



Supplementary material

TRPV2 calcium channel gene expression and outcomes in gastric cancer patients: a clinically relevant correlation

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Methods

Table S1. Clinical characteristics of patients by gene expression dataset.

Parameters	KMplot (n = 593)	GSE15460 (n = 248)	GSE62254 (n = 300)	STAD-TCGA (n = 385)
GENDER				
Female	138 (23.3)	87 (35.1)	101 (33.7)	133 (34.5)
Male	360 (60.7)	161 (64.9)	199 (66.3)	250 (64.9)
AGE				
(Mean ± SD)	-	65.4 ± 12.5	61.9 ± 11.3	65.4 ± 10.4
TREATMENT				
Only surgical	174 (29.3)	-	219 (73.0)	38 (9.9)
Adjuvant	153 (25.8)	-	80 (26.7)	27 (7.0)
LAUREN'S HISTOLOGY				
Intestinal	179 (30.2)	138 (55.6)	150 (50.0)	170 (44.1)
Diffuse	106 (17.9)	86 (34.7)	142 (47.3)	77 (20.0)
Mixed	25 (4.2)	22 (3.7)	8 (2.7)	-
N STAGE				
N0	38 (6.4)	-	38 (12.7)	116 (30.1)
N1+N2+N3	175 (29.5)	-	262 (87.3)	258 (67.0)
M STAGE				
M0	186 (31.4)	-	273 (91.0)	342 (88.8)
M1	31 (5.2)	-	27 (9.0)	25 (6.5)
TUMOR STAGE				
I	39 (6.6)	42 (16.9)	30 (10.0)	50 (13.0)
II	49 (8.3)	40 (16.1)	96 (32.0)	125 (32.5)
III	217 (36.6)	91 (36.7)	95 (31.7)	155 (40.3)
IV	74 (12.5)	73 (29.4)	77 (29.4)	39 (10.1)

