Supplementary Figure 1: Large view of liver and heart section images (Figure 1A, B).

Supplementary Figure 2: Large view of lung and kidney section images (Figure 1C, D).

Supplementary Figure 3: Large view of spleen and brain section images (Figure 1E, F).

Supplementary Figure 4: Volcano plots for multiple organs in the four liver injury models. Number of significantly upregulated and downregulated genes was indicated on the top of the volcano plots.

Supplementary Figure 5: Gene Ontology analysis for liver transcriptome in the four liver injury models.

Supplementary Figure 6: Pathway enrichment for genes changed in multiple organs after acute liver injury. According to the P-value, top 5 pathways were showed.

Supplementary Figure 7: Venn plots for up- and down-regulated genes in different models of the same organ. Genes co-upregulated in three models were indicated.

Supplementary Figure 8: PLS-DA score plots for serum metabolome of the 4 acute liver injury models.

Supplementary Figure 9: PCA plots. (A) PCA plots for pulmonary transcriptome in BDL model. (B-C) PCA plots for renal transcriptome in BDL and LR models. (D-E) PCA plots for brain transcriptome in BDL and LR models.
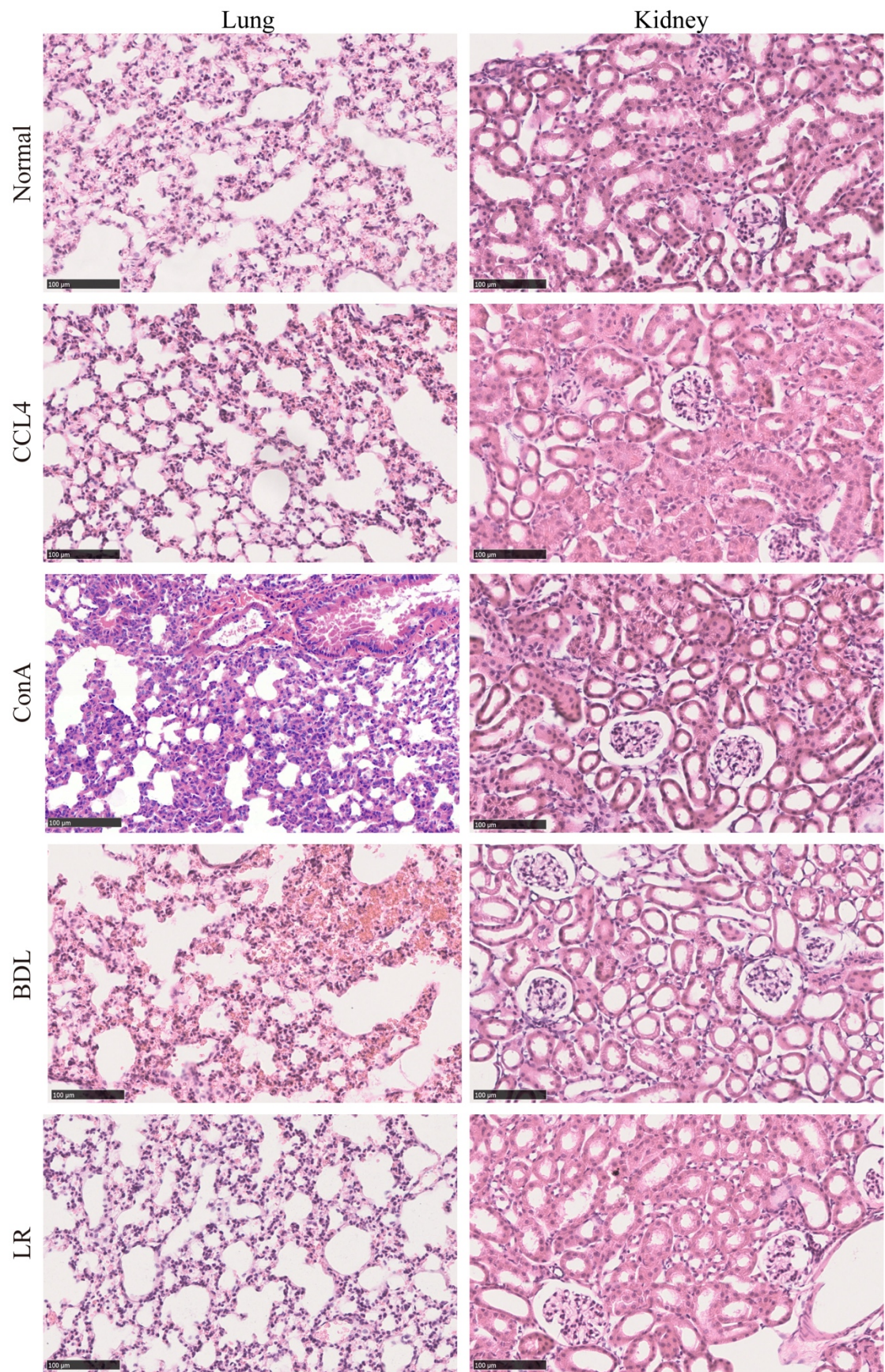
Supplementary Figure 10: Protein-protein interaction for genes co-changed in the renal transcriptome of BDL and LR models.

