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| **Manuskript 1 (Research Article):**  Martin Kuric (MK), Susanne Beck, Doris Schneider, Wyonna Rindt, Marietheres Evers, Jutta Meißner-Weigl, Sabine Zeck, Melanie Krug, Marietta Herrmann, Tanja Nicole Hartmann, Ellen Leich, Maximilian Rudert, Denitsa Docheva, Anja Seckinger, Dirk Hose, Franziska Jundt, Regina Ebert1 (2023): Keep it Together: Describing Myeloma Dissemination *in vitro* with hMSC-Interacting Subpopulations and their Aggregation/Detachment Dynamics, **Cancer Research Communications (submitted, under peer review)** | | | | | |
| **Participated in** | **Author Initials,** Responsibility decreasing from left to right | | | | |
| Study Design | Martin Kuric | Regina Ebert | Wyonna Rindt |  |  |
| Methods Development | Martin Kuric | Doris Schneider |  |  |  |
| Data Collection | Martin Kuric | Doris Schneider |  |  |  |
| Data Analysis and Interpretation | Martin Kuric | Susanne Beck | Regina Ebert |  |  |
| Manuscript Writing  Writing of Introduction  Writing of Materials & Methods  Writing of Discussion  Writing of First Draft | Martin Kuric | Regina Ebert |  |  |  |

**Explanations**: The content of this publication significantly exceeds the usual scope (~29 pages Supplemental). It includes not only research findings but also survival data and protocols of new, established methods and their validations. The contribution of Martin Kuric was pivotal and predominant in all aspects of this work. Doris Schneider assisted in the experimental procedures. Susanne Beck analyzed the raw data from RNAseq and survival data, which were interpreted, depicted, and summarized by Martin Kuric.

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| **Manuscript 2 (Data Analysis Software)**:Martin Kuric, Regina Ebert (2023): plotastic: Bridging Plotting and Statistics in Python, **Journal of Open Source Software (submitted)** | | | | | |
| **Participated in** | **Author Initials,** Responsibility decreasing from left to right | | | | |
| Idea, Architectural Design | Martin Kuric |  |  |  |  |
| Software Development  Feature Implementation  Unit-testing | Martin Kuric |  |  |  |  |
| Distribution of Software Writing of Documentation Packaging Upload on PyPi | Martin Kuric |  |  |  |  |
| Manuscript Writing  Writing of Statement of Need  Writing of Example  Writing of Overview | Martin Kuric | Regina Ebert |  |  |  |

**Explanations:** The software was entirely created by MK, comprising more than 8000 lines in total (including ~2000 unit-testable lines) and is comparable in size to a typical web application. The release involves submission to the peer-reviewed journal (JOSS), version control using GitHub, and compilation and deployment on PyPi.

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| **Manuscript 3 (Research Letter)**:Daniela Simone Maichl, Julius Arthur Kirner, Susanne Beck, Wen-Hui Cheng, Melanie Krug, Martin Kuric, Carsten Patrick Ade, Thorsten Bischler, Franz Jakob, Dirk Hose, Anja Seckinger, Regina Ebert & Franziska Jundt (2023): Identification of NOTCH-driven matrisome-associated genes as prognostic indicators of multiple myeloma patient survival, **Blood Cancer Journal 13:134 (published)** | | | | | |
| **Participated in** | **Author Initials,** Responsibility decreasing from left to right | | | | |
| Study Design  Methods Development | Daniela Simone |  |  |  |  |
| Data Collection | Daniela Simone |  |  |  |  |
| Data Analysis and Interpretation | Daniela Simone | Susanne Beck |  | Martin Kuric |  |
| Manuscript Writing  Writing of Introduction  Writing of Materials & Methods  Writing of Discussion  Writing of First Draft | Daniela Simone |  |  | Martin Kuric |  |

**Explanations:** Martin Kuric was provided with processed but complex-to-visualize data. He plotted multidimensional diagrams using python and fine-adjusted them using professional design software (Affinity Publisher, Serif Ltd).

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The doctoral researcher and the primary supervisor confirm the correctness of the above mentioned assessment.

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Doctoral Researcher’s Name Date Place Signature

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Primary Supervisor’s Name Date Place Signature