

## **Spa-RQ: an Image Analysis Tool to Visualise and Quantify Spatial Phenotypes Applied to Non-Small Cell Lung Cancer**

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**Figure S1. Depiction of Spa-R\_optimizer configuration.** (a) Data list showing the default optimizer settings of Spa-R generated by multimodal image registration with MATLAB function `imregtform`. (b) Display of Spa-R\_optimizer's user-friendly interface, which enables adjustment on five optimizer parameters. (c) Image set comparing the registration quality at different PyramidLevels (L). Left: a pair of reference and target images (size>500MB). Right upper lane: the images registered at PyramidLevels 1-5 (L1-5). Right lower lane: zoom-in overlapped images to compare registration quality, with reference image at back (at 100% opacity) and registered image in front (at 70% opacity). Asterisks indicate low (\*), medium (\*\*) or high (\*\*\*) registration quality. Tissue sections of reference and target images are 12  $\mu\text{m}$  apart. (d-g) Bar charts showing the registration speed with different values of iterations (d), InitialRadius (e), Epsilon (f) or GrowthFactor (g) at PyramidLevels ranged L2-4. The registration quality is indicated by asterisks as in (c). Red outlines indicate default settings (in d, e-g). The same image set as used in (c) was used.

**Figure S2. Depiction of the spatial activation of MAPK and mTOR in GEMM PAC samples.** (a) Scatterplot showing areas (%) of p4EBP1, pAKT, pERK and pp38 in ASCs, PACs, or IACs. Data are presented as mean  $\pm$  standard deviation (SD) of average marker expression in all tumours per histotype found within one animal, individual dots represent individual GEMMs. (b) Bar plot showing the spatial expression of p4EBP1 and pERK in GEMM PACs. Individual tumours are plotted, grouped per animal. Dashed black line indicates a 15% OL level. (c) Pie chart illustrating the classification of murine PACs according to MAPK/mTOR and Null spatial phenotypes.

**Figure S3. Overview of MAPK, AKT, mTOR and p38 activation and depiction of the spatial activation of MAPK and p38 pathways in clinical samples.** (a) Schematic summary of p4EBP1, pAKT, pERK and pp38 visual analyses in human ASC and PAC samples. Red bar and grey bars indicate presence or absence of expression of the indicated markers,

