The Proto-Oncogene ERG in Megakaryoblastic Leukemias

Liat Rainis,1,2 Tsutomu Toki,3 John E. Pimanda,4 Ester Rosenthal,1 Keren Machol,1,2 Sabine Strehi,5 Berthold Göttgens,4 Etsuro Ito,3 and Shai Izraeli1,2,5

1Department of Pediatric Hematology-Oncology, Safra Children’s Hospital and Hematology Institute, Sheba Cancer Research Center, Sheba Medical Center, Tel-Hashomer, Israel; 2Sackler School of Medicine, Tel-Aviv University, Tel-Aviv, Israel; 3Department of Pediatrics, Hirosaki University School of Medicine, Hirosaki, Japan; 4Department of Haematology, Cambridge Institute for Medical Research, University of Cambridge, Cambridge, United Kingdom; and 5Children’s Cancer Research Institute, Vienna, Austria

Abstract
Aneuploidy is one of the hallmarks of cancer. Acquired additions of chromosome 21 are a common finding in leukemias, suggesting a contributory role to leukemogenesis. About 10% of patients with a germ line trisomy 21 (Down syndrome) are born with transient megakaryoblastic leukemia. We and others have shown acquired mutations in the X chromosome gene GATA1 in all these cases. The gene or genes on chromosome 21 whose overexpression promote the megakaryoblastic phenotype are presently unknown. We propose that ERG, an Ets transcription factor situated on chromosome 21, is one such candidate. We show that ERG is expressed in hematopoietic stem cells, megakaryoblastic cell lines, and in primary leukemic cells from Down syndrome patients. ERG expression is induced upon megakaryocytic differentiation of the erythroleukemia cell lines K562 and UT-7, and forced expression of ERG in K562 cells induces erythroid to megakaryoblastic phenotypic switch. We also show that ERG activates the gpIb megakaryocytic promoter and binds the gpIIb promoter in vivo. Furthermore, both ERG and ETS2 bind in vivo the hematopoietic enhancer of SCL/TAL1, a key regulator of hematopoietic stem cell and megakaryocytic development. We propose that trisomy 21 facilitates the occurrence of megakaryoblastic leukemias through a shift toward the megakaryoblastic lineage caused by the excess expression of ERG, and possibly by other chromosome 21 genes, such as RUNXI and ETS2, in hematopoietic progenitor cells, coupled with a differentiation arrest caused by the acquisition of mutations in GATA1. (Cancer Res 2005; 65(17): 7596-602)

Introduction
Numerical chromosomal aberrations (aneuploidy) are common in cancer (1). Their significance for oncogenesis is revealed by genetic syndromes of aneuploidy and cancer (2). The classic constitutional aneuploidy that shows predisposition to certain kinds of cancer is trisomy 21, also called Down syndrome. Children with Down syndrome have a marked risk for childhood leukemia (reviewed in ref. 3). Thus, additional copies of chromosome 21 are leukemogenic.

At least 10% of children with Down syndrome are born with a transient megakaryoblastic leukemia (transient myeloproliferative disorder) that resolves spontaneously. In about one fifth of these patients, it recurs as acute megakaryoblastic leukemia (3). Acquired mutations in GATA1 in the leukemic blasts are detected in virtually all these cases (refs. 4–6; reviewed in ref. 7). GATA1 is a transcription factor that regulates megakaryocytic differentiation and the mutations observed are believed to cause accumulation of poorly differentiated megakaryocytic precursors (4).

Strikingly, GATA1 is located on chromosome X; therefore, genetic interaction of GATA1 with one or more genes on chromosome 21 presumably contributes to the development of Down syndrome megakaryoblastic leukemia. However, the gene(s) on chromosome 21 that promote the megakaryoblastic leukemias of Down syndrome are currently unknown. Healthy infants with Down syndrome have a significantly higher platelet count compared with normal infants (8). This observation suggests that trisomy 21 may cause developmental skewing toward the megakaryocytic lineage during hematopoietic development. This “promegakaryocytic” pressure caused by trisomy 21 may in turn enhance the selection and proliferation of cells carrying an acquired “differentiation arresting” mutation in GATA1 (9).

