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Title Establishing gene expression for early and high-throughput prediction of the hematological acute radiation syndrome

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Text

We aimed to predict the later occurring hematological acute radiation syndrome (HARS) and its severity based on early detected changes in gene expression. Using

peripheral blood from baboons irradiated with 2.5 or 5 Gy (whole body equivalent dose) we examined changes in gene expression occurring 1 and 2 days after exposure in relation to unexposed blood samples (pre-exposure samples). Utilizing whole genome microarrays and validating candidate genes with qRT-PCR finally allowed us to identify a set of 29 baboon genes forwarded for cross-species validation using human samples. Within this presentation we will provide first results on this cross-species validation and share preliminary results on our envisioned 1,000 sample exercise to examine the feature of high-throughput diagnostic of the HARS using gene expression.