Supplementary table 1: Document of primer sequence.
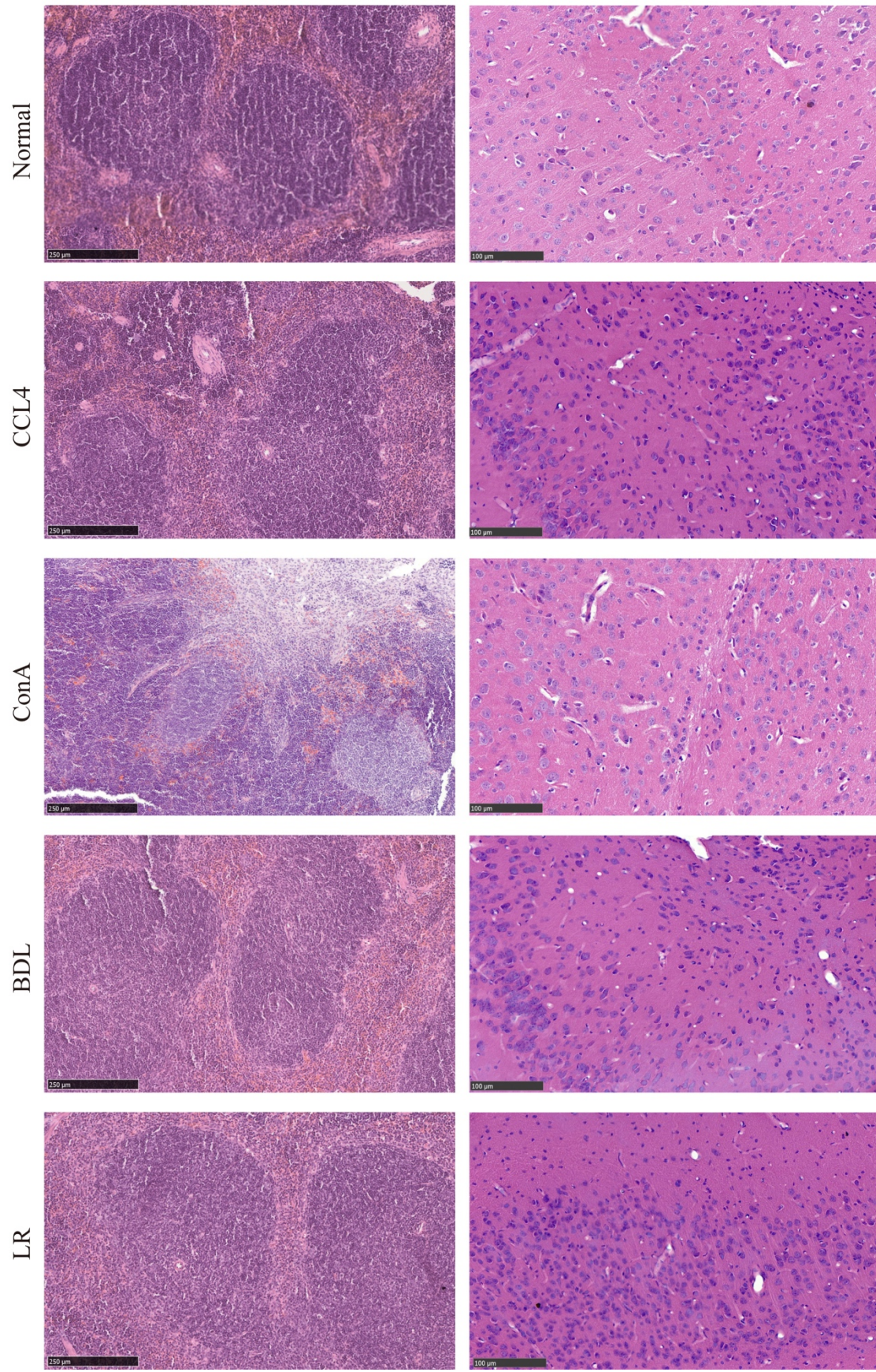
