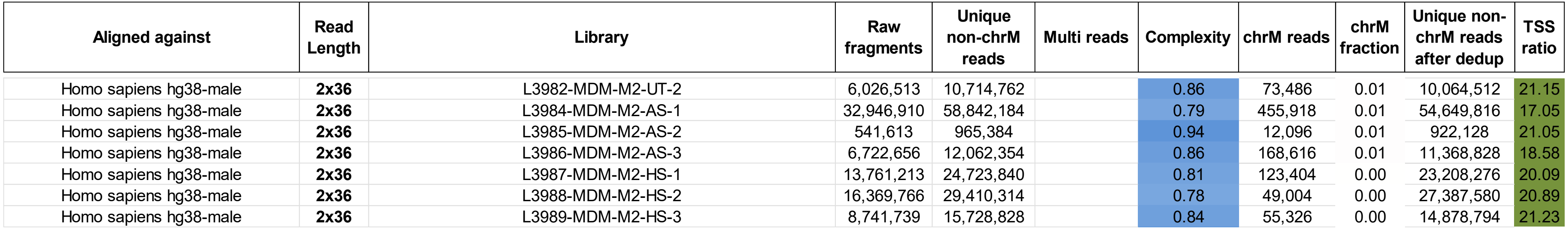
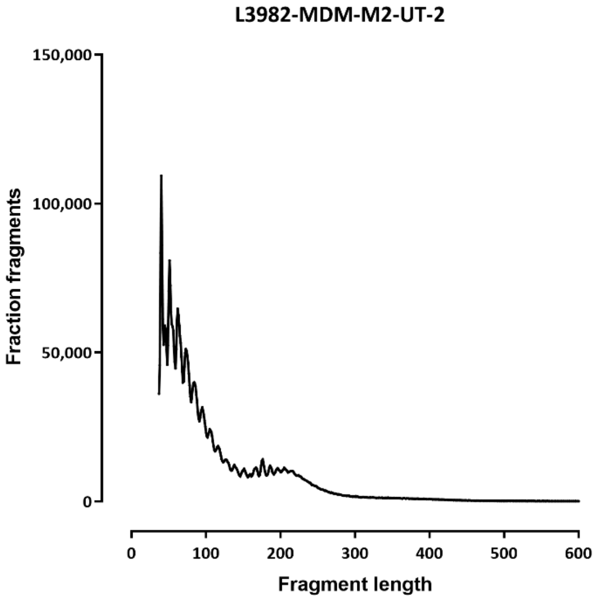
Dataset stats



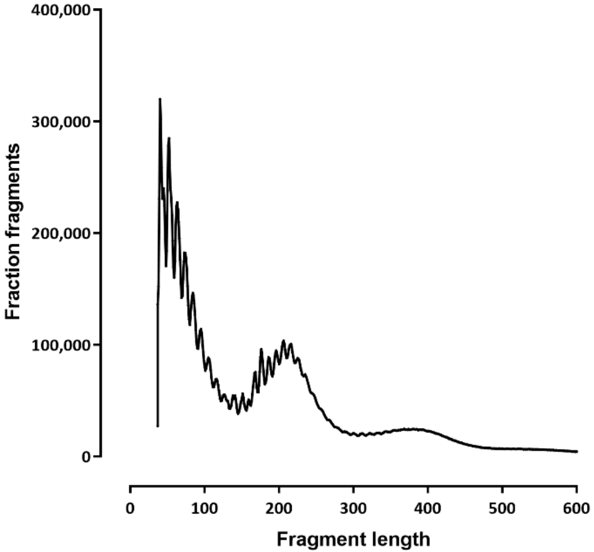
Aligned against	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio
Homo sapiens hg38-male	**2x36**	L3982-MDM-M2-UT-2	6,026,513	10,714,762		0.86	73,486	0.01	10,064,512	21.15
Homo sapiens hg38-male	**2x36**	L3984-MDM-M2-AS-1	32,946,910	58,842,184		0.79	455,918	0.01	54,649,816	17.05
Homo sapiens hg38-male	**2x36**	L3985-MDM-M2-AS-2	541,613	965,384		0.94	12,096	0.01	922,128	21.05
Homo sapiens hg38-male	**2x36**	L3986-MDM-M2-AS-3	6,722,656	12,062,354		0.86	168,616	0.01	11,368,828	18.58
Homo sapiens hg38-male	**2x36**	L3987-MDM-M2-HS-1	13,761,213	24,723,840		0.81	123,404	0.00	23,208,276	20.09
Homo sapiens hg38-male	**2x36**	L3988-MDM-M2-HS-2	16,369,766	29,410,314		0.78	49,004	0.00	27,387,580	20.89
Homo sapiens hg38-male	**2x36**	L3989-MDM-M2-HS-3	8,741,739	15,728,828		0.84	55,326	0.00	14,878,794	21.23

