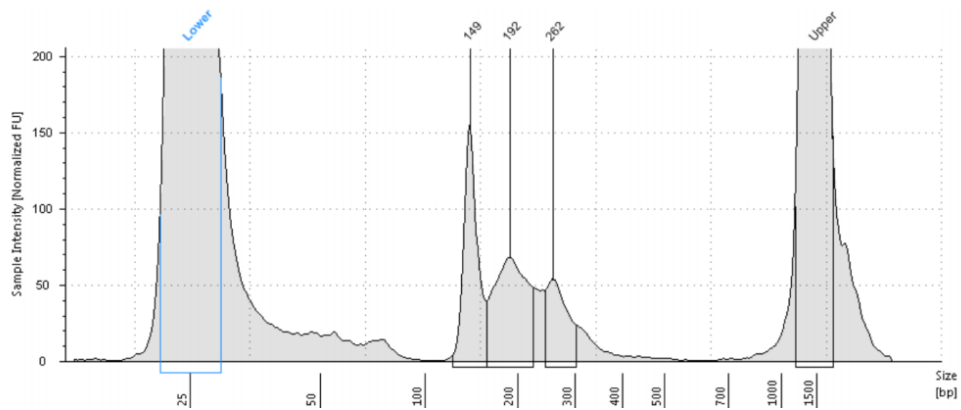


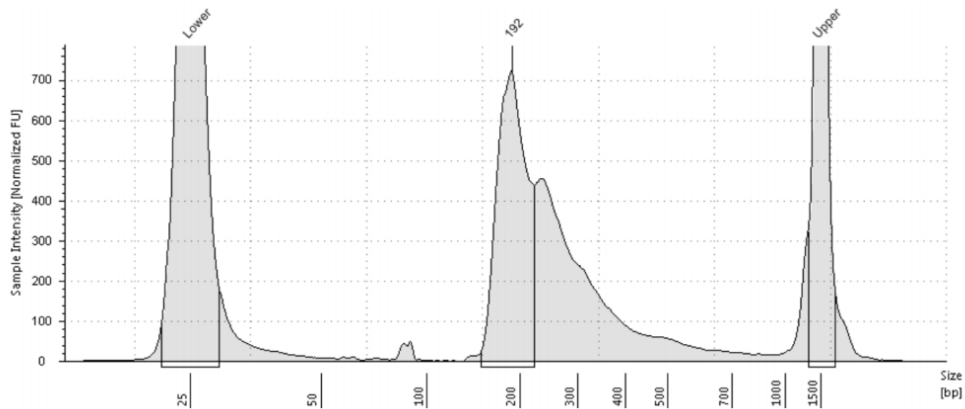
Dataset stats

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
Saccharomyces cerevisiae	2x36	L1922-H4S47C_250M_30min	5,410,268	94,008	191,328	0.89	4,815,630	0.98	85,210	1.25
Saccharomyces cerevisiae	2x36	L1923-H4S47C_50M_30min	5,949,115	1,624,878	1,559,848	0.85	5,211,516	0.76	1,527,670	1.40
Saccharomyces cerevisiae	2x36	L1924-H4S47C_5M_30min	39,416,206	27,421,912	18,629,814	0.63	7,008,758	0.20	24,567,102	1.28
Saccharomyces cerevisiae	2x36	L1925-H4S47C_250M_30min_low_enzyme	7,469,933	29,342	297,372	0.80	7,558,552	1.00	23,726	1.29
Saccharomyces cerevisiae	2x36	L1926-H4S47C_50M_30min_low_enzyme	14,977,598	533,058	1,248,582	0.84	18,150,640	0.97	478,240	1.37
Saccharomyces cerevisiae	2x36	L1927-H4S47C_5M_30min_low_enzyme	21,680,170	12,105,190	14,158,758	0.72	6,926,016	0.36	11,036,142	1.28
Saccharomyces cerevisiae	2x36	L1928-H4S47C_250M_5min	7,141,255	180,814	362,926	0.75	8,507,968	0.98	139,152	1.30
Saccharomyces cerevisiae	2x36	L1929-H4S47C_50M_5min	6,394,217	927,564	1,029,336	0.86	6,651,834	0.88	854,260	1.37
Saccharomyces cerevisiae	2x36	L1930-H4S47C_5M_5min	7,997,046	3,241,688	4,169,122	0.82	5,217,260	0.62	2,980,586	1.30

