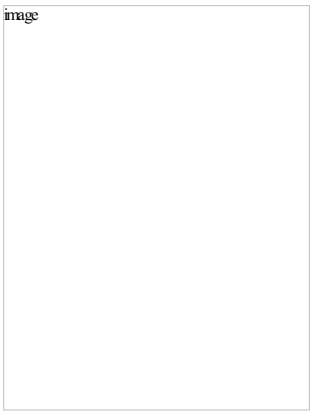

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# Circulating tumour DNA for detecting minimal residual disease in multiple myeloma

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## Abstract
Circulating tumour DNA faithfully recapitulates somatic mutations detected in bone marrow aspirates from patients with newly diagnosed or relapsed/recurrent myeloma. Extending these methods to enable detection of minimal residual disease will require increased sensitivity and breadth of genomic assays to maximize information content from small quantities of cell-free DNA; as well as definition of a clinically-meaningful ctDNA concentration in comparison with conventional bone marrow cell-count thresholds. This review describes the use of cell-free DNA sequencing in myeloma to date, identifies challenges associated with pushing limit of detection of these assays into the realm of detecting minimal residual disease, and describes potential strategies to overcome these challenges.

**Key words**
Cell-free circulating tumour DNA; multiple myeloma; cancer genomics; mutations; epigenetics