

General mapping stats

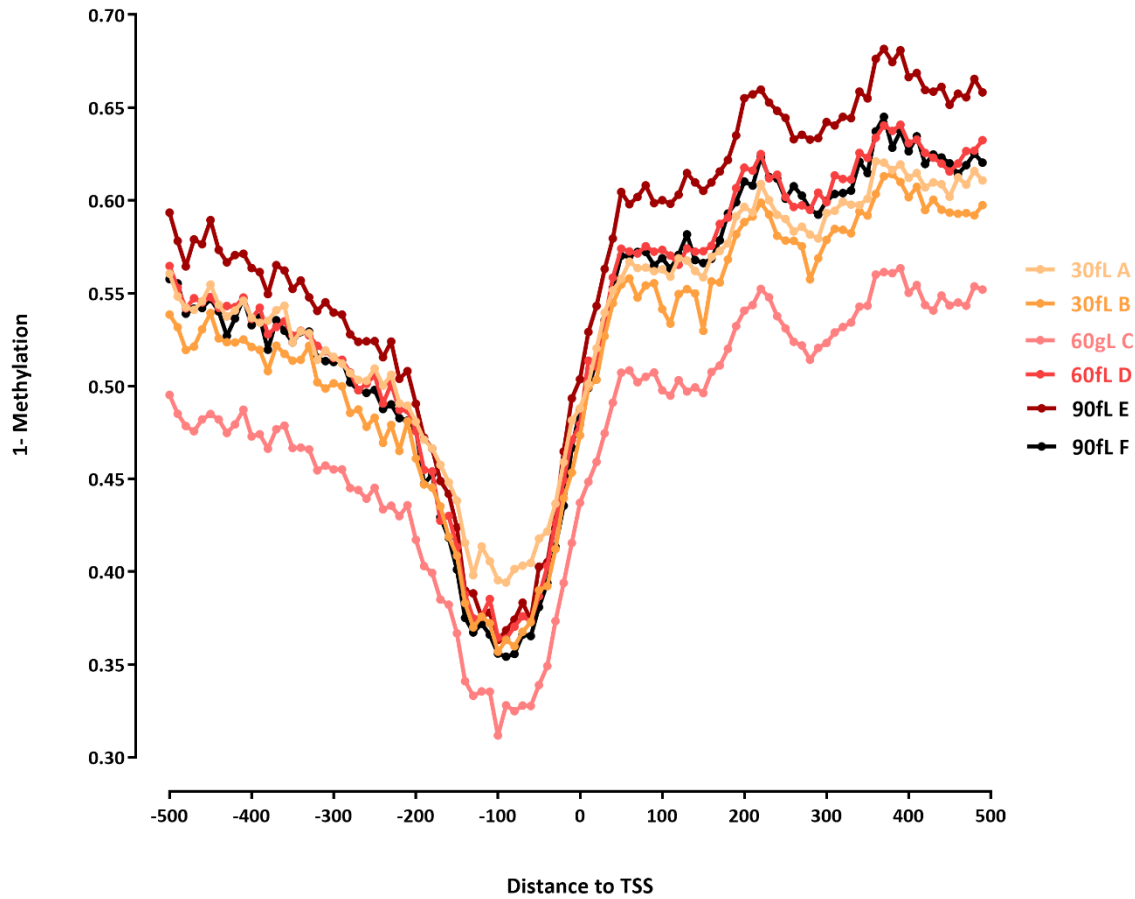
Species	#	CpG %	CHG%	CHH%	Complexity	Read Length	Mean alignment Length	Unique	Unique deduped	Multi	Raw fragments	Alignment fraction	Notes
Saccharomyces_cerevisiae+Candida_glabrata, both	L1231-30fL_A_dSMF				0.86	2x150-trim	107.50	115,016	103,378		22,301,120	0.26%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1232-30fL_B_dSMF				0.88	2x150-trim	112.68	114,030	104,082		18,296,585	0.31%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1233-60fL_C_dSMF				0.90	2x150-trim	129.17	1,175,490	1,082,068		23,699,593	2.48%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1234-60fL_D_dSMF				0.88	2x150-trim	89.86	279,182	250,612		23,332,194	0.60%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1235-90fL_E_dSMF				0.88	2x150-trim	92.53	418,268	373,756		23,461,107	0.89%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1236-90fL_F_dSMF				0.85	2x150-trim	84.67	443,470	383,788		23,220,953	0.95%	Bismark bowtie2
Saccharomyces_cerevisiae+Candida_glabrata, both	L1231-30fL_A_dSMF				0.82	2x150-trim	124.02	34,358,945			22,301,120	77.03%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, both	L1232-30fL_B_dSMF				0.83	2x150-trim	124.55	28,095,760			18,296,585	76.78%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, both	L1233-60fL_C_dSMF				0.79	2x150-trim	128.28	37,765,648			23,699,593	79.68%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, both	L1234-60fL_D_dSMF				0.86	2x150-trim	110.29	35,038,344			23,332,194	75.09%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, both	L1235-90fL_E_dSMF				0.85	2x150-trim	107.47	34,683,161			23,461,107	73.92%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, both	L1236-90fL_F_dSMF				0.85	2x150-trim	101.68	34,404,210			23,220,953	74.08%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1231-30fL_A_dSMF				0.81	2x150-trim	123.99	31,287,280			22,301,120	70.15%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1232-30fL_B_dSMF				0.83	2x150-trim	124.49	25,944,904			18,296,585	70.90%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1233-60fL_C_dSMF				0.78	2x150-trim	128.23	33,229,223			23,699,593	70.11%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1234-60fL_D_dSMF				0.85	2x150-trim	110.10	31,691,089			23,332,194	67.91%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1235-90fL_E_dSMF				0.84	2x150-trim	107.20	31,724,367			23,461,107	67.61%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, sacCer3	L1236-90fL_F_dSMF				0.84	2x150-trim	101.34	31,057,273			23,220,953	66.87%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1231-30fL_A_dSMF				0.89	2x150-trim	124.39	3,071,665			22,301,120	6.89%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1232-30fL_B_dSMF				0.90	2x150-trim	125.24	2,150,856			18,296,585	5.88%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1233-60fL_C_dSMF				0.88	2x150-trim	128.67	4,536,425			23,699,593	9.57%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1234-60fL_D_dSMF				0.90	2x150-trim	112.05	3,347,255			23,332,194	7.17%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1235-90fL_E_dSMF				0.89	2x150-trim	110.31	2,958,794			23,461,107	6.31%	bwameth
Saccharomyces_cerevisiae+Candida_glabrata, Candida	L1236-90fL_F_dSMF				0.88	2x150-trim	104.80	3,346,937			23,220,953	7.21%	bwameth

