

id

==> idpig.txt <==

gen	pig's generation
par	parity of the sow that the pig was born from
ear	ear notch (in form of litter-pig)
old_idpig	old pig id
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idsire	new pig id of the sire of the pig (in form of litter-pig)
iddam	new pig id for the dam giving birth to this pig (in form of litter-pig)
dam_sire_gen	the generation of the dam and sire giving birth to this pig
dam_sire_par	the parity of the dam giving birth to this pig
sex	1=boar, 2= gilt, 3=barrow
line	1= low RFI line, 2= high RFI line, 3=non-York
grp	contemporary group for grow-finish performance data
barn	barn on farm that pigs were housed in during grow-finish
finish_pen	pen within finishing barn that pig was located
diet	diet the pig was fed: 1= High Energy-Low Fiber 2=Low Energy-High Fiber
f_date	date when piglet was born, mm/dd/yyyy
litter	litter number
birth_wt	weight of piglet at birth (kg)
teats	total number of teats of the piglet
wean_date	date when the piglet was weaned, mm/dd/yyyy
wean_wt	weaning weight (kg)
fost_dam	ear notch number of the sow that the piglet was fostered to (in form of litter-pig)
dod	date pig died or was euthanized
castrate	1=yes, default=no

feeding_behavior

==> all 2 hour behavior.txt <==

idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
adfi	average daily feed intake over the whole test period
adfi1	average daily feed intake for the first half of the test period
adfi2	average daily feed intake for the second half of the test period
afiv	average feed intake per visit over the whole test period
afiv1	average feed intake per visit for the first half of the test period
afiv2	average feed intake per visit for the second half of the test period
afrv	average feeding rate per visit over the whole test period
afrv1	average feeding rate per visit for the first half of the test period
afrv2	average feeding rate per visit for the second half of the test period
anvd	average number of visits per day over the whole test period
anvd1	average number of visits per day for the first half of the test period
anvd2	average number of visits per day for the second half of the test period

aotd	average occupation time per day over the whole test period
aotd1	average occupation time per day for the first half of the test period
aotd2	average occupation time per day for the second half of the test period
aotv	average occupation time per visit over the whole test period
aotv1	average occupation time per visit for the first half of the test period
aotv2	average occupation time per visit for the second half of the test period
thr	two hour block (1 is for midnight to 2 am, 2 is for 2 am to 4 am, 3 is for 4 am to 6 am, etc.)
anv2h	average number of visits per 2 hr block over the whole test period
aot2h	average occupation time per 2 hr block over the whole test period
afi2h	average feed intake per 2 hr block over the whole test period
anv2h1	average number of visits per 2 hr block for the first half of the test period
aot2h1	average occupation time per 2 hr block for the first half of the test period
afi2h1	average feed intake per 2 hr block for the first half of the test period
anv2h2	average number of visits per 2 hr block for the second half of the test period
aot2h2	average occupation time per 2 hr block for the second half of the test period
afi2h2	average feed intake per 2 hr block for the second half of the test period

rfi

==> all RFI info.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
testlng	test length for feed efficiency (day)
onwt	ontest weight (kg)
offwt	offtest weight (kg)
ondate	ontest date
onage	ontest age (day)
offage	offtest age (day)
adg	average daily gain (kg/day) during test period
metamidw	average of $\text{onweight}^{0.75}$ and $\text{offweight}^{0.75}$ (kg); average of all $(\text{predicted_wt})^{0.75}$ for entire test-period
adfiind	average daily feed intake predicted from old procedure (quadratic regression on pig by pig basis) between onage and offage (kg/day)
offbf	ultrasound backfat (cm) at off-test
offlma	ultrasound longissimus muscle area (cm^2) at off-test
offscandate	off-test scan date

calcr

==> calcr_genotype.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
genotype	genotype at calcr locus

