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Transcriptome analysis reveals the important roles of two-component system, flagellar assembly, active efflux system and outer membrane proteins in the anti-quinolone ability of *Vibrio harveyi* from Orange-spotted Grouper

Xiaochen Tang[1], Yu Ding[1]

[1] Fisheries College of Guangdong Ocean University, Guangdong Provincial Key Laboratory of Aquatic Animal Disease Control and Healthy culture, Southern Marine Science and Engineering Guangdong Laboratory (Zhanjiang), Guangdong Key Laboratory of Control for Disease of Aquatic Economic Animals, Zhanjiang, China

Correspondence
Yu Ding
Fisheries College, Guangdong Ocean University, 40 Jiefang East Road, Zhanjiang, Guangdong Province 524000, P R China.
Tel: +86-759-2383509; **Fax**: +86-759-2383507; **E-mail**: dingyuddd@163.com;

Table S1 Statistical analysis of the transcriptome sequencing and assembly

Summary	VR	VS
Raw reads	24,366,080	32,074,449
Clean reads	23,371,075	29,171,777
Error rate	4.08 %	9.04 %
Q30 (%)	91.28	88.41
GC content (%)	47.53	47.45
Mapped Reads	17,350,434	21,799,154
Mapped Ratio	74.24%	74.73%

Table S2 Annotation statistics of predicted genes

Annotated Database	Annotated_Number	300<=length<1000	length>=1000
COG	2086	967	1112
GO	1895	861	1028
KEGG	1485	653	827
Pfam	2330	1109	1216
Swissprot	2057	947	1105
nr	2507	1209	1283
All_Annotated	2509	1210	1283