Note: I could not map the reads with Bismarck

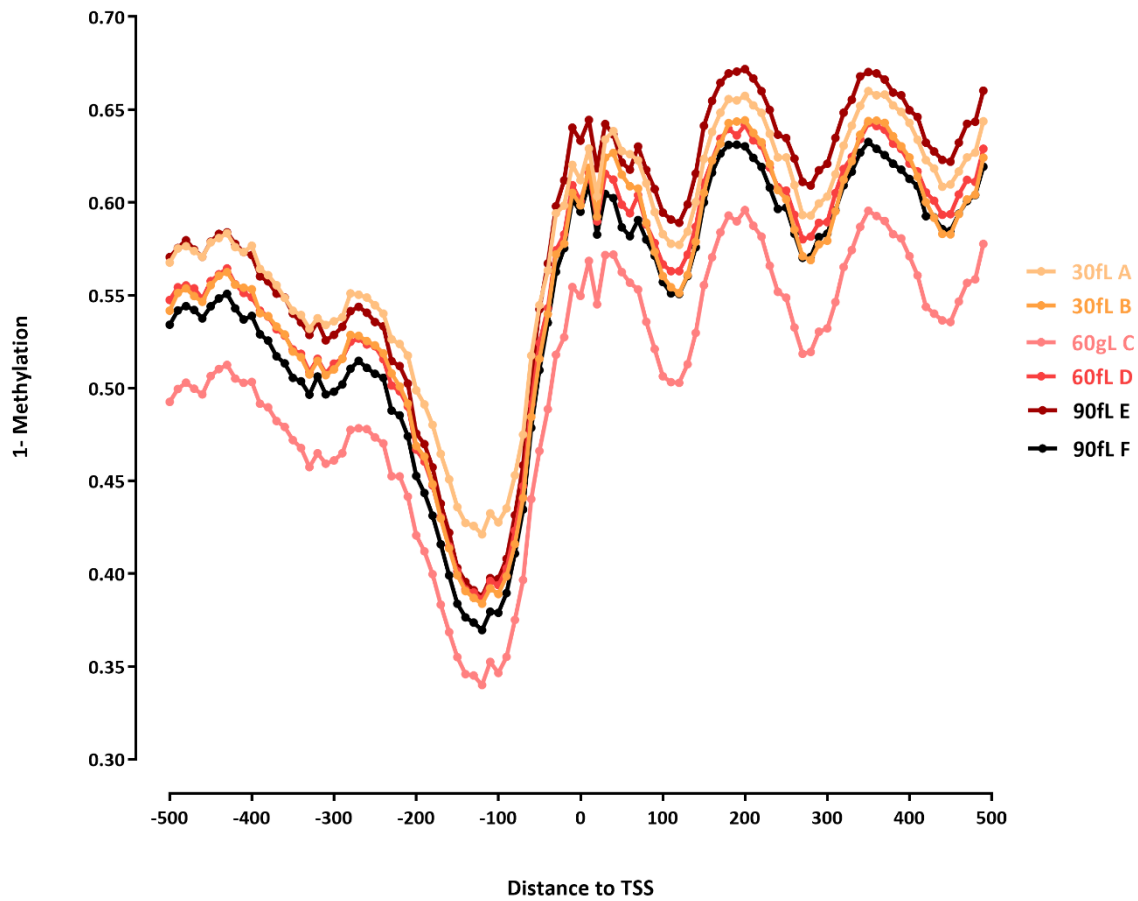
BWAmeth, on the other hand, works.