carcass

==> carcass.txt <==

idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
slaughter_date	slaughter date
weight	carcass weight (kg) [lbs?]
length	carcass length (cm) [inches?]
bf_10	backfat (cm) at 10th rib [inches?]
bf_last_rib	backfat (cm) at last rib [inches?]
bf_last_lum	backfat (cm) at last lumbar [inches?]
lma	longissimus muscle area (cm ²) [inches ² ?]
color	Loin color, National Pork Board standards, 5-point scale (1=pale pinkish gray to white; 5=dark purplish red)
firmness	Loin firmness, National Pork Board standards, 5-point scale (1=soft; 5=very firm)
marbling	Loin marbling, National Pork Board standards, 10-point scale (1=1.0% intramuscular fat; 10=10.0% intramuscular fat)
pH	Loin pH post-rigor, lower=more acidic (timing of collection unknown)
min_Y*	Loin, minolta Y: not needed suggest to not include in database
Hunter_L	Loin color value based on reflectance: 0=black, 100= pure white
HCW	Hot Carcass Weight (weight after dressing): units=lbs
trim	note if significant trimming was done on a carcass at the slaughter plant

cbc

==> CBC.txt <==

see <http://www.webmd.com/a-to-z-guides/complete-blood-count-cbc>

idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
Wn2BI	days from weaning to bleeding (day)
WBC	white blood cell count (x 10 ³ /ul)
RBC	red blood cell count (x10 ⁶ /ul)
hemoglobin	hemoglobin molecule fills up the red blood cells (gm/dl)
hematocrit	the amount of space (volume) red blood cells take up in the blood (%)
MCV	mean corpuscular volume (fl)
MCH	mean corpuscular hemoglobin(pg)
MCHC	mean corpuscular hemoglobin concentration (gm/dl)
RDW	Red cell distribution width(%)
platelet_auto	Platelet (thrombocyte) count(x10³)
MPV	Mean platelet volume (fl)
neutrophil	neutrophil count (x10 ³ /ul)
lymphocyte	lymphocyte count (x10 ³ /ul)
monocyte	monocyte count (x10 ³ /ul)
eosinophil	eosinophil count (x10 ³ /ul)
basophil	basophil count (x10 ³ /ul)
unidentifiedCells	unidentified cells count (x10 ³ /ul)
platelets_clumped	platelets clumped or not

dam_mate

==> dam mate info.txt <==

idmate	mating id
iddam	new pig id for the dam
tag	sow ear tag
idsire	new pig id for the mating sire
for_gen	generation the mating will give birth to
for_parity	parity the mating will give birth to
bred_date	date dam was bred, mm/dd/yyyy
sftwt	weight of sow when moved into farrowing house (kg)
sfbf	backfat thickness of sow when moved into farrowing house (cm)
swwt	weight of sow at weaning (kg)
swbf	backfat thickness of sow at weaning (cm) (mm?)
sfi	sow feed intake during lactation (lbs)
pfi	piglet feed intake during lactation (lbs)
litter	litter number of piglets
wn_date	date when litter was weaned
f_wt_date	date sow moved into farrowing house
f_pen	farrowing pen of sow, room-pen
f_date	date when litter was born
KSU_wt_date*	wean date of piglets sent to KSU for PRRS challenge
row	pen's row; row in which the barn is located at the Madrid farm?
gestation_pen	gestation pen of sow in gestation barn
diet	diet the dam was fed
comm	1=farrow before weighing, 2=dudded, 3=death, 4=lame, 6=sold
comm1	? I don't see this in any of my dam files
cull_date	date sow was removed from the breeding herd or died
category	1=primary, 2=alternative
pt_result	pregnancy test result?
pt_date	pregnancy test date?
comm_origin	?
old_ear	old ear, in format of 123-04-00S

genotyping

==> genotyped pig.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
dataset	genotyping batch, range: 1-10
sample_id	id of the sample

