Scoring of cluster 1_1

Scoring of cluster 2_0

92.6

1.2

0.0

Samp6.bin.7.orig.fa *

2355761.0

27386.0

88.6

- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

genome

Normalized Score

Scoring of cluster 3_0

Scoring of cluster 4_0

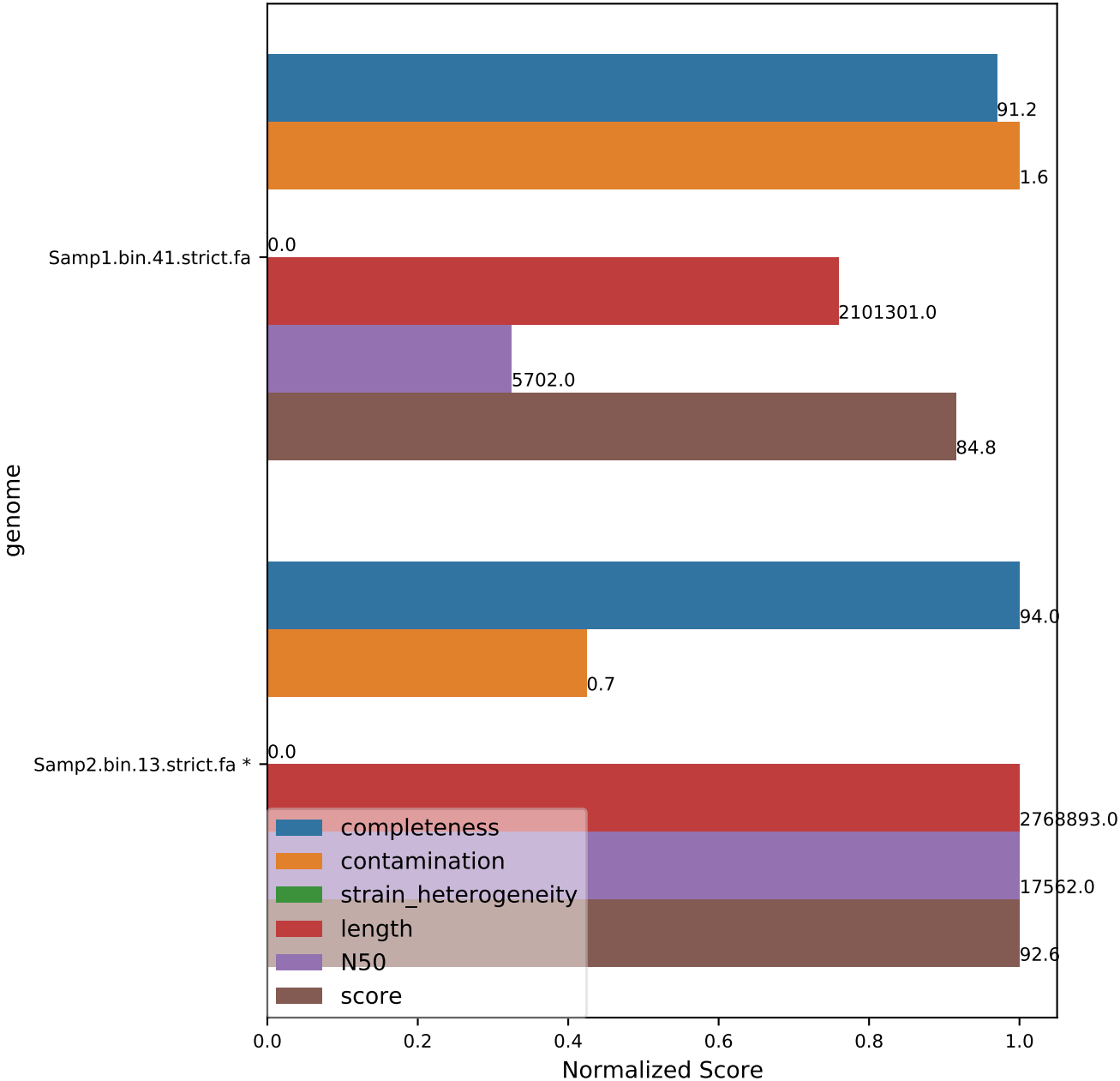Scoring of cluster 5_0

Scoring of cluster 6_1
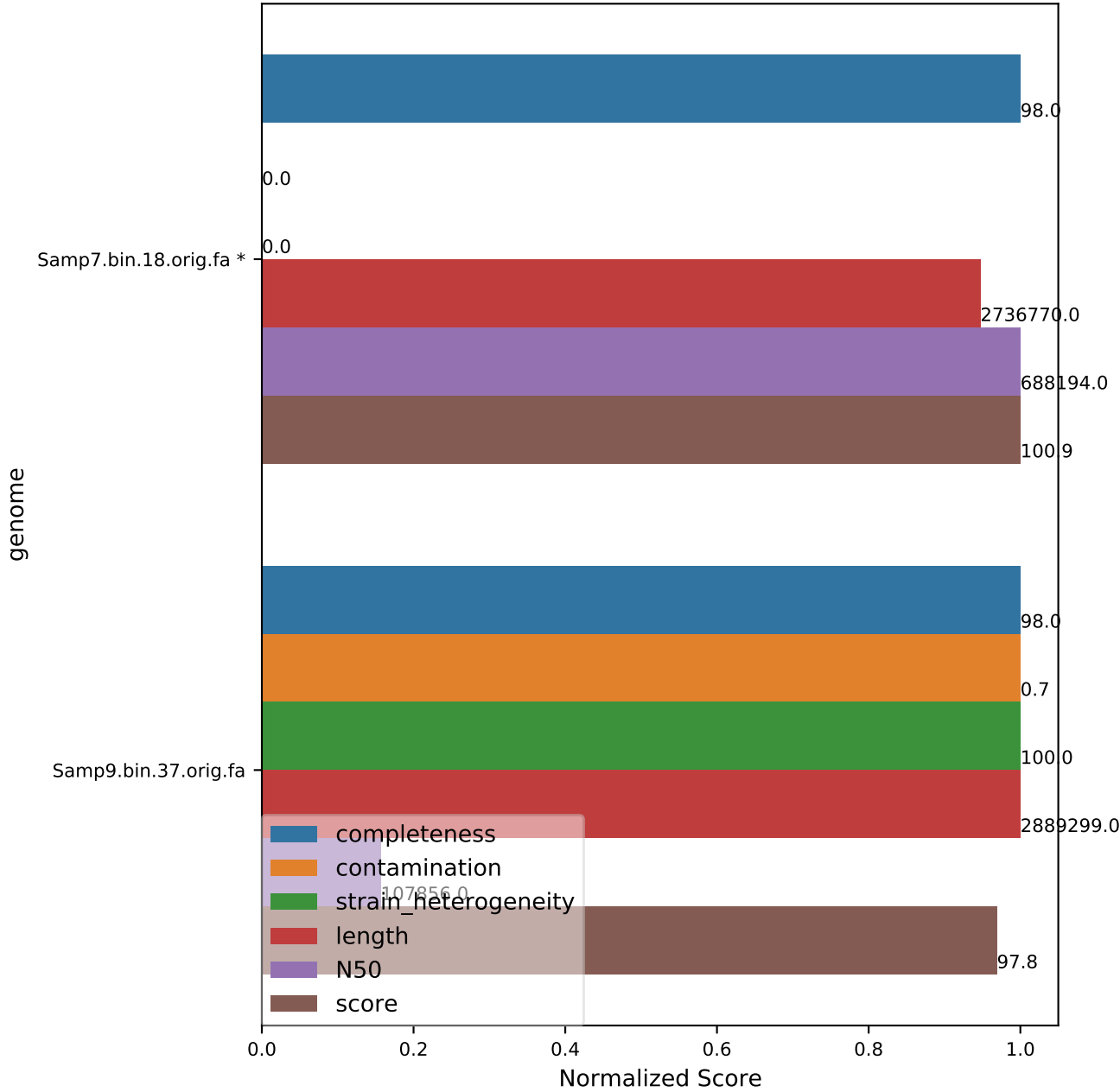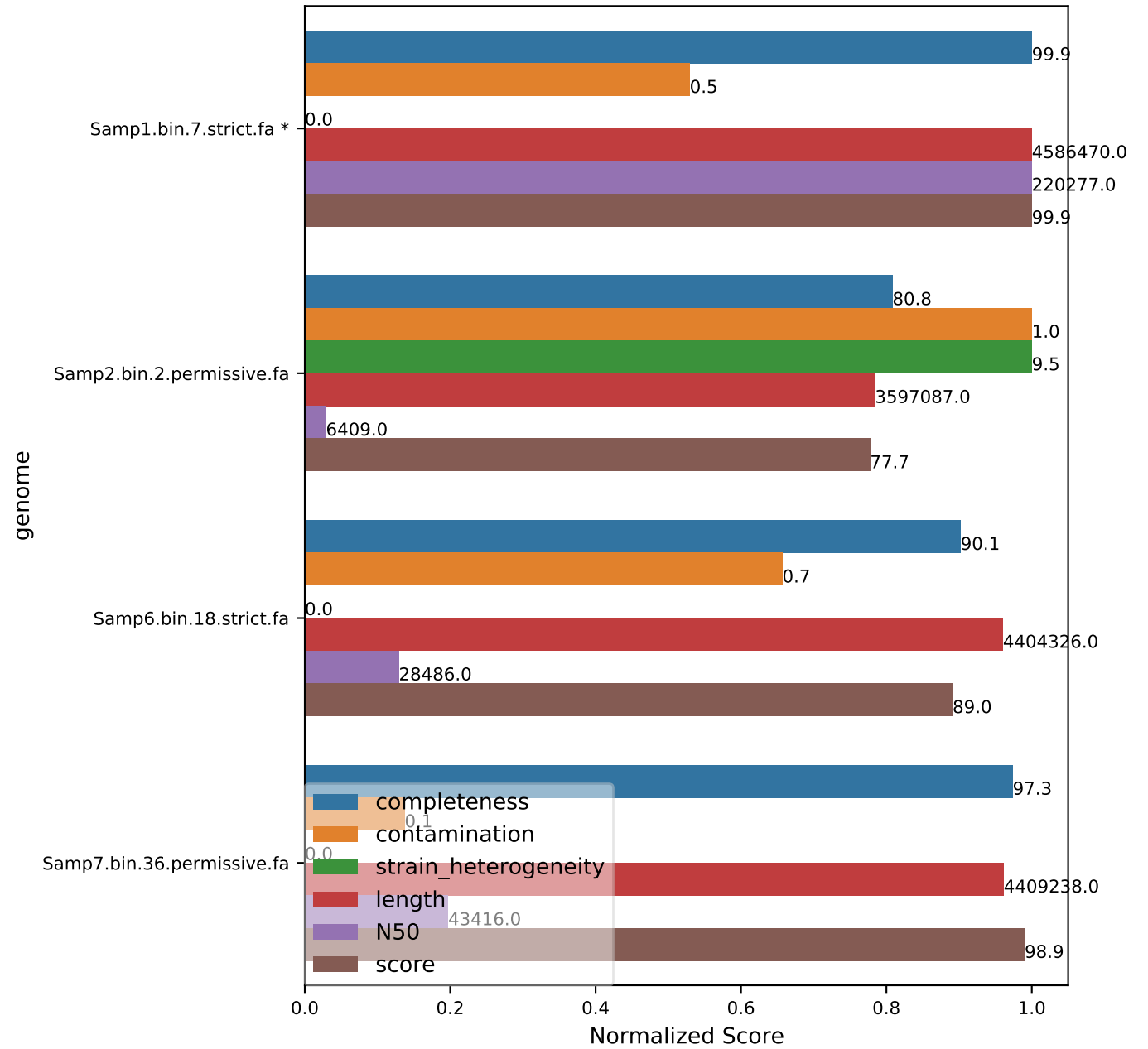
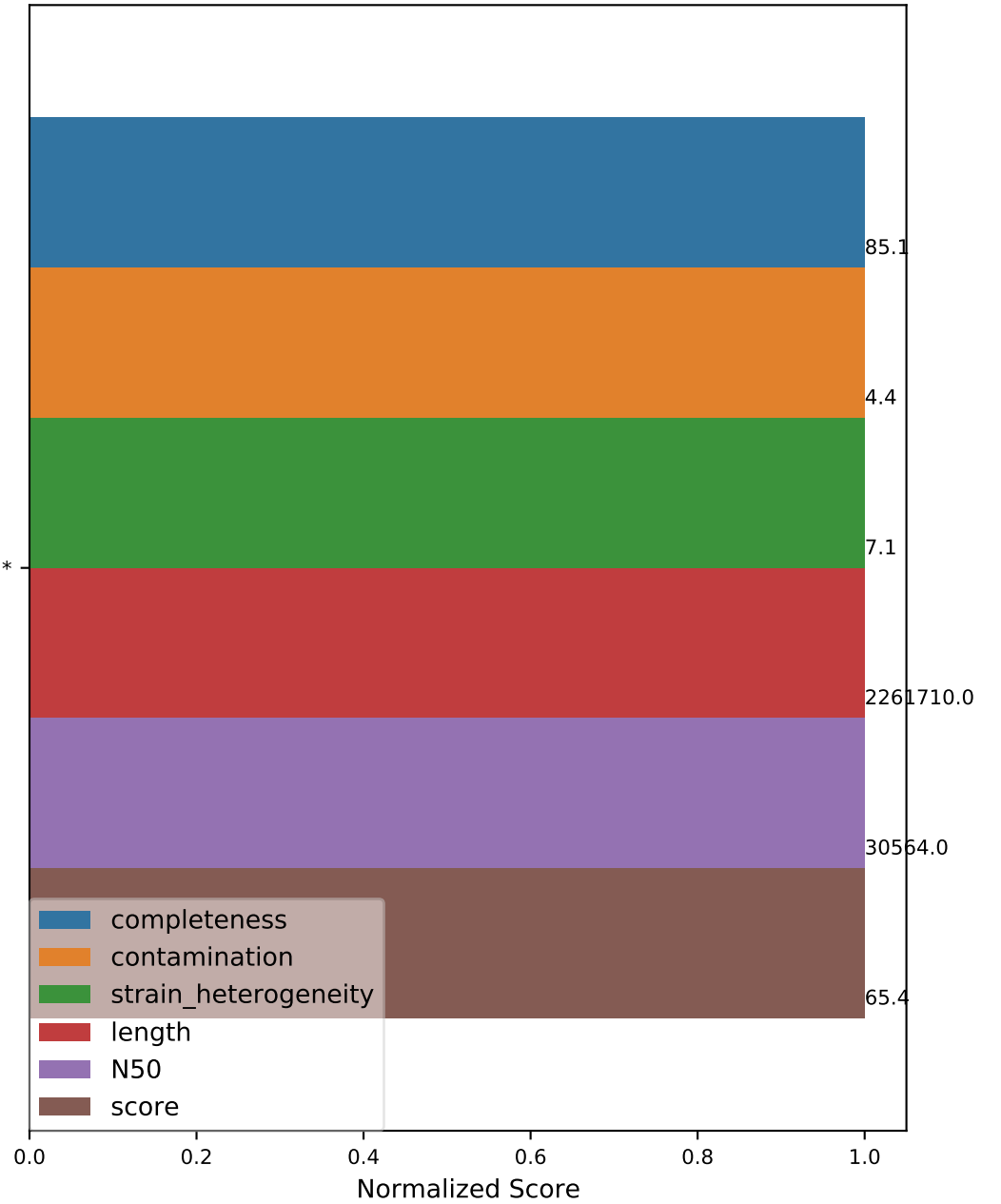Scoring of cluster 7_1

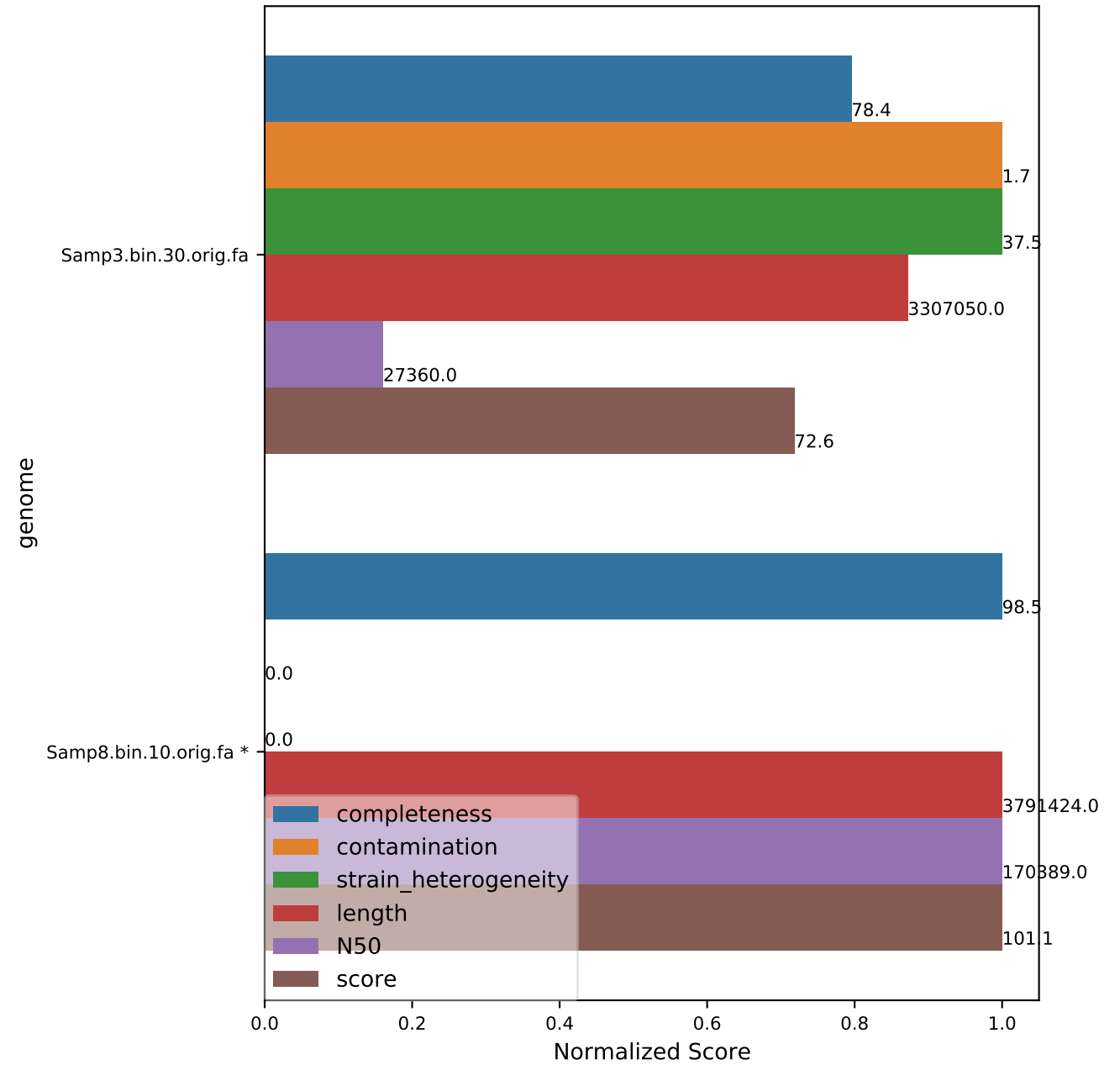Scoring of cluster 8_1

Scoring of cluster 9_1

Scoring of cluster 10_1

Samp1.bin.7.strict.fa *
- completeness: 99.9
- contamination: 0.5
- strain_heterogeneity: 0.0
- length: 4586470.0
- N50: 220277.0
- score: 99.9

Samp2.bin.2.permissive.fa
- completeness: 80.8
- contamination: 1.0
- strain_heterogeneity: 9.5
- length: 3597087.0
- N50: 6409.0
- score: 77.7

Samp6.bin.18.strict.fa
- completeness: 90.1
- contamination: 0.7
- strain_heterogeneity: 0.0
- length: 4404326.0
- N50: 28486.0
- score: 89.0

Samp7.bin.36.permissive.fa
- completeness: 97.3
- contamination: 0.1
- strain_heterogeneity: 0.0
- length: 4409238.0
- N50: 43416.0
- score: 98.9

Legend: completeness, contamination, strain_heterogeneity, length, N50, score
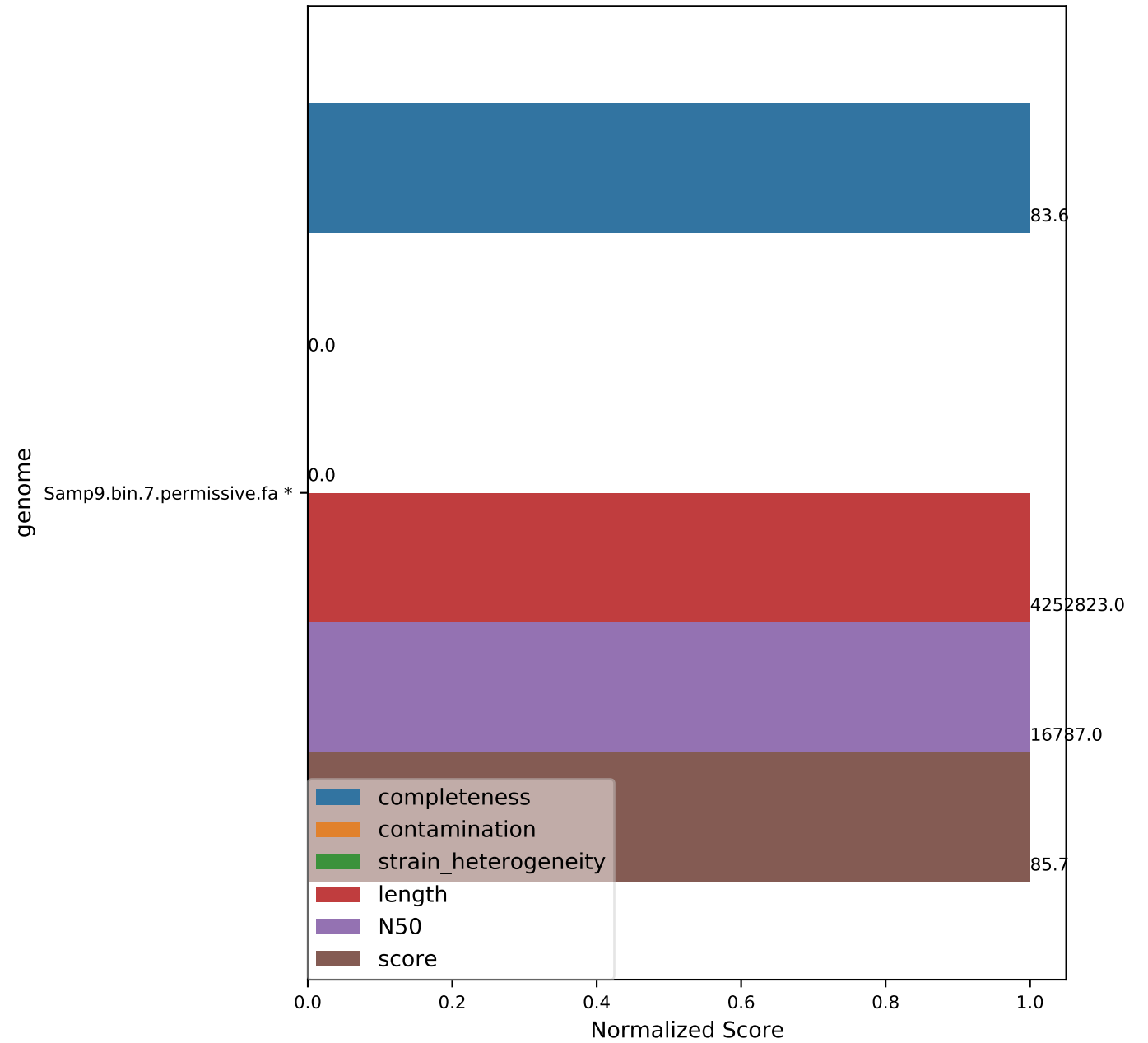
genome

