

Figure S6: Phenotypic and genomic characteristics of two morphologically distinct Shef-*LMS* 01 cultures **A and B**: Photomicrographs of haematoxylin & eosin-stained sections of the parent tumour, a <u>primary leiomyosarcoma</u> taken at low- (x100) and high- (x400) magnification, respectively. Scale bars = 1mm.

Cultures were established in washes of initially non-adherent cells taken off original tissue setups in a slope and flask designated w_s and w_1 variants respectively. **C and D:** Phase contrast micrographs of the w_s and w_1 variant cells at passage 69 and 56, respectively. Scale Bars = 100 μ m **E:** Growth curve and doubling time of w_1 and w_2 variant tumour cells at passage 63 and 54 respectively as evaluated by MTT proliferation assay. Doubling Times = 44.62 and 27.44 hours respectively **F:** Genomic Copy number profile of w_s variant cells at passage 27 compared with the parent tumour from which the culture was

F: Genomic Copy number profile of w_s variant cells at passage 27 compared with the parent tumour from which the culture was derived. The overlaid red and blue lines represent the moving average of log₂ ratios of the cultured cells and parent tumour tissue, respectively. Deviations above and below the horizontal baseline represent amplifications and deletions, respectively. Relative amplitude of deviation shows the log₂ ratio and represents DNA copy number at the corresponding genomic locus.

Copy number analysis was performed on the Agilent® 4 x 180K DNA microarray platform and data analysed using Agilent® Genomic Workbench Software v6.0. Growth Curve fitting and doubling time calculation were done using GraphPad® Prism Software (v6.0) based on experiments done in quadruplicate.