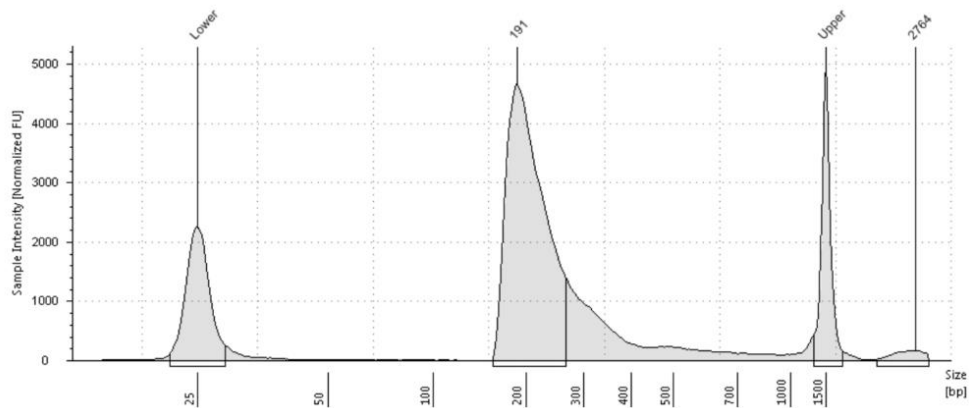
A1: L1922



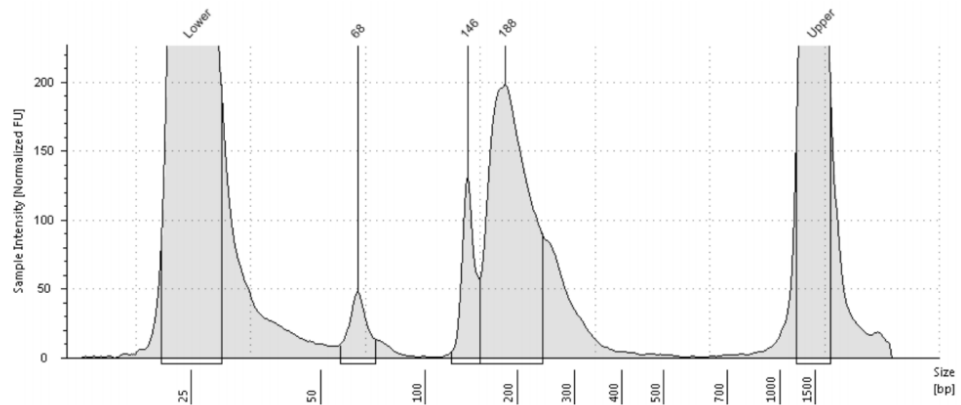
B1: L1923



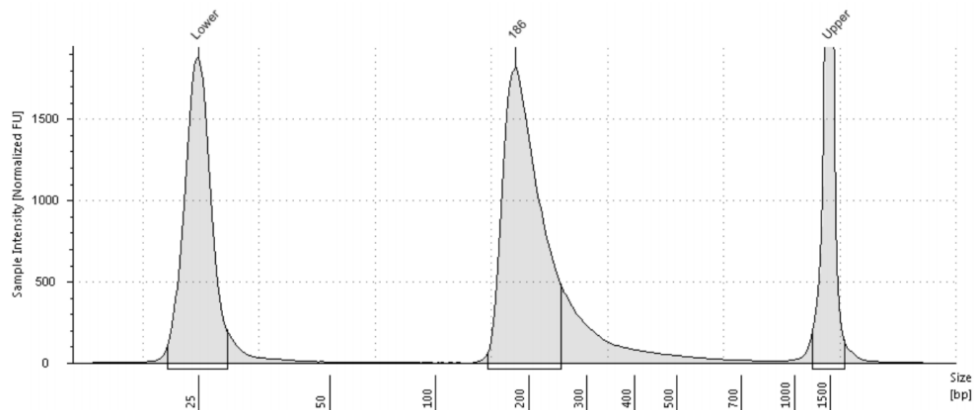
CI: L1924



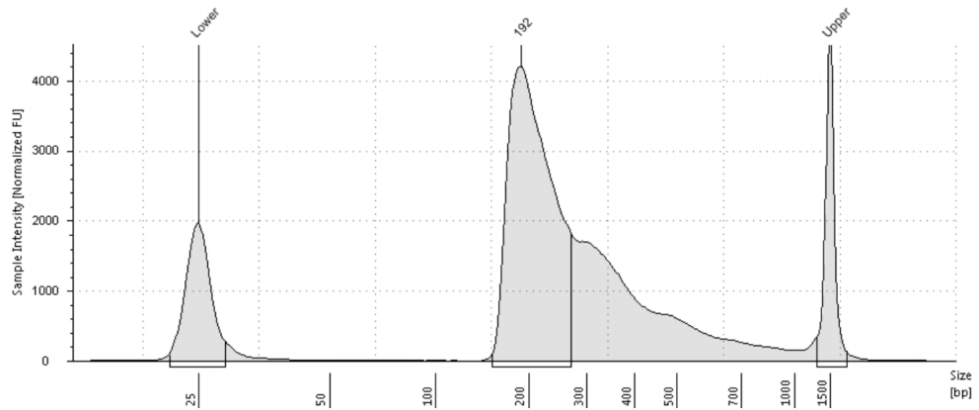
DI: L1925



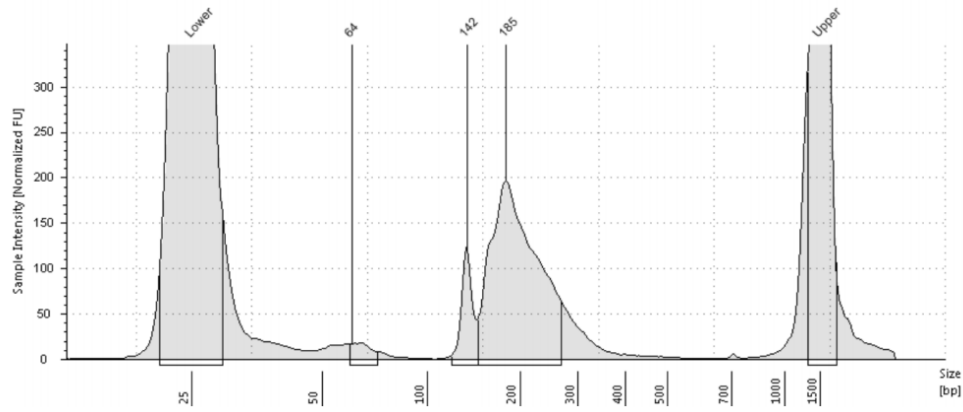
EI: L1926



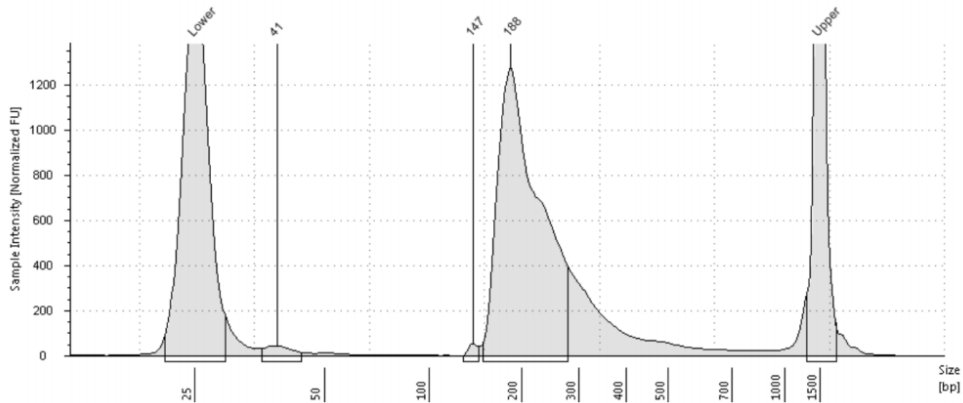
F1: L1927



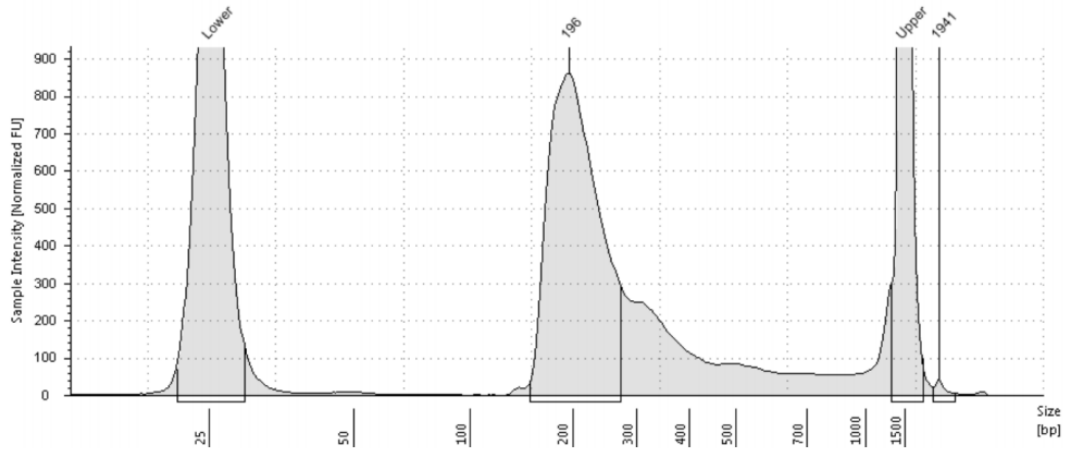
G1: L1928



H1: L1929

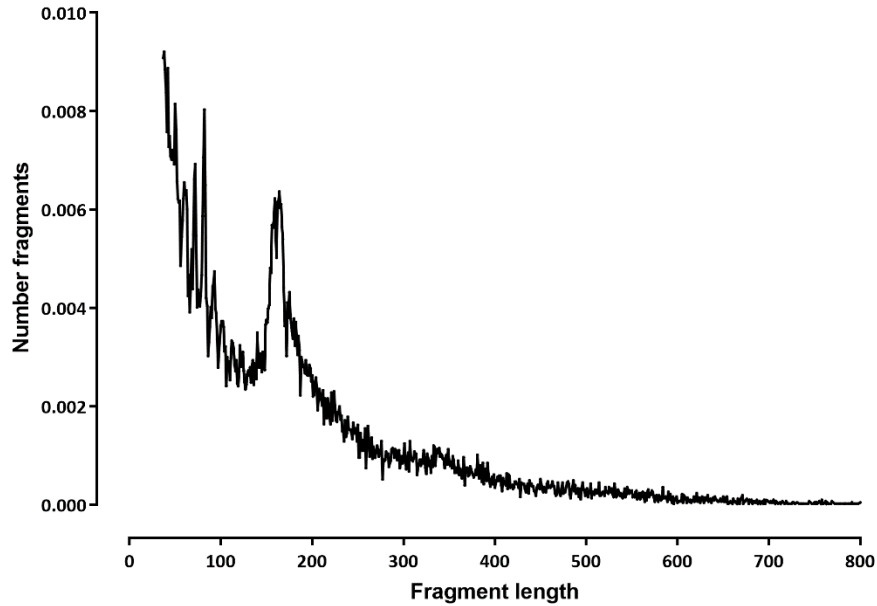


A2: L1930

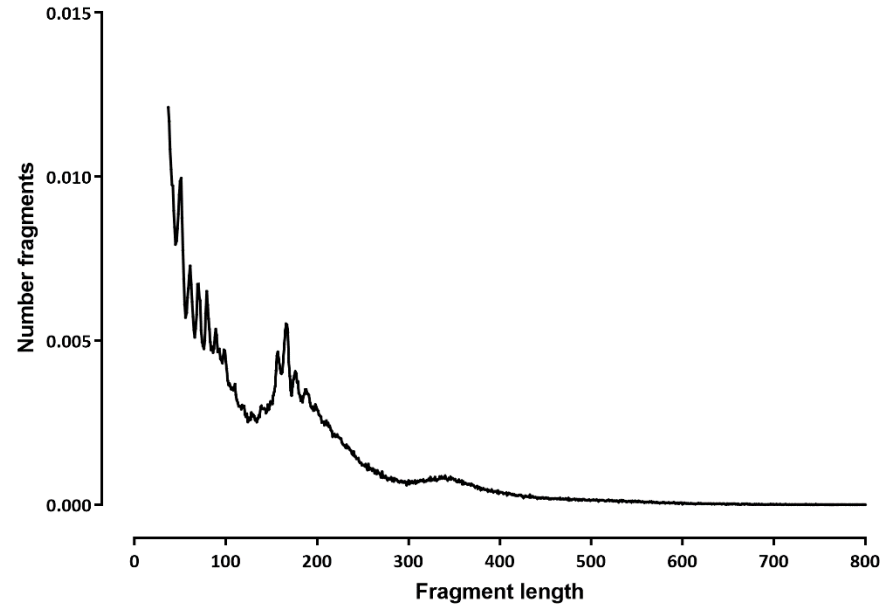


Fragment length

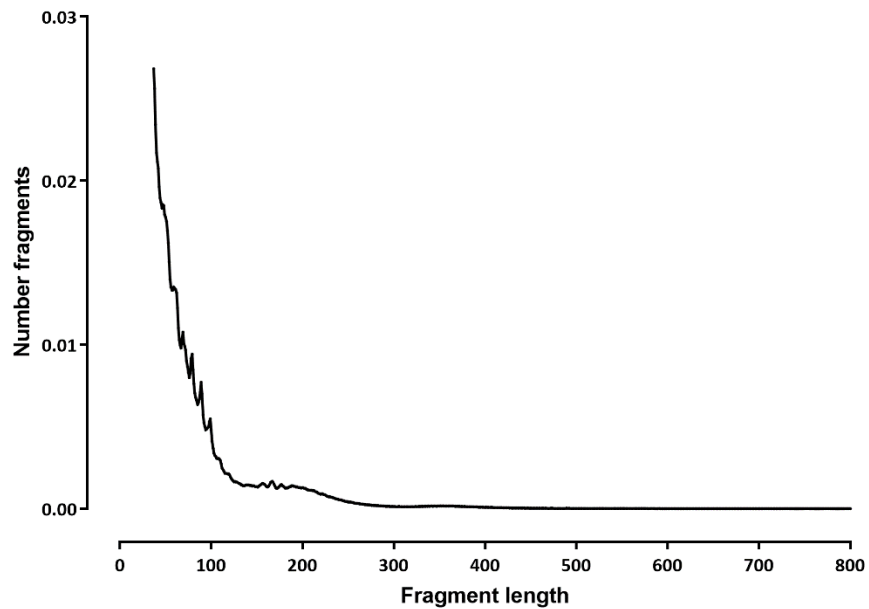
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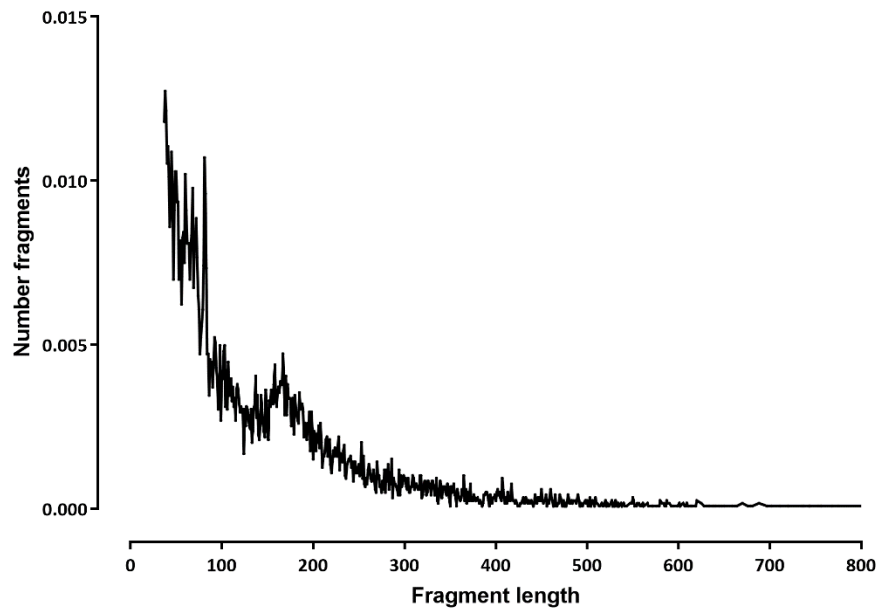
L1923-H4S47C_50M_30min



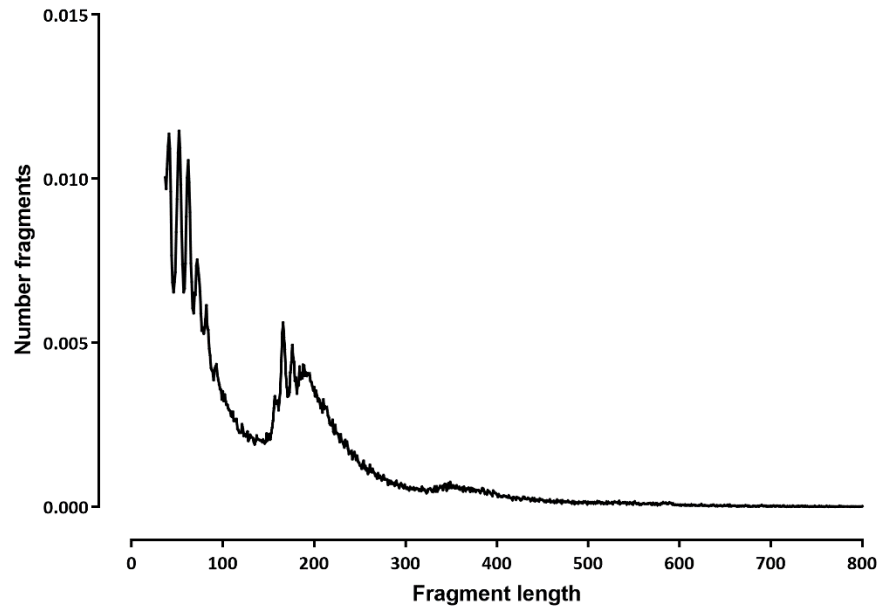
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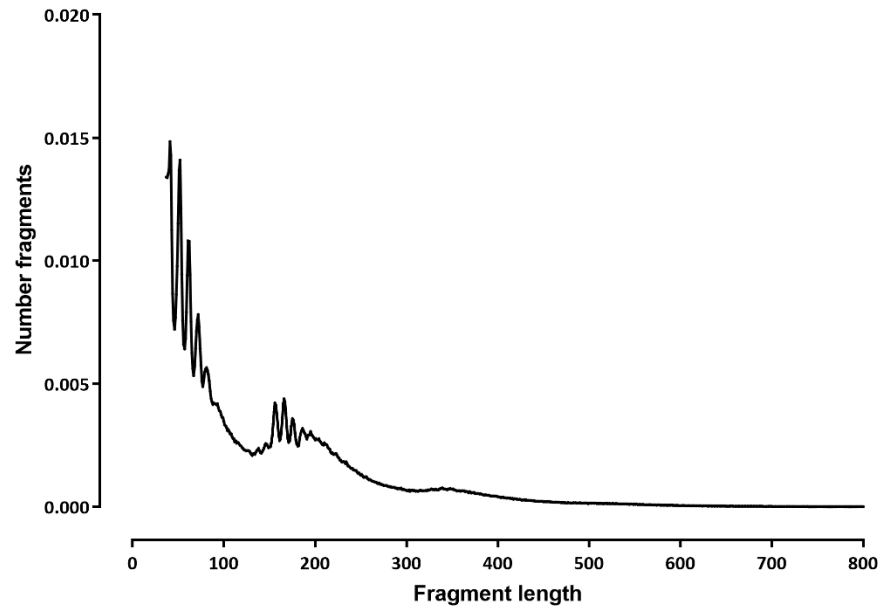
L1925-H4S47C_250M_30min_low_enzyme



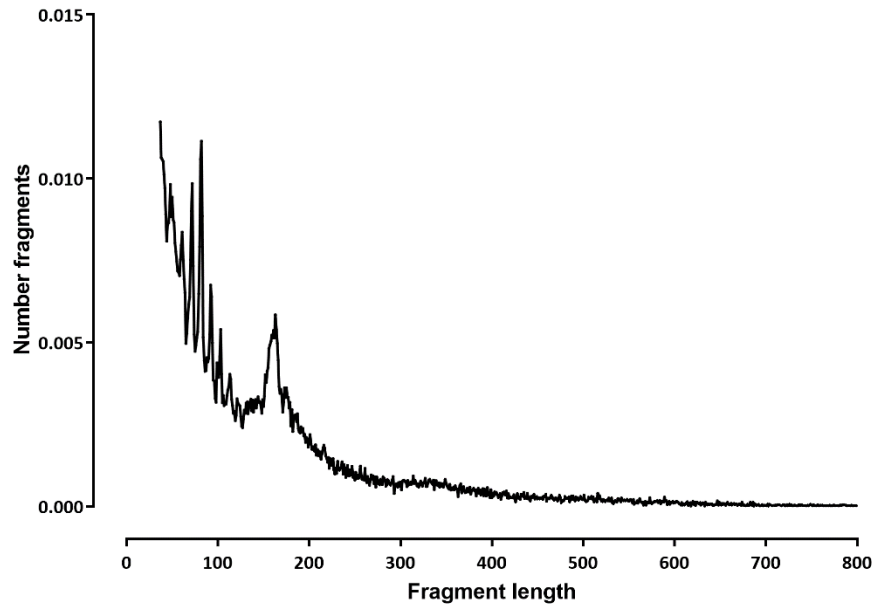
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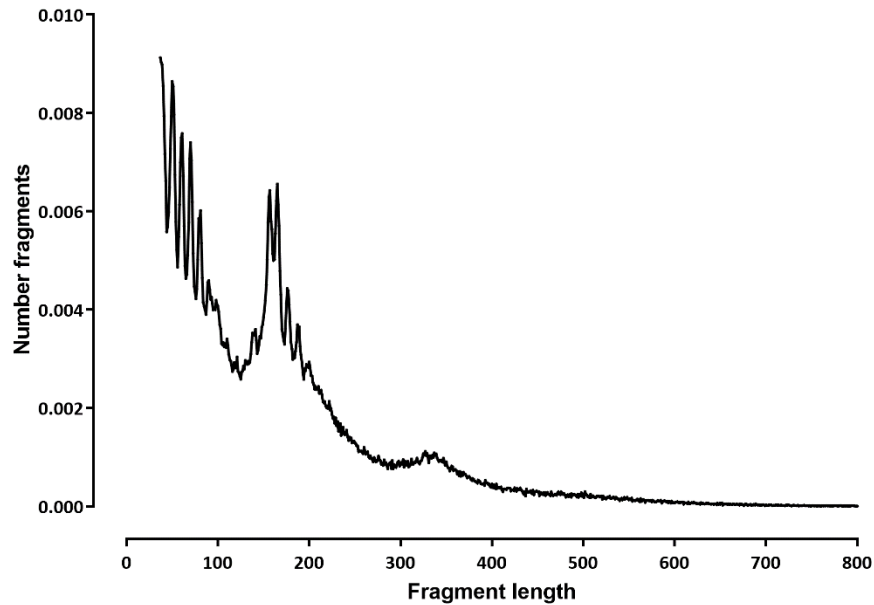
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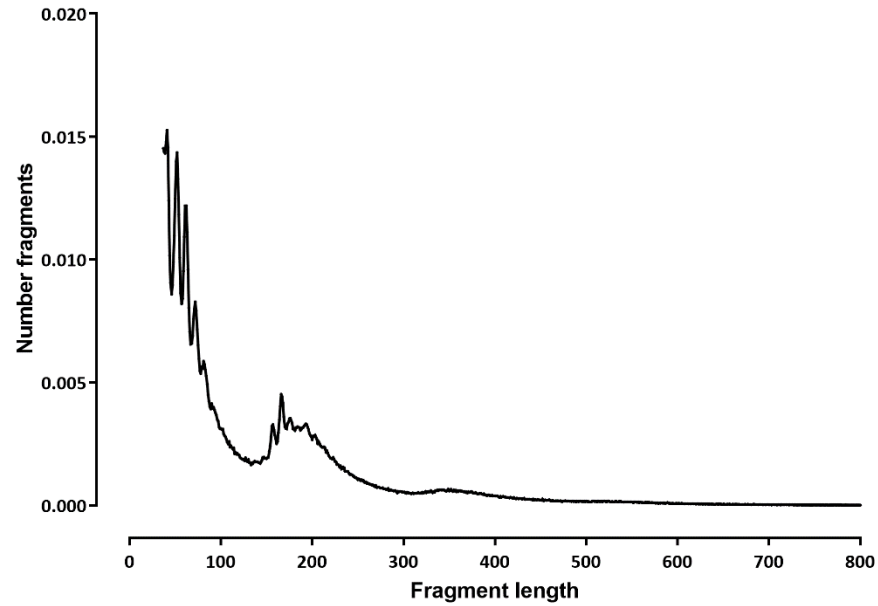
L1928-H4S47C_250M_5min



