

Table S1. The average of estimates of heritability (h^2), additive genetic variance (σ^2_g), residual variance (σ^2_e), and phenotypic variance (σ^2_p) for carcass traits, primal cut yields, and composite traits using bivariate models in Hanwoo cattle.

Trait	h^2	σ^2_g	σ^2_e	σ^2_p
Carcass traits				
CW	0.28	304.63	783.36	1087.99
EMA	0.47	29.23	33.48	62.70
BFT	0.58	7.31	5.40	12.71
MS	0.59	1.44	1.01	2.45
Primal cut yields				
TLN	0.35	0.14	0.27	0.42
SLN	0.43	5.32	7.15	12.47
STLN	0.39	0.31	0.50	0.81
CHK	0.21	1.80	6.66	8.46
BSK	0.51	3.18	3.06	6.24
TRD	0.52	2.23	2.05	4.28
BRD	0.50	5.48	5.38	10.86
SK	0.50	1.10	1.10	2.20
FK	0.29	4.63	11.54	16.18
RB	0.27	9.88	27.10	36.99
Composite traits				
HVC ¹	0.34	15.76	30.04	45.80
MVC ²	0.36	51.6	93.23	144.83
LVC ³	0.36	9.16	16.54	25.70

CW, carcass weight; BFT, backfat thickness; EMA, eye muscle area; MS, marbling score; TLN, tenderloin; SLN, sirloin; STLN, striploin; CHK, chuck; BSK, brisket; TRD, top round; BRD, bottom round; SK, shank; FK, flank; RB, rib; ¹ HVC, (CHK+SLN+STLN+TLN); ² MVC, (BSK+TRD+BRD+RB); ³ LVC, (FK+SK).