LEGENDS TO SUPPLEMENTARY FIGURES

FIGURE S1. **Event-free survival plots for 15 *ABC* genes associated with neuroblastoma patient outcome.** Kaplan-Meier plots were generated for each of 23 individual ABC family genes whose expression levels in 251 neuroblastoma tumours were extracted from microarray data (23). For each gene, the cut-point used to determine 'high'; or 'low' expression is indicated as upper quartile, lower quartile, or upper decile. $p<0.05$ was used as the criterion for inclusion in the cluster analysis displayed in Fig. 1. Those genes whose expression was not associated with clinical outcome were: *ABCA3, ABCB1, ABCB4, ABCC2, ABCC7, ABCC8, ABCD4 and ABCF1*.

FIGURE S2. **MYCN regulates *ABCA12* transcription through an indirect mechanism.** *ABCA12* mRNA expression was assessed in SK-N-BE(2)C cells depleted of MYCN. *(A)* Western blotting showing MYCN levels in cells treated with a MYCN specific siRNA. *(B)* mRNA levels of control genes and *ABCA12* isoforms were determined by RQ-PCR in cells depleted of MYCN and compared to those of undepleted cells. *(C)* Chromatin immunoprecipitation was performed in SK-N-BE(2)C cells. Several DNA regions of the *ABCA12* promoters were tested for IP enrichment. Results represent the average of three independent ChIP experiments in which each region was amplified by RQ-PCR in duplicate ± SE. Promoter diagram: bent arrow, transcription start site; red arrow, canonical E-box; black arrow, non-canonical E-box; open boxes, amplicons indicated with a capital letter; chromosome and coordinates (bp) are also given.

FIGURE S3. **Specificity of *MYCN* ChIP assay.** *(A)* Quantitative ChIP was applied to TET21/N cells exposed to tetracycline and hence repressed for MYCN expression. Fold enrichment is relative to the pre-immune serum. Results represent the average of five independent ChIP experiments in which each region was amplified by RQ-PCR in triplicate ± SE. Promoter diagram: bent arrow, transcription start site; red arrow, canonical E-box; black arrow, non-canonical E-box; open boxes, amplicons indicated with a capital letter; chromosome and coordinates (bp) are also given *(left and middle panel).* Dual cross-linking ChIP for the *ABCC*3 gene promoter using MYCN, MAX or Sp1 antibodies in TET/21N cells repressed for *MYCN* expression. Results represent the average of three independent ChIP experiments. In all cases, positive ChIP results for MYCN were dependent on *MYCN* expression (*right panel). (B)* Quantitative ChIP and quantitative dual cross-linking ChIP was performed for *APEX-1* and *p21CIP/WAF,* respectively.

FIGURE S4. **MYCN does not associate with promoters of the *ABCA1, ABCA6, ABCA7* or *ABCD2* genes.** Dual cross-linking ChIP was performed for the *ABCA1, ABCA6, ABCA7* and *ABCD2* gene promoters using MYCN, MAX or SP1 antibodies in TET/21N cells in the presence of MYCN. Fold enrichment of immunoprecipitated DNA regions was calculated as described above. Results represent the average of three independent ChIP experiments.

FIGURE S5. **Human *ABCC3* promoter sequence.** The identified Sp1 binding sites (BS) were found in the promoter region close to the TSS from -39 to +490bp. Site directed mutagenesis was used to mutate the Sp1 BS found in the human *ABCC3* promoter. In red are highlighted the nucleotides mutated and the sequence of the oligonucleotides used are listed below.

FIGURE S6. **c-MYC associates with the promoters of multiple *ABC* gene family members.** *(A)* Quantitative ChIP was applied to P493-6 cells in which c-MYC was either expressed (-tet) or not (+tet) and binding of transcription factors was compared between the two conditions. Fold enrichment is relative to the pre-immune serum. Results represent the mean ± SE of four independent ChIP experiments in which each region was amplified by RQ-PCR in triplicate ± SE. Promoter diagram: bent arrow, transcription start site; red arrow, canonical E-box; black arrow, non-canonical E-box; open boxes, amplicons indicated with a capital letter; chromosome and coordinates (bp) are also given. *(B)* Dual cross-linking ChIP for the *ABCC*3 gene promoter using c-MYC, MAX or Sp1 antibodies. Results represent the mean ± SE of three independent ChIP experiments.

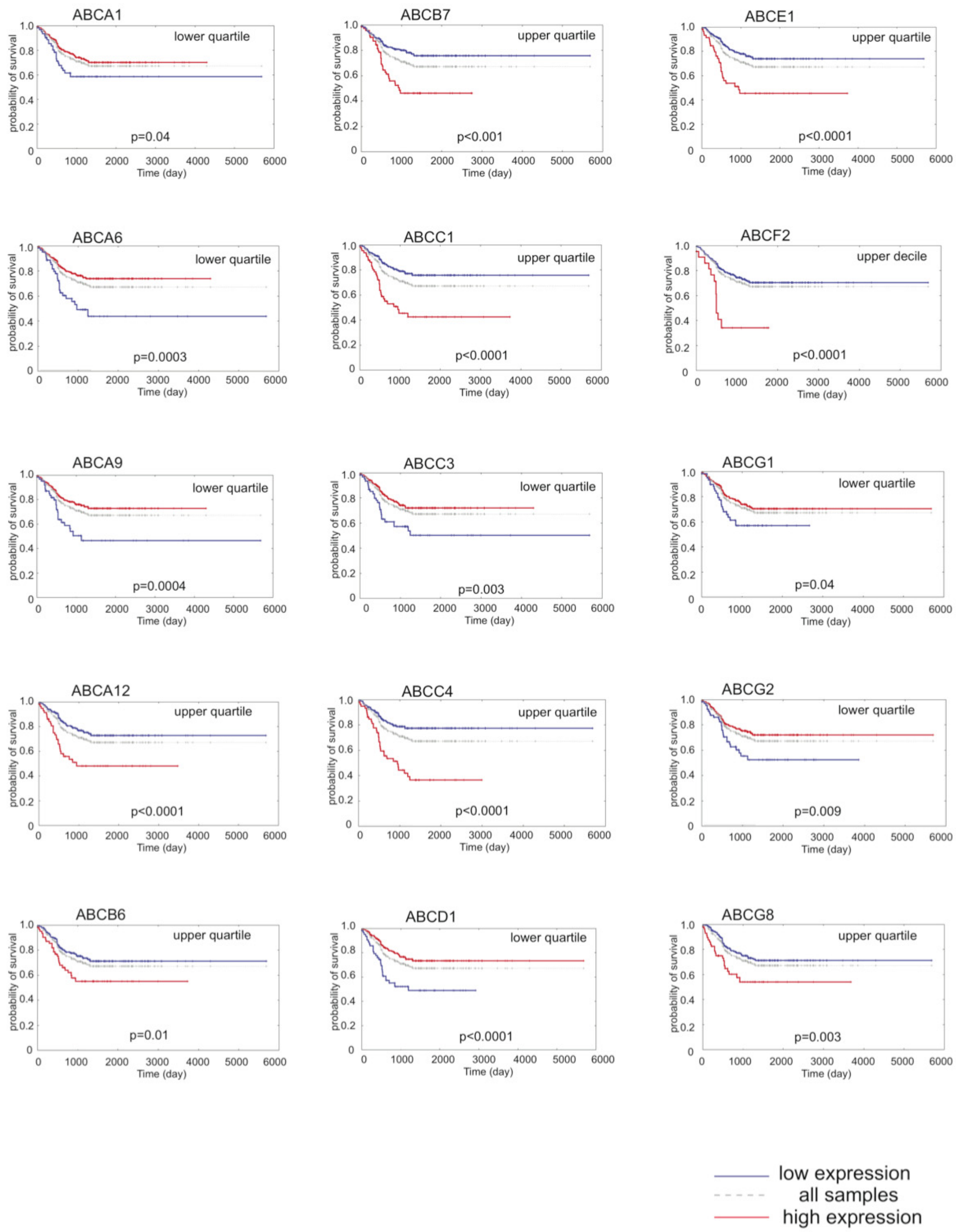
ABCA1
lower quartile
p=0.04
ABCB7
upper quartile
p<0.001
ABCE1
upper quartile
p<0.0001
ABCA6
lower quartile
p=0.0003
ABCC1
upper quartile
p<0.0001
ABCF2
upper decile
p<0.0001
ABCA9
lower quartile
p=0.0004
ABCC3
lower quartile
p=0.003
ABCG1
lower quartile
p=0.04
ABCA12
upper quartile
p<0.0001
ABCC4
upper quartile
p<0.0001
ABCG2
lower quartile
p=0.009
ABCB6
upper quartile
p=0.01
ABCD1
lower quartile
p<0.0001
ABCG8
upper quartile
p=0.003
probability of survival
Time (day)
low expression
all samples
high expression