L1929-H4S47C_50M_5min

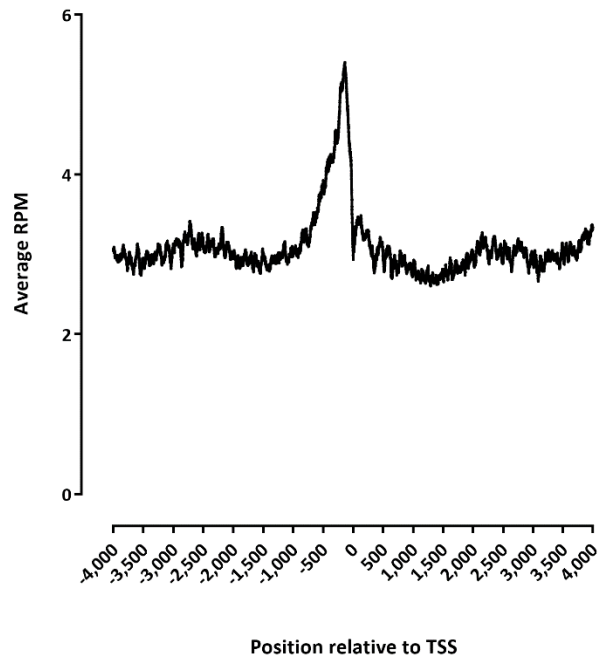


L1930-H4S47C_5M_5min

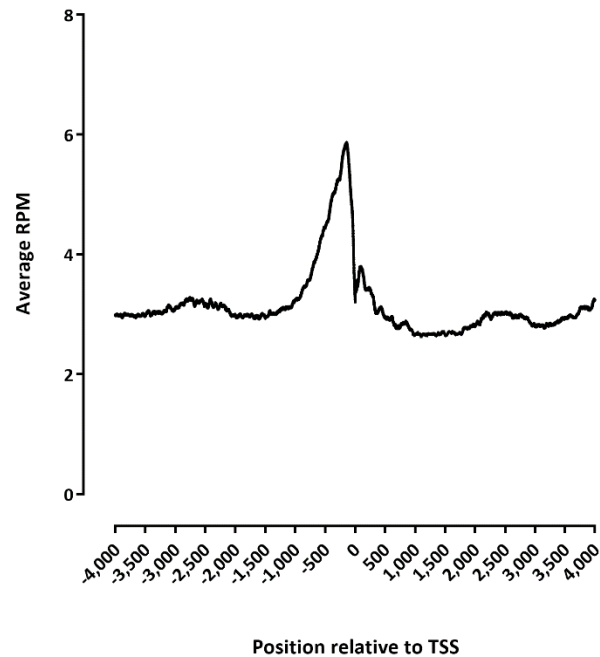


TSS profiles

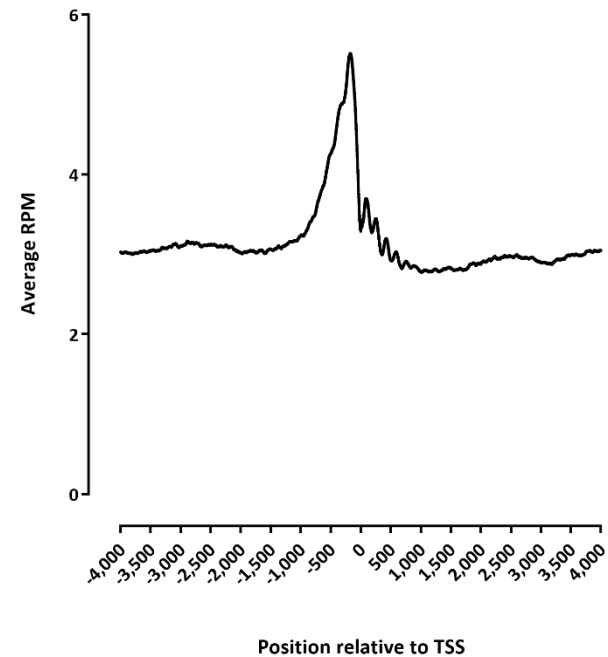
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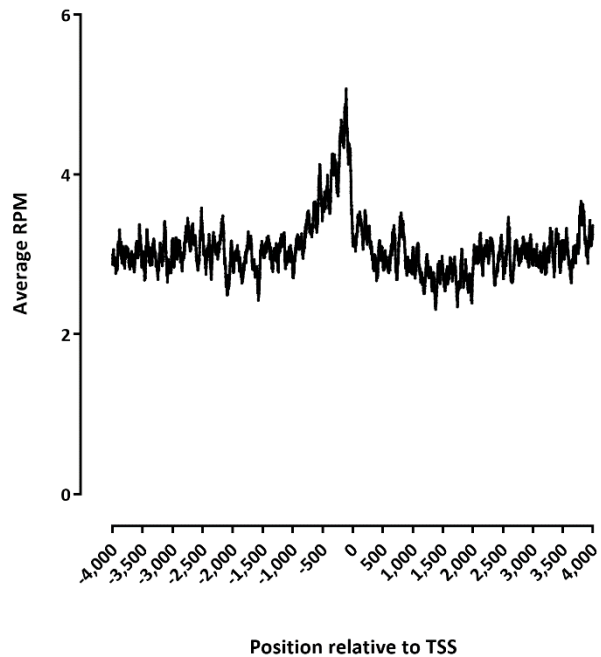
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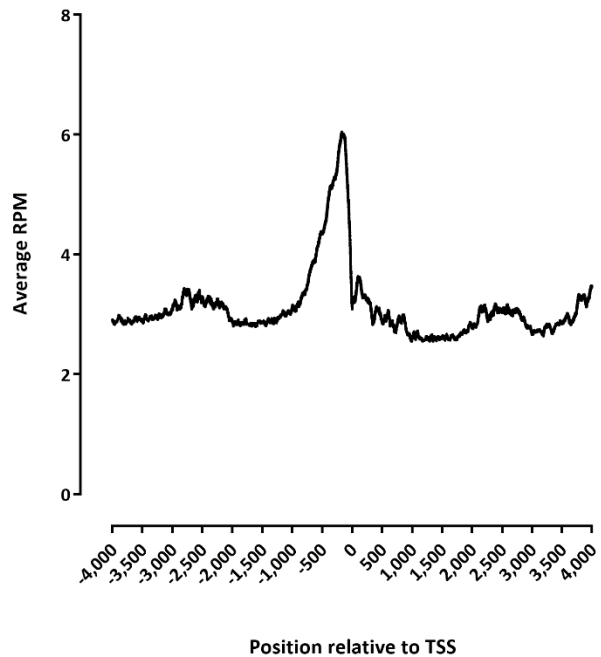
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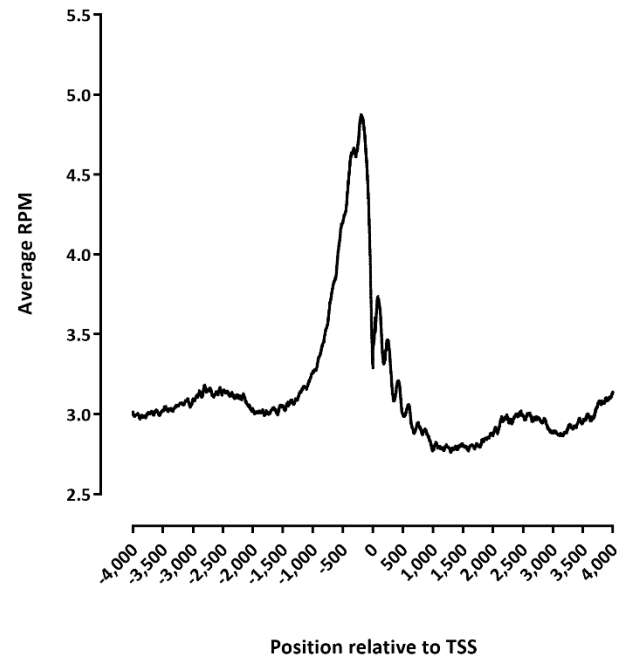
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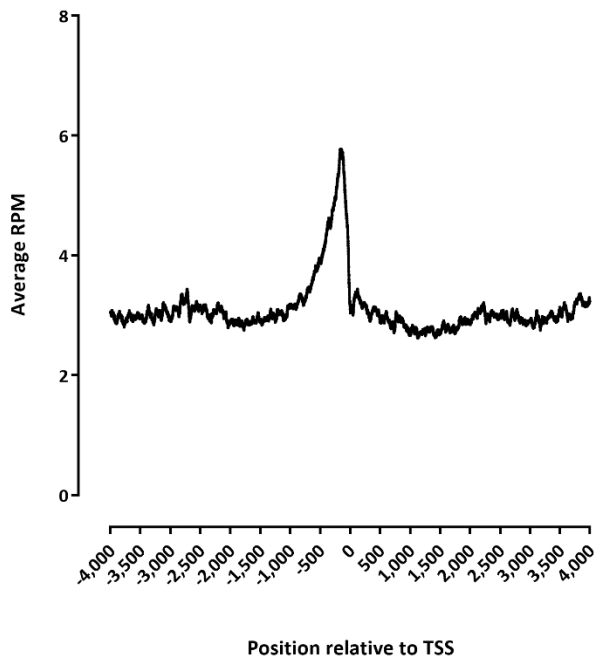
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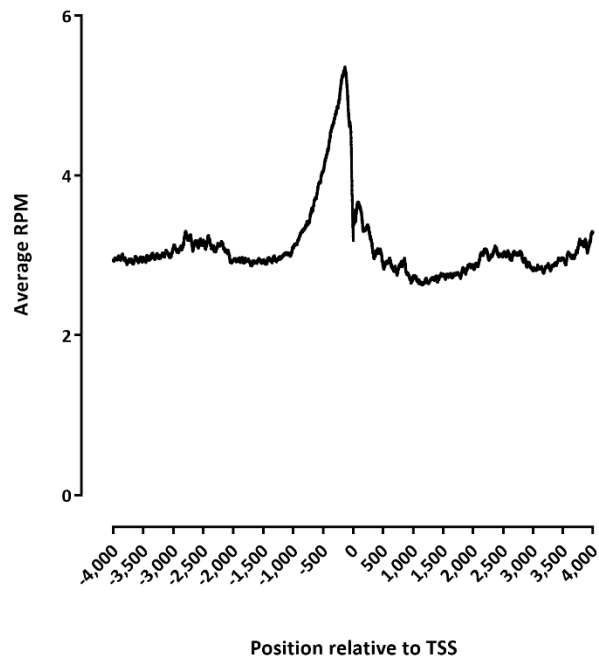
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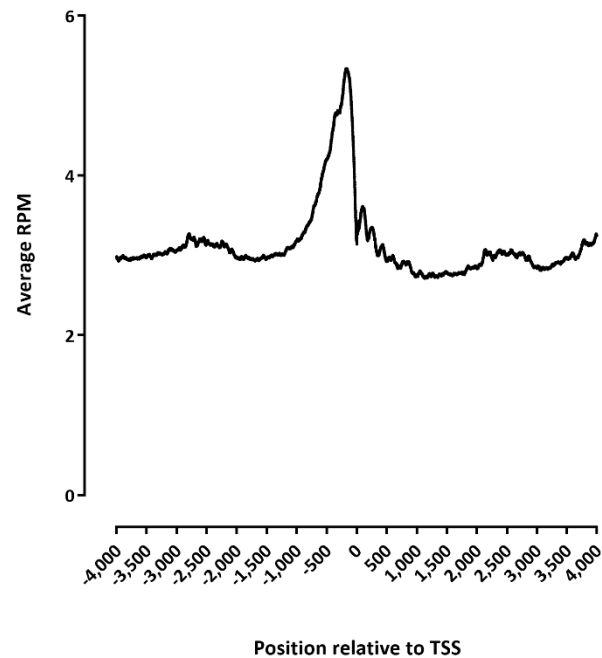
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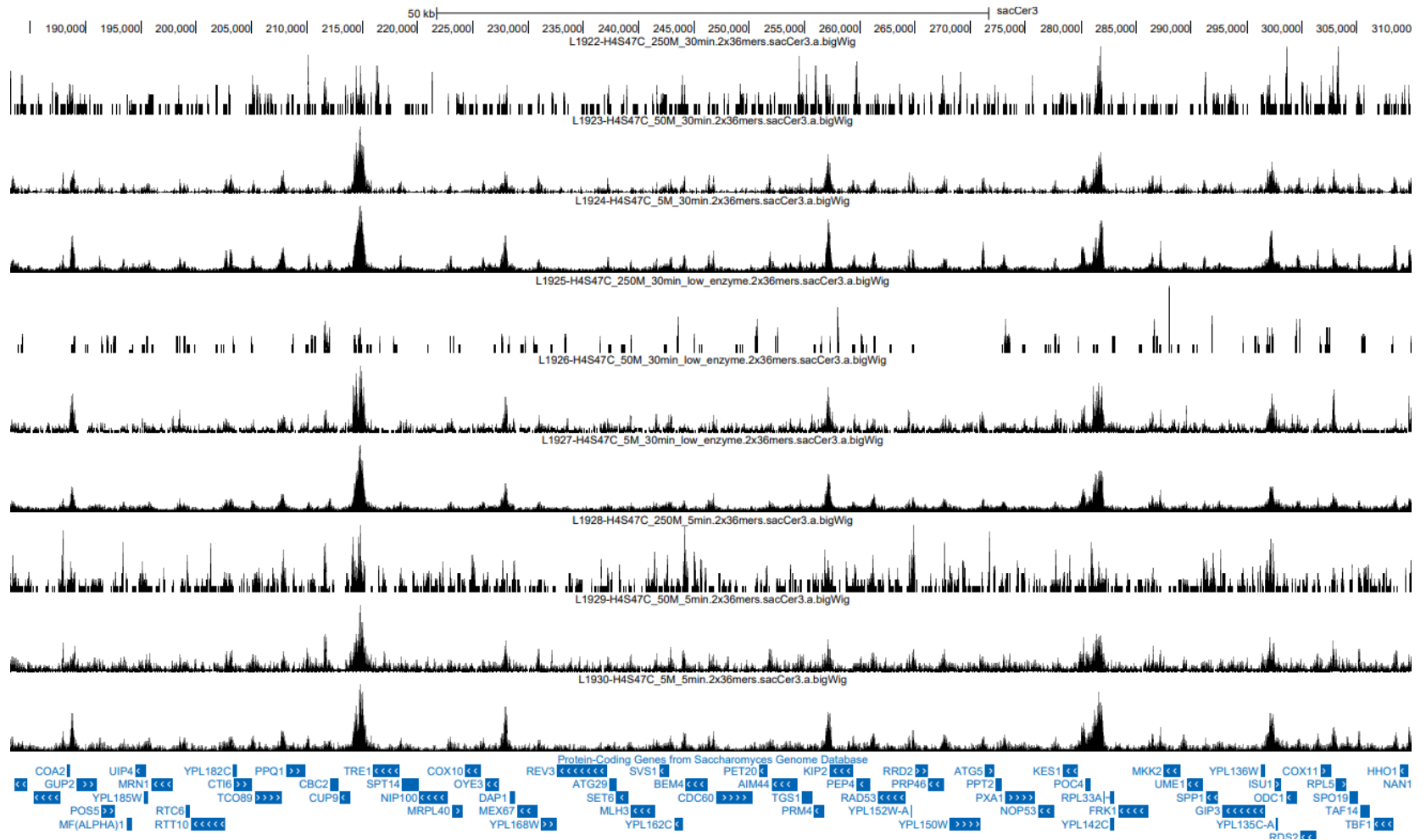
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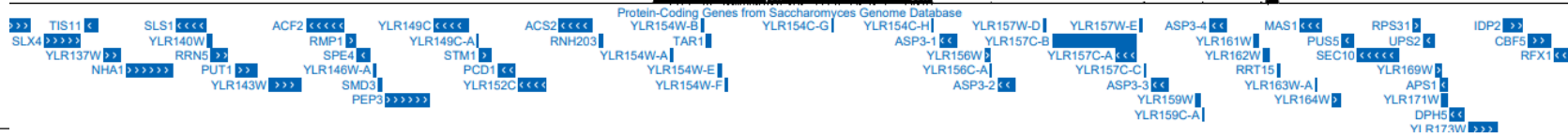
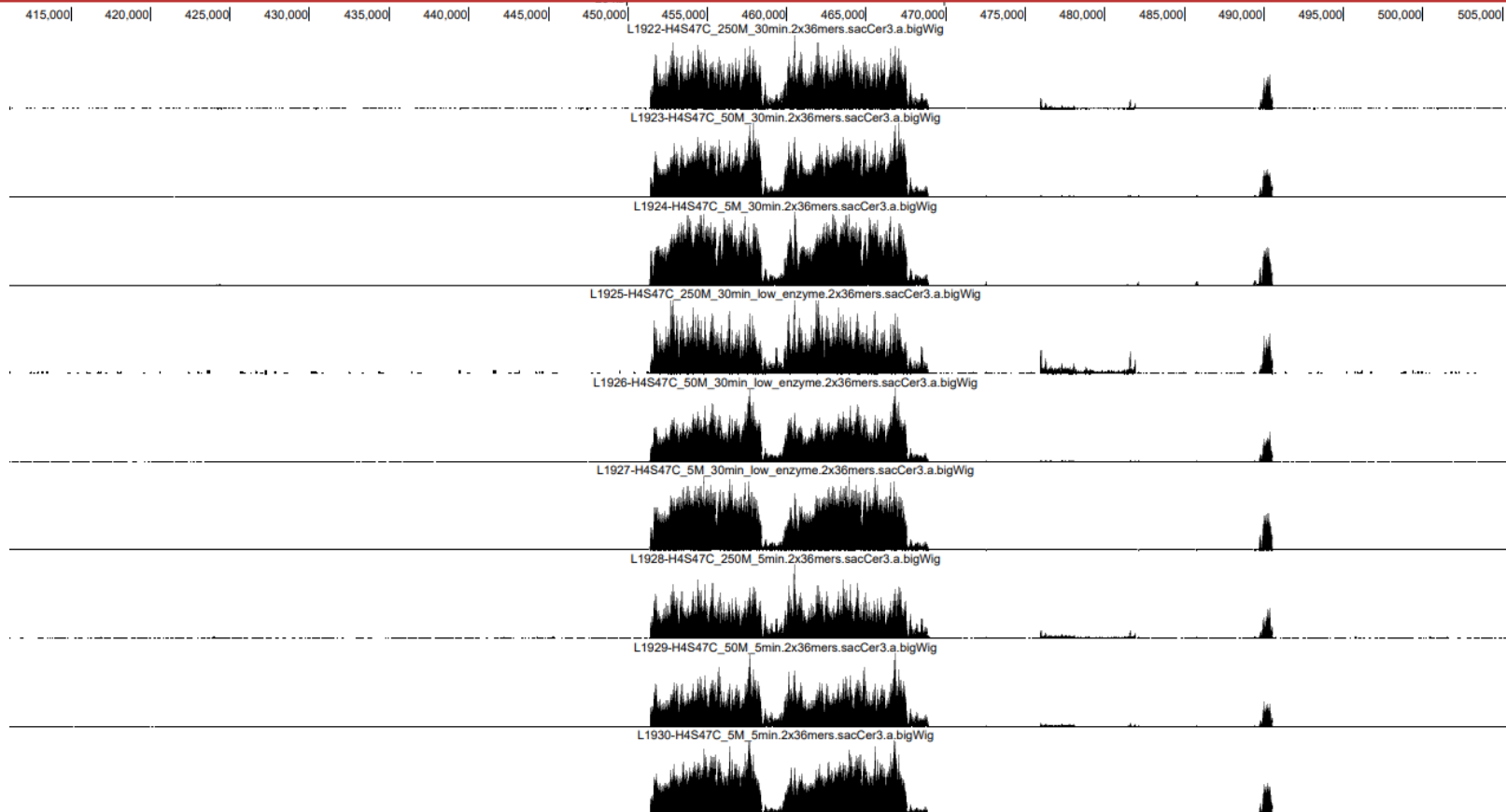
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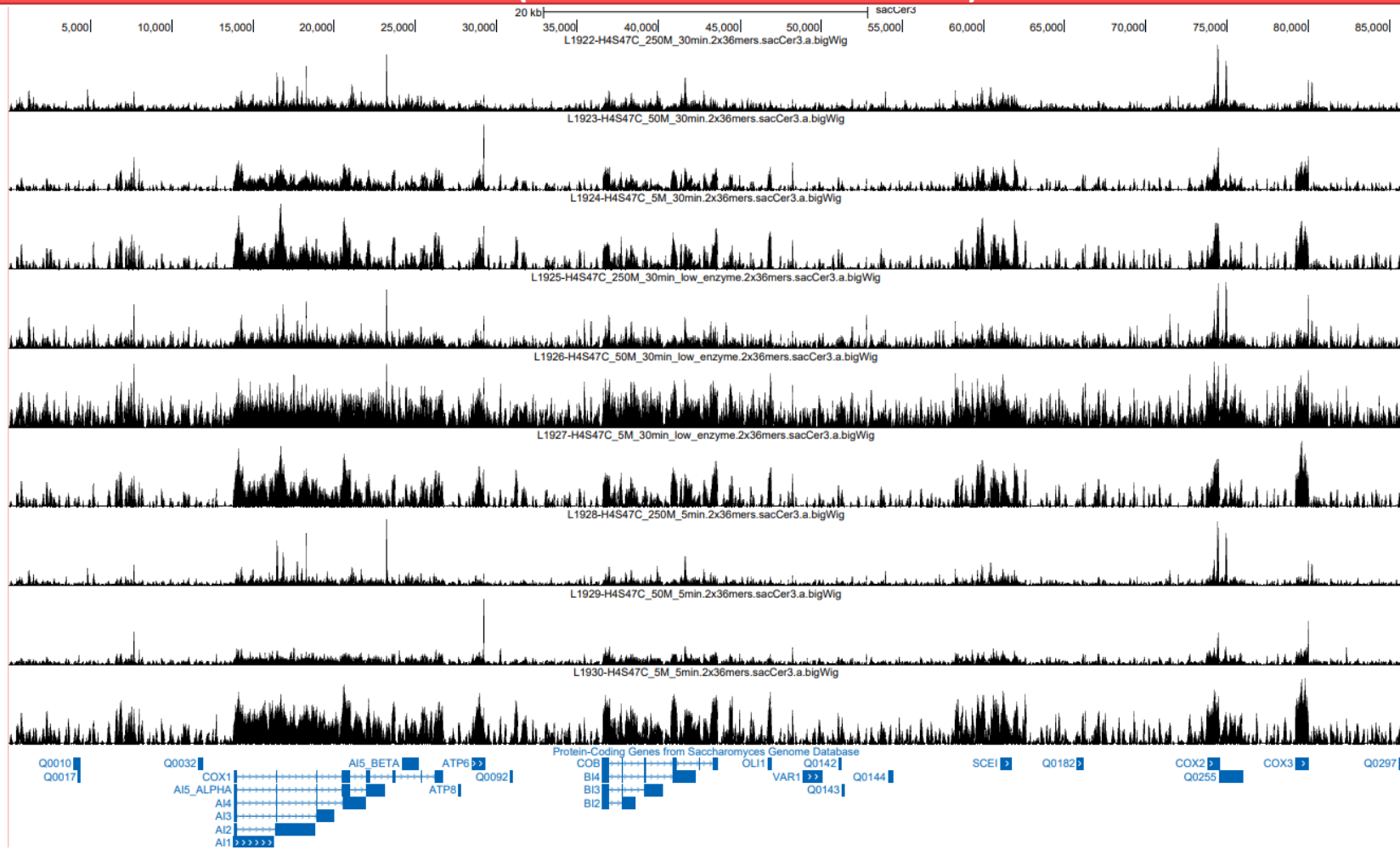
Snapshots



