

**Zuin et al., Table S1**

***Parameters for peak calling with SWEMBL***

	<b>CTCF</b>	<b>RNA Pol II</b>	<b>SMC1A</b>	<b>SMC3</b>	<b>NIPBL</b>
#Sequence length	36	36	36	36	36
#Fragment length	150	150	150	150	150
#Background	0.000000	0.000000	0.000000	0.000000	0.000000
#Position Background	0.010000	0.010000	0.010000	0.010000	0.010000
#Long Background	0.050000	0.050000	0.050000	0.050000	0.050000
#Threshold	5.000000	5.000000	5.000000	5.000000	5.000000
#Minimum count above bg	10	10	15	8	10
#Penalty increase	25	25	25	25	25
#Quality cutoff	0.000000	0.000000	0.000000	0.000000	0.000000
#Result cutoff	4.000000	4.000000	8.000000	4.000000	4.000000
#Penalty factor	1.000000	1.000000	1.000000	1.000000	1.000000