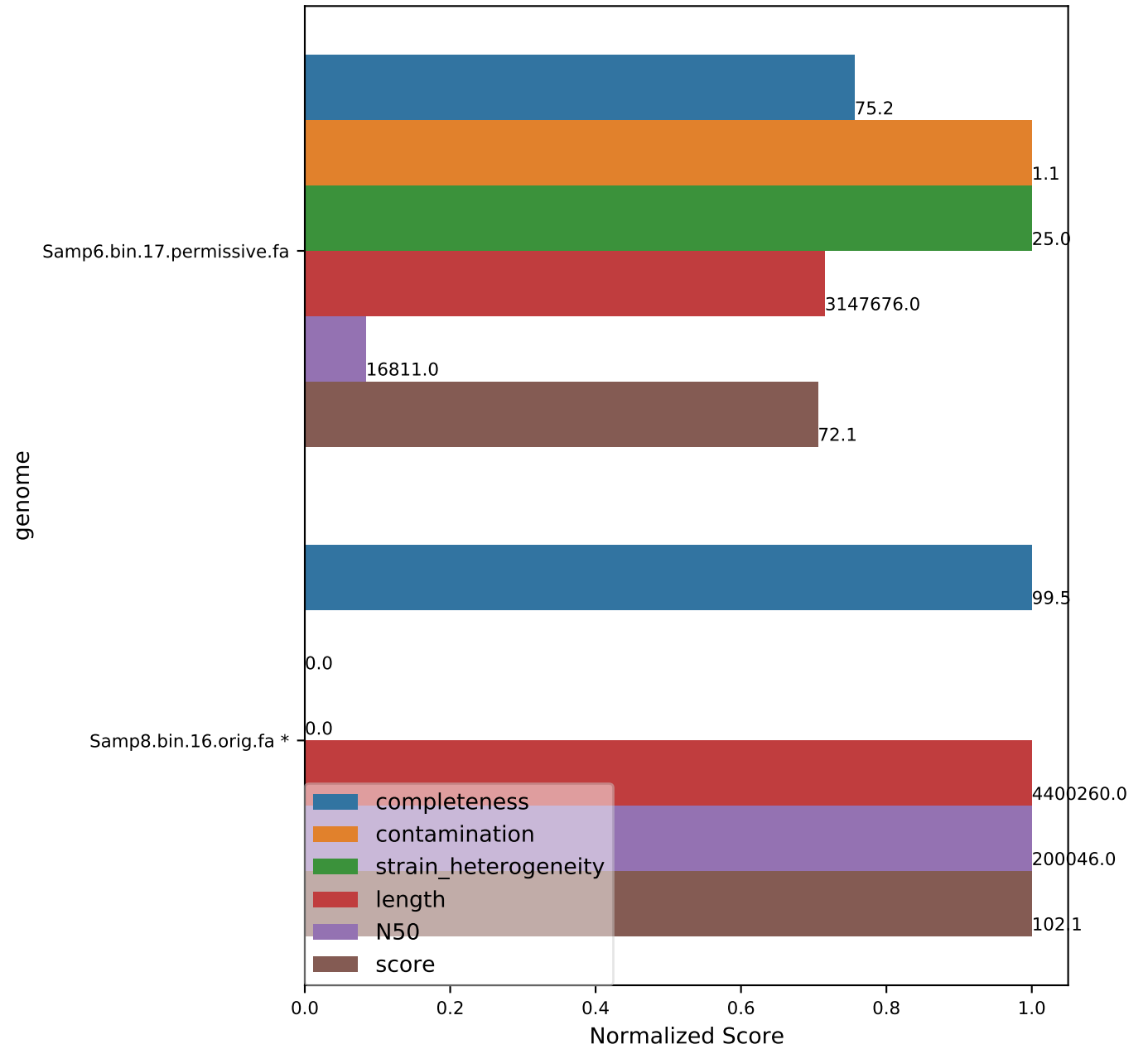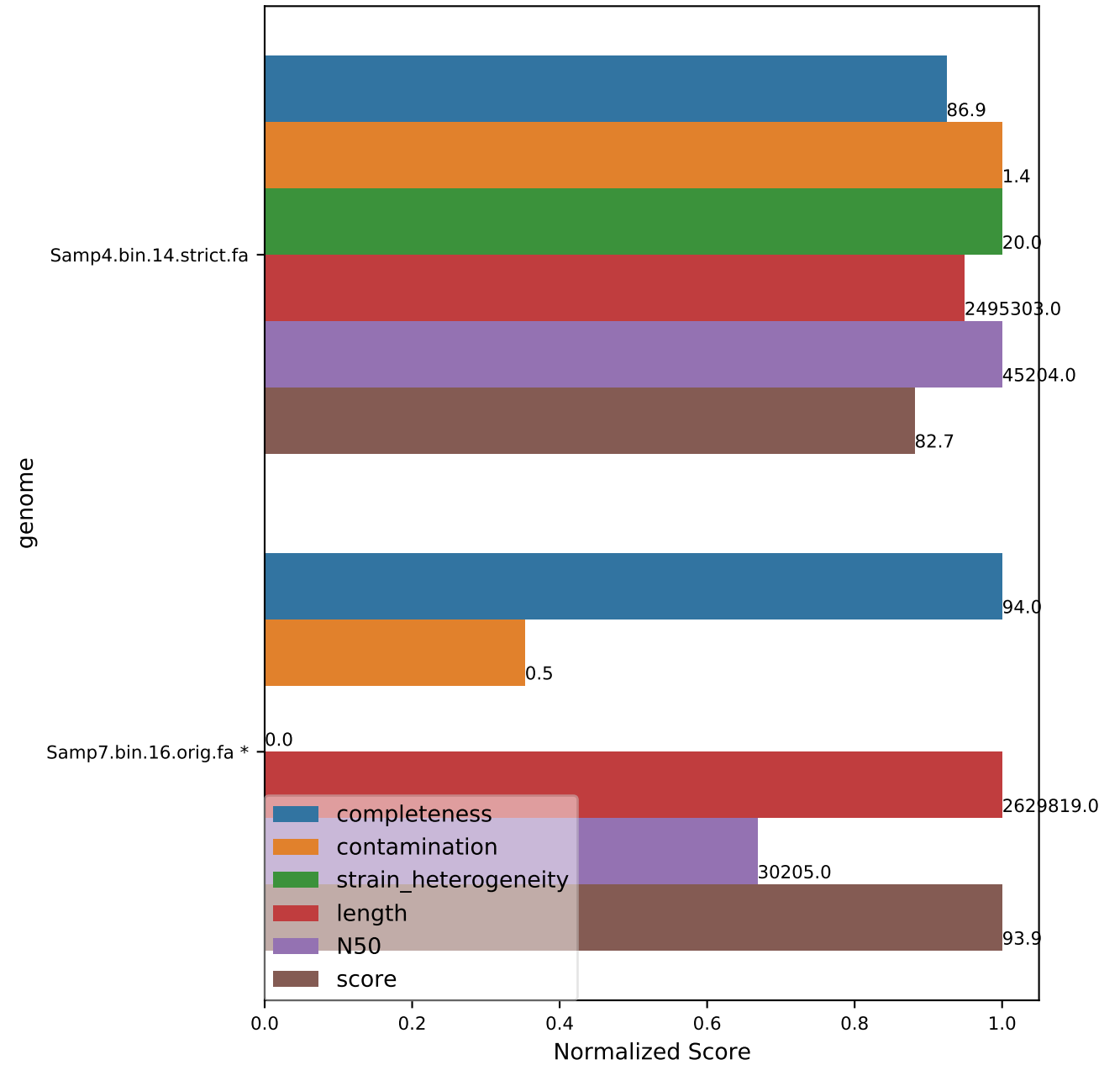Normalized Score

Scoring of cluster 11_0

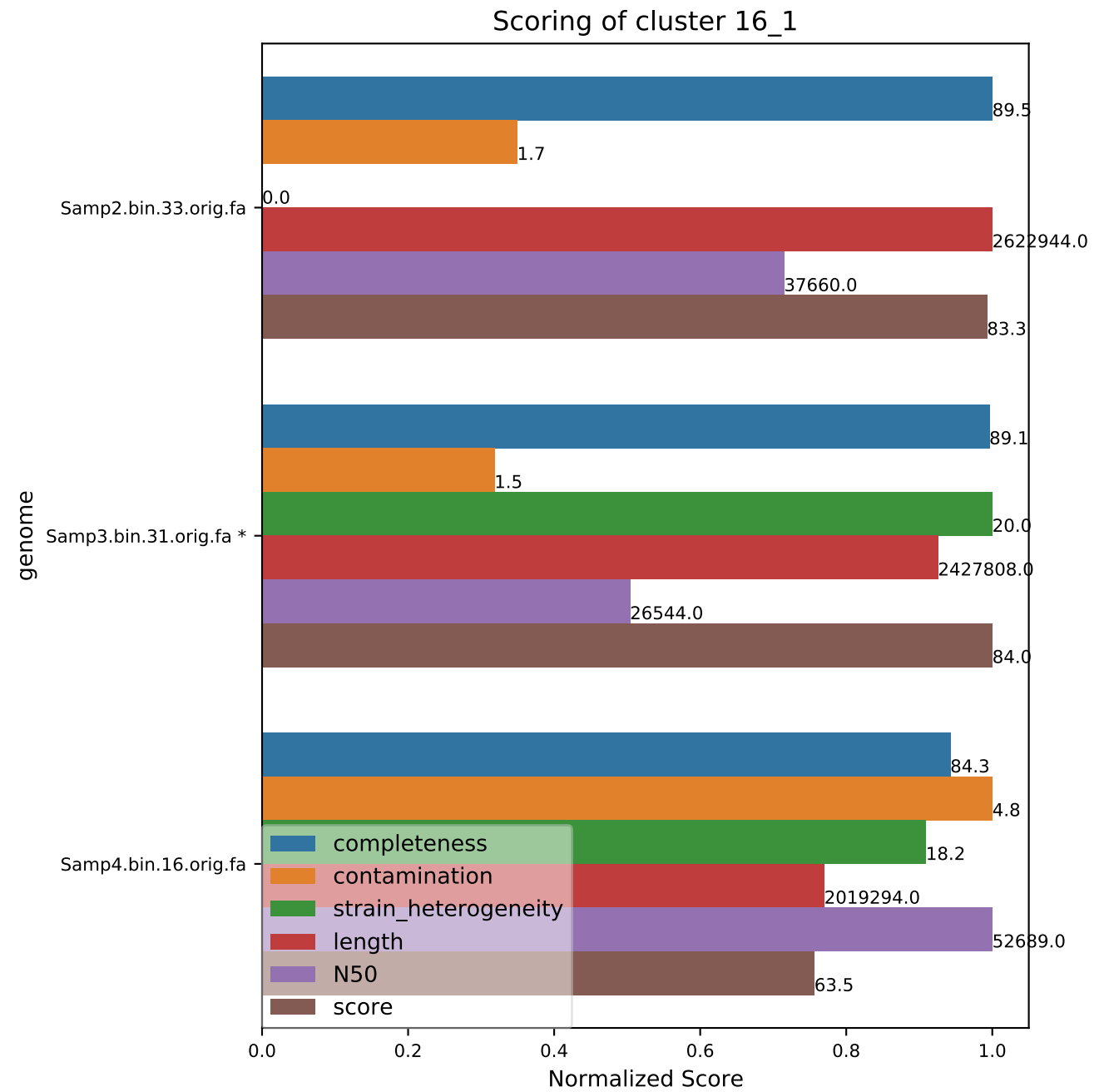Scoring of cluster 12_1

Scoring of cluster 13_1
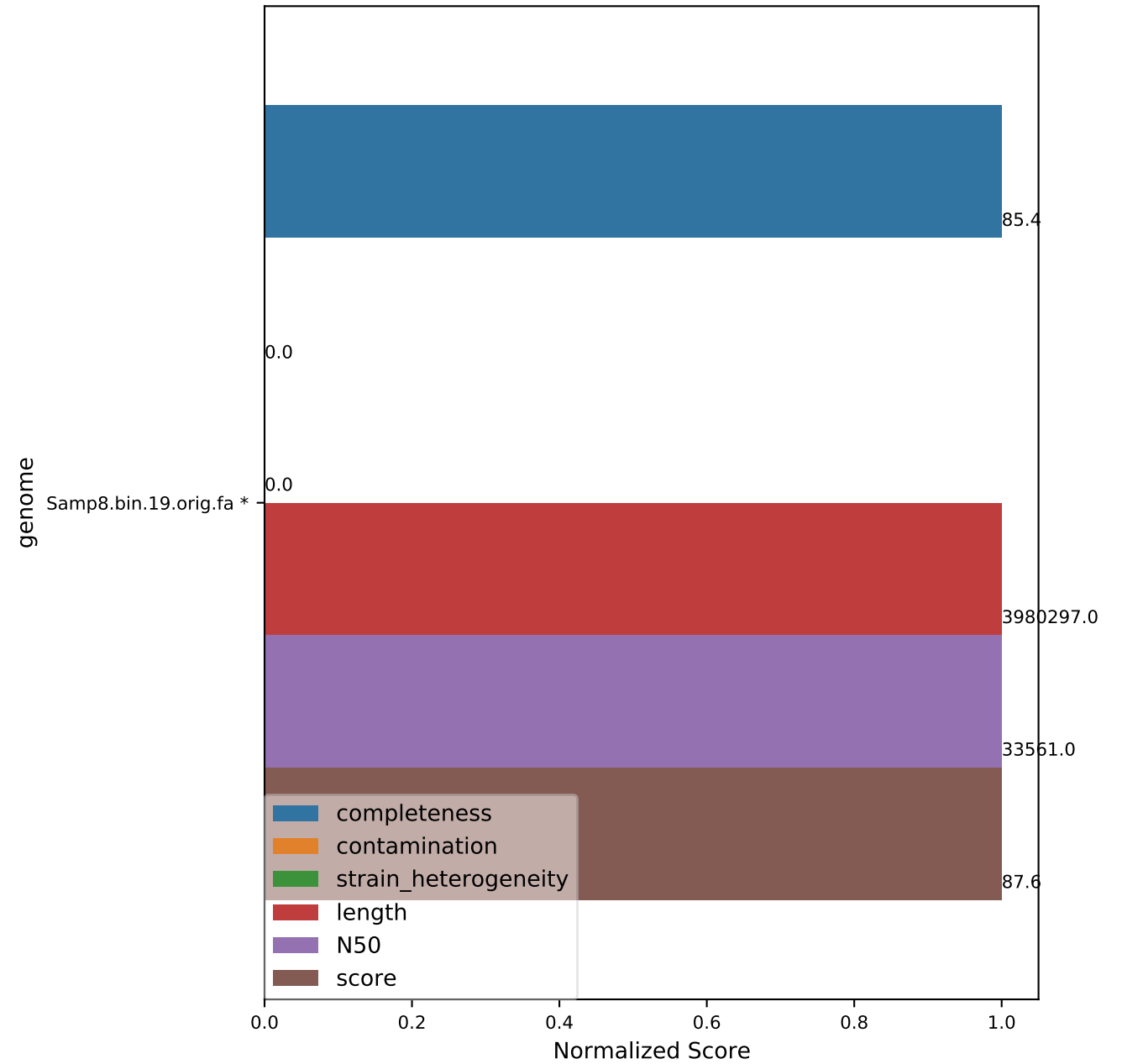
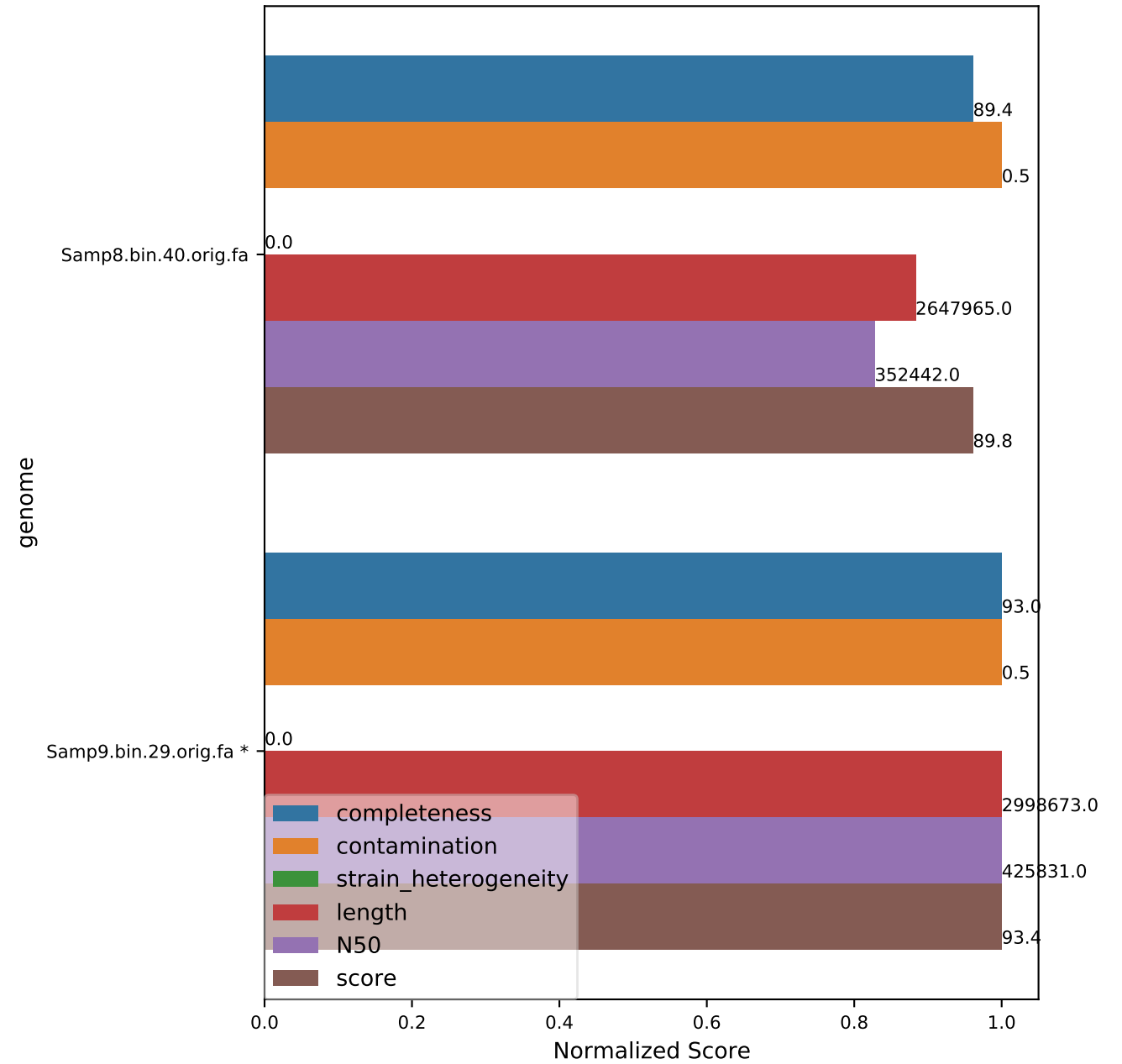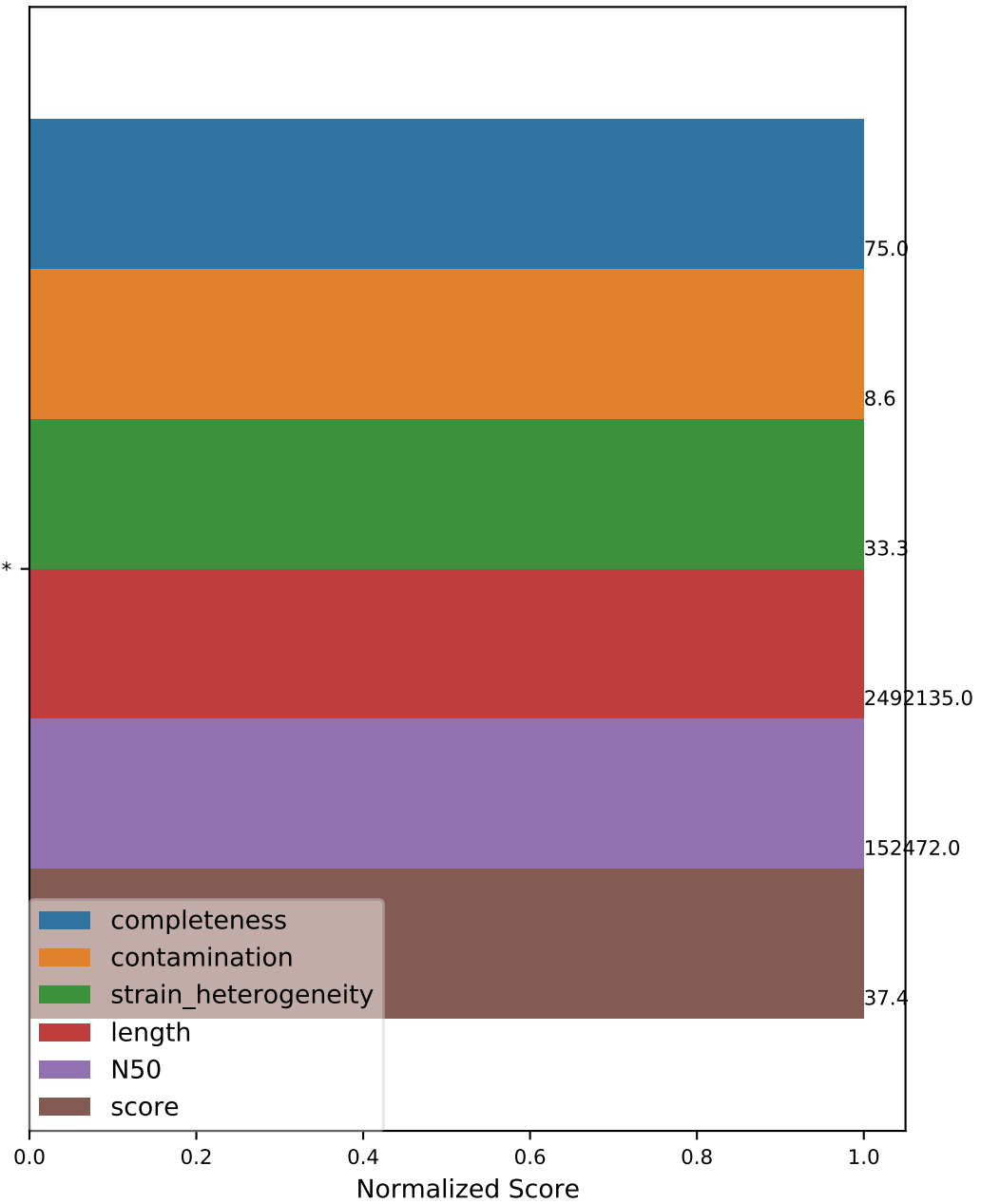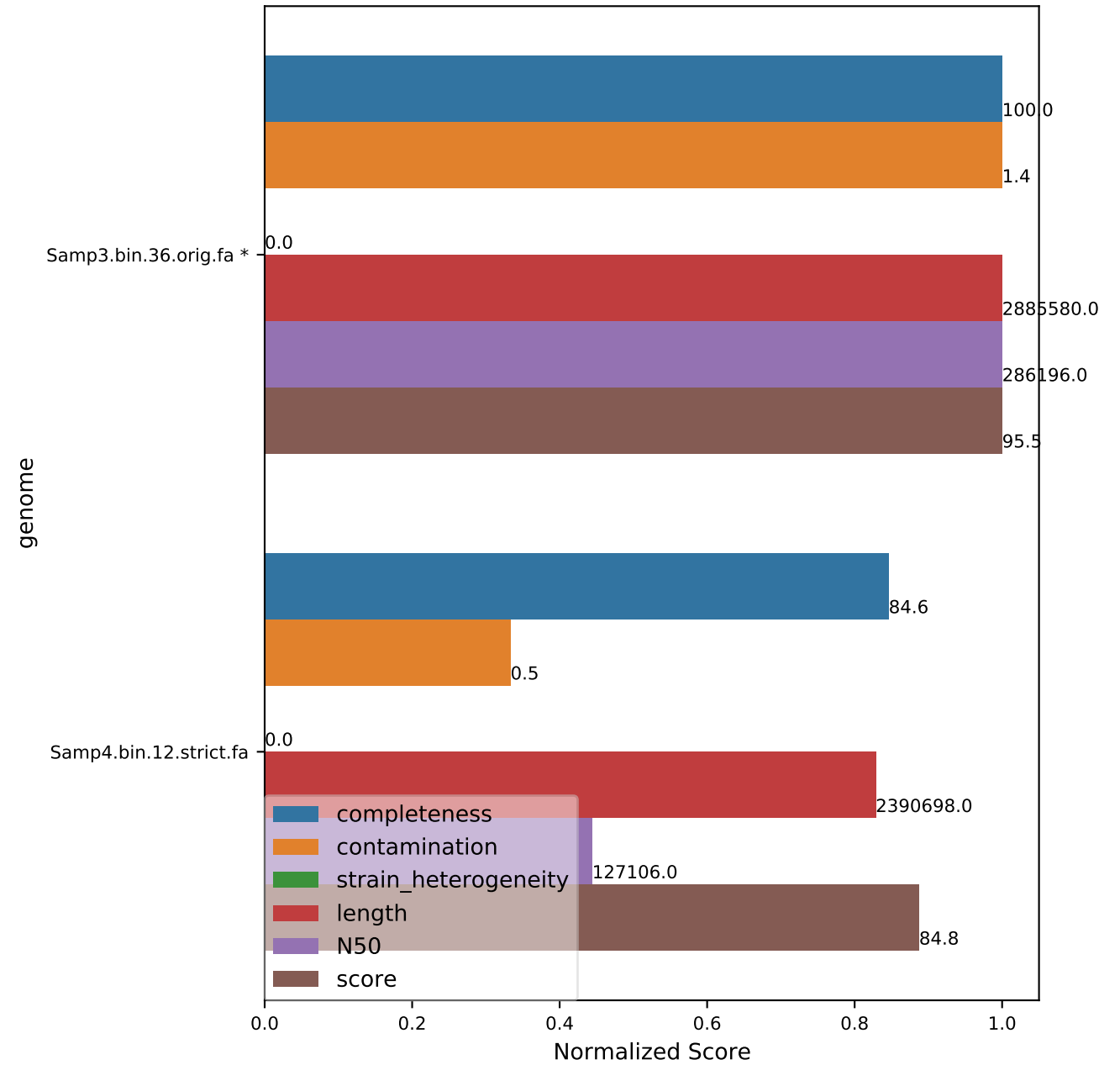Scoring of cluster 13_2

