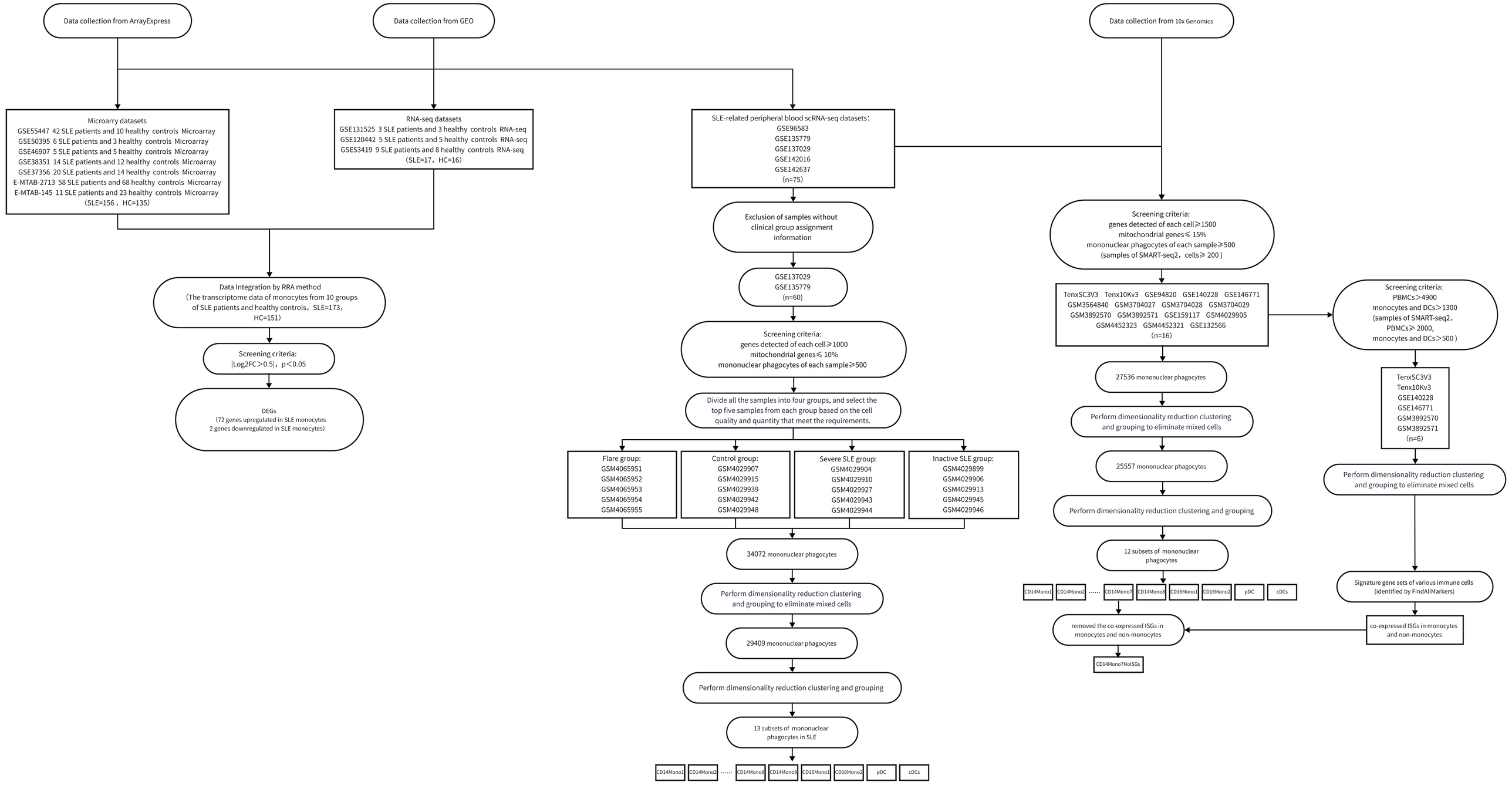
Data collection from ArrayExpress
Data collection from GEO
Data collection from 10x Genomics
Microarry datasets
GSE55447 42 SLE patients and 10 healthy controls Microarray
GSE50395 6 SLE patients and 3 healthy controls Microarray
GSE46907 5 SLE patients and 5 healthy controls Microarray
GSE38351 14 SLE patients and 12 healthy controls Microarray
GSE37356 20 SLE patients and 14 healthy controls Microarray
E-MTAB-2713 58 SLE patients and 68 healthy controls Microarray
E-MTAB-145 11 SLE patients and 23 healthy controls Microarray
(SLE=156 , HC=135)
RNA-seq datasets
GSE131525 3 SLE patients and 3 healthy controls RNA-seq
GSE120442 5 SLE patients and 5 healthy controls RNA-seq
GSE53419 9 SLE patients and 8 healthy controls RNA-seq
(SLE=17，HC=16)
SLE-related peripheral blood scRNA-seq datasets:
GSE96583
GSE135779
GSE137029
GSE142016
GSE142637
(n=75)
Data Integration by RRA method
(The transcriptome data of monocytes from 10 groups
of SLE patients and healthy controls，SLE=173，
HC=151)
Screening criteria:
|Log2FC＞0.5|，p＜0.05
DEGs
(72 genes upregulated in SLE monocytes
2 genes downregulated in SLE monocytes)
Exclusion of samples without
clinical group assignment
information
GSE137029
GSE135779
(n=60)
Screening criteria:
genes detected of each cell⩾1000
mitochondrial genes⩽ 10%
mononuclear phagocytes of each sample⩾500
Divide all the samples into four groups, and select the
top five samples from each group based on the cell
quality and quantity that meet the requirements.
Flare group:
GSM4065951
GSM4065952
GSM4065953
GSM4065954
GSM4065955
Control group:
