

Table S1. Pig trait values dependent on breed effect (mean±S.D).

Index	PLW (96)	PUŁ (150)	PL (96)	Total (336)
Water exudation (%)	35.6 ± 7.6 ^A	28.8 ± 2.50 ^B	36.2 ± 6.54 ^A	33.4 ± 0.44
Meat color L*(lightness)	53.8 ± 2.43 ^A	55.1 ± 3.73 ^B	55.1 ± 2.31 ^B	54.8 ± 3.10
Meat color b*(yellowness)	2.37 ± 0.91 ^A	2.94 ± 1.17 ^B	2.45 ± 0.68 ^A	2.65 ± 1.02
pH 45 min (<i>longissimus dorsi</i>)	6.30 ± 0.19 ^A	6.16 ± 0.21 ^B	6.28 ± 0.16 ^A	6.23 ± 0.20
pH 24 h (<i>longissimus dorsi</i>)	5.59 ± 0.11 ^A	5.52 ± 0.09 ^B	5.61 ± 0.10 ^A	5.57 ± 0.11
pH 45 min (<i>semimembranosus</i>)	6.33 ± 0.16 ^A	6.21 ± 0.07 ^B	6.28 ± 0.14 ^A	6.22 ± 0.19
pH 24 h (<i>semimembranosus</i>)	5.62 ± 0.12 ^A	5.56 ± 0.11 ^B	5.65 ± 0.10 ^A	5.60 ± 0.11
IMF (%)	1.34 ± 0.41 ^A	1.70 ± 0.46 ^B	1.12 ± 0.14 ^C	1.41 ± 0.43
Carcass yield (%)	77.2 ± 2.71 ^A	74.5 ± 2.28 ^B	76.2 ± 2.27 ^C	75.7 ± 2.47
Loin mass (kg)	6.18 ± 0.58 ^A	5.06 ± 0.43 ^B	5.95 ± 0.60 ^C	5.62 ± 0.73
Ham mass (kg)	9.28 ± 0.62 ^A	8.78 ± 0.62 ^B	9.23 ± 0.40 ^A	9.05 ± 0.61
Average backfat thickness (cm)	1.31 ± 0.31 ^{Aa}	1.55 ± 0.42 ^B	1.23 ± 0.28 ^{Ab}	1.40 ± 0.38
Loin eye area (cm²)	52.2 ± 5.37	51.9 ± 5.53	53.4 ± 4.50	52.4 ± 5.22
Lean meat percentage (%)	61.0 ± 3.01 ^{Aa}	60.1 ± 3.08 ^{Ab}	62.4 ± 2.21 ^B	61.1 ± 2.95
Primary cuts (kg)	24.1 ± 1.27 ^A	22.2 ± 1.45 ^B	24.0 ± 1.09 ^A	23.2 ± 1.57
Average daily gain (g/day)	924 ± 107 ^A	778 ± 141 ^B	945 ± 105 ^A	865 ± 146
Feed conversion (kg/kg)	2.69 ± 0.22 ^A	3.04 ± 0.33 ^B	2.75 ± 0.20 ^A	2.86 ± 0.32
Daily feed intake (kg)	2.48 ± 0.30 ^A	2.33 ± 0.31 ^B	2.59 ± 0.25 ^C	2.44 ± 0.31
Age at slaughter (day)	167 ± 16.4 ^A	184 ± 21.2 ^B	165 ± 19.9 ^A	174 ± 22.6

Mean± standard deviation. Within rows, in each column, means denoted by different letter superscripts differ
^{AB}P<0.01; ^{ab}P<0.05. PLW – Polish Large White, PUŁ – Puławska, PL – Polish Landrace.

Table S2. The frequencies of genotypes and alleles in *FASN* gene.

