Figure S1. Overview of RNA-Seq mapping in channel catfish (*Ictalurus punctatus*).
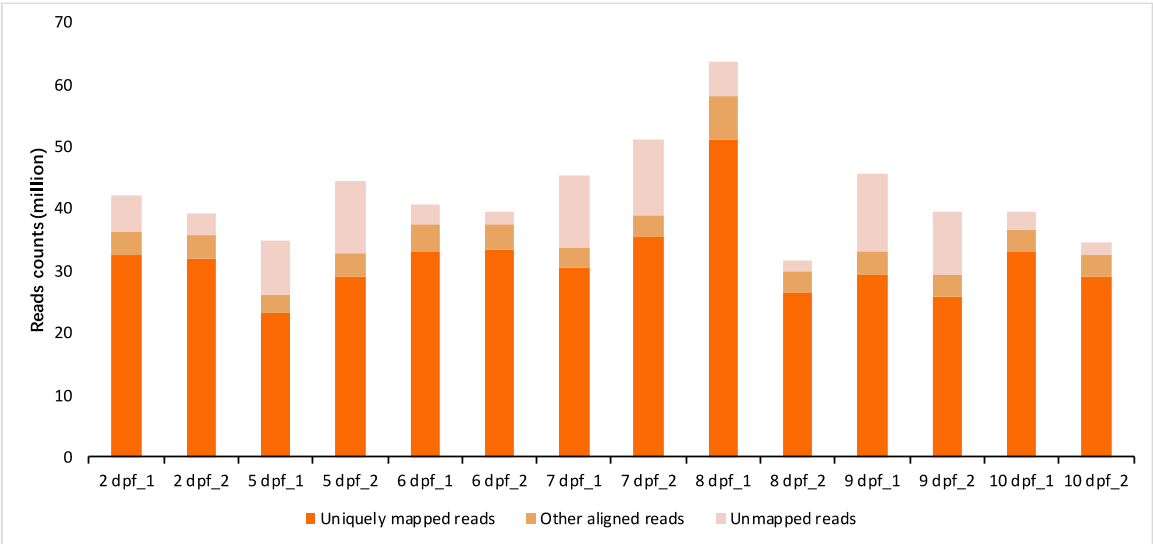
Figure S2. Analysis of network topology for different soft thresholding powers in channel catfish (*Ictalurus punctatus*). In the left diagram, y-axis is the scale-free fit index as a function of the soft-thresholding power (x-axis). The right diagram shows the mean connectivity (degree, y-axis) as a function of the soft-thresholding power (x-axis).
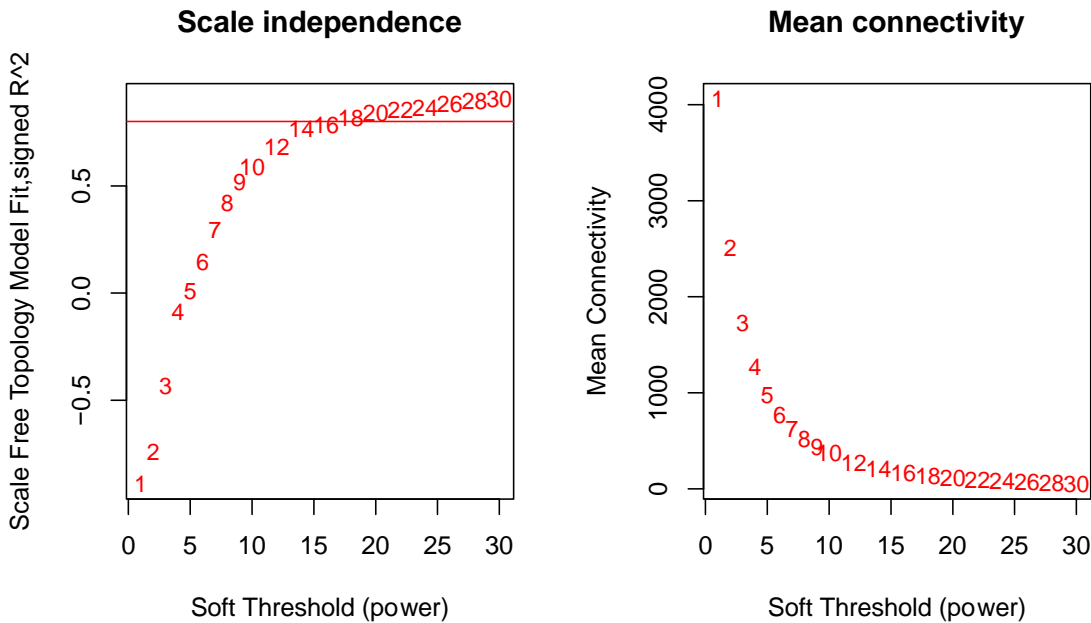
Sampling	No. of raw reads	No. of clean reads	%GC	No. of mapped reads	Mapping rate (%)
CC2-1	91,669,324	42,131,732	49	36,303,934	86.16%
CC2-2	89,890,166	39,249,396	50	35,763,124	91.12%
CC5-1	64,585,468	34,709,236	48	261,03,146	75.21%
CC5-2	84,453,314	44,511,770	48	32,883,240	73.87%
CC6-1	100,421,168	40,793,066	50	37,564,304	92.08%
CC6-2	94,323,974	39,364,512	48	37,419,614	95.06%
CC7-1	87,494,136	45,224,692	47	33,714,328	74.55%

CC7-2	98,318,154	51,048,372	47	39,055,300	76.51%
CC8-1	116,489,572	63,382,006	50	58,254,748	91.91%
CC8-2	73,963,212	31,525,758	49	29,772,108	94.44%
CC9-1	92,613,334	45,676,882	47	33,003,294	72.26%
CC9-2	79,448,748	39,374,808	48	29,202,904	74.17%
CC10-1	89,215,722	39,707,608	49	36,730,700	92.5%
CC10-2	95,788,206	34,652,038	48	32,555,886	93.95%