Fig. S1

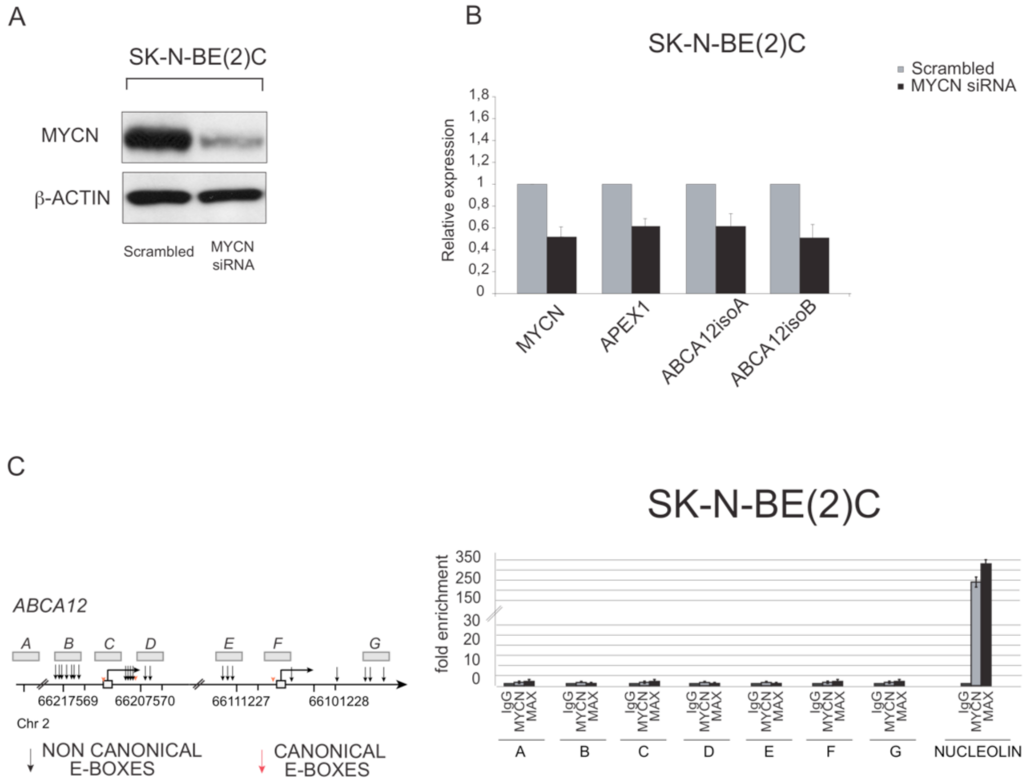
A
SK-N-BE(2)C
MYCN
β-ACTIN
Scrambled
MYCN siRNA
B
SK-N-BE(2)C
Scrambled
MYCN siRNA
Relative expression
MYCN
APEX1
ABCA12isoA
ABCA12isoB
C
ABCA12
66217569
66207570
66111227
66101228
Chr 2
NON CANONICAL E-BOXES
CANONICAL E-BOXES
SK-N-BE(2)C
fold enrichment
IgG
MYCN
MAX
NUCLEOLIN