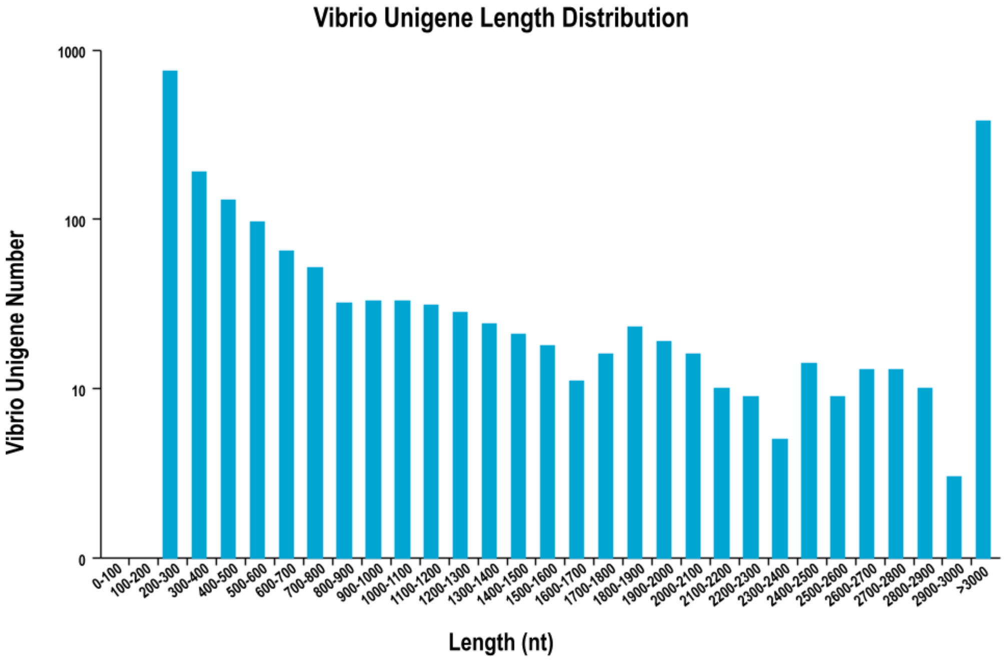

Figure S1 Length distribution of obtained Unigenes

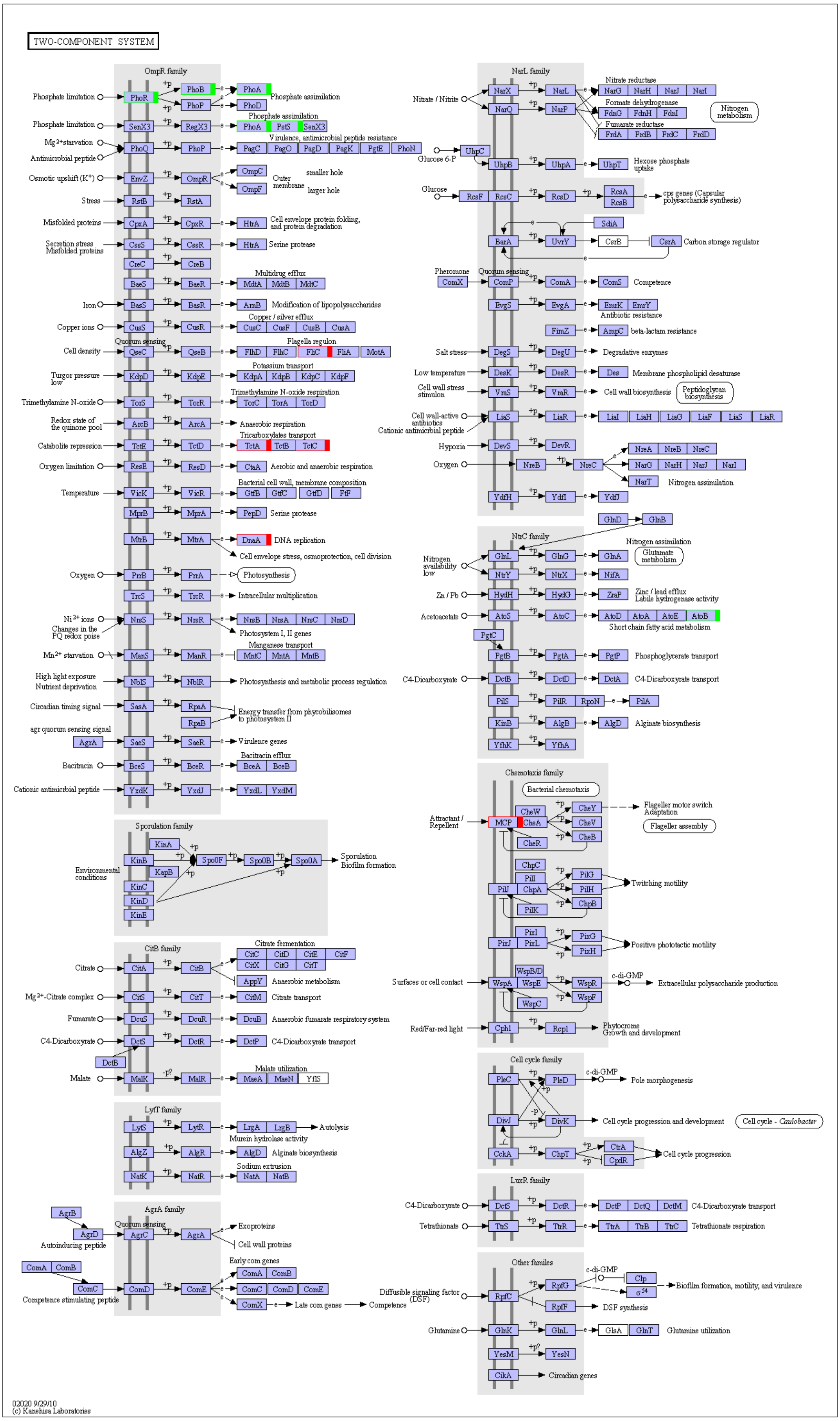