rDNA (with multireads normalized)

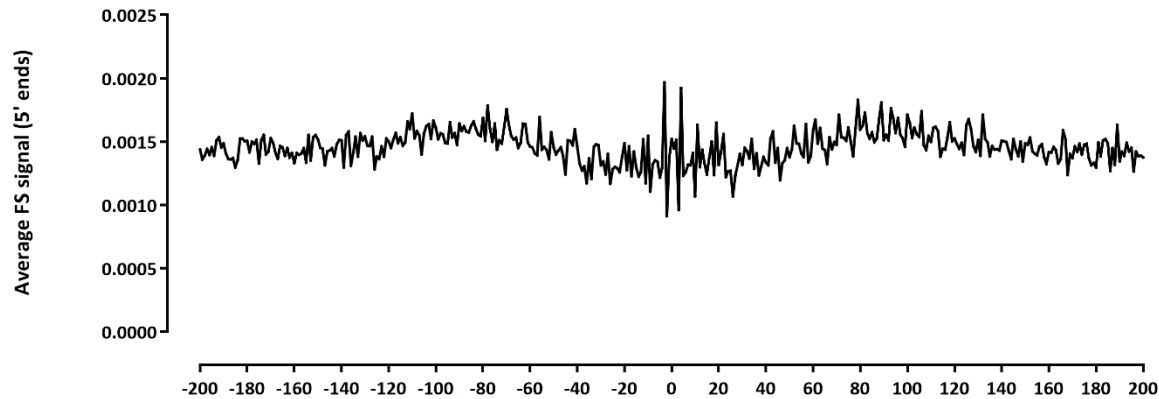


chrM (with multireads normalized)

