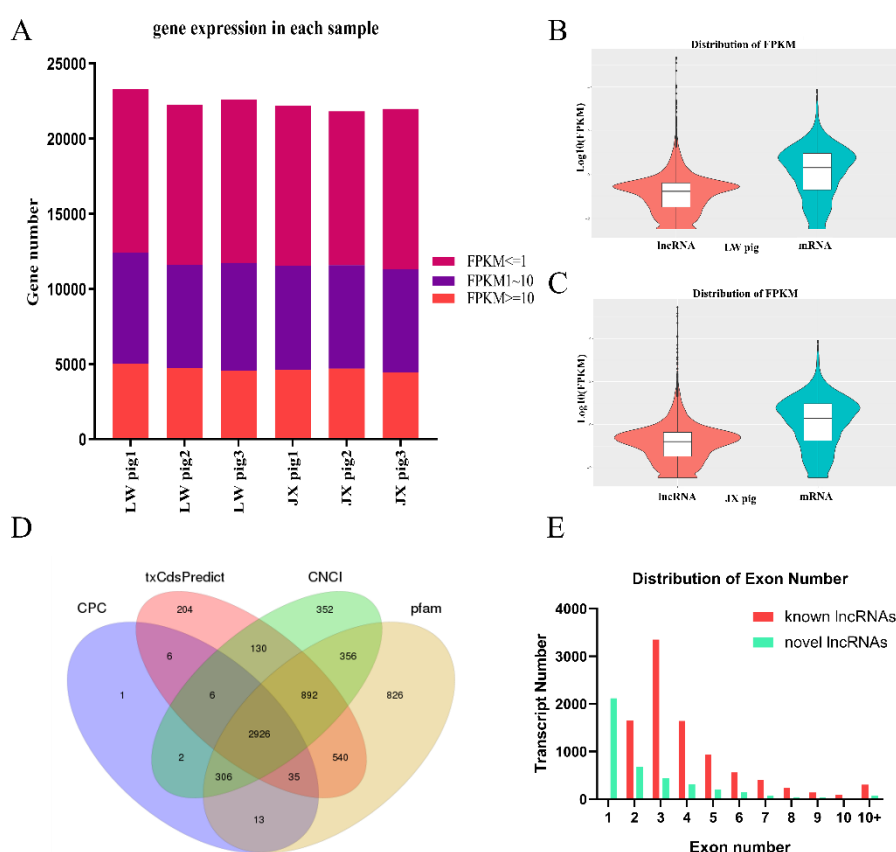


Supplementary Table 1 Summary of raw reads after quality control and mapping to the reference genome

Sample	Raw reads	Clean reads	Clean Read ratio	Total mapped reads	Uniquely mapped reads	Gene number (FPKM ≥ 1)
LW_SF1	163,015,236	152,234,246	93.39%	95.07%	90.22%	12,446
LW_SF2	165,689,668	152,444,042	92.01%	94.17%	87.20%	11,643
LW_SF3	166,398,866	152,161,886	91.44%	93.61%	86.05%	11,765
JX_SF1	161,091,938	152,250,878	94.51%	91.85%	84.79%	11,579
JX_SF2	159,503,542	151,692,558	95.10%	92.13%	85.59%	11,593
JX_SF3	162,238,544	151,565,872	93.42%	85.76%	92.91%	11,310

Supplementary Fig. 1 Characterization of subcutaneous adipocyte transcript in JX and LW pigs.

A. Statistics of gene number according FPKM value among samples. **B&C.** Expression levels of mRNAs and lncRNAs indicated by $\log_{10}(\text{FPKM})$. **D.** Coding potential analysis of candidate lncRNAs was performed by using four conventional tools (CPC, txCdsPredict, CNCI and pfam). **E.** The exon number distribution of lncRNAs and mRNAs.



Supplementary Table 2 The top 50 expressed genes based on FPKM values of JX pigs

Gene Symbol	JX FPKM	LW FPKM
<i>LGALS1</i>	7773.65	5996.48
<i>EEF1A1</i>	7619.98	7326.90
<i>RPLP1</i>	6549.92	6488.11
<i>COL1A2</i>	4718.12	3841.24
<i>TMSB10</i>	4644.90	3826.81
<i>RPS27</i>	4523.23	3835.24
<i>RPS19</i>	4066.84	3764.01
<i>RPS29</i>	4003.07	3260.87
<i>RPLP0</i>	3943.62	3998.98
<i>FTL</i>	3832.95	5374.78
<i>RPS12</i>	3806.12	3966.53
<i>S100A6</i>	3637.09	2384.64
<i>TMSB4X</i>	3636.53	3053.08
<i>RPS8</i>	3292.06	2947.65
<i>RPL35</i>	2814.35	2665.29
<i>SERF2</i>	2701.96	2186.65
<i>ACTA2</i>	2617.83	2866.17
<i>RPL37</i>	2610.21	2327.09
<i>VIM</i>	2584.89	2895.58
<i>CTSK</i>	2492.33	1347.09
<i>RPL23</i>	2463.26	2098.41
<i>RACK1</i>	2461.45	2535.88
<i>RPL26</i>	2431.31	2471.48
<i>GAPDH</i>	2372.44	1881.21
<i>RPLP2</i>	2338.30	2351.18
<i>RPS28</i>	2299.64	2339.39
<i>RPL17</i>	2207.27	2018.07
<i>TAGLN</i>	2200.39	2563.98
<i>RPS26</i>	2179.53	2113.36
<i>SPARC</i>	2138.17	1846.41
<i>RPL10A</i>	2046.68	1866.33
<i>RPS21</i>	2011.14	2327.65
<i>RPS15A</i>	1973.47	1926.65
<i>RPS18</i>	1967.31	1847.04
<i>RPS27A</i>	1890.97	1752.33
<i>RPS24</i>	1853.98	1812.61
<i>RPL29</i>	1830.74	1703.81
<i>RPS11</i>	1806.13	1548.39
<i>MYL6</i>	1797.12	1745.54
<i>RPL31</i>	1694.36	1500.56

