

**Table S1** Details of primers used for qRT-PCR experiments

<b>Gene</b>	<b>Description</b>	<b>Primer</b>
18S rRNA	18S rRNA	GCTGATATCAACGCCAAC GACAAGCCCCTCCTGAAAT
FP1V-1	Foot protein 1 variant 1	TGCAAAAGACGCCGTATGT TGGGTTCTTCAGACAGGGA
FP1V-2	Foot protein 1 variant 2	AACCATGGACTGCTTGGAG TGTTCTTCCTGTCTTGC
FP4V-1	Foot protein-4 variant-1	TGCAGTCTTGGTCGTCTG AACGTCGGTAGTAGTGCCT
PLC-β	Phospholipase C beta	CTTCTTCCTTGCTGCC TTGACCTGATGAATCCTGCT
MAGL	Monoacylglycerol lipase	TAGTGCTGTTGTCCCTGTC TGTTGGTGTGATGCAGTGA
PKA	cAMP-dependent protein kinase	AGCGATGTCCAATTCAAGCT AGGGGTAAGTGGGGAGAAA

**Table S2** Summary of RNA-seq data for attached (AT) and unattached (UAT) *P. viridis*

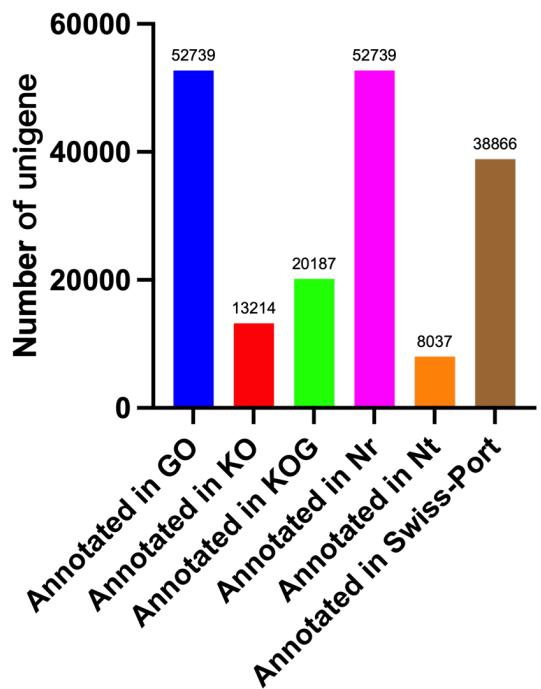
<b>Sample</b>	<b>Raw Reads</b>	<b>Clean Reads</b>	<b>Clean Bases(Gb)</b>	<b>Q20 (%)</b>	<b>GC Content (%)</b>
AT1	54,698,918	53,115,242	7.97	96.78	36.92
AT2	48,519,088	47,122,664	7.07	96.9	36.61
AT3	48,129,850	46,757,870	7.01	97.19	36.49
UAT1	49,478,510	48,079,108	7.21	96.97	36.44
UAT2	50,581,238	49,069,894	7.36	96.78	36.57
UAT3	46,959,760	46,136,128	6.92	97.08	36.28

