

Table S2. Sequencing data and selected reference genome sequence alignment results.

Samples	Total Reads	Mapped Reads	Uniq Mapped Reads	Multiple Map Reads	Reads Map to '+'	Reads Map to '-'
hybrid	41 702	28 144 612	27 150 517	994 095	13 990 952	14 051 936
tilapia (NA)	610	(67.49%)	(65.11%)	(2.38%)	(33.55%)	(33.70%)
<i>O.niloticus</i>	42 152	31 130 747	30 155 953	974 794	15 495 455	15 542 463
(N)	458	(73.85%)	(754%)	(2.31%)	(36.76%)	(36.87%)
<i>O.aureus</i>	47 006	30 915 223	29 873 658	1 041 565	15 329 543	15 483 390
(A)	714	(65.77%)	(63.55%)	(2.22%)	(32.61%)	(32.94%)