	Genotype			Alleles	
	GG	AG	AA	G	A
PL	-	0,42 (39)	0,58 (54)	0,21	0,79
PLW	0,11 (10)	0,73 (65)	0,16 (14)	0,48	0,52
PUL	0,66 (100)	0,3 (46)	0,04 (6)	0,81	0,19

Table S3. The frequencies of genotypes and alleles in *SCD* gene.

	Genotype			Alleles	
	GG	AG	AA	G	A
PL	0,91 (74)	0,09 (7)	-	0,96	0,04
PLW	0,82 (55)	0,18 (12)	-	0,91	0,09
PUL	0,66 (99)	0,32 (49)	0,02 (3)	0,82	0,18

Table S4. The frequencies of genotypes and alleles in *ACACA* gene.

	Genotype			Alleles	
	TT	CT	CC	T	C
PL	0,62 (49)	0,35 (28)	0,03 (2)	0,80	0,20
PLW	0,74 (64)	0,24 (21)	0,01 (1)	0,87	0,13
PUL	0,57 (87)	0,36 (55)	0,07 (10)	0,75	0,25

Table S5. Association of *FASN* mutation and analyzed traits (LSM±S.E.).

Index	Genotype	PLW	PUŁ	PL	Total	GLM	
						<i>FASN</i>	Breed
IMF (%)	GG	1.36±0.11	1.66±0.05	-	1.56±0.06	ns	***
	AG	1.31±0.05	1.75±0.08	1.11±0.02	1.58±0.05		
	AA	1.44±0.11	1.52±0.19	1.15±0.02	1.56±0.07		
Meat color a* (redness)	GG	16.0±0.49	15.8±0.11	-	16.8±0.20	ns	ns
	AG	16.8±0.27	15.7±0.14	16.3±0.14	16.7±0.16		
	AA	17.0±0.42	15.9±0.32	16.5±0.16	16.6±0.18		
pH 24 h (<i>longissimus dorsi</i>)	GG	5.61±0.03	5.52±0.01	-	5.49±0.02	ns	***
	AG	5.59±0.01	5.53±0.01	5.61±0.01	5.49±0.01		
	AA	5.59±0.03	5.52±0.04	5.61±0.02	5.49±0.02		
pH 24 h (<i>semimembranosus</i>)	GG	5.62±0.04	5.57±0.04	-	5.60±0.02	ns	***
	AG	5.63±0.02	5.56±0.02	5.65±0.01 ^a	5.59±0.02		
	AA	5.61±0.04	5.53±0.01	5.65±0.02 ^b	5.58±0.02		
Ham mass (kg)	GG	9.30±0.18	8.80±0.16	-	8.84±0.08 ^A	ns	***
	AG	9.21±0.08	8.72±0.07	9.18±0.06	9.05±0.07 ^B		
	AA	9.27±0.15	8.96±0.06	9.29±0.05	9.26±0.08 ^C		
Loin eye area (cm ²)	GG	52.4 ± 1.60	51.9 ± 1.63	-	51.9 ± 0.80	ns	***
	AG	52.6 ± 0.70	51.9 ± 0.71	53.2 ± 0.6	52.5 ± 0.63		
	AA	49.3 ± 1.36	54.6 ± 0.56	53.2 ± 0.5	52.3 ± 0.80		
Lean meat percentage (%)	GG	61.8 ± 0.86	60.3 ± 0.98	-	60.4 ± 0.47 ^A	ns	***
	AG	60.9 ± 0.37	60.0 ± 0.43	62.4 ± 0.34	61.0 ± 0.37 ^{AB}		
	AA	61.0 ± 0.73	61.0 ± 0.34	62.1 ± 0.30	61.8 ± 0.47 ^B		
Primary cuts (kg)	GG	24.4 ± 0.34	22.3 ± 0.35	-	22.5 ± 0.17 ^A	ns	***
	AG	24.0 ± 0.15	22.1 ± 0.15	23.8 ± 0.13	23.3 ± 0.14 ^B		
	AA	23.7 ± 0.29	22.9 ± 0.112	24.0 ± 0.12	23.9 ± 0.17 ^C		