<i>TPT1</i>	1691.53	1711.40
<i>LGMN</i>	1687.39	1505.92
<i>RPL19</i>	1670.74	1663.57
<i>RPL14</i>	1668.24	1461.85
<i>RPS7</i>	1659.94	1549.12
<i>RPL13A</i>	1633.30	1450.34
<i>RPL7A</i>	1596.69	1705.34
<i>RPS14</i>	1585.58	1712.99
<i>RPS23</i>	1573.66	1499.43
<i>RPL7</i>	1550.16	1597.54

Supplementary Table 3 The top 25 up- and 25 down-regulated DEGs between the two breeds

Gene Symbol	JX FPKM	LW FPKM	Log2foldchange (JX/LW)	Up/Down	p-value
<i>RPS17</i>	123.4733	0	13.93041	Up	1.00E-300
<i>LDHB</i>	27.63	0.01	11.44782	Up	1.00E-300
<i>PTCD1</i>	1.05	0	10.33495	Up	3.2075E-101
<i>TCEAL2</i>	1.063333	0.03	5.191806	Up	4.04242E-47
<i>SYNPR</i>	8.793333	0.243333	5.167654	Up	1.00E-300
<i>SLC7A3</i>	1.006667	0.026667	5.137354	Up	3.9766E-99
<i>CCT2</i>	6.656667	0.21	4.984293	Up	1.00E-300
<i>DDX24</i>	1.69	0.1	4.086367	Up	5.9132E-192
<i>CIQTNF3</i>	25.73667	1.62	3.992309	Up	1.00E-300
<i>HTR2A</i>	1.466667	0.093333	3.718916	Up	1.276E-165
<i>RAMP1</i>	29.14667	2.566667	3.534632	Up	1.00E-300
<i>AWN</i>	7.866667	0.766667	3.37453	Up	4.0885E-167
<i>CA4</i>	5.216667	0.53	3.309405	Up	3.292E-191
<i>H3-3A</i>	8.103333	0.993333	3.153083	Up	4.4083E-102
<i>CD207</i>	2.556667	0.3	3.120928	Up	1.87208E-85
<i>TLCD4</i>	1.056667	0.126667	3.047772	Up	1.94E-227
<i>CALCB</i>	9.816667	0.783333	3.013125	Up	8.83E-185
<i>FRMD7</i>	2.306667	0.296667	2.952308	Up	3.1136E-186
<i>FAM237A</i>	4.18	0.736667	2.803847	Up	1.00E-300
<i>CYP2J34</i>	1.663333	0.24	2.802589	Up	1.05445E-92
<i>IGFBP4</i>	7.84	1.143333	2.782304	Up	1.1733E-155
<i>MCHR1</i>	2.68	0.403333	2.759758	Up	1.6859E-105
<i>CHI3L2</i>	4.853333	0.756667	2.694868	Up	1.9531E-236
<i>CRSP-2</i>	2.85	0.416667	2.640654	Up	5.43953E-47
<i>MAB21L2</i>	1.09	0.183333	2.572675	Up	9.66647E-84
<i>SLA-DRA</i>	0	5.22	-11.1169	Down	2.9928E-154
<i>LGALS13</i>	0	12.00333	-10.8663	Down	2.5382E-135
<i>KRT5</i>	0.036667	61.10667	-10.6362	Down	1.00E-300
<i>GBP2</i>	0	1.756667	-10.4668	Down	1.1703E-109
<i>F13A1</i>	0.006667	4.14	-9.24995	Down	1.00E-300

