Supplementary Table 1 Reverse causal association between PPD and gut microbiota.

Exposure	Outcome	Methods	SNPs	Beta	SE	OR (95%CI)	P-value	Heterogeneity		Horizontal pleiotropy	
								Cochran's Q	P	Egger intercept	P
PPD	Family *Veillonellaceae*	IVW	14	-0.006	0.035	0.99(0.93-1.06)	0.853	10.107	0.685	0.013	0.564
		MR Egger	14	-0.138	0.225	0.87(0.56-1.35)	0.550	9.756	0.637		
		Weighted median	14	0.005	0.047	1.01(0.92-1.10)	0.914	-	-		
		Weighted mode	14	0.014	0.083	1.01(0.86-1.19)	0.867	-	-		
PPD	Class *Alphaproteobacteria*	IVW	14	0.049	0.047	1.05(0.96-1.15)	0.299	14.138	0.364	0.012	0.697
		MR Egger	14	0.172	0.313	1.19(0.64-2.20)	0.592	13.954	0.304		
		Weighted median	14	0.054	0.061	1.06(0.94-1.19)	0.381	-	-		
		Weighted mode	14	0.055	0.102	1.06(0.86-1.29)	0.601	-	-		
PPD	Genus *Family XIII AD3011 group*	IVW	14	0.021	0.038	1.02(0.95-1.10)	0.578	13.925	0.379	0.046	0.071
		MR Egger	14	-0.444	0.238	0.64(0.40-1.02)	0.087	10.013	0.615		
		Weighted median	14	-0.019	0.051	0.98(0.89-1.08)	0.706	-	-		
		Weighted mode	14	-0.036	0.086	0.96(0.81-1.14)	0.683	-	-		

Supplementary Table 2 SNP genes of *Family XIII AD3011 group*.

SNP	chromosome_name	chromosome _position	distance	is_mapped_gene	is_closest_gene	is_intergenic	is_upstream	is_downstream	source	mapping_method
rs11126423	ACTG2	2	73968424	48559	FALSE	FALSE	TRUE	TRUE	FALSE	Ensembl
rs11126423	STAMBP	2	73968424	94765	FALSE	FALSE	TRUE	TRUE	FALSE	Ensembl
rs11126423	DGUOK-AS1	2	73968424	0	TRUE	FALSE	FALSE	FALSE	FALSE	Ensembl
rs11126423	RNA5SP97	2	73968424	218	FALSE	TRUE	TRUE	TRUE	FALSE	Ensembl
rs11126423	DGUOK	2	73968424	9463	FALSE	FALSE	TRUE	TRUE	FALSE	Ensembl
rs11126423	TET3	2	73968424	16486	FALSE	TRUE	TRUE	FALSE	TRUE	Ensembl
rs11126423	LOC107985898	2	73968424	17181	FALSE	FALSE	TRUE	FALSE	TRUE	NCBI
rs11126423	LOC100420774	2	73968424	90605	FALSE	FALSE	TRUE	TRUE	FALSE	NCBI
rs16940167	AQP9	15	58391498	205587	FALSE	TRUE	TRUE	TRUE	FALSE	Ensembl
rs16940167	LIPC	15	58391498	19071	FALSE	TRUE	TRUE	FALSE	TRUE	Ensembl
rs16940167	ALDH1A2	15	58391498	0	TRUE	FALSE	FALSE	FALSE	FALSE	Ensembl
rs16940167	LIPC-AS1	15	58391498	43392	FALSE	FALSE	TRUE	FALSE	TRUE	Ensembl
rs16940167	RPL28P4	15	58391498	190564	FALSE	TRUE	TRUE	TRUE	FALSE	NCBI