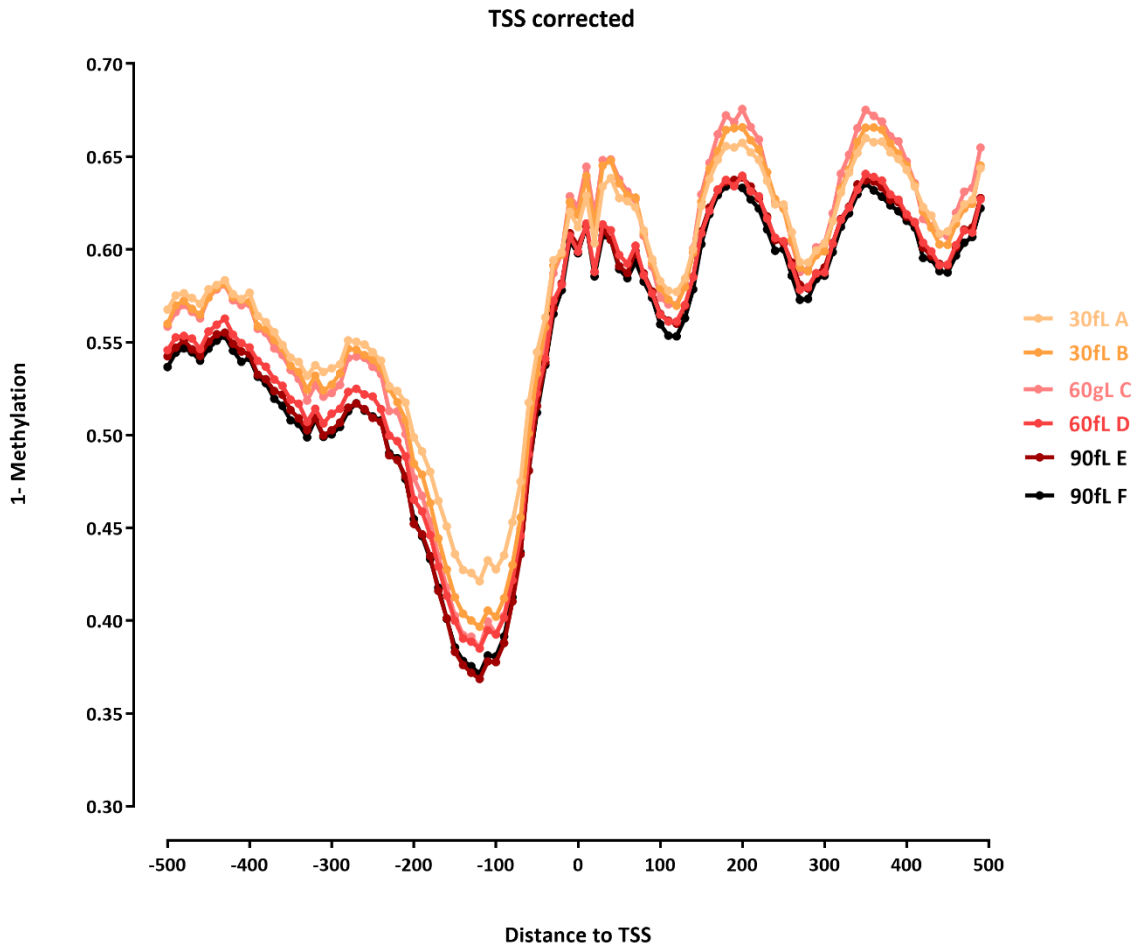
My guess is that something is not 100% right with the EM-seq adaptor trimming, but I have not been able to figure out what exactly

