

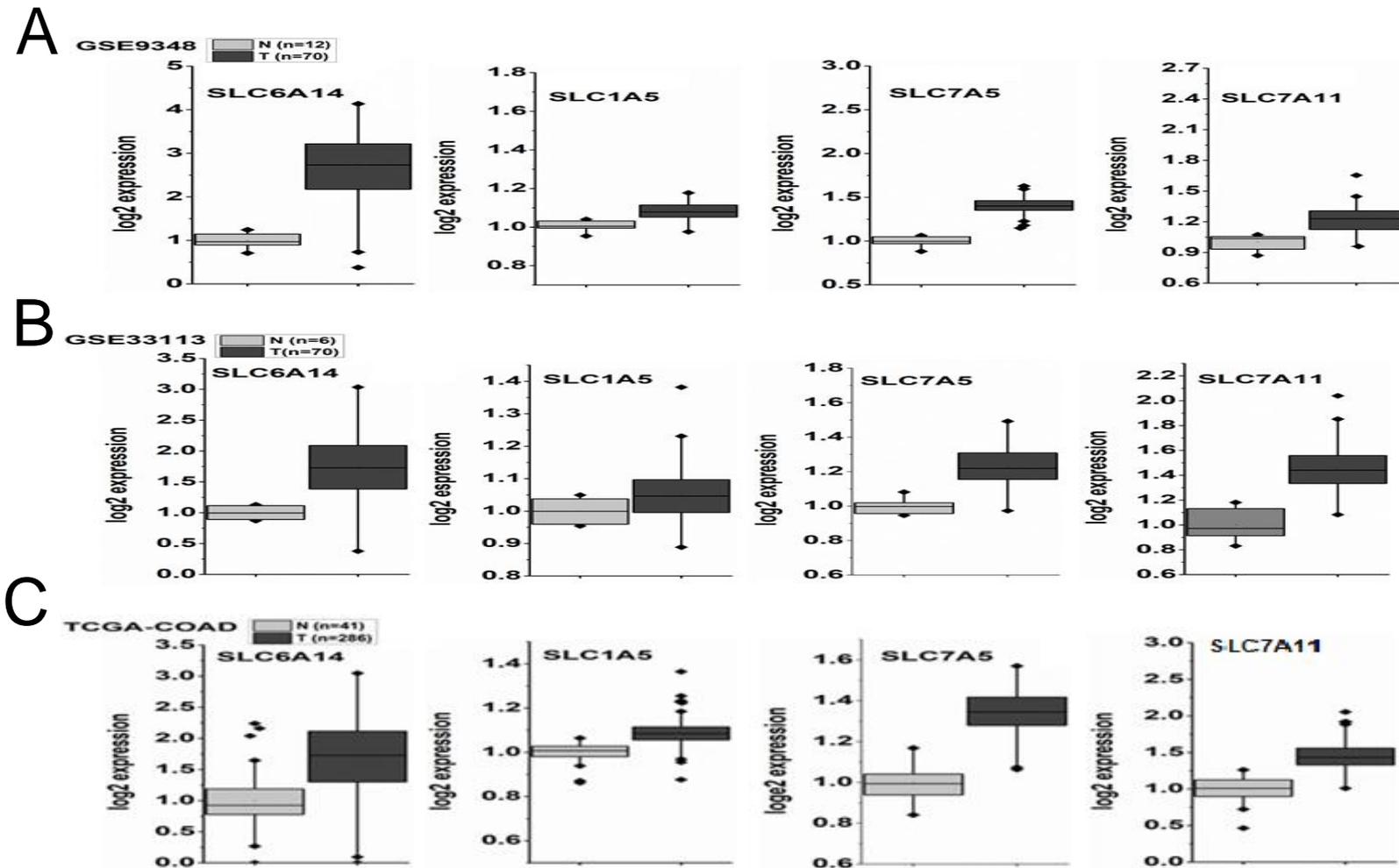
Target	Primer sequence (5'-3')
hASNS	CTGCTAGAAAGGTGGCAGATCA
	CCAGAGAAGATCACCACGCTA
hCHOP	TCCAGCCACTCCCCATTATC
	GCAGGGTCAAGAGTGGTGAA
hβ-catenin	GCTTGAATGAGACTGCTGAT
	TCCATACCCAAGGCATCCTG
hCyclinD1	GGAGCTGCTGCAAATGGA
	GGAGGGCGGATTGGAAATGA
hSLC6A14	ATCGTCTGGCAAGGTGGTAT
	TGAGTGGCAGCATCTTTCCAT
hGAPDH	CCACTCCTCCACCTTTGAC
	ACCCTGTTGCTGTAGCCA
h18S	CCCGTTGAACCCCATTCGT
	GCCTCACTAAACCATCCAATCGGTA
hSLC6A14 promoter	ATTGCAAACGTACCTACACAGC
	ACCGGAAGGGACTAAAGTGAG
mSlc6a14 WT/genotype	AGCTCCTTTCTCAGCCTTCGGAAT
	TCCTTGTCAGCCAGTGAGGAACAA
mSlc6a14 KO/genotype	CATGTTCTTATTGGGCCTACC
	CCTGCCATAGCCTCAGGTTACTC
WT Apc ^{Min/+} genotype	GCCATCCCTTCACGTTAG
Mutant Apc ^{Min/+} genotype	TTCTGAGAAAGACAGAAGTTA
Apc ^{Min/+} common/genotype	TTCCACTTTGGCATAAGC
hSLC1A1	TGGTGCTAGGCATTACCACA
	CCGGATACGTTGGAATCCAGT
hSLC1A5	GAGACTCCAAGGGGCTCGC
	CACAAGCAGGTTGGCTCGAAG

