

Table S3 Gene expression involved in nutrition synthesis and transport and cellular information processing in yellow and red bacteriomes and the remaining body tissues.

Trinity ID	FPKM (FC)			Gene	Product	EC number	Function
	body	red	yellow				
DN151056_c1_g2	20.1	26.3 (-)	104.9 (5.4)	PANK	pantothenate kinase	2.7.1.33	CoA synthesis
DN155361_c0_g1	15.9	18.5 (-)	8.6 (-)	PPCS	phosphopantothenate-cysteine ligase	6.3.2.5	
DN155009_c0_g2	15.2	19.7 (-)	20.6 (-)	PPCDC	phosphopentothenoylecysteine decarboxylase	4.1.1.36	
DN143829_c0_g1	9.6	13.1 (-)	29.6 (2.9)	COASY	bifunctional coenzyme A synthase	2.7.7.3 & 2.7.1.24	
DN155712_c2_g2	13.2	6.8 (-)	861.7 (69.8)	GDH	glutamate dehydrogenase, mt	1.4.1.3	NH ₃ recycling
DN154114_c1_g1	201.9	149.1 (-)	134.9 (-)	GS	glutamine synthetase	6.3.1.2	
DN158059_c0_g3	39.8	502.1 (12.8)	126.7 (3.4)	GOGAT	glutamate synthase (NADPH)	1.4.1.13	
DN149933_c0_g1	2.3	39 (23)	24.8 (11.3)	ASR	isoaspartyl peptidase/L-asparaginase	3.4.19.5 & 3.5.1.1	
DN145636_c0_g2	2.9	22.9 (9.1)	3.4 (-)	GADL1	acidic amino acid decarboxylase GADL1	4.1.1.11	β-alanine synthesis
DN158110_c2_g1	4.6	1.9 (-)	1988.2 (455.1)	PAH	Phenylalanine hydroxylase	1.14.16.1	Tyrosine synthesis
DN149170_c0_g2	3.1	0.6 (-)	24 (7.5)	RAD51	DNA repair protein RAD51 homolog 3	N/A	DNA repair & replication
DN159094_c0_g1	1.1	0.6 (-)	7.2 (10.6)	HFM1	ATP-dependent DNA helicase HFM1	3.6.4.12	
DN74806_c0_g1	1.5	0.1 (-)	5.4 (3.7)	PIF1	ATP-dependent DNA helicase PIF1	3.6.4.12	
DN154852_c1_g2	5.9	11.8 (-)	40.9 (6.5)	LIG3	DNA ligase 3	6.5.1.1	
DN162793_c6_g2	4	7.3 (-)	26.3 (8)	DHX30	ATP-dependent RNA helicase DHX30	3.6.4.13	
DN159064_c0_g4	5.5	9.7 (-)	52.5 (9.8)	DHX36	ATP-dependent RNA helicase DHX36	3.6.4.13	
DN136421_c0_g1	1.3	4.7 (-)	16 (12.1)	RPB1	DNA-directed RNA polymerase II subunit RPB1	2.7.7.6	Transcription
DN158446_c2_g1	2.7	1.9 (-)	9.1 (3.7)	ALAS	alanine--tRNA ligase, mt	6.1.1.7	Aminoacyl-tRNA formation
DN141869_c0_g2	6.8	2.6 (-)	291.4 (48.5)	ASPS	aspartate--tRNA ligase	6.1.1.12	
DN142995_c0_g2	18.8	46.2 (2.5)	63 (3)	ARGS	arginine--tRNA ligase	6.1.1.19	