Note: I need to get more reads for the UT condition. The others are done though.

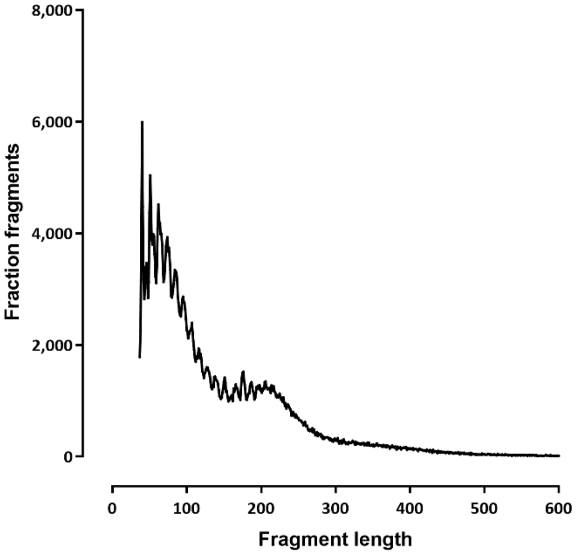
And enrichment is fantastic


L3982-MDM-M2-UT-2
150,000
100,000
50,000
0
Fraction fragments
0
100
200
300
400
500
600
Fragment length