Scoring of cluster 14_1

genome

Samp6.bin.17.permissive.fa

75.2
1.1
25.0
3147676.0
16811.0
72.1

Samp8.bin.16.orig.fa *

99.5
0.0
0.0
4400260.0
200046.0
102.1

- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

Normalized Score

Scoring of cluster 15_1

Scoring of cluster 16_1

Scoring of cluster 17_1
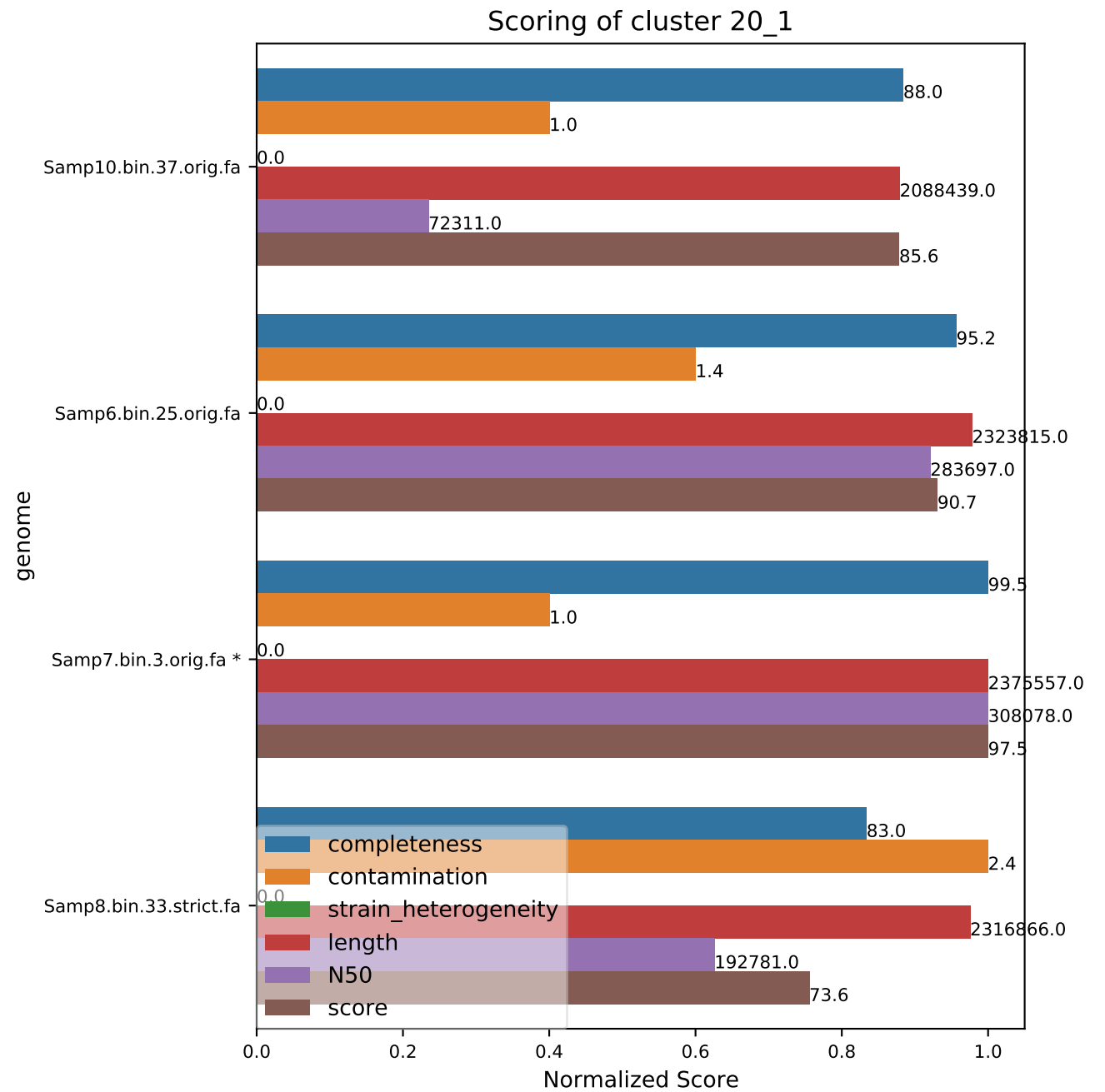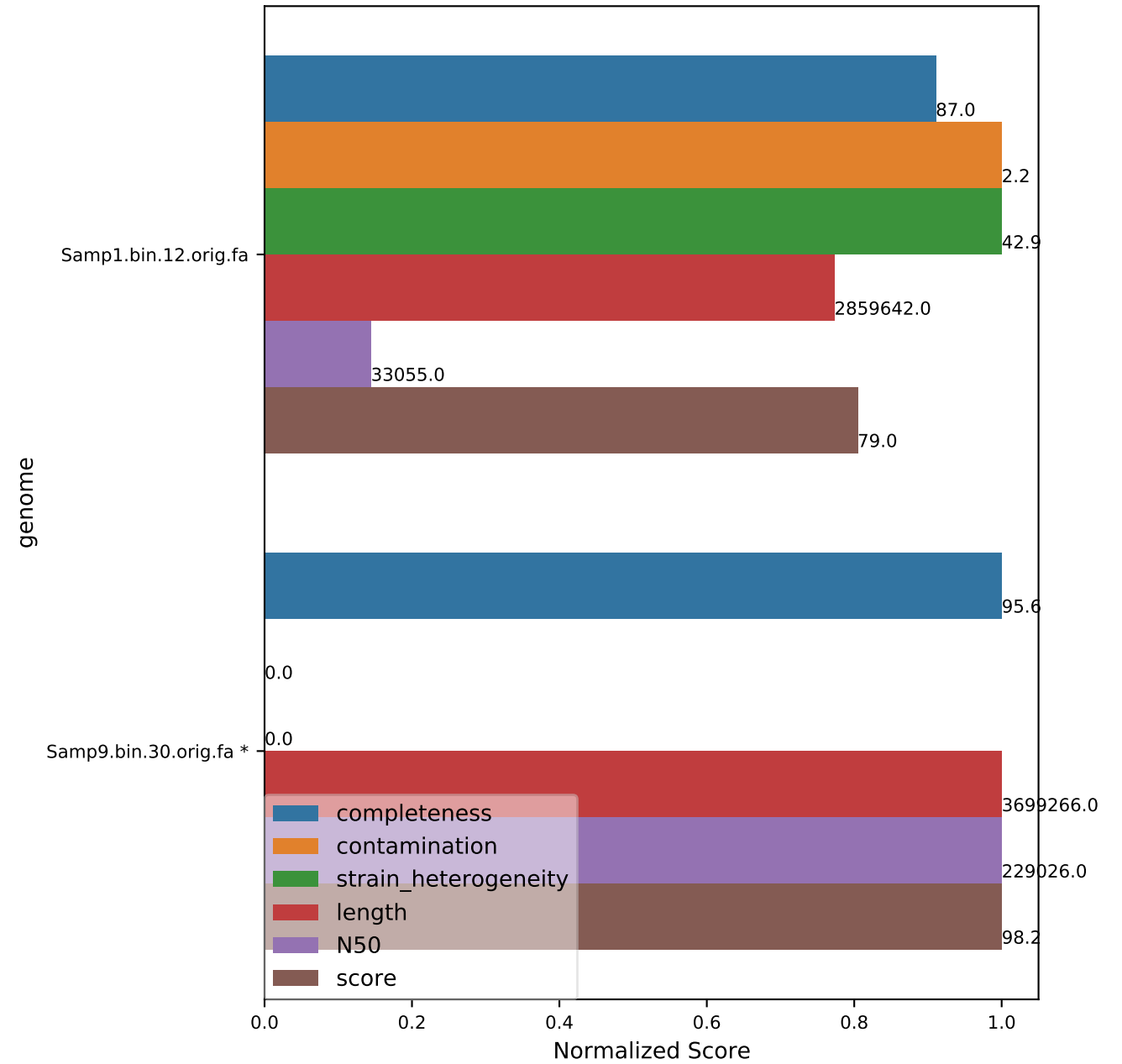
Scoring of cluster 18_0
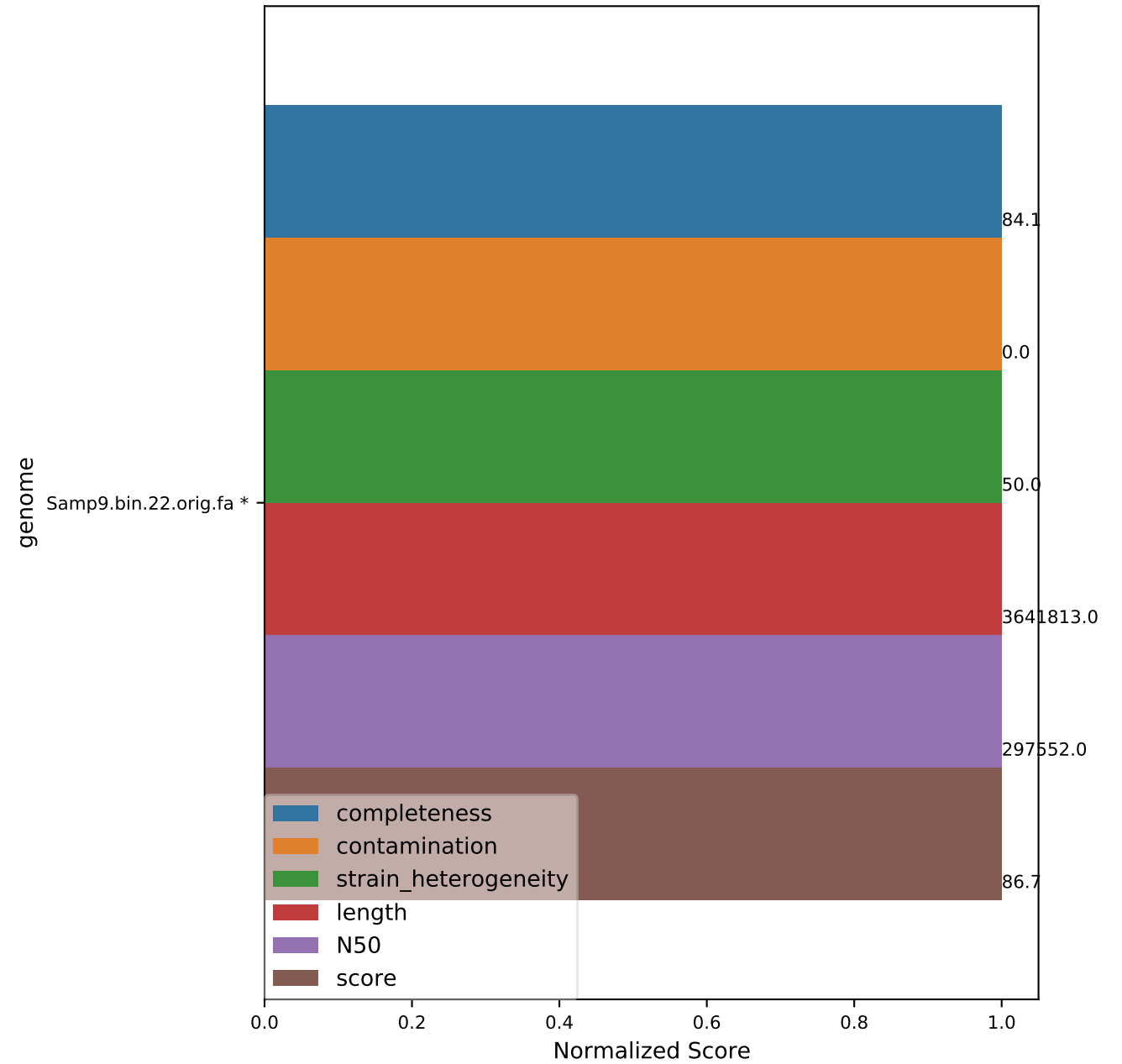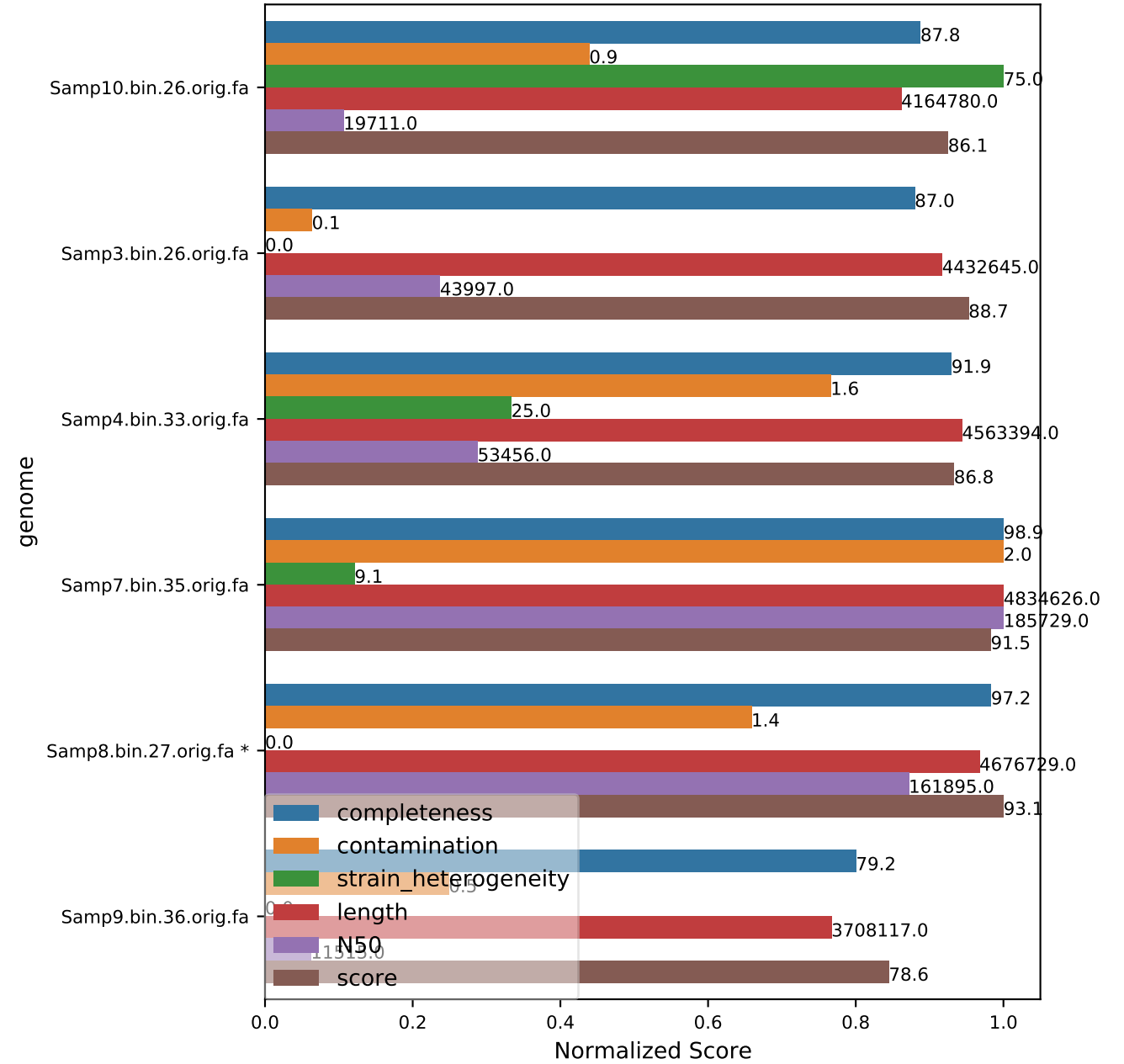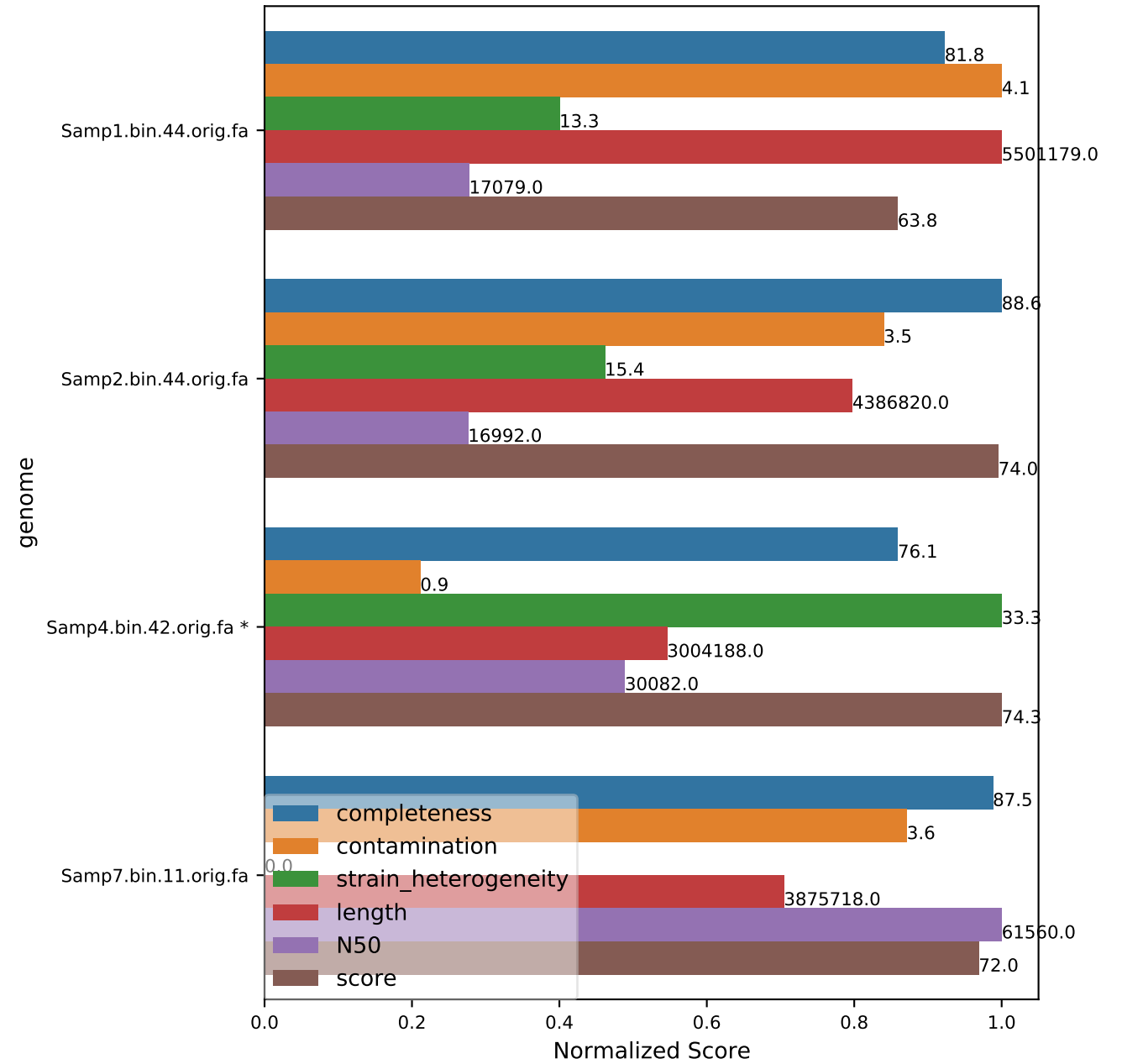
Scoring of cluster 19_1

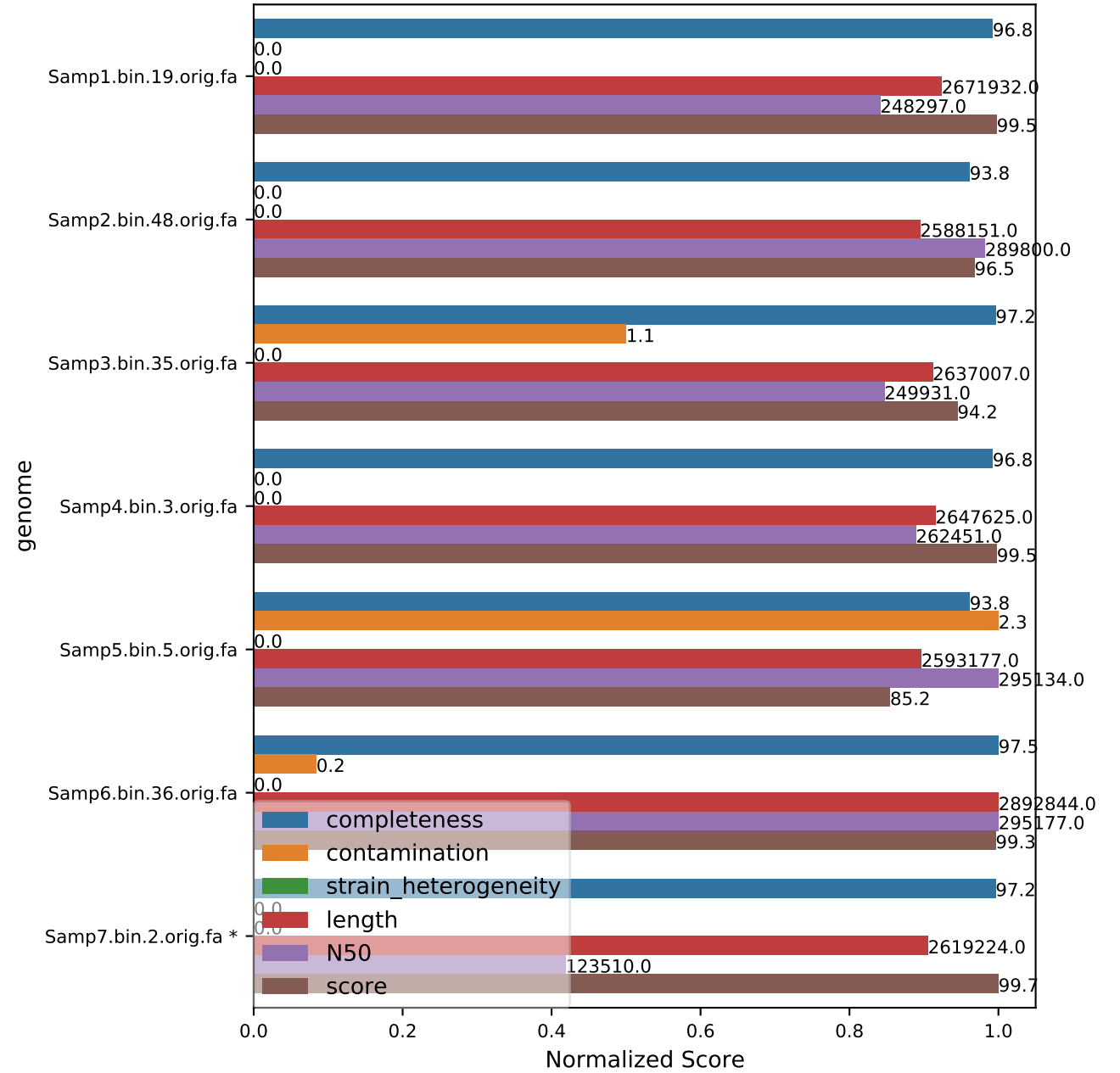Scoring of cluster 20_1

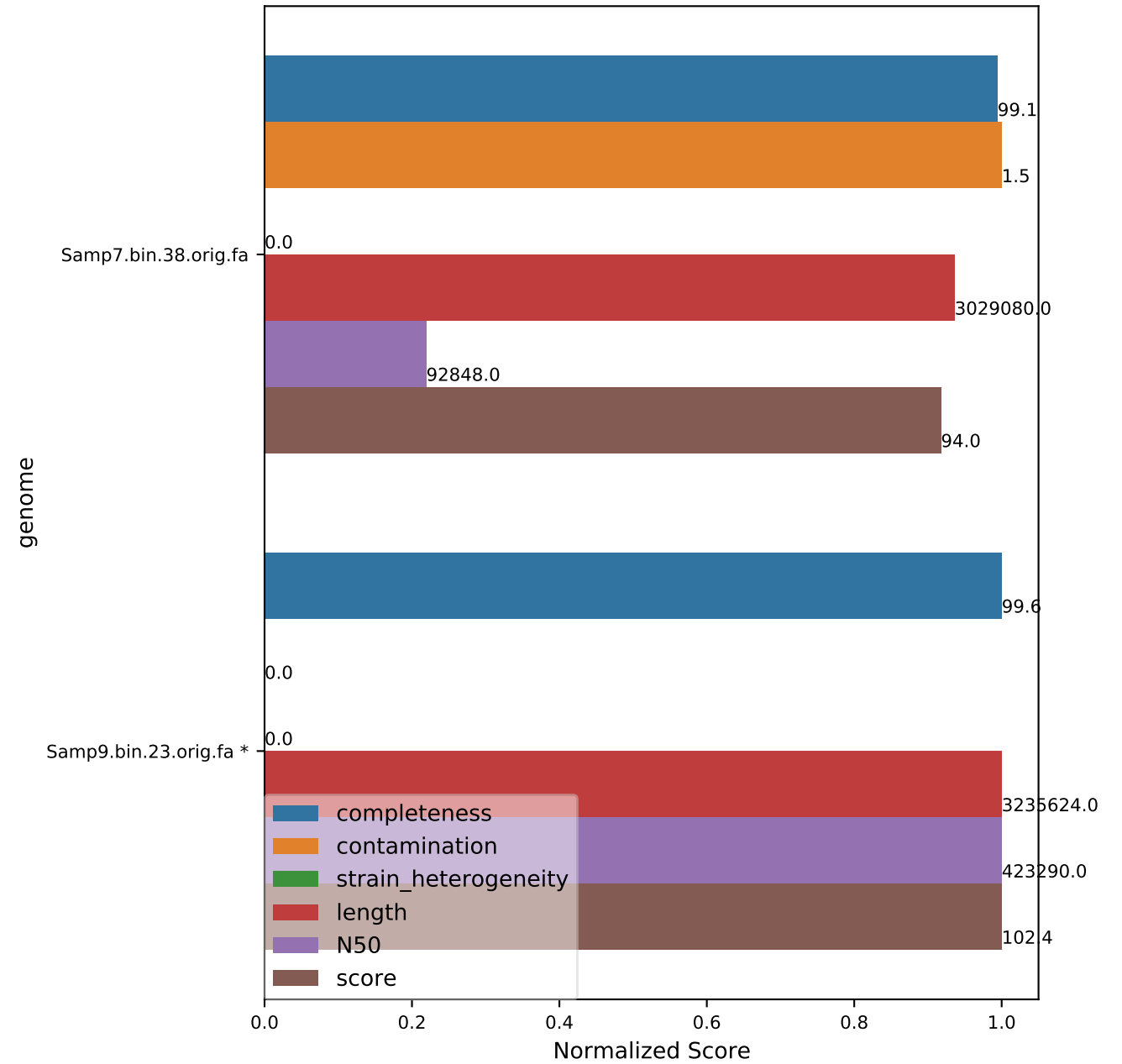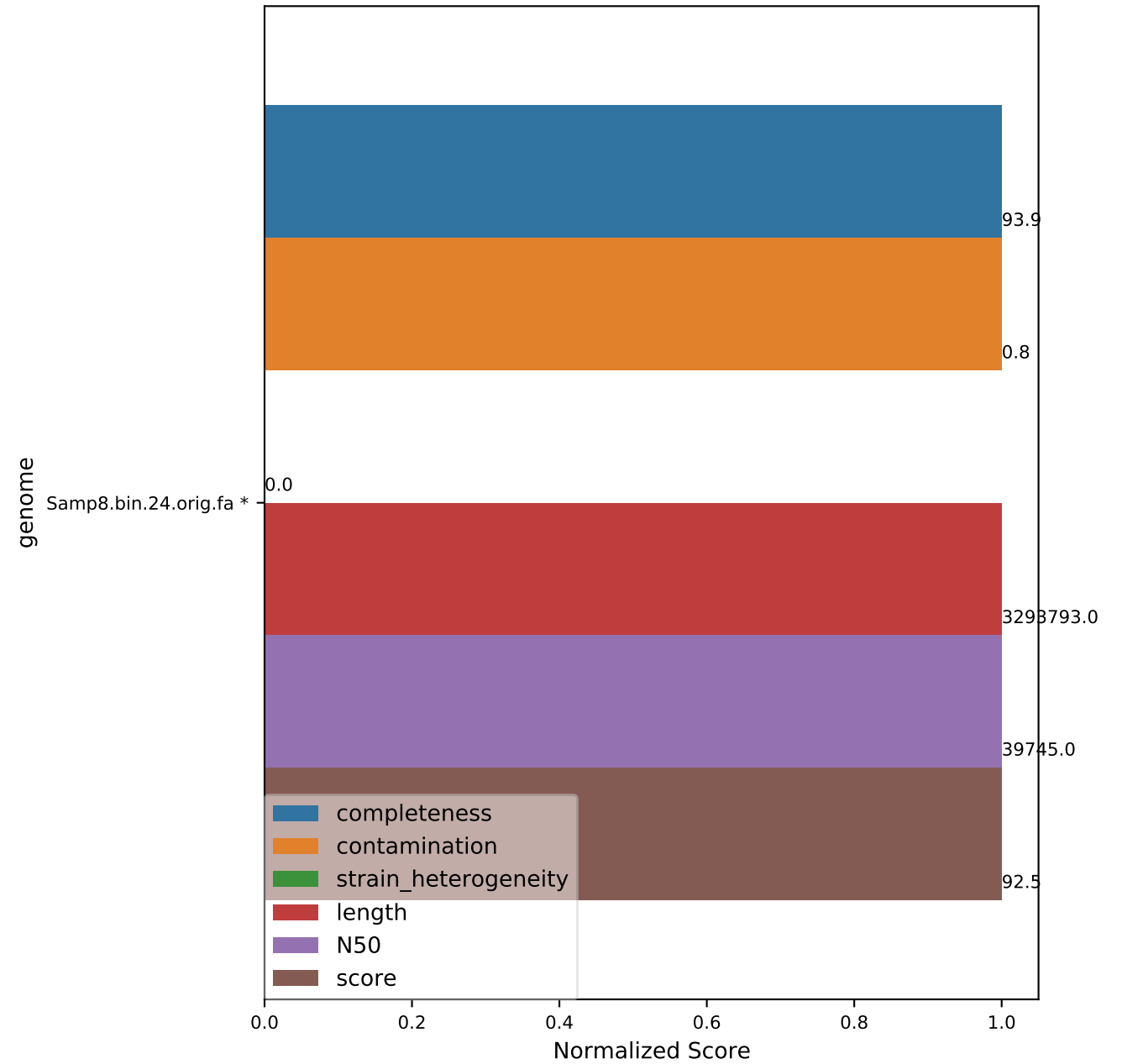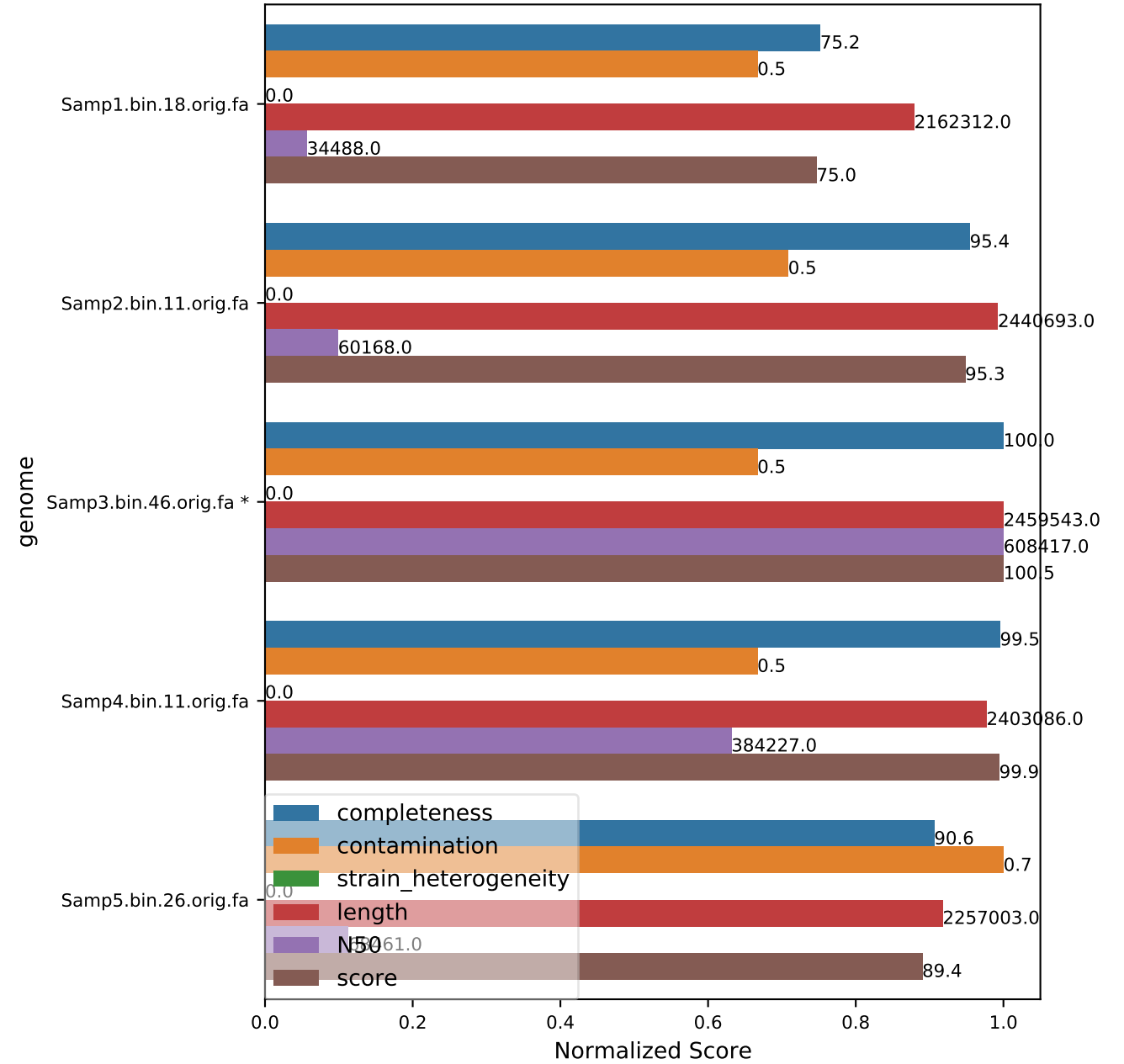Scoring of cluster 21_1