<i>CCL24</i>	0	1.023333	-9.02396	Down	2.06749E-50
<i>LY86</i>	0	1.72	-8.84923	Down	8.40197E-46
<i>KRT8</i>	0.013333	5.806667	-8.7705	Down	1.00E-300
<i>UBC</i>	1.89	408.48	-7.78886	Down	1.00E-300
<i>KRT6A</i>	0.073333	15.13	-7.65769	Down	1.00E-300
<i>SLA-DRB1</i>	0.036667	7.326667	-7.56995	Down	1.00E-300
<i>COL17A1</i>	0.03	4.716667	-7.27099	Down	1.00E-300
<i>FAM199X</i>	0.046667	4.146667	-6.46552	Down	1.00E-300
<i>SPINK2</i>	0.146667	13.27333	-6.42799	Down	1.2244E-222
<i>SERPINB5</i>	0.016667	1.153333	-6.38226	Down	4.0301E-138
<i>TNFRSF1A</i>	0.04	3.26	-6.28061	Down	2.1574E-281
<i>TCEAL9</i>	0.07	6.156667	-6.26086	Down	2.5601E-258
<i>FEM1B</i>	0.063333	4.51	-6.17989	Down	1.00E-300
<i>MARCO</i>	0.066667	4.646667	-6.05679	Down	1.2251E-299
<i>SIGLEC1</i>	0.023333	1.183333	-5.81012	Down	1.00E-300
<i>SLA-DQAI</i>	0.05	2.55	-5.68548	Down	2.5189E-135
<i>TIMD4</i>	0.033333	1.343333	-5.51382	Down	2.53182E-66
<i>GRAP</i>	0.046667	2.16	-5.4968	Down	7.0625E-172
<i>PGM5</i>	0.093333	3.87	-5.38985	Down	1.00E-300
<i>TMSB15B</i>	0.083333	3.463333	-5.38117	Down	7.4745E-90

Supplementary Table 4 The potential target genes of DELs

The table was provided in a XLSX file independently.

Supplementary Table 5 Sequences of Q-PCR primers for protein-coding genes and lncRNAs

Name	Sequence
ITGB3-RTF	GAAAAGGACTACCGCCCCTC
ITGB3-RTR	CACTCACAGTACTTGCCCGT
LRP10-RTF	ACCAAGACCGGATCCTTTTCC
LRP10-RTR	CCACAGGCCAGGTGTAGTTT
C1QTNF3-RTF	GAATACATGGAGGTGAGCGGA
C1QTNF3-RTR	TCCACAGTCCCAGTTCTAGC
LCN2-RTF	ATTGCCTCACCTTCCTGGAT
LCN2-RTR	GGAGACTTAGGGCCATGGTTG
PLIN1-RTF	GTACAACCAGCTGCGCAAGAA
PLIN1-RTR	AGGTTCTTCTGGTTTGCAGGAG
PLIN4-RTF	ATAAGGCCAGGGAGCTGAGA
PLIN4-RTR	GGACCCAAAGAAGCTGCTCA
ISG15-RTF	GGTGAGGAACGACAAGGGTC
ISG15-RTR	GGCTTGAGGTCATACTCCCC
STEAP1-RTF	AGCAGTTTGGGCTTCTCAGT
STEAP1-RTR	GACCTGTTGATACGCCCAGT

ACKR3-RTF	GCTCTAAGGCAGTGATCGCA
ACKR3-RTR	GCTCCGAGTAGTCGAAGACG
KCNK12-RTF	CCGTAGTCCCCAGCAGATTC
KCNK12-RTR	AGATGGGGTTTAGTGGCAGC
MGP-RTF	TATCGCCACAGCAGAGATGG
MGP-RTR	TTGTAGGCGGCGTTGTATCC
REST-RTF	CAGAAGCAACTTGCACCACC
REST-RTR	TTGGTGTTTCCTGGCCACTT
LTCONS_00084841-RTF	AATCTCGTTCATCCATTC
LTCONS_00084841-RTR	ATGTCAAAGTGAAGAAATTC
LTCONS_00045964-RTF	CACAGCTTCATGCCCATTTGT
LTCONS_00045964-RTR	GGGAGATTTAGGCTCCCGAT
LTCONS_00048531-RTF	AACCTCCCGCAATGTCTCAA
LTCONS_00048531-RTR	TTGTGTTTCAGGTTGCGGTCT
LTCONS_00084076-RTF	GCTTACTCGGTGGCCATCG
LTCONS_00084076-RTR	CGAGTCAGAGGGAAACAAAGC
XR_002337668.1-RTF	CAGGTGCTTCTCTTGGGACG
XR_002337668.1-RTR	TGTGGGCCAGGTTCTTACAC
XR_002340445.1-RTF	GCCGCCAAGAAACGAAAACA
XR_002340445.1-RTR	GGGACCCTCAATGGTCTTGG
XR_001306655.2-RTF	TGCTGAGACGAGTGATGGCT
XR_001306655.2-RTR	ACAGGGCCACTCTCAAGTTT
XR_002346227.1-RTF	CCGGCCGCGGTATTTGA
XR_002346227.1-RTR	CTGGGACATCTGAGTTGCGG
XR_001299446.2-RTF	CAAATCCCGCAGTGTTCTCA
XR_001299446.2-RTR	TGGGGCAAGGCATCGAAAT
XR_303007.3-RTF	GGATCAGTGGGCTCAGTCTTT
XR_303007.3-RTR	GTGTTTCATCAGACGATCCCCA