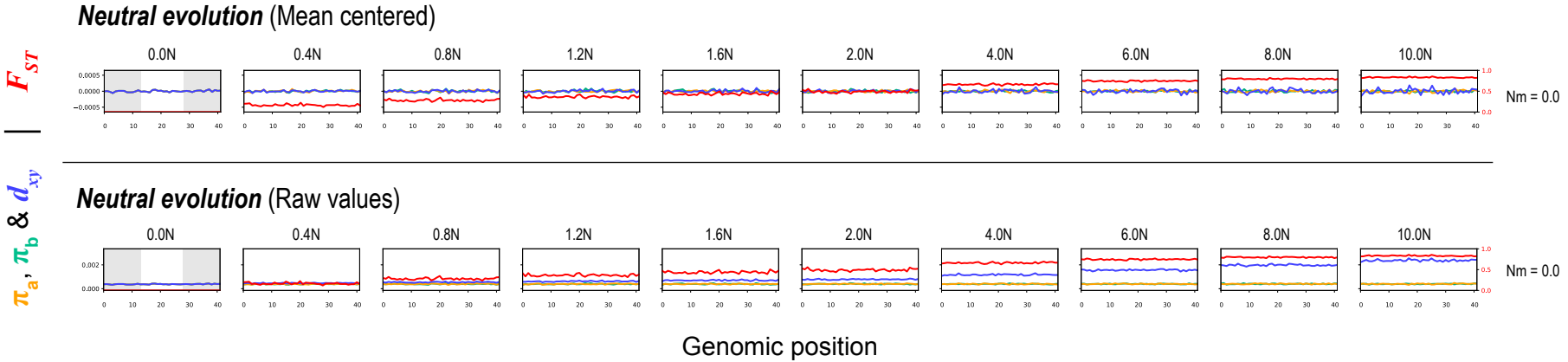
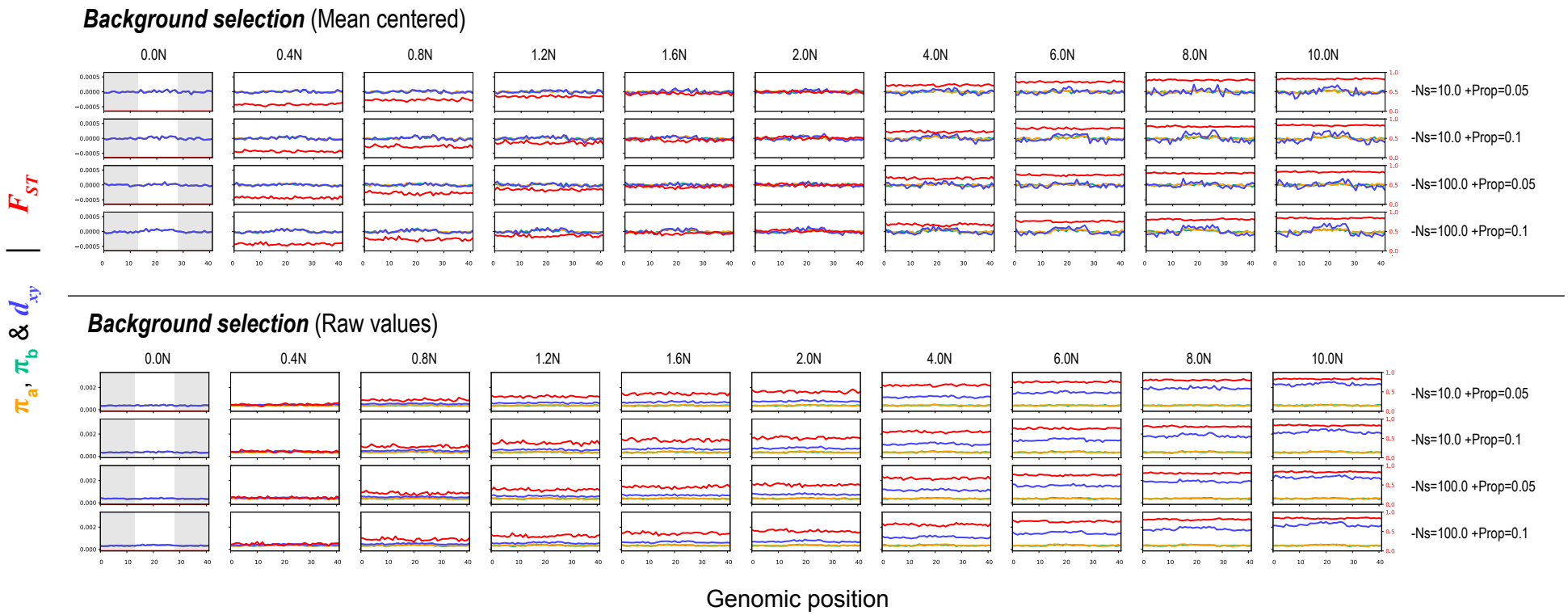
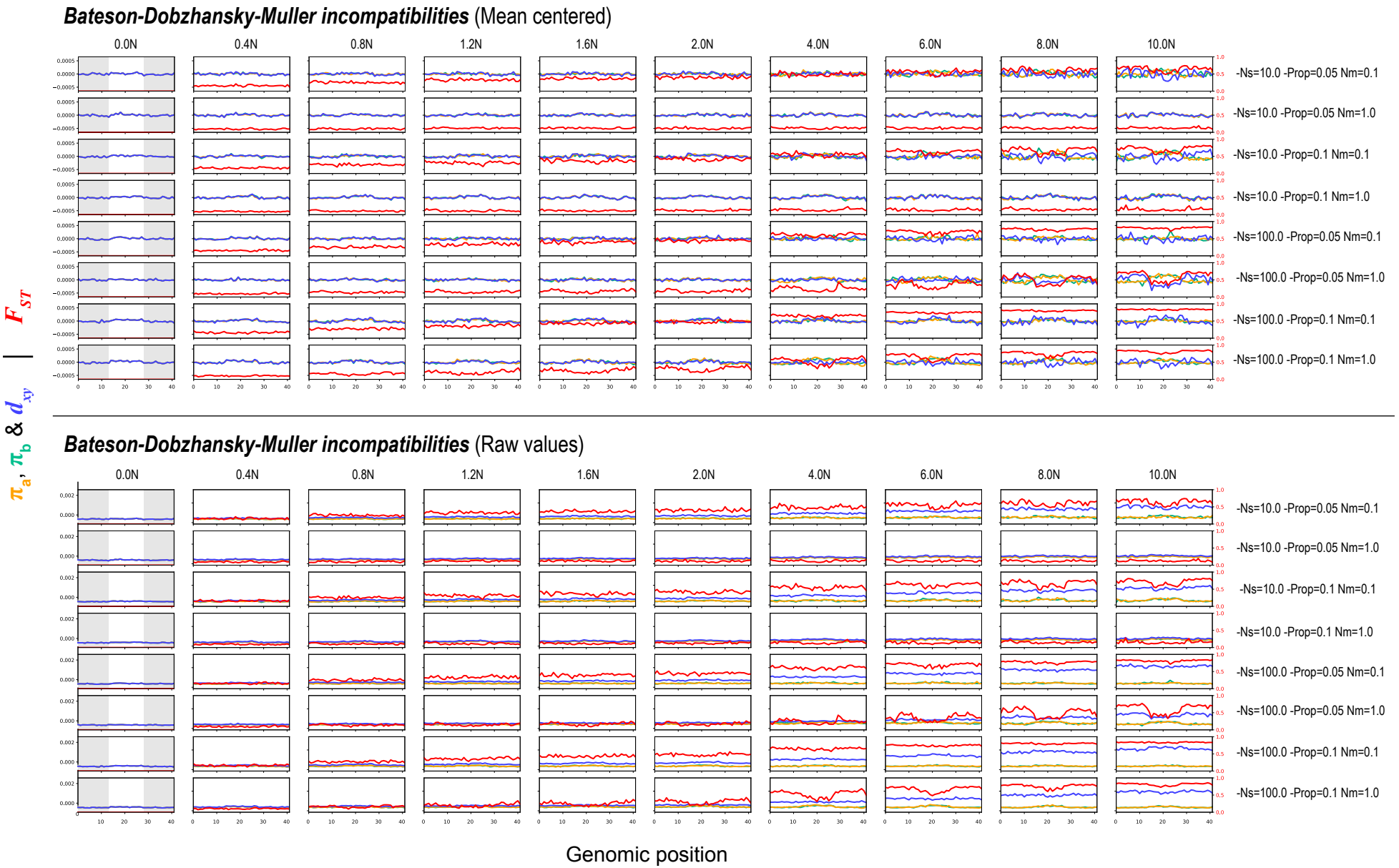
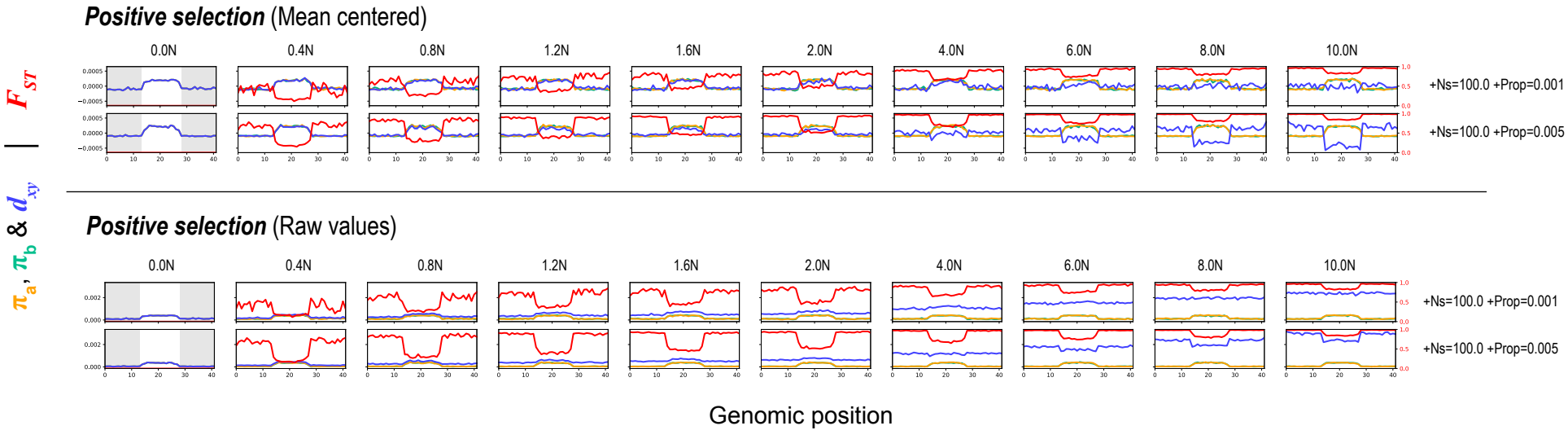
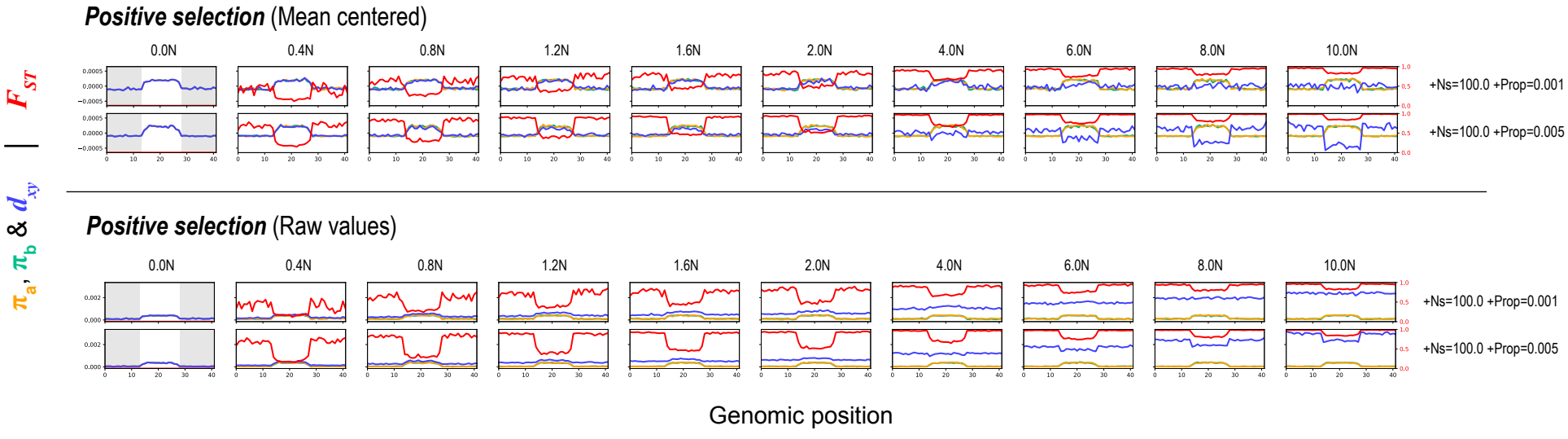
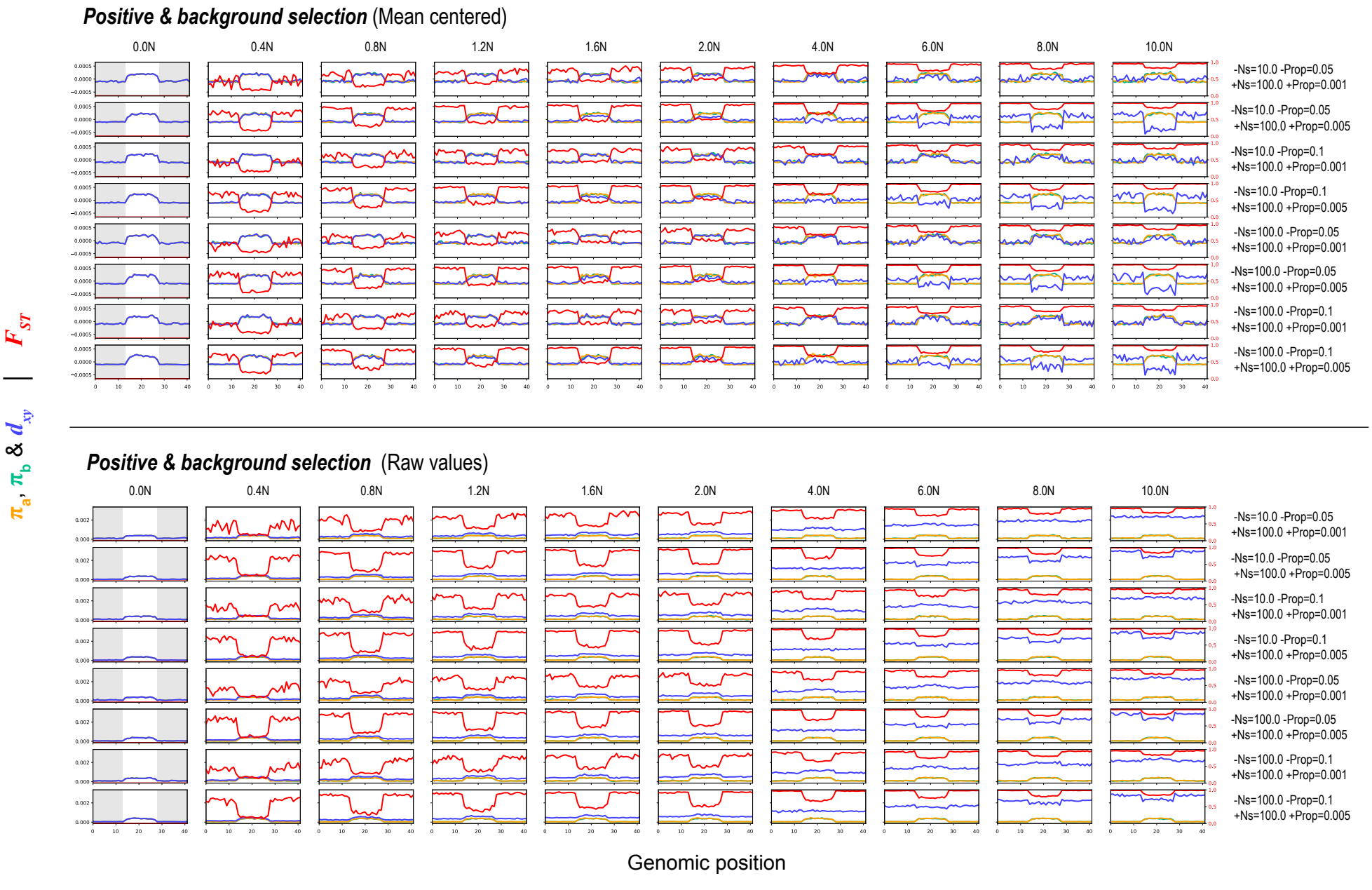

Neutral evolution (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
Nm = 0.0
Neutral evolution (Raw values)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