One gene, RUNXI, located in the “critical Down syndrome region” on chromosome 21, is a known key regulator of hematopoiesis and megakaryopoiesis and is commonly mutated and translocated in leukemias (10, 11). Haploinsufficiency of RUNXI causes thrombocytopenia in human and in mouse models (12, 13) and overexpression facilitates megakaryocytic differentiation (10). However, unlike other types of leukemias, acute megakaryoblastic leukemia has not been associated with RUNXI abnormalities. Moreover, the leukemogenic properties of RUNXI have been generally associated with loss of function (11), whereas there is an excess of an additional copy of RUNXI in trisomy 21.

The ERG gene, located on chromosome 21q22, encodes a transforming proto-oncogene (14) that is also expressed in hematopoietic stem cells and endothelial cells. Its close family member, FLI1 (located at chromosome 11q24), is required for normal megakaryopoiesis (15). In patients with Ewing sarcoma, either FLI1 or ERG fuses with the EWS gene to create a chimeric oncogenic protein (16). Thus, at least in the context of this particular chromosomal translocation, FLI1 and ERG are interchangeable. ERG has also been associated with rare cases of leukemias, such as the TLS(FUS)-ERG fusion gene in megakaryoblastic leukemias (17, 18). ERG was also recently reported to be overexpressed in myeloid leukemias with complex karyotypes (19).

We, therefore, hypothesized that increased expression of ERG in hematopoietic progenitors caused by excess copies of chromosome 21 may contribute to the development of megakaryoblastic leukemias.
Materials and Methods

Cell lines. CMK, Dami, Meg-01, and 416B cells were grown in RPMI containing 10% fetal bovine serum (FBS) with additional antibiotics and 2 mmol/L L-glutamine. UT-7/EPO (20) and UT-7/TPO (21) cell lines were maintained in Iscove’s modified Dulbecco’s medium (Invitrogen Life Technologies, Carlsbad, CA) supplemented with 10% FBS (Invitrogen Life Technologies) and 1 unit/mL of human recombinant erythropoietin (Kirin, Gunma, Japan) or 10 g/mL of human recombinant thrombopoietin (Kirin, respectively). Isolation of cord blood CD34+ cells and megakaryocytic genes (e.g., MPL, PF4, TXAS) were expressed in UT-7/TPO, whereas those genes were not amplified in UT-7/EPO.

Patient samples. The patients were described by us previously (5). The study was approved by the institutional review board.

Platelet extraction. Ten milliliters of fresh blood extracted into EDTA were centrifuged at 120 x g for 10 minutes. The supernatant was transferred into 50 mL of 5 mmol/L EDTA in PBS and centrifuged again at 600 x g for 5 minutes. The supernatant was discarded and total RNA was extracted from the pelleted platelets with TRIzol Reagent (Life Technologies).

Reverse transcription-PCR analysis. Reverse transcription-PCR (RT-PCR) was done as previously described (5). Primer sequences and PCR conditions are available upon request.

Megakaryocytic induction of K562 cells. K562 cells (2 x 10^6 cells/mL) were induced with 15 nmol/L phorbol 12-myristate 13-acetate (PMA, Sigma Chemical, St. Louis, MO) for 77 hours as described (10).

Forced expression of ERG in K562. K562 cells (7 x 10^5) were coelectroporated with 10 μg of pMSCV-IRES hCD2 and 40 μg of each of the indicated plasmids: pCEFL-HA-ERG3, pCEFL-HA-ERG3ΔETS, and pKC3-FLI1. Seventy-two hours after electroporation, the cells were analyzed by flow cytometry by a standard protocol.

Plasmids and constructs. pKC3-FLI1 was provided by Dr. Olivier Delattre (Institut Curie, Paris, France). pXM-GATA1 was provided by Dr. Peter Aplan (NIH, Bethesda, MD). pCEFL-GATA1s was generated by inserting an GATA1s cDNA fragment BamHI-NcoI into pCEFL. pCEFL-HA-ERG3 was generated by inserting an ERG-3 cDNA fragment, HX tagged, and flanked by MfeI sites into the EcoRI site of pCEFL. pCEFL-HA-ERG3ΔETS was generated by cutting pCEFL-HA-ERG3 with NdeI and religating to create an ERG3 mutant that lacks the ETS DNA-binding domain. The gpIbα5′-567lac reporter plasmid was provided by Dr. G. Roth.