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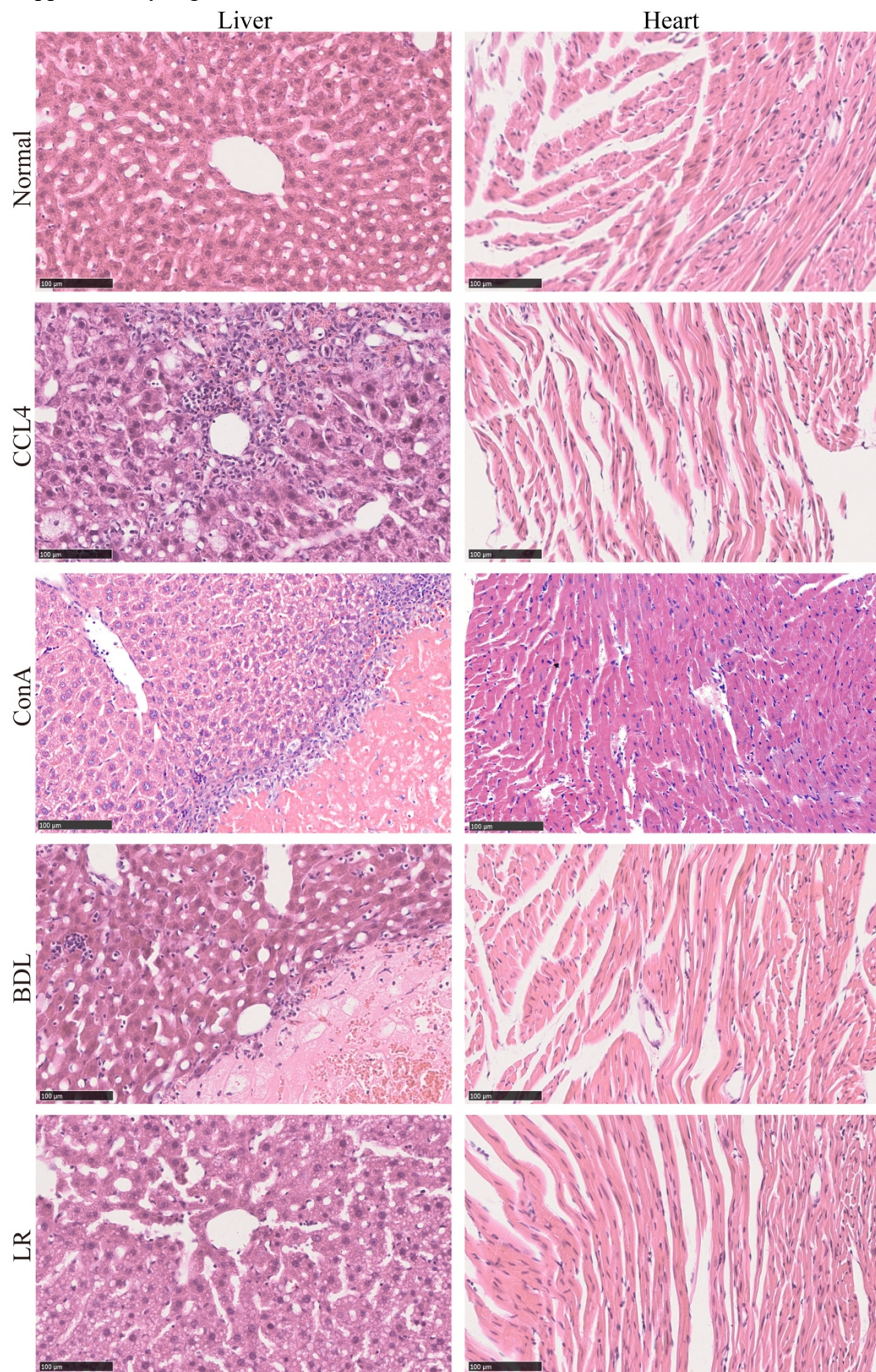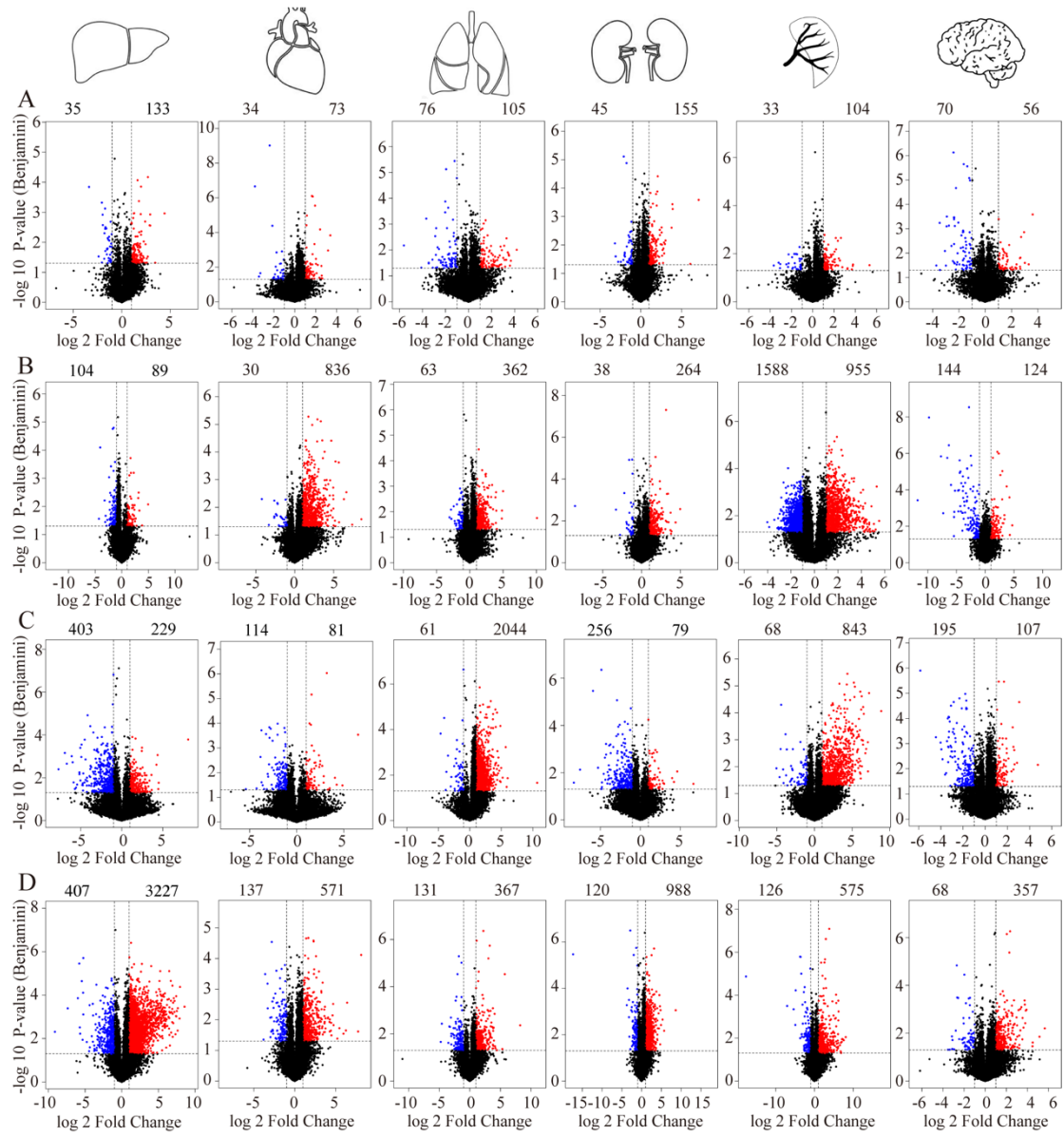
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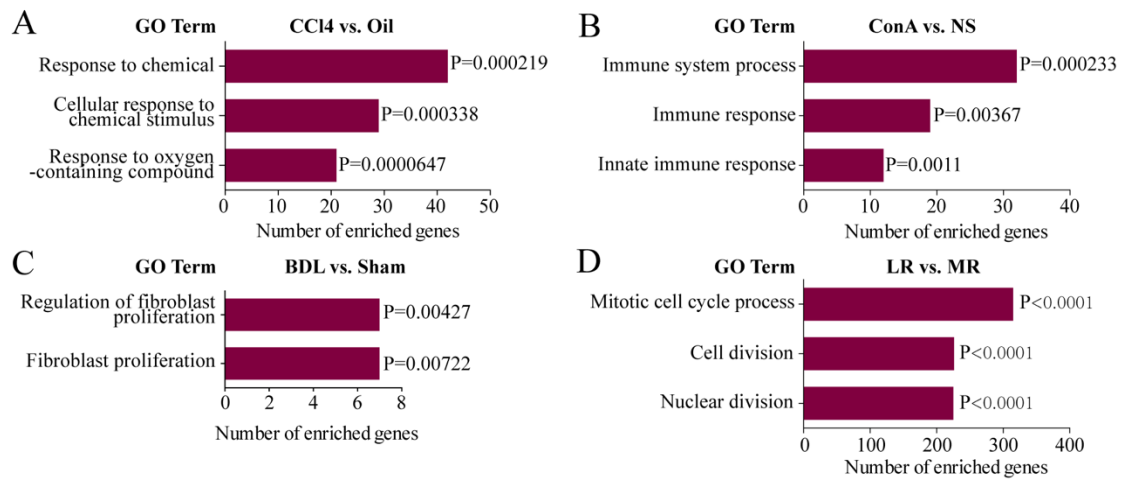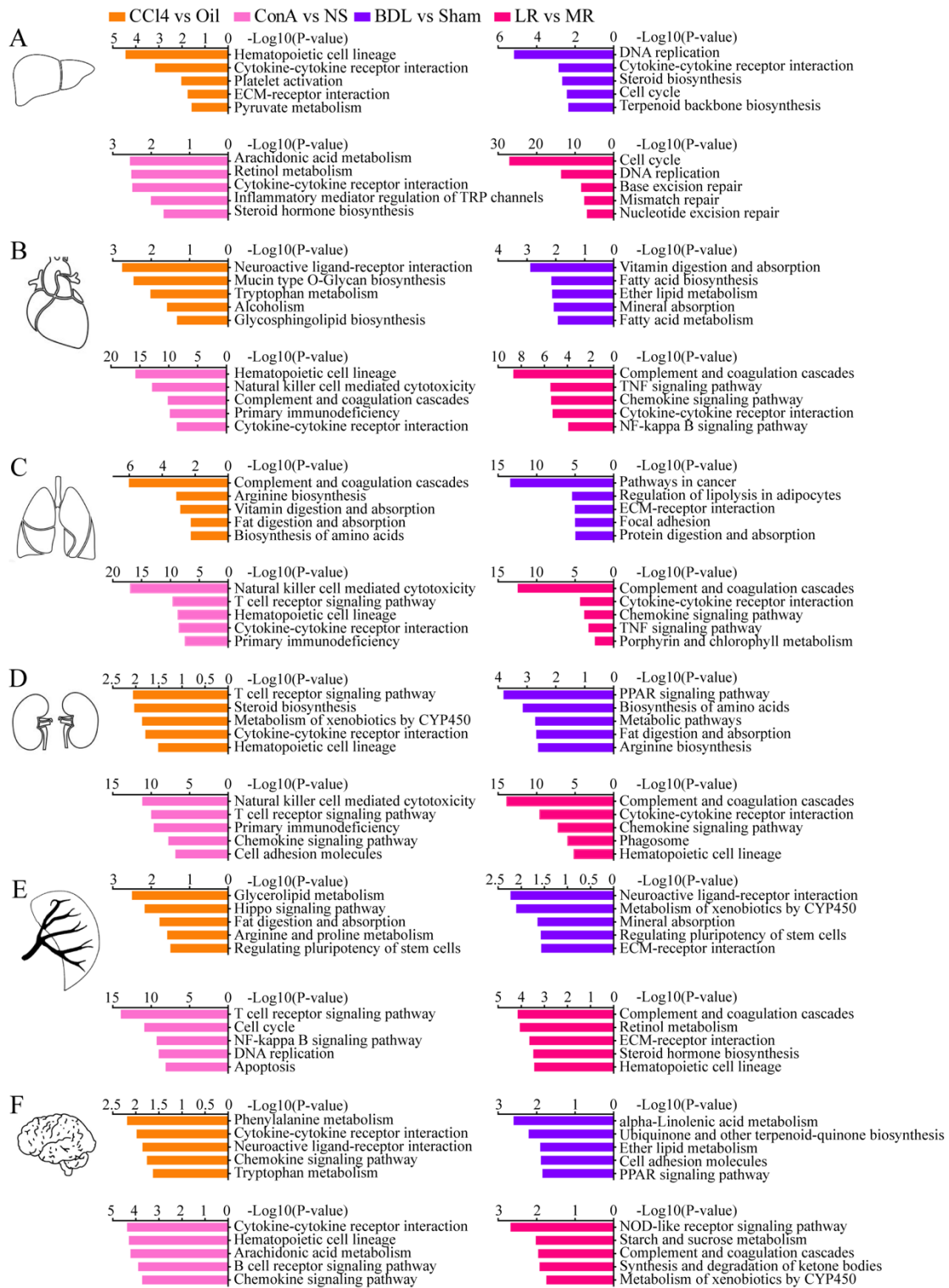
Supplementary Figure 3

