

Table S7. Summary of mapping rate of full-length sequencing reads to Japanese flounder reference genome.

Sample	Total reads	Total mapped	Unmapped	Multiple mapped	Uniquely mapped	Reads map to '+'	Reads map to '-'
R	212319	184371 (86.84%)	27948 (13.16%)	2938 (1.38%)	181433 (85.45%)	100678 (47.42%)	80755 (38.03%)
S	183681	155400 (84.6%)	28281 (15.4%)	1578 (0.86%)	153822 (83.74%)	81780 (44.52%)	72042 (39.22%)