Supplementary Table S2. Gene differences and overlap between the 3 groups (scr, Plcγ1 shRNA1, Plcγ1 shRNA 2) analysed by gene expression profiling (364 probe sets).

Supplementary Table S3. Gene annotation of differentially methylated regions located in CGIs, CGI-shores and/or promoter regions identified by global methylome analysis in Plcγ1-deficient cells at d0 and/or d1 compared to controls.

Supplementary Table S4. List of genes associated with each GO-term cluster identified by gene-ontology clustering using the DAVID functional annotation tool (http://david.abcc.ncifcrf.gov/home.jsp).

Supplementary Table S5: Primer sequences for validation of methylation status of 17 selected DMRs (Fig. 5b) using MassArray.