ACCSCIENCE PUBLISHING

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ORIGINAL RESEARCH ARTICLE

Distinct metabolic subtypes of gastric cancer: Immune profiles, therapeutic response prediction, and a 60-gene classifier

Supplementary File

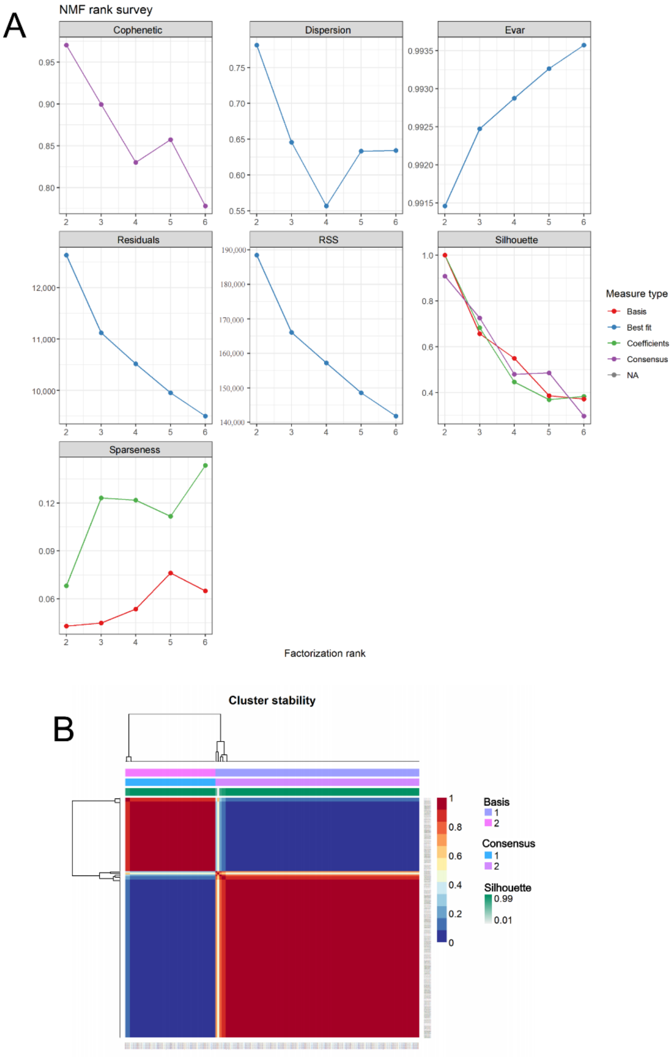

Figure S1. NMF clustering validation for gastric cancer metabolic subtype identification. (**A**) NMF rank survey parameters of the integrated Gene Expression Omnibus dataset. (**B**) Consensus clustering map of the TCGA-STAD cohort at the optimal clustering rank *k* = 2.

Abbreviations: Evar: Explained variance; NA: Not available; NMF: Non-negative matrix factorization; RSS: Residual sum of squares; TCGA-STAD: The Cancer Genome Atlas Stomach Adenocarcinoma.

Table S1. Clinicopathological characteristics of gastric cancer metabolic subtypes in the Asian Cancer Research Group cohort

Characteristic	*n*	Cluster 1	Cluster 2	*p*
Age				
<60	106	54	52	<0.0001
≥60	194	52	142	
Sex				
Female	101	43	58	0.0616
Male	199	63	136	
Status				
Alive	148	32	116	<0.0001
Dead	152	74	78	
Recurrence				
Recurrence	125	63	62	<0.0001
No recurrence	157	36	121	
Unknown	18	7	11	
Tumor location				
Antrum	150	42	108	0.0672
Body	107	45	62	
Cardia	30	13	17	
Multicentric	13	6	7	
Lauren classification				
Diffuse	135	75	60	<0.0001
Intestinal	148	25	123	
Mixed	17	6	11	
Pathological stage				
I	31	3	28	0.0012
II	165	55	110	
III	77	33	44	
IV	27	15	12	
MLH1 mutation				
Negative	66	6	60	<0.0001
Positive	234	100	134	
Molecular subtype				
MSI	68	9	59	<0.0001
EMT	46	46	0	
MSS/*TP53*$^-$	107	31	76	
MSS/*TP53*$^+$	79	20	59	

Abbreviations: EMT: Epithelial–mesenchymal transition; MSI: Microsatellite instability; MSS: Microsatellite stable.