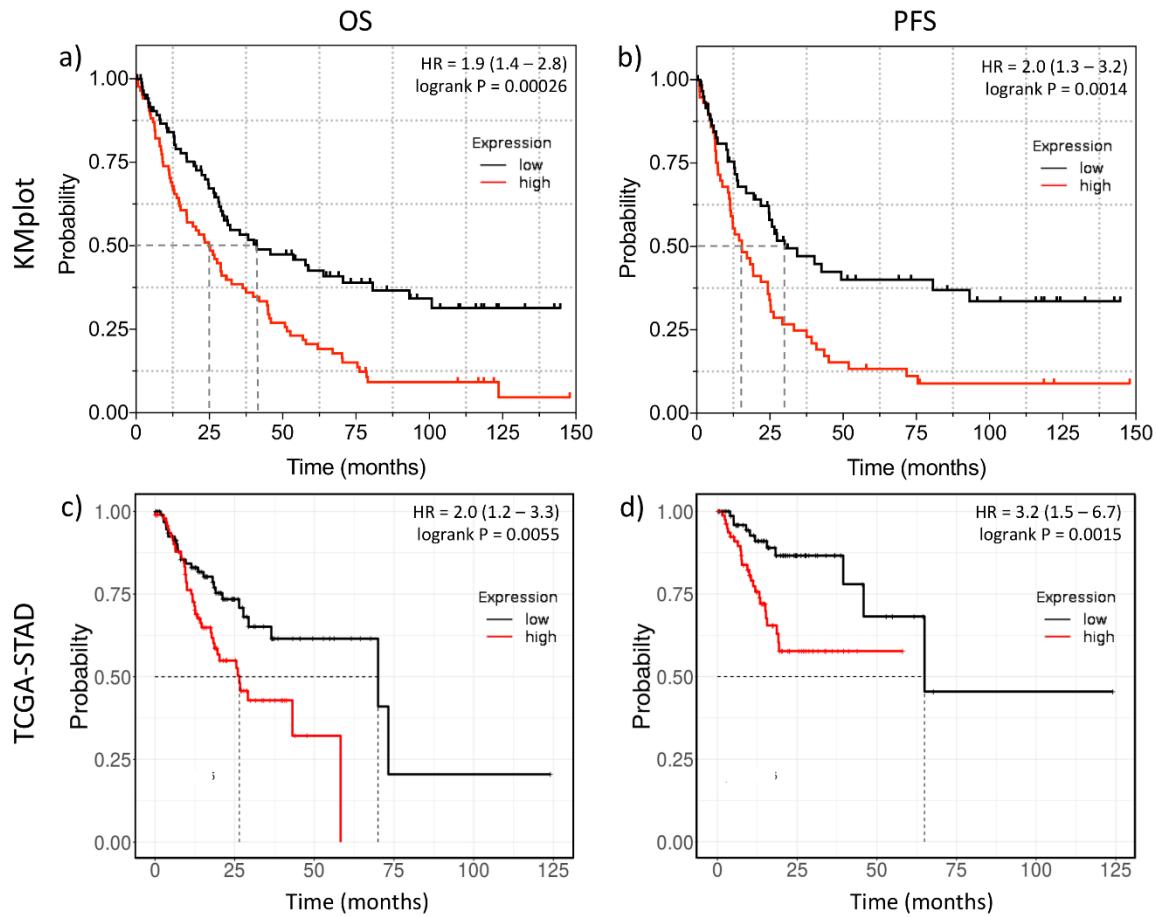


Figure S1. Prognostic relevance of a representative CaRG mRNA expression in gastric cancer patients. OS (**a**) and PFS (**b**) survival curves of the *NALCN* gene in the KMplot dataset (593 and 359 patients, respectively). OS (**c**) and PFS (**d**) survival curves of the *NALCN* gene in the TCGA-STAD dataset (383 and 320 patients, respectively). High and low expression cohorts represent samples falling in Q4 and Q1 of expression values.

Results

Table S2. CaRG list and selection criteria

Gene	Ca ²⁺ channel/transporter	Ca ²⁺ permeability	Ca ²⁺ channels subunit
<i>ANO6</i>		x	
<i>ATP13A2</i>		x	
<i>ATP13A3</i>		x	
<i>ATP13A4</i>		x	
<i>ATP13A5</i>		x	
<i>ATP2A1</i>	x		
<i>ATP2A2</i>	x		
<i>ATP2A3</i>	x		
<i>ATP2B1</i>	x		
<i>ATP2B2</i>	x		
<i>ATP2B3</i>	x		
<i>ATP2C1</i>	x		
<i>C19orf26</i>			x
<i>CACNA1B</i>			x
<i>CACNA1C</i>			x
<i>CACNA1D</i>			x
<i>CACNA1E</i>			x
<i>CACNA1F</i>			x
<i>CACNA1G</i>			x
<i>CACNA1H</i>			x
<i>CACNA1I</i>			x
<i>CACNA2D1</i>			x
<i>CACNA2D2</i>			x
<i>CACNA2D3</i>			x
<i>CACNA2D4</i>			x
<i>CACNB1</i>			x
<i>CACNB2</i>			x
<i>CACNB3</i>			x
<i>CACNB4</i>			x
<i>CACNG4</i>			x
<i>CACNG6</i>			x
<i>CACNG7</i>			x
<i>CACNG8</i>			x
<i>CCDC109B</i>			x
<i>CHRNA10</i>		x	
<i>GRIN1</i>			x
<i>GRIN2A</i>			x
<i>GRIN2B</i>			x
<i>GRIN2C</i>			x
<i>GRIN2D</i>			x
<i>GRIN3A</i>			x
<i>GRIN3B</i>			x
<i>ITPR1</i>	x		
<i>ITPR2</i>	x		
<i>ITPR3</i>	x		
<i>LETM1</i>	x		
<i>MCOLN2</i>	x		
<i>NALCN</i>		x	
<i>ORAI1</i>			x
<i>ORAI2</i>			x
<i>ORAI3</i>			x
<i>P2RX1</i>			x

<i>P2RX2</i>	x
<i>P2RX3</i>	x
<i>P2RX4</i>	x
<i>P2RX5</i>	x
<i>P2RX6</i>	x
<i>P2RX7</i>	x
<i>PKD1L1</i>	x
<i>PKDREJ</i>	x
<i>RYR1</i>	x
<i>RYR2</i>	x
<i>RYR3</i>	x
<i>SLC24A1</i>	x
<i>SLC24A2</i>	x
<i>SLC24A3</i>	x
<i>SLC24A4</i>	x
<i>SLC25A23</i>	x
<i>SLC25A25</i>	x
<i>SLC3A2</i>	x
<i>SLC8A1</i>	x
<i>SLC8A2</i>	x
<i>SLC8A3</i>	x
<i>STIM1</i>	x
<i>STIM2</i>	x
<i>TMC2</i>	x
<i>TMCO1</i>	x
<i>TMEM165</i>	x
<i>TMEM37</i>	x
<i>TMEM63C</i>	x
<i>TPCN1</i>	x
<i>TPCN2</i>	x
<i>TRDN</i>	x
<i>TRPA1</i>	x
<i>TRPC1</i>	x
<i>TRPC3</i>	x
<i>TRPC4</i>	x
<i>TRPC4AP</i>	x
<i>TRPC6</i>	x
<i>TRPM2</i>	x
<i>TRPM3</i>	x
<i>TRPM6</i>	x
<i>TRPM7</i>	x
<i>TRPM8</i>	x
<i>TRPV2</i>	x
<i>TRPV3</i>	x
<i>TRPV4</i>	x
<i>TRPV6</i>	x

