wildtype	31 (84%)	18 (95%)	
DNMT3A			0.6
variant	2 (5.4%)	2 (11%)	
wildtype	35 (95%)	17 (89%)	
MTOR			0.6
variant	2 (5.4%)	2 (11%)	
wildtype	35 (95%)	17 (89%)	
NF1			0.6
variant	2 (5.4%)	2 (11%)	
wildtype	35 (95%)	17 (89%)	
TERT			0.6
variant	2 (5.4%)	2 (11%)	
wildtype	35 (95%)	17 (89%)	
BRCA2			0.7
variant	5 (14%)	1 (5.3%)	
wildtype	32 (86%)	18 (95%)	
CDK4			0.7
variant	6 (16%)	2 (11%)	
wildtype	31 (84%)	17 (89%)	
GNAS			0.7
variant	4 (11%)	1 (5.3%)	
wildtype	33 (89%)	18 (95%)	
KRAS			0.7
variant	5 (14%)	1 (5.3%)	
wildtype	32 (86%)	18 (95%)	
NOTCH1			0.7
variant	4 (11%)	1 (5.3%)	
wildtype	33 (89%)	18 (95%)	
PTEN			0.7
variant	7 (19%)	2 (11%)	
wildtype	30 (81%)	17 (89%)	
PIK3CA			0.8
variant	10 (27%)	4 (21%)	
wildtype	27 (73%)	15 (79%)	
BAP1			>0.9
variant	3 (8.1%)	2 (11%)	
wildtype	34 (92%)	17 (89%)	
BRCA1			>0.9
variant	3 (8.1%)	1 (5.3%)	
wildtype	34 (92%)	18 (95%)	
CDK12			>0.9
variant	3 (8.1%)	1 (5.3%)	
wildtype	34 (92%)	18 (95%)	

FGFR1			>0.9
variant	3 (8.1%)	2 (11%)	
wildtype	34 (92%)	17 (89%)	
IRS2			>0.9
variant	3 (8.1%)	1 (5.3%)	
wildtype	34 (92%)	18 (95%)	
MDM2			>0.9
variant	3 (8.1%)	1 (5.3%)	
wildtype	34 (92%)	18 (95%)	
NOTCH2			>0.9
variant	3 (8.1%)	1 (5.3%)	
wildtype	34 (92%)	18 (95%)	

¹n (%)

²Pearson's Chi-squared test; Fisher's exact test

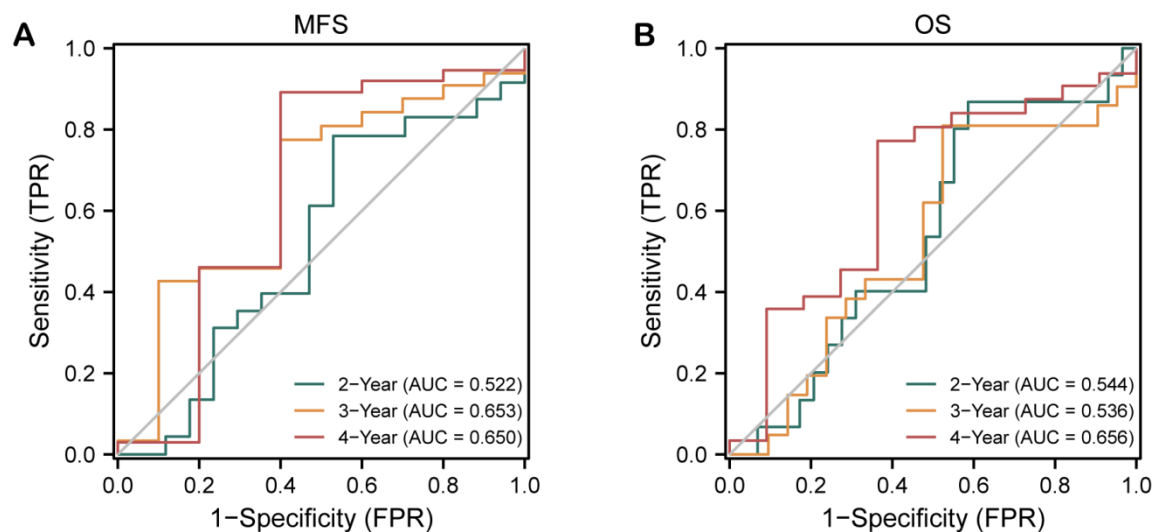


Figure S1. Receiver operating characteristic (ROC) curves for MFS and OS.

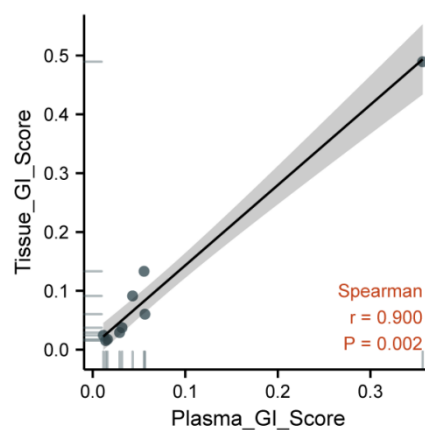


Figure S2. Correlation analysis of GI_Scores between 9 paired plasma cfDNA and primary tumor tissues.