Fig. S2

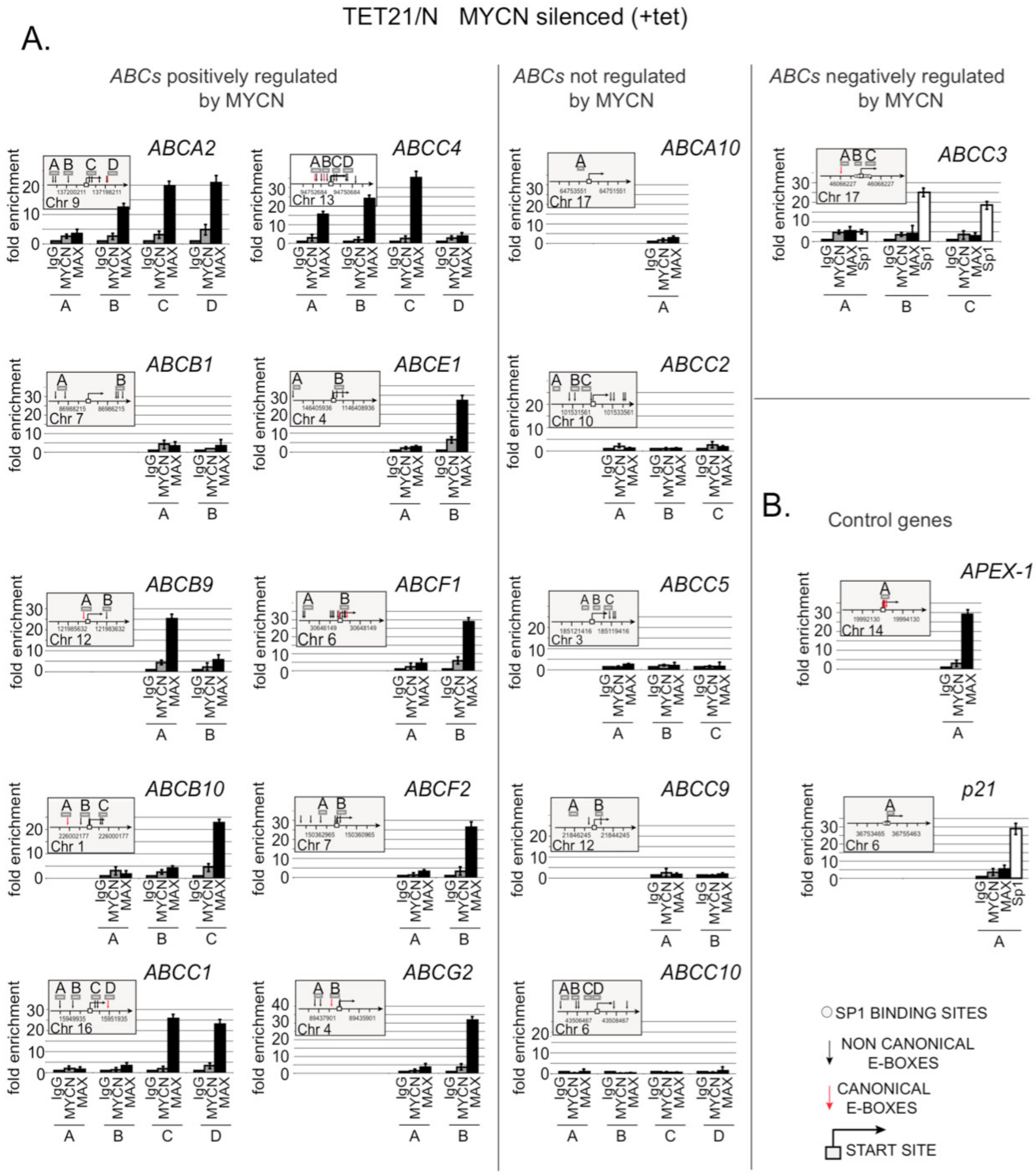
TET21/N MYCN silenced (+tet)
A.
ABCs positively regulated by MYCN
ABCs not regulated by MYCN
ABCs negatively regulated by MYCN
ABCA2
ABCC4
ABCA10
ABCC3
ABCB1
ABCE1
ABCC2
ABCB9
ABCF1
ABCC5
ABCB10
ABCF2
ABCC9
ABCC1
ABCG2
ABCC10
fold enrichment
IgG
MYCN
MAX
Sp1
B.
Control genes
APEX-1
p21
SP1 BINDING SITES
NON CANONICAL E-BOXES
CANONICAL E-BOXES
START SITE

Fig. S3

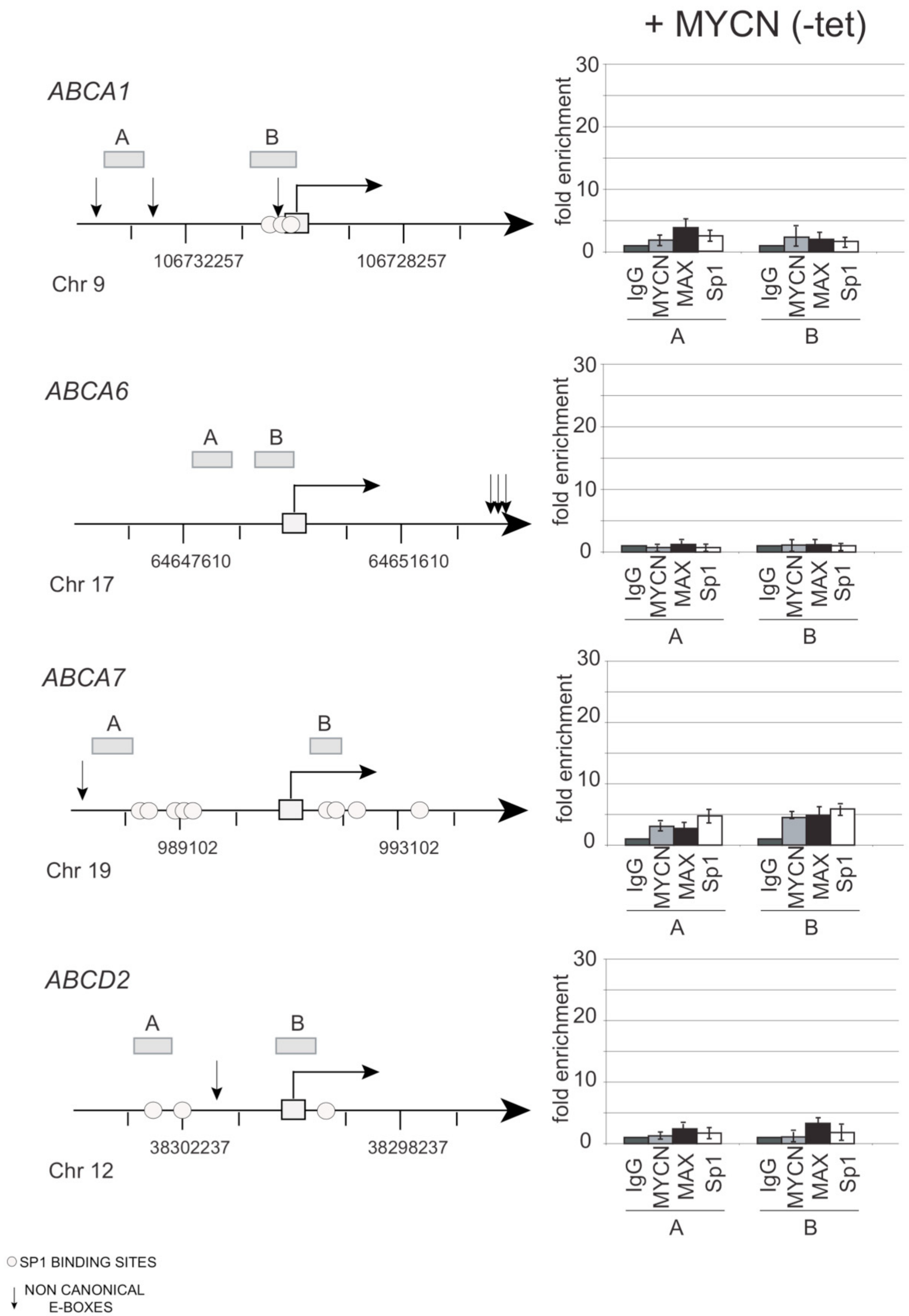
+ MYCN (-tet)
ABCA1
A
B
106732257
106728257
Chr 9
fold enrichment
30
20
10
0
IgG
MYCN
MAX
Sp1
A
B
ABCA6
64647610
64651610
Chr 17
ABCA7
989102
993102
Chr 19
ABCD2
38302237
38298237
Chr 12
SP1 BINDING SITES
NON CANONICAL
E-BOXES

