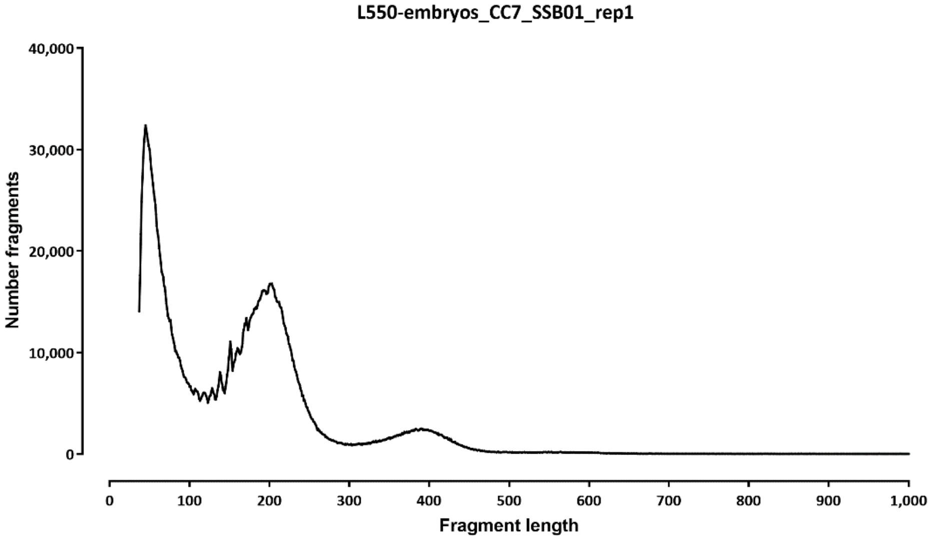
Dataset stats

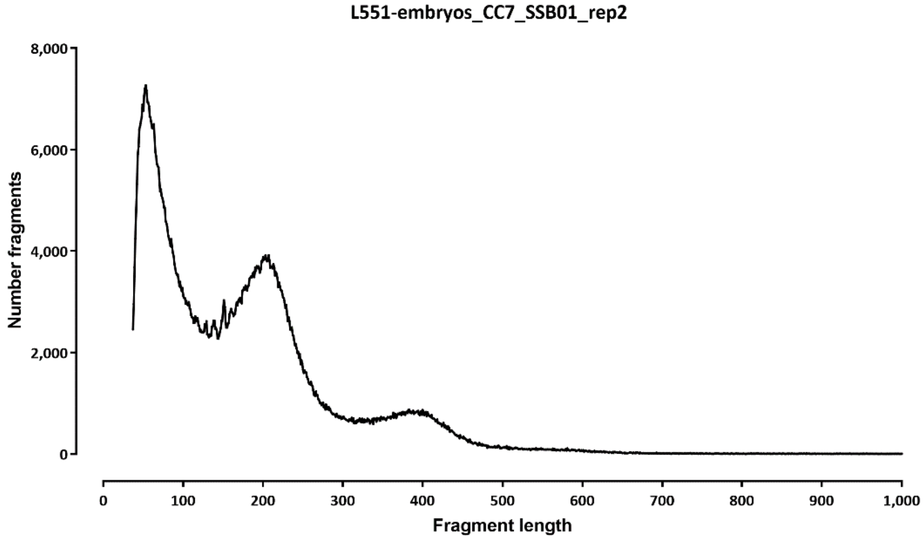
Species	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio	MACS default peaks	FRiP (MACS)
***Aiptasia pallida* 1.0**	**2x36**	L550-embryos_CC7_SSB01_rep1	6,628,608	6,136,750		0.93			5,950,942		8,749	78,776
***Aiptasia pallida* 1.0**	**2x36**	L551-embryos_CC7_SSB01_rep2	2,546,337	1,945,922		0.94			1,881,346		3,453	52,490
***Aiptasia pallida* 1.0**	**2x36**	L552-embryos_CC7_Apo_rep1	2,206,132	1,357,800		0.94			1,299,898		1,737	40,110
***Aiptasia pallida* 1.0**	**2x36**	L553-embryos_CC7_Apo_rep2	3,200,828	2,745,918		0.94			2,652,542		4,422	60,535
***Aiptasia pallida* 1.0**	**2x36**	L558-embryos_CC7_SSB01_rep3	6,291,806	889,466		0.95			861,382		1,046	33,670
***Aiptasia pallida* 1.0**	**2x36**	L559-embryos_CC7_Apo_rep3	1,279,673	963,202		0.95			929,402		1,284	39,067