Scoring of cluster 22_0

Scoring of cluster 23_1

Samp10.bin.26.orig.fa	completeness 87.8
	contamination 0.9
	strain_heterogeneity 75.0
	length 4164780.0
	N50 19711.0
	score 86.1
Samp3.bin.26.orig.fa	completeness 87.0
	contamination 0.1
	strain_heterogeneity 0.0
	length 4432645.0
	N50 43997.0
	score 88.7
Samp4.bin.33.orig.fa	completeness 91.9
	contamination 1.6
	strain_heterogeneity 25.0
	length 4563394.0
	N50 53456.0
	score 86.8
Samp7.bin.35.orig.fa	completeness 98.9
	contamination 2.0
	strain_heterogeneity 9.1
	length 4834626.0
	N50 185729.0
	score 91.5
Samp8.bin.27.orig.fa *	completeness 97.2
	contamination 1.4
	strain_heterogeneity 0.0
	length 4676729.0
	N50 161895.0
	score 93.1
Samp9.bin.36.orig.fa	completeness 79.2
	contamination 0.5
	strain_heterogeneity 0.0
	length 3708117.0
	N50 11515.0
	score 78.6

Legend: completeness, contamination, strain_heterogeneity, length, N50, score

X-axis: Normalized Score
Y-axis: genome

Scoring of cluster 24_1
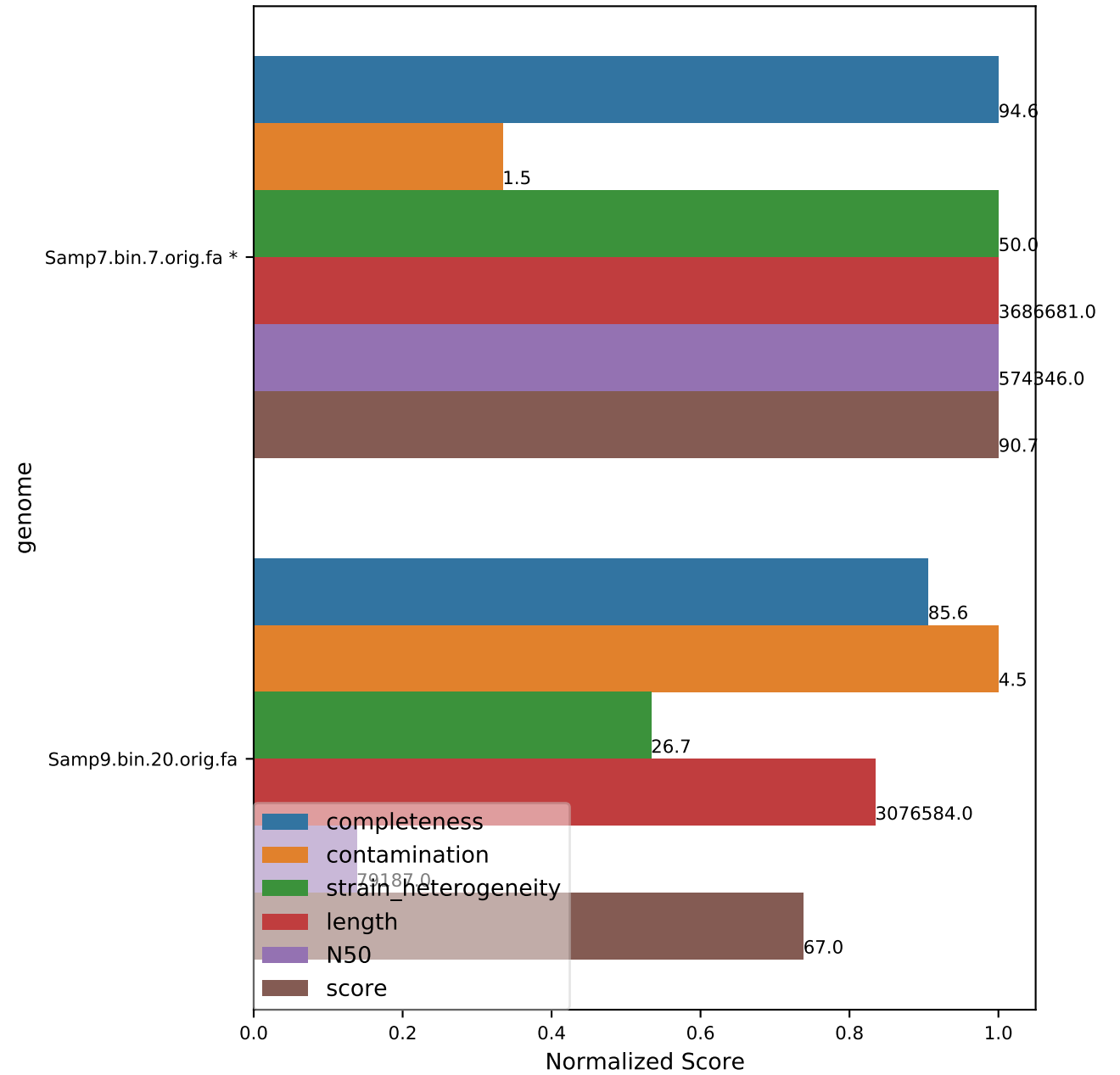
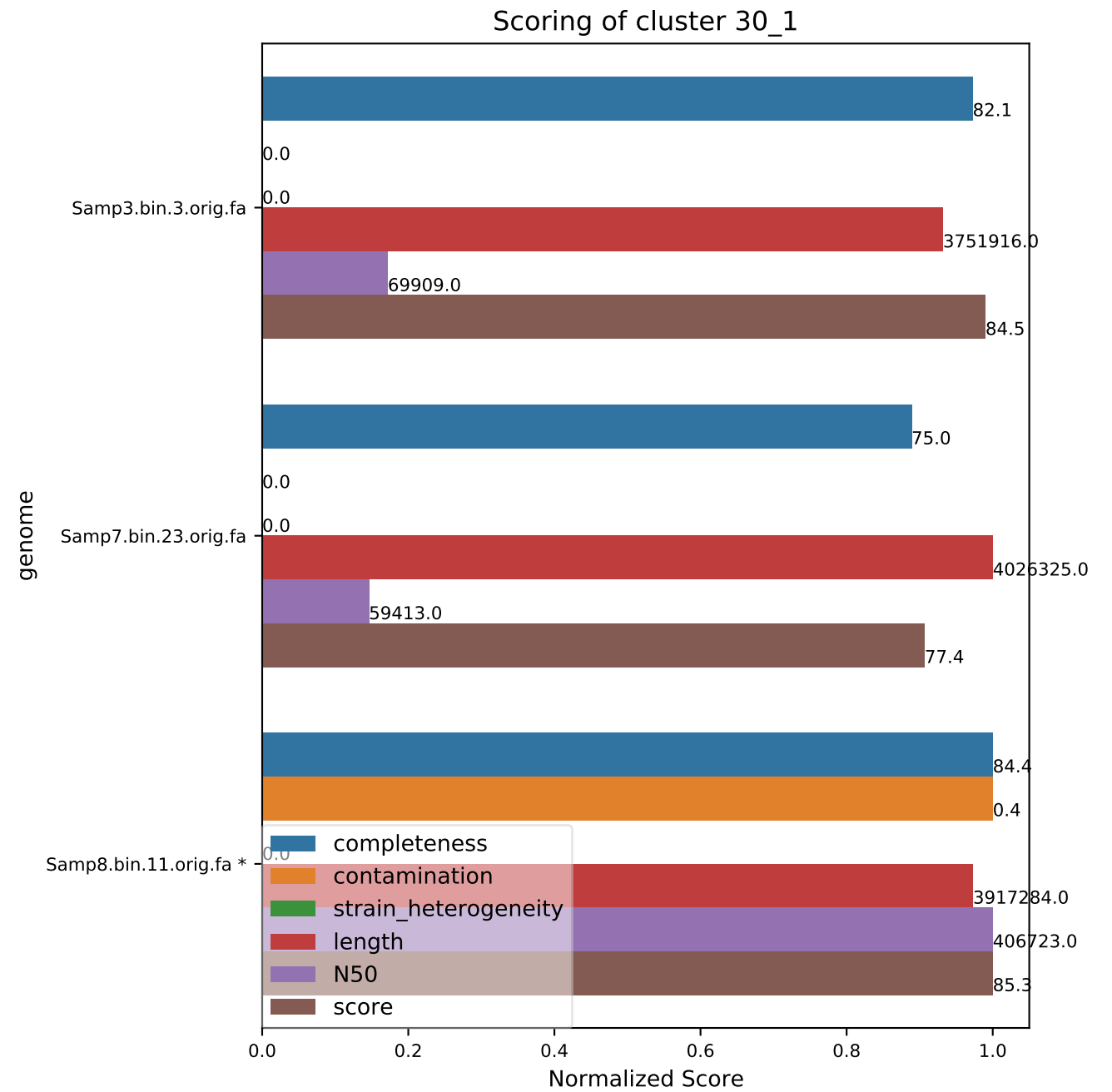Scoring of cluster 25_1

Scoring of cluster 26_1
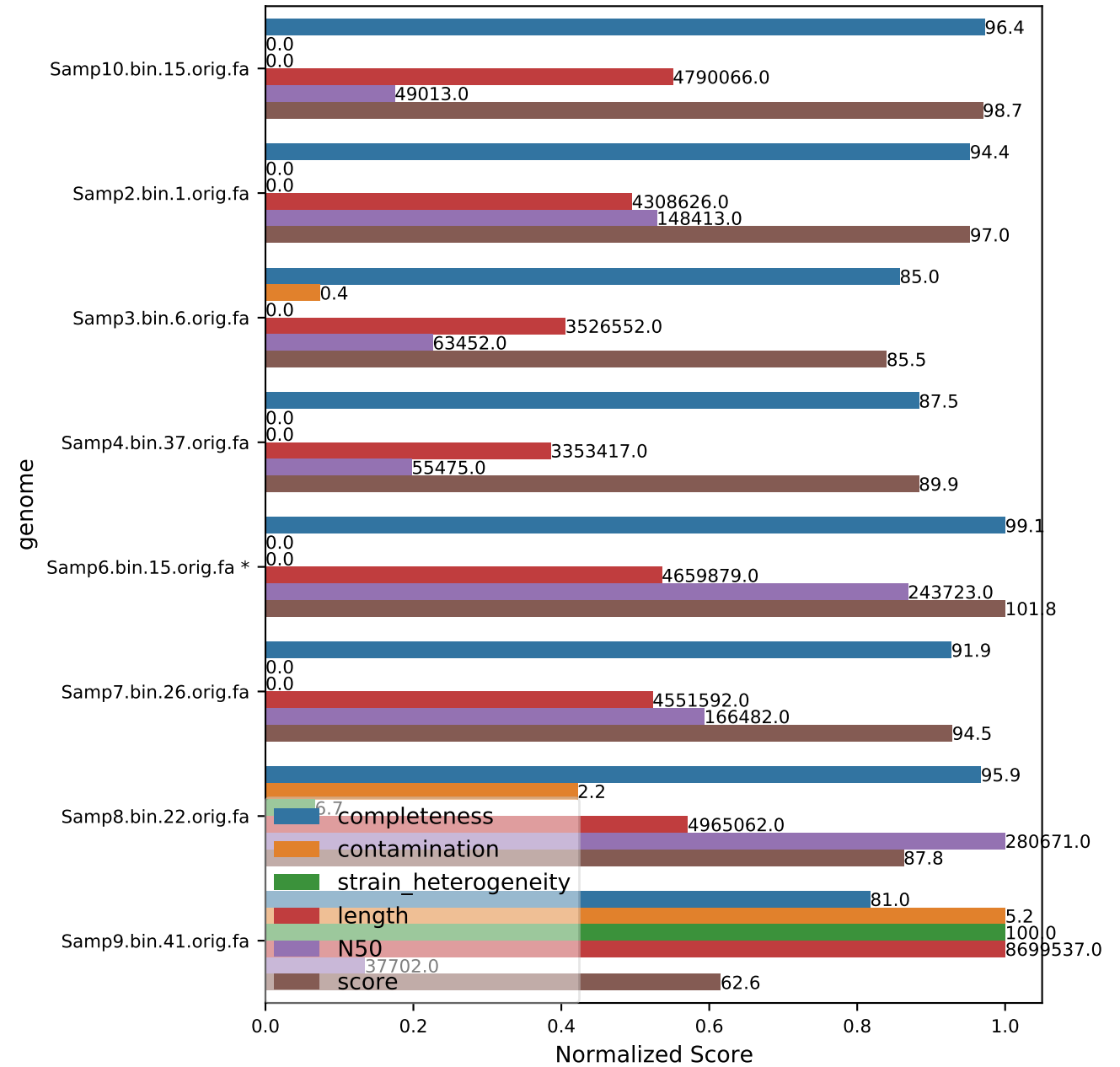
Scoring of cluster 27_0
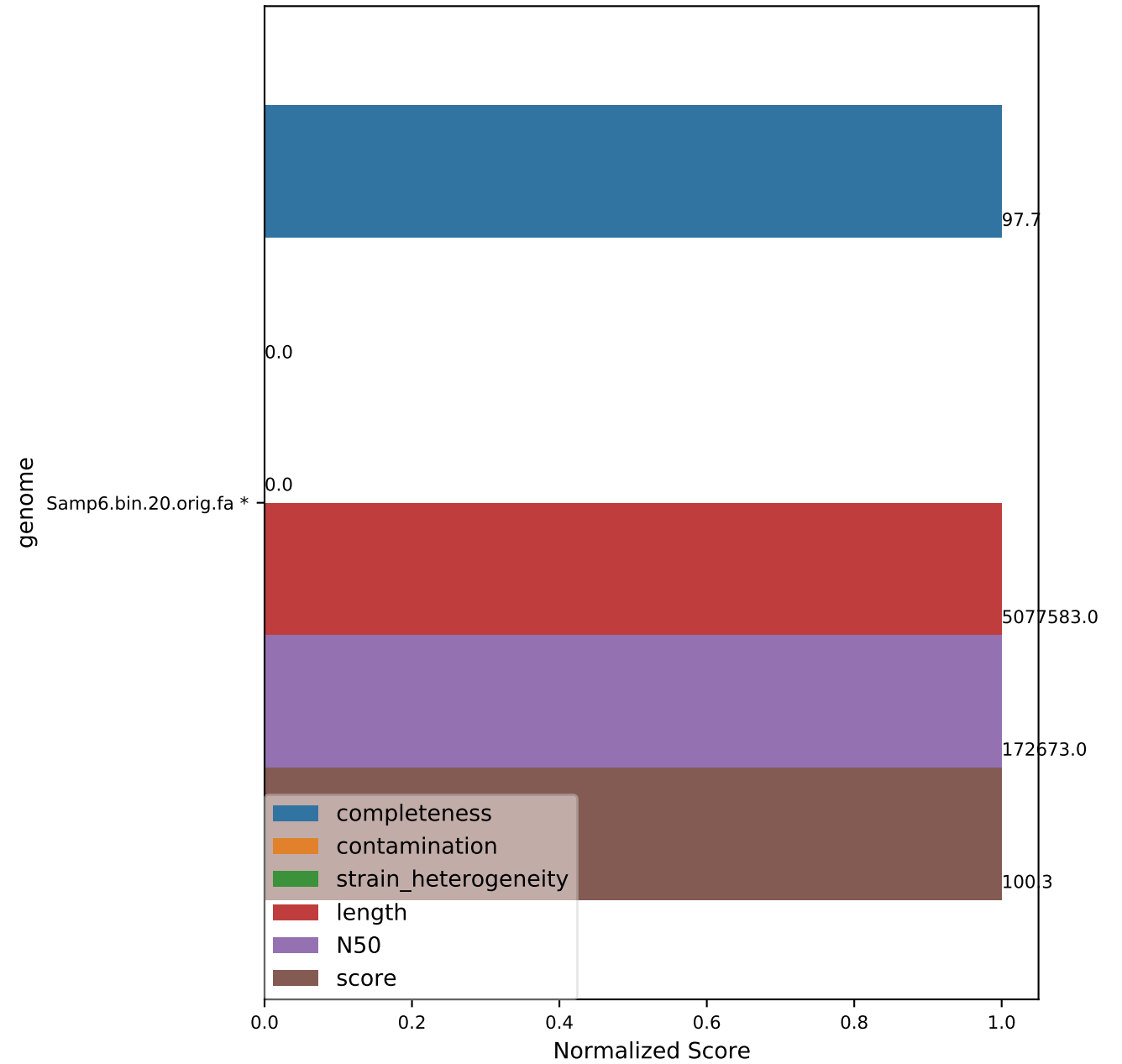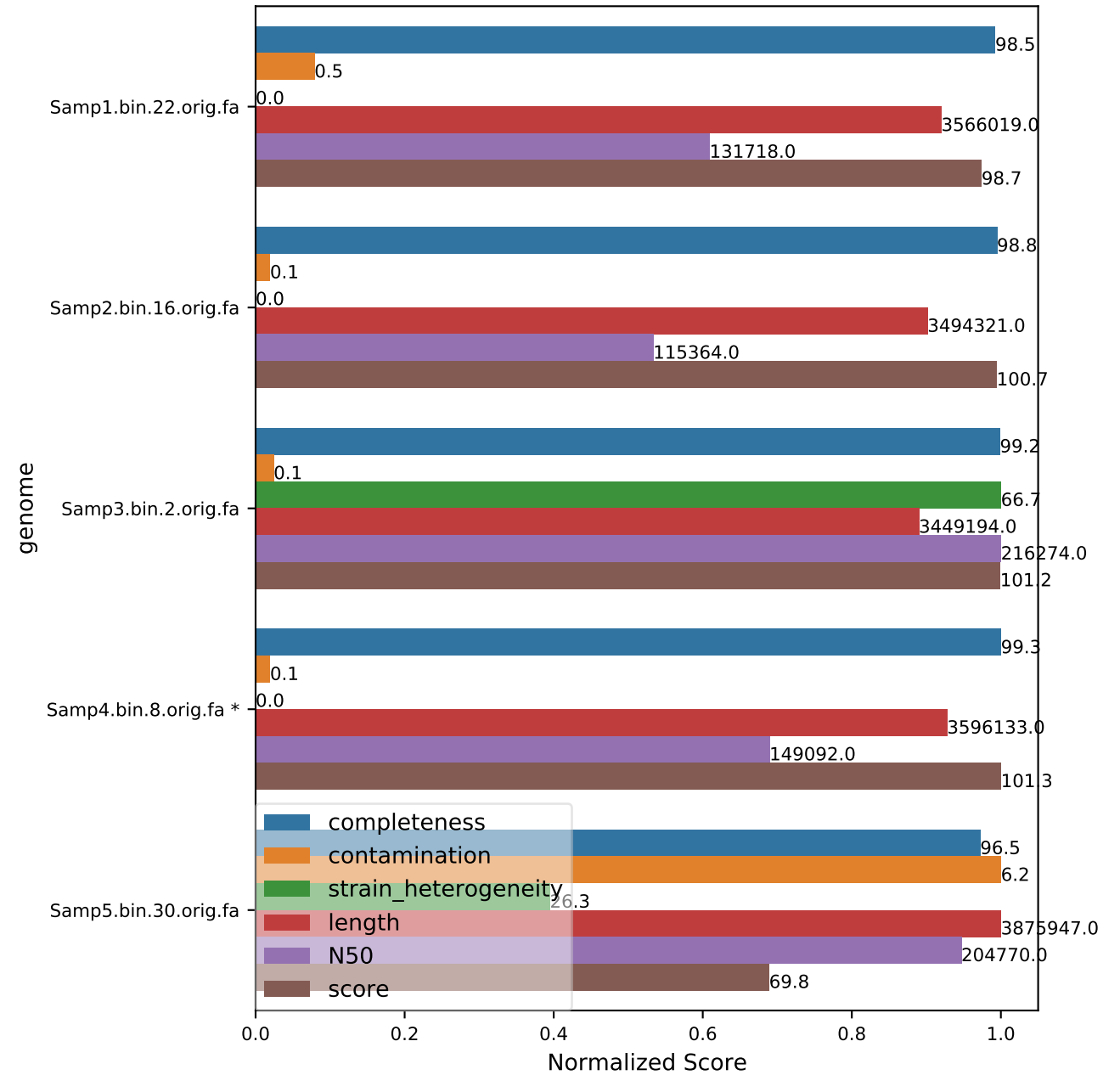
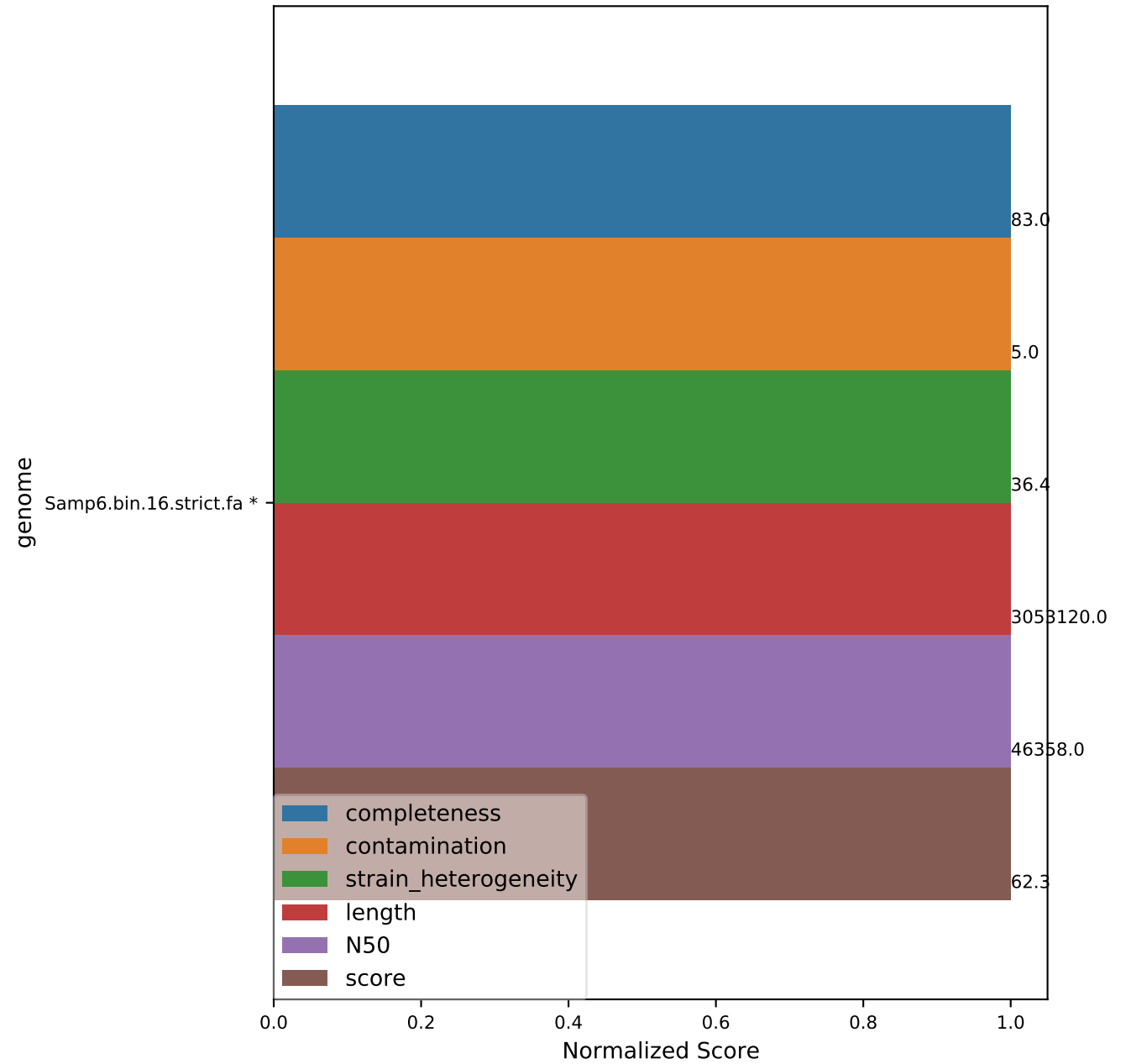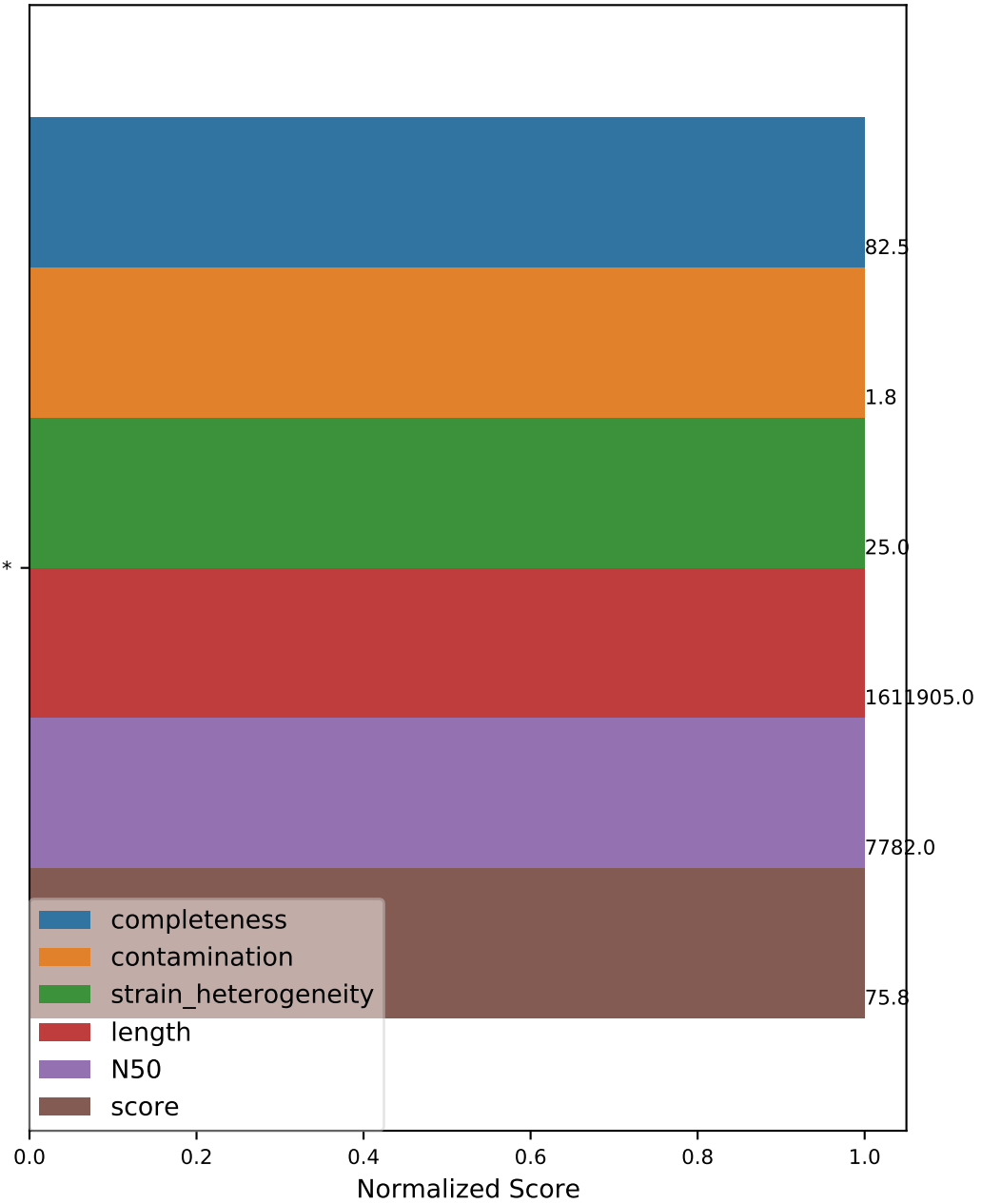Scoring of cluster 28_1