Transient transfection and reporter assays. Transient transfection of HeLa cells was carried out in 24-well plates by using JetPEI (Polyplus-Transfection, Illkirch, France) reagent according to the instructions of the
manufacturer. HeLa cells were transfected with 170 ng of the gp1bα5
V5-567luc reporter plasmid (23) and 335 ng of the expression plasmids
encoding ERG3, ERG3ΔETS, GATA1, and GATA1s as indicated. The total
amount of DNA in each transfection was kept constant at 1.34 μg by adding
the pcDNA3 backbone. Cells were harvested 24 hours after transfection, and 10 μL of lysate was assayed for luciferase activity by using the Luciferase
Reporter Assay System kit (Promega, Madison, WI).

Antibodies and protein analysis. Ten micrograms of nuclear extracts
from the transfected HeLa cells were analyzed by 10% SDS-PAGE and
transferred to nitrocellulose membrane. Following transfer, the membrane
was blocked overnight in 10% skim milk–TBS–0.05% Tween 20 and incubated
with anti–GATA-1 antibody M20 (1:1,000 dilution, Santa Cruz Biotechnology,
Santa Cruz, CA) for 1 hour. The membrane was washed thrice with PBS–TWEEN 20, and subjected to chemiluminescence detection (Pierce, Rockford, IL). The
membrane was then stripped and reprobed with anti-ERG antibody C17
(1:5,000 dilution, Santa Cruz Biotechnology) and anti-Emerin antibody
(1:5,000 dilution, Santa Cruz Biotechnology) for loading control.

Chromatin immunoprecipitation assays. Real-time PCR-based quan-
titative chromatin immunoprecipitation analysis was done as previously
described (24, 25) using the murine myeloid progenitor cell line, 416B
(2 × 10⁶ cells per immunoprecipitation). Normal rabbit IgG, anti-Fli1, anti-
Erg, and anti-Ets 2 antibodies were purchased from Santa Cruz
Biotechnology and the anti–acetyl histone H3 antibody from Upstate
Biotechnology (Lake Placid, NY). One microliter aliquots of each
immunoprecipitate sample were used for SYBR green quantitative real-
time PCR analysis (using a Stratagene MX3000 thermocycler). PCR products
were quantified relative to a standard curve generated by titrating input
chromatin. All reactions were validated by postamplification denaturation
curves to confirm single product yield (data not shown). Forward and
reverse primers (5’ to 3’) used for real-time PCR were as follows. Stem
cell leukemia (SCL) +19, CCATACATTGCAAGGCATCC and AGCAGT-
CCTACATGGGCTAA; GPIIb promoter, CTTCCAGCGCATCAGCC and
TTTCCCTTTGCCAGTCC; Endogen untranslated region (UTR), GTCCCAGAAACAC and GGGCAGTTCTGAAATGG.

Results

ERG expression in megakaryocytic and erythroid leukemias.
To establish the pattern of ERG expression in leukemic cells, we
surveyed several leukemic cell lines for its expression by RT-PCR
(Fig. 1A). ERG was expressed in the three megakaryoblastic
leukemia cell lines (CMK, Meg-01, and Dami) and the pre-B ALL
cell line 697. CMK (derived from Down syndrome) and Meg-01
[derived from a blast crisis of chronic myelogenous leukemia
(CML)] contain trisomy 21, whereas Dami is reported to have two
copies of chromosome 21. ERG was low to absent in myeloid
leukemia cell lines U937 and HL-60 (not shown), in K562 (a cell line
derived from erythroleukemia blast crisis of CML), in a T-cell ALL
cell line derived from erythroleukemia blast crisis of CML), in a T-cell ALL
line SUPT1, and in the mature B-cell leukemia cell lines Rajii
and Daudi (not shown).