**Table S3** Summary of de novo assembly of the *P. viridis* transcriptome

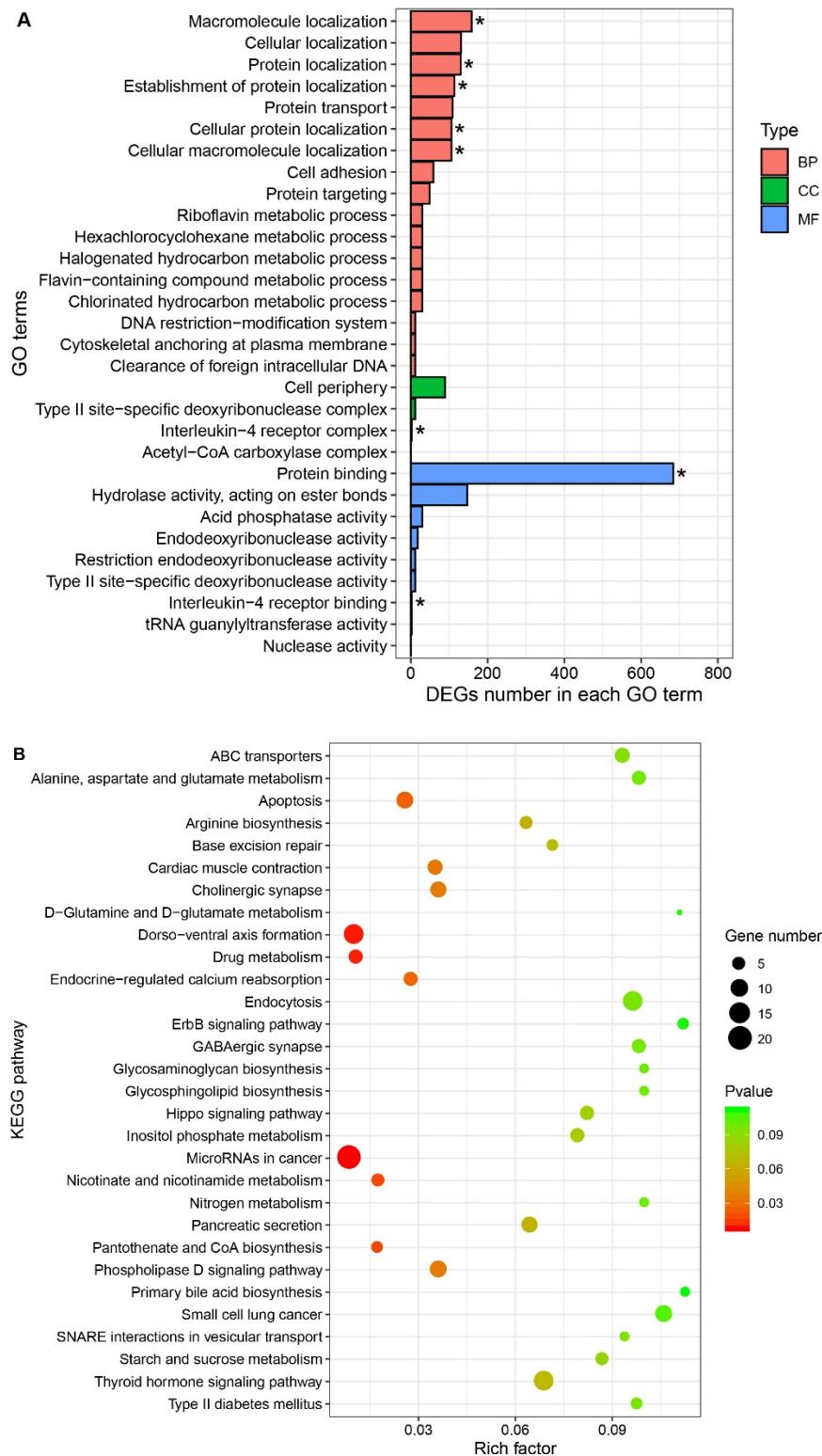
	Min Length(nt)	Mean Length(nt)	Median Length(nt)	Max Length(nt)	N50	Total number	Total length(nt)
<b>Transcripts</b>	201	795	361	65,553	1,592	335,166	266,499,739
<b>Unigenes</b>	201	1,232	689	65,553	2,074	181,179	223,159,074

**Table S4** Genes of GPCRs closely related with cannabinoid receptors in *P. viridis*

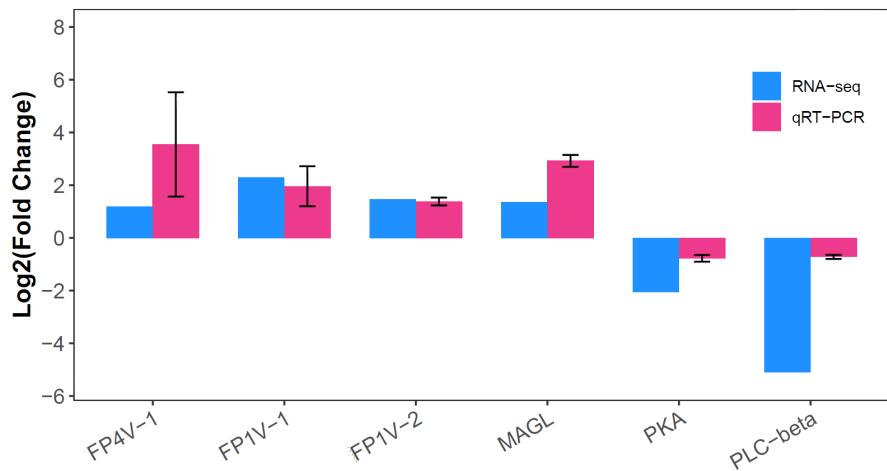
Transcript ID	log2 ratio	P value	Gene description	Gene name
Cluster-34876.0	-0.47407	0.73082	Sphingosine 1-phosphate receptor 1	S1PR1
Cluster-23089.0	0.20429	0.87862	Adenosine receptor A2b	ADORA2b
Cluster-56369.0	-1.3193	0.25979	Adenosine receptor A3-like	ADORA3-like
Cluster-10988.0	0.30964	0.70866	Adenosine receptor A2b-like	ADORA2b-like



**Figure S1** Functional annotation of genes in databases.



**Figure S2** Analysis of the differentially expressed genes (DEGs) between attached (AT) and unattached (UAT) mussel groups. (A) Top 30 enriched GO terms. BP: biological process; CC: cellular component; MF: molecular function. \*\* indicates  $P$  value  $\leq 0.001$ . \* indicates  $P$  value  $\leq 0.01$ . (B) Top 30 enriched KEGG pathways.



**Figure S3** Confirmation of RNA-seq results by qRT-PCR.

FP4V-1: foot protein 4 variant 1; FP1V-1: foot protein 1 variant 1; FP1V-2: foot protein 1 variant 2; MAGL: monoacylglycerol lipase abhd6-B-like; PKA: cAMP-dependent protein kinase catalytic subunit; PLC-beta: phospholipase C beta.