#### Supplementary Figure Legends

# Supplementary Figure S1. Aberrant *DNMT3B* expression and global DNA methylation in primary neuroblastoma tumors

A, RT-PCR examination of aberrant *DNMT3B* transcripts expressed in neuroblastoma (NB) and ganglioneuroblastoma (GNB) patient samples were normalized to the *GAPDH* housekeeping gene, and *DNMT3B* was amplified from exons 6 and 11 to identify the wild-type and aberrant *DNTM3B* transcripts specifically. DNA sizing is shown on the left and *DNMT3B* isoforms are shown on the right. B, Southern blot of RT-PCR shown in Figure 1A of aberrant *DNMT3B* transcripts expressed in neuroblastoma (NB) and ganglioneuroblastoma (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms amplified in the RT-PCR. C, Southern blot of RT-PCR shown in Supplementary Figure 1A of aberrant *DNMT3B* transcripts expressed in neuroblastoma (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms amplified in the RT-PCR. C, Southern blot of RT-PCR shown in Supplementary Figure 1A of aberrant *DNMT3B* transcripts expressed in neuroblastoma (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms amplified in the RT-PCR. C, Southern blot of RT-PCR shown in Supplementary Figure 1A of aberrant *DNMT3B* transcripts expressed in neuroblastoma (NB) and ganglioneuroblastoma (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms (GNB) patient samples using a probe spanning exons six and seven to detect all of the known aberrant isoforms amplified in the RT-PCR.

## Supplementary Figure S2. *DNMT3B7* expression levels in primary neuroblastoma tumors and induced cells

A, Expression of *DNMT3B7* in primary ganglioneuroblastoma (GNB), ganglioneuroma (GN), and neuroblastoma tumors (NB) low, intermediate and high risk as determined by real-time RT-PCR. The data are summarized in the table on the right of the graph. B, Expression of *DNMT3B7* (RNA) as determined by real-time RT-PCR or DNMT3B7 (protein) as determined by quantitation of Western blot shown in Figure 2B using Image J in induced LA1-55n cells. The data are summarized in the table on the right of the graph.

## Supplementary Figure S3. Establishment of KCNR neuroblastoma cells overexpressing DNMT3B7.

SMS-KCNR cells were transduced with a constitutive *DNMT3B7* or control vector. Parental SMS-KCNR, vector control and *DNMT3B7* expressing cells were grown and counted daily for three days.

#### Supplementary Figure S4. Analyses of SMS-KCNR cell xenografts

A, Microvascular Density of SMS-KCNR xenografts. B, Percent of cells in G0 in SMS-KCNR xenografts. C, Apoptosis by TUNEL assay in SMS-KCNR xenografts.

**Supplementary Figure S5. DNA methylation of Satellite 2 repetitive elements.** Southern blotting analysis of DNA methylation of Satellite 2 repetitive elements. *Mspl* digests DNA regardless of methylation. *Hpall* is a methylation sensitive isoschizomer of *Mspl*. Horizontal lines are drawn to indicate the level of methylation. All three lanes digest to the same degree in the *Mspl* digested lanes. The bracket on the right of the figure indicates the level of hypermethylation in the *DNMT3B7*-expressing cell lines.

# Supplementary Figure S6. *DNMT3B7* expression in LA1-55n transduced cells by RNA-Sequencing

RNA-Sequencing reads aligned to the *DNMT3B* genomic locus in the control and two *DNMT3B7*-expressing LA1-55n cells.

# Supplementary Figure S7. Endogenous levels of *DNMT1, DNMT3A*, and *DNMT3B* in *DNMT3B7*-expressing LA1-55n cells

A. Relative expression of endogenous *DNMT1* in *DNMT3B7*-expressing or vector control LA1-55n cells at day 0 and day 21 determined by real-time. B, Relative

expression of endogenous *DNMT3A* in *DNMT3B7*-expressing or vector control LA1-55n cells at day 0 and day 21 determined by real-time. C, Relative expression of endogenous *DNMTB* in *DNMT3B7*-expressing or vector control LA1-55n cells at day 0 and day 21 determined by real-time.

#### Supplementary Figure S8. Relative DNA methylation by mass spectrometry

The methylation level of *EEA1* and *RXRB* was determined by quantitative mass spectrometry of PCR amplified bisulfite-treated DNA of *DNMT3B7*-expressing or vector control LA1-55n cells at day 21. Mass spectrometry was performed in technical duplicate. In the top panel, the average percent methylation levels are graphed +/- standard error. In the table at the bottom of the figure, the raw values from the mass spectrometry experiment are given.

#### Supplementary Figure S9. Effect of ATRA on global DNA methylation

Global DNA methylation by mass spectrometry of the *DNMT3B7*-expressing LA1-55n cells or control, treated with ATRA or vehicle control for seven days. Samples were normalized to vehicle controls.