Fig. S4

```
Wt   -100 ...CGCTGTCGCAACCCGCGGACGGGGGCAGGGAGACCGGACCCAGAGGCACTGGGGTAGGG  -40
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  -100 ...CGCTGTCGCAACCCGCGGACGGGGGCAGGGAGACCGGACCCAGAGGCACTGGGGTAGGG  -40
                        Sp1 BS-1                        TSS-> Sp1 BS-2
Wt   -39     CTCGGCAGGGCGGGTCCGGGCGGAGCGCGGGGTGCGGAGGGCGGAGGCGGCTCCGGCG   +18
             ||||||||    ||||||    |||||||||||||||||||||||    |||||||||
Mut  -39     CTCGGCAGCTACGGTCCGCTACGAGCGCGGGGTGCGGAGGGCGGACTACGCTCCGGCG   +18

Wt   +19     CCCGCTCTGCCCGCCGCTGGTCCGACCGCGCTCGCCTTCCTTGCAGCCGCGCCTCGGC   +77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +19     CCCGCTCTGCCCGCCGCTGGTCCGACCGCGCTCGCCTTCCTTGCAGCCGCGCCTCGGC   +77

Wt   +78     CCCATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGTAAGGCGCGGG +137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +78     CCCATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGTAAGGCGCGGG +137

Wt   +138    GCTCCGGGGTCACTGCGCGGGGGCCAGGGTCGGCCGGCTTCGCCCGGTCCCCGCCGCCTG +197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +138    GCTCCGGGGTCACTGCGCGGGGGCCAGGGTCGGCCGGCTTCGCCCGGTCCCCGCCGCCTG +197

Wt   +198    CCTTCCCGCGGGGCCGGCAGGTATCCCGGGACGGAGCCCCTGAGACGGCCTGGGCGCCCG +257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +198    CCTTCCCGCGGGGCCGGCAGGTATCCCGGGACGGAGCCCCTGAGACGGCCTGGGCGCCCG +257
                 Sp1 BS-3
Wt   +258    GGAGGGGGCGATGGCTCGGGAGGGAGGTTGGCTGCGCCGCCCGGAGCCGGGTCCCACG   +316
             ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +258    GGAGGGCTACATGGCTCGGGAGGGAGGTTGGCTGCGCCGCCCGGAGCCGGGTCCCACG   +316

Wt   +317    CGGTGTCGGGGACCTGCCCTGCTCTGCCCTTCCCGGCTGCAGCACTGGGGAGCCCGGGAA +376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +317    CGGTGTCGGGGACCTGCCCTGCTCTGCCCTTCCCGGCTGCAGCACTGGGGAGCCCGGGAA +376
                                      Sp1 BS-4
Wt   +377    AGTGAGGAAGAGTGCGCGGCTGGGGCGCAAAGGCACAGTGCGTGGCTGGGTGAGTCGGC  +435
             |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Mut  +377    AGTGAGGAAGAGTGCGCGGCTGGCTACCAAAGGCACAGTGCGTGGCTGGGTGAGTCGGC  +435
                                               Sp1 BS-5
Wt   +436    TCCATCCCAGCCCCTCCGTCGGGTGCGGAAGGGGCGTTTCGCAATCAGCCGCGGGTTCC  +494
             ||||||||||||||||||||||||||||||||    |||||||||||||||||||||||
Mut  +436    TCCATCCCAGCCCCTCCGTCGGGTGCGGAAGGCTACTTTCGCAATCAGCCGCGGGTTCC  +494

Wt   +495    TGATGGAGGGTCTTCCCTCAGCATCTGCCTCAGGTTAGGACTCGGTTGCCCACCTGGGCA +554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Mut  +495    TGATGGAGGGTCTTCCCTCAGCATCTGCCTCAGGTTAGGACTCGGTTGCCCACCTGGGCA +554

Wt   +555    TGGATTGCCCCCAGGGCATCCAGAGCACCTGCTCAACCAGGTGTTT...  +600
             ||||||||||||||||||||||||||||||||||||||||||||||
Mut  +555    TGGATTGCCCCCAGGGCATCCAGAGCACCTGCTCAACCAGGTGTTT...  +600
```

