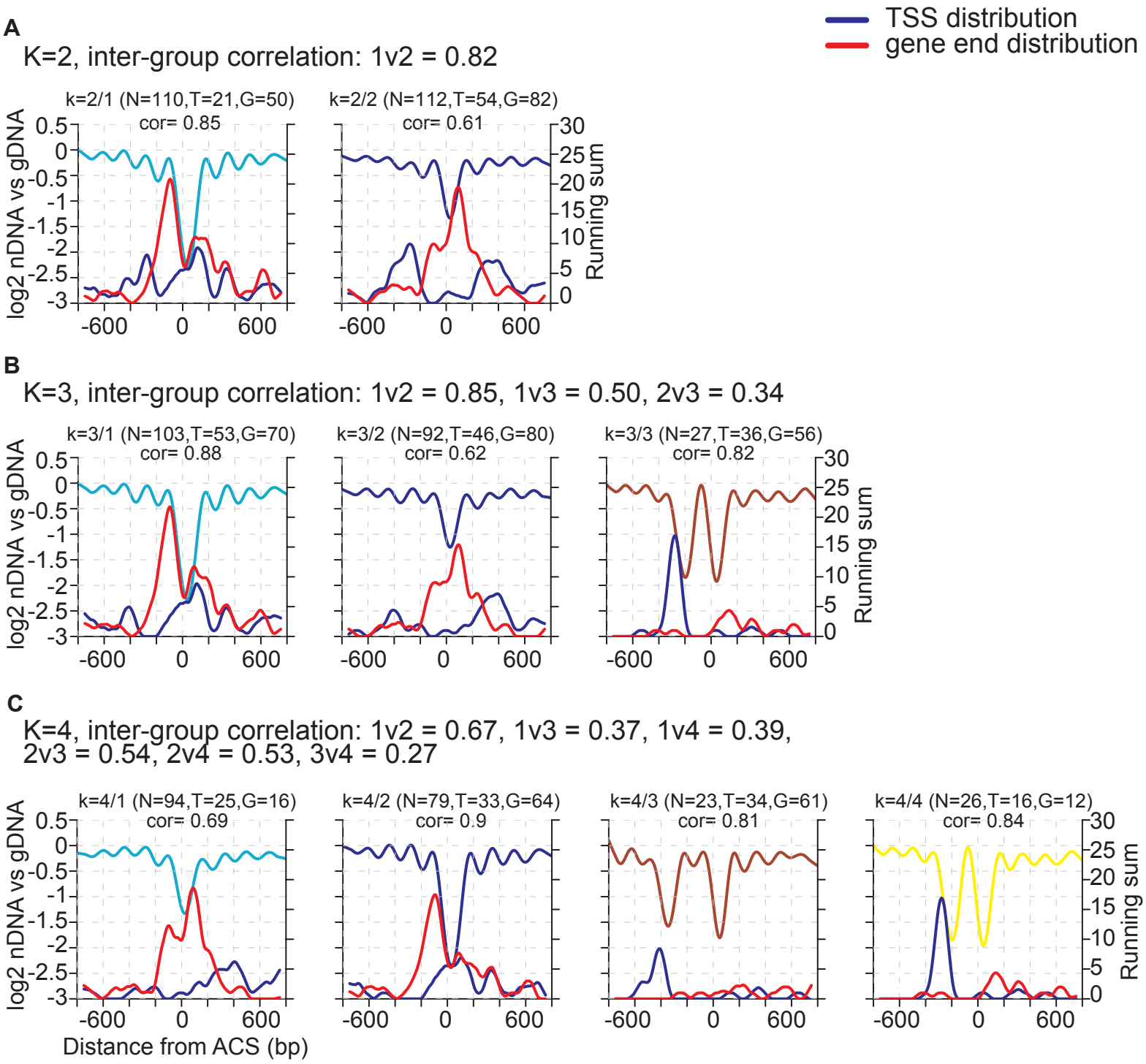
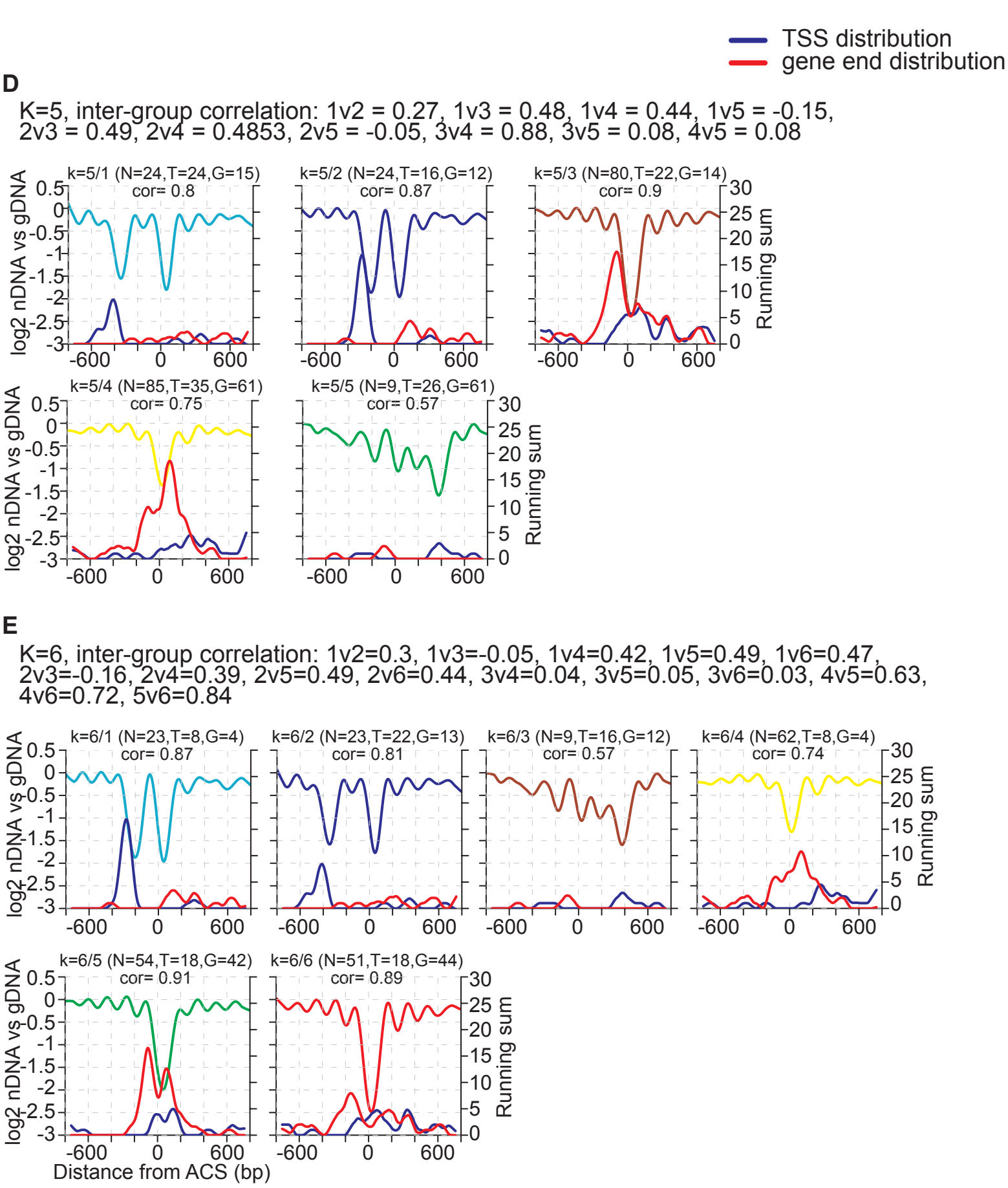

A
K=2, inter-group correlation: 1v2 = 0.82
TSS distribution
gene end distribution
k=2/1 (N=110,T=21,G=50)
cor= 0.85
k=2/2 (N=112,T=54,G=82)
cor= 0.61
log2 nDNA vs gDNA
Running sum
B
K=3, inter-group correlation: 1v2 = 0.85, 1v3 = 0.50, 2v3 = 0.34
k=3/1 (N=103,T=53,G=70)
cor= 0.88
k=3/2 (N=92,T=46,G=80)
cor= 0.62
k=3/3 (N=27,T=36,G=56)
cor= 0.82
C
K=4, inter-group correlation: 1v2 = 0.67, 1v3 = 0.37, 1v4 = 0.39,
2v3 = 0.54, 2v4 = 0.53, 3v4 = 0.27
k=4/1 (N=94,T=25,G=16)
cor= 0.69
k=4/2 (N=79,T=33,G=64)
cor= 0.9
k=4/3 (N=23,T=34,G=61)
cor= 0.81