igf

==> igf-1.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	

igf1	igf-1 concentration (ng/mL)
batch	batch IGF1 samples were sent to company in; sometimes this is combined with plate
plate	plate on which IGF1 was assayed
sample_no	lab sample number assigned to IGF1 samples, chronological within batch
test_date	igf-1 measuring date; date IGF1 assay was run
imf	
==> imf.txt <==	
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
imf	Ultrasound intramuscular fat
mcr4	
==> mc4r_genotype.txt <==	
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
genotype	genotype at mc4r locus
meat_qual	
==> meat_quality.txt <==	
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
sequence	processing order
HCW	Hot Carcass Weight (kg?) [lbs]
BFMM	backfat depth (mm)
LEMM	loin eye depth (mm)
PLEAN	calculated percent fat-free lean (%)
pH	loin pH, 48 hours post-mortem
drip_loss_percent	loin moisture loss in retail package after 24 hours of storage, (%)
WHC_percent	loin percent water loss at 40,000xG (%)
wetness	loin wetness, National Pork Board standards, 3-point scale (1=wet; 3=dry)
firmness	loin firmness, National Pork Board standards, 3-point scale (1=soft; 3=very firm)
color	loin color, National Pork Board standards, 6-point scale (1=pale pinkish gray to white; 6=dark purplish red)
marbling	loin marbling, National Pork Board standards, 10-point scale (1=1.0% intramuscular fat; 10=10.0% intramuscular fat)
D65L	lightness score of loin, D65 light source: 0=black, 100=white
D65a	lightness score of loin, D65 light source,: +=red, -=green
D65b	lightness score of loin, D65 light source: +=yellow, -=blue
CL	lightness score of loin, C-illuminant light source: 0=black, 100=white
Ca	lightness score of loin, C-illuminant light source, : +=red, -=green
Cb	lightness score of loin, C-illuminant light source: +=yellow, -=blue

purge_percent	purge of a vacuum packaged chop (loin) after 1 week
SpH	Sensory pH: loin pH after aging 10 days
cook_loss	loin, % cook loss=[(raw weight - cooked weight)/raw weight]x100
JCS	Japanese color score of loin: 1-5 scale, 1=pale, 5=dark
L	star(*) value of loin after 10 days aging, D75 light source: 0=black, 100=white
a	* value of loin after 10 days aging, D75 light source: '+=red, -=green
b	* value of loin after 10 days aging, D75 light source: '+=yellow, -=blue
juic	loin juiceness: unanchored 15-unit scale (greater values indicate a greater juiciness)
tend	loin tenderness: unanchored 15-unit scale (greater values indicate a greater tenderness)
chew	loin chewiness: unanchored 15-unit scale (greater values indicate a greater chewiness)
pork_flav	loin pork flavor: unanchored 15-unit scale (greater values indicate a greater pork flavor)
off_flav	loin off flavor: unanchored 15-unit scale (greater values indicate a greater off flavor)
SP	star probe (kg): force utilized to compress sample to 20% of its (loin) original height
fat_percent	lipid content in loin (%)
mst_percent	% moisture determined by proximate composition (AOAC, 1990)

mix

==> miscaneous.sorted.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
fdr_type	feeder type, FIRE=fire feeder, CONV=conventional?
bleed_date	bleeding date (between 33-42 days)
sick_wn_bled	health status when bled
pretestwt	pretest weight (kg)
pretestdate	pretest date
post_wn_date	date of post weaning weight (one wk after weaning)
post_wn_wt	weight one week after weaning (kg)
total_wt	total weighted with the recording person (kg)
tare_wt	weight of the recording person (kg)
saw	?
transp	transponder number
transp2	2nd transponder number
transp3	3rd transponder number
tattoo	tattoo number for slaughter
marker_color	color used to sort animals into groups?
slaughter_grp	slaughter group
barn_from	barn which pig came from?
on_temp	on-test temperature?
temp2	tempurate on date2

