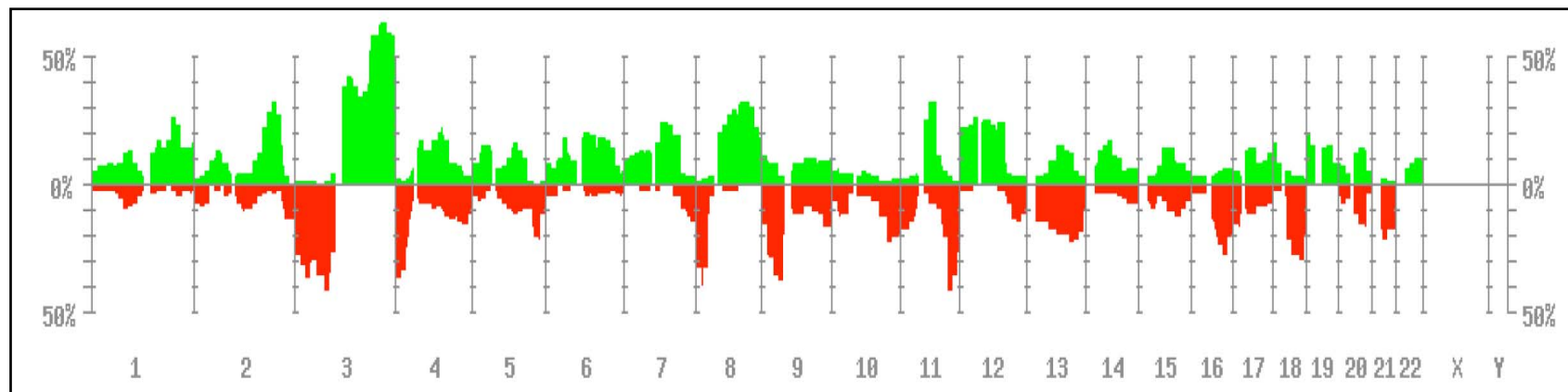


Chromosomal gains and losses in head and neck squamous carcinoma (HNSCC)

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Entity of chromosomal aberrations in 117 HNSCC detected by chromosomal CGH

Chromosomal changes were detected along chromosomes 1-22 (x-axis) and plotted against their occurring frequency (%; y-axis). DNA gains are shown in green, DNA losses in red.

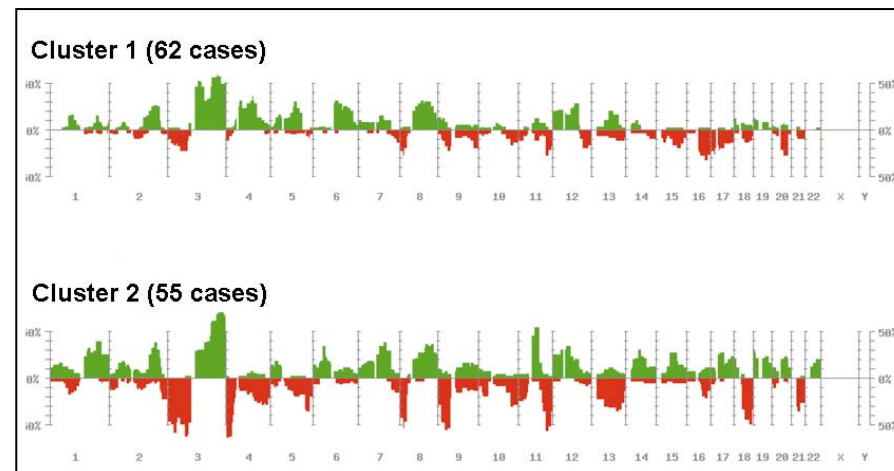
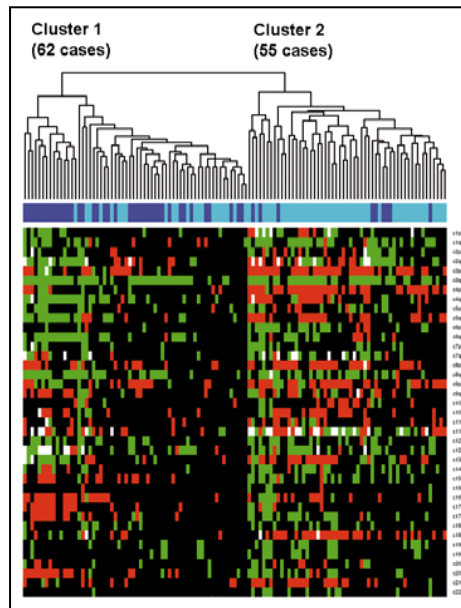


