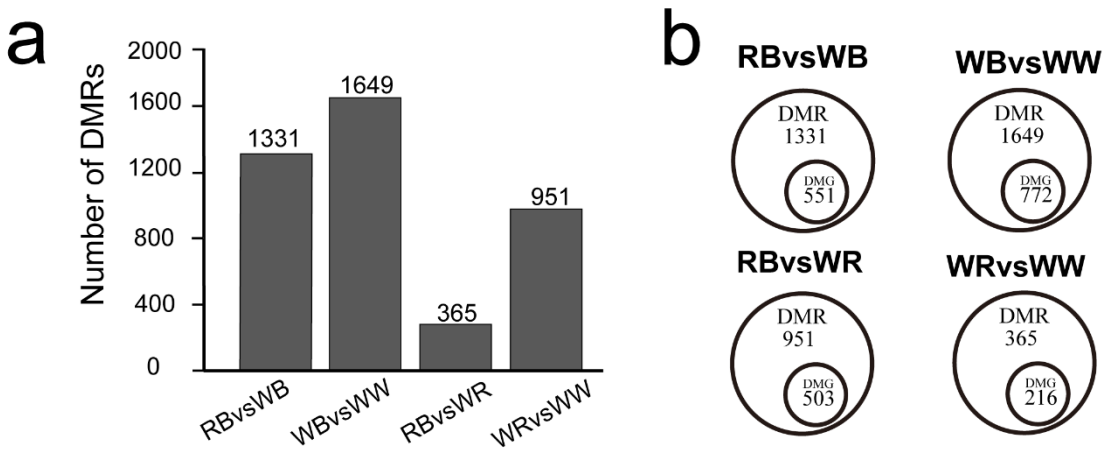
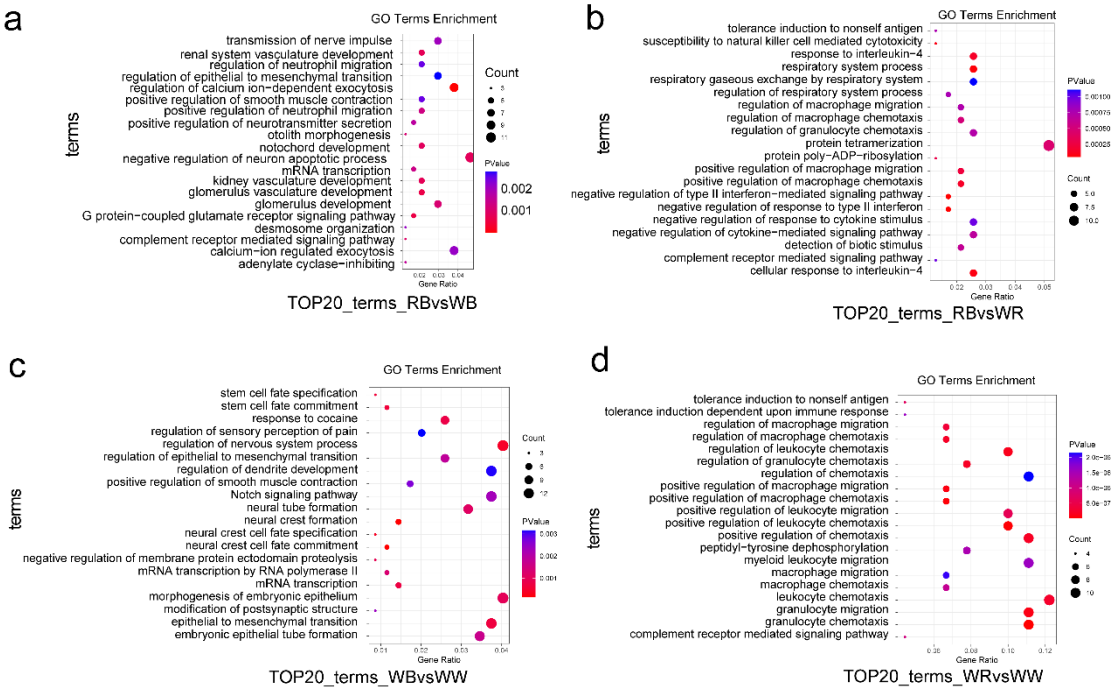
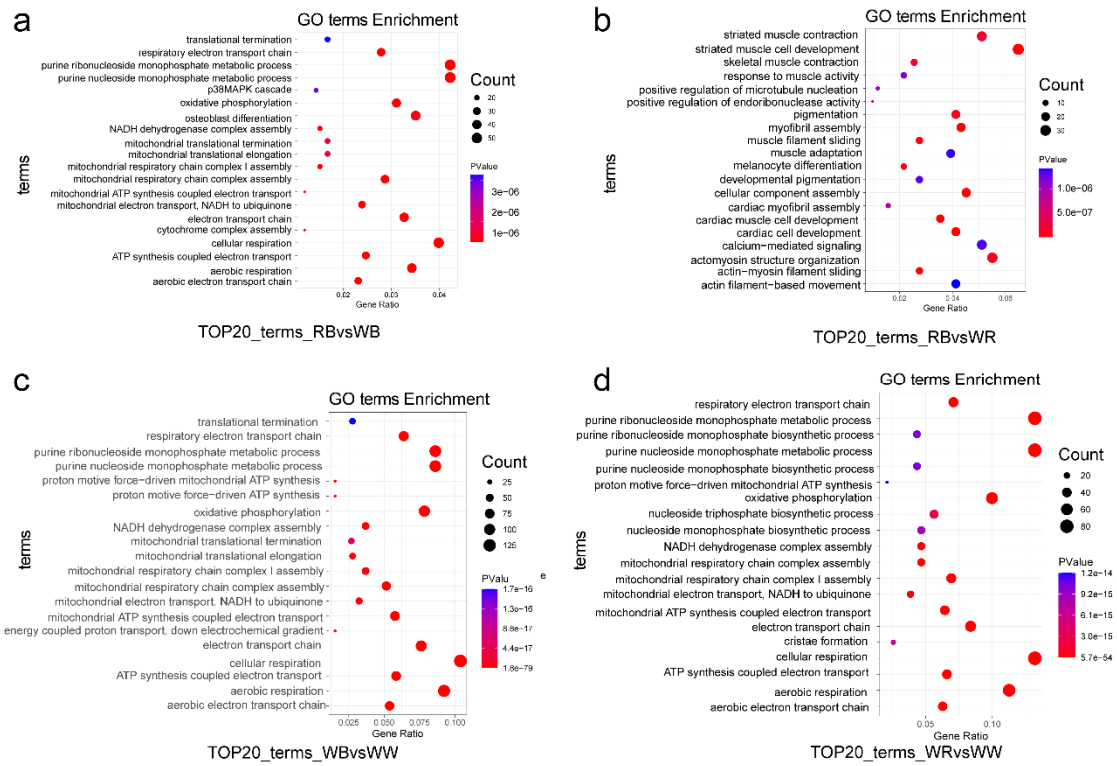