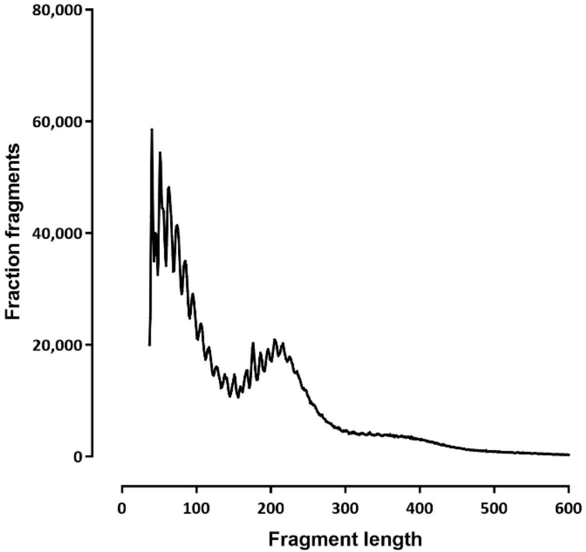
L3984-MDM-M2-AS-1

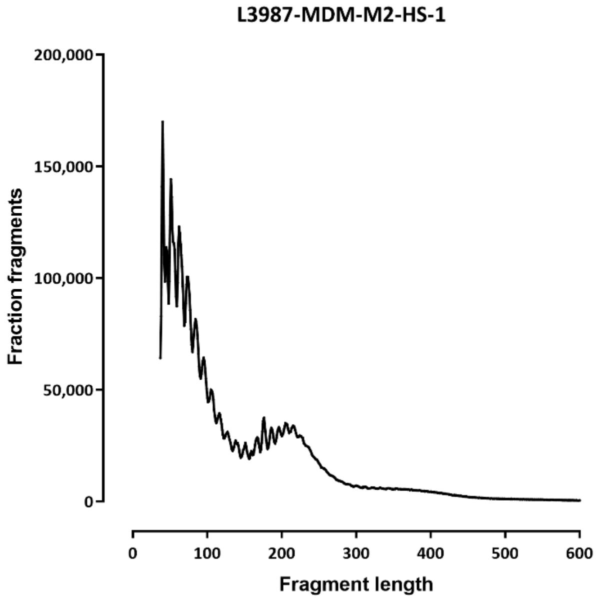


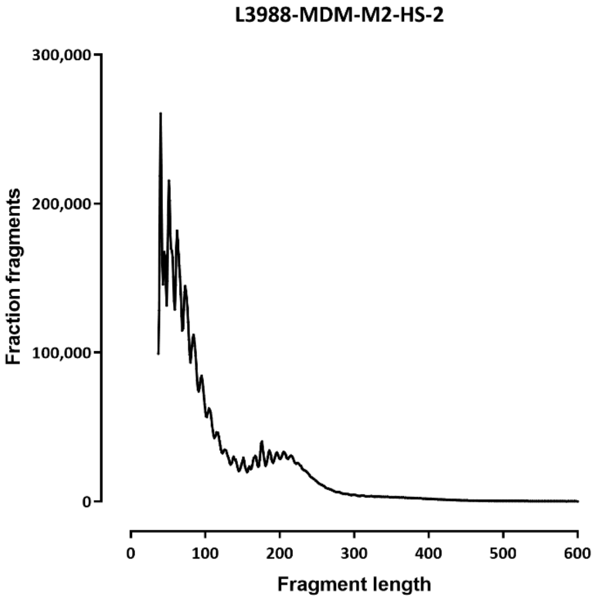
L3985-MDM-M2-AS-2

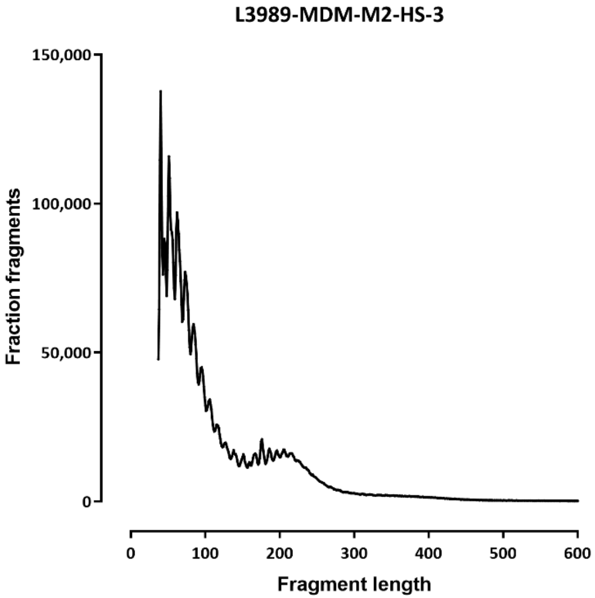


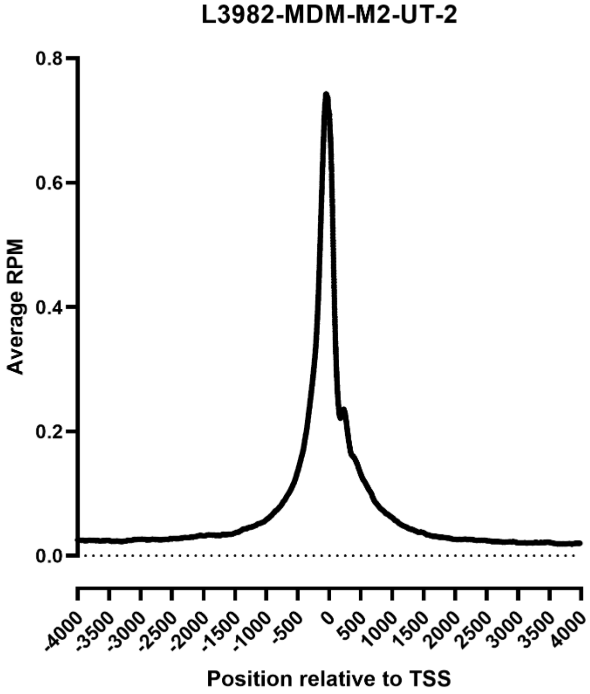
L3986-MDM-M2-AS-3

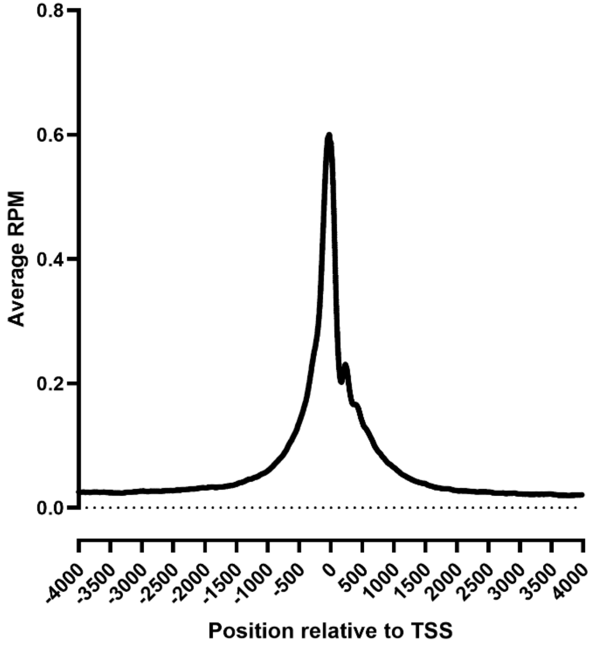