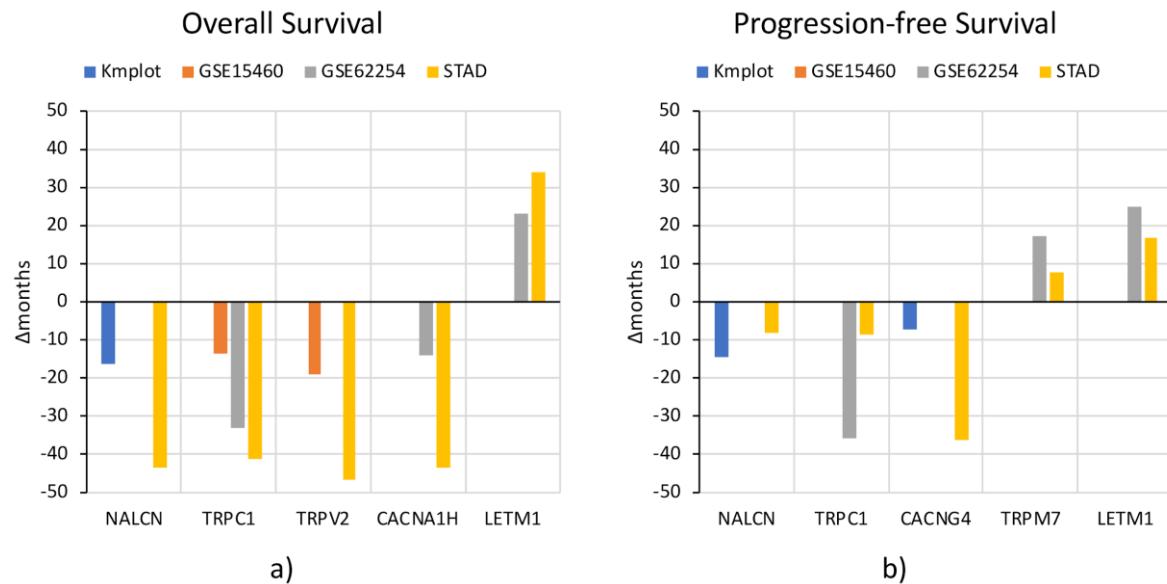


Figure S2. Differences of OS (a) and PFS (b) duration between high and low expression cohorts of each prognostic CaRG. Differences were calculated between median survival times of the two cohorts. If cohorts did not reach median survival, restricted mean (rmean) of survival times were considered.

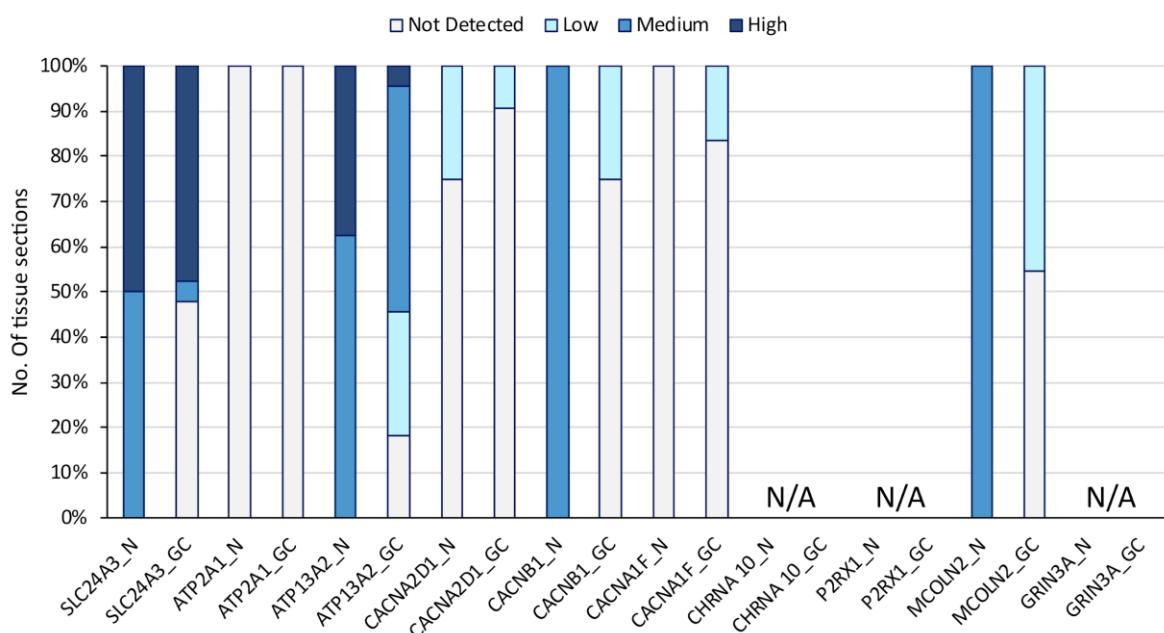


Figure S3. Differential protein expression in normal stomach (N) and gastric cancer (GC) tissue sections from the HPA database of CaRGs with significant prognostic value in subgroup analysis. Colors represent the intensity of staining.