Note: these will need quite a bit deeper sequencing

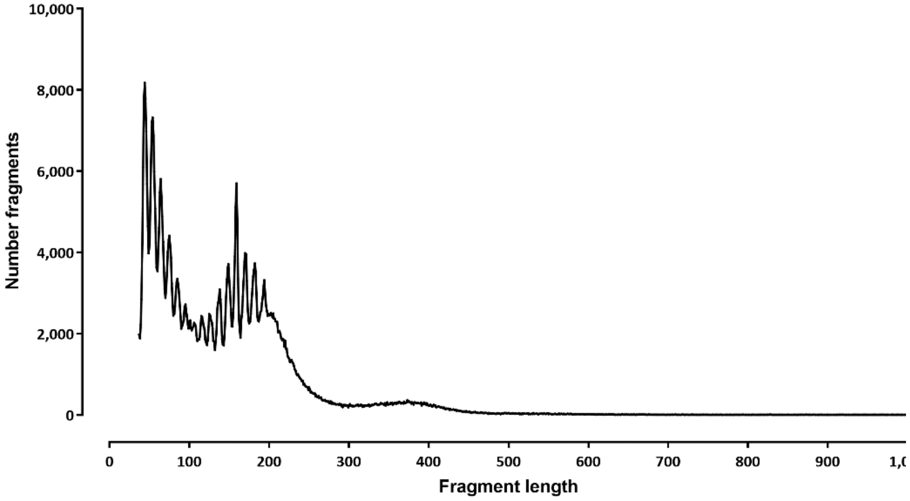
	Raw fragments	SSB01 mapping reads	SSB01 mapping fraction
L550-embryos_CC7_SSB01_rep1	6,628,608	60,154	0.907%
L551-embryos_CC7_SSB01_rep2	2,546,337	27,572	1.083%
L552-embryos_CC7_Apo_rep1	2,206,132	2,882	0.131%
L553-embryos_CC7_Apo_rep2	3,200,828	4,372	0.137%
L558-embryos_CC7_SSB01_rep3	6,291,806	3,120	0.050%
L559-embryos_CC7_Apo_rep3	1,279,673	1,934	0.151%