L3987-MDM-M2-HS-1

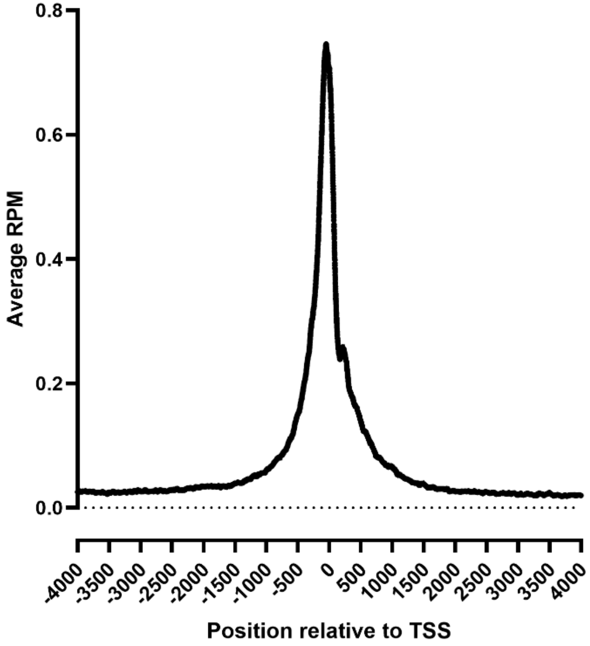

L3988-MDM-M2-HS-2


L3989-MDM-M2-HS-3

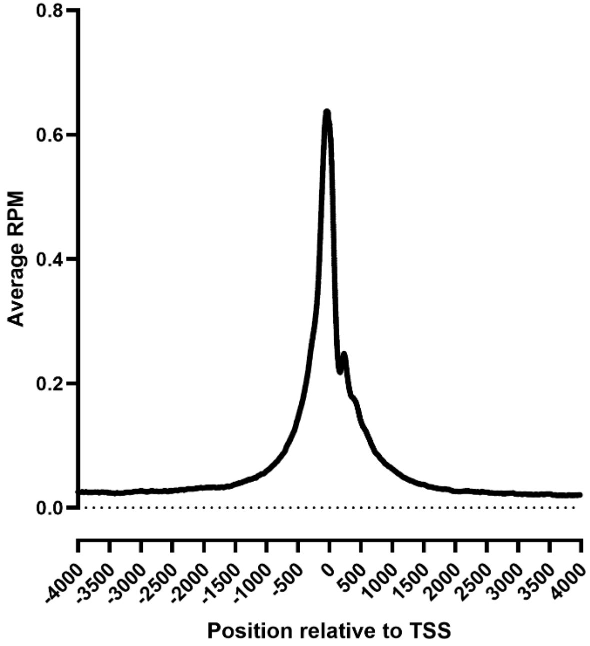

L3982-MDM-M2-UT-2
Average RPM
0.8
0.6
0.4
0.2
0.0
-4000
-3500
-3000
-2500
-2000
-1500
-1000
-500
0
500
1000
1500
2000
2500
3000
3500
4000
Position relative to TSS



