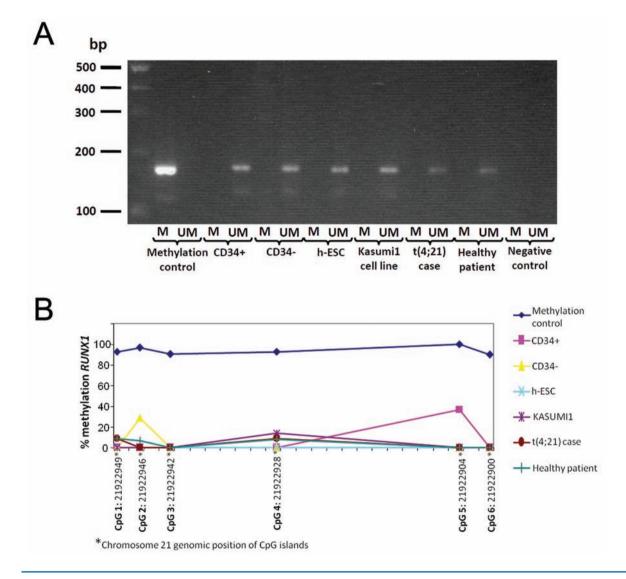
Abrogation of RUNX1 gene expression in de novo myelodysplastic syndrome with t(4;21)(q21;q22)

Ana Rio-Machín,¹* Juliane Menezes,¹* Alba Maiques-Diaz,¹ Xabier Agirre,² Bibiana I. Ferreira,¹ Francesco Acquadro,¹ Sandra Rodriguez-Perales,¹ Karmele A. Juaristi,³ Sara Álvarez¹ and Juan C. Cigudosa¹

¹Molecular Cytogenetics Group, Human Cancer Genetics Program, Centro Nacional Investigaciones Oncológicas (CNIO) - Centro de Investigación de Enfermedades Raras (CIBERER), Madrid; ²Division of Oncology, Department of Hematology Service and Area of Cell Therapy, Center for Applied Medical Research (CIMA), University of Navarra, Pamplona, Navarra: and ³Hematology Service, Hospital Alcorcón Foundation, Madrid, Spain

Citation: Rio-Machín A, Menezes J, Maiques-Diaz A, Agirre X, Ferreira BI, Acquadro F, Rodriguez-Perales S, Juaristi KA, Álvarez S and Cigudosa JC. Abrogation of RUNX1 gene expression in de novo myelodysplastic syndrome with t(4;21) (q21;q22). Haematologica 2012;97(4):534-537. doi:10.3324/haematol.2011.050567



Online Supplementary Figure S1. Methylation Specific PCR and pyrosequencing. (A) Methylation-specific PCR was carried out to assess RUNX1 proximal promoter methylation using specific RUNX1 promoter primers for methylation and unmethylation (MF: 5'- TTCGGGTTGCGTATAGTAGC; MR: 5'- ATAAAC-CCGACCGAAAAAAT; UMF: 5'- GTTTGGGTTGTGTATAGTAGT; UMR: 5'- TATAAACCCAACCAAAAAAAT). For methylation-specific PCR reaction, we included universal methylated DNA (CpGenome Universal Methylated DNA, Millipore, Temecula, CA, USA) as positive control, and normal blood DNA as negative control. Quality controls for bisulphite conversion were performed for each reaction. (B) The second methylathion analysis of the RUNX1 proximal promoter was realized by bisulphite genomic pyrosequencing of the corresponding six CpG islands located within the fragment amplified by MSP. Following sodium bisulphite treatment, the specific region was PCR amplified using specific primers for modified DNA (Forward: 5'- GGTTAGTATGTAGGTTTGGATG and Reverse: 5'- CTATAAATAAAAATAACCTAAAAATAAAC) and PCR products were sequenced. The positive control also corresponds to the universal methylated DNA. In both analyses we included DNA from CD34⁻ and CD34⁻ cells isolated from cord blood, AND2 human embryonic stem cell line, AML Kasumi1 cell line, the studied case and DNA from the patient in remission. No methylation within the RUNX1 proximal promoter was observed in any of these cases. We conclude that this epigenetic mechanism is not involved in the inactivation of the remaining gene copy in the patient.

Online Supplementary Table S1. Deleted genes on chromosome 4 and 21 reveled by aCGH.

	Ch4	Description
	CXCL9	chemokine (C-X-C motif) ligand 9
6.6Mb	CXCL10	chemokine (C-X-C motif) ligand 10
	CXCL11	chemokine (C-X-C motif) ligand 11
	ASAHL	N-acylethanolamine acid amidase
	SDAD1	SDA1 domain containing 1
	ART3	ADP-ribosyltransferase 3
	GENX-3414	starch binding domain 1
	FLJ25770	coiled-coil domain containing 158
	ShrmL	shroom family member 3
	SEPT11	septin 11
	CCNI	cyclin I
	CCNG2	cyclin G2
	CXCL13	chemokine (C-X-C motif) ligand 13
	CNOT6L	CCR4-NOT transcription complex, subunit 6-like
	MRPL1	mitochondrial ribosomal protein L1
	FRAS1	Fraser syndrome 1
	ANXA3	annexin A3
	BMP2K	BMP2 inducible kinase
	PAQR3	progestin and adipoQ receptor family member III
	GK2	glycerol kinase 2
	GDEP	gene differentially expressed in prostate (non-coding RNA)
	ANTXR2	anthrax toxin receptor 2
	PRDM8	PR domain containing 8
	FGF5	fibroblast growth factor 5
	MGC35043	uncharacterized protein C4orf22
	PRKG2	protein kinase, cGMP-dependent, type II
	BMP3	bone morphogenetic protein 3
	RASGEF1B	RasGEF domain family, member 1B
	HNRNPD	heterogeneous nuclear ribonucleoprotein D
	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like
	MASA	enolase-phosphatase 1
	SCD5	stearoyl-CoA desaturase 5
Ch21		Description
2.3Mb	KCNE2	potassium voltage-gated channel, Isk-related family, member 2
	KCNE1	potassium voltage-gated channel, Isk-related family, member 1
	C21orf51	family with sequence similarity 165, member B
	DSCR1	regulator of calcineurin 1
	CLIC6	chloride intracellular channel 6
	RUNX1	runt-related transcription factor 1
	C21orf18	SET domain containing 4
	CBR1	carbonyl reductase 1
	CBR3	carbonyl reductase 3
	C21orf51	family with sequence similarity 165, member B
	CHAF1B	chromatin assembly factor 1, subunit B (p60)
	ZCWCC3	MORC family CW-type zinc finger 3