**ABSTRACT INSTRUCTIONS (delete all red text before submitting).**

* Replace the text in the example below. Do not change any formatting (font type, size, justification, margins or line and paragraph spacing etc).
* All elements must be included exactly as indicated in the example.
* **The main text should not exceed 300-words (inclusive of references) and must fit within this single page.** *Title, authors, and affiliations are not included in the word count.*
* Abstracts should contain a statement of the problem, brief methods, clear results, and a statement of the conclusions or significance of the findings. No figures are allowed.
* Non-compliant abstracts will be rejected and returned.

**Abstract Title – Bold, font size 14**

**G-quadruplex DNA structures, genomic imprinting and allelic drop-out in PCR**

**Authors – font size 12, with presenting author underlined.**

Stevens, A.J.1, Stuffrein-Roberts, S.1, Miller, A.L.1, Gibb, A.1, Doudney, K.1, Bagshaw, A.1, Aitchison, A.1, Eccles, M.R.2, Filichev, V.V.3, Kennedy, M.A.1

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**Main text – font size 12, justified, single line spacing**

During analysis of the promoter region of the human *MEST* gene, we noted apparent non-Mendelian behaviour of three closely linked single nucleotide polymorphisms (SNPs)1. *MEST* plays a role in mammalian development and maternal behaviour. It is genomically imprinted, with the maternally inherited allele permanently switched off. When we genotyped these SNPs in many subjects, no heterozygotes were observed, despite the use of multiple PCR-based methods and several different primer pairs. Experiments with mixing the genomic DNA from different individuals proved that the assays could detect both alleles simultaneously. This indicates that the observed homozygosity was likely resulting from consistent allelic dropout of one allele in every subject.

It is possible that the DNA (CpG) methylation likely to occur on the imprinted allele could play a role in altering the outcome of genotyping results; however, this phenomenon alone cannot explain the pattern of allelic dropout. Therefore, we examined the region containing the three SNPs for evidence of secondary structures that might also be a factor in allelic dropout. The region is GC-rich, and using several prediction algorithms2 it appeared likely that it has a propensity for forming G-quadruplex (G4) structures. These arise from the formation of G-tetrads by hydrogen bonding of four G residues, either within or between strands, and the subsequent stacking of these into higher order structures. We hypothesized that DNA methylation may interact to stabilize such secondary structures and block the *Taq* polymerase from actively replicating one template strand.

**Optional references – font size 10, Calibri. Title in Italics (Note if included: references are included in the 300-word limit)**

1. Stuffrein-Roberts, S., *Allelic expression patterns in psychatric candidate genes*. PhD Thesis in Pathology. 2008, University of Otago: Christchurch. p. 216.

2. Kikin, O., L. D'Antonio and P.S. Bagga (2006). *QGRS Mapper: a web-based server for predicting G-quadruplexes in nucleotide sequences*. Nucleic acids research. 34: W676-82.