

Table S2. Summary of sequencing read alignment to the goat reference genome.

Sample	Total reads	Total mapped	Multiple mapped	Unique mapped
D1_1	122652950	119526217(97.45%)	11359329(9.26%)	108166888(88.19%)
D1_2	121783280	118365352(97.19%)	11693696(9.6%)	106671656(87.59%)
D1_3	119676092	116299281(97.18%)	11002117(9.19%)	105297164(87.99%)
D1_4	120264076	117157837(97.42%)	12697214(10.56%)	104460623(86.86%)
D1_5	120479764	117342955(97.4%)	12589812(10.45%)	104753143(86.95%)
W2_1	120859436	117162548(96.94%)	12277063(10.16%)	104885485(86.78%)
W2_2	123705754	120370171(97.3%)	12269044(9.92%)	108101127(87.39%)
W2_3	118304356	115202551(97.38%)	12025689(10.17%)	103176862(87.21%)
W2_4	136724132	132755116(97.1%)	15714255(11.49%)	117040861(85.6%)
W2_5	122445796	119027235(97.21%)	12710898(10.38%)	106316337(86.83%)
W4_1	120410174	116902441(97.09%)	11231241(9.33%)	105671200(87.76%)
W4_2	117388094	114165989(97.26%)	10431646(8.89%)	103734343(88.37%)
W4_3	120185204	116771445(97.16%)	12150598(10.11%)	104620847(87.05%)
W4_4	123101152	119636922(97.19%)	12345381(10.03%)	107291541(87.16%)
W4_5	123580984	120356723(97.39%)	12473458(10.09%)	107883265(87.3%)
W8_1	121955756	118574248(97.23%)	13868028(11.37%)	104706220(85.86%)
W8_2	119109088	116160798(97.52%)	13173902(11.06%)	102986896(86.46%)
W8_3	115449396	112576636(97.51%)	12046959(10.43%)	100529677(87.08%)
W8_4	119620226	116392152(97.3%)	13430024(11.23%)	102962128(86.07%)

W8_5	120674068	117566378(97.42%)	12965052(10.74%)	104601326(86.68%)
W12_1	119033274	115840121(97.32%)	13042473(10.96%)	102797648(86.36%)
W12_2	119799184	116198233(96.99%)	11636839(9.71%)	104561394(87.28%)
W12_3	119656710	116673515(97.51%)	10534177(8.8%)	106139338(88.7%)
W12_4	114642794	111662013(97.4%)	11230955(9.8%)	100431058(87.6%)
W12_5	122363858	119161730(97.38%)	10878213(8.89%)	108283517(88.49%)