hSLC6A15	CAAAGGCATTCAGTCTTCTGGA
	AGCATTATTTCAAGCTTAGGGGTA
hSLC6A19	CTCTTCACGCCCAACGTCA
	ACCGATGTGAAGCCGTTGAT
hSLC6A20	GTGTTTCGCCTGCATCTCGTA
	GACCAGGAAACTACCTCCGC
hSLC7A5	CGCTCTTCCCCACCTGC
	GACACATCACCCCTTCCCGAT
hSLC7A8	CAGAGTCTGGCCTTCGGCTC
	CCAGCCAGAAGTACTCTCCTTTG
hSLC7A9	AGCCTGGCGTTTTACAATGG
	AGGCAGGTTTCTGTAAGGGTT
hSLC7A11	TGTGTGGGGTCCTGTCACTA
	CAGTAGCTGCAGGGCGTATT
hSLC36A1	TTGGAATGGTTCTGCCCTG
	CAGCAGCTTAACTGACTGGT
hSLC36A2	ACTGCTGGCTGTACCAGTCT
	GGATGAGGATGGCCAGGAGG
hSLC38A1	TTTGGAGTCGTAGGAGTTACATCT
	TGGAAACTGGAGGAAGAGAAAGA
hSLC38A2	GCAGTGGAATCCTTGGGCTT
	ATAAAGACCCTCCTTCATTGGCA
hSLC38A3	GCTCCAGAACATCGGAGCCAT
	TTCCCGTTCATGTACCAGTCC
hSLC38A5	GTTGGGGCCATGTCCAGTTA
	AGTGTTTCATGAGGGCGAGG