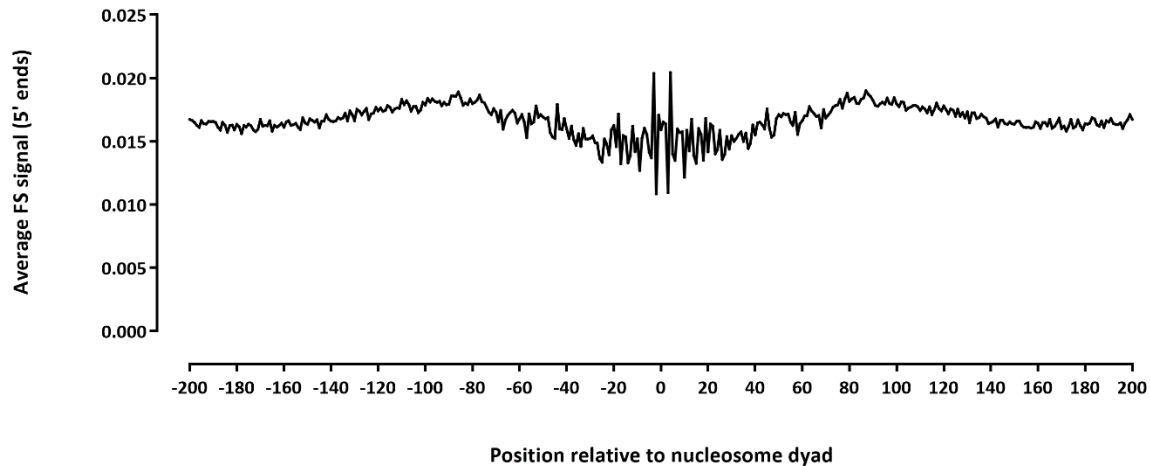


Chemical map

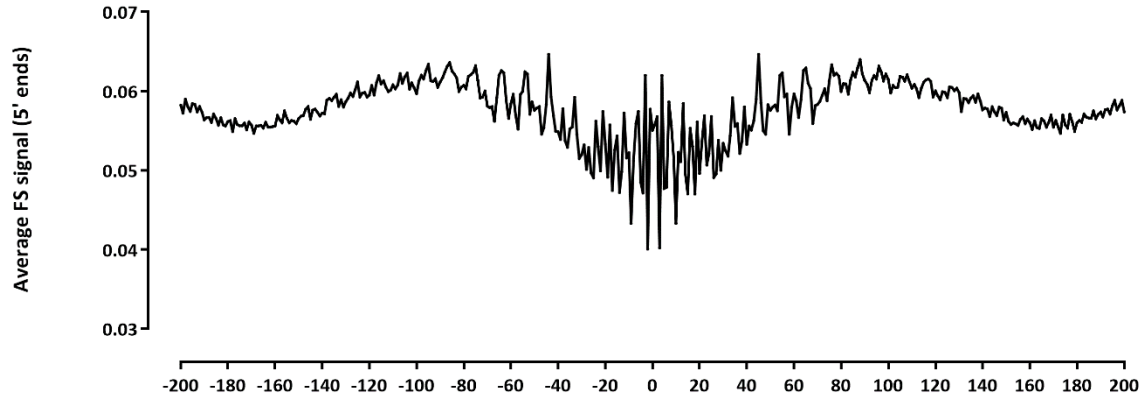
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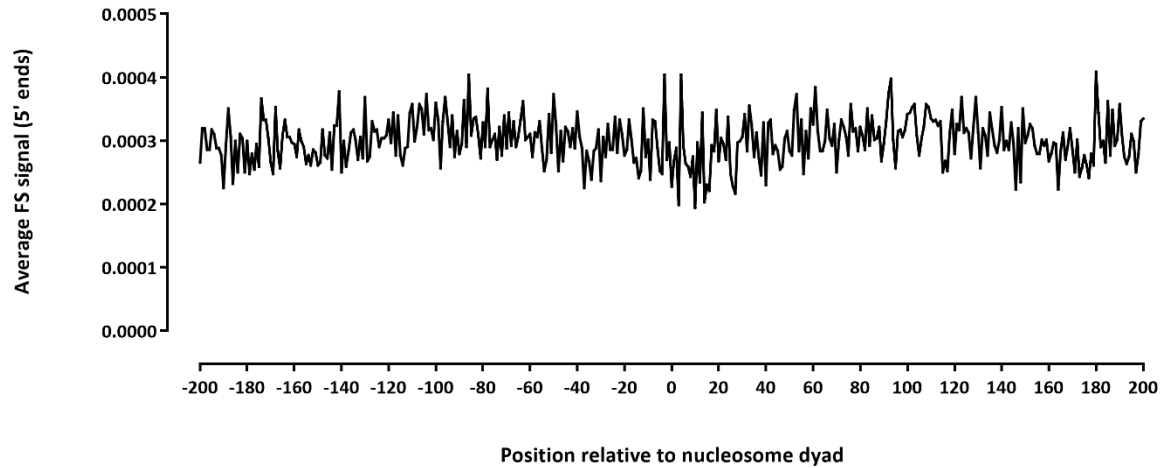
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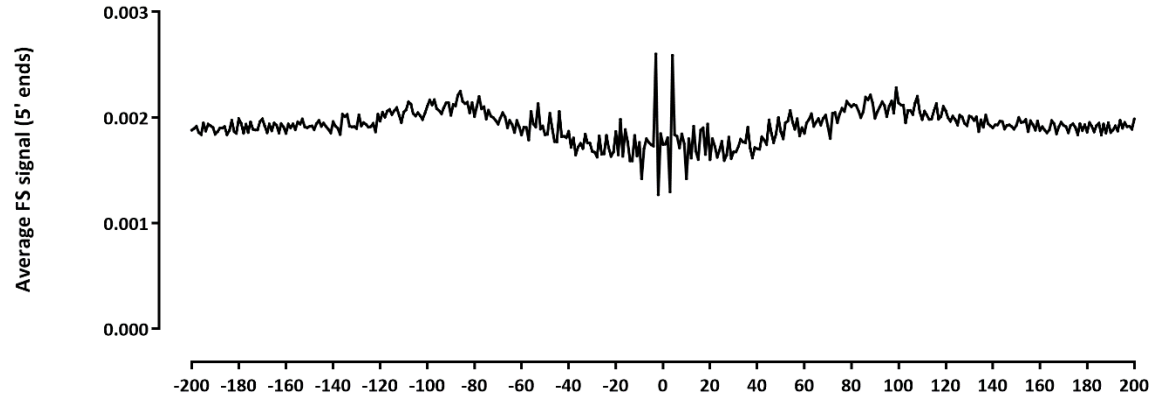
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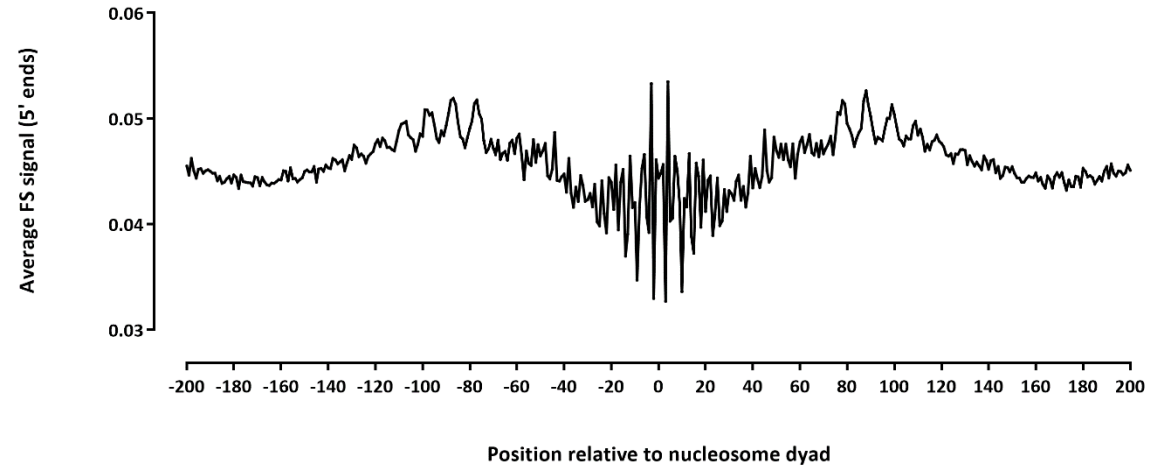
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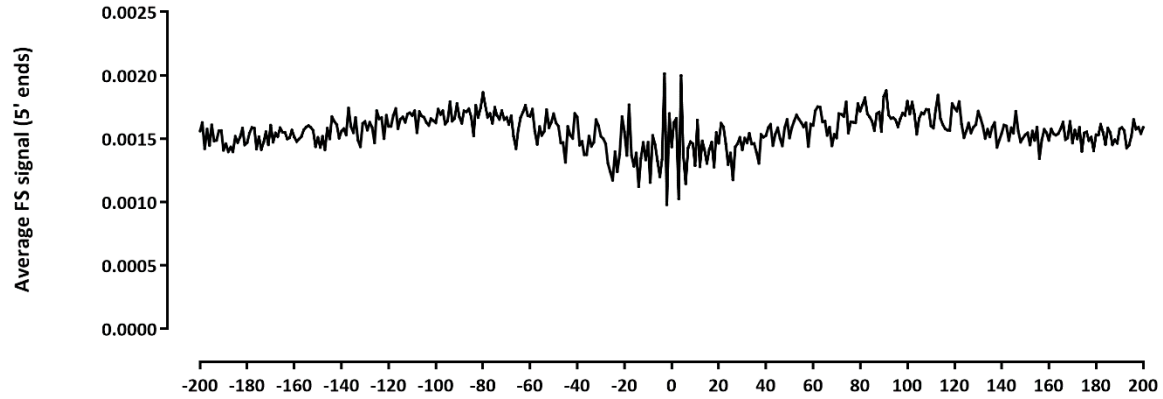
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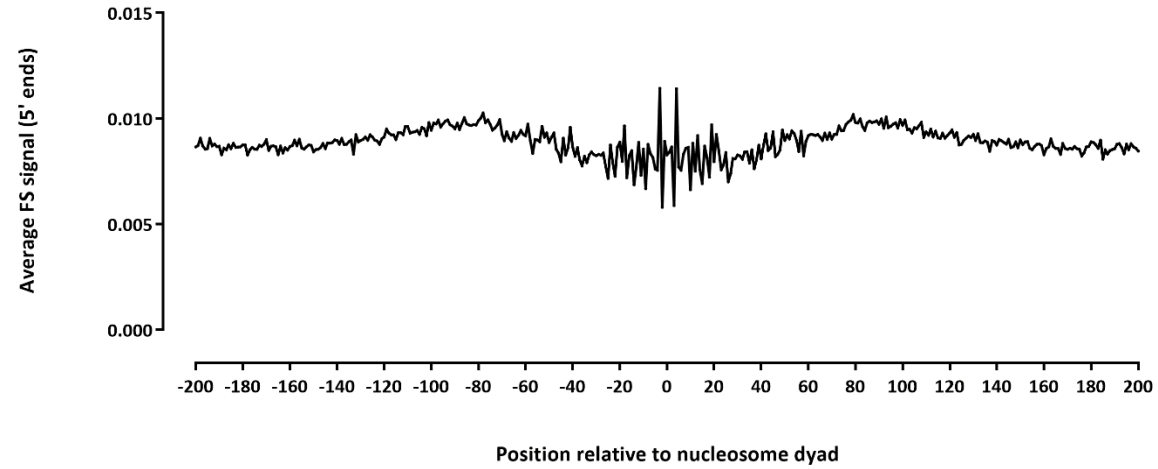
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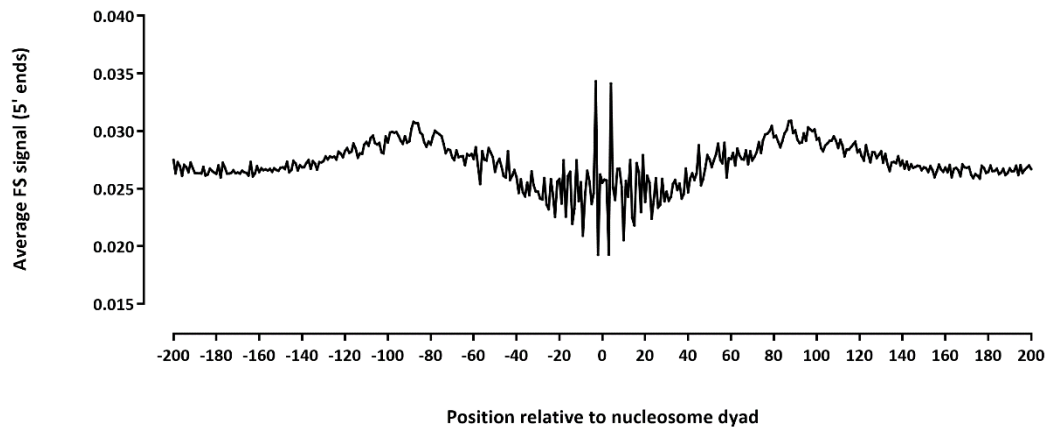
L1928-H4S47C_250M_5min



L1929-H4S47C_50M_5min

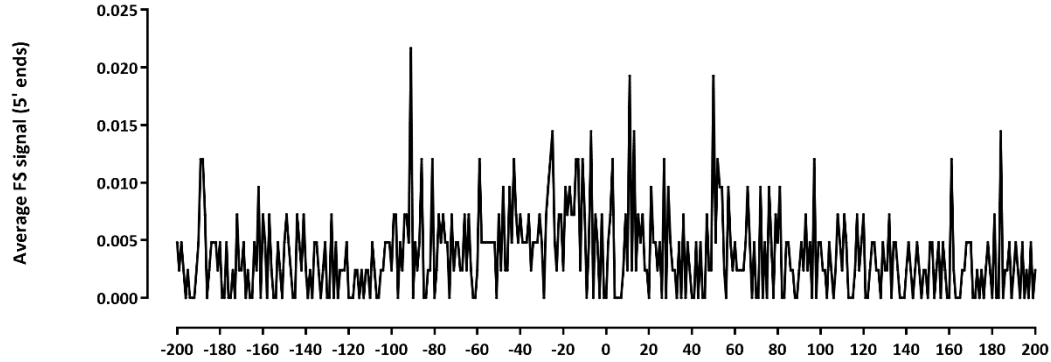


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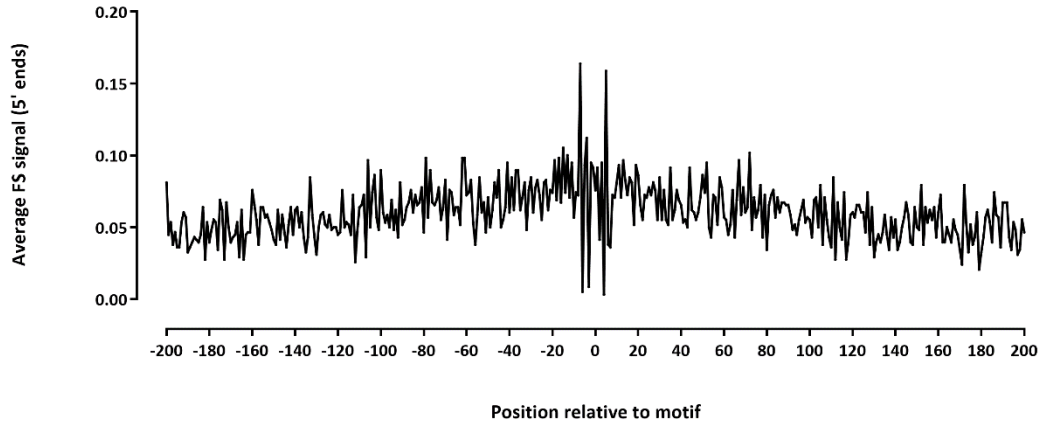


Footprints ABF1

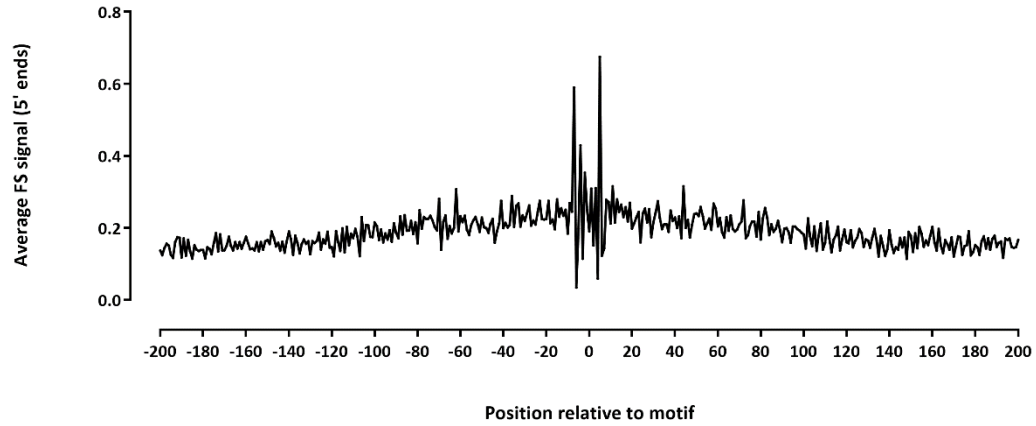
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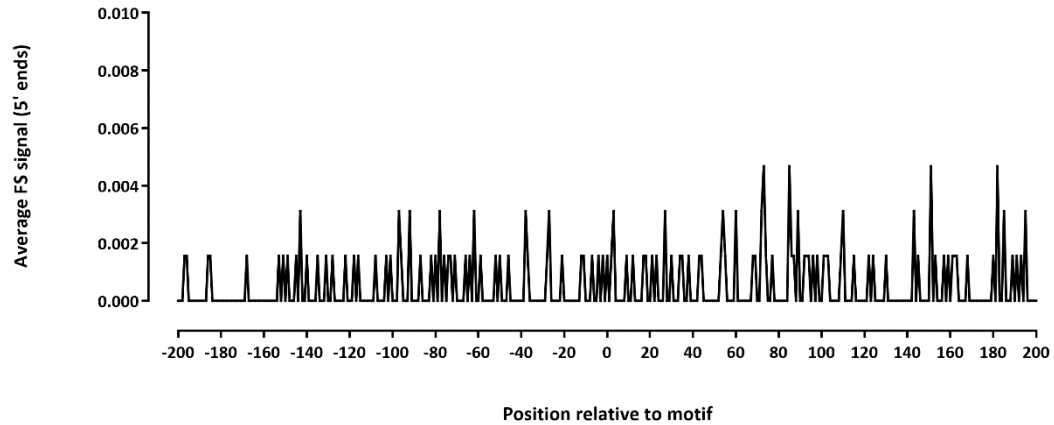
L1923-H4S47C_50M_30min