Specific aberration patterns lead to separation of HNSCC cases in two main clusters

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Hierarchical cluster analysis reveals two main clusters (Cluster 1 and 2) depending on chromosomal changes. Clustering also correlates to the patients anaemic status.

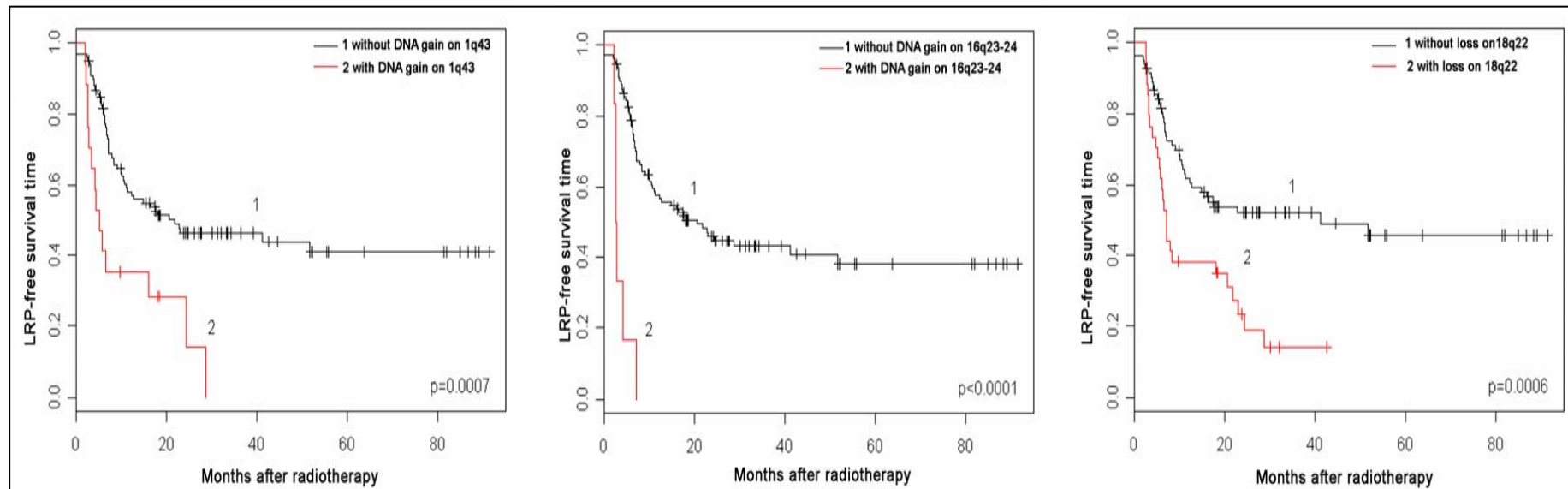
DNA gains (green) and losses (red) are arranged by tumour groups, coloured bars indicate tumours from anaemic (light blue) and nonanaemic (dark blue) patients



Chromosomal changes correlate to reduced LRP-survival times after radiotherapy

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Kaplan-Meier survival curves show significant impact of DNA gains on chromosomes 1q43 and 16q23-24 and DNA loss on chromosome 18q22 on LRP-free survival of HNSCC patients after radiotherapy