Nm = 0.0
Genomic position

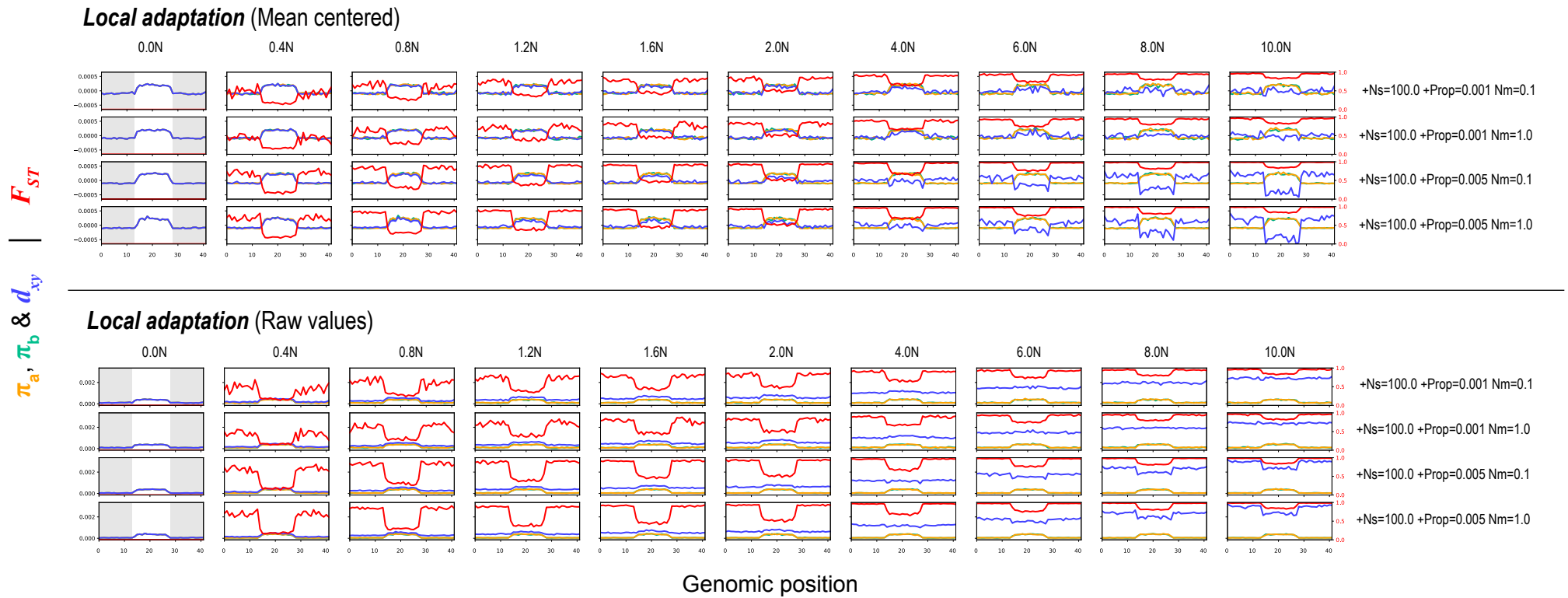

Background selection (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
-Ns=10.0 +Prop=0.05
-Ns=10.0 +Prop=0.1
-Ns=100.0 +Prop=0.05
-Ns=100.0 +Prop=0.1
F_{ST}
Background selection (Raw values)
π_a, π_b & d_{xy}
Genomic position


Bateson-Dobzhansky-Muller incompatibilities (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
