

# High-Resolution Melt

High-Resolution Melt or HRM analysis as it will be referred to herein is a hugely powerful technique for the detection of [mutations](#), [polymorphisms](#) and epigenetic differences in double-stranded DNA samples.

Saito et al. examined the efficacy of a pre-screening method for high-resolution melting (HRM) analysis of [TP53 mutation](#) before [direct sequencing](#) using samples from patients with [diffuse glioma](#). Surgical samples from 64 [diffuse gliomas](#) were classified based on the [World Health Organization Classification of Tumors of the Central Nervous System 2016](#) and the [cIMPACT-NOW \(the Consortium to Inform Molecular and Practical Approaches to CNS Tumor Taxonomy-not official WHO\)](#) update. TP53 mutations from [exon 5](#) to exon 8 were assessed by direct [sequencing](#). The results of HRM and p53 immunohistochemistry (IHC) analysis were compared by recording the sensitivity, specificity, and false-negative and false-positive rates. Direct sequencing detected TP53 mutations in 18 of 64 samples (28.1%): diffuse astrocytoma, IDH-mutant (n = 3); diffuse astrocytoma, IDH-wild type (n = 1); anaplastic astrocytoma, IDH-mutant (n = 3); anaplastic astrocytoma, IDH-wild type (n = 4); and glioblastoma, IDH-wild type (n = 7). A total of 22 mutations was detected in the 18 samples; 4 samples exhibited duplicate missense mutations. Sensitivity and specificity were 0.96 and 0.96, respectively, for HRM analysis; they were 0.89 and 0.52, respectively, for p53 IHC. Overall accuracy was 0.98 for HRM and 0.63 for IHC. HRM analysis is a good pre-screening method for the detection of TP53 mutation before direct sequencing <sup>1)</sup>.

<sup>1)</sup>

Saito K, Yokogami K, Maekawa K, Sato Y, Yamashita S, Matsumoto F, Mizuguchi A, Takeshima H. High-resolution melting effectively pre-screens for TP53 mutations before direct sequencing in patients with diffuse glioma. Hum Cell. 2021 Jan 17. doi: 10.1007/s13577-020-00471-2. Epub ahead of print. PMID: 33454902.

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