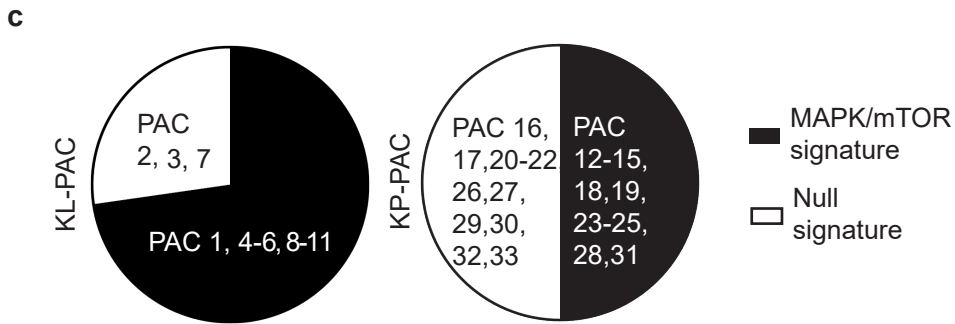
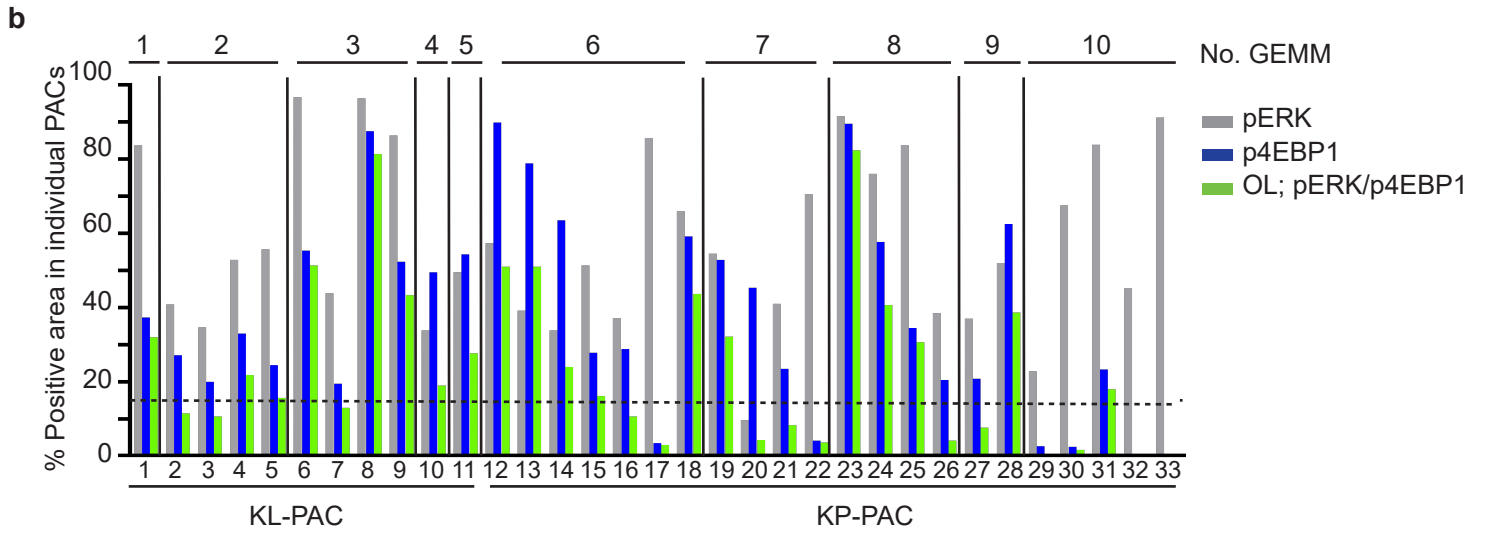
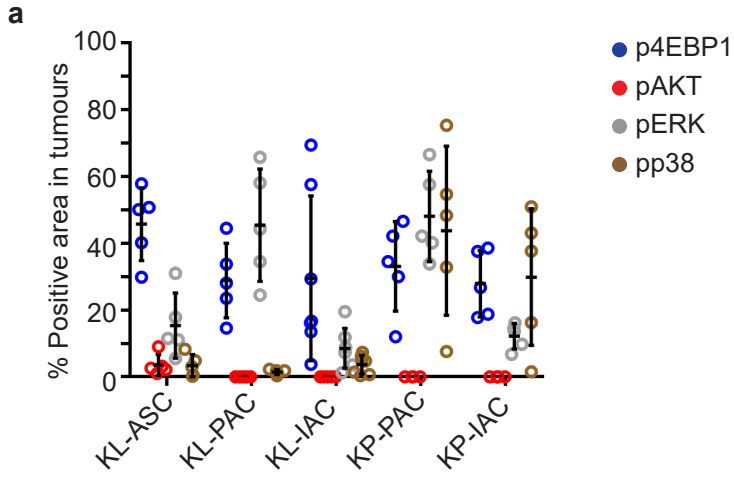
respectively. Replicate spots are marked by a dividing line in the bar. (b) Representative images illustrating p4EBP1, pAKT, pERK and pp38 expression in samples shown in (a). ‘++’ indicates strong staining; ‘+’ indicates weak staining; ‘-’ indicates absence of expression. (c) Left: scatterplot depicting the areas (%) of pp38, pERK, pAKT, as well as pp38/pERK and pp38/pAKT OL in 13 individual clinical ASCs. Right: images of pp38 and pERK staining in eight pp38<sup>positive</sup> clinical ASCs. (d) Left: scatterplot depicting the areas (%) of pp38, pERK, and pp38/pERK overlap in 25 individual clinical PACs. Right: images of pp38 and pERK staining in 10 pp38<sup>positive</sup> clinical PACs. Scale bar, 500  $\mu$ m.

**Figure S4. Overview of *KRAS* mutation status of clinical samples and their distribution in the spatial signature classes.** (a) Bar plot showing that 3 *KRAS* mutant and 2 *KRAS* wildtype ASC samples (5 of 13 ASCs in total) located to both MAPK/mTOR and Null signature classes. (b) Bar plot showing that within PACs of known *KRAS* status (15 out of 25), *KRAS* mutant samples (5 of 15) have a Null signature.





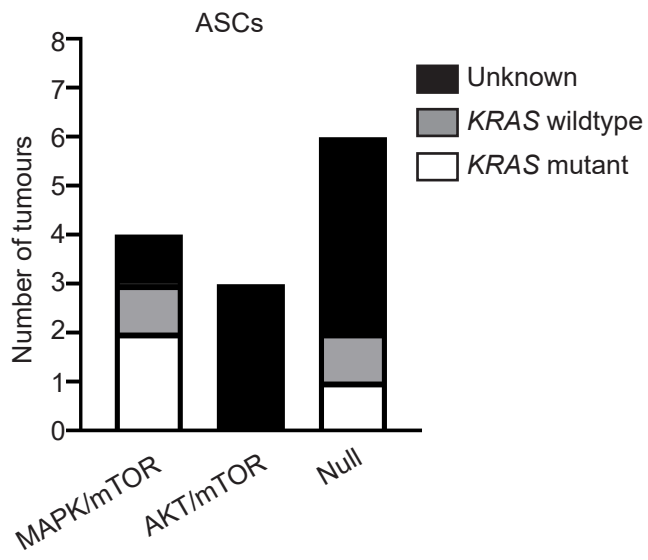
**FIGURE S2**





**FIGURE S4**

**a**



**b**

