adapted if needed. 724 CT features were calculated using radomics software. To test if features were different for EGFR+, KRAS+ or WT patients one way ANOVA (initially without correction for multiple testing) was performed using a 5% significance level. A pair-wise comparison (t-test) identified significantly different groups.

Results: 51 EGFR+, 47 KRAS+ and 32 WT patients were included. 41 features were significantly different between EGFR+, KRAS+ and WT patients. One feature is a first order gray-level statistics feature (7% of feature subgroup total), two are gray-level co-occurrence matrix based (9%), two gray-level size-zone matrix based (18%), one Laplacian-of-Gaussian transform based (0.5%) and 35 are wavelet transform based features (7%). Statistics for the significant features are shown in Table 1. One easy to interpret significantly different feature for EGFR+ compared to WT patients was the median Hounsfield Unit (HU). EGFR+ patients had a median HU which is on average 54±23 HU higher compared to WT patients, see Figure 1. KRAS+ patients did not have a significantly different median HU compared to EGFR+ or WT patients.

Table 1: Mean values and standard deviation of EGFR+, KRAS+ and WT patients for the selected features.

<table>
<thead>
<tr>
<th>Feature inside primary tumor</th>
<th>EGFR+ Mean ± std</th>
<th>KRAS+ Mean ± std</th>
<th>WT type Mean ± std</th>
<th>Different group</th>
</tr>
</thead>
<tbody>
<tr>
<td>GLCM_inclination-2</td>
<td>0.21±0.01</td>
<td>0.18±0.06</td>
<td>0.25±0.07</td>
<td>EGFR+ vs. both</td>
</tr>
<tr>
<td>GLDMkehlin150</td>
<td>0.57±0.13</td>
<td>0.43±0.14</td>
<td>0.64±0.13</td>
<td>EGFR+ vs. both</td>
</tr>
<tr>
<td>GLDM_kerniess150</td>
<td>3.3±2.07</td>
<td>1.0±0.17</td>
<td>5.4±2.27</td>
<td>EGFR+ vs. WT</td>
</tr>
<tr>
<td>GLDM_kerniess150</td>
<td>3.3±2.07</td>
<td>1.0±0.17</td>
<td>5.4±2.27</td>
<td>EGFR+ vs. WT</td>
</tr>
<tr>
<td>(fl_prime_0.mes.0.0.0)</td>
<td>0.55±0.25</td>
<td>0.78±0.34</td>
<td>0.95±0.59</td>
<td>EGFR+ vs. WT</td>
</tr>
</tbody>
</table>

Figure 1: This image shows the difference in intensity between a WT patient (upper, median: 890 HU) and an EGFR+ patient (lower, median 61 HU).

Conclusion: We showed that there are differences in radiomic CT features between EGFR+, KRAS+ and WT NSCLC. The next step will be to externally validate (work in progress) a robust radiomic signature, based on standard CT imaging. Also this allows to monitor radiomic signature evolution under treatment.

SP-0610
Gene expression alterations to carbon ion and X-irradiation
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Hadron therapy is an advanced technique in the field of radiotherapy that makes use of charged particles such as protons and carbon ions. The inverted depth-dose profile and the sharp dose fall-off after the Bragg peak offered by charged particle beams allow for a more precise localization of the radiation dosage to the tumor as compared to the conventional used photons. As a consequence, the surrounding healthy tissue receives a much lower dose. Besides this ballistic advantage, the use of high-linear energy transfer (LET) carbon ion beams offers also a biological advantage, i.e. a higher relative biological effectiveness (RBE) as compared to conventional low-LET photon therapy.

Carbon ion radiation is thus more effective in inducing DNA damage, cell cycle arrest and cell death, thereby accounting for highly lethal effects, even in tumors that are resistant to X-ray irradiation.

The response of an irradiated cell depends on the dose, dose-rate, radiation quality, the lapse between the radiation-induced stress and the analysis, and the cell type. In this context, genome-wide studies can contribute in exploring differences in signaling pathways and to unravel high-LET-specific genes. Several studies within SCK-CEN and outside have already compared changes in gene expression induced by different radiation qualities. Overall, the number of differentially expressed genes as well as the magnitude of (dose-dependent) gene expression changes was found to be more pronounced after irradiation with particle beams.

Currently, the Radiobiology Unit of SCK-CEN is deeply investigating the effect of low- and high-LET radiation on the gene expression of different cancer cell lines in vitro. Our results clearly demonstrate a dose-dependent downregulation in several genes involved in cell migration and motility after carbon ion irradiation. A higher number of genes as well as more pronounced changes in their expression levels were found after carbon ion irradiation compared to X-rays. Further research are currently investigating whether the observed molecular changes also influence the cellular ‘behavior’ after irradiation in terms of cell migration and motility after irradiation, since these are prominent characteristics of cancer progression and metastasis.

Assessing both the risks and advantages of high-LET irradiation can contribute to the study of the biological effect on the tumor and will lead to further acceptance and improvement of the clinical outcome of hadron therapy.

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SP-0611
Normal tissue response in particle therapy
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Particle therapy as cancer treatment, with either protons or heavier ions, provide a more favourable dose distribution compared to X-rays. While the physical characteristics of particle radiation have been the aim of intense research, less focus has been on the actual biological responses particle irradiation gives rise to. Protons and high LET radiation have a higher radiobiological effect (RBE), but RBE is a complex quantity, depending on both biological and physical parameters. One of the central questions in particle therapy is whether the tumor and the normal tissue has a differential RBE due to the difference in α/β ratio. Most of the data to enlighten this is in vitro data, and there is very limited in