Scoring of cluster 29_1

Scoring of cluster 30_1

Scoring of cluster 31_1

Samp10.bin.15.orig.fa
96.4
0.0
0.0
4790066.0
49013.0
98.7

Samp2.bin.1.orig.fa
94.4
0.0
0.0
4308626.0
148413.0
97.0

Samp3.bin.6.orig.fa
85.0
0.4
0.0
3526552.0
63452.0
85.5

Samp4.bin.37.orig.fa
87.5
0.0
0.0
3353417.0
55475.0
89.9

Samp6.bin.15.orig.fa *
99.1
0.0
0.0
4659879.0
243723.0
101.8

Samp7.bin.26.orig.fa
91.9
0.0
0.0
4551592.0
166482.0
94.5

Samp8.bin.22.orig.fa
95.9
2.2
6.7
4965062.0
280671.0
87.8

Samp9.bin.41.orig.fa
81.0
5.2
100.0
8699537.0
37702.0
62.6

genome

Legend:
- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

Normalized Score
0.0 0.2 0.4 0.6 0.8 1.0

Scoring of cluster 32_0

Scoring of cluster 33_1

Scoring of cluster 34_0

Scoring of cluster 35_0

Scoring of cluster 36_1
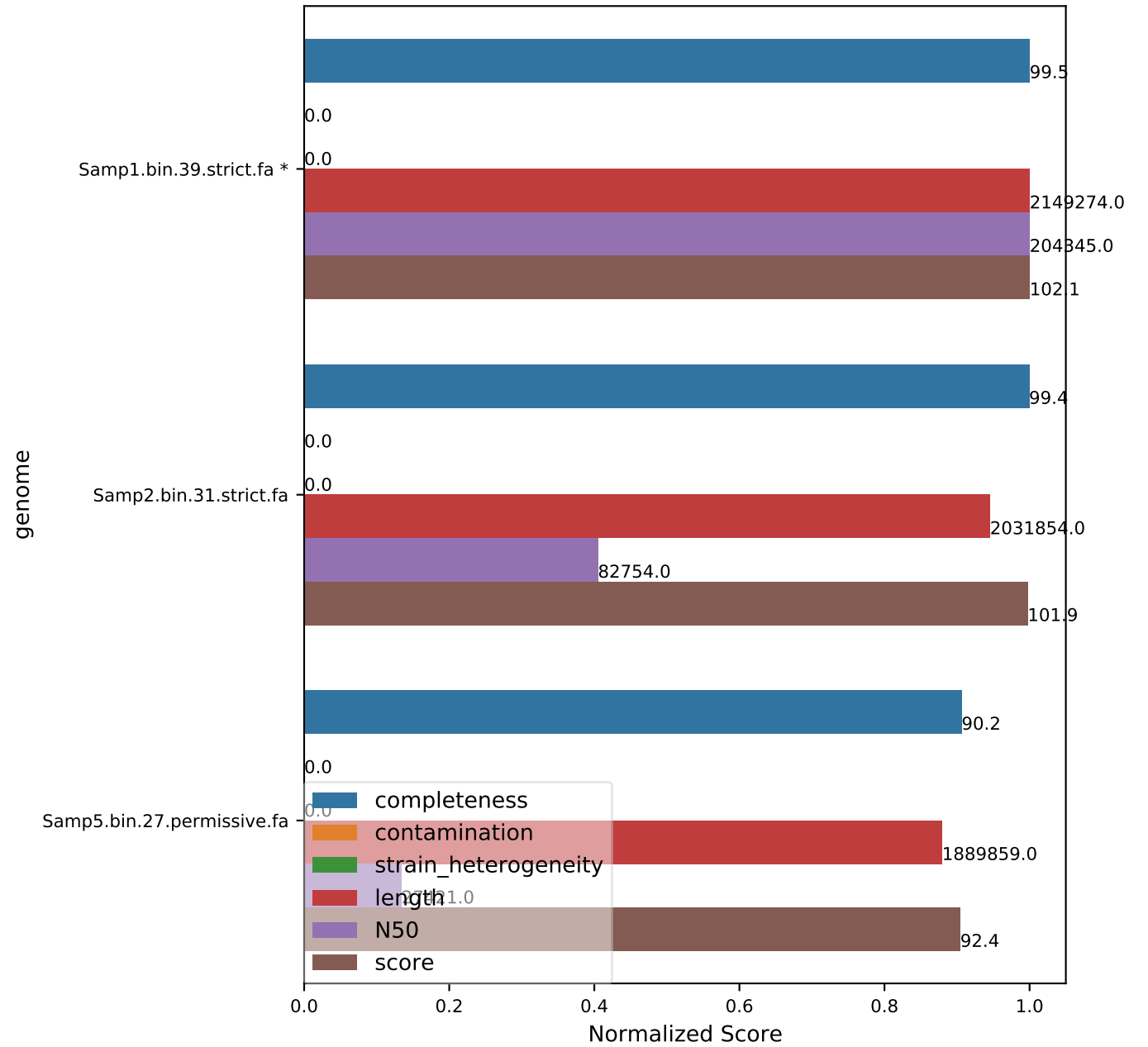
Scoring of cluster 37_1
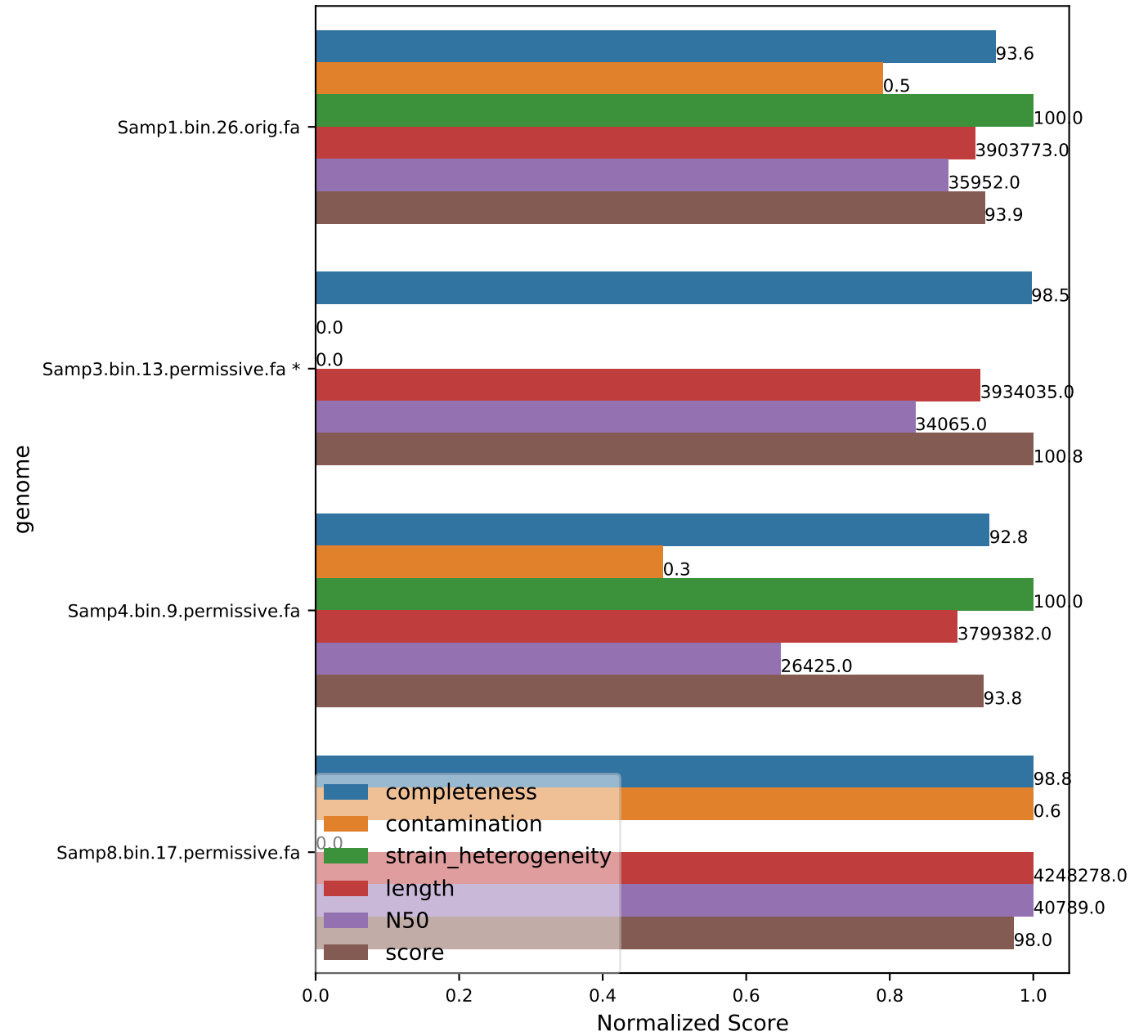