Figure 3. Forced expression of ERG in
K562 cells. A, RT-PCR analysis of K562
cells transfected with an empty
pMSCV-IRES-CD2 vector or with a vector
encoding ERG-3. gpIb, gpIIb, and gpIIIa
are megakaryocytic markers. h-actin is
used as a control for the amount of cDNA.
B, RT-PCR of K562 cells transfected with
mammalian expression vectors encoding
ERG3. A mutant ERG3 lacking the Ets
domain and FLI-1, demonstrating
expression of the three genes in the
transfected K562 cells. C, flow cytometry
analysis of the transfected K562 cells.
The histograms show the percentage of
CD41- and CD61-positive cells out of the
transfected (CD2-positive) cells. Forced
expression of ERG3 induced the
expression of both CD41 and CD61. D, flow cytometry of K562 cells
cotransfected with an empty pMSCV-IRES
CD2 vector and each of the three indicated
plasmids. Columns, percentage of CD2-
positive cells expressing CD41, CD61, and
glycophorin A, respectively. ERG3
induces the expression of CD61 and
CD41 and dramatically reduce the
expression of the erythroid marker
glycophorin A in a way dependent on
the presence of an intact Ets domain.
There are at least five isoforms of ERG generated by alternative splicing and translation initiation sites (see Supplementary Data; refs. 14, 26). ERG isoforms showed differential expression between samples. In the CMK cell line (Fig. 1B) and in primary samples of Down syndrome–acute megakaryoblastic leukemia (Fig. 1C), mostly expression of ERG-3 was detected. ERG-2 was the only isoform detected in Dami, whereas both isoforms were expressed in the Meg-01 cell line. ERG-3 was also detected in normal platelets (Fig. 1B), in CD34+ hematopoietic cells purified from umbilical cord blood, and in megakaryoblasts generated in vitro (Fig. 1D). ERG3 expression was low to absent in erythroblast differentiated Down syndrome–acute megakaryoblastic leukemia (Fig. 1C), in the Meg-01 cell line. ERG-3 was also detected in normal platelets (Fig. 1B), whereas both isoforms were expressed in the CMK cell line (Fig. 1D). These findings implicate ERG-3 as the major hematopoietic isoform. ERG expression in platelets and in megakaryoblasts suggests that it may have a role in normal megakaryopoiesis.

The erythroid and the megakaryocytic lineages are closely related and originate from a common megakaryoblastic erythroid progenitor (MEP; ref. 27). K562 cells can be induced to undergo megakaryocytic differentiation by treatment with phorbol esters. This assay is commonly used to study megakaryocytic differentiation (10). As shown in Fig. 2A, ERG expression (interestingly ERG-2 and not ERG-3) was induced in differentiated K562 cells. gplIla levels were also increased in treated K562 cells, indicating that they underwent megakaryocytic differentiation. To further study the differential expression of ERG between megakaryoblastic and erythroid leukemia, we analyzed two sublines of the multipotential MEP leukemia cell line UT-7. ERG3 and typical megakaryocytic genes (e.g., MPL, PF4, TX4S) were expressed in UT-7/TP0, whereas these genes were not amplified in UT-7/EP0 (Fig. 2B). Thus, ERG is induced upon megakaryocytic differentiation of leukemic progenitor cells.

Overexpression of ERG induces phenotypic shift of erythroleukemia cells toward the megakaryocytic lineage. To examine whether ERG plays a direct role in induction of the leukemic megakaryoblastic phenotype, we cotransfected K562 cells with expression vectors of ERG3 and CD2 (as a marker for transfected cells). As shown in Fig. 3, overexpression of ERG-3 resulted in induction of the megakaryocytic genes gpIIb, gpIIb, and gplIla and expression of CD41 and CD61 antigens (representing the protein products of the gpIIb and gpIIa genes, respectively) on the surface of transfected cells (Fig. 3A and C). The extent of induction of megakaryocytic markers was higher than the positive control (FLI-1) and completely dependent on the presence of the Ets domain in ERG-3 (Fig. 3B and D). Strikingly, the induction of megakaryocytic markers by ERG-3 was associated with down-regulation of the erythroid marker glycoporphin A (Fig. 3D). Thus, ectopic expression of ERG-3 in K562 cells caused a phenotypic shift from the erythroid to the megakaryocytic lineage.

ERG activates and occupies megakaryocytic gene promoters. We next examined the role of ERG in activating megakaryocytic gene promoters. ERG3 activated a gpIIb5′-567luc reporter plasmid. HeLa cells were transfected with 170 ng of the gpIIb5′-567luc reporter plasmid and 335 ng of the expression plasmids encoding ERG3, ERG3ETS, GATA1, and GATA1s as indicated. The total amount of DNA in each transfection was kept constant at 1.34 μg by adding the pcDNA3 backbone. Cells were harvested 24 hours after transfection and assayed for luciferase activity. The results shown are a summary of three experiments done in triplicate. Columns, average fold increase in firefly luciferase relative to a value of 1 for the reporter alone; bars, SE. ERG3 activates the reporter plasmid and synergizes with GATA1. Its activity depends on the presence of the Ets motif. All the transcription factors added transactivate the reporter plasmid in a statistically significant manner (P < 0.05), except ERG3ETS. The bottom part shows Western blot analysis using nuclear extracts and the antibodies indicated on the left.