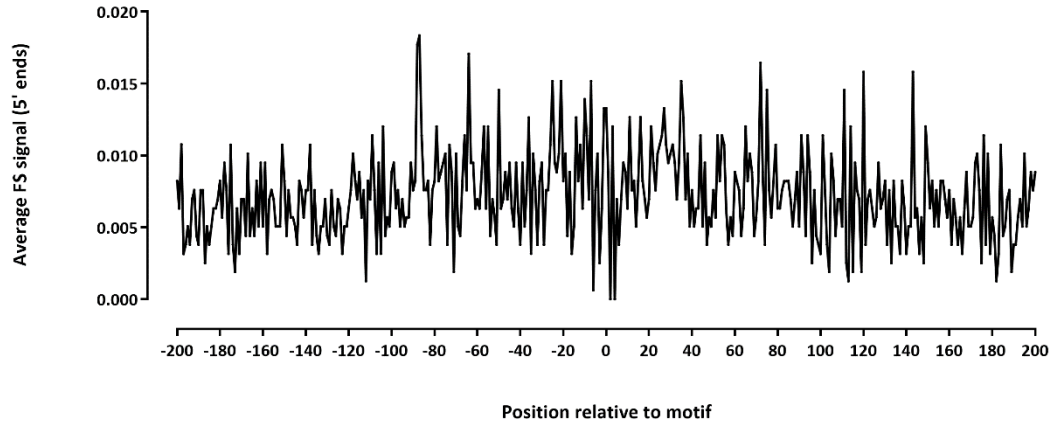
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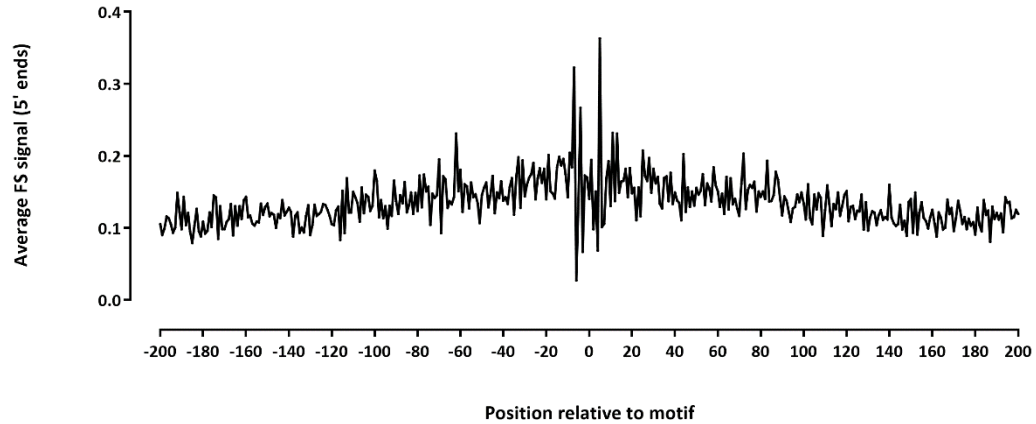
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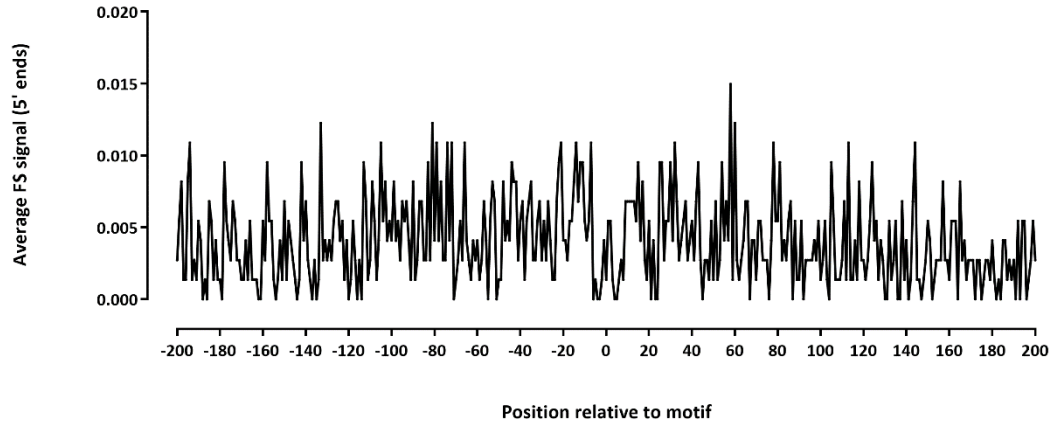
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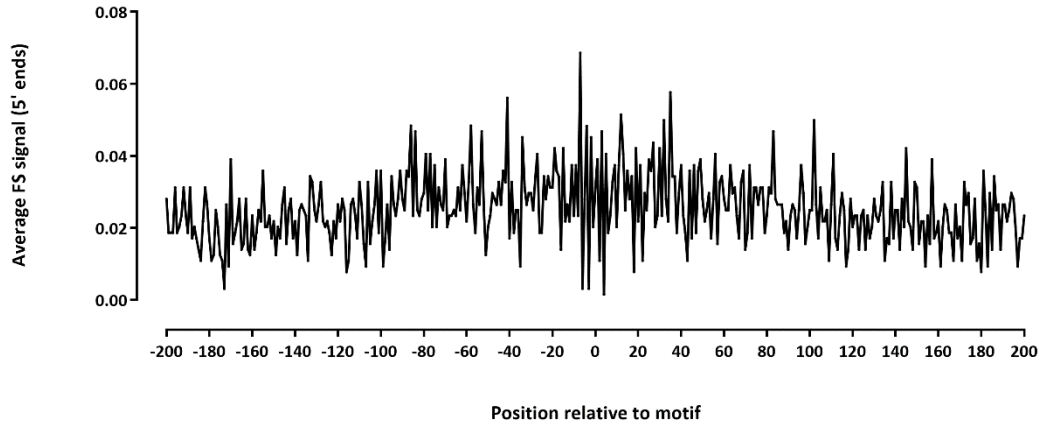
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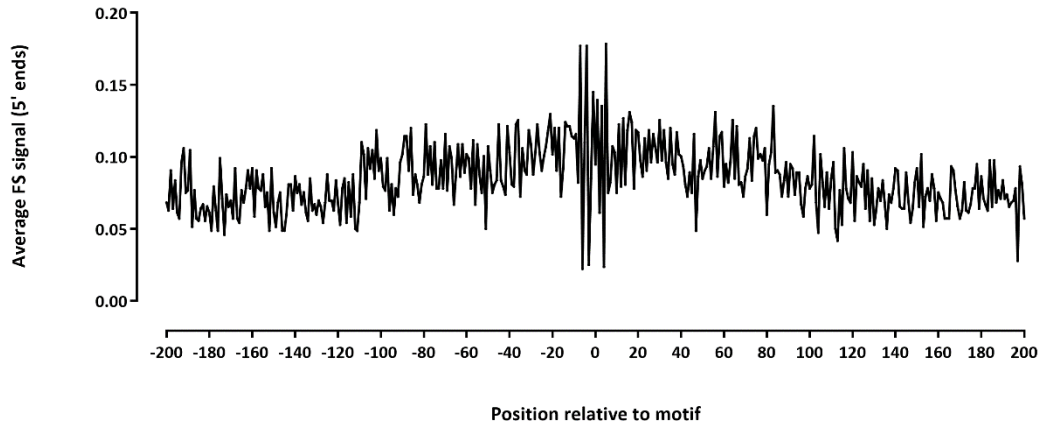
L1928-H4S47C_250M_5min



L1929-H4S47C_50M_5min

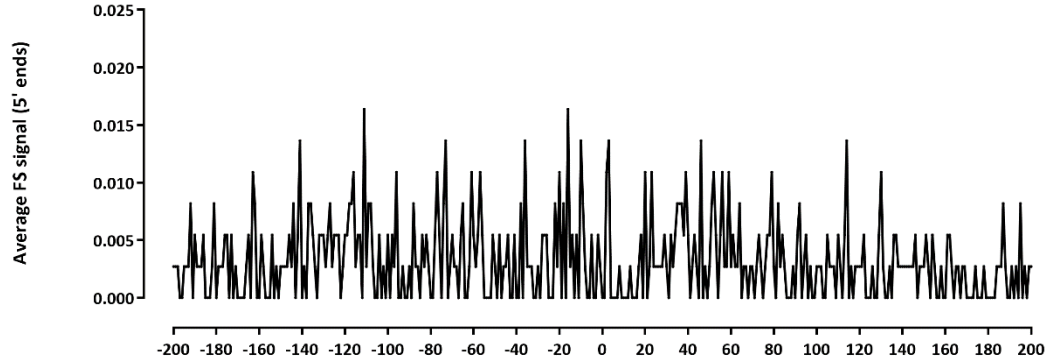


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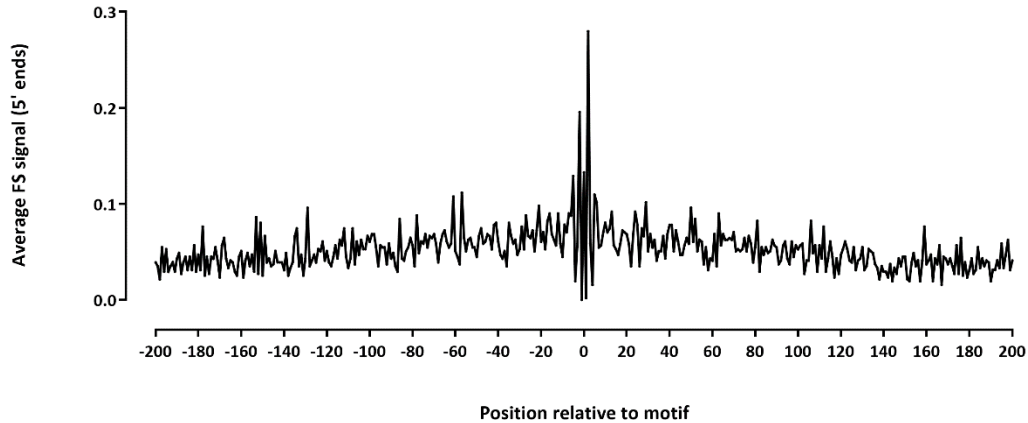