wt AGGG CTCGGCAGGG CGGGTCCGGG CGGAGCGCGG GGT — Sp1 BS-1
mut AGGG CTCGGCAGCT ACGGTCCGCT ACGAGCGCGG GGT

wt CGGAGG GCGGAGGCGG CTCCGGCGCC — Sp1 BS-2
mut CGGAGG GCGGACTACG CTCCGGCGCC

wt GCCCGGGA GGGGGCGATG GGCTCGGG — Sp1 BS-3
mut GCCCGGGA GGGCTACATG GGCTCGGG

wt GTG CGCGGCTGGG GCGCAAAGGC ACAGTG — Sp1 BS-4
mut GTG CGCGGCTGGC TACCAAAGGC ACAGTG

wt GGTG CGGAAGGGGC GTTTCGCAAT CAGC — Sp1 BS-5
mut GGTG CGGAAGGCTA CTTTCGCAAT CAGC

Fig. S5

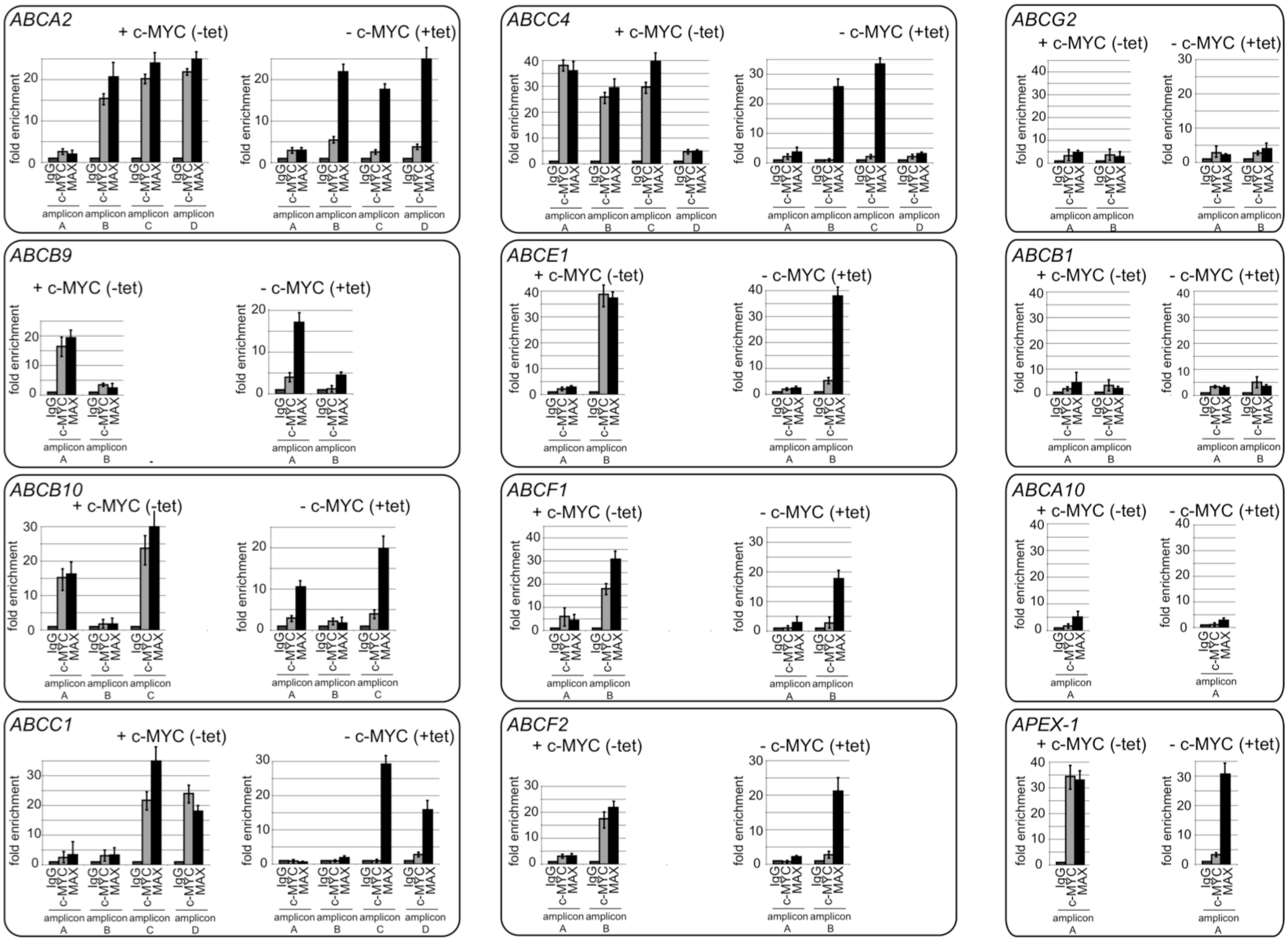
ABCA2
+ c-MYC (-tet)
- c-MYC (+tet)
ABCC4
ABCG2
ABCB9
ABCE1
ABCB1
ABCB10
ABCF1
ABCA10
ABCC1
ABCF2
APEX-1
fold enrichment
IgG
c-MYC
MAX
amplicon A
amplicon B
amplicon C
amplicon D

Fig. S6

Table S1. DNA sequence of primers and TaqMan assay codes of assays used for quantitative RT-PCR

Primers for RQ-PCR on Cell Line RNA	
ABCA1 F	ACCACTGTTACCAGAGGAGATGC
ABCA1 R	CACTCACCAACCTTGCCAACTTC
ABCA2 F	GGTGTGCGTCCTGGCGAG
ABCA2 R	CATCTTGAAGGTGCTGGTCTTGC
ABCA3 F	GTCGCAGAGCACCTTTATTTC
ABCA3 R	GTATCAGCACCTTGGAGCC
ABCA4 F	TTCATCGGCATCAACAGCAGTG
ABCA4 R	TTCTTCCCAATCAGGTCCCAGTG
ABCA5 F	GGAACGAACACAAGAAGATAGAGTAG
ABCA5 R	CCAGTAAGCAGACCGAACAATAC
ABCA6 F	GTTCCTTCATATACCTTGCTTG
ABCA6 R	ATTCTCTGTAGTGCTCCTGG
ABCA7 F	GCAGGCACCTACAGCGGAG
ABCA7 R	CTGTGGTCGGCTCGTCCAG
ABCA8 F	CTGGAAAGGGCTGAGGAAAGG
ABCA8 R	ACTAACCGTGTGATGGCAACC
ABCA9 F	TCGCCATCACACGGTTAG
ABCA9 R	CCAATACATCTCAGCCTTCC
ABCA10 F	ATGTTTGTTTTGGTGGTATGC
ABCA10 R	TTGCGAAAGAATGAAAGC
ABCA12 F iso A	ACCTCGCACCTCGAAACCTTCC
ABCA12 R iso A	AAGCAGATCTTGTGGGCCATAGGG
ABCA12 F iso B	ATTTCCAACAAAAGAGCATAGATG
ABCA12 R iso B	CCCAGGTCAAATTAATGAGGAG
ABCA13 F	TCAAGGATAAAACAAGCACGC
ABCA13 R	CTAACAAGGAGATTCAAAATAGAAAATG
ABCB1 F	CATCATCAAGTGGAGAGAAATCATAG
ABCB1 R	TTAGCAAGGCAGTCAGTTACAG
ABCB2 F	GATGTCTCCTTTGCCTACCC
ABCB2 R	CGTCTACCTCTGTGTCATAGC
ABCB3 F	TGGTGGGGTGGAGAGGTGGGG
ABCB3 R	TGATGGGACAGGCAGCAAAATAGCAAC
ABCB4 F	ACACAAACCAGACAGCATCAAAGG
ABCB4 R	CTCTTCCCACAGCCACTACTTCC
ABCB5 F	ACCAACTCACTTCCTCTGC
ABCB5 R	CTGCCGTAAAATAATCCCTGC
ABCB6 F	ACACCATCGCCGACAATATCCG
ABCB6 R	GCAGCAGCCTCCACCTCATC
ABCB7 F	TCGGTTCCTCTTTCCTCGCTC
ABCB7 R	TGCCTTTTCCCAATCTCTGCC
ABCB8 F	CCAGGAGCCACCAGCACAAG
ABCB8 R	GAGCAGGAGCAGCCGCAG
ABCB9 F	CTTCGCCAATGAGGAGGAGGAGGAG
ABCB9 R	CTGTAGACGGAGCCCACGG
ABCB10 F	AACAGCGGATTGCATTGCC
ABCB10 R	ACACCGTTCTTCCATCCATCAGG
ABCB11 F	AAGGGAAGGTGATGATAGATGG
ABCB11 R	TGAGCGGAGGAACTGGAC

