**Genome-wide association analysis reveals genomic regions on Chromosome 13 affecting litter size and candidate genes for uterine horn length in Erhualian pigs**

X. Ma, P. H. Li, M. X. Zhu, L. C. He, S. P. Sui, S. Gao, G. S. Su, N. S. Ding, Y. Huang, Z. Q. Lu, X. G. Huang, and R. H. Huang

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**Supplementary Table S1** *Three populations* *for genotyping of rs81447100*

|  |  |  |
| --- | --- | --- |
| Population | Farm | N1 |
| Erhualian | Changzhou Jiaoxi Cooperatives of Erhualian Pigs | 144 |
| Changshu Animal Husbandry and Veterinary Station | 111 |
| Sutai Enterprise Co., Ltd | 58 |
| Sutai | Sutai Enterprise Co., Ltd | 173 |
| Yorkshire | Laizhou farm of Fujian Yichun Corporation | 488 |

1N, sows number

**Supplementary Table S2** *Significant SNP and genes identified in this study1*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Phenotypes2 | Top SNP2 | Chromosome | Position (bp) | Genes located within ±1 Mb3 |
| TNB-2~7\NBA2~7 | rs80882306 | 7 | 11 531 743 | *MCUR1, RNF182, JARID2, DTNBP1* |
| NBA-2~7 | rs81447100 | 13 | 88 653 330 | *MRPS22, COPB2, RBP2, RBP1,* *CLSTN2, TRIM42, SLC25A36,* |
| TNB-2~7 | rs81406385 | 8 | 18 169 869 | *DHX15* |
| NBA-2~7 | [rs81215583](http://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?rs=81215583) | 13 | 79 276 382 | *FBLN2, NUP210, IQSEC1, KIAA1257, ACAD9, EFCC1,* ***RPN1****, HMCES, COPG1, H1FX, RAB7A, DNAJB8, GATA2, SEC61A1, KBTBD12, TPRA1, MGLL, ABTB1, PODXL2, MCM2* |
| TNB-2~7 | rs81260290 | 1 | 278 190 574 | *RPS16, ZNF462, RAD23B, KLF4* |
| NBA-2~7 | rs81447231 | 13 | 90433453 | *SLC25A36, SPSB4, PXYLP1, ZBTB38, RASA2, RNF7,* ***GRK7****, GK5, XRN1, ATR, PLS1, TRPC1, PCOLCE2* |
| NBA-2~7 | rs80952566 | 17 | 30 670 293 | *PARD3, CUL2, CREB, CCNY, GJD4* |
| NBA-1 | rs80890206 | 5 | 34 298 027 | *IRAK3, HELB, GRIP1* |
| TNB-1\NBA-1 | rs80927364 | 4 | 143 188 763 | *CLCA2, ODF2L, ZNHIT6, CYR61,* ***DDAH1****, BCL10, SYDE2, MCOLN3, WDR63* |
| TNB-2~7\NBA-2~7 | rs81274366 | 10 | 63 120 836 | *PARD3, CUL2, CREB, CCNY, GJD4* |
| TNB-2~7  TNB-2~7\NBA-2~7 | rs81289648  rs81434499 | 16  12 | 81 255 133  37 502 410 | *MTRRR, FASTKD3, C5orf49, ADCY2, PAPD7, SDR5A1, NSUN2, UBE2QL1, MED10*  *TRIM37, CLTC, DHX40, GDPD1, SMG8, PRR11, SKA2, PTRH2, VMP1, TBX4, TBX2, TUBD1, RPS6KB1, RNDT1, MED13, INTS2* |

