

### Supplementary Material to “A comprehensive transcriptome analysis of skeletal muscles in two Polish pig breeds differing in fat and meat quality traits”

**Table S5** - Correlation coefficient r between FPKMs of DEGs in *semimembranosus* and pig production traits.

Trait	Differentially expressed genes																
	ASS1	UCLH1	LIPE	HES1	LXRA	MAOB	SCRF2	VCAN	APOD	LIMK1	PEX11G	PPP11R1	HP	OAS2	PVALB	CNN1	GPX3
<b>Fattening traits</b>																	
age at slaughter	<u>0.69**</u>	0.22	0.23	-0.40	0.35	0.43	-0.33	-0.16	<u>0.80***</u>	0.26	0.40	-0.32	<u>0.75***</u>	<u>-0.67**</u>	-0.36	-0.31	<u>0.76***</u>
daily gain (g/kg)	-0.49	0.31	-0.49	0.63**	-0.38	-0.51*	0.42	0.57*	-0.54*	-0.53*	-0.57*	<u>0.85***</u>	-0.35	-0.54*	0.52*	0.70**	-0.53*
feed gain ration (g/day)	0.55*	0.33	0.32	-0.51*	0.23	0.54*	-0.46	-0.59*	0.46	0.41	0.52*	<u>-0.76***</u>	0.19	0.44	-0.31	-0.62**	0.54*
feed intake (kg)	0.48	0.24	0.28	-0.51*	0.15	<u>0.66**</u>	-0.51*	-0.55*	0.53*	0.56*	0.46	<u>-0.72**</u>	0.35	0.49	-0.36	-0.46	0.50*
<b>Slaughter traits</b>																	
weight of ham (kg)	-0.43	-0.59*	-0.39	0.36	-0.54*	-0.16	0.33	0.46	-0.23	-0.18	-0.63**	0.38	-0.30	0.23	0.26	0.61*	-0.31
Meat percentage (%)	-0.29	-0.42	-0.32	0.36	-0.41	-0.53*	0.53*	0.55*	-0.40	<u>-0.68**</u>	-0.58*	0.40	-0.19	-0.11	0.41	0.25	-0.27
<b>Semimembranosus</b>																	
firmness by Warner-Bratzler	-0.15	-0.08	0	0.49	-0.11	-0.34	0.60*	0.35	-0.24	-0.31	-0.22	0.44	-0.22	-0.09	0.26	0.24	-0.12
harness by TPA	0	-0.21	0.49	0.43	0.50	-0.23	-0.07	-0.11	0.11	0.12	0.28	0.55*	0.26	-0.10	-0.01	0.15	-0.03
pH24	-0.34	-0.15	0.17	0.30	-0.02	-0.28	-0.10	-0.32	-0.65**	0.27	0.04	0.05	<u>-0.70**</u>	<u>-0.69**</u>	0.04	0.15	-0.46

\*-  $P \leq 0.05$ ; \*\*-  $P \leq 0.01$ , \*\*\*-  $P \leq 0.001$ . underlined values were significant after Bonferroni correction. In additional LIPE gene although it was not validated by qPCR was correlated with pig traits. The transcript levels were showed as normalized FPKM values.