Scoring of cluster 38_0
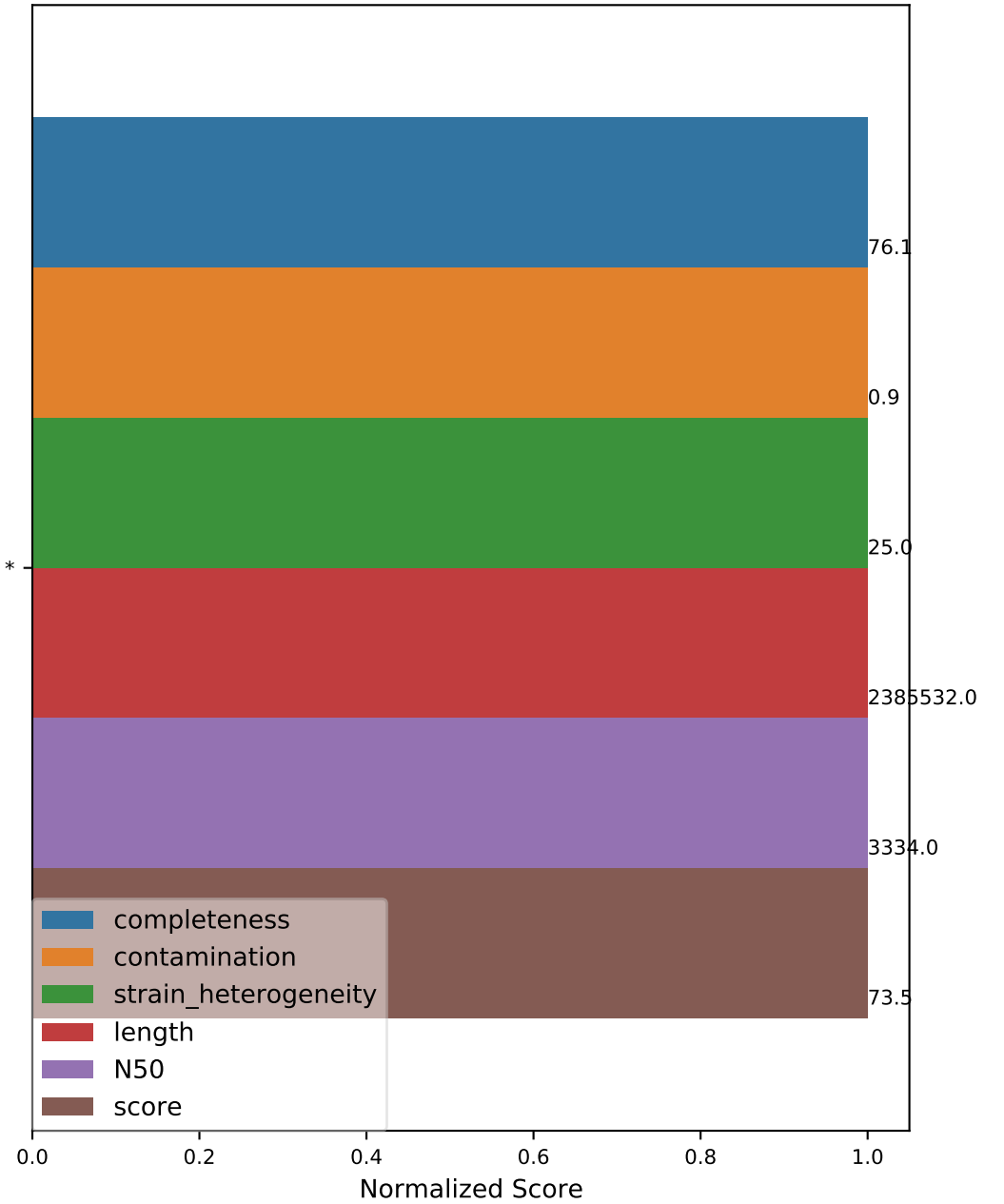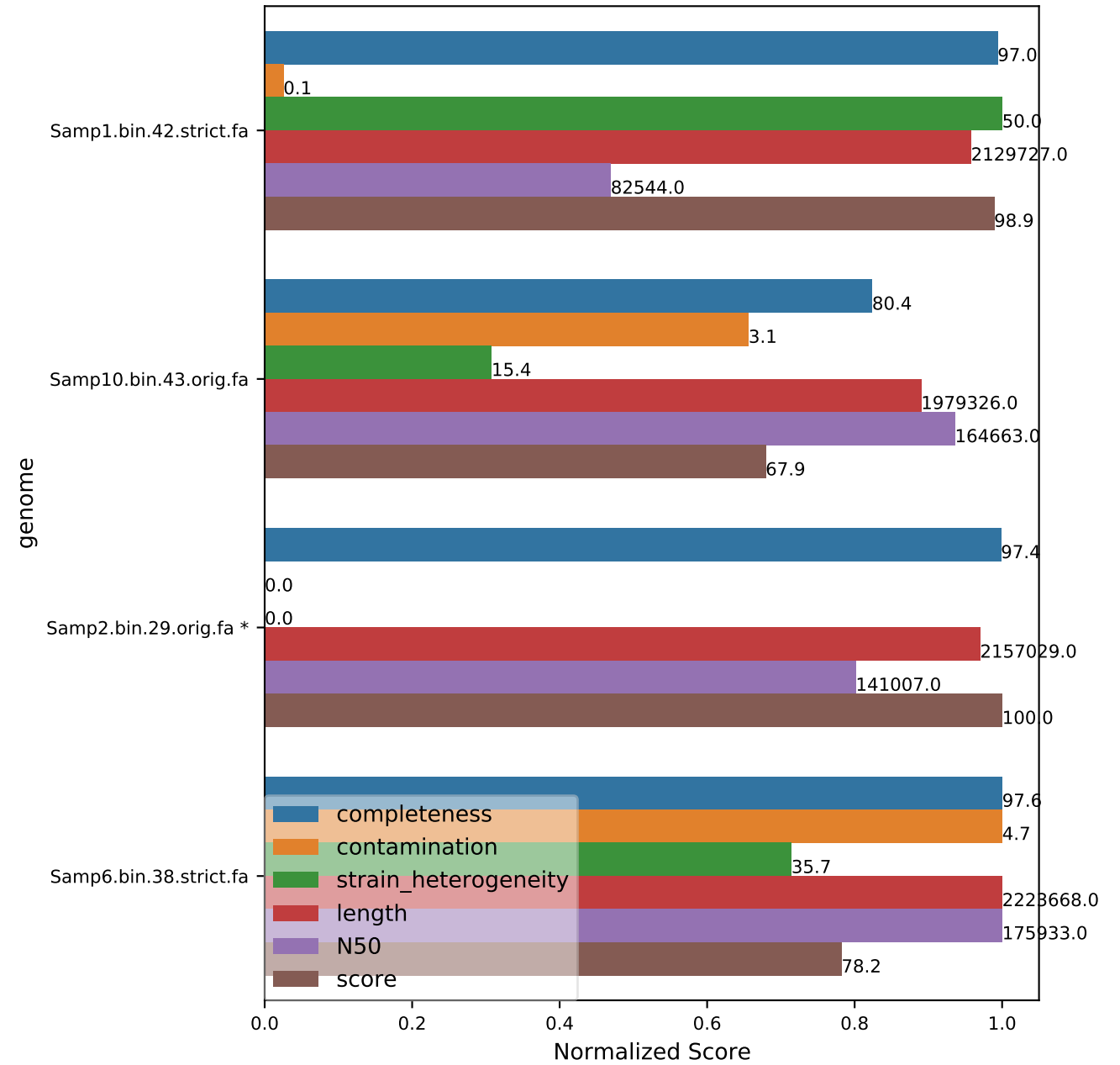
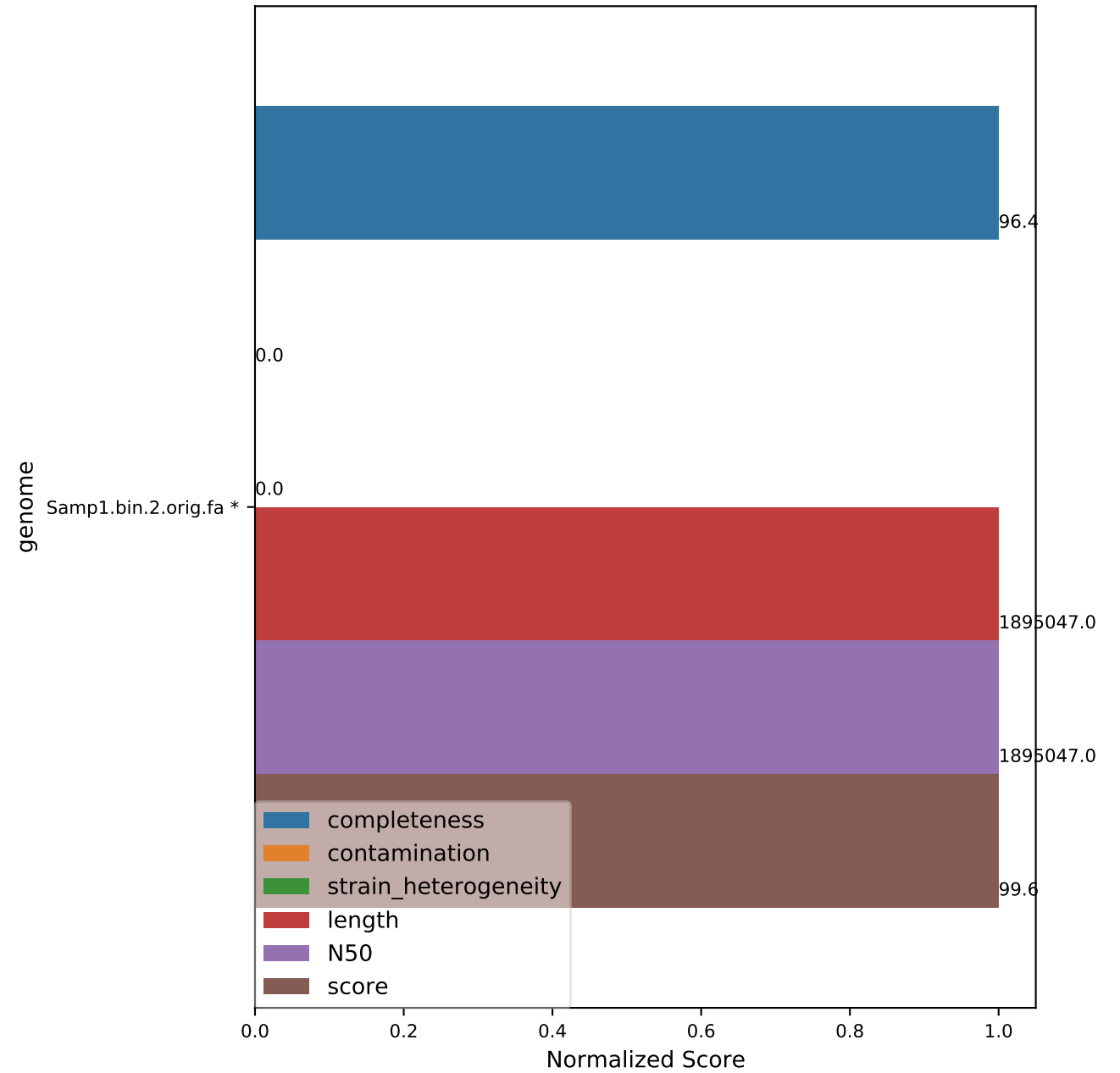Scoring of cluster 39_1
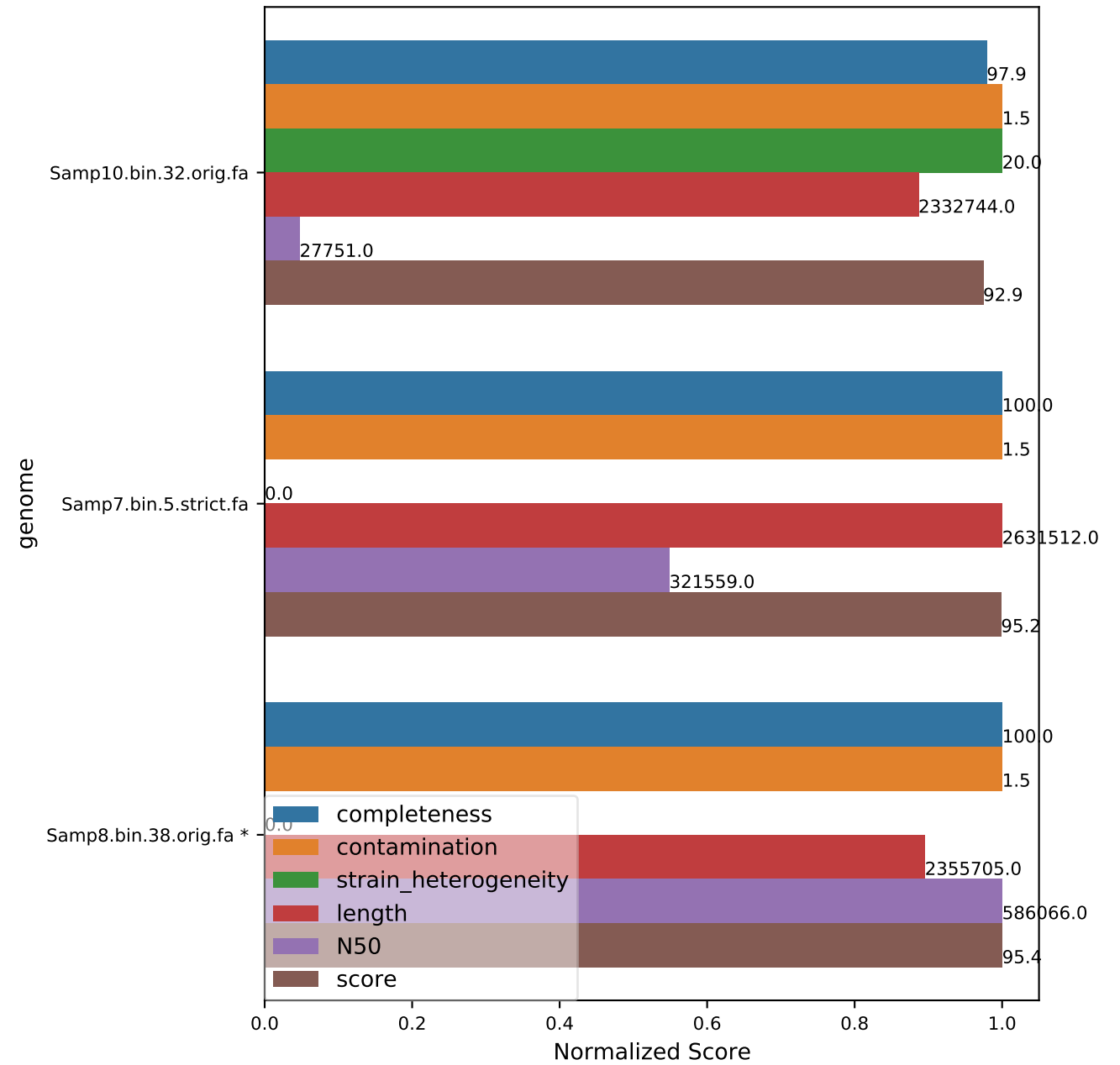
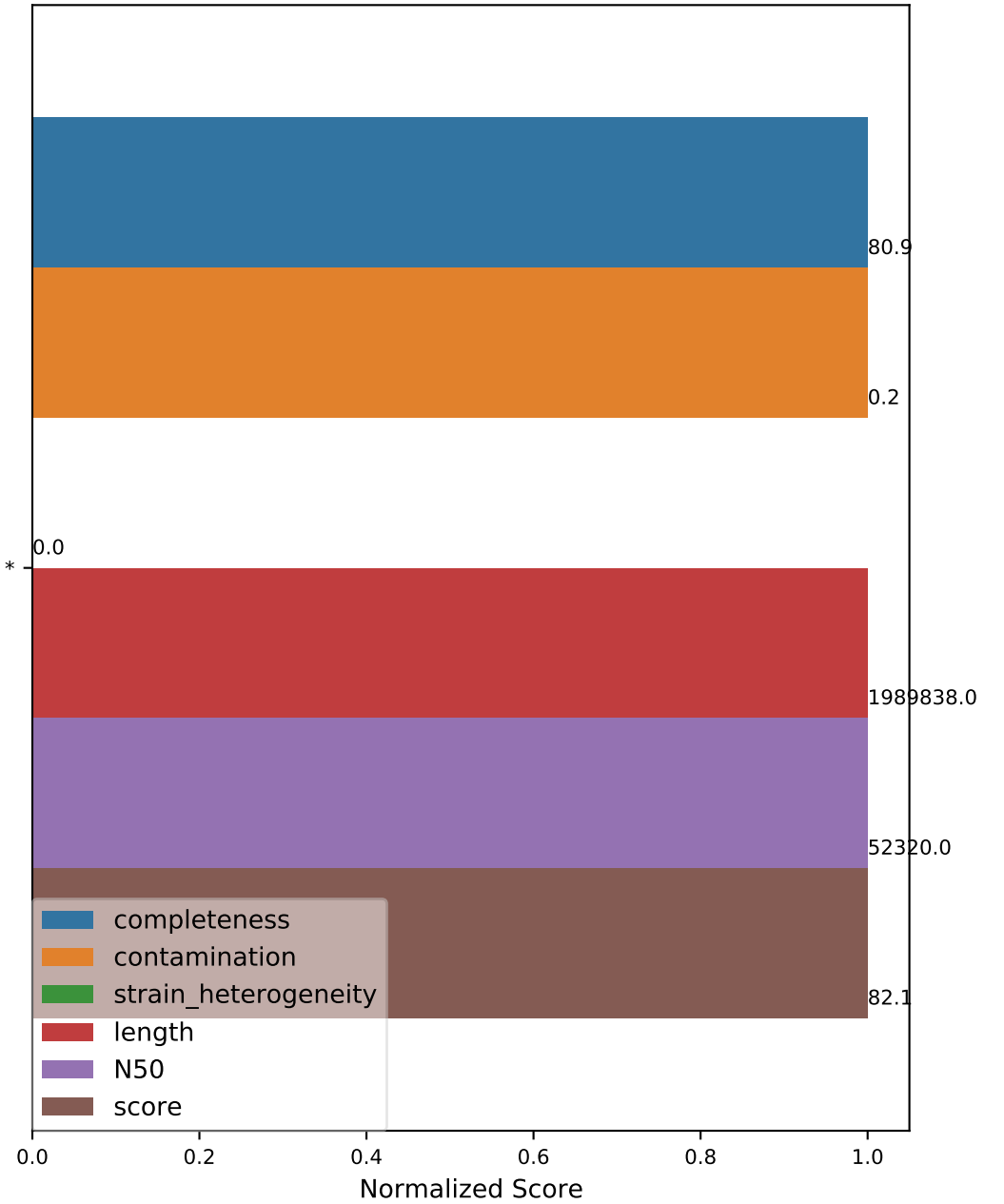Scoring of cluster 40_1
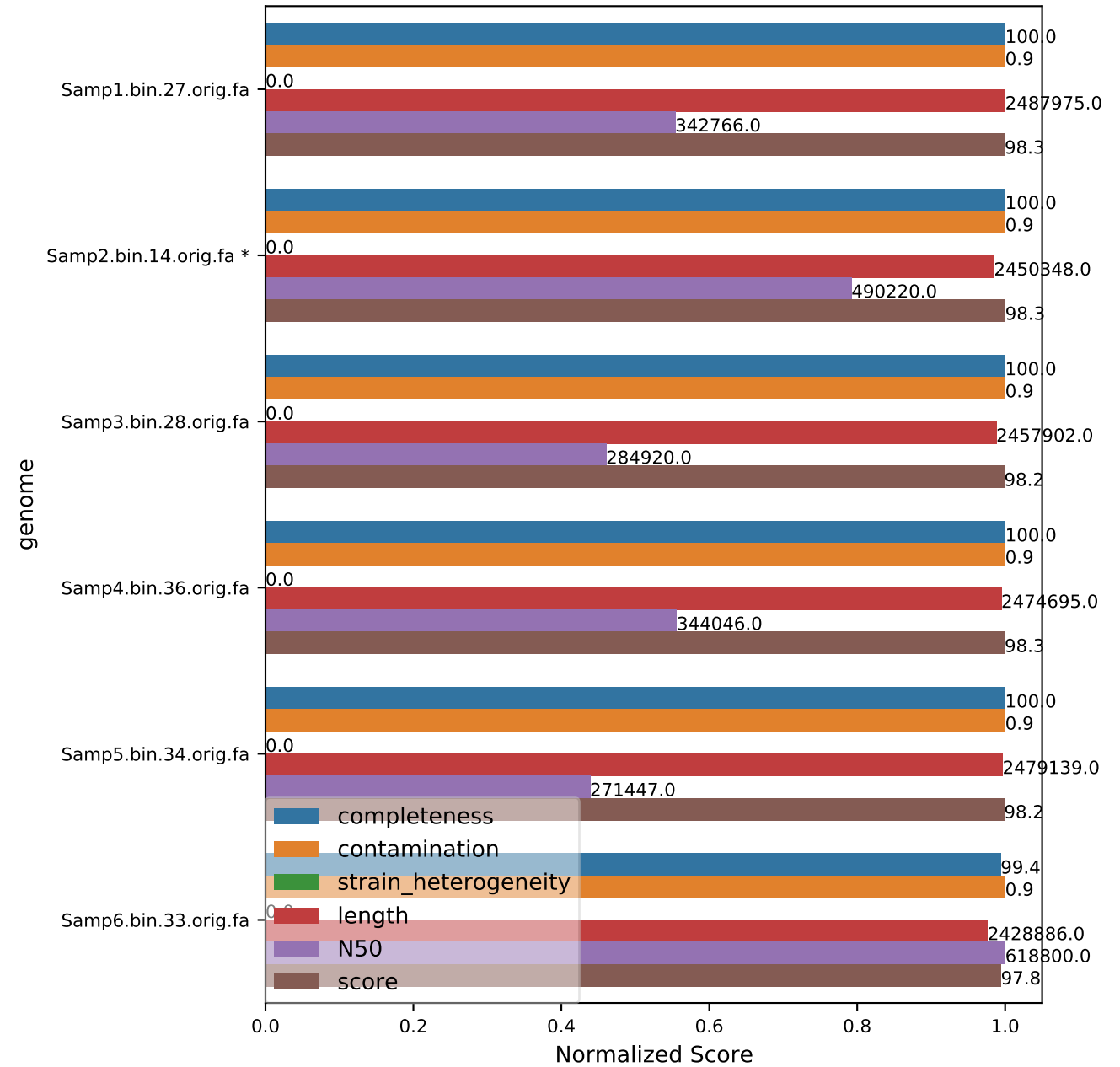
Scoring of cluster 41_1
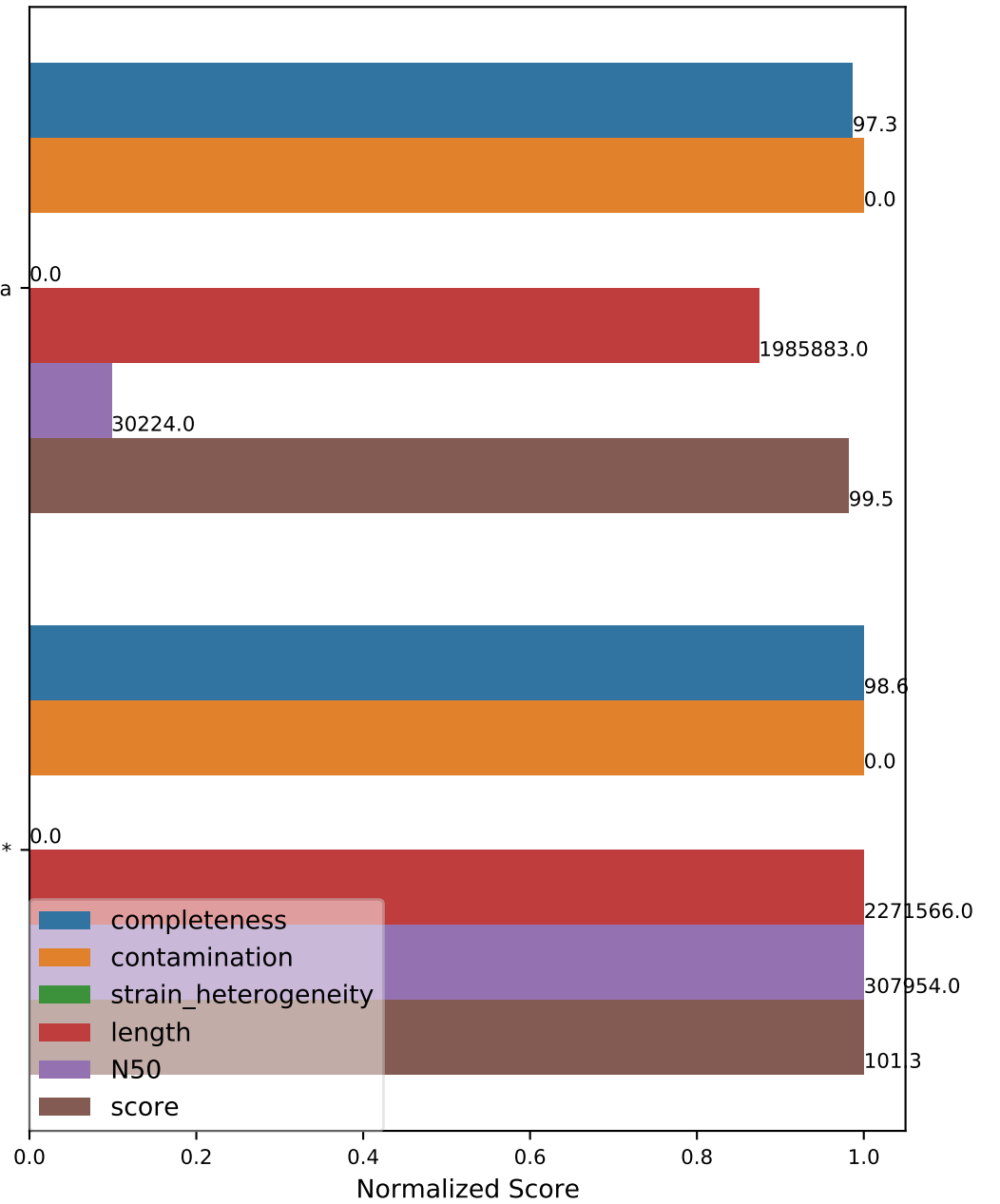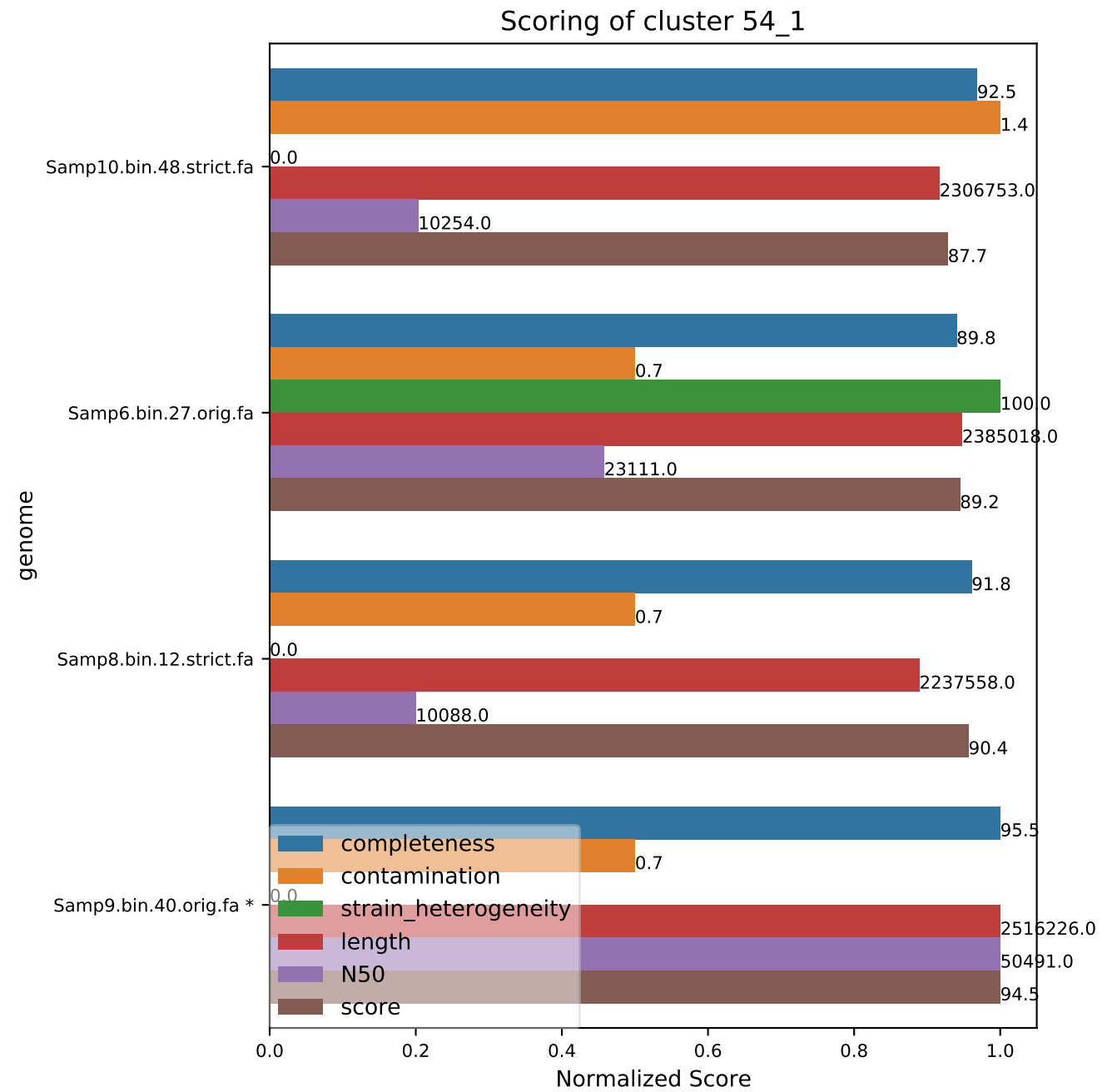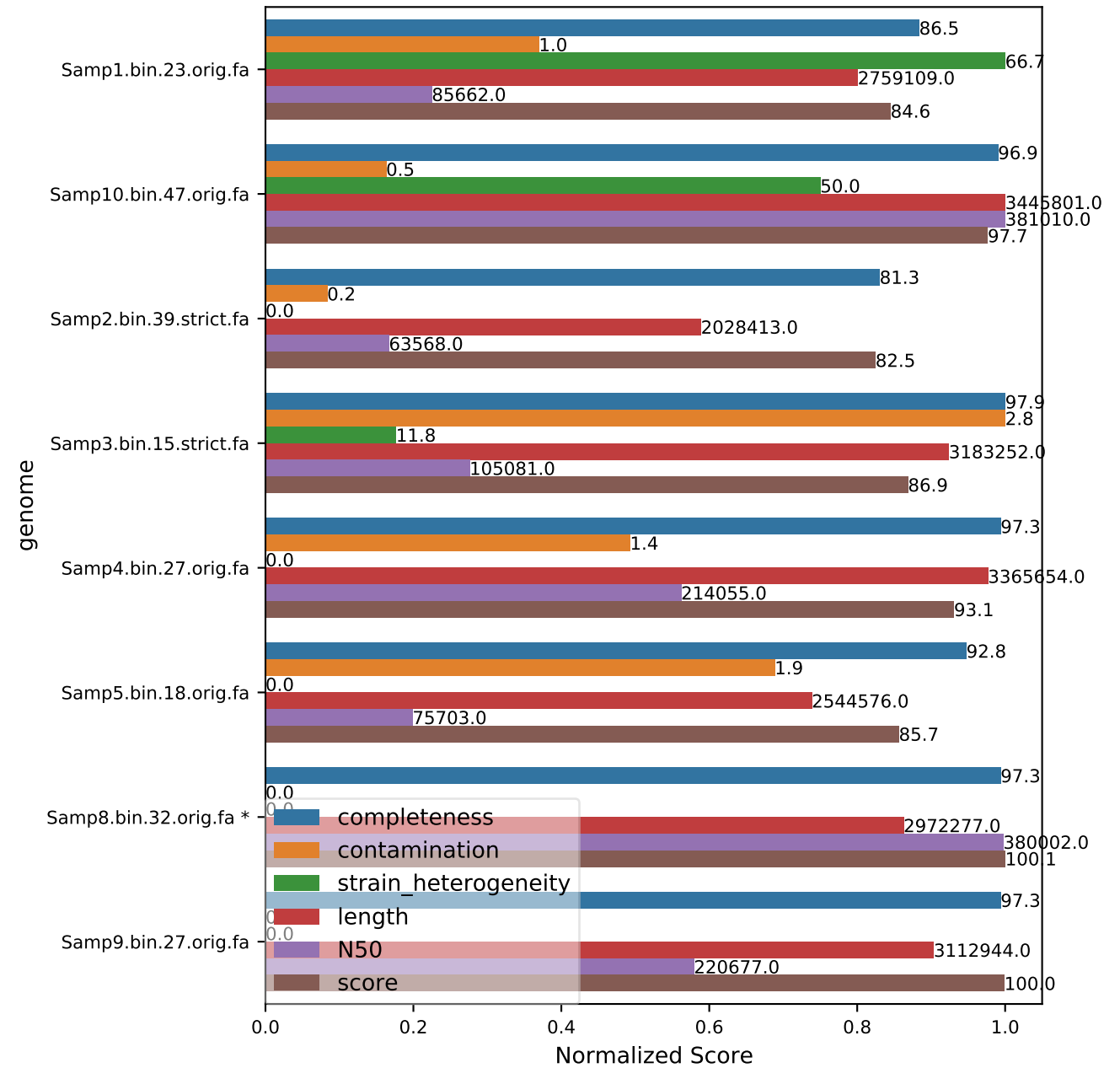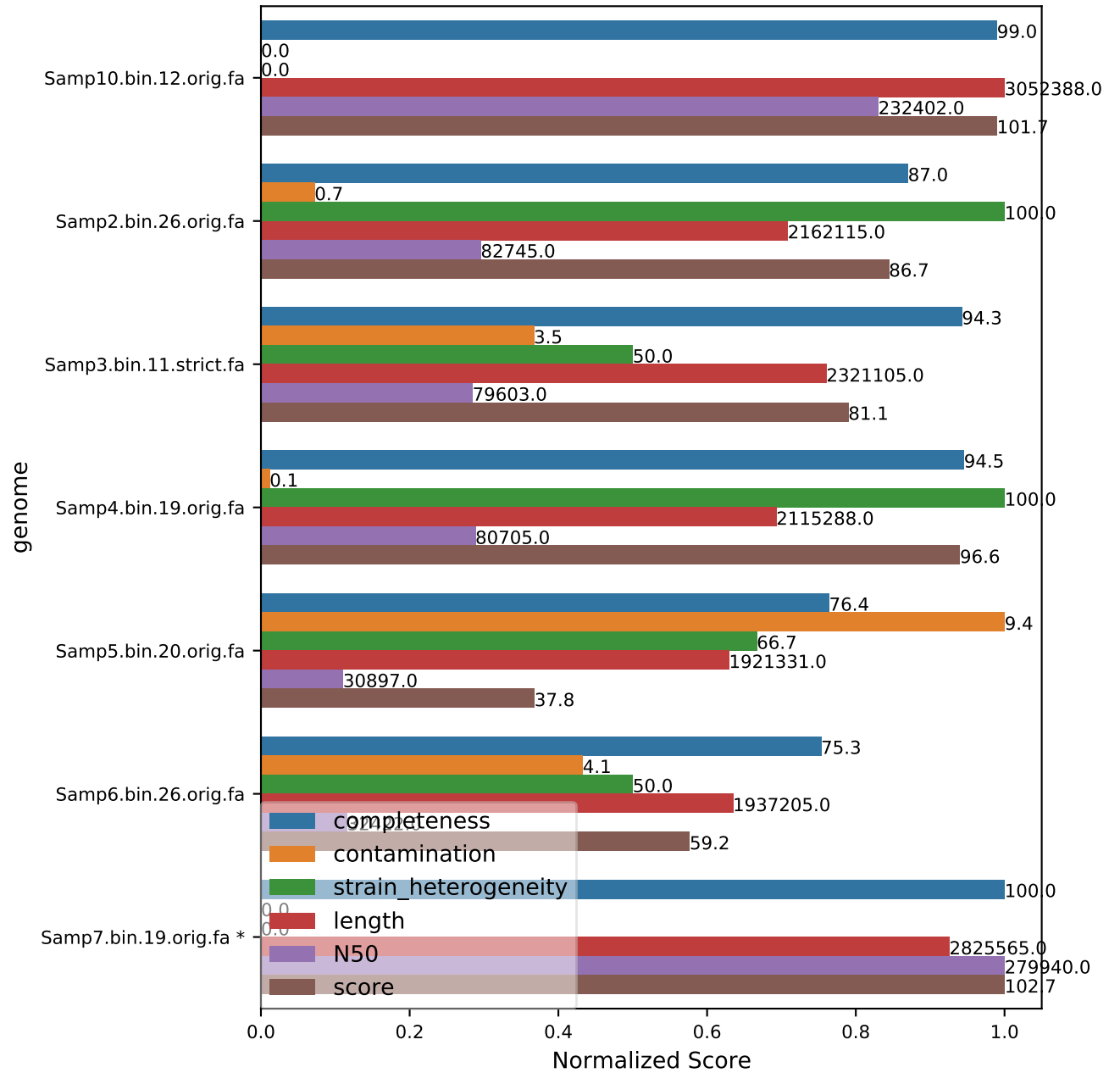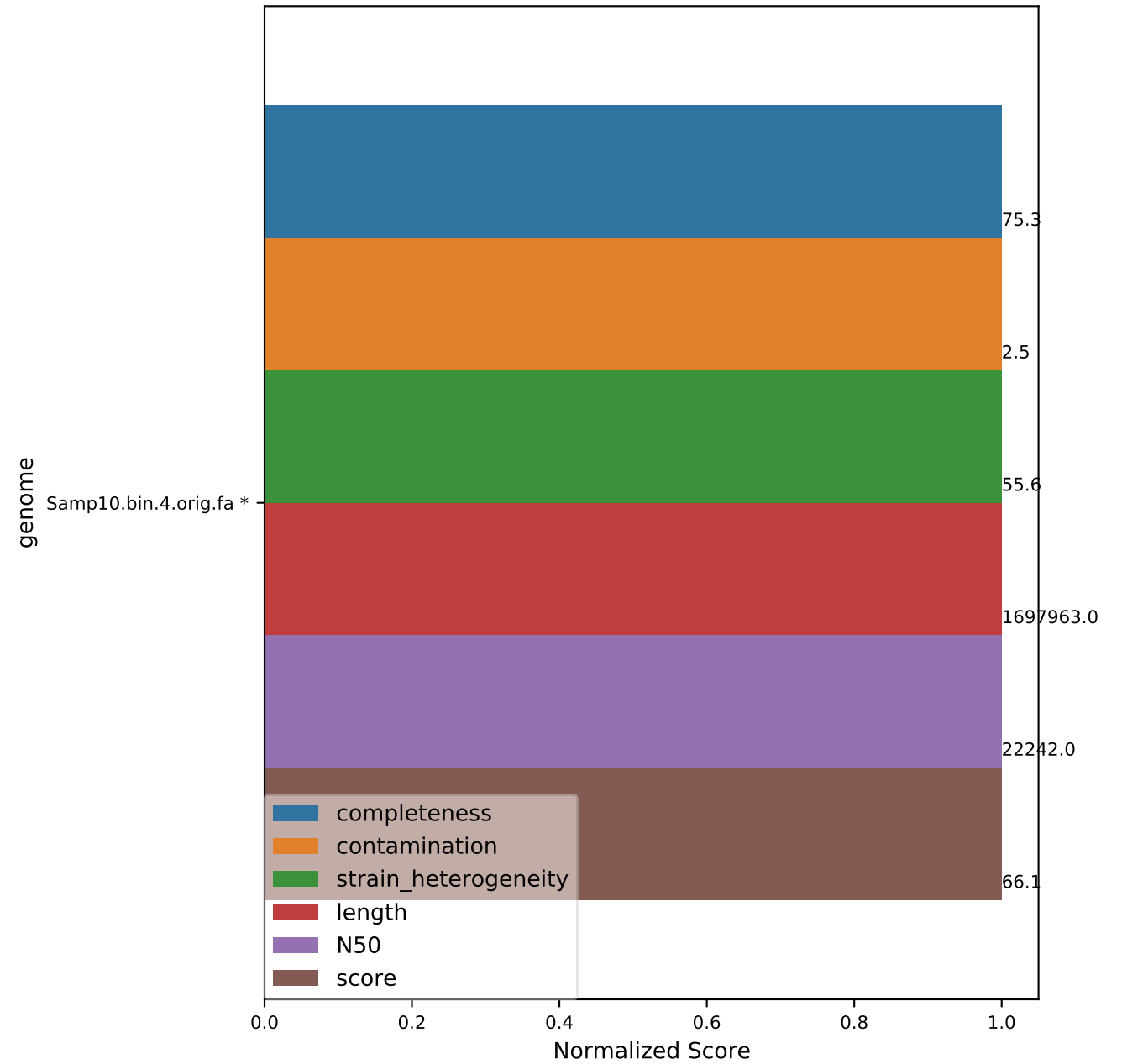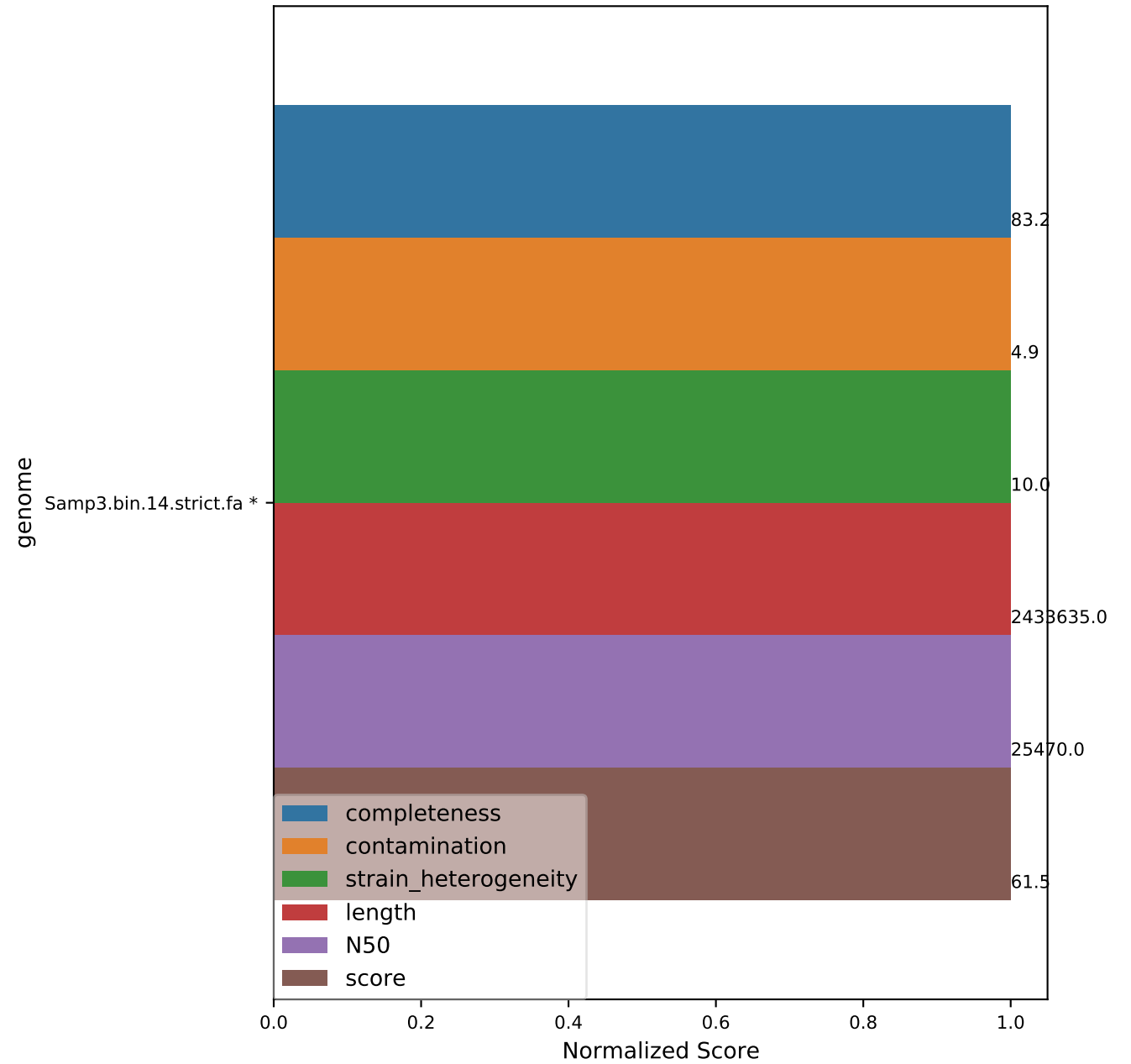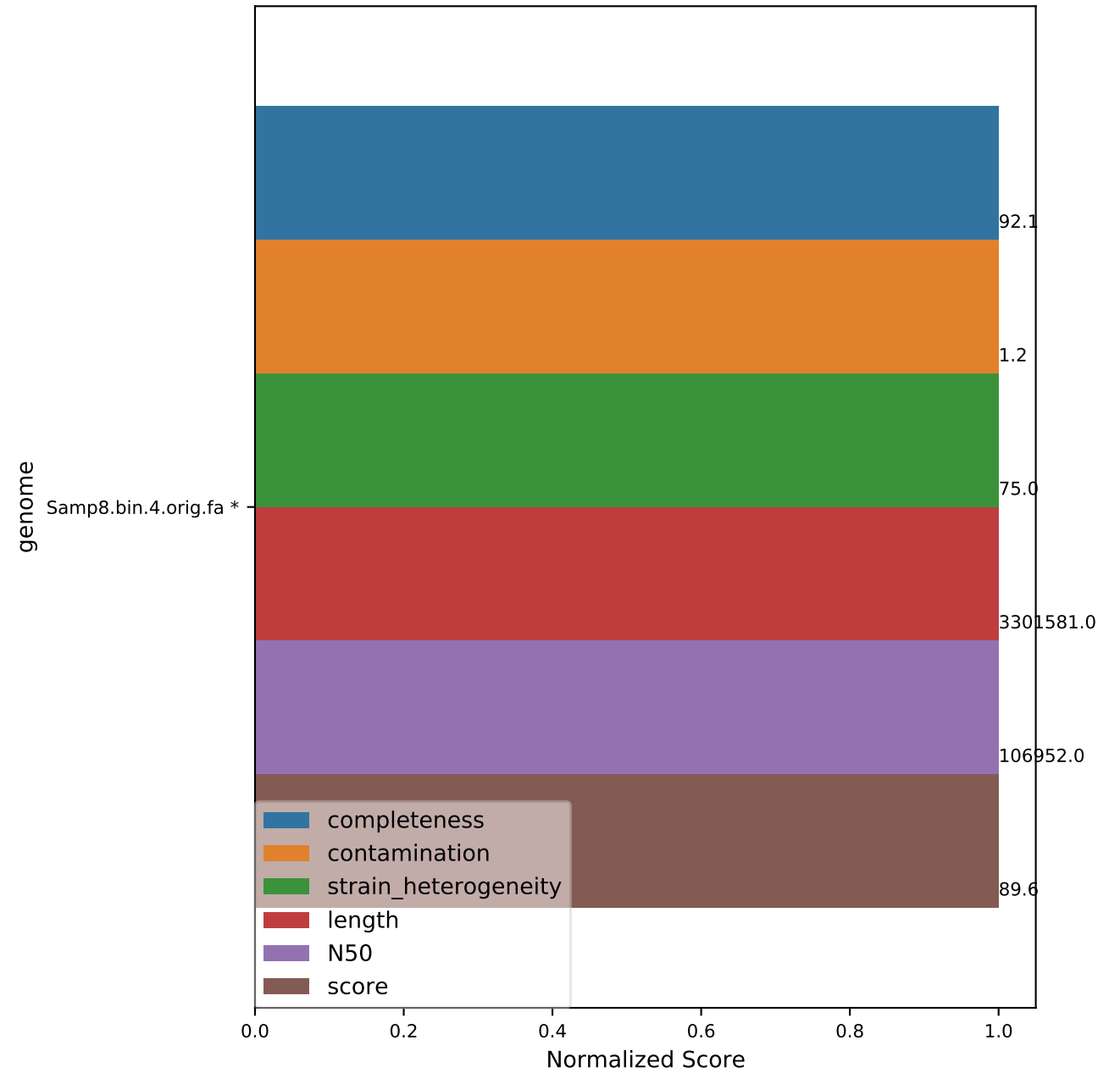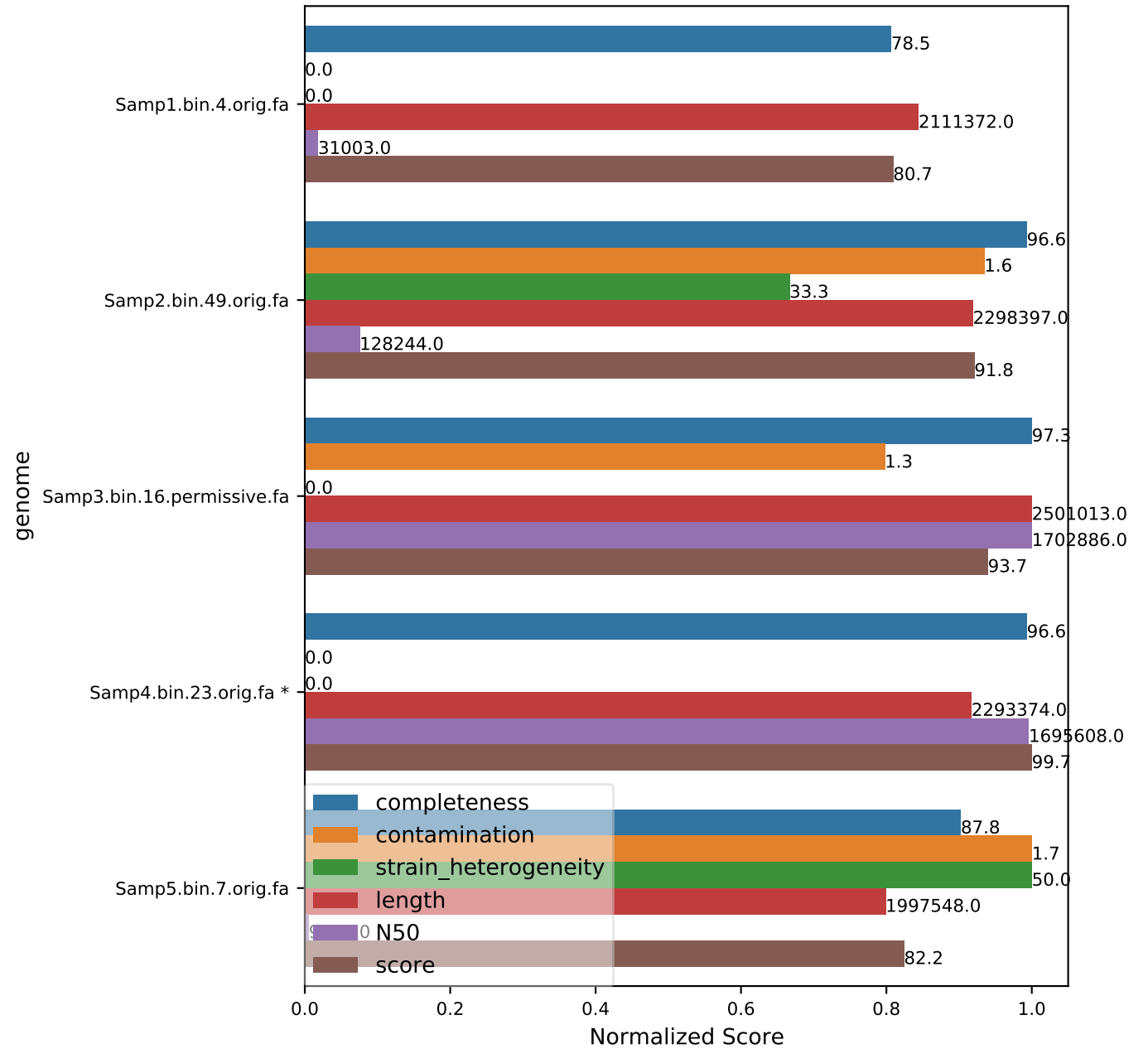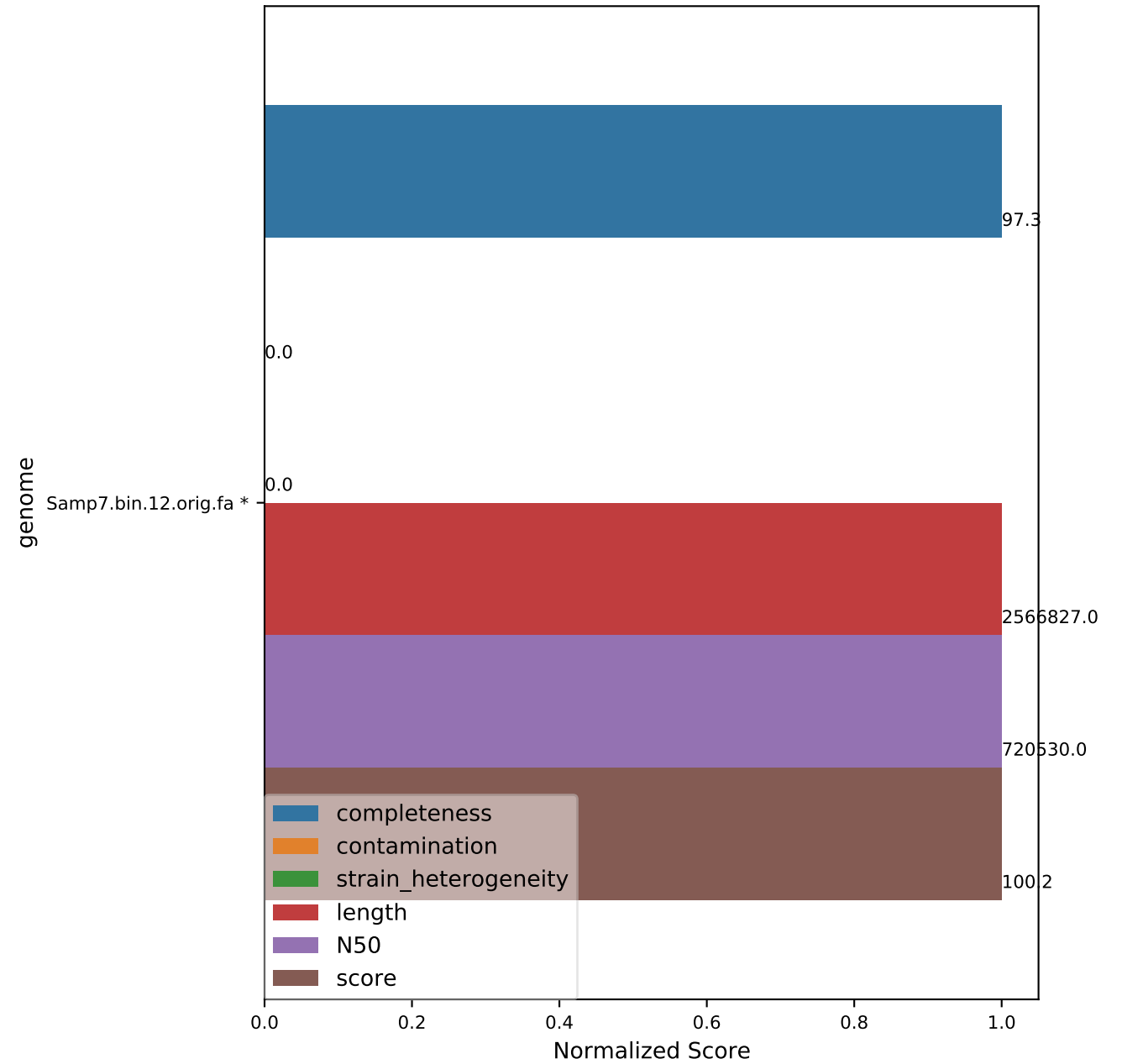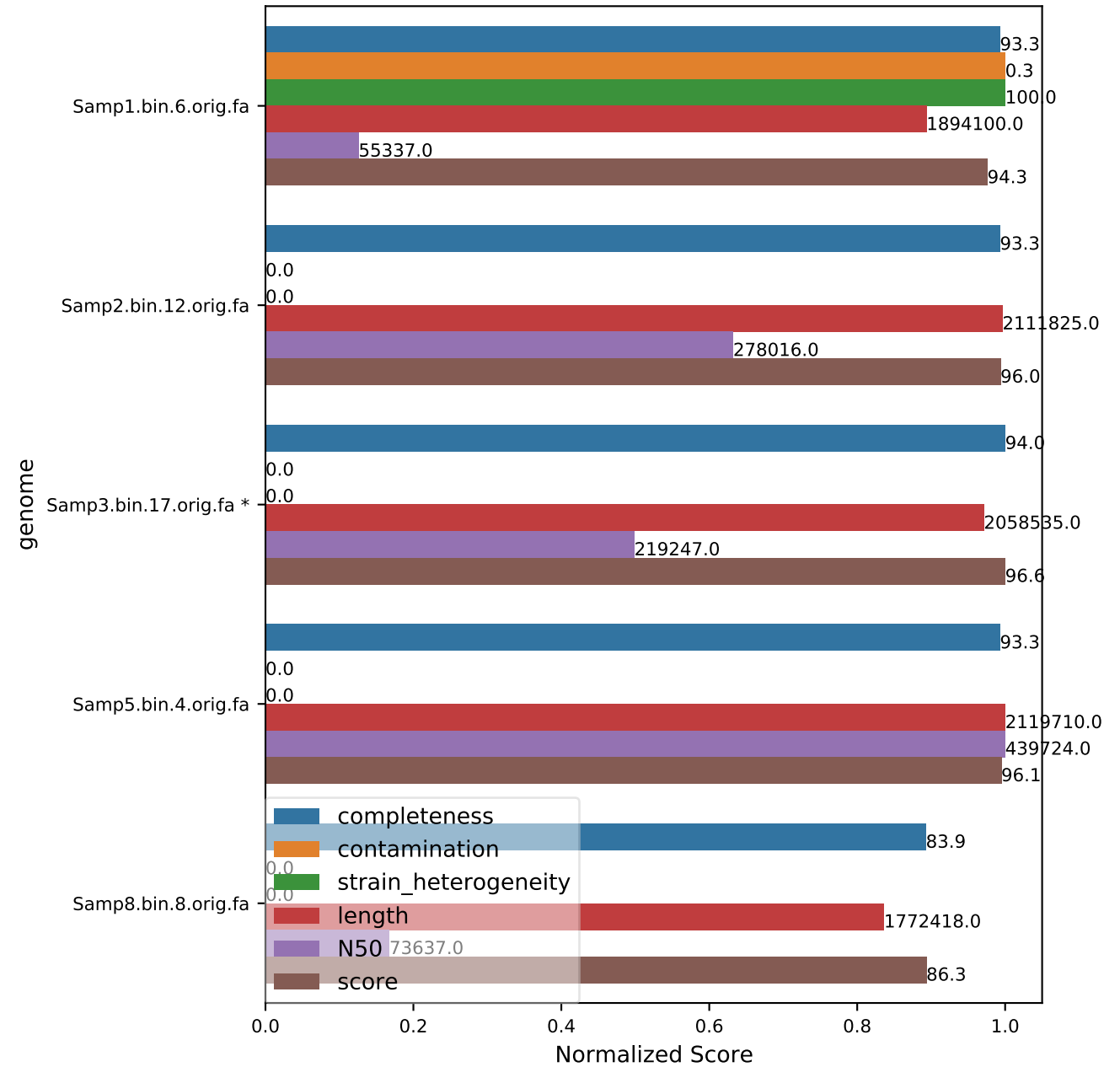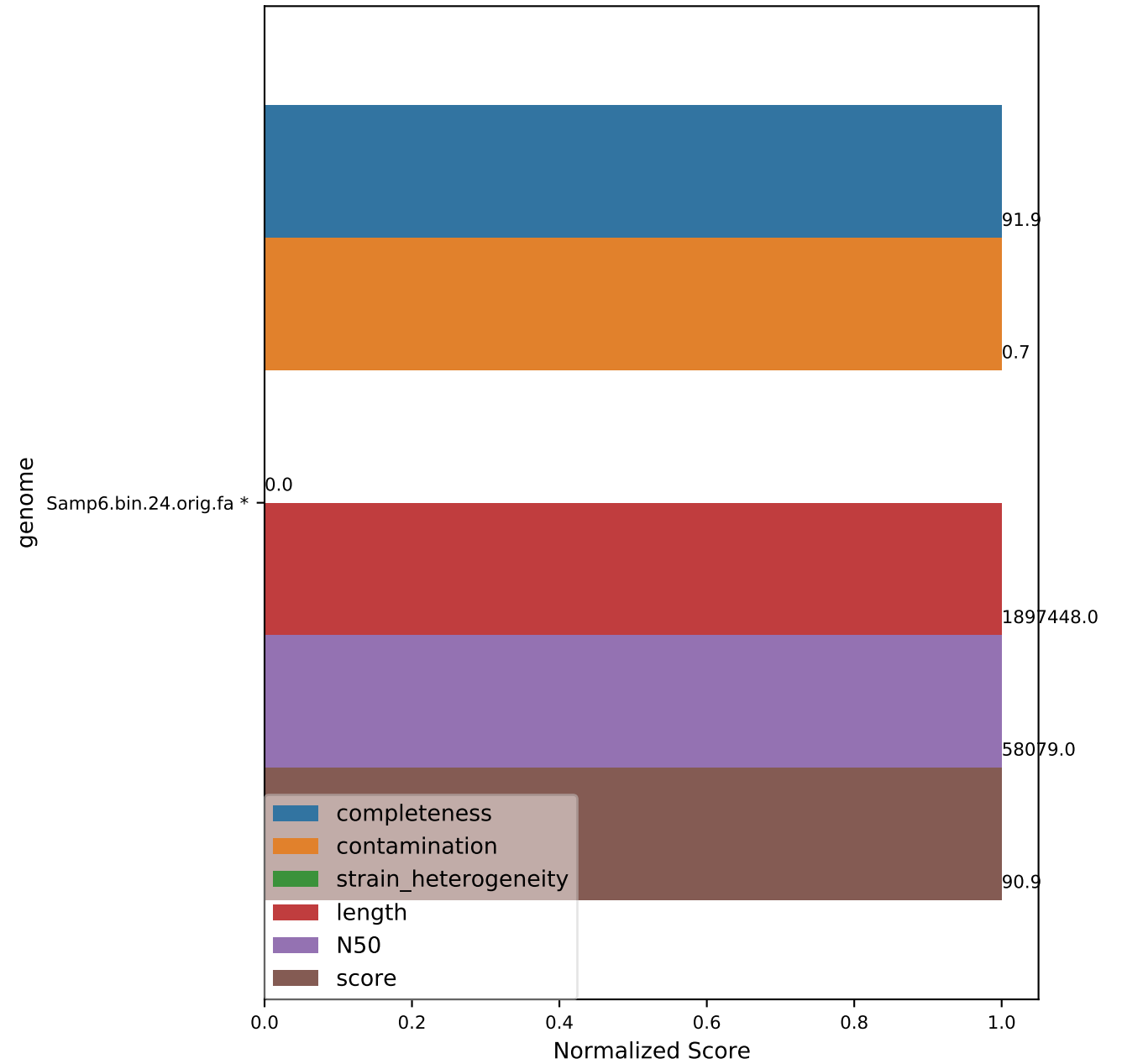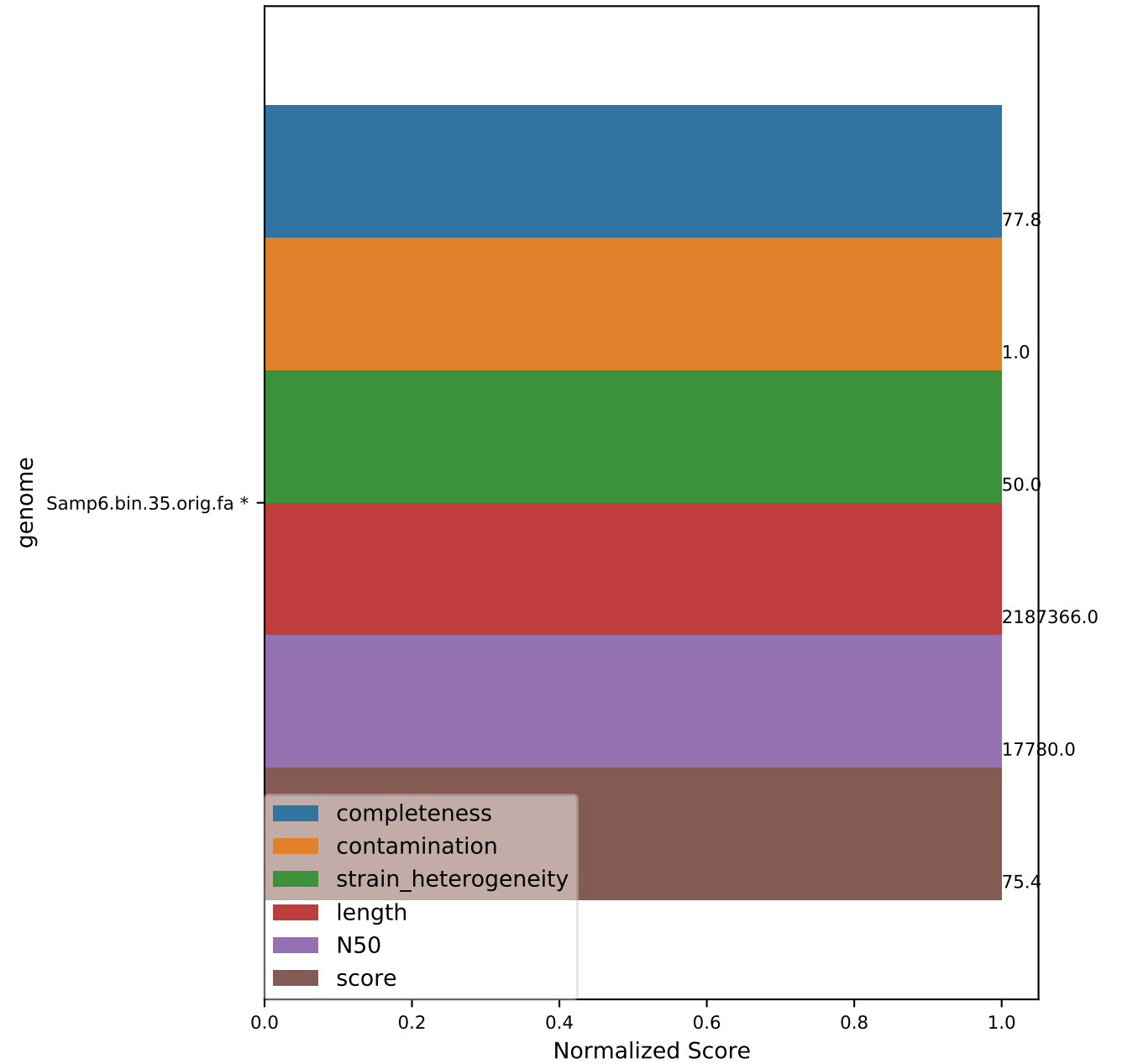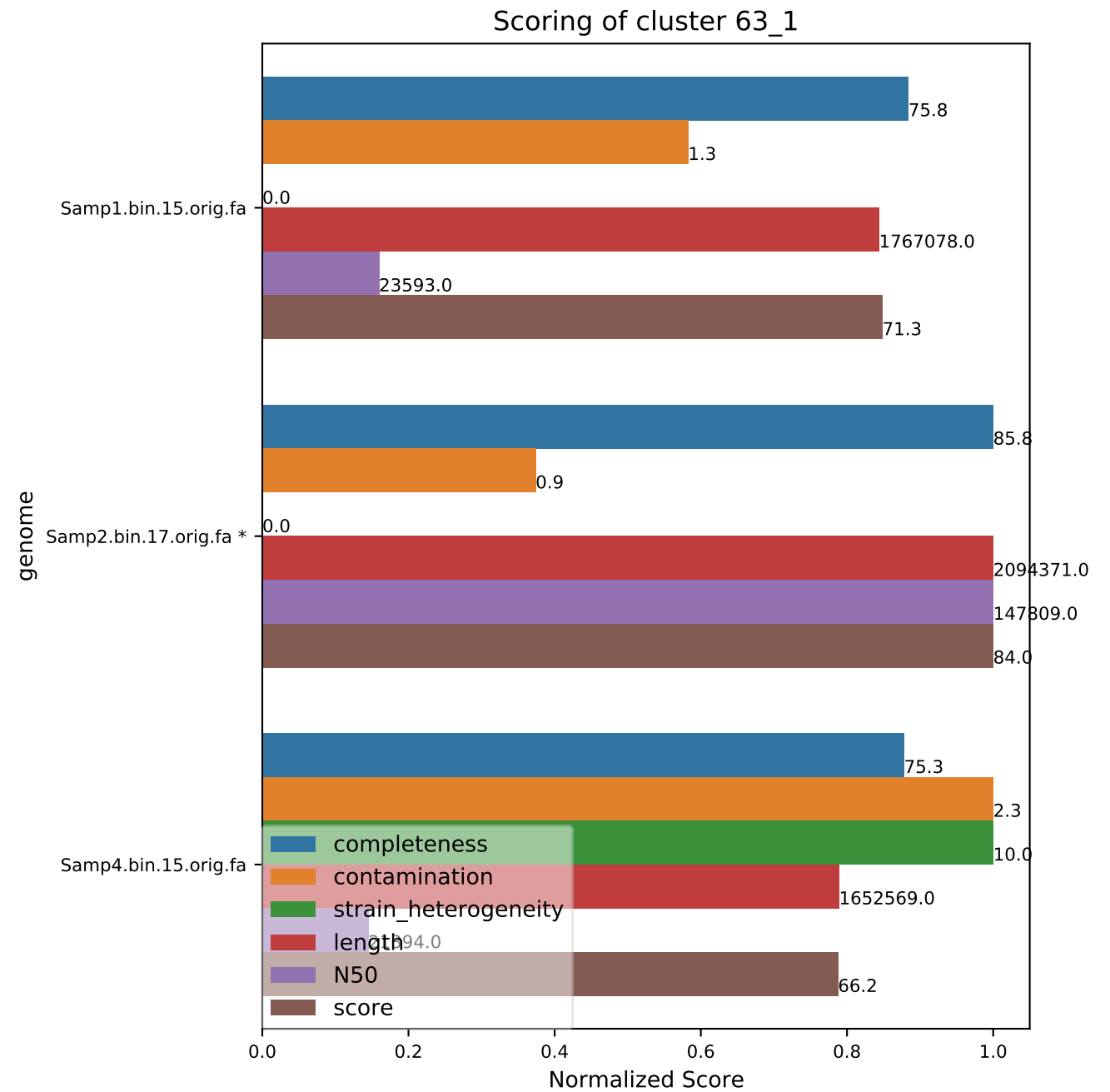
Scoring of cluster 42_0