ABCC1 F	CCAAACCCAGACAACCAAAAC
ABCC1 R	GGAAGCACCAGGAAACCAC
ABCC2 F	TCAGCGAGACCGTATCAGG
ABCC2 R	TCACCAGCCAGTTCAGGG
ABCC3 F	GTCTCCTGTATGTGGGTCAAAGTG
ABCC3 R	CTGTGGCGAGCGTATCTTGTTG
ABCC4 F	ATGATTTGCTGCCGCTGAC
ABCC4 R	CTGACACCTCTCTTCTGCTTTG
ABCC5 F	CAAGAGACCATCCGAGAAGC
ABCC5 R	GAAACACACAAGCCAATCCG
ABCC6 F	AGGAGATAGAGGAGAAGGAGAACAGAACC
ABCC6 R	CAGAGGAAGAGGAAGAGTGCGTAGAGG
ABCC7 F	GCAACAGTGGAGGAAAGCC
ABCC7 R	TGGGTTCATCAAGCAGCAAG
ABCC8 F	AAGATCCAGATCCAGAACCTGAGC
ABCC8 R	TGTCCACCATGCGGAAGAAGG
ABCC9 F	TTGGTGTTGCCTTTTATTTTATCC
ABCC9 R	CCGAATGGTGGTGAGTCC
ABCC10 F	CCTTCATCCTCAACATCCTCC
ABCC10 R	GCAAACTGGCACCTCTGG
ABCC11 F	CGTGGCTTTTGGCATTTCC
ABCC11 R	GGGTCTCTTGTCTCTGTATTTC
ABCC12 F	CATCACCTATCACCTCCTCTAC
ABCC12 R	GGCTTGCGTCTCTGTTCC
ABCC13 F	GACTCTGGCTGCTATGTGG
ABCC13 R	CTCGCTTCCTCTCTCAACC
ABCD1 F	AGCCTTCACTATTGCCCG
ABCD1 R	CTTCCTCCACCCTGATGTTG
ABCD2 F	AACCCTGACCAATCTCTTAGG
ABCD2 R	GCACATACCGCAAATAGCC
ABCD3 F	ACAGAAGATACAGTTGAGTTTGG
ABCD3 R	CAGGTTACAGTGATTGAAGCC
ABCD4 F	CGACCTGTCCACGACGCTC
ABCD4 R	TGCTGTGTCTGCTGGCTCTG
ABCE1 F	TAACCCACCTAAAAGAACGAAATG
ABCE1 R	AAACGACAGCACAAGCAAATC
ABCF1 F	ACTGCTGATGCTGGTGAG
ABCF1 R	GCCTGCTTGGTGGACTTC
ABCF2 F	GTTTGAGGGTGGTATGATGC
ABCF2 R	CTGCTGAATGAGTCTGAAGTC
ABCF3 F	AGTGTGCGAGAGGAGTGC
ABCF3 R	AAGCCCAGCGAGAATGAC
ABCG1 F	TGGGTTTGTGGGTGTCTCG
ABCG1 R	ACGGTGCCTGGTGCTAAG
ABCG2 F	CTTCTTCCTGACGACCAACC
ABCG2 R	TCTGTAGTATCCGCTGATGTATTC
ABCG4 F	ATCCTGACGATCTATGGCATGGAG
ABCG4 R	GTAACGCAGCACAAGGTAGGC
ABCG5 F	TTGTCGTCCTCCTGGTGG
ABCG5 R	TTCCCGTTCCTTGCTTTGG

ABCG8 F	TATGGAAAGCAGAGACGAAGG
ABCG8 R	

Table S2: DNA sequence of primers used for quantitative ChIP.

abca1 amplicon A F	CTGGAGGTGGGAAGAGAAGTAGG
abca1 amplicon A R	AGATTCATAGAAGACTCAGGACAGACC
abca1 amplicon B F	CGGAAAGCAGGATTTAGAGGAAGC
abca1 amplicon B R	GCAGAGGTTACTATCGGTCAAAGC
abca2 amplicon A F	ACTACATTACGGAGAAATTCTGGCG
abca2 amplicon A R	CCTCATAGACTTGGCTGCGGG
abca2 amplicon B F	GGAGGGCGGTGGACAATAAACATCTGAG
abca2 amplicon B R	TCTGGCGGAGGCTGTAGGAACTGG
abca2 amplicon C F	GCCTGTCCTCTGTCGCTCTCTAC
abca2 amplicon C R	GGGTCTCCTGTGTGCTTTGTAAAC
abca2 amplicon D F	GGGAGGTGGCTCGGTCGTGTC
abca2 amplicon D R	AGGAGGGGAGGCGGAGAGATGC
abca12 amplicon A F	GCCATTCTCCTGCCTCAGTCTC
abca12 amplicon A R	TAACACGGTGAAACCCTGTCTCTAC
abca12 amplicon B F	TCCATGAAGAAACAAGCGATAGTAG
abca12 amplicon B R	AGCGTAGAGTATTCAGAAAGATCATC
abca12 amplicon C F	GAAATGTCTTGGATCAGCCTGTGTC
abca12 amplicon C R	GGTCCCACCTTTCATCACAATGTAC
abca12 amplicon D F	AAAGGAATTGGTTTCTGGGAGTTG
abca12 amplicon D R	AAAGTGCTGGTTTCTGTGTGATG
abca12 amplicon E F	ATACTAGGAACTACCCAGATGGC
abca12 amplicon E R	AAACTCAATGTGTATTCCAGCAATAG
abca12 amplicon F F	ACGTGGTAGTCAATCTTCATTATAG
abca12 amplicon F R	ATCAAAATAATCCCGATGGTCAAG
abca12 amplicon G F	AGATAGAGGCGTGAACTTGAAAGAC
abca12 amplicon G R	AAGGAAGTCAGGATCTAGGCTCAG
abcb1 amplicon A F	TCTCGTCTAACCAGTTGTCTATCTTC
abcb1 amplicon A R	TACCAGCATTTATTATTAAGTTTAGTGAGG
abcb1 amplicon B F	TGGGACATCTGAAATG
abcb1 amplicon B R	AAGGGTACATATTAGGACAACAGTCATTC
abcb9 amplicon A F	TCCCTCCTCCACTACCCCTCTC
abcb9 amplicon A R	TCTTTCTCCGCAGACCGTTTCC
abcb9 amplicon B F	GAGTGGTGGAAGTATGTGGGATTTG
abcb9 amplicon B R	AAGGGCAGTTAGGCGGGTAATG
abcb10 amplicon A F	GCACTAAAATGTTTATGTTGATTATTGAGG
abcb10 amplicon A R	ATTTGAAGACAGGCGTGGTCG
abcb10 amplicon B F	GCTCGTGTCGTTCCCAAGTTC
abcb10 amplicon B R	GCTGTCACCCGCCTTATCG
abcb10 amplicon C F	CGTGTCACCGCCGCCTCTCCTG
abcb10 amplicon C R	GCCTAAGCCAAAACAGATGCTCCCACTAAG

