

➤ SubQperior mouse tumor models

Imagine syngeneic models with almost no tumor ulceration, nearly 100% take rate, and homogeneous tumor growth.

We have developed our tumor models with an implantation method overcoming all common problems researchers experience with subcutaneous tumor models. The solution is simple: change the injection site from subcutaneous to mammary fat pad and experience an impressive difference: get beautiful growth curves and with the ease of calipering tumor size. SubQperior = superior to subcutaneous.

➤ Tumor cell line Hepa1-6

Origin: liver / mouse C57BL/6
Description: hepatoma

➤ Study example

Comparison of HEPA1-6 tumor growth characteristic after subcutaneous vs. subQperior implantation shows growth of subQperior tumors whereas subcutaneous implantation of HEPA1-6 cells does not result in growth.

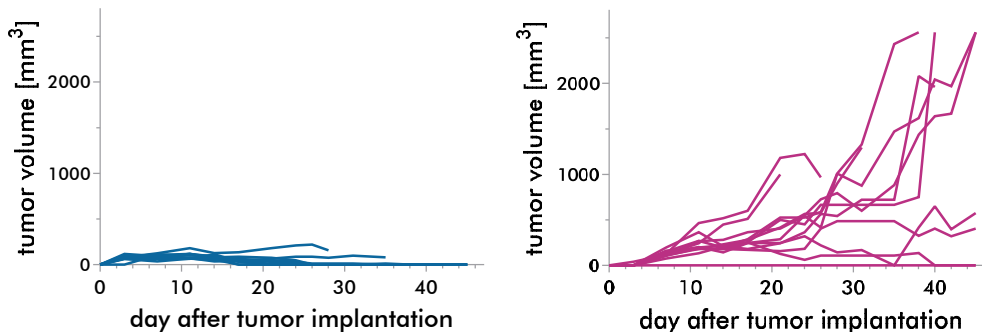


Figure 1: C57BL/6 mice were implanted subcutaneously (left) and into the mammary fat pad (subQperior; right) with Hepa1-6 cells. Data are displayed as single growth curves.

➤ Quality assurance

- Routine authentication of tumor cell lines by STR profiling
- Mycoplasma testing of tumor cells by PCR just prior to implantation
- Routine health monitoring of sentinel animals (according to FELASA guide lines)
- Animal work according to the 5R rules (reduce, refine, replace, responsible, remember)

Note: Graphs depicted are derived from study examples. Each study is a biological system of its own and subject to intrinsic variation.

➤ please turn over <

➤ Study example – Immune Checkpoint Inhibitors

Mice bearing HEPA1-6 cells implanted in the mammary fat pad were treated with anti-mPD-1. Treatment started after randomization when tumor volumes had reached a size of approximately 68 mm³.

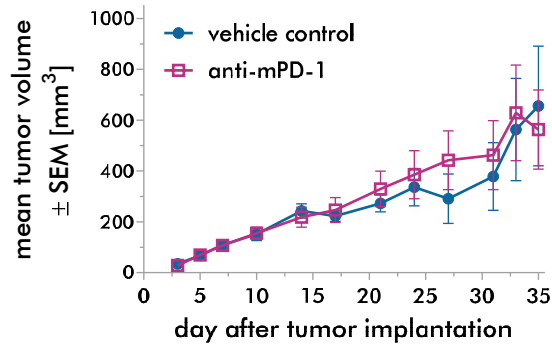


Figure 2: HEPA1-6 tumors were treated with anti-mPD-1. Tumor growth was monitored by calipering.

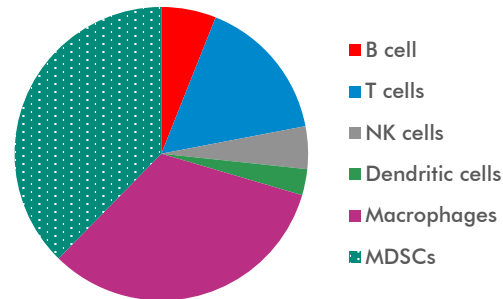


Figure 3: Flow cytometry analysis of HEPA1-6 primary tumor tissue showing the relative distribution of the major immune cell populations.

➤ Immune cell populations infiltrating HEPA 1-6 tumors

At tumor model endpoint, primary tumor tissues were appropriately processed and analyzed by flow cytometry for determination of T cell, B cell, macrophage, NK cell, dendritic cell and myeloid cell populations.

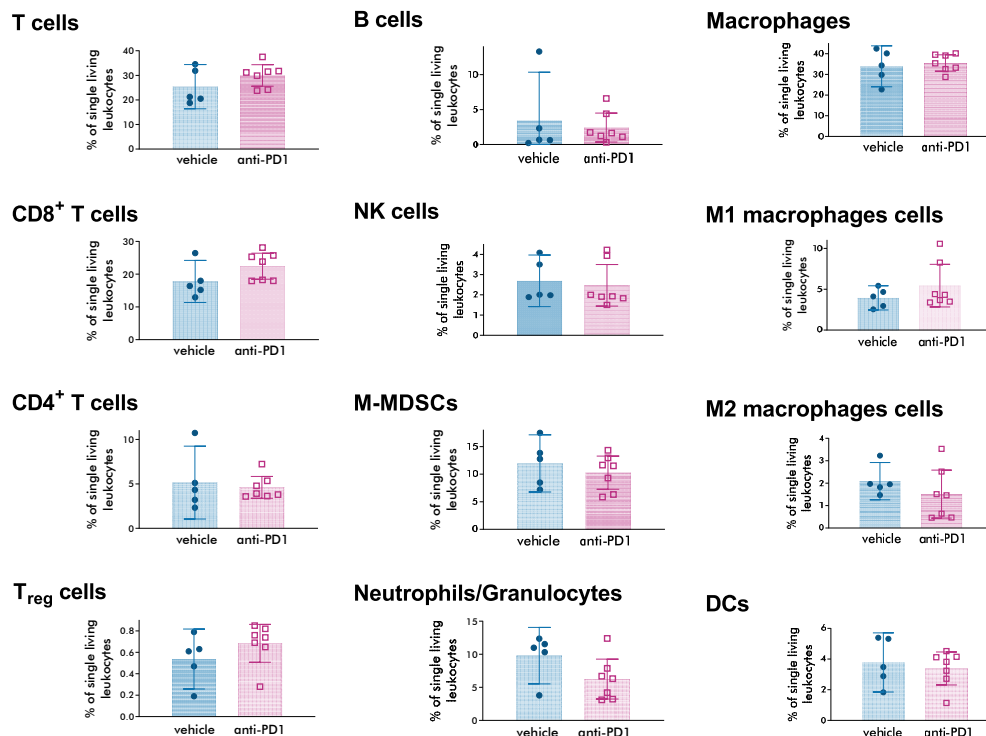


Figure 4: Flow cytometry analysis of Hepa1-6 primary tumor tissue is depicted as percentage of living immune cell tumor infiltrate. For each immune population, data are displayed as mean bar together with their corresponding + 95% CI.