Scoring of cluster 43_1
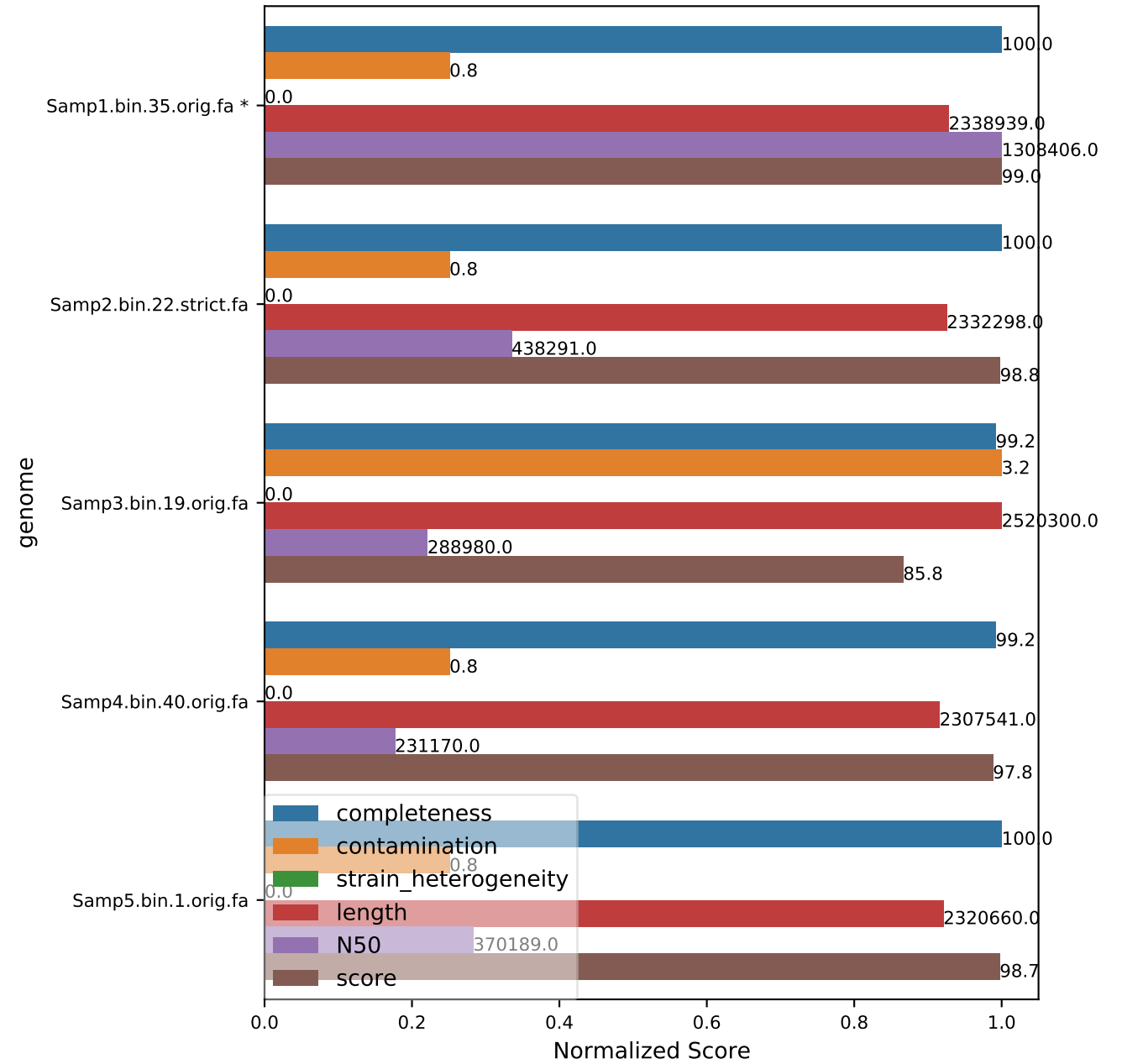
Samp1.bin.35.orig.fa *
- 100.0
- 0.8
- 0.0
- 2338939.0
- 1308406.0
- 99.0