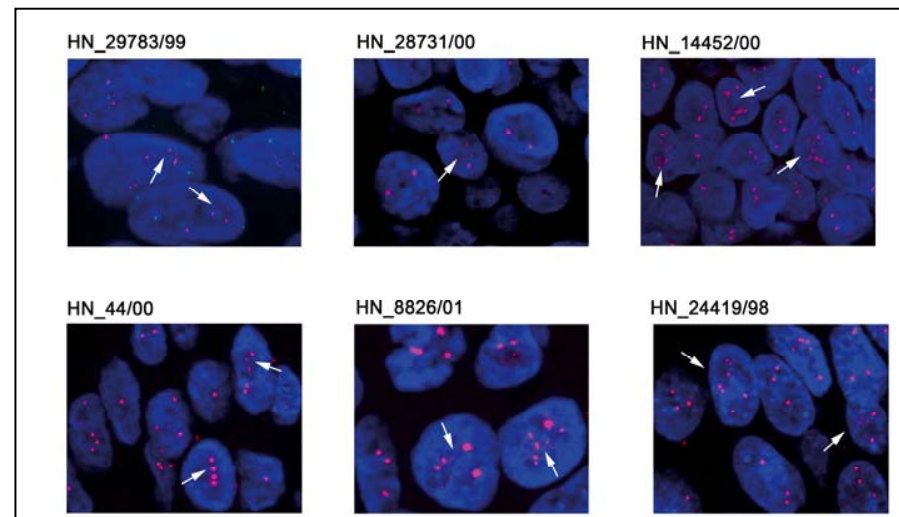
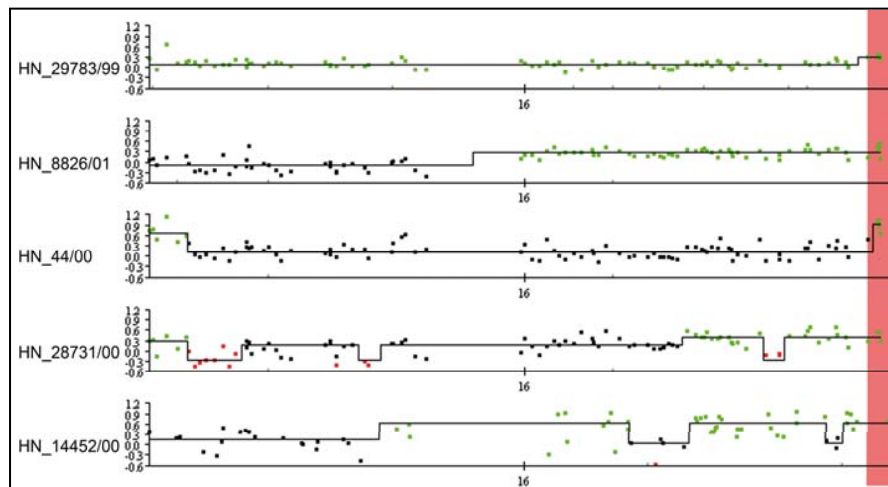
Analysis at higher molecular resolution and identification of candidate genes

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Array-CGH and FISH analysis of HNSCC tissue sections confirm DNA gain on chromosome 16q24.3 and verify the amplification of the identified candidate gene *FANCA*.

1 Mb BAC Array-CGH profiles display a minimal region of DNA gain on chromosome 16q24.3 (red bar). Dots represent log₂-ratios of BAC clones indicating no alteration (black), deletion (red) and DNA gain (green)

FANCA FISH-analysis with clone RP11-354M24 reveals amplified signals (red) in all investigated HNSCC cases with DNA gain on 16q24.3



Identification of further candidate genes on chromosomes 1q43 and 18q22 and functional studies to investigate the role of the candidate gene *FANCA* for the sensitivity of cells to ionising radiation

Development of a specific array for the Fanconi anaemia/BRCA1 pathway as a diagnostic tool to detect these prognostic markers in tumours