ERG binds the stem cell leukemia hematopoietic enhancer. The current study is driven by the hypothesis that increased expression of ERG in hematopoietic progenitors of Down syndrome patients enhances the formation of megakaryocytic precursors. The SCL/TAL1 gene encodes a bHLH transcription factor required for the development of hematopoietic stem cells (29, 30). Both gain- and loss-of-function experiments have established that SCL/TAL1 directs megakaryocytic development (31–33). Göttgens et al. (25) have previously shown that expression of SCL/TAL1 in hematopoietic stem and progenitor cells is controlled by a 3′ enhancer element (+19 enhancer). The activity of the +19 enhancer was critically dependent on conserved Ets and GATA consensus binding sites that we had previously shown to be bound in vivo by GATA2, FLI-1, and ELF1 (but not PU.1) in hematopoietic progenitor cells (25). By performing additional chromatin immunoprecipitation experiments, we have now shown that both ERG and ETS2 are bound to this enhancer in vivo at a similar level as FLI1 (Fig. 5A and B). Thus, the induction of megakaryocytic genes by ERG results from direct binding to their promoters.

Discussion

This is the first study associating ERG expression with megakaryopoiesis and megakaryoblastic leukemias. We found ERG to be expressed in hematopoietic stem cells, megakaryoblasts...

![Figure 4. ERG3 activates a gpIIb5′-567luc luciferase reporter plasmid. HeLa cells were transfected with 170 ng of the gpIIb5′-567luc reporter plasmid and 335 ng of the expression plasmids encoding ERG3, ERG3ETS, GATA1, and GATA1s as indicated.](image-url)
and platelets, and in megakaryoblastic leukemia cells including primary transient leukemia cells of Down syndrome. The expression of ERG was induced upon megakaryocytic differentiation of erythroleukemia cells. Forced expression of ERG in erythroleukemia cells caused a phenotypic shift toward the megakaryocytic lineage. The induction of megakaryocytic markers was most likely the consequence of direct binding and activation as shown by luciferase reporter assays and chromatin immunoprecipitation. Finally, we have shown that ERG is bound in vivo to the enhancer of the stem cell and megakaryocytic transcription factor SCL/TAL1. Together, these findings are consistent with the hypothesis that excess copies of the ERG gene in hematopoietic progenitors push the hematopoietic development into the megakaryocytic lineage and, in collaboration with mutated GATA1, contribute to the clonal megakaryoblastic proliferation observed in at least 10% of infants with Down syndrome.

ERG has been reported to regulate genes involved in chondrogenesis and angiogenesis and functions as a modulator of endothelial cell differentiation (26, 34–37). It has not been previously associated with hematopoiesis, although it was detected in DNA-microarray gene expression analysis of the slow-dividing CD133-positive hematopoietic stem cells (38). Different isoforms of ERG are expressed by alternative splicing and the utilization of different 5' UTRs. We have observed that ERG3 is the dominant isoform in normal and malignant hematopoietic cells. ERG3 differs from the nonhematopoietic isoform ERG2 by an additional exon and a different 5' UTR and the first few amino acids. Both ERG2 and ERG3 were shown to activate Ets binding sites in vitro to a similar degree (14), and we have observed similar results with ERG2 in luciferase reporter and K562 transfection experiments (not shown). Interestingly, ERG-3 has been previously reported to be the major isoform expressed in endothelial cells (26). Thus, it seems that ERG3 is the major hematoendothelial ERG isoform.

We have confirmed the absence of ERG expression in mature lymphoid or myeloid cells (26) as well as in myeloid and mature B-cell leukemias. However, we have observed expression of ERG3 in a pre-B leukemia cell line. This is consistent with the data obtained by microarray gene expression analysis of primary ALL samples (39, 40). Interestingly, the highest levels of ERG expression were observed in hyperdiploid ALL, uniformly harboring three to four copies of chromosome 21. The possible role of ERG in ALL needs further investigation.