Supplementary Figure S1. The number of DMRs and DMR-associated genes in each comparison group. (a)The number of DMRs in each comparison group. (b) The number of DMR-associated genes in each comparison group.



Supplementary Figure S2. The TOP20 GO enrichment terms of DMGs in each group. (a) The TOP20 GO enrichment terms of DMGs in RBvsWB. (b) The TOP20 GO enrichment terms of DMGs in RBvsWR. (c) The TOP20 GO enrichment terms of DMGs in WBvsWW. (d) The TOP20 GO enrichment terms of DMGs in WRvsWW.



Supplementary Figure S3. The TOP20 GO enrichment terms of DEGs in each group. (a) The TOP20 GO enrichment terms of DEGs in RBvsWB. (b) The TOP20 GO enrichment terms of DEGs in RBvsWR. (c) The TOP20 GO enrichment terms of DMGs in WBvsWW. (d) The TOP20 GO enrichment terms of DEGs in WRvsWW.

Supplementary Table S1. MBD-seq_quality_control_metrics

SampleID	Raw Reads	Clean Reads	Q30(%)
RB1	28,498,814	27,148,628	89.76%
RB2	40,437,721	38,931,104	90.12%
RB3	55,116,855	53,074,000	90.15%
WB1	31,330,174	30,243,676	90.07%
WB2	36,951,445	35,724,510	90.38%
WB3	32,517,977	31,236,791	89.72%
WW1	15,557,937	15,557,937	93.65%
WW2	42,500,345	40,752,767	91.66%
WW3	40,842,013	39,391,525	91.59%
WR1	26,968,065	26,377,136	92.08%
WR2	23,948,518	23,194,124	91.94%
WR3	21,006,809	20,234,406	91.76%

Supplementary Table S2. RNA-seq_quality_control_metrics

SampleID	Raw Reads	Clean Reads	Q30(%)
RB1	25,686,388	24,609,068	91.45%
RB2	28,241,420	27,682,050	90.85%
RB3	22,805,740	22,159,402	90.21%
WB1	24,766,382	23,783,860	91.26%
WB2	26,337,432	25,824,716	90.98%
WB3	21,428,528	20,971,270	90.81%
WW1	39,642,101	38,764,648	88.35%
WW2	25,190,430	24,652,398	90.80%
WW3	34,148,372	33,590,668	91.12%
WR1	20,178,300	19,862,756	91.11%
WR2	21,912,906	21,173,668	90.95%
WR3	32,459,772	31,629,760	91.26%