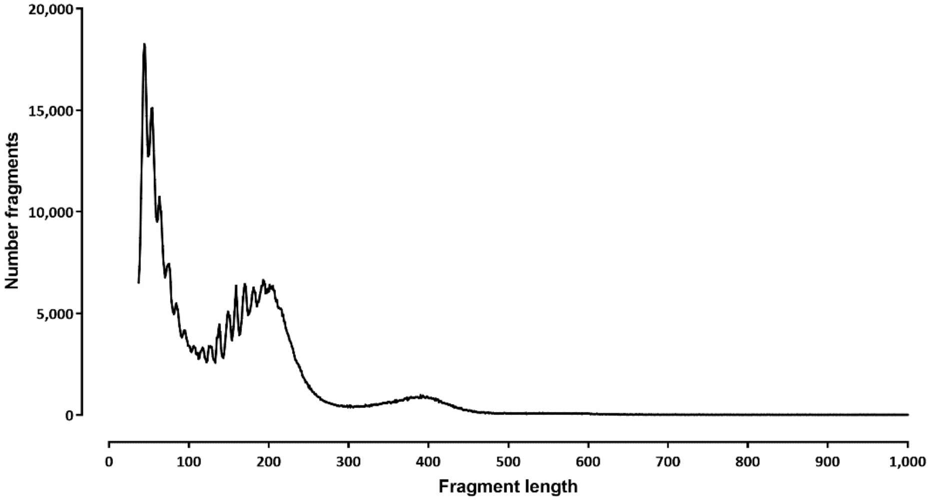


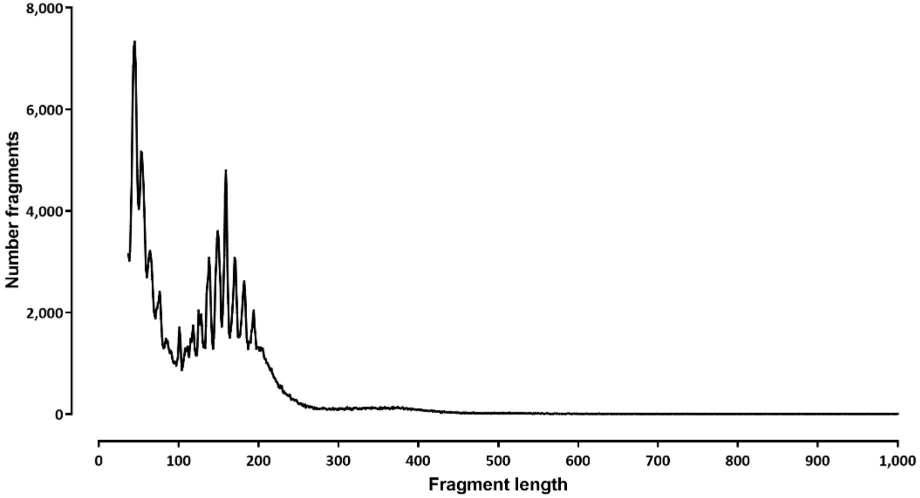
L550-embryos_CC7_SSB01_rep1



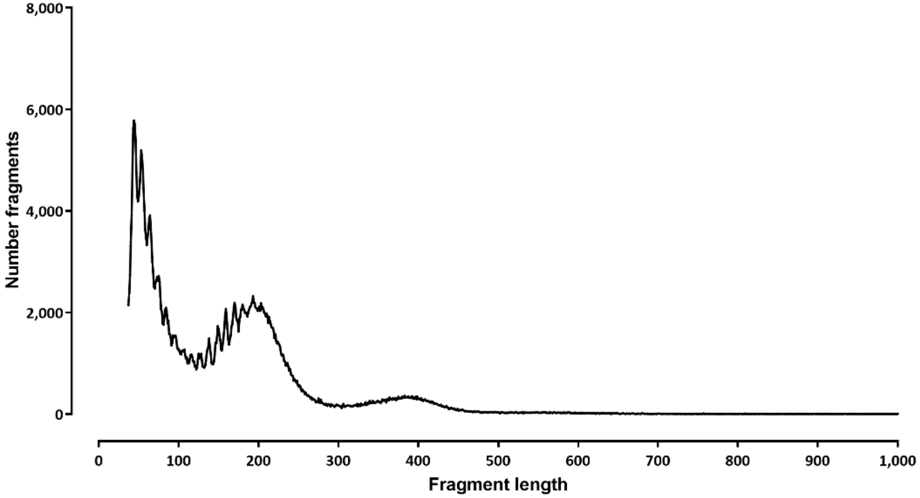
L551-embryos_CC7_SSB01_rep2


L552-embryos_CC7_Apo_rep1


L553-embryos_CC7_Apo_rep2

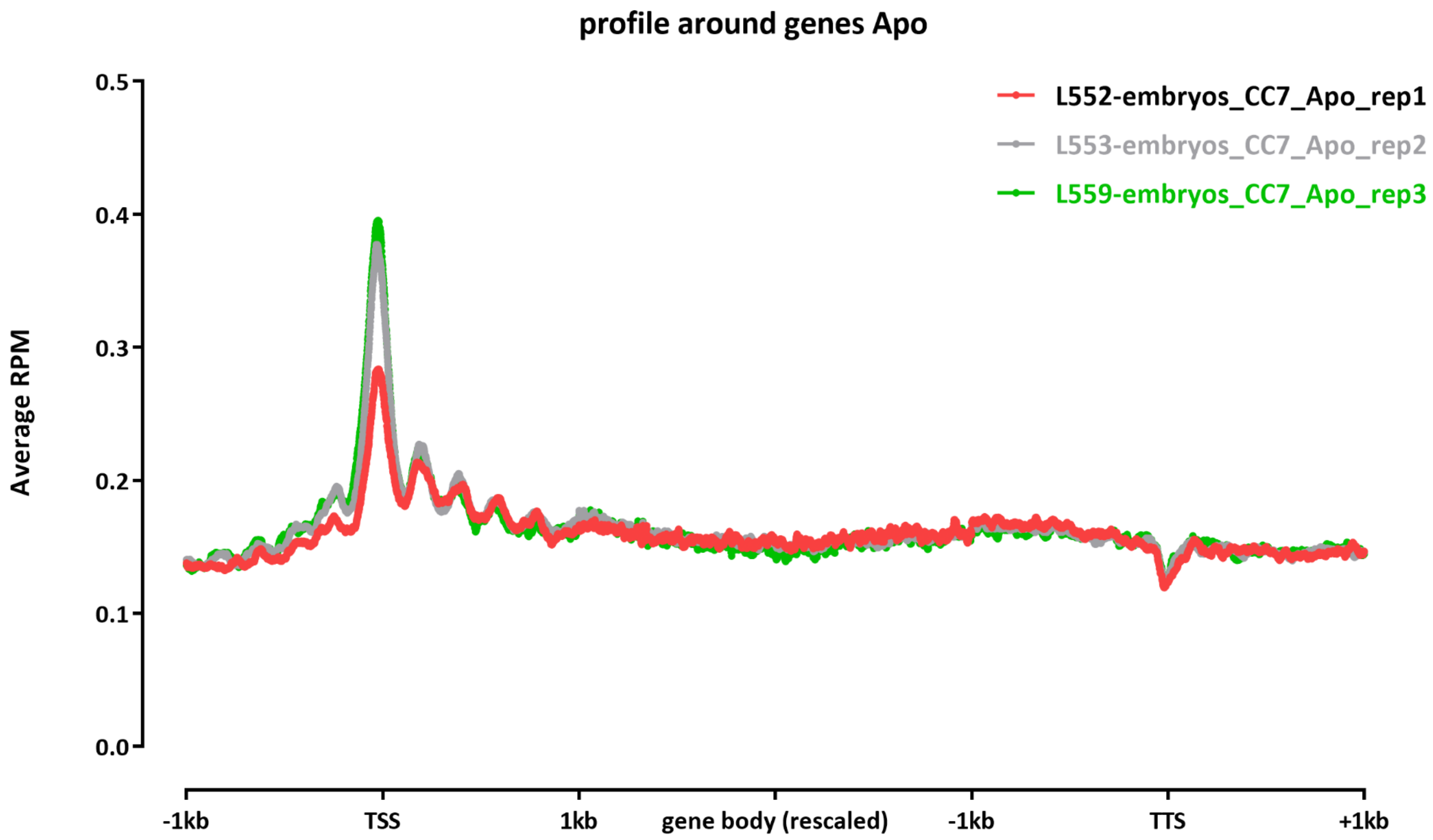


