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Erratum

In the paper 'Expression and parental imprinting of the H19 gene in human rhabdomyosarcoma' by Stefano Casola *et al*., *Oncogene* 1997, **14:** 1503–1510, Figure 1c was incorrectly reproduced. The correct reproduction is shown below

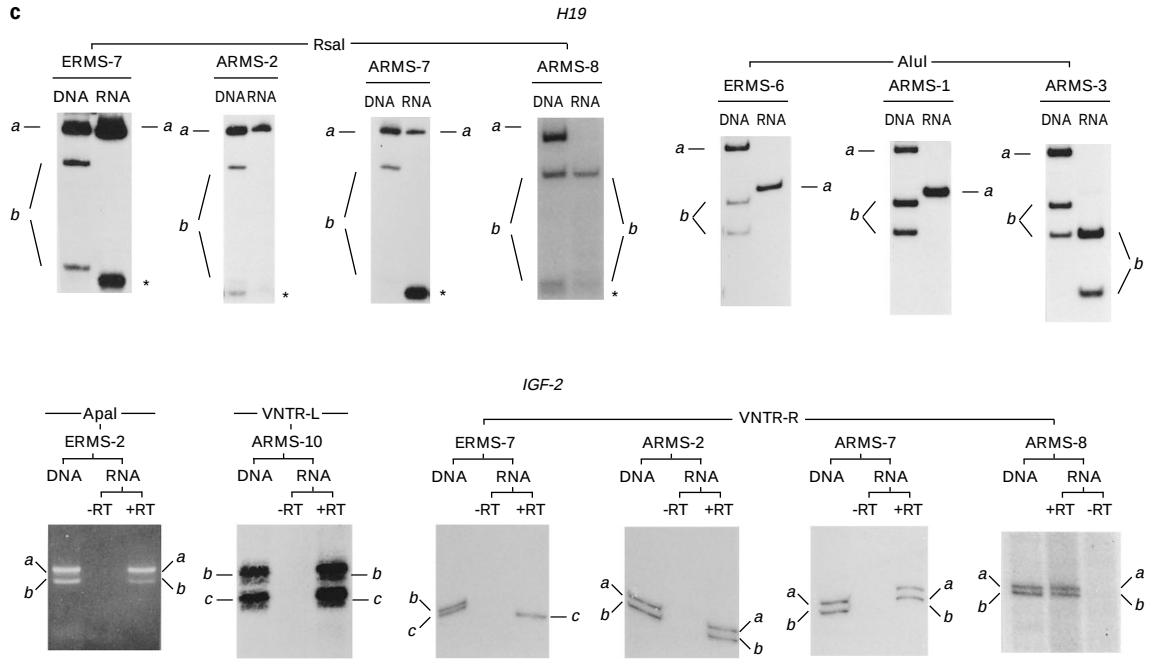

Figure 1 Representative results of an analysis of allele-specific expression of the *H19* and *IGF-2* genes in normal striated muscle and RMS. *H19* and *IGF-2* alleles were analysed by PCR and RT–PCR in bioptic samples of normal striated muscle tissue (**a**), in the informative RMSs showing loss of the constitutional heterozygosity (**b**) and in the RMSs retaining the heterozygosity (**c**). *H19* alleles were detected in DNA and RNA extracted from tissues by standard methods (Sambrook *et al*., 1989; Chomczynski and Sacchi, 1987), using primers specific for the RsaI RFLP (Zhang and Tycko, 1992): A: 5′-GCACTAAGTCATTTGCACTG-3′ (sense) and B: 5′-GGTCGGAGCTTCCAGACTAG-3′ (antisense) or with primers specific for the AluI RFLP (Zhang and Tycko, 1992): C: 5′-TGCTGCACTTTACAACCACTG-3′ (sense) and D: 5′-GTGGCCATGAAGATGGAGTC-3′ (antisense). The fast migrating band observed in all of the lanes corresponding to the RsaI RFLP and indicated by an asterisk is an artefact, probably due to primer oligomerization. 0.5 μg of genomic DNA was amplified in 25 μl with 1 unit Taq DNA polymerase (Stratagene) and in the presence of [^{32}P]dGTP, using an initial denaturation step of 2 min 30 s at 95°C followed by 30–35 cycles at 94°C for 1 min, 58°C for 1 min and 72°C for 1 min. PCR products were digested with either RsaI or AluI and electrophoresed on a 6% non denaturing polyacrylamide gel. For detection of the expressed alleles, 0.5–1 μg total RNA were reverse transcribed using 200 units of Superscript RT (BRL) in the presence of 500 nM random hexamers (Boehringer), 10 mM DTT, 50 mM Tris-HCl-pH 8.3, 75 mM KCl, 3 mM $MgCl_2$, 0.5 mM dNTP-lithium salt (Boehringer) and 20 units of RNase inhibitor (Promega). One fiftieth of first strand cDNA was amplified following the conditions used for genomic DNA except that the number of cycles were increased to 35–40. The presence of each allele in the cDNA was identified as described for genomic DNA. To control for contamination by genomic DNA, all RNA samples were run in duplicate with or without addition of reverse transcriptase. RNA samples found contaminated with genomic DNA were treated for 30 min with 1 unit of RQ RNase-free DNase (Promega) at 37°C in the presence of 40 mM Tris-HCl-pH 7.6, 10 mM NaCl, 6 mM $MgCl_2$, 100 mM $CaCl_2$. *IGF-2* alleles were detected using primers specific for the ApaI RFLP or for the VNTR present in an untranslated region of the gene, as previously described (Pedone *et al*., 1994b). See Table 1 for complete results and details on the polymorphisms