Table S2. Amino acid mutation sites of *MUC16* in cluster 1

HGNC	Amino acid position	Variant classification[a]	Number of mutations	Total[b]	Domain label[c]
MUC16	12,955	Missense_Mutation	1	35	Tandem repeat region
	13,755	Missense_Mutation	1	35	Tandem repeat region
	13,842	Missense_Mutation	1	35	Tandem repeat region
	12,694	Missense_Mutation	1	35	Tandem repeat region
	13,120	Missense_Mutation	1	35	Tandem repeat region
	12,704	Missense_Mutation	1	35	Tandem repeat region
	13,043	Missense_Mutation	1	35	Tandem repeat region

Notes: [a]Classification of single nucleotide variant loci. [b]Number of samples in each cluster; [c]Domains containing mutations.
Abbreviation: HGNC: HUGO Gene Nomenclature Committee.

Table S3. Amino acid mutation sites of *MUC16* in cluster 2

HGNC	Amino acid position	Variant classification[a]	Number of mutations	Total[b]	Domain label[c]
MUC16	13,865	Missense_Mutation	2	169	Tandem repeat region
	13,161	Missense_Mutation	1	169	Tandem repeat region
	13,337	Missense_Mutation	1	169	Tandem repeat region
	12,815	Missense_Mutation	1	169	Tandem repeat region
	12,500	Missense_Mutation	1	169	Tandem repeat region
	12,344	Missense_Mutation	1	169	Tandem repeat region
	13,537	Missense_Mutation	1	169	Tandem repeat region
	13,005	Missense_Mutation	1	169	Tandem repeat region
	12,977	Missense_Mutation	1	169	Tandem repeat region
	13,599	Missense_Mutation	1	169	Tandem repeat region
	12,820	Missense_Mutation	1	169	Tandem repeat region
	12,326	Missense_Mutation	1	169	Tandem repeat region
	12,135	Missense_Mutation	1	169	Tandem repeat region
	12,966	Missense_Mutation	1	169	Tandem repeat region
	12,535	Missense_Mutation	1	169	Tandem repeat region
	12,248	Missense_Mutation	1	169	Tandem repeat region
	12,991	Missense_Mutation	1	169	Tandem repeat region
	12,740	Missense_Mutation	1	169	Tandem repeat region
	12,619	Missense_Mutation	1	169	Tandem repeat region
	13,507	Missense_Mutation	1	169	Tandem repeat region
	12,711	Missense_Mutation	1	169	Tandem repeat region
	13,539	Missense_Mutation	1	169	Tandem repeat region
	13,647	Missense_Mutation	1	169	Tandem repeat region
	12,999	Missense_Mutation	1	169	Tandem repeat region
	14,081	Missense_Mutation	1	169	Tandem repeat region
	13,078	Missense_Mutation	1	169	Tandem repeat region

(*Cont'd...*)

Table S3. (*Continued*)

HGNC	Amino acid position	Variant classification[a]	Number of mutations	Total[b]	Domain label[c]
MUC16	12,602	Splice_Site	1	169	Tandem repeat region
	14,341	Missense_Mutation	1	169	SEA
	14,351	Frame_Shift_Ins	1	169	SEA

Notes: [a]Classification of single nucleotide variant loci. [b]Number of samples in each cluster; [c]Domains containing mutations.
Abbreviations: HGNC: HUGO Gene Nomenclature Committee; SEA: Sea-urchin sperm protein, enterokinase, and agrin.