k=4/4 (N=26,T=16,G=12)
cor= 0.84
Distance from ACS (bp)


TSS distribution
gene end distribution
D
K=5, inter-group correlation: 1v2 = 0.27, 1v3 = 0.48, 1v4 = 0.44, 1v5 = -0.15, 2v3 = 0.49, 2v4 = 0.4853, 2v5 = -0.05, 3v4 = 0.88, 3v5 = 0.08, 4v5 = 0.08
k=5/1 (N=24,T=24,G=15)
cor= 0.8
k=5/2 (N=24,T=16,G=12)
cor= 0.87
k=5/3 (N=80,T=22,G=14)
cor= 0.9
k=5/4 (N=85,T=35,G=61)
cor= 0.75
k=5/5 (N=9,T=26,G=61)
cor= 0.57
log2 nDNA vs gDNA
Running sum
E
K=6, inter-group correlation: 1v2=0.3, 1v3=-0.05, 1v4=0.42, 1v5=0.49, 1v6=0.47, 2v3=-0.16, 2v4=0.39, 2v5=0.49, 2v6=0.44, 3v4=0.04, 3v5=0.05, 3v6=0.03, 4v5=0.63, 4v6=0.72, 5v6=0.84
k=6/1 (N=23,T=8,G=4)
cor= 0.87
k=6/2 (N=23,T=22,G=13)
cor= 0.81
k=6/3 (N=9,T=16,G=12)
cor= 0.57
k=6/4 (N=62,T=8,G=4)
cor= 0.74
k=6/5 (N=54,T=18,G=42)
cor= 0.91
k=6/6 (N=51,T=18,G=44)
cor= 0.89
log2 nDNA vs gDNA
Running sum
Distance from ACS (bp)

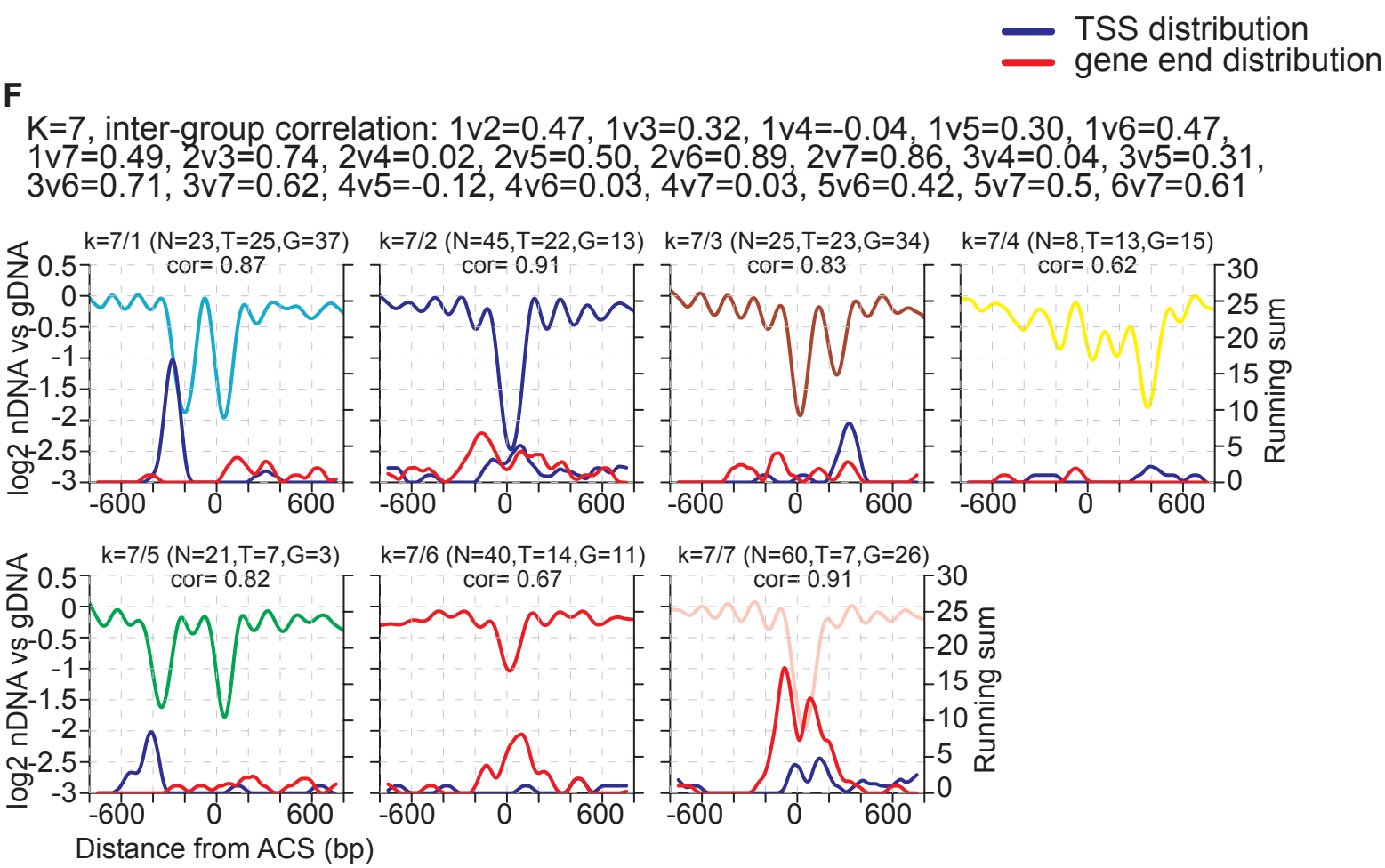


Figure S2. Subcluster average, TSS (—) and gene end (—) distribution obtained following kmeans clustering of the wild-type (k=2 to k=7) following 10,000 iterations. For each grouping the number of origins in each subcluster is indicated (N), along with the number of TSSs (T), gene ends (G), and the correlation of each subcluster against the average ACS profile (cor).