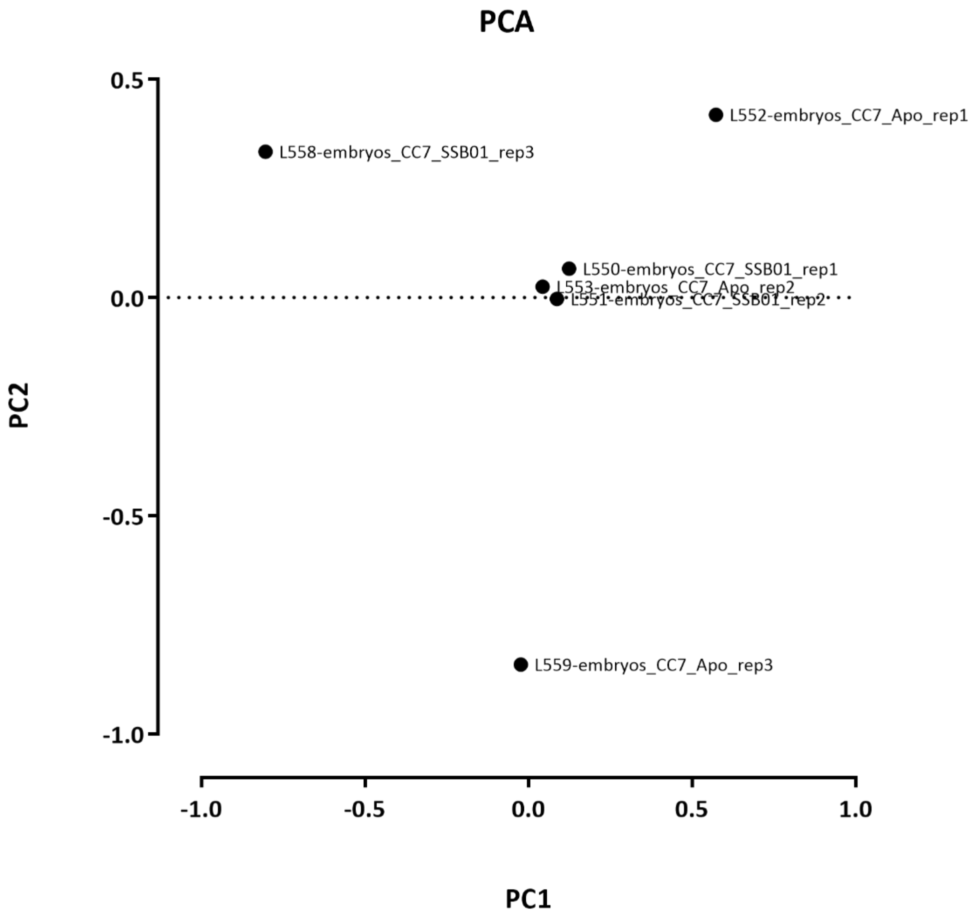
L558-embryos_CC7_SSB01_rep3



L559-embryos_CC7_Apo_rep3

profile around genes SSB01

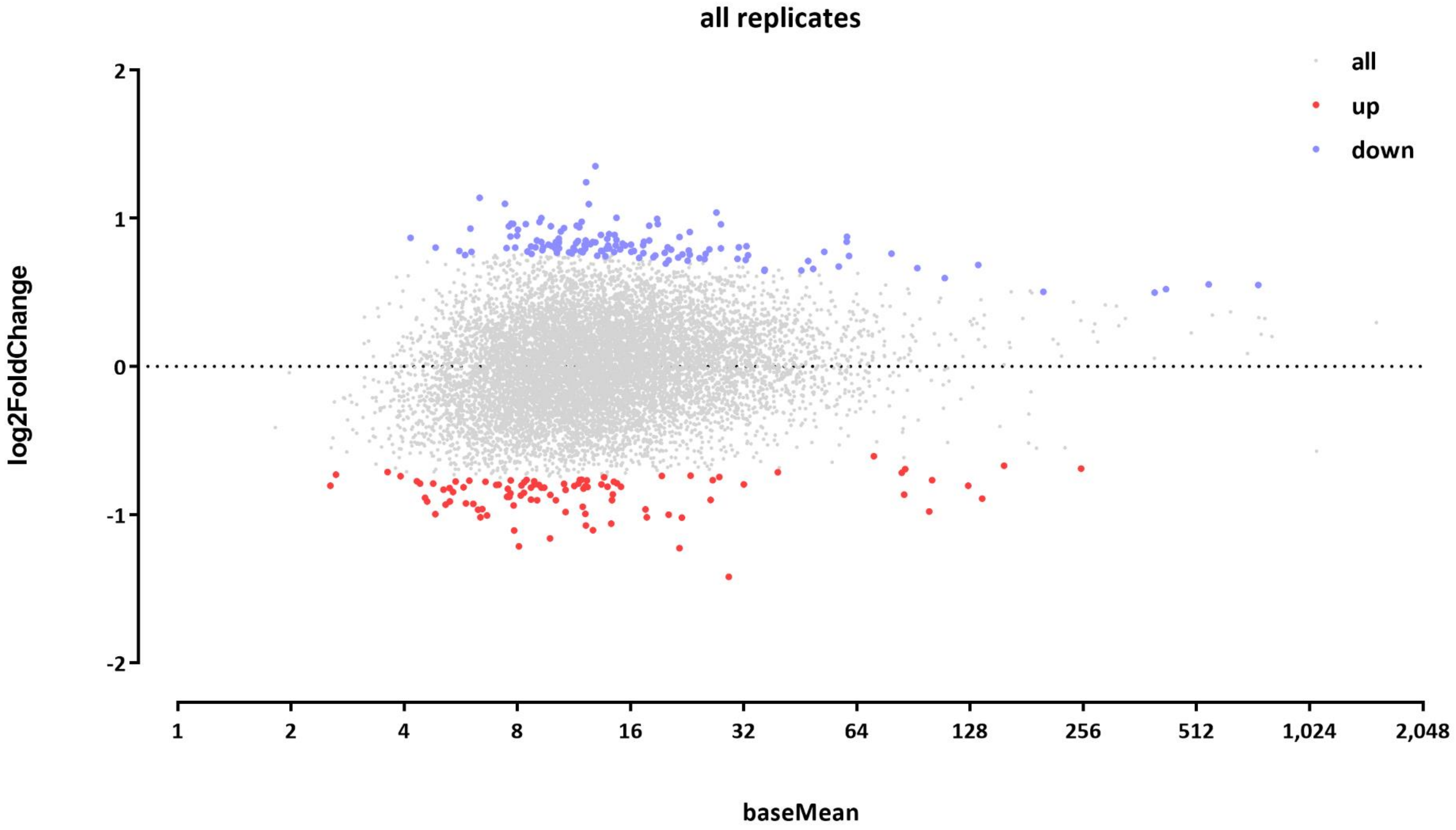

profile around genes Apo
Average RPM
0.5
0.4
0.3
0.2
0.1
0.0
L552-embryos_CC7_Apo_rep1
L553-embryos_CC7_Apo_rep2
L559-embryos_CC7_Apo_rep3
-1kb
TSS
1kb
gene body (rescaled)
-1kb
TTS
+1kb


PCA
PC2
0.5
0.0
-0.5
-1.0
PC1
-1.0
-0.5
0.0
0.5
1.0
L552-embryos_CC7_Apo_rep1
L558-embryos_CC7_SSB01_rep3
L550-embryos_CC7_SSB01_rep1
L553-embryos_CC7_Apo_rep2
L551-embryos_CC7_SSB01_rep2
L559-embryos_CC7_Apo_rep3

Number differential ATAC peaks

	A	B	p-adj		p-adj	
			up in B vs A	down in B vs A	up in B vs A	down in B vs A
all reps	**Apo**	**SSB01**	0	0	98	136
first 4 reps	**Apo**	**SSB01**	0	0	42	69

Using all replicates



Using just the first set of two reps per condition: