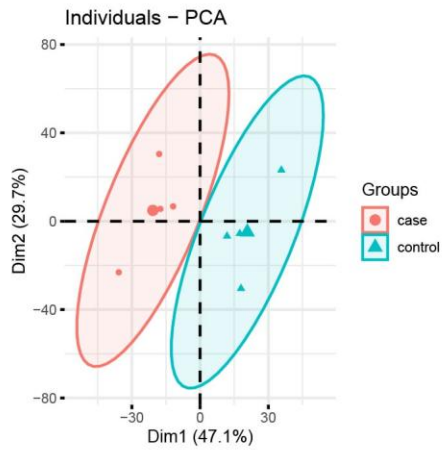
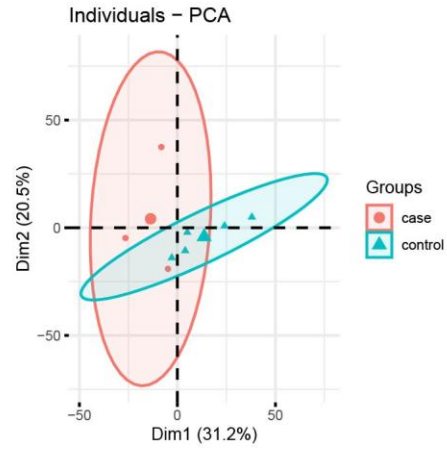


A



B



C

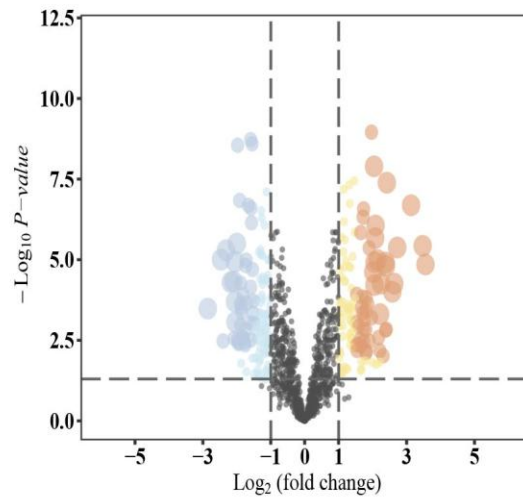


Figure S1. Identification and functional analysis of DEMs in BPD. (A-B) PCA plot for the GSE108755 gene expression dataset showing batch effects after and before. (C) Volcano plot depicting the expression patterns of DEMs. Yellow: upregulated genes; blue: downregulated genes.

Table S1. Clinical characteristics of infants with and without BPD

| Variable                          | NO-BPD (n=4)     | BPD (n=6)      | P-value* |
|-----------------------------------|------------------|----------------|----------|
| Gestational age (weeks)           | 28.86 ± 1.10     | 24.88 ± 1.06   | 0.002    |
| Birth weight (g)                  | 1150.00 ± 147.65 | 708.33 ± 53.45 | 0.004    |
| Male, n (%)                       | 1 (25.0)         | 4 (66.7)       | 0.527    |
| 1-min Apgar ≤3, n (%)             | 1 (25.0)         | 0 (0.0)        | 1.000    |
| Cesarean delivery, n (%)          | 3 (75.0)         | 2 (33.3)       | 0.527    |
| Mechanical ventilation >7d, n (%) | 0 (0.0)          | 6 (100.0)      | 0.005    |
| Total oxygen exposure (days)      | 38.00 ± 11.28    | 136.00 ± 56.32 | 0.004    |
| PDA, n (%)                        | 2 (50.0)         | 4 (66.7)       | 1.000    |
| Sepsis, n (%)                     | 2 (50.0)         | 6 (100.0)      | 0.222    |

**Table notes:** \*P values were calculated using the **Mann–Whitney U test** (continuous variables) and Fisher’s exact test (categorical variables), without multivariate adjustment.

This study has a small sample size (n=10) and inherent baseline imbalance between groups, which should be acknowledged as major limitations.

Continuous variables are presented as mean ± standard deviation; categorical variables are presented as n (%). PDA, patent ductus arteriosus.

Table S2. Peripheral blood gene expression ( $2^{-\Delta CT}$ ) analyzed by qRT-PCR

| Gene      | NO-BPD (n=4)    | BPD (n=6)       | P-value* |
|-----------|-----------------|-----------------|----------|
| ATF2      | $1.00 \pm 0.48$ | $1.62 \pm 1.33$ | 0.548    |
| SOX10     | $0.99 \pm 0.56$ | $1.01 \pm 0.63$ | 0.969    |
| GATA6     | $1.00 \pm 0.41$ | $1.34 \pm 0.78$ | 0.437    |
| GTF2I     | $1.00 \pm 0.63$ | $2.02 \pm 0.85$ | 0.042    |
| LOC135440 | $1.00 \pm 0.42$ | $2.65 \pm 2.73$ | 0.182    |

**Table notes:** \*P values were calculated using the **Mann–Whitney U test** (unadjusted comparison between groups).

Gene expression was normalized using the  $2^{-\Delta CT}$  method (mean  $\pm$  standard deviation).

A small sample size with baseline imbalance was noted as a major limitation of this study.

Table S3. Oligonucleotides used in this study for qRT-PCR analyses.

| Name             | Primer                  | purpose |
|------------------|-------------------------|---------|
| ATF2-F           | AATTGAGGAGCCTTCTGTTGTAG | PCR     |
| ATF2-R           | CATCACTGGTAGTAGACTCTBBC | PCR     |
| SOX10-F          | CCTCACAGATCGCCTACACC    | PCR     |
| SOX10-R          | CATATAGGAGAAGGCCGAGTAGA | PCR     |
| GATA6-F          | CTCAGTTCCTACGCTTCGCAT   | PCR     |
| GATA6-R          | GTCGAGGTCAGTGAACAGCA    | PCR     |
| GTF2I-F          | TTGTCGTCGGAAGTGAAGAG    | PCR     |
| GTF2I-R          | CGATTTGCCTBBCTTGTAGAT   | PCR     |
| LOC135440-F      | GAGGAAABBCCTGACAGAGT    | PCR     |
| LOC135440-R      | GCTTCCCAACTCTCCTGTCT    | PCR     |
| $\beta$ -actin-F | GAGCTACGAGCTGCCTGACG    | PCR     |
| $\beta$ -actin-R | TGCCABBCCAGTGATCTCCT    | PCR     |