abce1 amplicon A F	TCAGGAACTGGGCATCTTTCTAC
abce1 amplicon A R	TTTGATTCTGTGCTCTTTTGACTAC
abce1 amplicon B F	CGAGAATGGACCTAGATGCCGTAG
abce1 amplicon B R	ATCATTTCTATAAAGCCTGGGAGTGG
abcf1 amplicon A F	CTCTTGCCTCCTTCCTGTTTGTTC
abcf1 amplicon A R	TCTTCTACGCTCTTGGGATACTACTG
abcf1 amplicon B F	GCAAGGAAGAAACGAGCAGAGG
abcf1 amplicon B R	GCCCAGTCTCACTTAGGTCACG
abcf2 amplicon A F	AATGTAGGTAATGTGAAGTCCTTGAGAG
abcf2 amplicon A R	GCATTGTTAGGTTTCCACTGAAGC
abcf2 amplicon B F	GGAGACTCGGAGGGGACTCAC
abcf2 amplicon B R	CTCAGCGGCTCTTCTAATCTTAACATC
abcg2 amplicon A F	TGTATAGTCAATTTTCTTATCTAGGCTTCC
abcg2 amplicon A R	CCATCCCAACATCTACCTGCTG
abcg2 amplicon B F	GTAGTTAATCACTCTGGTTCATTCCGTTCG
abcg2 amplicon B R	TGCGGCTGGAGGTCACGATGG
abca10 amplicon A F	AGCAACATCACCAACCTTATATTTCCC
abca10 amplicon A R	TTAGTCAGTAAACACTCACTCAGTAAAGC
abcc1amplicon A F	TCCCTTAGAAACTCATTCACCCTTGG
abcc1 amplicon A R	ATAGGCAGACAGGTAGAGACAGAGG
abcc1 amplicon B F	ATGTCTCCAGGCTTCAGTTTCC
abcc1 amplicon B R	CCCGAGGTCACACAGTTAATAAGG
abcc1 amplicon C F	GATGGCTCCGACCCGCTCTGG
abcc1 amplicon C R	GCTCCGCAGGAACTGAGTCACC
abcc1 amplicon D F	TGATGTGCCCTACCTGACCCTCGG
abcc1 amplicon D R	AGAGAGAAACAGTCGTGTCCAGATTTGCC
abcc2 amplicon A F	CACCAGTGCCAAGAGAAGTATGC
abcc2 amplicon A R	TCACCAGAAGAGCCAGGAAAGG
abcc2 amplicon B F	CCAAGGCAGAAGGATTGTTGAAGC
abcc2 amplicon B R	AACAGAGTGGTGGCATCAGTCG
abcc2 amplicon C F	TCCCATTTGGCATACTACCTC
abcc2 amplicon C R	CACTGAAAGATGTCAACAGAGC
abcc3 amplicon A F	AGGAGAAGGAGAGCACTGACAAG
abcc3 amplicon A R	TGAATGGAAAGGGTAGGCAAAGC
abcc3 amplicon B F	CCCCACCTCTGCCCCAAAGTCC
abcc3 amplicon B R	CGCCCTGCCGAGCCCTACC
abcc3 amplicon C F	GATGGGCTCGGGAGGGAGGTTG
abcc3 amplicon C R	CTAGAGAAAAGAAGGTGGCAGGAAAC
abcc4 amplicon A F	CCACTGTTATCTGTTAGGCTTTAGGG
abcc4 amplicon A R	CTTCTCAGGACCAAACGACGG
abcc4 amplicon B F	CGCCTAGACTCGGATAGTGAATTTC
abcc4 amplicon B R	GGATGGAGAGGGTAGCAGAGC
abcc4 amplicon C F	GTCCCCGCCCGAAACAGGTCAC
abcc4 amplicon C R	CGCCACCCGCAGCAGAAAGCC
abcc4 amplicon D F	CTTTTGCCTCTTTGTGGGAATCTC
abcc4 amplicon D R	GGGGTGGTTTTAAGAAGGTAGAACTC
abcc5 amplicon A F	GGGTGGGACTGCTCTGCCTACG
abcc5 amplicon A R	TGCCTCTGCGAGACTGTCTGGAATC
abcc5 amplicon B F	TCTCCTGCCGCCGCCTCCTAG
abcc5 amplicon B R	TCCCGATCCTACCTGCCTGTCTTCC
abcc5 amplicon C F	TCTTGGAGGAGGAGATGGCTAGG

abcc5 amplicon C R	AGACACCACGCTAAAGGGATACG
abcc9 amplicon A F	GCAGGTTGGAGGTTGTGTAATACG
abcc9 amplicon A R	CAAACAGATGGGAGATGAGCAAAGG
abcc9 amplicon B F	CTAATGGCTGAGATTTGGGATAATGTTG
abcc9 amplicon B R	ACTGCTGCTGCTACCTGAAGG
abcc10 amplicon A F	GACTGGCACTACACTAAGCATTATCTC
abcc10 amplicon A R	GGCTCTACACTTACTGGTTCAATCAC
abcc10 amplicon B F	CCGTGGCTTAGTGGCTCCTG
abcc10 amplicon B R	CCTACCTGGCTCGTGTCTTCC
abcc10 amplicon C F	GGAAGACAAGGAGGCACATCG
abcc10 amplicon C R	GTTCTGAGGTAAAGTGGAGTAGGG
abcc10 amplicon D F	TCATTTTCTAAACTACCCACACCATTTC
abcc10 amplicon D R	CCCGTCTCAGCCTCCCAAAG
abca6 amplicon A F	ACTTTGATTTCCTGTTTTGCCATTC
abca6 amplicon A R	ATTTGTTGCTCCCACCCTCTTC
abca6 amplicon B F	TTCTTGTTCCTGCCTCCATCTTG
abca6 amplicon B R	TTTCTGTGTCTCTTTCTCCCTAAGC
abca7 amplicon A F	GACCCACACGCTCCCATTTC
abca7 amplicon A R	AACGCTCCTCGGCTTCTGC
abca7 amplicon B F	CCCACCGTCTCCCACCTATTC
abca7 amplicon B R	GAACAGCCACCAGGATGAAGAAG
abcd2 amplicon A F	TGACTGGAAATGTGTATGTATGTTGGG
abcd2 amplicon A R	CTGCTTGCTCTTCTGCTTGTGG
abcd2 amplicon B F	GTTCCTTCTCCCTCCTCGTCTC
abcd2 amplicon B R	GTAAGATTTCAGTAGATACCGCAAACAG