Allele: A – wild type; G – mutation; Within rows, in each column, means denoted by different letter superscripts differ ^{AB}P<0.01; ^{ab}P<0.05. PLW – Polish Large White, PUŁ – Puławska, PL – Polish. The linear model for mixed analysis was: $Y_{ijkl} = \mu + d_i + b_l + (d_i \cdot b_l) + \alpha(x_{ijk}) + e_{ijkl}$ where: Y_{ijk} – observation, μ – overall mean, d_i – fixed effect of genotype group, b_l – fixed effect of the breed, $(d_i \cdot b_l)$ – the interaction between d_i genotype group and breed, $\alpha(x_{ijk})$ – covariate for weight of the right side of the carcass, e_{ijkl} – random error. GLM model for analysis within breeds omitted b_j – fixed effect of breed and $(d_i \cdot b_j)$ – the interaction between d_i genotype group and breed. Landrace.

Table S6. Association of the ACACA mutation and analyzed traits (LSM \pm S.E).

Index	Genotype	PLW	PUŁ	PL	Total	GLM	
						ACACA	Breed
Water exudation (%)	CC	-	30.7 \pm 1.97	-	30.9 \pm 2.02		
	CT	37.3 \pm 1.76	30.6 \pm 0.85	36.2 \pm 1.29	33.5 \pm 0.99	ns	**
	TT	34.9 \pm 1.04	29.9 \pm 0.68	36.8 \pm 0.96	33.2 \pm 0.84		
Meat color L* (lightness)	CC	-	54.6 \pm 1.18	-	54.7 \pm 0.87		
	CT	53.7 \pm 0.52	55.3 \pm 0.51	55.5 \pm 0.44	55.1 \pm 0.69	ns	***
	TT	54.1 \pm 0.31	55.1 \pm 0.41	55.0 \pm 0.33	54.7 \pm 0.66		
Meat colour a* (redness)	CC	-	15.7 \pm 0.32	-	15.9 \pm 0.35		
	CT	16.7 \pm 0.35	15.7 \pm 0.14	16.3 \pm .19	16.1 \pm 0.17	ns	ns
	TT	16.7 \pm 0.21	15.8 \pm 0.11	16.5 \pm 0.14	16.3 \pm 0.15		
pH 24 h (longissimus dorsi)	CC	-	5.54 \pm 0.03	-	5.56 \pm 0.03	ns	***
	CT	5.62 \pm 0.02	5.52 \pm 0.01	5.63 \pm 0.02	5.57 \pm 0.02		
	TT	5.65 \pm 0.01	5.53 \pm 0.01	5.60 \pm 0.02	5.56 \pm 0.02		
pH 24 h (semimembranosus)	CC	-	5.58 \pm 0.03	-	5.59 \pm 0.03	ns	***
	CT	5.64 \pm 0.03	5.55 \pm 0.01	5.68 \pm 0.02 ^a	5.60 \pm 0.02		
	TT	5.62 \pm 0.02	5.57 \pm 0.01	5.63 \pm 0.02 ^b	5.60 \pm 0.02		
Loin mass (kg)	CC	-	5.06 \pm 0.11	-	5.41 \pm 0.13 ^a		
	CT	6.10 \pm 0.11	5.08 \pm 0.05	6.03 \pm 0.09	5.54 \pm 0.06 ^{ab}	ns	***
	TT	6.25 \pm 0.06	5.06 \pm 0.04	5.90 \pm 0.07	5.65 \pm 0.05 ^b		
Ham mass (kg)	CC	-	8.80 \pm 0.16	-	8.92 \pm 0.15		
	CT	9.37 \pm 0.13	8.73 \pm 0.07	9.28 \pm 0.09	9.00 \pm 0.07	ns	***
	TT	9.22 \pm 0.08	8.80 \pm 0.06	9.26 \pm 0.07	9.05 \pm 0.06		
Loin eye area (cm²)	CC	-	52.9 \pm 1.63	-	53.7 \pm 1.45		
	CT	51.4 \pm 1.20	52.4 \pm 0.71	53.6 \pm 0.7	52.5 \pm 0.71	ns	***
	TT	52.4 \pm 0.71	51.6 \pm 0.56	53.3 \pm 0.3	52.3 \pm 0.61		
Lean meat percentage (%)	CC	-	61.0 \pm 0.98	-	61.5 \pm 0.84		
	CT	61.7 \pm 0.63	59.8 \pm 0.43	62.4 \pm 0.39	60.9 \pm 0.41	ns	***
	TT	60.8 \pm 0.37	60.4 \pm 0.34	62.3 \pm 0.29	61.0 \pm 0.35		
Primary cuts (kg)	CC	-	22.4 \pm 0.35	-	22.9 \pm 0.31		
	CT	24.1 \pm 0.25	22.1 \pm 0.15	24.0 \pm 0.14	23.0 \pm 0.15	ns	***
	TT	24.1 \pm 0.15	22.3 \pm 0.112	23.9 \pm 0.11	23.3 \pm 0.13		
Feed conversion (kg/kg)	CC	-	3.03 \pm 0.10	-	2.98 \pm 0.08		
	CT	2.68 \pm 0.05	3.02 \pm 0.05	2.71 \pm 0.04	2.87 \pm 0.04	ns	***
	TT	2.67 \pm 0.03	3.06 \pm 0.04	2.75 \pm 0.03	2.86 \pm 0.03		
Age at slaughter (day)	CC	-	188 \pm 7	-	182 \pm 6 ^a		
	CT	165 \pm 4	185 \pm 3	166 \pm 4	176 \pm 3 ^{ab}	ns	***
	TT	168 \pm 2	183 \pm 2	162 \pm 3	173 \pm 3 ^b		