TSS Candida

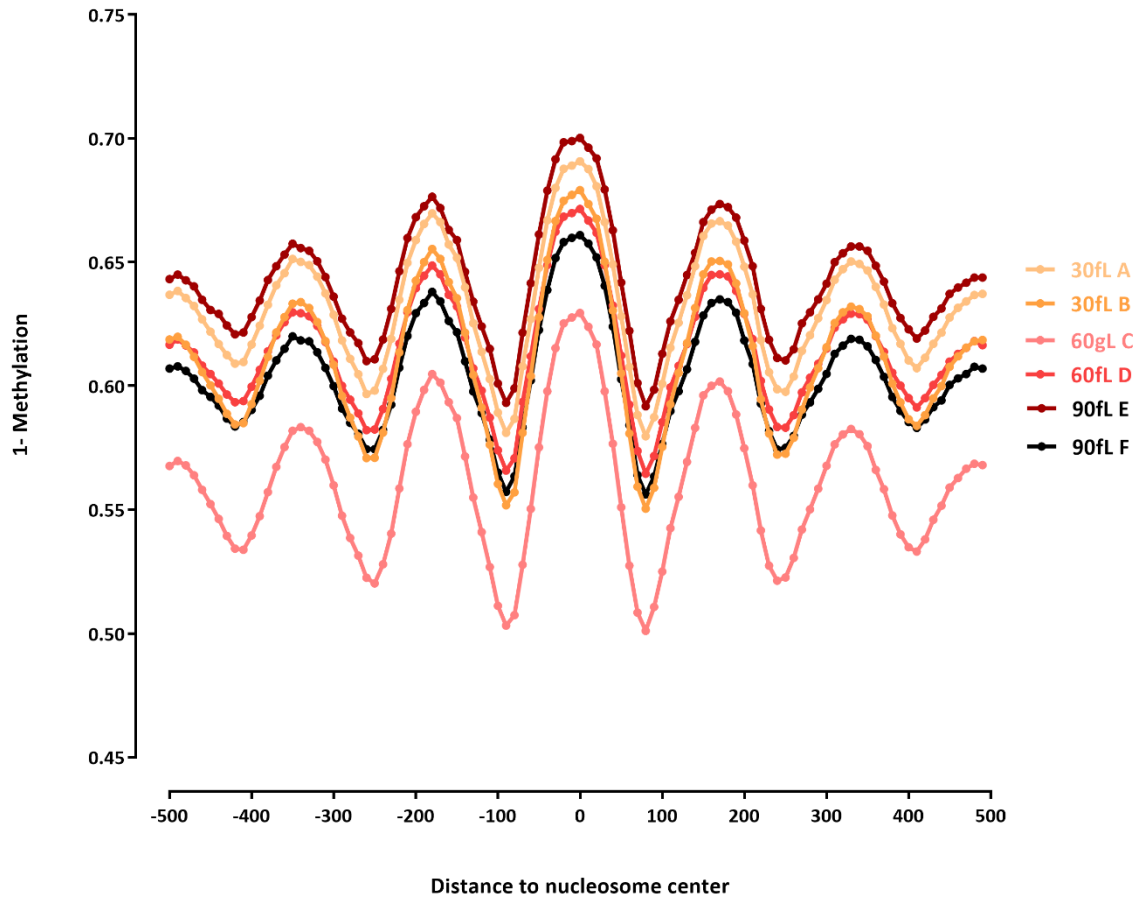


TSS





positioned nucleosomes



positioned nucleosomes corrected

