Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: The top 20 differentially expressed genes of the osteoblastic OS subclusters. The

"pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes

among all cells in the subjected subcluster and the other subclusters beyond, respectively.

The "avg_logFC" refers to the log fold-change of the average gene expression levels between

the subjected cell subcluster and the other subclusters, while the "p_val" refers to the

Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding

Bonferroni-corrected "p_value".

File name: Supplementary Data 2

Description: The top 20 differentially expressed genes of the chondroblastic OS subclusters.

The "pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated

genes among all cells in the subjected subcluster and the other subclusters beyond,

respectively. The "avg_logFC" refers to the log fold-change of the average gene expression

levels between the subjected cell subcluster and the other subclusters, while the "p_val"

refers to the Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the

corresponding Bonferroni-corrected "p_value".

File name: Supplementary Data 3

Description: The top 20 differentially expressed genes of the osteoclast subclusters. The

"pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes

among all cells in the subjected subcluster and the other subclusters beyond, respectively.

The "avg_logFC" refers to the log fold-change of the average gene expression levels between

the subjected cell subcluster and the other subclusters, while the "p_val" refers to the

Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding

Bonferroni-corrected "p_value".

File name: Supplementary Data 4

Description: The top 20 differentially expressed genes of the MSC subclusters. The "pct.1"

and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes among all

cells in the subjected subcluster and the other subclusters beyond, respectively. The

"avg_logFC" refers to the log fold-change of the average gene expression levels between the

subjected cell subcluster and the other subclusters, while the "p_val" refers to the Wilcoxon

Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding Bonferroni-

corrected "p_value".

File name: Supplementary Data 5

Description: The top 20 differentially expressed genes of the fibroblast subclusters. The

"pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes

among all cells in the subjected subcluster and the other subclusters beyond, respectively.

The "avg_logFC" refers to the log fold-change of the average gene expression levels between

the subjected cell subcluster and the other subclusters, while the "p_val" refers to the

Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding

Bonferroni-corrected "p_value".

File name: Supplementary Data 6

Description: The top 20 differentially expressed genes of the myeloid cell subclusters. The

"pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes

among all cells in the subjected subcluster and the other subclusters beyond, respectively.

The "avg_logFC" refers to the log fold-change of the average gene expression levels between the subjected cell subcluster and the other subclusters, while the "p_val" refers to the Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding Bonferroni-corrected "p_value".

File name: Supplementary Data 7

Description: The top 20 differentially expressed genes of the T&NK subclusters. The "pct.1" and "pct.2" refer to the percent of cells (%) that are positive for the indicated genes among all cells in the subjected subcluster and the other subclusters beyond, respectively. The "avg_logFC" refers to the log fold-change of the average gene expression levels between the subjected cell subcluster and the other subclusters, while the "p val" refers to the Wilcoxon Rank Sum test results (two-sided test) and "p_val_adj" is the corresponding Bonferronicorrected "p_value".