The erythroid and megakaryocytic lineages are closely related. Both originate in a common MEP progenitor cell. The mechanisms directing the choice of development from the MEP stage are unclear because many of the critical transcription factors, such as GATA1 and FOG1, are expressed in both lineages (27, 41). We have observed striking differential expression of ERG between these two lineages. Moreover, forced expression of ERG in erythroleukemia cells caused up-regulation of megakaryocytic markers coupled with down-regulation of glycophorin A, an erythroid marker. Thus, ERG may regulate the differentiation of MEP along the megakaryocytic pathway. This hypothesis needs to be studied further in appropriate nonleukemic models.

Figure 5. In vivo binding of chromosome 21 Ets family transcription factors to the gpllb promoter and SCL +19 enhancer in the hematopoietic progenitor cell line 416B. A, diagram of the murine gpllb and SCL loci indicating the location of the gpllb and SCL clusters of conserved Ets and GATA sites. Open boxes, noncoding exons; filled boxes, coding exons. The triangles mark the position of the sequences of the gpllb promoter and the SCL enhancer, respectively. B, the gpllb promoter is bound in vivo by Fli1 and ERG, and the SCL +19 enhancer by Fli1, ERG, and Ets2. Chromatin immunoprecipitates were analyzed by quantitative real-time PCR. Rabbit IgG served as a negative control and antibodies against K9 acetylated histones as a positive control. The fold enrichment shown is normalized against the negative control IgG samples and corrected for the enrichment seen when performing quantitative PCR for a neutral region of the genome (see Materials and Methods).
In the current study, we have observed ERG binding in vivo to the SCL +19 enhancer that regulates SCL expression in hematopoietic stem and progenitor cells (25). Both gain- and loss-of-function studies have shown that SCL/TAL1 is a key regulator of megakaryocytic development (31–33, 42). In particular, previous studies have shown that overexpression of SCL/TAL1 in primary multipotential myeloid progenitor cells drives their subsequent differentiation toward the megakaryocytic lineage (32, 33). Our data are, therefore, consistent with the notion that, at least in part, ERG may mediate a promegakaryopoietic effect through regulating the levels of SCL expression in hematopoietic progenitors. Incidentally, we also noted binding of Ets2 to the SCL +19 enhancer, suggesting that Ets2, also located in the critical region of chromosome 21, may represent an additional candidate gene involved in the development of Down syndrome megakaryoblastic leukemia.

The pattern of ERG expression is reminiscent of the expression pattern of the chromosome 21 gene RUNX1. Both are expressed in hematopoietic stem cells and in megakaryocytic and lymphoid progenitors (11, 43). Forced expression of RUNX1 in the K562 erythroleukemia cell line accelerated its megakaryocytic differentiation in response to thrombopoietin (10). In contrast, ERG induced megakaryocytic differentiation in the absence of additional growth factors. Conditional knockout experiments in mice have shown that RUNX1 expression in early hematopoietic progenitor regulates their differentiation toward the lymphoid and the megakaryocytic lineages (12). A similar assessment of ERG function needs to be done. Because RUNX1 is known to cooperate with Ets transcription factors (44–46), the potential functional and biochemical interactions between RUNX1 and ERG warrant further studies.

Several studies have shown a linear correlation between gene copy number and gene expression (1, 39, 47). How could trisomy 21, resulting in an average 1.5 x increase in expression of multiple genes, cause a dramatic phenotype of 10% incidence of congenital leukemia? We hypothesize (Fig. 6) that the excess of several chromosome 21 genes regulating megakaryopoiesis induces these leukemias in Down syndrome. This hypothesis is consistent with the thrombocytosis observed in the majority of healthy infants with Down syndrome (8). Thus, increased expression of RUNX1, ERG, and perhaps other genes (e.g., ETS2) in fetal liver hematopoietic progenitors promotes megakaryopoiesis and increases the pool of early megakaryocytic cells, whereas the acquired GATA1 mutations and the overexpression of the chromosome 21 transcription factor BACH1 (48) block further differentiation, leading to marked accumulation of megakaryoblasts. This model, testable by animal experiments or by studies of human fetal liver cells from Down syndrome embryos, could serve as a general paradigm by which the carcinogenic effects of numerical chromosomal changes reflect collaborative activities of several genetic elements on the amplified or deleted chromosomes.

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