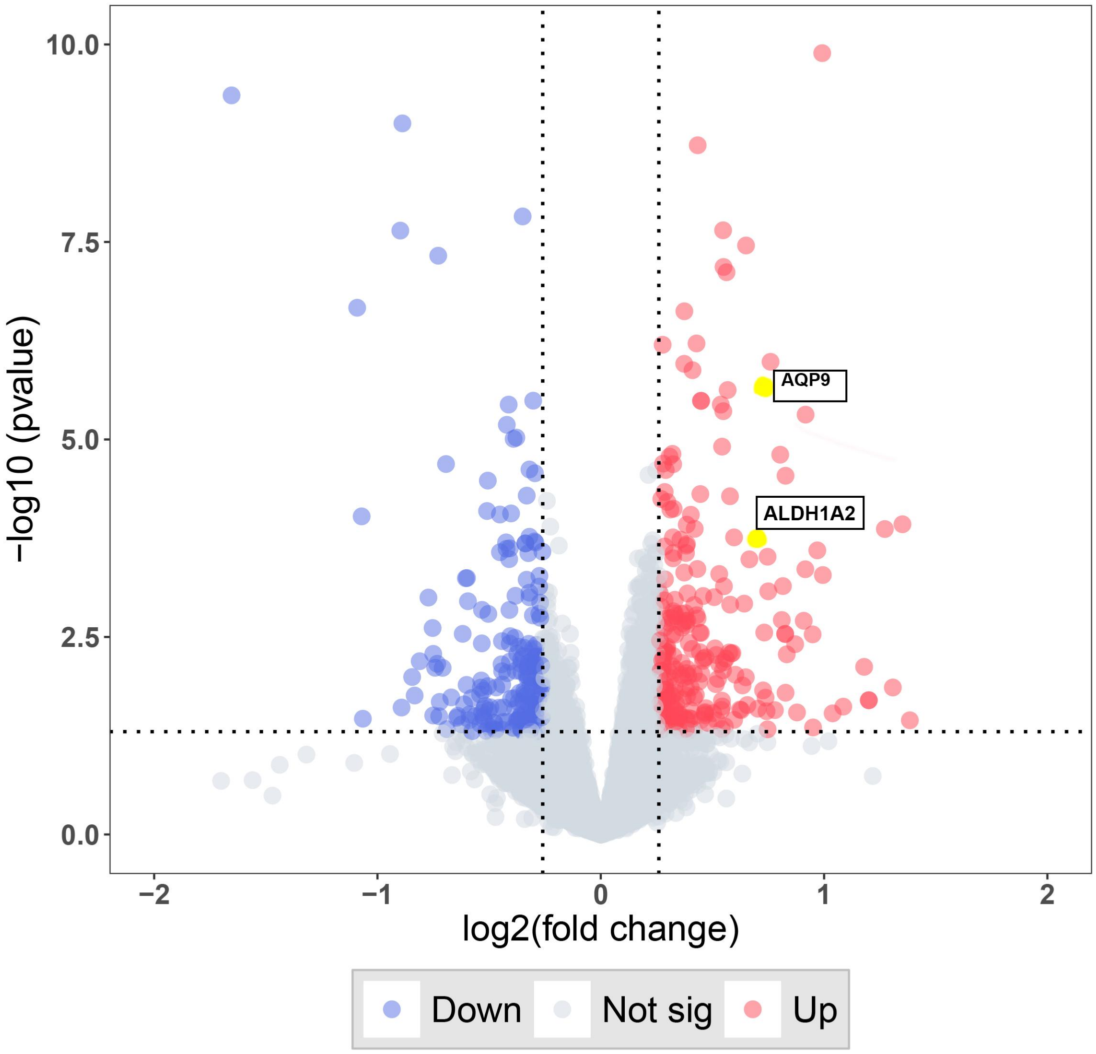
Supplementary Table 3 The relevance scores of the top 20 pathogenic genes.

Gene Symbol	Relevance score
BDNF	42
FKBP5	38
COMT	32
NR3C1	30
TNF	25
MTHFR	21
CRHR1	21
OXTR	20
LEP	20
IL1B	19
IL10	18
CREB1	16
NR3C2	14
DISC1	13
SOD1	12
PER3	12
GHRL	12
CLOCK	12
HP1BP3	11
IDO1	11

Supplementary Table 4 MR estimates for the association between the gut microbiota and PPD (threshold of $p < 1 \times 10^{-8}$)

Gut microbiota (exposure)	Methods	SNPs	Beta	SE	OR (95%CI)	P-value
order Bifidobacteriales	IVW	2	-0.247	0.190	0.78(0.54-1.13)	0.194
family Bifidobacteriaceae	IVW	2	0.25	0.190	0.78(0.54-1.13)	0.194
genus Bifidobacterium	IVW	2	0.242	0.186	1.24(0.56-1.13)	0.192

MR, mendelian randomization; IVW, inverse-variance weighted; SNP, single nucleotide polymorphisms; Beta, The effect size of the exposure on PPD; SE, standard errors; OR, odd ratio; CI, confidence interval; PPD, postpartum depression.



Supplementary Figure 1. Volcano plot showing differentlly expressed genes (DEGs) in hypothalamus of mice in GSE70732. The up-regulated (red) or down-regulated (blue) genes between PPD vs. Control groups.