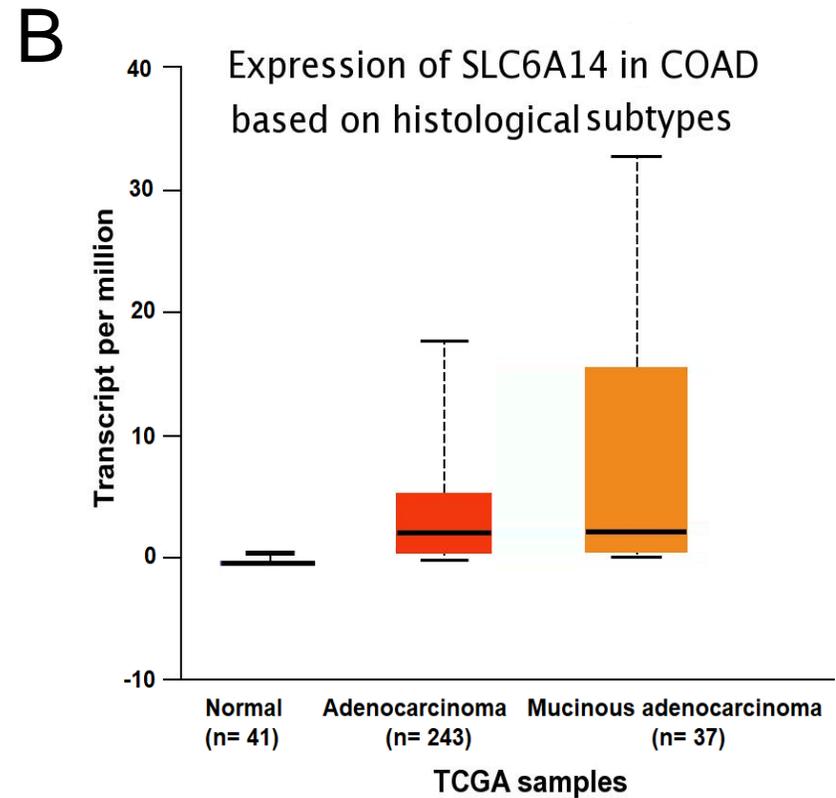
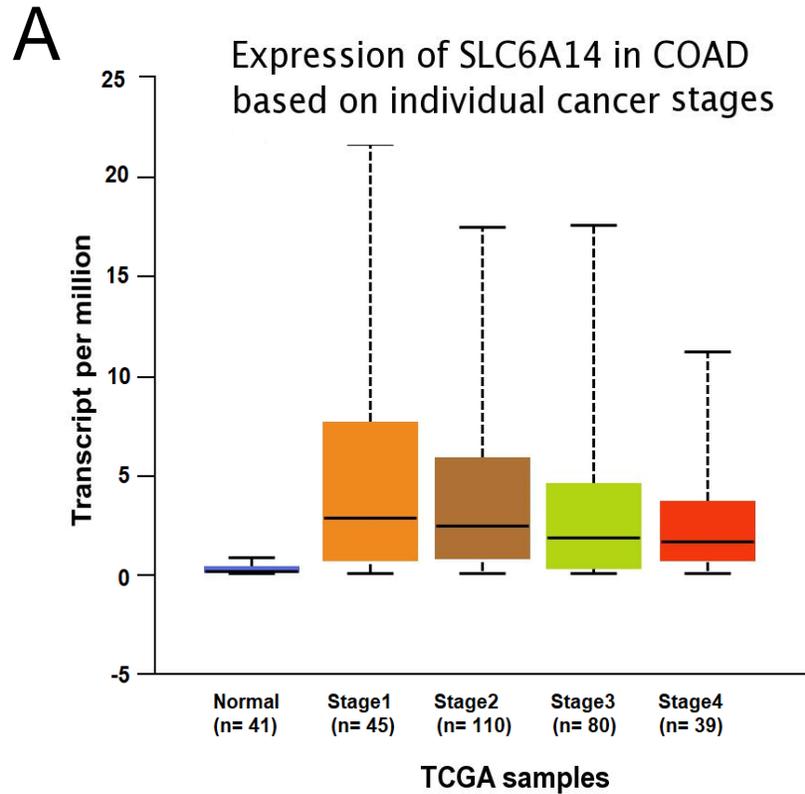
Supplementary Table S1. Sequences of PCR Primers used in this study.