Footprints CBF1

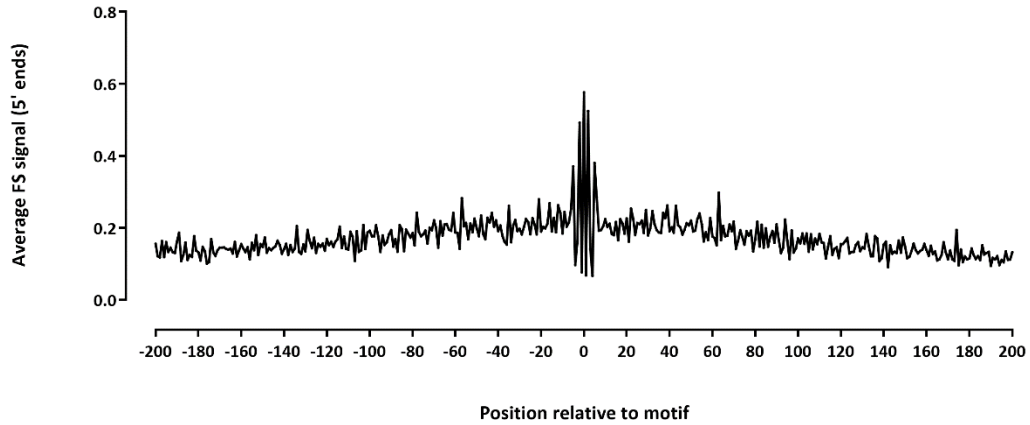
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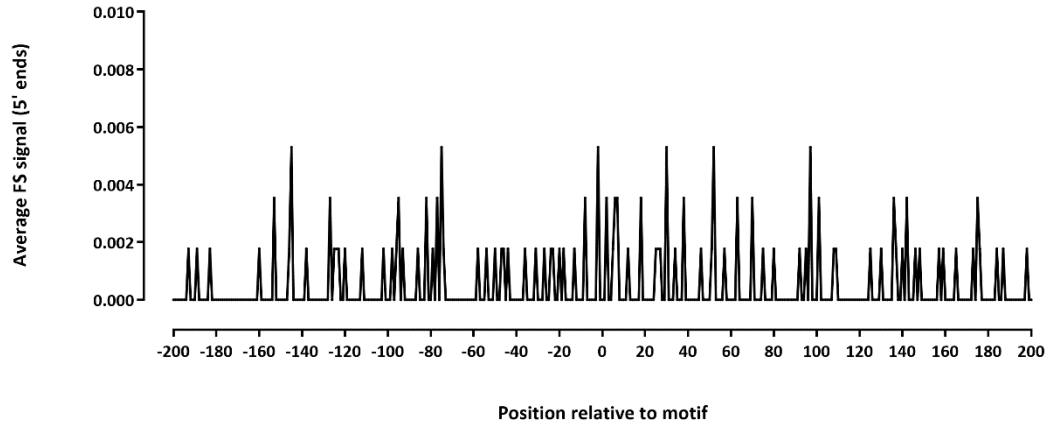
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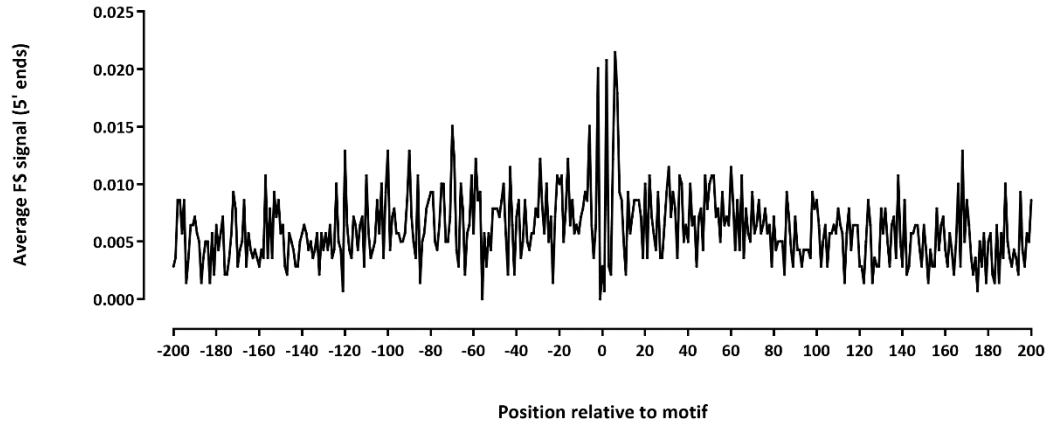
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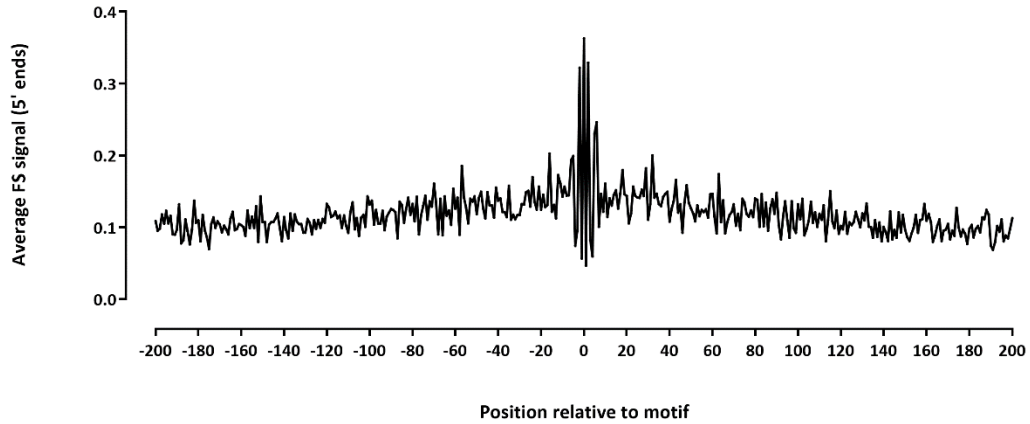
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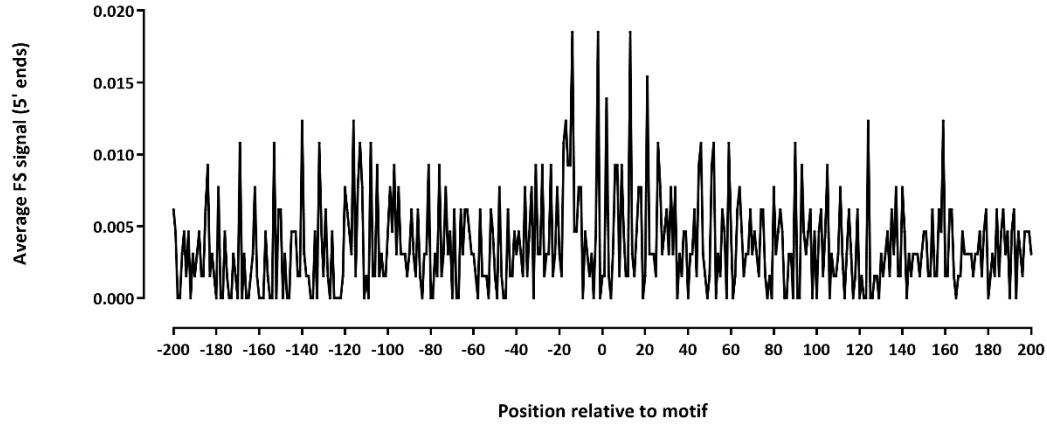
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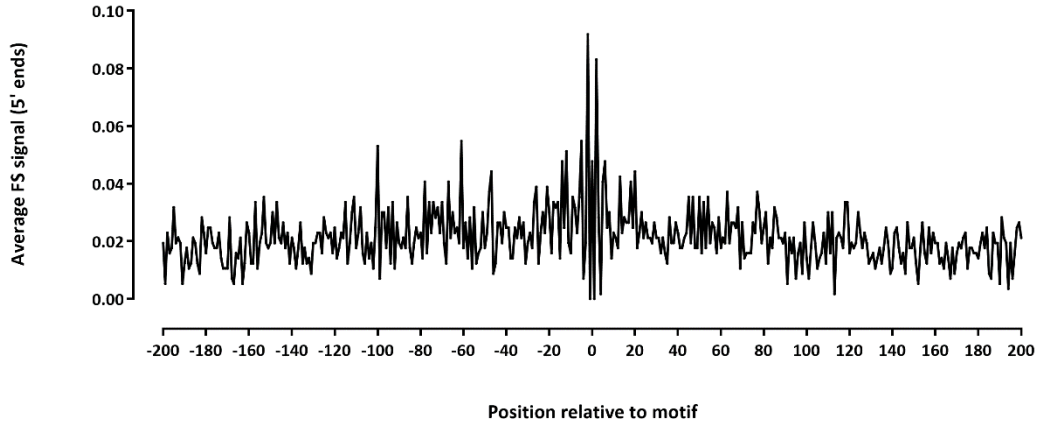
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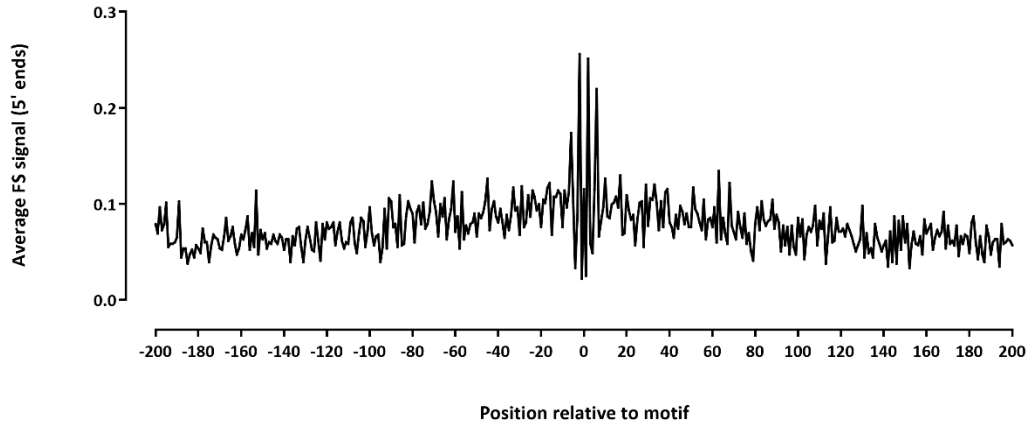
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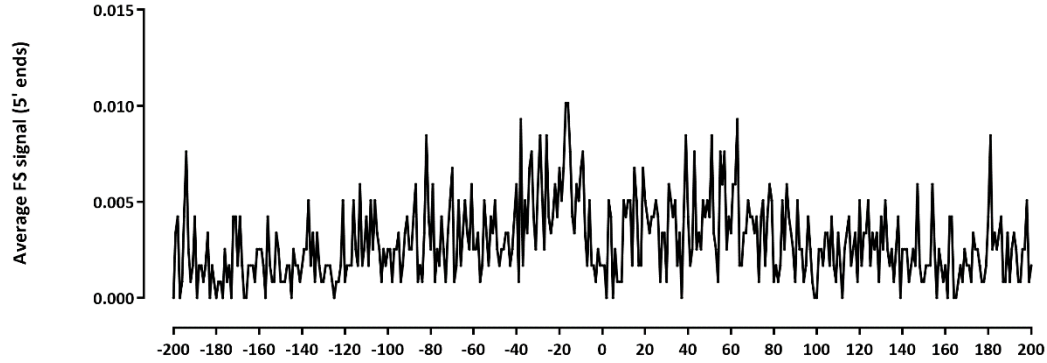


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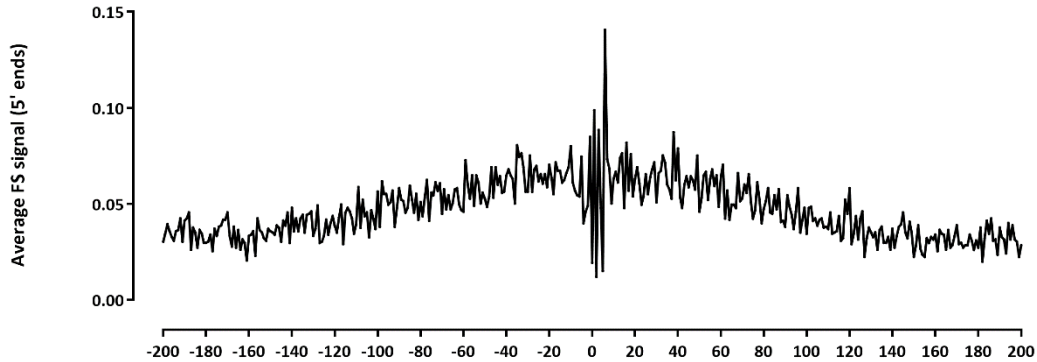


Footprints REB1

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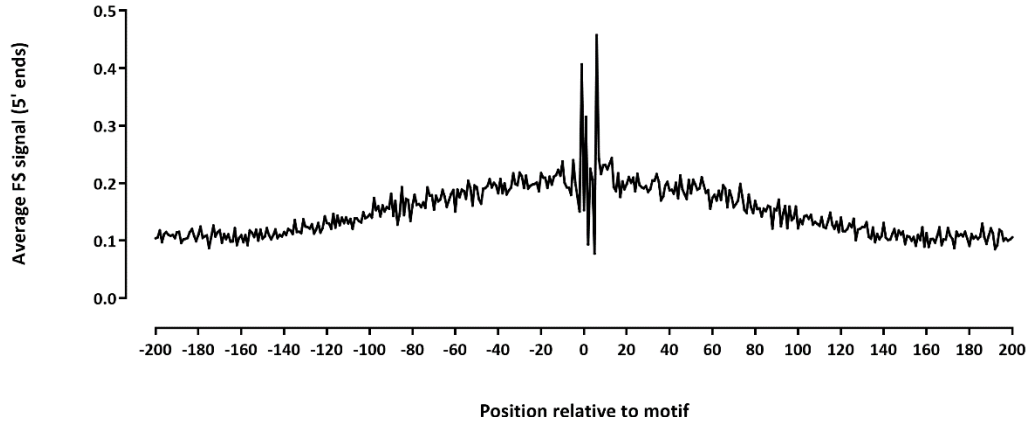


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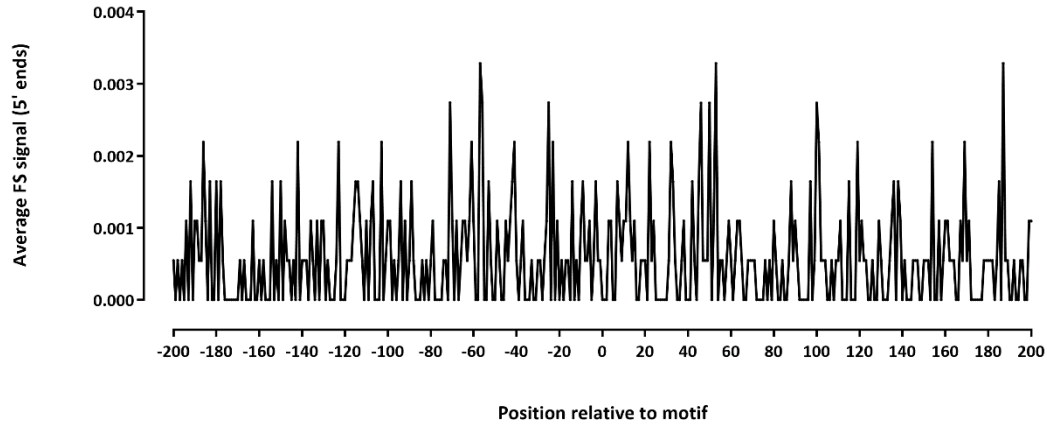


Position relative to motif

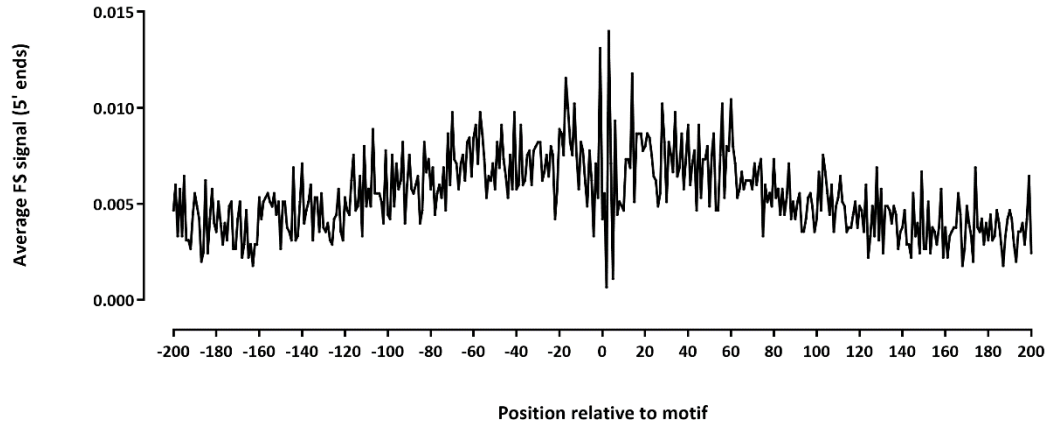
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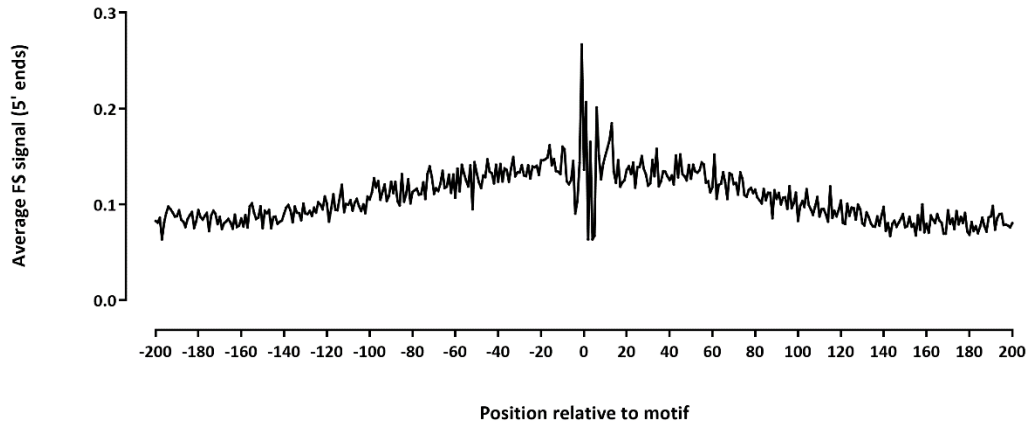
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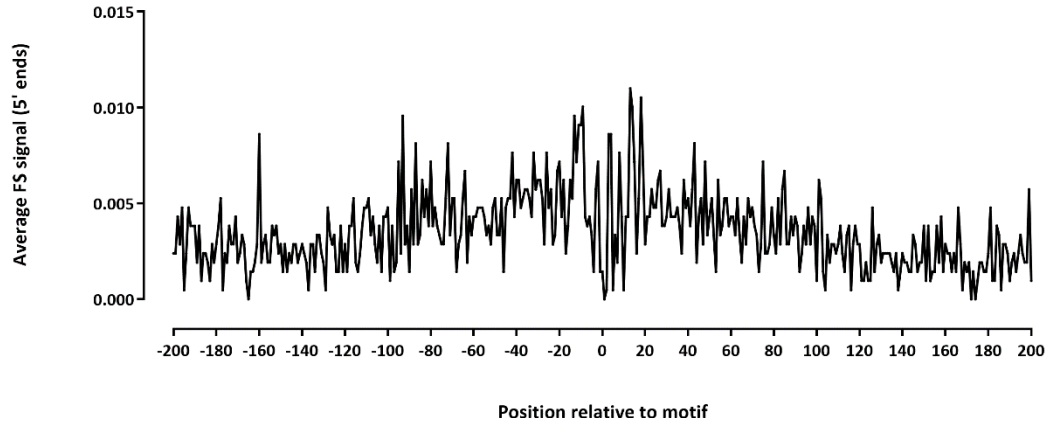
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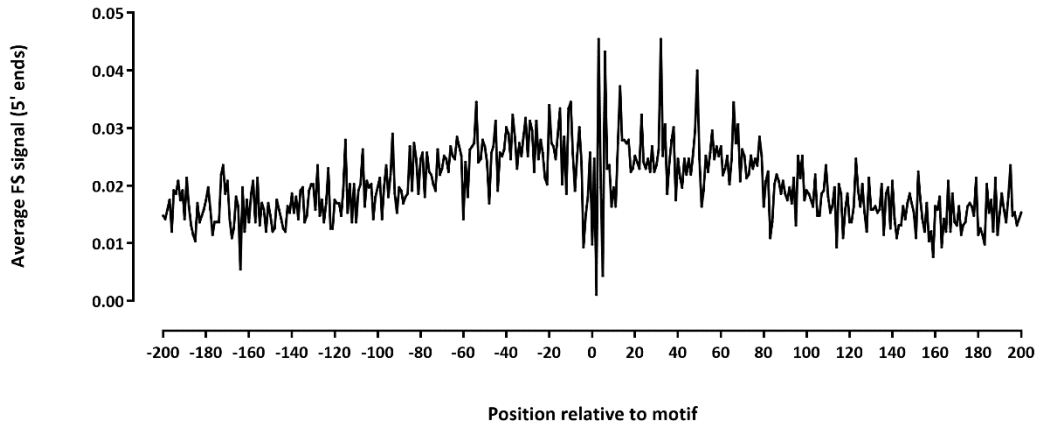
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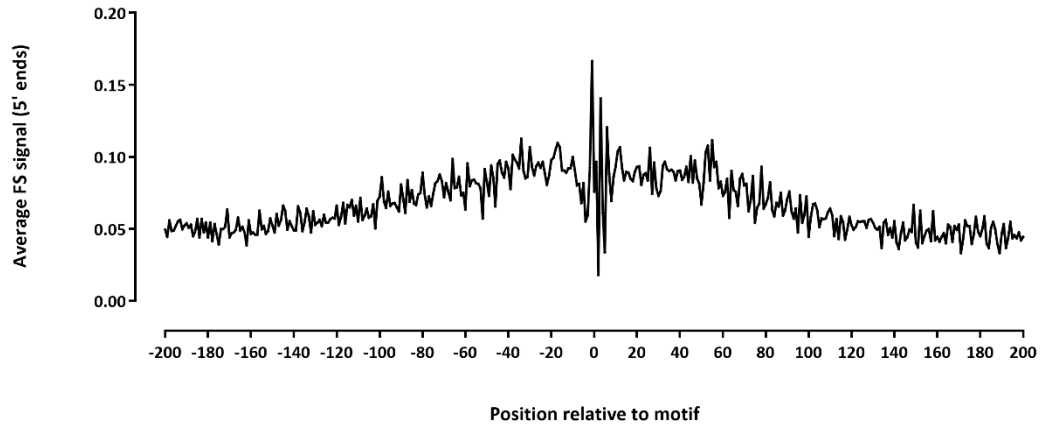
L1928-H4S47C_250M_5min