GSM4029907
GSM4029915
GSM4029939
GSM4029942
GSM4029948
Severe SLE group:
GSM4029904
GSM4029910
GSM4029927
GSM4029943
GSM4029944
Inactive SLE group:
GSM4029899
GSM4029906
GSM4029913
GSM4029945
GSM4029946
34072 mononuclear phagocytes
Perform dimensionality reduction clustering
and grouping to eliminate mixed cells
29409 mononuclear phagocytes
Perform dimensionality reduction clustering and grouping
13 subsets of mononuclear
phagocytes in SLE
CD14Mono1
CD14Mono2
.....
CD14Mono8
CD14Mono9
CD16Mono1
CD16Mono2
pDC
cDCs
Screening criteria:
genes detected of each cell⩾1500
mitochondrial genes⩽ 15%
mononuclear phagocytes of each sample⩾500
(samples of SMART-seq2，cells⩾ 200)
TenxSC3V3 Tenx10Kv3 GSE94820 GSE140228 GSE146771
GSM3564840 GSM3704027 GSM3704028 GSM3704029
GSM3892570 GSM3892571 GSE159117 GSM4029905
GSM4452323 GSM4452321 GSE132566
(n=16)
27536 mononuclear phagocytes
Perform dimensionality reduction clustering
and grouping to eliminate mixed cells
25557 mononuclear phagocytes
Perform dimensionality reduction clustering and grouping
12 subsets of mononuclear
phagocytes
CD14Mono1
CD14Mono2
.....
CD14Mono7
CD14Mono8
CD16Mono1
CD16Mono2
pDC
cDCs
removed the co-expressed ISGs in
monocytes and non-monocytes
CD14Mono7NoISGs
Screening criteria:
PBMCs＞4900
monocytes and DCs＞1300
(samples of SMART-seq2，
PBMCs⩾ 2000,
monocytes and DCs＞500)
TenxSC3V3
Tenx10Kv3
GSE140228
GSE146771
GSM3892570
GSM3892571
(n=6)
Perform dimensionality reduction clustering
and grouping to eliminate mixed cells
Signature gene sets of various immune cells
(identified by FindAllMarkers)
co-expressed ISGs in monocytes
and non-monocytes