Table S3. Data values ($\ln 2^{-\Delta(\Delta Ct)}$) of ABC transporter genes expression used to generate the hierarchical clustering in TET21N cell line.

	tet 0h	tet 12h	tet 24h	tet 48h
abca2	0	-0.25812327	-0.142139767	-0.328504067
abcb1	0	-0.549046837	-0.967584026	-1.03563749
abcb7	0	-0.053928342	-0.265703166	-0.360252765
abcb9	0	-0.162518929	-0.253602759	-0.436955775
abcb10	0	-0.562118918	-0.494296322	-1.108662625
abcc1	0	-0.266573109	-0.391562203	-0.507497834
abcc4	0	-0.717439873	-0.415515444	-0.400477567
abcd3	0	-0.061875404	-0.556287998	-0.653926467
abce1	0	-0.597837001	-0.502526821	-1.427116356
abcf1	0	-0.251671635	-0.349557476	-0.536143432
abcf2	0	-0.405465108	-0.567984038	-0.488846717
abcf3	0	-0.252744021	-0.333144447	-0.567984038
abcg2	0	-0.661648514	-0.510825624	-0.572701027
abca4	0	-0.030459207	-0.005012542	-0.083381609
abca5	0	0.055119299	0.013245227	-0.15082289
abca10	0	0.097126711	0.243730185	0.499562431
abcb2	0	0.126632651	0.117783036	0.292669614
abcb4	0	0.412109651	-0.174353387	-0.13926207
abcb6	0	-0.356674944	0.039220713	-0.010050336
abcb8	0	-0.006688988	0.070769071	0.116300456
abcc2	0	0.186479567	0.21913553	0.242946179
abcc5	0	-0.051293294	-0.139262067	0.099845335
abcc9	0	0.3074847	0.223143551	-0.083381609
abcc10	0	0.262364264	0.273836666	0.357674444
abca1	0	0.792992516	1.10856262	0.947789399
abca3	0	0.292669614	0.966983846	0.817574759
abca6	0	0.420900916	1.474763009	1.550395372
abca7	0	0.954228571	1.362684495	1.4762874
abca8	0	0.168335315	0.536493371	0.864295437
abcg8	0	0.207014169	0.21511138	0.848011891
abcc3	0	0.656223826	1.398716881	1.623998064
abcd1	0	0.159848701	0.894726554	0.53454215
abcd2	0	1.057790294	0.938052224	1.387543581
abcd4	0	0.593326845	0.708035793	0.970778917
abcg4	0	0.688134639	0.623261053	0.675492245

Table S4. Data values ($\ln 2^{-\Delta(\Delta Ct)}$) of ABC transporter genes expression used to generate the hierarchical clustering in 6 neuroblastoma cell lines.

	SKNBE	LAN1	SHSY5Y	SHNSK	SHEP
MYCN	6.42	-1.68	-2.18	-10.08	7.52
abca2	0.73	0.93	-0.12	-0.07	-0.37
abcb9	2.96	1.46	-1.79	-1.99	-0.64
abcb10	-0.48	-0.28	0.62	-0.78	1.22
abcc1	1.74	1.74	0.04	-0.36	-1.16
abcc4	1.72	1.82	-1.08	0.02	-1.28
abce1	1.22	0.82	-1.58	-0.18	-0.28
abcf1	-0.26	0.44	-0.26	0.24	-0.16
abcf2	1.8	-0.2	-0.8	0.4	0.6
abcg2	4.08	3.08	-1.12	-4.32	-1.72
abcc3	-1.61	-6.01	-2.56	2.84	5.34

Table S5. Data values ($ln2^{-\Delta(\Delta Ct)}$) of ABC transporter genes expression used to generate the hierarchical clustering in P493-6 cell line.

	P493-6 0h	P493-6 12h	P493-6 24h	P493-6 24h
abca2	0	-0.531879033	-0.602392817	-0.506667614
abca3	0	-0.57664809	-0.476948729	-0.696449289
abcb9	0	-0.202524264	-0.430782916	-0.405465108
abcb10	0	-0.446287103	-0.644357016	-0.502526821
abcc1	0	-0.371063681	-0.570392986	-0.65082289
abcc2	0	-0.776528789	-0.425667815	-0.415515444
abcc4	0	-0.366244395	-0.366244395	-0.510825624
abcd3	0	-0.456758402	-0.415515444	-0.488846717
abce1	0	-0.916290732	-0.836248024	-0.713349888
abcf1	0	-0.405465108	-0.292136423	-0.274436846
abcf2	0	-0.755022584	-0.84397007	-0.950192284
abcf3	0	-0.588787165	-0.423120043	-0.980829253
abcb6	0	0.067658648	0.317240875	0.414314723
abcb7	0	0.009950331	0.086177696	-0.097980408
abcb8	0	0.016529302	0.136859183	0.058268908
abcc5	0	0.116300456	0.322083499	0.326902786
abcc7	0	-0.349557476	0.364643114	0.548121409
abcd4	0	0.292669614	0.446820294	0.585933096
abcg4	0	-0.606969484	0.364643114	0.395414772
abca1	0	0.613382212	0.749842524	1.281859343
abca4	0	1.145283808	1.212932546	1.065859502
abca5	0	0.681411924	0.925580779	1.191900223
abca7	0	1.158975438	1.659497112	1.986046194
abca10	0	-0.090654368	0.259796869	0.598836501
abcb2	0	0.538440791	0.622366998	0.631271777
abcb3	0	0.262364264	0.955511445	1.029619417
abcc6	0	0.770108222	0.802001585	1.208960346
abcc8	0	0.862889955	0.88376754	-0.030459207
abcc10	0	0.185095484	0.385262401	0.733969175
abcc11	0	0.810930216	1.17557333	1.643742716
abcd1	0	0.90691357	1.151626324	1.470941835
abcg1	0	0.116300456	0.714314723	0.904218151