temp2_date	date of 2nd temperature collection
therm	
scanner	individual who collected ultrasound scan: 1=Jennifer, 2=Dallas, 3=Jenelle, 4=Emily
comment	
comm	1=mummy, 2=stillborn, 3=death, 4=sold
	1=crushed/laid on, 2=starved, 3=failure to thrive, 4=euthanize, 5=killed by sow, 6=dead at weaning, 7=dead due to sickness, 8=anemic
comm2	1=other, 2=spraddle legs, 3=missing/deformed feet, 4=clef palate, 5=cripple/deformed legs, 6=low birth weight, 7=stepped on, 8=sick, 9=deformed head, 10=poor doing/failure to thrive
comm3	1=belly rupture, 2=rupture, 3=lame, 4=runt, 5=cauliflower ear, 6=sickness, 7=one testicle, 8=abscess, 9=shaker
comm4	
comm_after_offset	

rfi_rnaseq

==> RNAseq meta-data.txt <==

idsample	sample id
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
blk	block of experimental design
ord	order in block
pre_conc	RNA concentration after RNA prep, before globin depletion (ng/ul)
pre_RIN	RIN after RNA prep, before globin depletion
post_conc	RNA concentration after globin depletion (ng/ul)
post_RIN	RIN after globin depletion
RNA_date	RNA prep date
GD_date	globin depletion date
lane	lane where RNA sequenced
seq_year	RNA-seq year

scan

==> scan.txt <==

idscan	scan id
idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
bf	backfat (cm)
lma	longissimus muscle area (cm ²)
date	scan date

scid

==> SCID.txt <==

idpig	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
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diagnosis status of scid genotyping: normal, carrier, SCID, or unknown

==> sire info.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
tag	ear tag
pen	
category	
boar_group	
rank	
comment	
old_ear	old ear label, in format of XXX-XX-00S OR in text for alias

weight

==> weight_adg.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
wt	weight (kg)
wt_date	weigh date
adg	average daily gain (kg/day)

blood_inventory

==> bloodsampleG89.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
bleed_no	bleeding sequence: 1st, 2nd, ...
bleed	
alternative	
Tempus_tube_in_box	box label for Tempus tube
pos_in_box	position in box
copy	copy of each blood sample
location	box location
comment_wn_bleed	health status when bled
comment	

lps_rfi

==> lps.stimulate.animal.txt <==

	new pig id, a combination of parity, generation and ear notch (since generation 0, in the format of one digit for parity, two digits for generation, six digits for ear notch)
idpig	
ear_tag	ear tag
exp_grp	experiment group: chall, challenge; con, control
prep_no	RNA preparation group number
onwt	onweight for feed efficiency (FE) test (kg)

onage	onage for FE test
Ondate	ondate for FE test
Midwt	midweight (kg)
MidwtDate	midweight date
Offwt	offweight (kg)
Offdate	offdate
total_FI	total feed intake
testIngth	test length (day)
pen	pen for test
room	room for test
offbf	offscan backfat (cm)
growth	
adg	average daily gain
adfi	average daily feed intake
adga	average daily gain adjusted
offbfa	offtest bakcfat adjusted
crate_no	crate number
wt_trt	weight when LPS stimulated (kg)

lps_inventory

==> LPS_challenge_sample_inventory.txt <==

eartag	ear tag
bulk	
hpt	hours post treatment (hour)
boxID	boxID
location	box location
comnt	comment

lps_rnaseq

==> LPS_RNASeq_meta.txt <==

idsample	sample id
eartag	ear tag
hpt	hours post treatment (hour)
RNA_date	RNA extraction date
kit	kit number
pre_conc	RNA concentration after prep and before globin depletion (ng/ul)
pre_RIN	RIN after prep and before globin depletion
post_conc	RNA cocentration after globin depletion (ng/ul)
post_RIN	RIN after globin depletion
lane	RNA-seq sequencing lane
comnt	comment