Figure S2 DEGs in two-component system

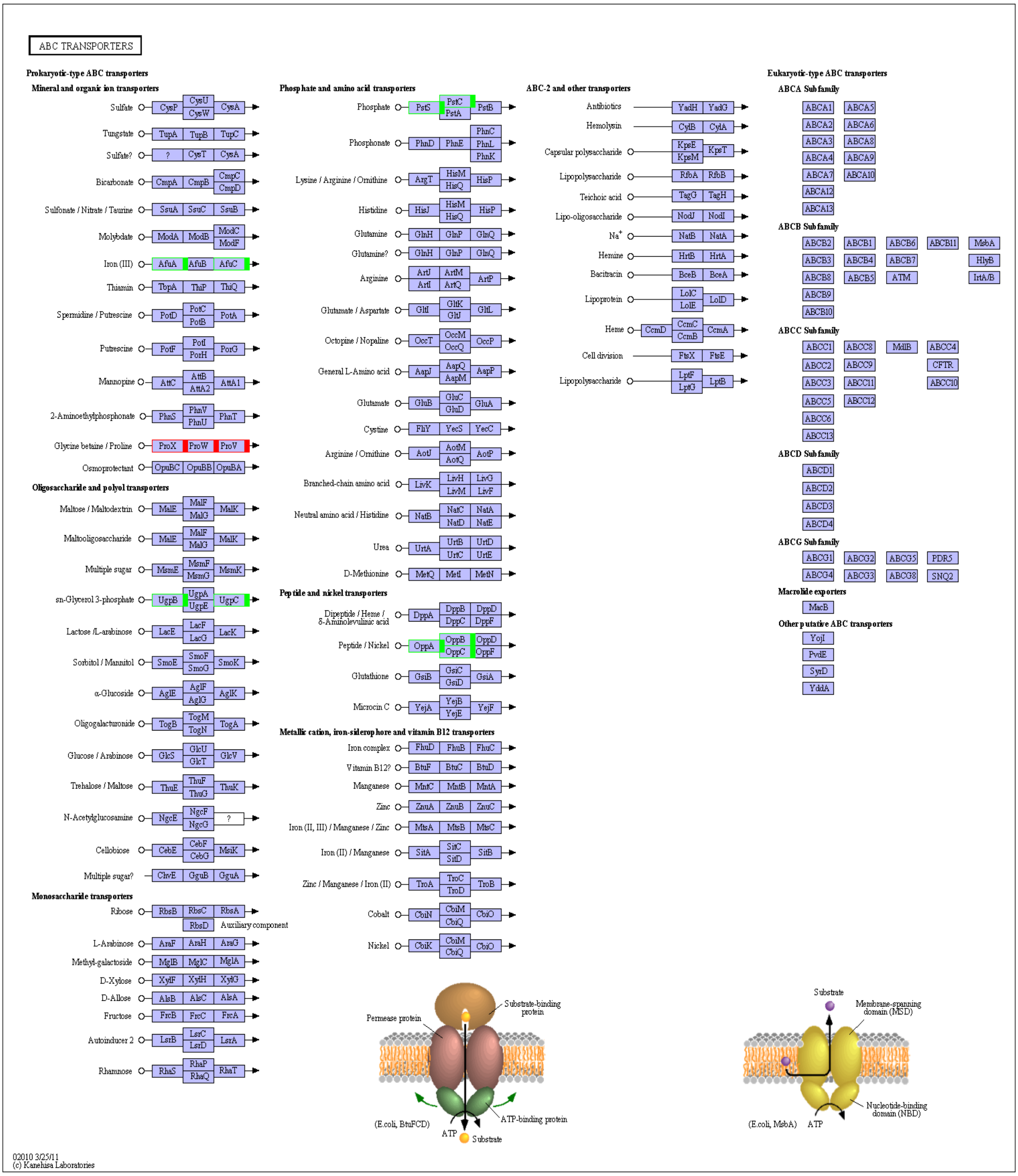

