Supplemental figure legends

Figure S1. Publication per year with fitted exponential curve.

Figure S2. Single-cell RNA-Seq publication per year.

Figure S3. Publications per disease II. Number of identified primary research publications per rheumatic disease using different HTS assays labeled as "Other" in Figure 3.

Figure S4. Publications per journal. Number of identified primary research publications per journal using different HTS assays in rheumatic disease. Assay abbreviations as in Figure 3.

Figure S5. Samples per SRA project. Each point represents a SRA project depositing HTS data from a certain number of samples. On the upper side, the total number of projects for each disease is depicted. The median number of samples across all projects within a disease is depicted inside the boxplot. Disease abbreviations as in Figure 4.

Figure S6. Species information for HTS data on SRA. Disease abbreviations as in Figure 4.

Figure S7. Phenotypic information for HTS data on SRA. Disease abbreviations as in Figure 4.

Figure S8. Information about raw sequencing data availability in publication.

Figure S9. Sequencing platform information for HTS data on SRA. Disease abbreviations as in Figure 4.

Figure S10. Read layout information for HTS data on SRA. Disease abbreviations as in Figure 4.

Figure S11. Tissue source of HTS data on SRA II. Distribution of tissues subject to sequencing in publicly available datasets on SRA labeled as "Other" in Figure 5. Disease abbreviations as in Figure 5.

Figure S12. Availability of patient characterization for SLE RNA-Seq data.