

Top SET Subfamilies of Amphimedon by Max Fold Change in Log2 TPM

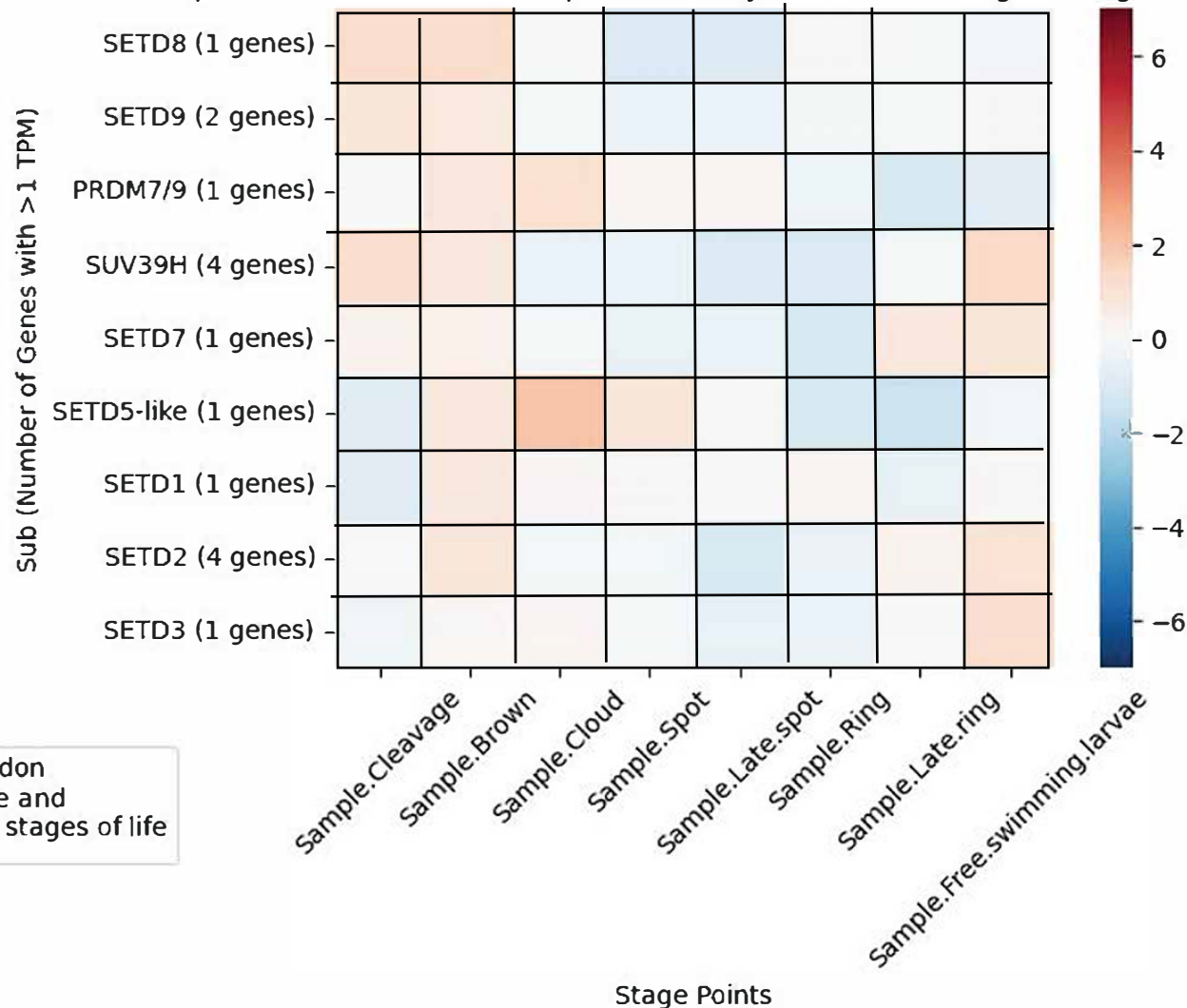


Fig 1. SET Subfamilies of Amphimedon transformed using maxfold change and ranked by prevalence within early stages of life

Subfamily_CDDID	Gene_Name_y	Sample.Cleavage	Sample.Brown	Sample.Cloud	Sample.Spot	Sample.Late.spot
Sample.Ring	Sample.Late.ring	Sample.Free.swimming.larvae				
cd10518	SETD1	126.75200000000001	171.633	192.154	144.292	100.847
		116.33699999999999				
		163.44299999999998	353.281			
cd10527	SETD3	43.738	39.011	21.214	16.527	16.517
		20.052	20.881999999999998	25.26		
cd10528	SETD8	3.977	12.175	30.376	13.543	8.059
		3.072	2.193	5.826		
cd10529	SETD5-like	67.503	69.147	46.762	35.163	38.088
		22.514	87.295	92.778		
cd10530	SETD7	5.983	12.001	5.386	5.458	2.763
		4.355	8.58	13.334		
cd10531	SETD2	49.643	147.265	101.035	92.163	88.467
		102.043	59.422000000000004			
		94.57600000000001				
cd10534	PRDM7/9	8.775	8.485	3.216	1.344	1.493
		3.618	3.014	2.641		
cd10537	SETD9	27.166	21.343	8.657	8.719	6.008999999999995
		5.787	10.788	32.001		
cd10538	SUV39H	22.654	41.183	48.65	27.751	27.464
		17.308	10.425	13.015		