Allele: C – wild type, T – mutation. Within rows, in each column, means denoted by different letter superscripts differ^a $P<0.01$; ^{ab} $P<0.05$. PLW – Polish Large White, PUŁ – Puławska, PL – Polish Landrace. The linear model for mixed analysis was: $Y_{ijkl} = \mu + d_i + b_i + (d_i \cdot b_i) + \alpha(x_{ijk}) + e_{ijkl}$ where: Y_{ijk} – observation, μ – overall mean, d_i –fixed effect of genotype group, b_j – fixed effect of the breed, $(d_i \cdot b_i)$ – the interaction between d_i genotype group and breed, $\alpha(x_{ijk})$ – covariate for

weight of the right side of the carcass, e_{ijkl} – random error. GLM model for analysis within breeds omitted b_j – fixed effect of breed and $(d_i \cdot b_j)$ – the interaction between d_i genotype group and breed.

Table S7. Association of SCD mutation and analyzed traits (LSM±S.E.).

Index	Genotype	PLW	PUŁ	PL	Total	GLM SCD	Breed
Meat colour a* (redness)	AA	-	-	-	-		
	AG	16.4 ± 0.43	15.9 ± 0.15	16.2 ± 0.39	16.0 ± 0.21	ns	*
	GG	16.7 ± 0.23	15.7 ± 0.11	16.4 ± 0.12	16.2 ± 0.16		
pH 24 h (longissimus dorsi)	AA	-	-	-	-		
	AG	5.62 ± 0.03	5.52 ± 0.01	5.68 ± 0.04	5.55 ± 0.02	ns	***
	GG	5.59 ± 0.02	5.52 ± 0.01	5.61 ± 0.01	5.57 ± 0.02		
pH 45 min (semimembranosus)	AA	-	-	-	-		
	AG	6.32 ± 0.05	6.13 ± 0.03	6.27 ± 0.05	6.18 ± 0.03	ns	***
	GG	6.32 ± 0.03	6.12 ± 0.02	6.29 ± 0.02	6.22 ± 0.03		
pH 24 h (semimembranosus)	AA	-	-	-	-		
	AG	5.67 ± 0.04	5.56 ± 0.02	5.68 ± 0.04	5.59 ± 0.02	ns	***
	GG	5.63 ± 0.02	5.56 ± 0.01	5.65 ± 0.01	5.61 ± 0.02		
Carcass yield (%)	AA	-	-	-	-		
	AG	77.7±0.33 ^a	74.2±0.09	77.1±0.24 ^A	75.2±0.15	ns	**
	GG	77.1±0.18 ^b	74.6±0.06	76.3±0.07 ^B	75.8±0.12		
Average backfat thickness (cm)	AA	-	-	-	-		
	AG	1.39 ± 0.08	1.55 ± 0.06	1.35 ± 0.10	1.50 ± 0.06	ns	***
	GG	1.30 ± 0.04	1.56 ± 0.04	1.23 ± 0.03	1.39 ± 0.05		
