

Supplementary online information for "QTL analysis of osteochondrosis traits in the elbow joint of pigs"

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1 Results

Here a complete list of QTLs exceeding the 5% chromosome-wide threshold is provided.

SSC	SURF	THICK	BONE	FISS	SAGIT	RADI
1	***	***	o	o		***
2	o	**				
3	o	o				
4	***	***	***	***		o
5	o		o	*		
6	o	o				*
7	***	o	o	**	*	***
8		o				
9	o					
10	o	o	*	***		
13	o	o				*
14	o			o		o
15	o	***				o
16		o	o			

Table S1: Traits and SSCs where a QTL exceeded the 5% chromosome-wide threshold ("o"), 5% genome-wide threshold ("*"), 1% genome-wide threshold ("**") and 0.1% genome-wide threshold ("***").

The genome scan revealed 43 pairs of traits and SSCs where a QTL exceeded the 5% chromosome-wide threshold with 18, 13 and 11 of these also exceeding the 5%, 1% and 0.1% genome-wide threshold, respectively (see Table S1). In addition, there were three cases where a second QTL exceeded a 5% chromosome-wide threshold, given an already existing first QTL on the chromosome. Thus, in total 46 QTLs were detected. The estimated positions of the QTLs with associated 95% confidence intervals are shown in Table S2.

SSC	trait	position	pct.	chr	trait	position	pct.
1	SURF	51 ([39; 58])	3.8%	7	SURF	61 ([54; 64])	2.8%
1	THICK	53 ([44; 60])	3.1%	7	THICK	11 ([0; 26])	1.5%
1	BONE	55 ([28; 84])	2.7%	7	BONE	63 ([51; 64])	1.3%
1	FISS	49 ([34; 60])	2.0%	7	FISS	57 ([51; 64])	1.9%
1	RADI	27 ([20; 44])	3.6%	7	SAGIT	29 ([18; 36])	1.7%
2	SURF	11 ([0; 24])	1.3%	7	RADI	31 ([20; 36])	3.8%
2	THICK	15 ([6; 22])	1.7%	8	THICK	45 ([22; 70])	1.2%
3	SURF	27 ([6; 36])	2.0%	9	SURF	69 ([62; 82])	1.3%
3	THICK	63 ([0; 22] \cup [54; 76])	1.5%	10	SURF	81 ([62; 100])	1.6%
4	SURF	79 ([62; 83])	2.9%	10	THICK	59 ([34; 90])	1.4%
4	THICK	75 ([65; 88])	3.8%	10	BONE	75 ([70; 86])	1.7%
4	BONE	23 ([16; 32]) 2nd QTL	1.8%	10	FISS	83 ([76; 100])	3.1%
4	BONE	71 ([58; 80])	2.7%	13	SURF	81 ([75; 86])	1.1%
4	FISS	69 ([53; 90])	2.5%	13	THICK	85 ([75; 92])	1.3%
4	RADI	41 ([28; 44])	2.4%	13	RADI	93 ([82; 100])	1.7%
5	SURF	27 ([18; 48])	1.7%	14	SURF	43 ([28; 96])	1.5%
5	BONE	53 ([40; 54])	1.6%	14	FISS	55 ([40; 72])	1.1%
5	FISS	23 ([18; 42])	2.5%	14	RADI	83 ([64; 96])	1.3%
6	SURF	13 ([4; 126])	0.9%	15	SURF	55 ([46; 78])	1.2%
6	THICK	37 ([20; 54])	1.4%	15	THICK	53 ([48; 78])	2.3%
6	RADI	51 ([34; 90])	1.4%	15	RADI	83 ([66; 100])	1.6%
6	RADI	119 ([110; 144]) 2nd QTL	2.6%	16	THICK	37 ([14; 38])	1.4%
7	SURF	5 ([0; 14]) 2nd QTL	2.2%	16	BONE	23 ([2; 38])	1.0%

Table S2: List of QTLs exceeding the 5% chromosome-wide threshold. The QTL positions with associated 95% confidence regions correspond to the peaks of the log-likelihood ratio curves. Percentage of phenotypic variation explained by the QTL is also provided. For the three cases with two QTLs, those considered to be the second QTLs are marked as such. In one case the confidence region was not an interval (there was a second peak, but not a significant second QTL) and this is shown as a set union, \cup , of two intervals.