Data files of work described in the manuscript:

Increased cell size, structural complexity and migration of cancer cells acquiring fibroblast organelles by cell-projection pumping

Hans Zoellner[1,2*], Belal Chami[1], Elizabeth Kelly[1], Malcolm A.S. Moore[2]

[1] The Cellular and Molecular Pathology Research Unit, Oral Pathology and Oral Medicine, School of Dentistry, Faculty of Medicine and Health, The University of Sydney, Westmead Hospital, Westmead, NSW 2145, Australia
[2] Cell Biology, The Memorial Sloan Kettering Cancer Center, 430 E 67th St, RRL 717, New York, NY

Explanatory Notes on Data Files Provided

At the time these files were uploaded to the University of Sydney Research Repository 27th of October, 2019), this work was in-press in the open-access on-line journal PLoS One.

A pre-print of the manuscript was also available at: bioRxiv
doi: http://biorxiv.org/cgi/content/short/770693v1

FACS, proliferation and migration data are provided in two separate MS Excel files titled:

- Migration Data: which contains calculations for distance migrated in scratch assays
- FACS Proliferation and Scatterplots: which contains data for FACS forward and side scatter analysis, as well as proliferation assays and scatterplots for all data

For purposes of clarity, the manuscript describes experiments numbered 1 to 9 with SAOS-2, and these differ from the experimental code numbers appearing in files, ranging from Exp 32 to Exp 50. In addition, single experiments with H3122 and A672, represent experiments originally coded Exp 35 and Exp 36 respectively.

Experimental Coding for Cell Populations Studied

Experimental coding for sub-populations of cells separated by FACS, as well as for control populations were as follows:
F: Control Fibroblasts
TC: Control Tumour Cells
FS: Tumour cells spiked with fibroblasts at levels found by post-sort analysis to contaminate tumour cell populations isolated by FACS sorting from co-cultures
MF: Fibroblasts isolated by FACS sorting after co-culture with tumour cells
MH: Tumour cells isolated by FACS sorting after co-culture with fibroblasts and with high levels of fibroblast labelling
MM: Tumour cells isolated by FACS sorting after co-culture with fibroblasts and with moderate levels of fibroblast labelling
ML: Tumour cells isolated by FACS sorting after co-culture with fibroblasts and with low levels of fibroblast labelling

Please note, that in experiments 40, 41, 46, 47, and 50 with SAOS-2, tumour cells were sorted into three (ML, MM, MH) as opposed to only two (ML, MH) sub-populations. In these experiments, MM populations often migrated more quickly compared with MH cells. We have determined that this is due to the confounding effect of cell division halving acquired

fluorescence. We have confirmed this effect in current and ongoing single cell tracking studies. In these cases, we have compared ML with MM cells for purposes of clarity.