Data set	Amino acid transporters	logFC	p value
GSE9348	SLC6A14	6.309173	4.15E-06
	SLC1A5	2.115759	0.101
	SLC7A5	2.649015	0.0531
	SLC7A11	2.342878	0.0343
GSE33113	SLC6A14	3.326173	0.00262
	SLC1A5	2.074127	0.0954
	SLC7A5	2.340183	0.082
	SLC7A11	2.741603	0.586
TCGA-COAD	SLC6A14	3.143338	0.0332
	SLC1A5	2.121997	0.134
	SLC7A5	2.537145	0.103
	SLC7A11	2.715731	0.334

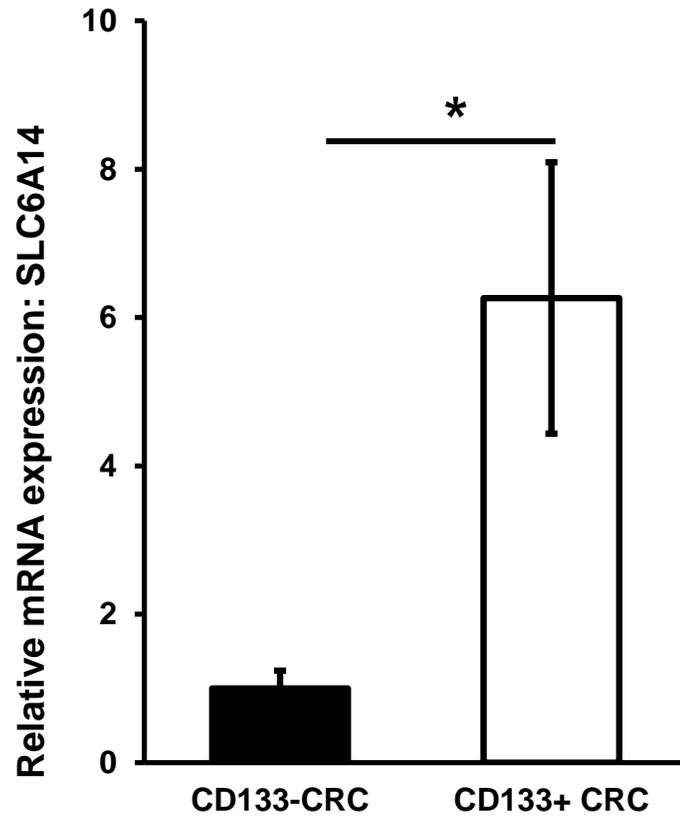
Supplementary Table S2. log₂ of fold changes (logFC) in the expression of SLC6A14, SLC1A5, SLC7A5 and SLC7A11 in colon cancer. Publicly available gene expression data sets (GSE9348, GSE33113 and TCGA-COAD) were used to analyze the fold changes. The values of $p < 0.05$ indicates the statistical significance of fold changes in the expression between tumor tissues and the corresponding normal tissues.