DN161509_c0_g3	3	3.8 (-)	21 (7)	CYSS	cysteine--tRNA ligase, mt	6.1.1.16	
DN79877_c0_g1	10.6	13 (-)	59.3 (6.1)	GLTX	glutamate--tRNA ligase, mt	6.1.1.17	
DN159506_c0_g2	18	50.1 (-)	80.8 (4.3)	GLYS	glycine--tRNA ligase	6.1.1.14	
DN161391_c0_g2	26.5	25.1 (-)	122.3 (4.6)	HISS	histidine--tRNA ligase	6.1.1.21	
DN155807_c0_g4	49.3	88 (-)	127.9 (2.6)	LYSS	lysine--tRNA ligase	6.1.1.6	
DN159445_c0_g1	12.6	42.9 (3.2)	271.6 (12.1)	METG	methionine--tRNA ligase	6.1.1.10	
DN163232_c1_g2	50.5	102 (-)	133.2 (2.8)	THRS	threonine--tRNA ligase	6.1.1.3	
DN140792_c0_g1	11.9	23.2 (-)	164.9 (17.1)	TFSM	elongation factor Ts, mt	N/A	Translation
DN160209_c1_g1	0.4	0.5 (-)	193.1 (445.7)	GUF	translation factor GUF1 homolog, mt	N/A	
DN155796_c0_g1	1.1	0.1 (-)	26.6 (24.3)	PAT-1	proton-coupled amino acid transporter	N/A	Amino acid transporter
DN162498_c0_g1	0.8	2.6 (-)	13.4 (19.7)	PAT-2	proton-coupled amino acid transporter	N/A	
DN162674_c0_g1	1.2	0.1 (-)	63.9 (52)	PAT-3	proton-coupled amino acid transporter	N/A	
DN146974_c0_g1	4.4	48.4 (10.6)	0.1 (-)	PAT-4	proton-coupled amino acid transporter	N/A	
DN159316_c0_g3	2.1	0.2 (-)	74.4 (34.3)	PAT-5	proton-coupled amino acid transporter	N/A	
DN158278_c0_g1	39.3	0.8 (-)	108.5 (4)	PAT-6	proton-coupled amino acid transporter	N/A	
DN146033_c0_g1	0	0 (-)	47 (891.4)	PAT-7	proton-coupled amino acid transporter	N/A	
DN161028_c1_g1	0.4	58.3 (157.6)	0 (-)	PAT-8	proton-coupled amino acid transporter	N/A	
DN153641_c3_g1	0	0 (-)	83 (11,585.2)	PAT-9	proton-coupled amino acid transporter	N/A	
DN154753_c0_g4	2.3	1.2 (-)	1242 (512)	PAT-10	proton-coupled amino acid transporter	N/A	
DN157783_c0_g2	5.9	0.7 (-)	135.4 (27.9)	PAT-11	proton-coupled amino acid transporter	N/A	
DN144557_c0_g1	0	0 (-)	51.6 (955.4)	BAT-1	b(0,+)-type amino acid transporter	N/A	
DN149645_c0_g4	5.6	43.7 (8)	1.5 (-)	BAT-2	b(0,+)-type amino acid transporter	N/A	
DN155947_c0_g1	10.6	1.7 (-)	25.2 (3)	YLAT-1	Y+L amino acid transporter	N/A	
DN127352_c0_g1	24.9	11.7 (-)	451.2 (13.9)	YLAT-2	Y+L amino acid transporter	N/A	
DN160184_c0_g1	4.8	270 (45.3)	87.8 (13)	YLAT-3	Y+L amino acid transporter	N/A	

DN61104_c0_g1	0.1	4.1 (36.9)	0 (-)	VGLUT-1	vesicular glutamate transporter	N/A	
DN129212_c0_g1	1.3	0.7 (-)	98.4 (73.5)	VGLUT-2	vesicular glutamate transporter	N/A	
DN148784_c0_g3	4.2	0.1 (-)	83.3 (19.7)	VGLUT-3	vesicular glutamate transporter	N/A	
DN96956_c0_g1	0	0.2 (-)	2.9 (39.4)	NBAT	neutral and basic amino acid transporter	N/A	
DN156988_c0_g1	10.2	75.8 (7.5)	9.9 (-)	SNAT	sodium-coupled neutral amino acid transporter	N/A	
DN160184_c0_g1	4.8	270 (45.3)	87.7 (13)	LAT	large neutral amino acids transporter	N/A	
DN126771_c0_g1	0.3	0 (-)	23.8 (55.7)	CAT	cationic amino acid transporter	N/A	
DN149876_c0_g2	0	0 (-)	26.4 (1049.1)	MBAT	mt basic amino acids transporter	N/A	
DN155727_c0_g3	0	0.4 (-)	436.1 (57,052.4)	TRET-1	facilitated trehalose transporter Tret1	N/A	
DN40504_c0_g1	0.2	4.5 (21.1)	0 (-)	TRET-2	facilitated trehalose transporter Tret1	N/A	
DN152415_c1_g1	5	2.2 (-)	21.5 (4.6)	TRET-3	facilitated trehalose transporter Tret1	N/A	
DN122455_c0_g2	1.1	0.2 (-)	51 (48.5)	TRET-4	facilitated trehalose transporter Tret1	N/A	
DN142534_c1_g1	21	4.5 (-)	1351.3 (64)	TRET-5	facilitated trehalose transporter Tret1	N/A	
DN154019_c3_g2	0.7	250.7 (337.8)	0.4 (-)	TRET-6	facilitated trehalose transporter Tret1	N/A	
DN144255_c2_g2	4.8	1.1 (-)	23.2 (4.9)	TRET-7	facilitated trehalose transporter Tret1	N/A	
DN152297_c0_g2	0.6	145.5 (274.4)	0.1 (-)	TRET-8	facilitated trehalose transporter Tret1	N/A	
DN157015_c2_g1	4	0.8 (-)	128 (39.4)	TRET-9	facilitated trehalose transporter Tret1	N/A	
DN146821_c0_g2	100.8	230 (-)	587.4 (4.9)	TRET-10	facilitated trehalose transporter Tret1	N/A	
DN133791_c0_g1	8.9	1 (-)	95.8 (11.3)	TRET-11	facilitated trehalose transporter Tret1	N/A	
DN164039_c0_g1	3.9	52.6 (13)	8.3 (-)	TRET-12	facilitated trehalose transporter Tret1	N/A	
DN135736_c7_g1	0.5	1.3 (-)	2470.2 (5,042.8)	TRET-13	facilitated trehalose transporter Tret1	N/A	
DN140222_c0_g1	25.2	4.6 (-)	74.8 (3)	TRET-14	facilitated trehalose transporter Tret1	N/A	
DN155037_c0_g1	19.3	11 (-)	208.4 (10.6)	TRET-15	facilitated trehalose transporter Tret1	N/A	
DN149209_c0_g1	52.3	254.2 (4.6)	14.2 (-)	TRET-16	facilitated trehalose transporter Tret1	N/A	
DN142743_c0_g1	0	0.1 (-)	17.3 (1,910.9)	TRET-17	facilitated trehalose transporter Tret1	N/A	

