

Table 2 Overview of the sequencing and assembly

Item	W1	W3	R1	R3
Total raw reads	59 276 174	56 792 504	60 929 858	44 011 092
Adaptor percentage (%)	0.01	0.03	0.02	0.02
Low Quality percentage (%)	2.85	2.66	2.43	2.08
Total Clean Reads	57 575 196	55 265 234	59 436 460	43 087 310
Total raw length (bp)	7 409 521 750	7 099 063 000	7 616 232 250	5 501 386 500
Total clean length (bp)	7 196 899 500	6 908 154 250	7 429 557 500	5 385 913 750
Q30 percentage (%)	91.13	91.52	91.81	93.42
N percentage (%)	0.00	0.00	0.00	0.00
GC percentage (%)	51.16	50.16	50.60	50.65
Unmapped Reads	7 454 416	19 091 220	19 578 556	9 564 356
Unique Mapped Reads	5 447 531	13 131 590	12 761 953	4 811 709
Multiple Mapped Reads	467 177	814 550	1 602 701	485 175
Total Mapped Reads	5 914 708	1 3946 140	14 364 654	5 296 884
Total unigenes	35 618	45 142	41 265	38 588
Percentage of total Unigenes (%)	66.90	84.79	77.51	72.48

Note: W1: White meat and fruit stage; W3: White meat maturity stage; R1: Red meat and fruit stage; R3: Red meat maturation stage