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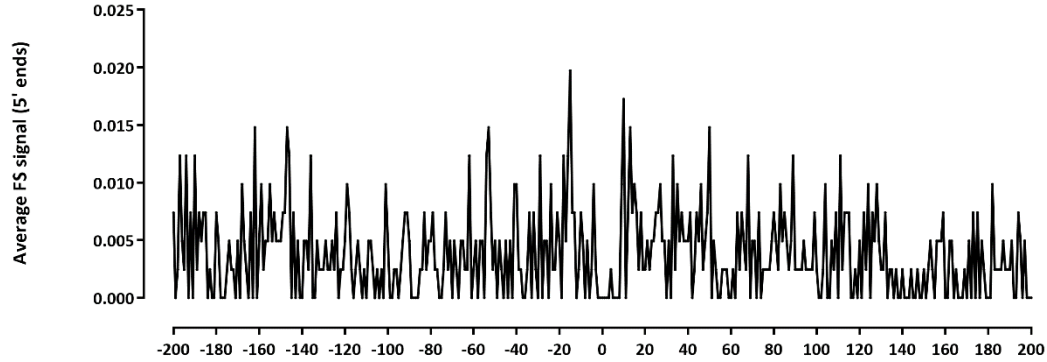


L1930-H4S47C_5M_5min

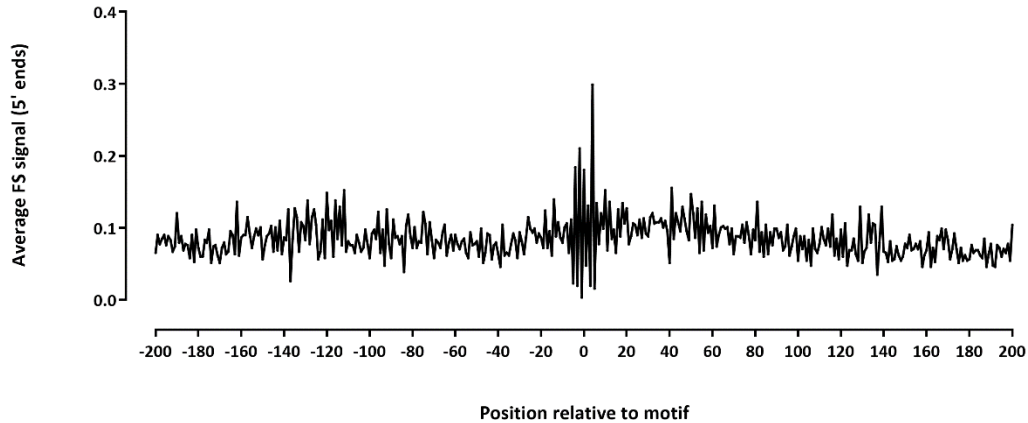


Footprints RAP1

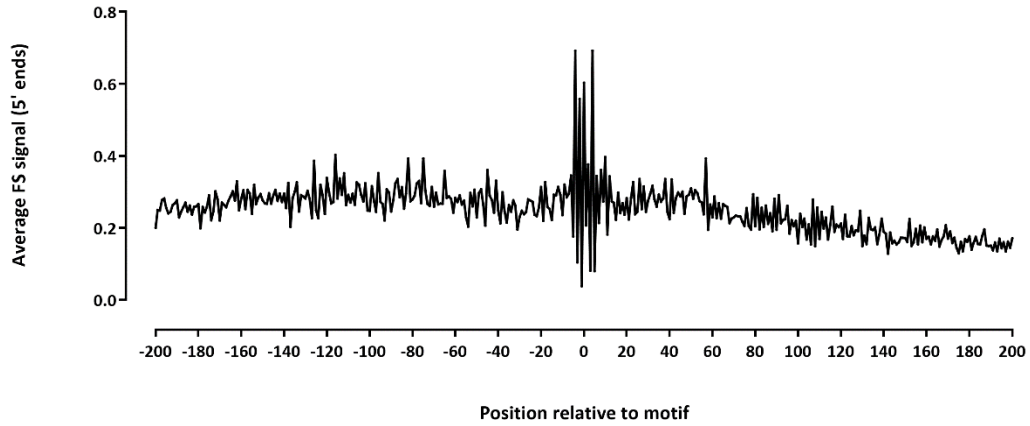
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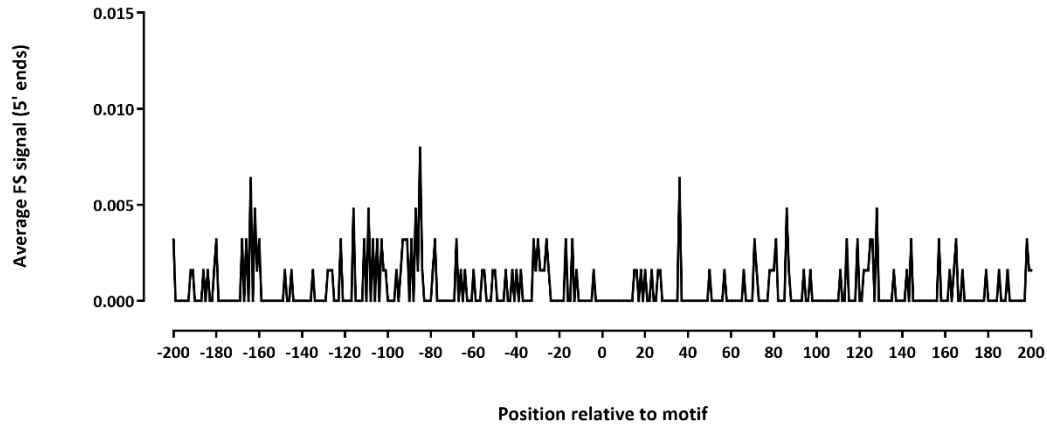
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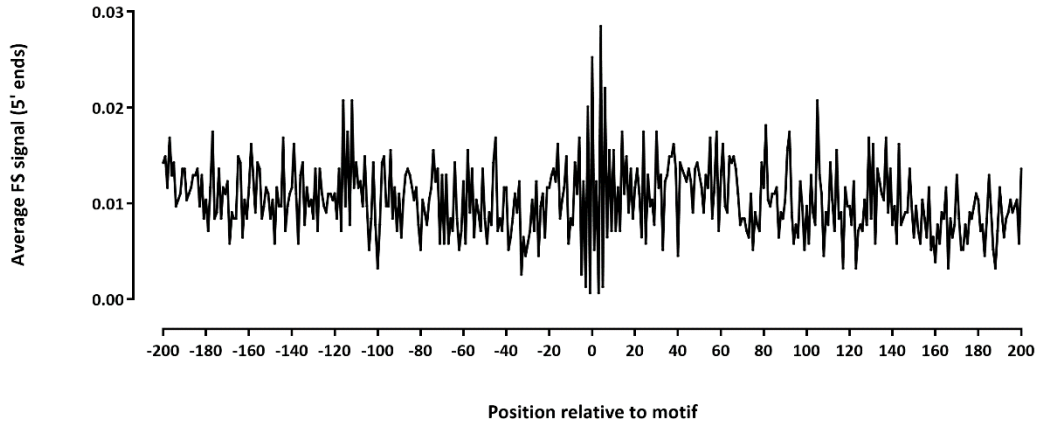
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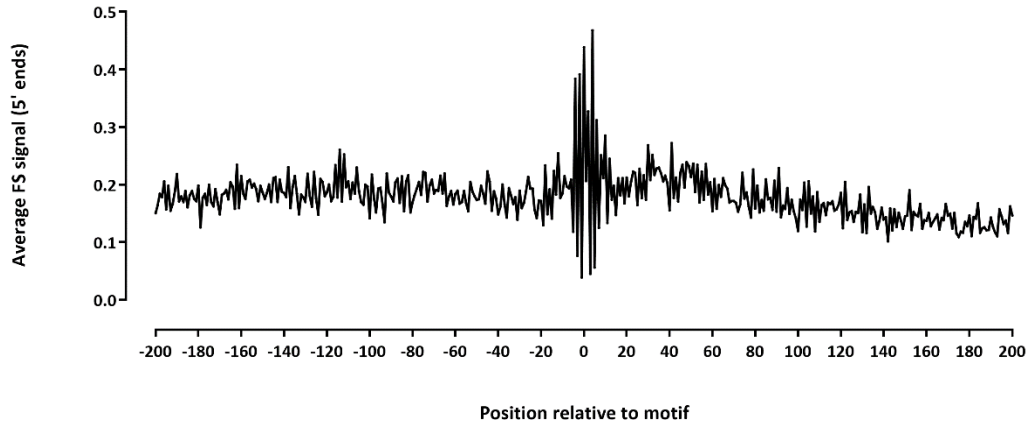
L1925-H4S47C_250M_30min_low_enzyme



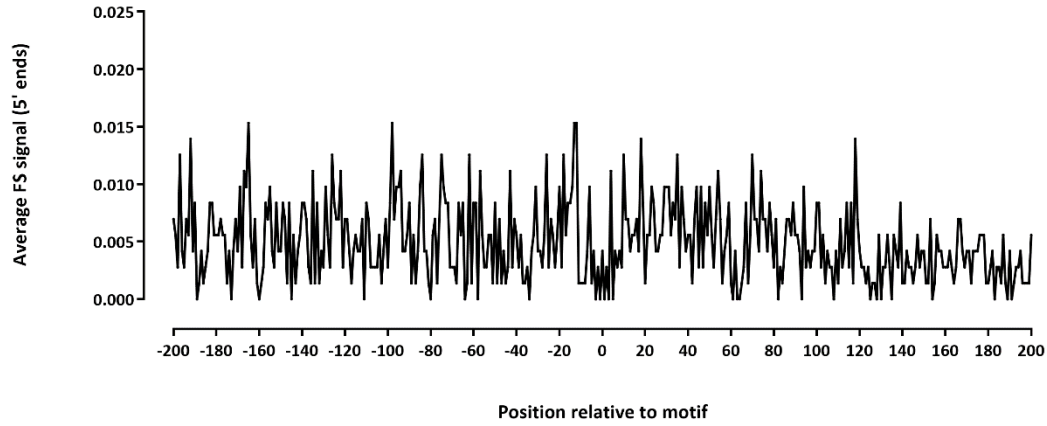
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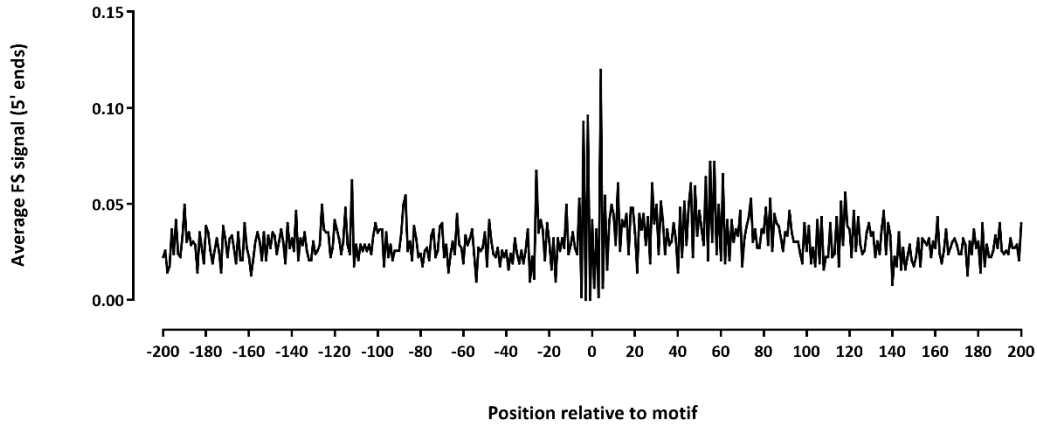
L1927-H4S47C_5M_30min_low_enzyme



L1928-H4S47C_250M_5min



L1929-H4S47C_50M_5min



L1930-H4S47C_5M_5min