DN125872_c0_g1	0.3	0.3 (-)	260.8 (891.4)	TRET-18	facilitated trehalose transporter Tret1	N/A	
DN148937_c0_g4	0.2	3 (16)	0.3 (-)	TRET-19	facilitated trehalose transporter Tret1	N/A	
DN150256_c0_g2	2.1	0.8 (-)	134.6 (68.6)	TRET-20	facilitated trehalose transporter Tret1	N/A	
DN147727_c0_g1	1.4	4.3 (-)	10.5 (7.5)	TRET-21	facilitated trehalose transporter Tret1	N/A	
DN147762_c2_g2	1.2	1.3 (-)	16 (13)	TRET-22	facilitated trehalose transporter Tret1	N/A	
DN129091_c0_g1	9.1	35.6 (3.7)	56.2 (6.5)	TRET-23	facilitated trehalose transporter Tret1	N/A	
DN150151_c0_g4	0	0 (-)	30.1 (418.8)	SMVT-1	sodium-dependent multivitamin transporter	N/A	
DN114993_c0_g1	0.3	48 (151.2)	102.8 (345.6)	SMVT-2	sodium-dependent multivitamin transporter	N/A	
DN143224_c1_g3	6.6	67.5 (11)	9.8 (-)	SMVT-3	sodium-dependent multivitamin transporter	N/A	
DN161485_c1_g2	2.7	85.8 (29)	5.2 (-)	SMVT-4	sodium-dependent multivitamin transporter	N/A	
DN159586_c1_g3	4.5	45.7 (12.6)	9.2 (-)	THIT-1	thiamine transporter	N/A	Vitamin transport
DN140997_c0_g3	1.7	796.9 (450.1)	2.9 (-)	THIT-2	thiamine transporter	N/A	
DN154958_c0_g1	6.8	24.7 (3.5)	5.5 (-)	PCFT-1	proton-coupled folate transporter	N/A	
DN134396_c0_g1	4.1	0.2 (-)	20.5 (5.2)	PCFT-2	proton-coupled folate transporter	N/A	
DN150212_c2_g1	5.2	17.3 (4.3)	0.5 (-)	PCFT-3	proton-coupled folate transporter	N/A	
DN154058_c2_g1	16.4	199.3 (11.3)	49.1 (3)	TREH-1	trehalase	3.2.1.18	trehalose hydrolysis
DN154236_c0_g2	14.7	266.4 (18.4)	149 (10.6)	TREH-2	trehalase	3.2.1.18	

Note: FPKM, fragments per kilobase per million; FC, fold change in expression of bacteriomes relative to body tissues; yellow, yellow bacteriome; red, red bacteriome; mt, mitochondrial; FC is represented with “-“ if p-value is higher than 0.001.