1 SNP, single nucleotide polymorphisms.

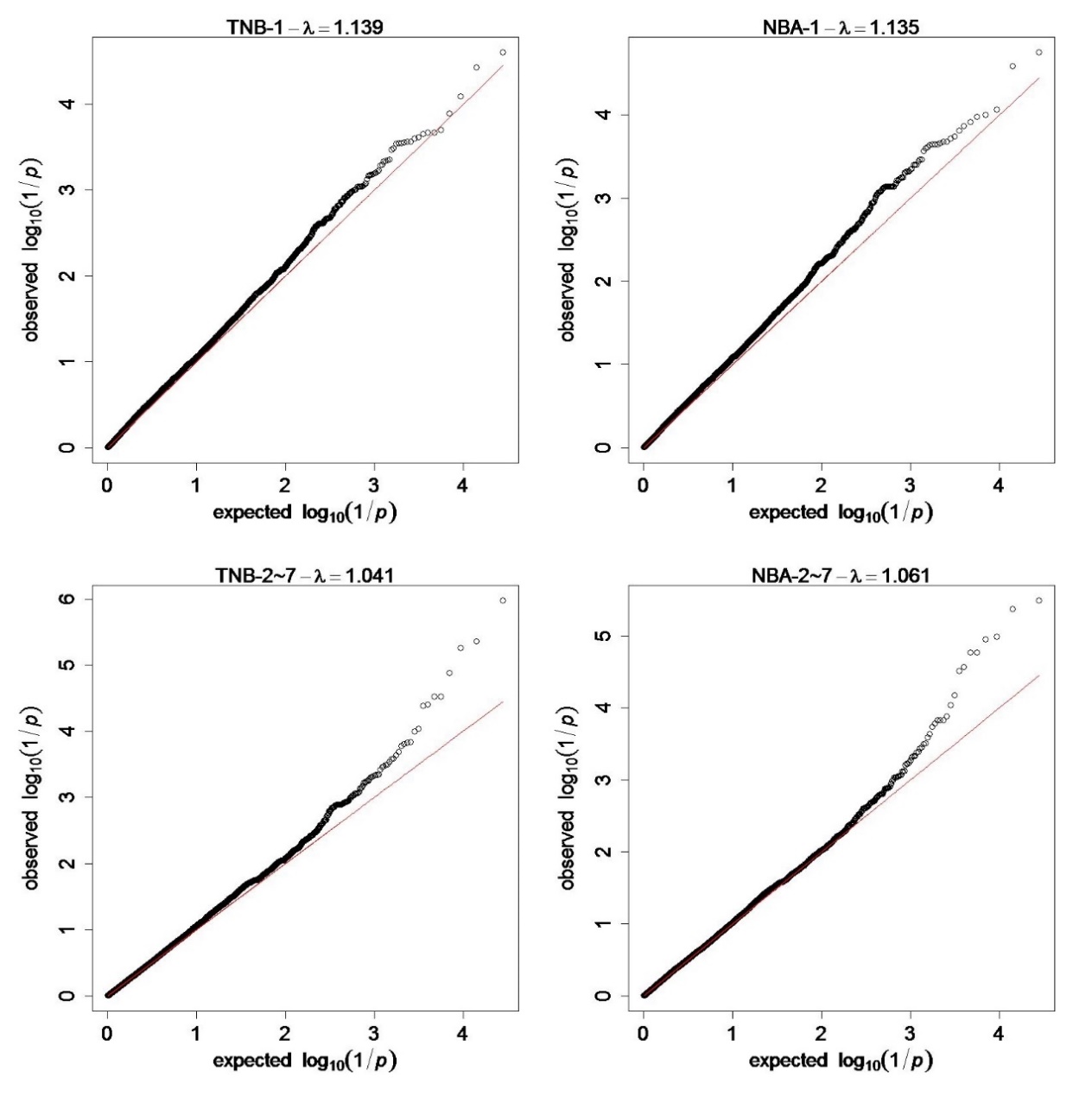
1 TNB-1, the 1st parity of total number born; NBA-1, the 1st parity of number born alive; TNB-2~7, the 2nd to 7th parity of total number born; NBA-2~7, the 2nd to 7th parity of number born alive.

3 Gene which is bolded represents the corresponding marker is in it, others mean the corresponding marker is not in it.



**Supplementary Figure S1** Image of uterine collected from a high- EBVTNB (a) and a low- EBVTNB sow (b). (a) Total uterine horn length is 278 cm. (b) Total uterine horn length is 434 cm. 1

1 EBVTNB, estimated breeding value of total number born



**Supplementary Figure S2** Quantile-quantile (Q-Q) plots of genome-wide association study for litter size. The black circles indicate single nucleotide polymorphisms markers. The red line in the QQ plots indicates the distribution of single nucleotide polymorphisms markers under the null hypothesis and the skew at the right edge indicates that these markers are stronger associated with the traits than it would be expected by chance.