

Appendix A. Table A4. Genotypes and alleles' frequencies of adaptation and growth markers.

Molecular marker (Genotype)	Observed			Expected			Chi square, $\chi^2$		
	Male	Femal e	Both	Male	Femal e	Both	p-value	p- value	p- value
<b>Adaptation trait markers</b>									
A. Halothane gene (HAL)							0.7000	0.8000	0.8000
<b>NN</b>	<b>0.8824</b>	<b>0.9600</b>	<b>0.9403</b>	<b>0.8858</b>	<b>0.9604</b>	<b>0.9412</b>			
Nn	0.1176	0.0400	0.0597	0.1107	0.0392	0.0579			
nn	0.0000	0.0000	0.0000	0.0035	0.0004	0.0009			
<b>N</b>	<b>0.9412</b>	<b>0.9800</b>	<b>0.9701</b>						
n	0.0588	0.0200	0.0299						
B. $\alpha$ (1, 2)-fucosyltransferase gene (FUT1)							0.1000	0.5000	0.0500
<b>AA</b>	<b>0.3333</b>	<b>0.0750</b>	<b>0.1455</b>	<b>0.2500</b>	<b>0.0564</b>	<b>0.0955</b>			
AG	0.3333	0.3250	0.3273	0.5000	0.3622	0.4271			
GG	0.3333	0.6000	0.5273	0.2500	0.5814	0.4774			
<b>A</b>	<b>0.5000</b>	<b>0.2375</b>	0.3091						
G	0.5000	0.7625	0.6909						
<b>Growth marker</b>									
A. Myogenic transcription factor (MYOG)							0.8000	0.3000	0.3000
AA	0.8333	0.7143	0.7353	0.8403	0.7347	0.7528			
AB	0.1667	0.2857	0.2647	0.1528	0.2449	0.2297			
<b>BB</b>	<b>0.0000</b>	<b>0.0000</b>	<b>0.0000</b>	<b>0.0069</b>	<b>0.0204</b>	<b>0.0175</b>			
A	0.9167	0.8571	0.8676						
<b>B</b>	<b>0.0833</b>	<b>0.1429</b>	<b>0.1324</b>						

Favorable genotypes and alleles are marked with bold.