Figure S3 DEGs in ABC transporters system

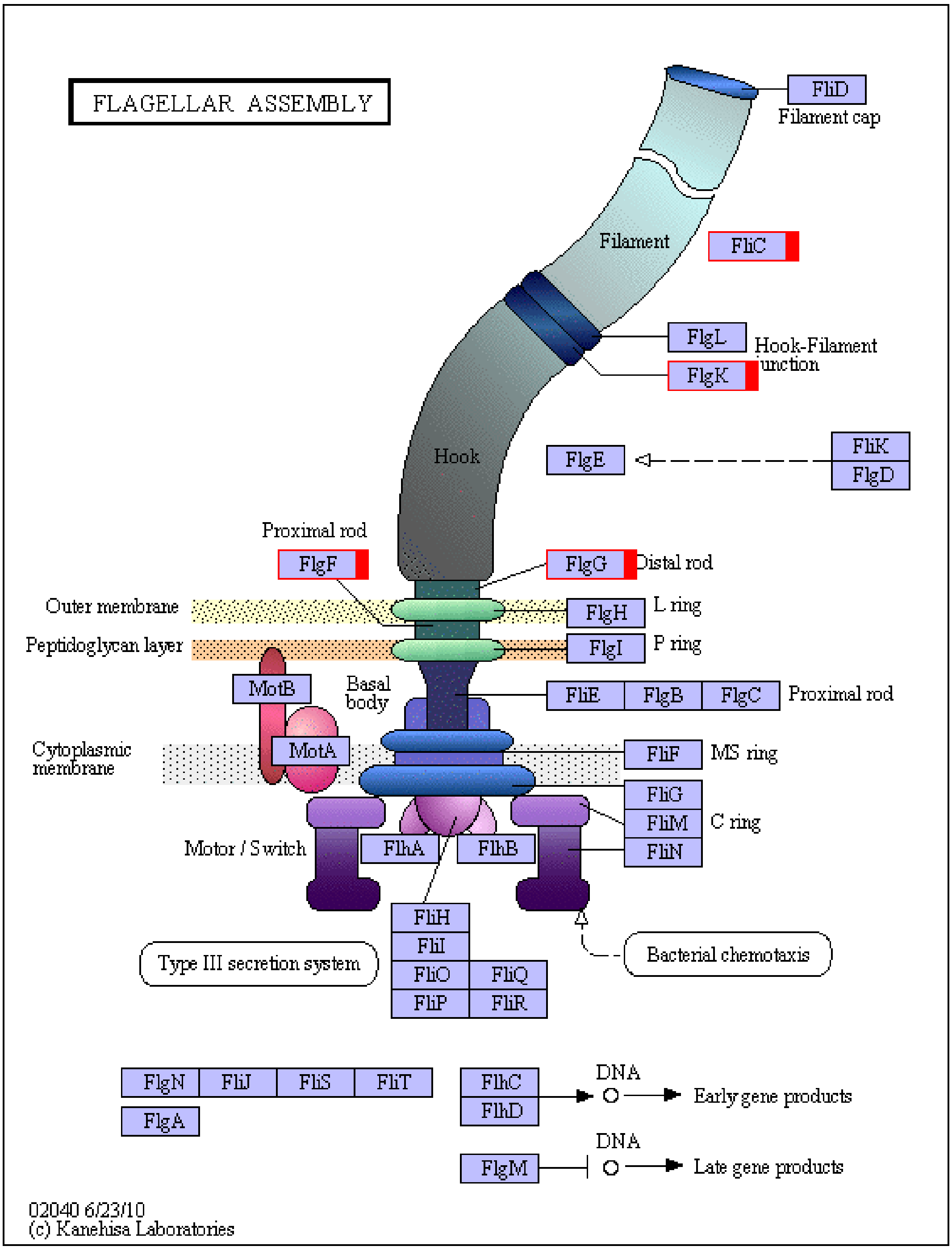

Figure S4 DEGs in flagellar assembly process