**Supplementary Table 1:** SPIA results on Colo741-KRas2 microarray data using control vs. G12D mutation.
The fold-change ratios of the control vs. G12D sets were computed and used as an input to SPIA. Using 5% cut off of the FDR-adjusted \( p \)-values, SPIA was unable find any significant pathway in the KEGG database. The FDR values with the Colo741-KRas2 dataset are around 34-35%, which is not significant according to authors.

<table>
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<tr>
<th>Pathway Name</th>
<th>KEGG ID</th>
<th>FDR</th>
<th>Status</th>
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