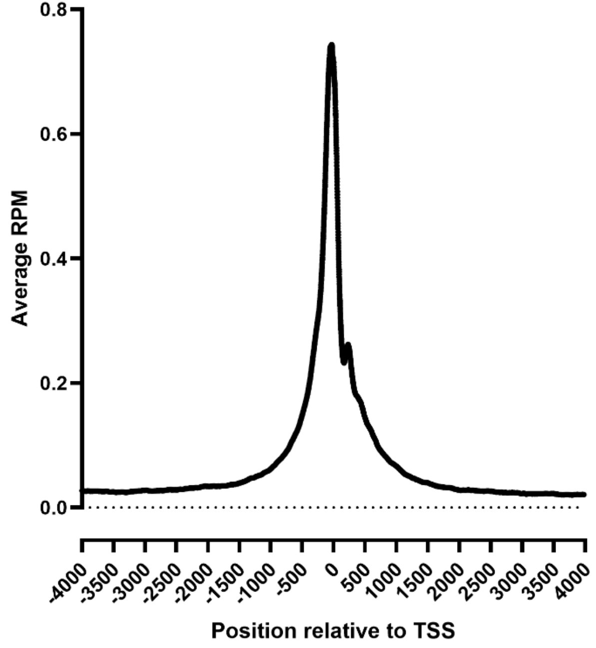
L3984-MDM-M2-AS-1



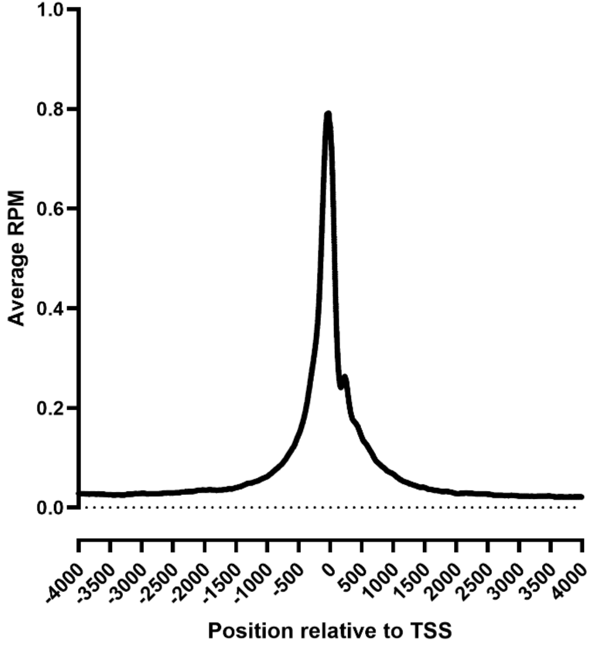
L3985-MDM-M2-AS-2



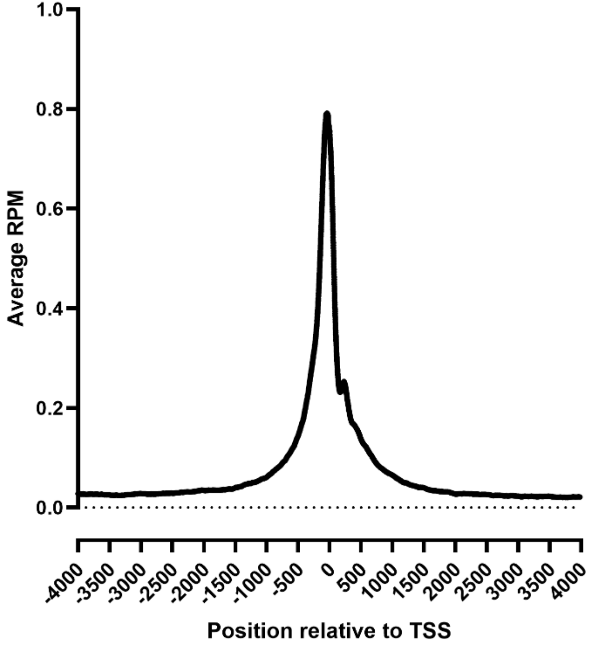
L3986-MDM-M2-AS-3



L3987-MDM-M2-HS-1



L3988-MDM-M2-HS-2



L3989-MDM-M2-HS-3