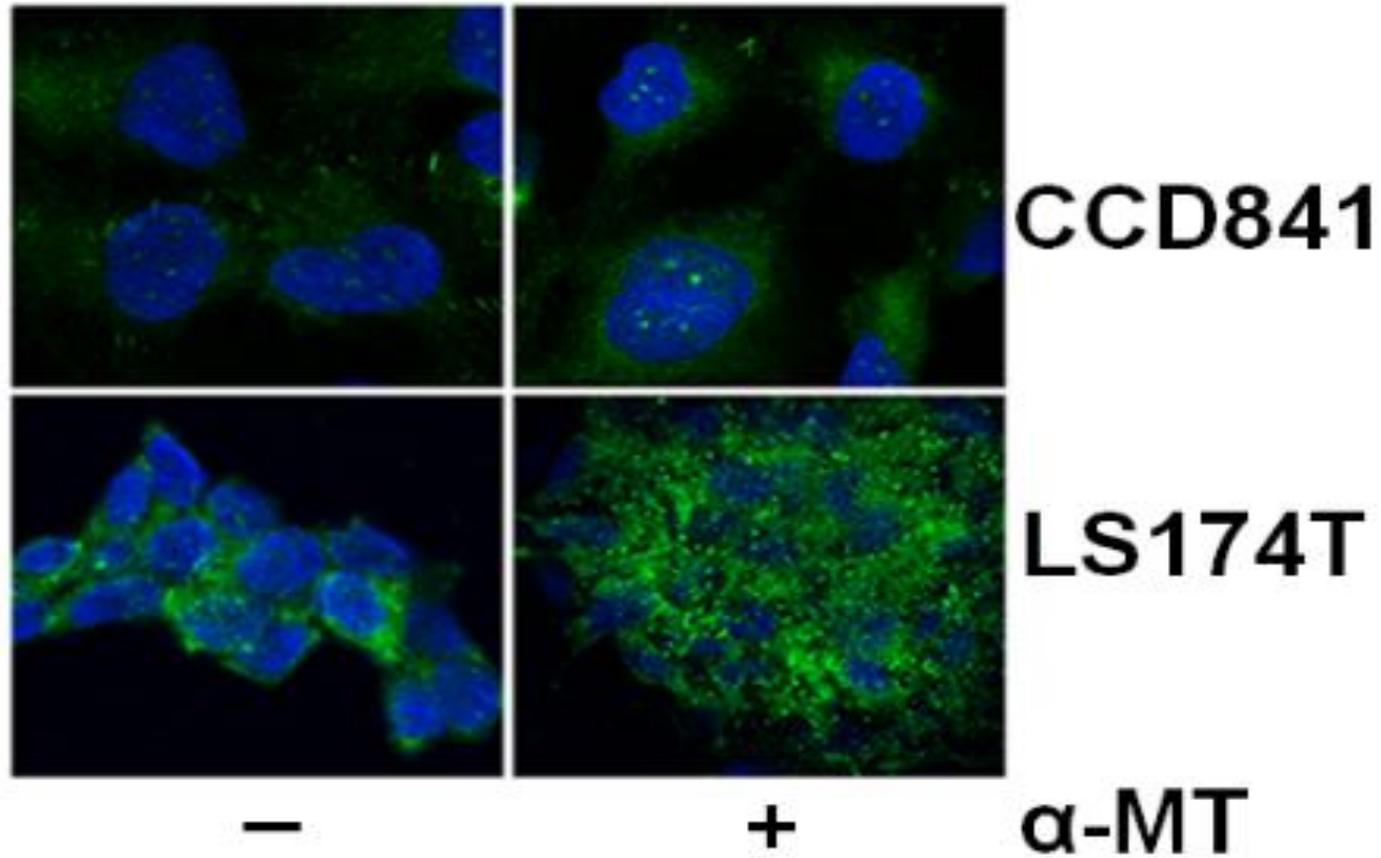
Supplementary Figure S1. Up-regulation of amino acid transporters in colon cancer. Box plots represent the log₂ expression of SLC6A14, SLC1A5, SLC7A5 and SLC7A11 in normal colon (N) vs colonic tumor (T) as assessed from publicly available microarray datasets GSE9348(A), GSE33113 (B), and TCGA (The Cancer Genome Atlas) colon cancer (TCGA-COAD) dataset (C). The horizontal line within each box indicates the median value and box edges represent the lower (25th) and upper (75th) quartile.



Supplementary Figure S2.(A) Box-whisker plots show the relative expression of SLC6A14 in normal and individual stages of colon adenocarcinoma (COAD). (B) Boxplots show relative expression of SLC6A14 in histological subtypes of COAD compared with normal colon tissue.

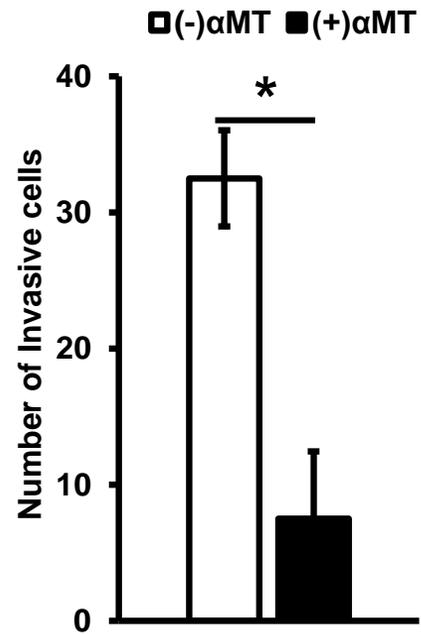


Supplementary Figure S3. Differential expression of SLC6A14 in CD133-positive vs CD133-negative colorectal cancer cells (CRCs). GSE34053 dataset was retrieved from NCBI gene expression omnibus (GEO) and subjected to analysis for SLC6A14 in CD133-positive CRCs (exhibit enhanced tumorigenicity) vs CD133-negative CRCs (exhibit low tumorigenicity).