Spleen   Brain

Normal

CCL4

ConA

BDL

LR

Supplementary Figure 4

Supplementary Figure 5

A   **GO Term**   **CCl4 vs. Oil**

Response to chemical — P=0.000219

Cellular response to chemical stimulus — P=0.000338

Response to oxygen -containing compound — P=0.0000647

0   10   20   30   40   50
Number of enriched genes

B   **GO Term**   **ConA vs. NS**

Immune system process — P=0.000233

Immune response — P=0.00367

Innate immune response — P=0.0011

0   10   20   30   40
Number of enriched genes

C   **GO Term**   **BDL vs. Sham**

Regulation of fibroblast proliferation — P=0.00427

Fibroblast proliferation — P=0.00722

0   2   4   6   8
Number of enriched genes

D   **GO Term**   **LR vs. MR**

Mitotic cell cycle process — P<0.0001

Cell division — P<0.0001

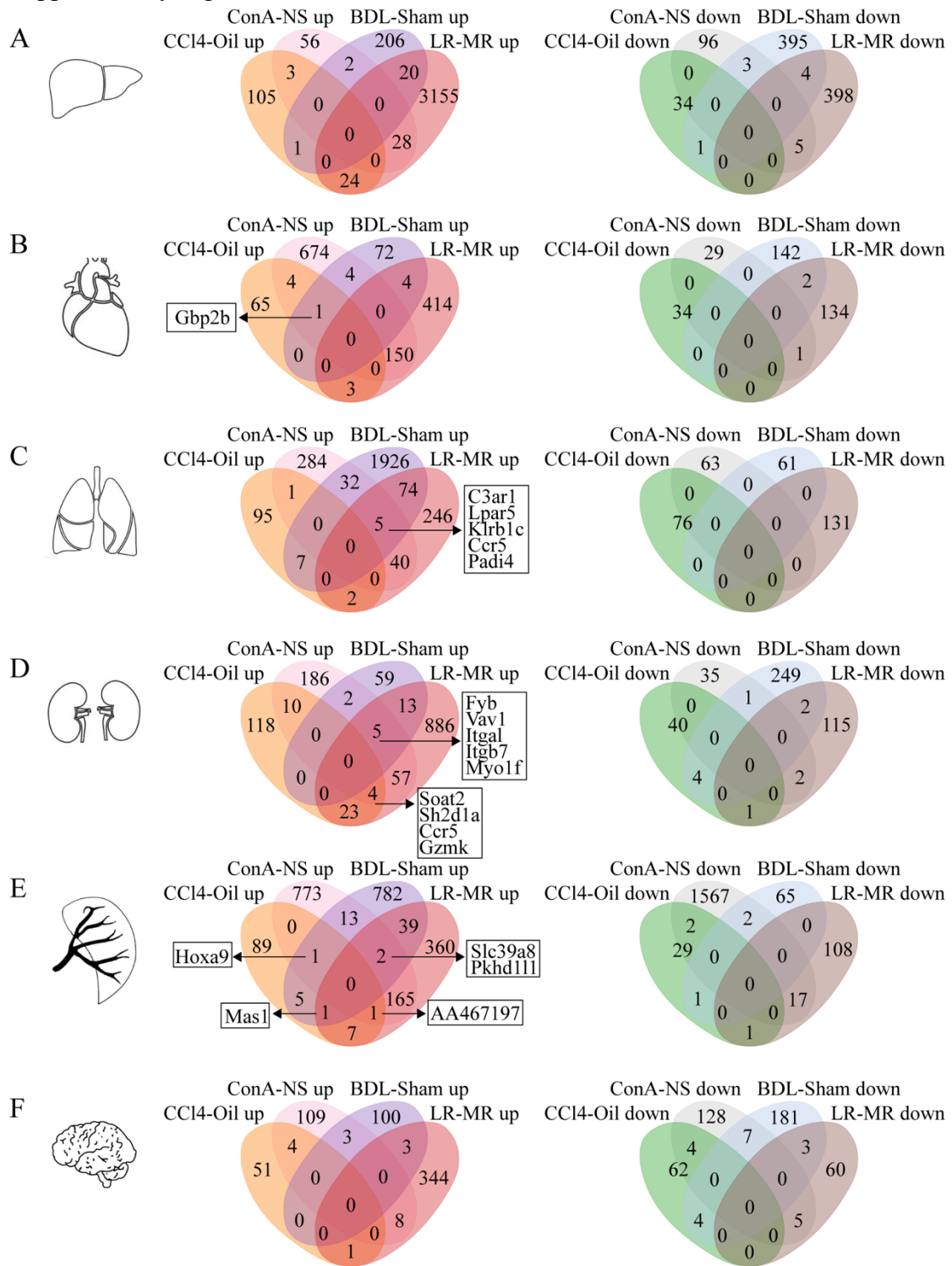Nuclear division — P<0.0001

0   100   200   300   400
Number of enriched genes

Supplementary Figure 6

Supplementary Figure 7

A

ConA-NS up BDL-Sham up
CCl4-Oil up 56 206 LR-MR up
3 2 20
105 0 0 3155
1 0 28
0 0
24

ConA-NS down BDL-Sham down
CCl4-Oil down 96 395 LR-MR down
0 3 4
34 0 0 398
1 0 5
0 0
0

B

ConA-NS up BDL-Sham up
CCl4-Oil up 674 72 LR-MR up
4 4 4
Gbp2b ← 65 1 0 414
0 0 150
0 0
3

ConA-NS down BDL-Sham down
CCl4-Oil down 29 142 LR-MR down
0 0 2
34 0 0 134
0 0 1
0 0
0

C

ConA-NS up BDL-Sham up
CCl4-Oil up 284 1926 LR-MR up
1 32 74
95 0 5 246 → C3ar1
7 0 40 Lpar5
0 0 Klrb1c
2 Ccr5
Padi4

ConA-NS down BDL-Sham down
CCl4-Oil down 63 61 LR-MR down
0 0 0
76 0 0 131
0 0
0 0
0

D

ConA-NS up BDL-Sham up
CCl4-Oil up 186 59 LR-MR up
10 2 13
118 0 5 886 → Fyb
0 57 Vav1
0 4 Itgal
0 Itgb7
23 Myo1f
→ Soat2
Sh2d1a
Ccr5
Gzmk

ConA-NS down BDL-Sham down
CCl4-Oil down 35 249 LR-MR down
0 1 2
40 0 0 115
4 0 2
0 0
1

E

ConA-NS up BDL-Sham up
CCl4-Oil up 773 782 LR-MR up
0 13 39
Hoxa9 ← 89 1 2 360 → Slc39a8
5 0 Pkhd1l1
Mas1 ← 1 1 165 → AA467197
7

ConA-NS down BDL-Sham down
CCl4-Oil down 1567 65 LR-MR down
2 2 0
29 0 0 108
1 0 17
0 0
1

F

ConA-NS up BDL-Sham up
CCl4-Oil up 109 100 LR-MR up
4 3 3
51 0 0 344
0 0 8
0 0
1

ConA-NS down BDL-Sham down
CCl4-Oil down 128 181 LR-MR down
4 7 3
62 0 0 60
4 0 5
0 0
0