Loin eye area (cm²)	AA	-	-	-	-		
	AG	52.4 ± 1.42	51.1 ± 0.74	52.9 ± 1.54	51.6 ± 0.86	ns	***
	GG	52.0 ± 0.76	52.2 ± 0.52	53.4 ± 0.47	52.5 ± 0.68		
Lean meat percentage (%)	AA	-	-	-	-		
	AG	59.9 ± 0.79	59.9 ± 0.46	61.4 ± 0.77	60.0 ± 0.50 ^a	ns	***
	GG	61.5 ± 0.42	60.4 ± 0.32	62.4 ± 0.24	61.3 ± 0.37 ^b		
Primary cuts (kg)	AA	-	-	-	-		
	AG	23.9 ± 0.31	22.0 ± 0.16	23.8 ± 0.30	22.5 ± 0.18 ^a	ns	***
	GG	24.2 ± 0.17	22.3 ± 0.11	24.0 ± 0.09	23.3 ± 0.15 ^b		
Average daily gain (g/day)	GG	-	-	-	-		
	AG	967±32	778 ± 21	906 ± 41	826 ± 23	ns	***
	AA	926±17	779 ± 15	948 ± 13	870 ± 18		
Feed conversion (kg/kg b. w.)	GG	-	-	-	-		
	AG	2.62 ± 0.07	2.99 ± 0.05	2.79 ± 0.08	2.90 ± 0.05	ns	***
	AA	2.68 ± 0.04	3.08 ± 0.03	2.76 ± 0.02	2.93 ± 0.03		
Daily feed intake (kg)	GG	-	-	-	-		
	AG	2.54 ± 0.10	2.31 ± 0.05	2.52 ± 0.10	2.37 ± 0.05	ns	***
	AA	2.48 ± 0.05	2.37 ± 0.03	2.60 ± 0.03	2.47 ± 0.04		
Age at slaughter (day)	GG	-	-	-	-		
	AG	163 ± 5	184 ± 3	159 ± 3	177 ± 4	ns	***
	AA	166 ± 3	184 ± 9	166 ± 2	174 ± 3		

Allele: A – wild type, G – mutation. Within rows, in each column, means denoted by different letter superscripts differ ^{AB}P<0.01; ^{ab}P<0.05. PLW – Polish Large White, PUŁ – Puławska, PL – Polish Landrace. The linear model for mixed analysis was: $Y_{ijkl} = \mu + d_i + b_t + (d_i \cdot b_t) + \alpha(x_{ijk}) + e_{jkl}$ where: Y_{ijk} – observation, μ – overall mean, d_i – fixed effect of genotype group, b_t – fixed effect of the breed, $(d_i \cdot b_t)$ – the interaction between d_i genotype group

and breed, $\alpha(x_{ijk})$ – covariate for weight of the right side of the carcass, e_{ijkl} – random error. GLM model for analysis within breeds omitted b_j – fixed effect of breed and $(d_i \cdot b_j)$ – the interaction between d_i genotype group and breed.
