

## ERRATUM

# The paternal chromosome 9 and the maternal chromosome 22 are preferentially rearranged in chronic myeloid leukaemia

R Olicio, MB Rivero and HN Seuáñez

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Due to a typesetting error, the data in Tables 1 and 2 of the above article were not aligned correctly. The correct tables are reproduced below.

**Correction to:** *Leukemia* (2004) 18, 1445–1448. doi: 10.1038/sj.leu.2403404

The Publisher would like to apologise for any inconvenience this may have caused.

**Table 1** Amplimers used for the amplification of chromosome 9 markers

<i>Amplimers</i>	<i>Amplimer reference</i>	<i>Cytogenetic allocation of amplified marker</i>	<i>Size of amplified fragment (bp)</i>	<i>Type of repeat</i>	<i>Annealing temperature (°C)</i>	<i>Maximum heterozygosity</i>
Mfd135CA*	GDB: 180704	9q31.1	116–150	Dinucleotide	53	0.8380
Mfd135GT						
C3B2-1*	GDB: 185718	9q31.3	105–137	Dinucleotide	52	0.8840
C3B2-2						
Mfd 178CA*	GDB: 180718	9q31.3	187–203	Dinucleotide	51	0.8030
Mfd178GT						
Mfd94CA*	GDB: 180558	9q33.1	135–159	Dinucleotide	55	0.8050
Mfd94GT						
Mfd77CA*	GDB: 180555	9q33.2	89–97	Dinucleotide	55	0.5530
Mfd77GT						
GSN.PCR1.1*	GDB: 178525	9q33.2	111–147	Dinucleotide	53	0.7610
GSN.PCR1.2						
1627-1*	GDB: 185720	9q33.3	136–154	Dinucleotide	55	0.8100
1627-2						
DBH.PCR2.1*	GDB: 196477	9q34.2	235–280	Dinucleotide	65	0.7238
DBH.PCR2.2						

\*Sense primer 5' labelled with 6-FAM.  
 bp = base pairs; GDB = Genome Database ([www.gdb.org](http://www.gdb.org)).

**Table 2** Amplimers used for the amplification of chromosome 22 markers

<i>Amplimers</i>	<i>Amplimer reference</i>	<i>Cytogenetic allocation of amplified marker</i>	<i>Size of amplified fragment (bp)</i>	<i>Type of repeat</i>	<i>Annealing temperature (°C)</i>	<i>Maximum heterozygosity</i>
F8WFP.PCR4.1**	GDB: 277263	22q11.1	329–349	Tetranucleotide	53	0.6100
F8WFP.PCR4.2						
TOP1P2.PCR1.1**	GDB: 188759	22q11.2	113–155	Dinucleotide	50	0.9200
TOP1P2.PCR1.2						
CYP2D8P.PCR2.1**	GDB: 180365	22q12.3	108–130	Dinucleotide	58	0.8000
CYP2D8P.PCR2.2						
MB-1F**	GDB: 270294	22q12.3	217–219	Dinucleotide	53	0.4712
MB-1R						
IL2RB.PCR1.1**	GDB: 188757	22q13.1	125–135	Dinucleotide	51	0.9100
IL2RB.PCR1.2						
TG-01**	GDB: 180405	22q13.1	149–163	Dinucleotide	56	0.9100
TG-02B						
CYP2D8P.PCR1.1**	GDB: 179878	22q13.3	98–116	Dinucleotide	51	0.8000
CYP2D8P.PCR1.2						

\*\*Sense primer 5' labelled with NED.  
 bp = base pairs; GDB = Genome Database ([www.gdb.org](http://www.gdb.org)).  
 TOP1P2.PCR1.1/1.2 amplify a marker that is distally located (bp 23 485 119–3 485 250) with respect to *BCR* (bp 21 847 702–21 982 691) according to <http://www.ensembl.org/Multi/blastview>.