Supplementary Figure 8

Supplementary Figure 9
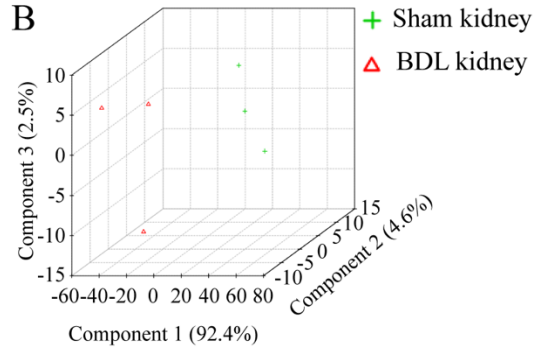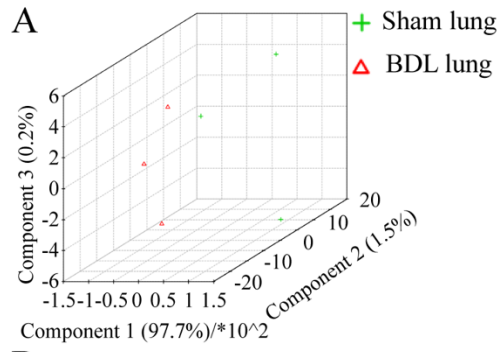
Supplementary Figure 10
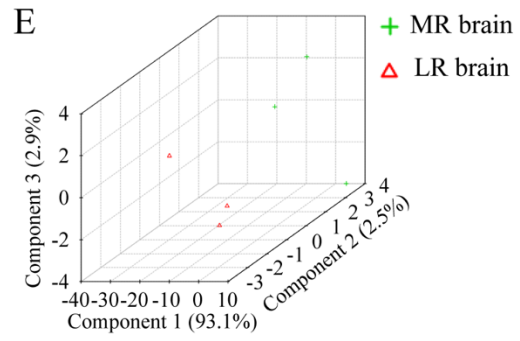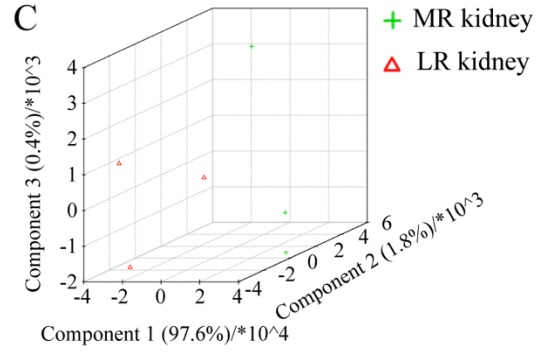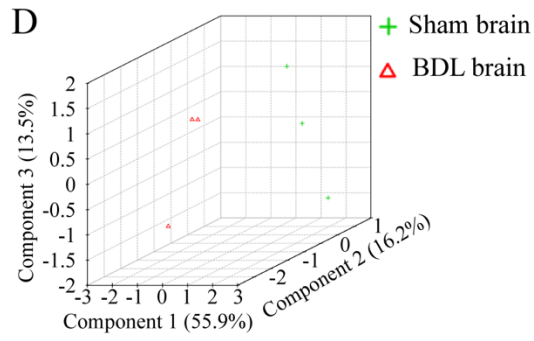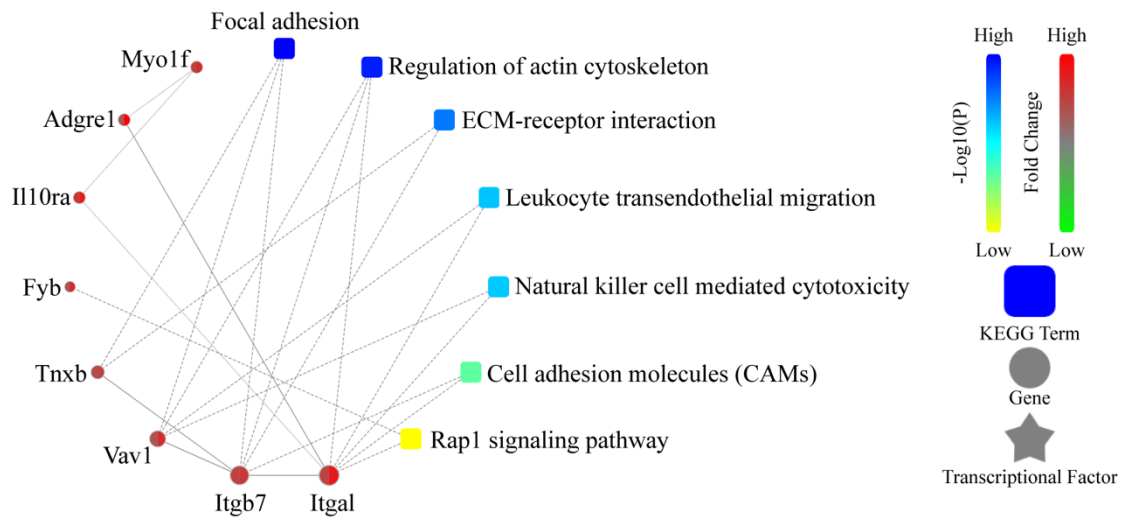
Supplementary Table 1

Name	Sequence
m-Itgb7-F	ACCTGAGCTACTCAATGAAGGA
m-Itgb7-R	CACCGTTTTGTCCACGAAGG
m-Hic1-F	GGCCATTCGAGGCAGCTAC
m-Hic1-R	AGGTTTAGCAGGTTGTCATGC
m-Esm1-F	CTGGAGCGCCAAATATGCG
m-Esm1-R	TGAGACTGTACGGTAGCAGGT
m-Caps2-F	TCTTTCTGGCTAATTCTGCAAGG
m-Caps2-R	CTTGGCGCAGTAACACTTTCT
m-Mup3-F	TTGGTTTTCTATTGCTGAAGCCT
m-Mup3-R	CCAATCGCAGTCATTTCGGTG
m-Itgb1-F	ATGCCAAATCTTGCGGAGAAT
m-Itgb1-R	TTTGCTGCGATTGGTGACATT
m-36B4-F	GGGCATCACCACGAAAATCTC
m-36B4-R	CTGCCGTTGTCAAACACCT
h-MYOF1-F	ACTACCTCAACCAATCGGACA
h-MYOF1-R	GCACTCAGAGTCTCACCAAAG
h-TNXB-F	GCCCTGCTCACTTGGACTG
h-TNXB-R	GGAGCCGTGCATTGTAGGAG
h-ITGAL-F	TGCTTATCATCATCACGGATGG
h-ITGAL-R	CTCTCCTTGGTCTGAAAATGCT
h-SNCA-F	AAGAGGGTGTTCTCTATGTAGGC
h-SNCA-R	GCTCCTCCAACATTTGTCACTT
h-36B4-F	AGCCACGCTGCTGAACAT
h-36B4-R	CAACATTGCGGACACCCT