Description of Additional Supplementary Files

Supplementary Data 1: Basic clinical and pathological characteristics of all patients and samples used in the study. % WD and % DD represent the proportion of the WD and DD components within DDLPS tumors after pathological analysis of the whole surgical specimen. Abbreviations: F: female. M: male; RP: retroperitoneum.

Supplementary Data 2: Patients and samples used for single-cell RNA-seq (scRNA-seq), bulk RNA-seq, immunohistochemistry (IHC), in situ multiplex immunofluorescence (IF), and shallow whole genome sequencing (WGS). A black box indicates that the sample was successfully processed and included in the analysis.

Supplementary Data 3: List of the twenty top marker genes of each cellular population. Statistical test: two-sided Wilcoxon rank sum test. Abbreviations: Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons. RBC: red blood cell.

Supplementary Data 4: Proportion of cell populations according to clinical and pathological covariates (two-sided moderated t test on logit transformed cell type proportions, left panel (A), and after global FDR correction for multiple testing, right panel (B)).

Supplementary Data 5: List of the twenty top marker genes in each myeloid cell cluster. Statistical test: two-sided Wilcoxon rank sum test with Bonferroni correction. Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 6: Number and proportion of the different myeloid cell populations detected in the series of 7 paired WD and DD samples analyzed by multiplex immunofluorescence. The proportions were calculated by normalization on the total number of cells detected and compared using Chi2 test.

Supplementary Data 7: List of the twenty top marker genes in each lymphoid cell cluster. Statistical test: two-sided Wilcoxon rank sum test with Bonferroni correction. Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 8: Number and proportion of the different lymphoid cell populations detected in the series of 7 paired WD and DD samples analyzed by in situ multiplex immunofluorescence. The proportions were calculated by normalization on the total number of cells, the total number of lymphocytes (CD4+ and CD8+ cells), the total number of CD4+ T cells or the total number of CD8+ T cells detected and compared using Chi2 test.

Supplementary Data 9: List of the 20 top marker genes in each tumor cell cluster (DDLPS-WD and DDLPS-DD samples only). Statistical test: two-sided Wilcoxon rank sum test with Bonferroni correction. Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 10: List of the genes specifically up-regulated in DDLPS-WD or DDLPS-DD samples used for Toppfun analysis. Statistical test: two-sided Wilcoxon rank sum test with Bonferroni correction. Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 11: List of the 25 most relevant pathways specifically up-regulated in DDLPS-WD o r DDLPS-DD samples. Toppfun analysis using the probability density function and FDR correction for multiple testing. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 12: Expression matrix of the 800 most variant genes identified by unsupervised clustering on bulk RNA-seq analysis of the larger cohort of adipocytic samples.

Supplementary Data 13: List of the 20 top marker genes in each tumor cell cluster (DDLPS-WD only). Statistical test: two-sided Wilcoxon rank sum test with Bonferroni correction. Pos: positive. Avg: average. p-val_adj: p-value with Bonferroni correction for multiple comparisons.

Supplementary Data 14: Number and proportion of tumor adipocyte stem cells expressing MDM2 together with other the stem cell markers CD55, CD44, CD34, and ALDH1 in the series of 7 WD DDLPS samples analyzed by multiplex immunofluorescence. The proportions were calculated by normalization on the total number of cells detected or on the number of MDM2+ cells.

Supplementary Data 15: List of the main copy number variations (CNV) identified in each sample by shallow Whole Genome Sequencing in the 296 chromosomal regions. The Log2 ratio of copy number is indicated for each CNV detected. Chr: chromosome; Mb: size of the chromosomal region in megabase; start and end indicate the genomic positions of the chromosomal region.

Supplementary Data 16: List of single nucleotide variations (SNV) identified in each sample by targeted DNA Sequencing. VAF: variant allele frequency.

Supplementary Data 17: Number and proportion of the different TGFB1-positive cell populations detected in the series of 7 paired WD and DD samples analyzed by multiplex immunofluorescence in situ. The proportions were calculated by normalization on the total number of cells or on the number of MDM2+ cells (tumor cells), CD3+ cells (T lymphocytes) and CD14+ cells (monocytes/macrophages) detected and compared using Chi2 test.