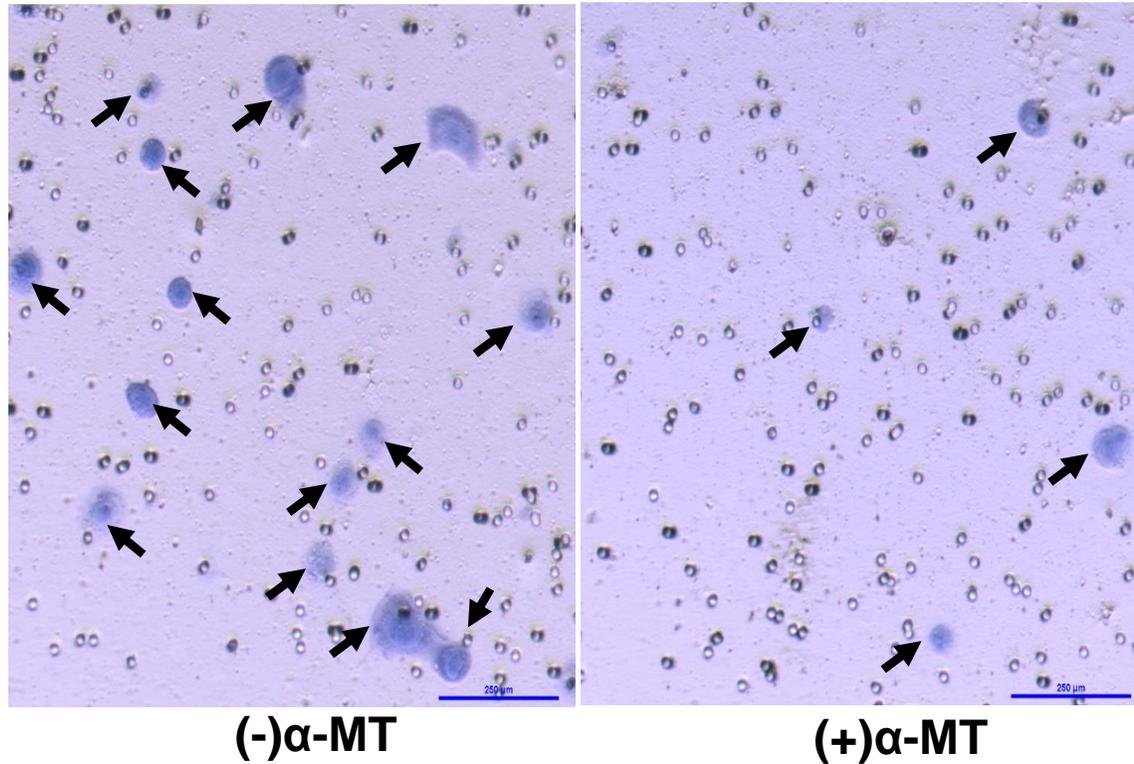


Supplementary Figure S4. Pharmacological blockade of SLC6A14 by α -MT induces autophagy in colon cancer. Immunofluorescence analysis to localize punctate form of LC3A/B in autophagosome in CCD841 and LS174T cells after treatment with and without 2.5 mM α -MT for 72 h.

A



B



Supplementary Figure S5. Effect of α-MT on invasion and migration of colon cancer cells. LS174T colon cancer cells were treated with or without 2.5 mM α-MT for 48 h in Matrigel-coated trans-well chambers. After 48 h of incubation, the invasive cells that have migrated to the other side were stained with crystal violet and observed and counted under the microscope ($\times 120$). Data are from two independent experiments done in triplicate. (A) Quantification of the cells that moved to the other side of the membrane; $*P < 0.05$. (B) The staining of the membrane with crystal violet for control and α-MT-treated cells in a representative experiment. Arrows indicate the cells that have migrated across the membrane and invaded the other side.