-Ns=10.0 -Prop=0.05 Nm=0.1
-Ns=10.0 -Prop=0.05 Nm=1.0
-Ns=10.0 -Prop=0.1 Nm=0.1
-Ns=10.0 -Prop=0.1 Nm=1.0
-Ns=100.0 -Prop=0.05 Nm=0.1
-Ns=100.0 -Prop=0.05 Nm=1.0
-Ns=100.0 -Prop=0.1 Nm=0.1
-Ns=100.0 -Prop=0.1 Nm=1.0
F_{ST}
π_a, π_b & d_{xy}
Bateson-Dobzhansky-Muller incompatibilities (Raw values)
Genomic position


Positive selection (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
+Ns=100.0 +Prop=0.001
+Ns=100.0 +Prop=0.005
Positive selection (Raw values)
+Ns=100.0 +Prop=0.001
+Ns=100.0 +Prop=0.005
Genomic position
F_{ST}
π_a, π_b & d_{xy}


Positive selection (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
+Ns=100.0 +Prop=0.001
+Ns=100.0 +Prop=0.005
Positive selection (Raw values)
+Ns=100.0 +Prop=0.001
+Ns=100.0 +Prop=0.005
Genomic position
F_{ST}
π_a, π_b & d_{xy}


Positive & background selection (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
-Ns=10.0 -Prop=0.05 +Ns=100.0 +Prop=0.001
-Ns=10.0 -Prop=0.05 +Ns=100.0 +Prop=0.005
-Ns=10.0 -Prop=0.1 +Ns=100.0 +Prop=0.001
-Ns=10.0 -Prop=0.1 +Ns=100.0 +Prop=0.005
-Ns=100.0 -Prop=0.05 +Ns=100.0 +Prop=0.001
-Ns=100.0 -Prop=0.05 +Ns=100.0 +Prop=0.005
-Ns=100.0 -Prop=0.1 +Ns=100.0 +Prop=0.001
-Ns=100.0 -Prop=0.1 +Ns=100.0 +Prop=0.005
F_{ST}
π_a, π_b & d_{xy}
Positive & background selection (Raw values)
Genomic position


Local adaptation (Mean centered)
0.0N
0.4N
0.8N
1.2N
1.6N
2.0N
4.0N
6.0N
8.0N
10.0N
+Ns=100.0 +Prop=0.001 Nm=0.1
+Ns=100.0 +Prop=0.001 Nm=1.0
+Ns=100.0 +Prop=0.005 Nm=0.1
+Ns=100.0 +Prop=0.005 Nm=1.0
F_{ST}
π_a, π_b & d_{xy}
Local adaptation (Raw values)
Genomic position