CDD_ID	Gene Name	Subfamily	CDD_ID
cd08161	SET	cd08161	
cd10518	SETD1-like	cd10518	
cd19169	SETD1	cd10518	
cd19204	SETD1A	cd10518	
cd19205	SETD1B	cd10518	
cd19170	KMT2A/2B	cd10518	
cd19206	KMT2A	cd10518	
cd19207	KMT2B	cd10518	
cd19171	KMT2C/2D	cd10518	
cd19208	KMT2C	cd10518	
cd19209	KMT2D	cd10518	
cd20072	SET1	cd10518	
cd10519	EZH	cd10519	
cd19168	EZH-like	cd10519	
cd19217	EZH1	cd10519	
cd19218	EZH2	cd10519	
cd10522	LegAS4-like	cd10522	
cd10524	Suv4-20-like	cd10524	
cd19184	KMT5B	cd10524	
cd19185	KMT5C	cd10524	
cd19186	Suv4-20	cd10524	
cd10527	LSMT	cd10527	
cd19176	SETD3	cd10527	
cd19177	SETD4	cd10527	
cd19178	SETD6	cd10527	
cd19179	RBCMT	cd10527	
cd19180	SpSET10-like	cd10527	
cd10528	SETD8	cd10528	
cd10529	SETD5-like	cd10529	
cd19181	SETD5	cd10529	
cd19182	KMT2E	cd10529	
cd19183	SpSET3-like	cd10529	
cd10530	SETD7	cd10530	
cd10531	SETD2-like	cd10531	
cd19172	SETD2	cd10531	
cd19173	NSD	cd10531	
cd19210	NSD1	cd10531	
cd19211	NSD2	cd10531	
cd19212	NSD3	cd10531	
cd19174	ASH1L	cd10531	
cd19175	ASHR3-like	cd10531	
cd10534	PRDM-like	cd10534	
cd10520	PRDM17	cd10534	
cd19187	PRDM1	cd10534	
cd19188	PRDM2	cd10534	
cd19189	PRDM4	cd10534	
cd19190	PRDM5	cd10534	
cd19191	PRDM6	cd10534	
cd19192	PRDM8	cd10534	
cd19193	PRDM7/9	cd10534	

cd19194 PRDM10 cd10534
cd19195 PRDM11 cd10534
cd19196 PRDM12 cd10534
cd19197 PRDM13 cd10534
cd19198 PRDM14 cd10534
cd19199 PRDM15 cd10534
cd19200 PRDM16/3 cd10534
cd19213 PRDM16 cd10534
cd19214 PRDM3 cd10534
cd19201 ZFPM cd10534
cd19215 ZFPM1 cd10534
cd19216 ZFPM2 cd10534
cd10537 SETD9 cd10537
cd10538 SETDB-like cd10538
cd10541 SETDB cd10538
cd10517 SETDB1 cd10538
cd10523 SETDB2 cd10538
cd10542 SUV39H cd10538
cd10525 SUV39H1 cd10538
cd10532 SUV39H2 cd10538
cd19473 DIM5-like cd10538
cd20073 Clr4-like cd10538
cd10543 EHMT cd10538
cd10533 EHMT2 cd10538
cd10535 EHMT1 cd10538
cd10544 SETMAR cd10538
cd10545 AtSUVH-like cd10538
cd10545 ATXR5/6-like cd10545
cd10540 SpSet7-like cd10540
cd20071 SMYD cd20071
cd10521 SMYD5 cd20071
cd10536 SMYD4 cd20071
cd19167 SMYD1/2/3-like cd20071
cd10526 SMYD1 cd20071
cd19202 SMYD2 cd20071
cd19203 SMYD3 cd20071

For this project, I am focusing on the SET Subfamilies and their expression throughout both of the Taxa. I did this by hand since the SET subfamilies had very few actual subfamilies to annotate. I looked up the information on the NCBI website using the superfamily number that was found in the first part of the project. I then created a Google Sheets file that had each Gene's Subfamily and its CDD_ID number. I then transferred this file to a .txt file and merged it with the rest of my tables, using the same code as project one. The difference with this one was that I was now looking at the subfamilies instead of the superfamilies, filtering out ones that did not align with the ones I was observing. However, I used the Top 20 Max Fold Change so i could see how many of these genes are used within each subfamily. I think my next move is to see what each of these subfamilies do and compare that to their trends in Amphemideon.