Samp2.bin.22.strict.fa
- 100.0
- 0.8
- 0.0
- 2332298.0
- 438291.0
- 98.8

Samp3.bin.19.orig.fa
- 99.2
- 3.2
- 0.0
- 2520300.0
- 288980.0
- 85.8

Samp4.bin.40.orig.fa
- 99.2
- 0.8
- 0.0
- 2307541.0
- 231170.0
- 97.8

Samp5.bin.1.orig.fa
- 100.0
- 0.8
- 0.0
- 2320660.0
- 370189.0
- 98.7

Legend:
- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

genome / Normalized Score
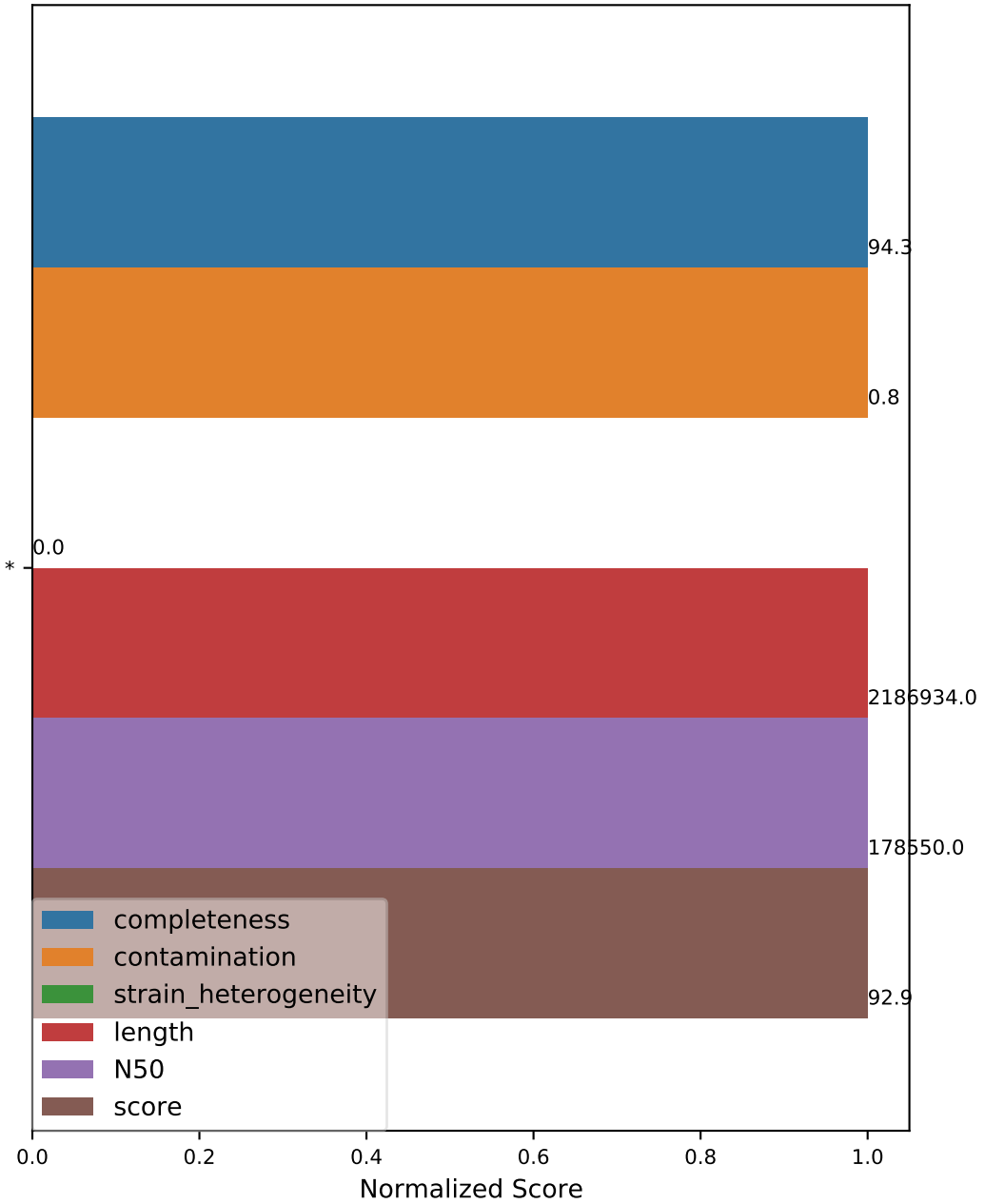
Scoring of cluster 43_2

Scoring of cluster 43_3
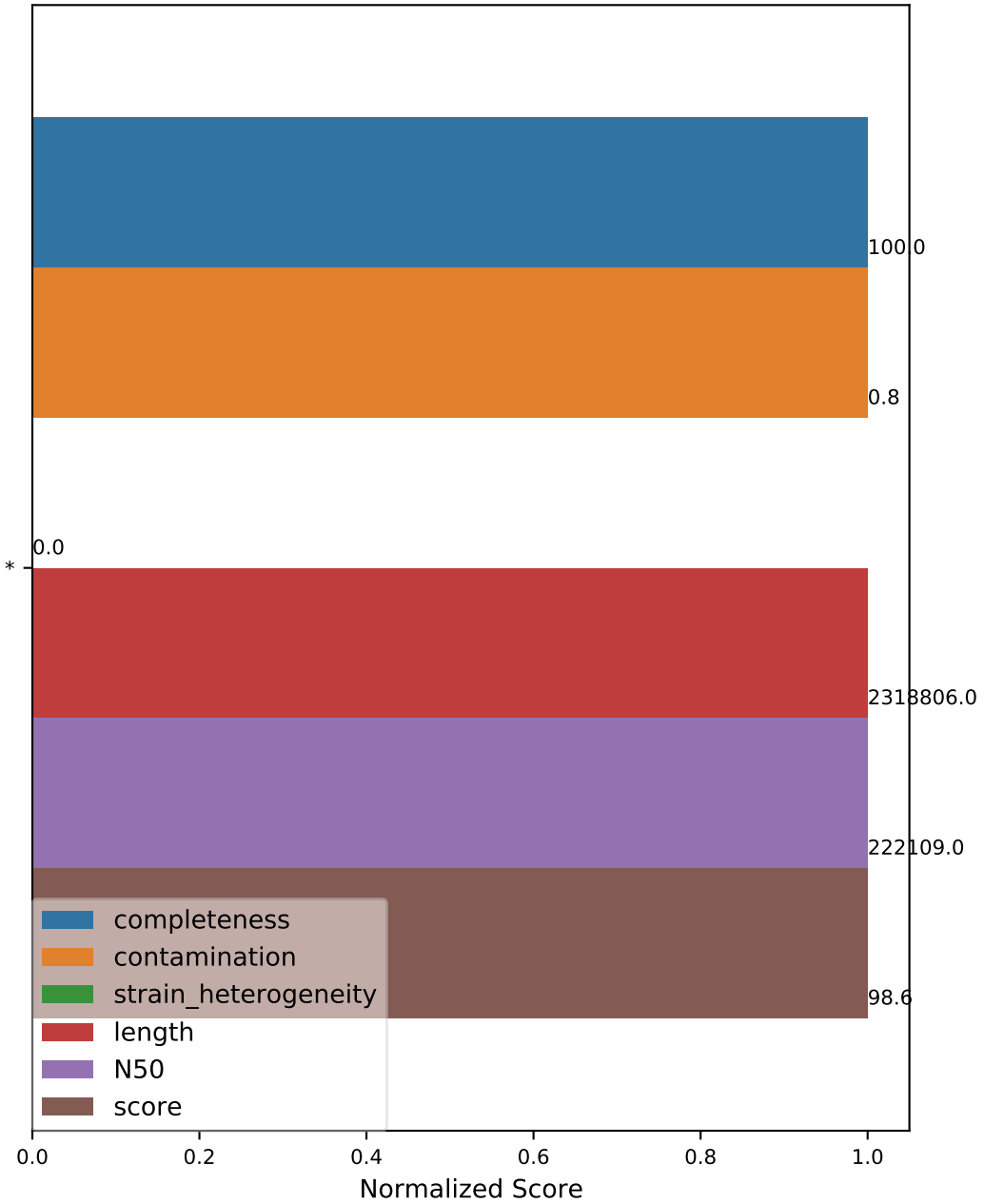
Scoring of cluster 43_4
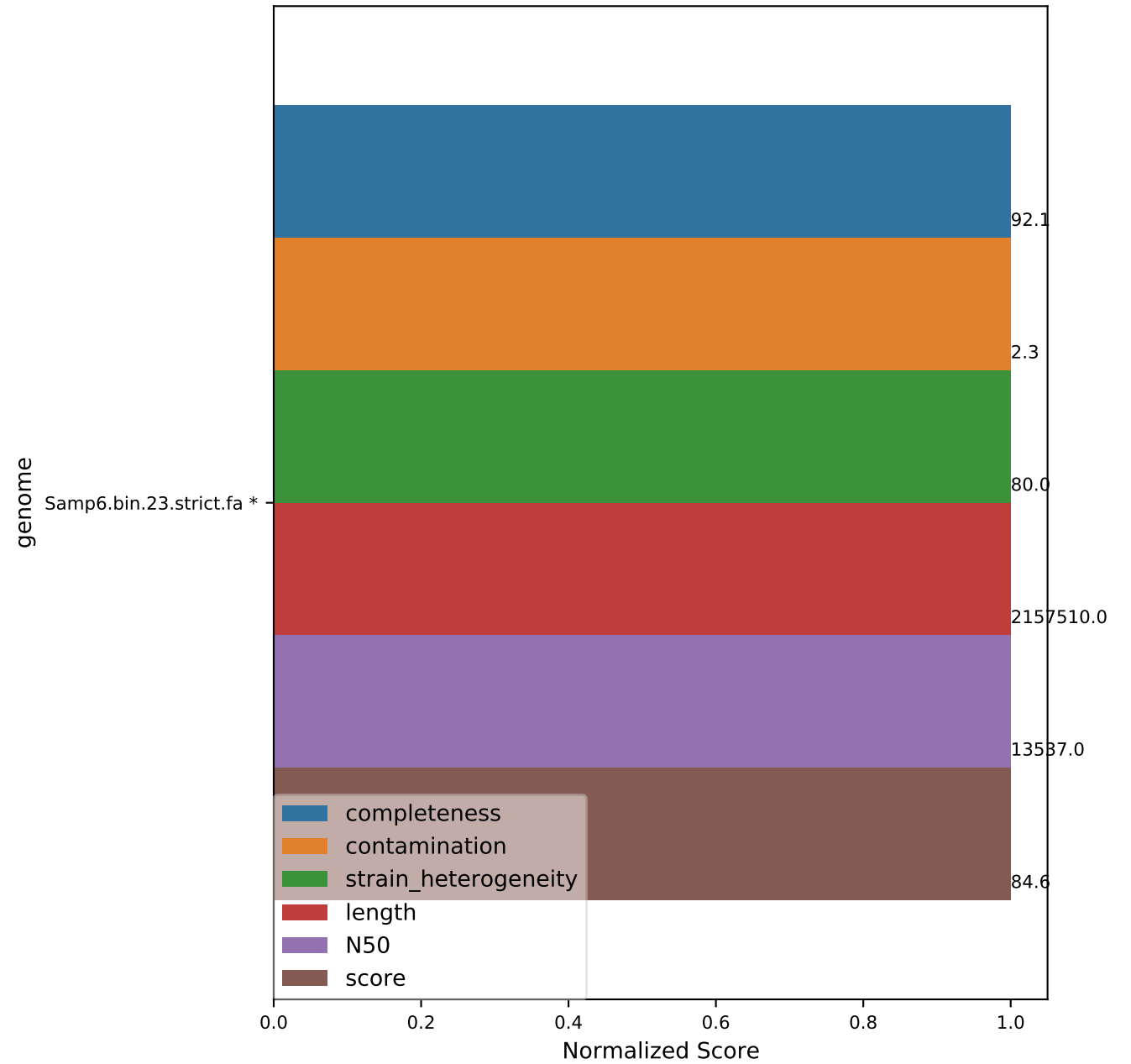
Scoring of cluster 43_5
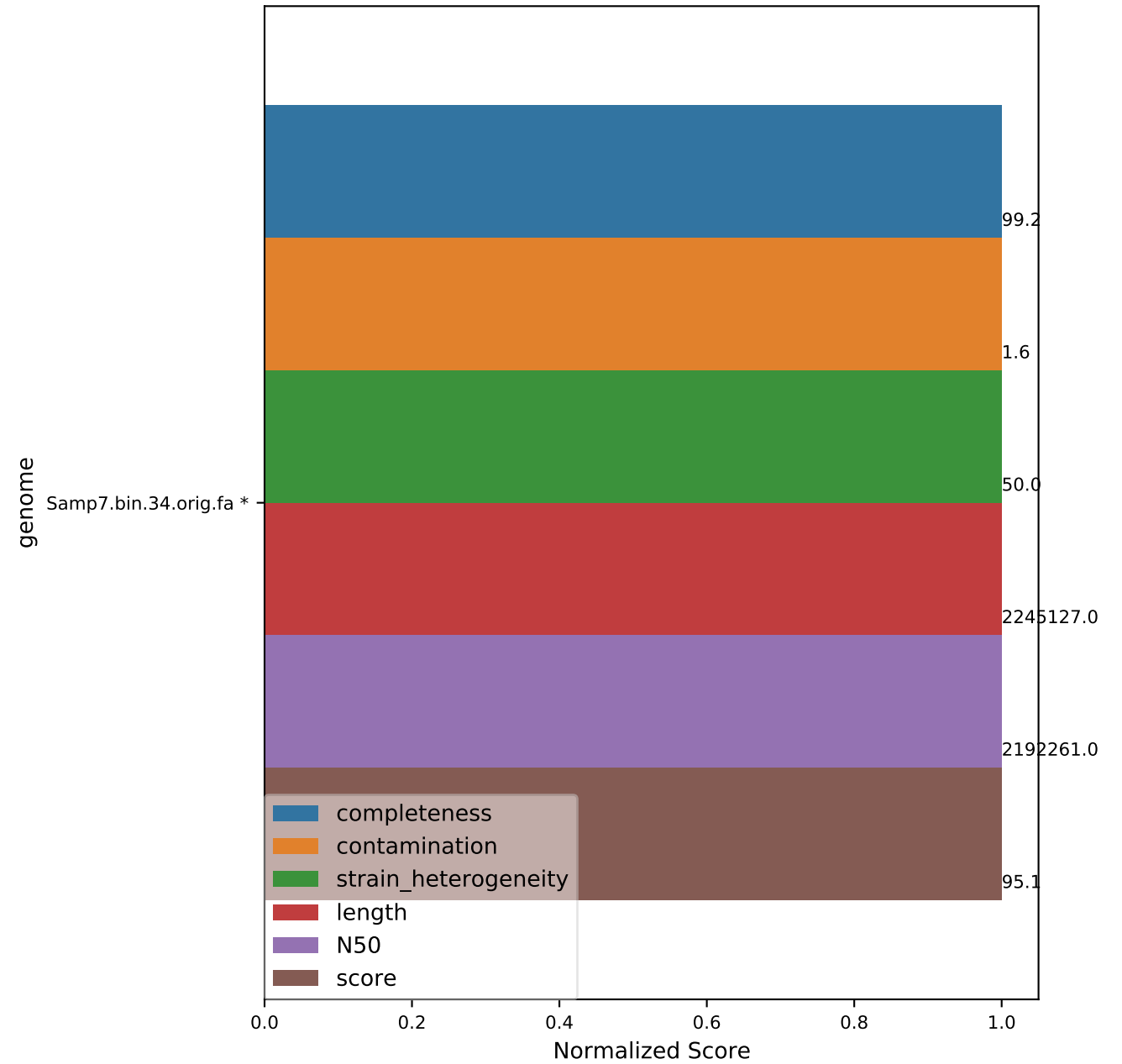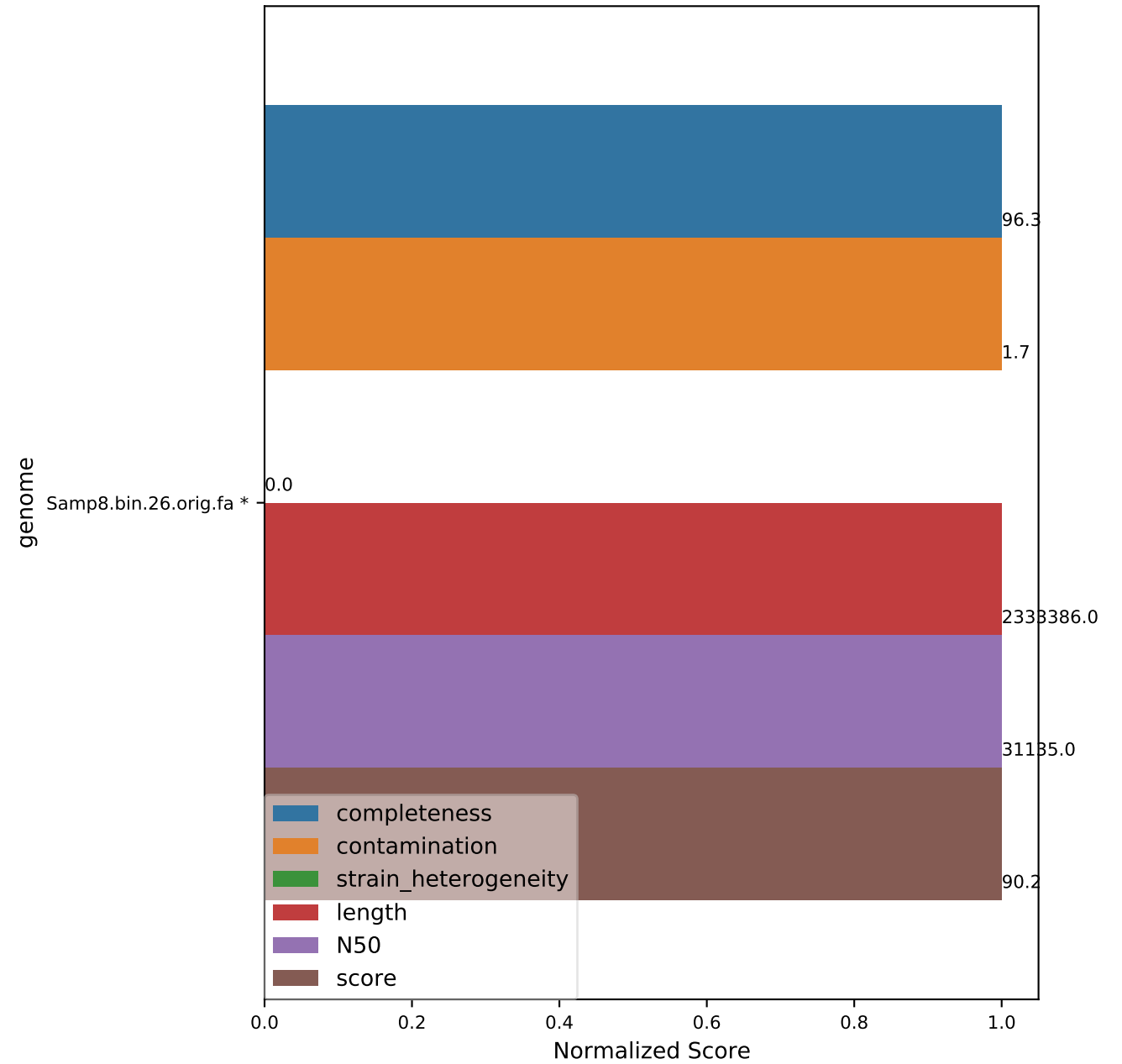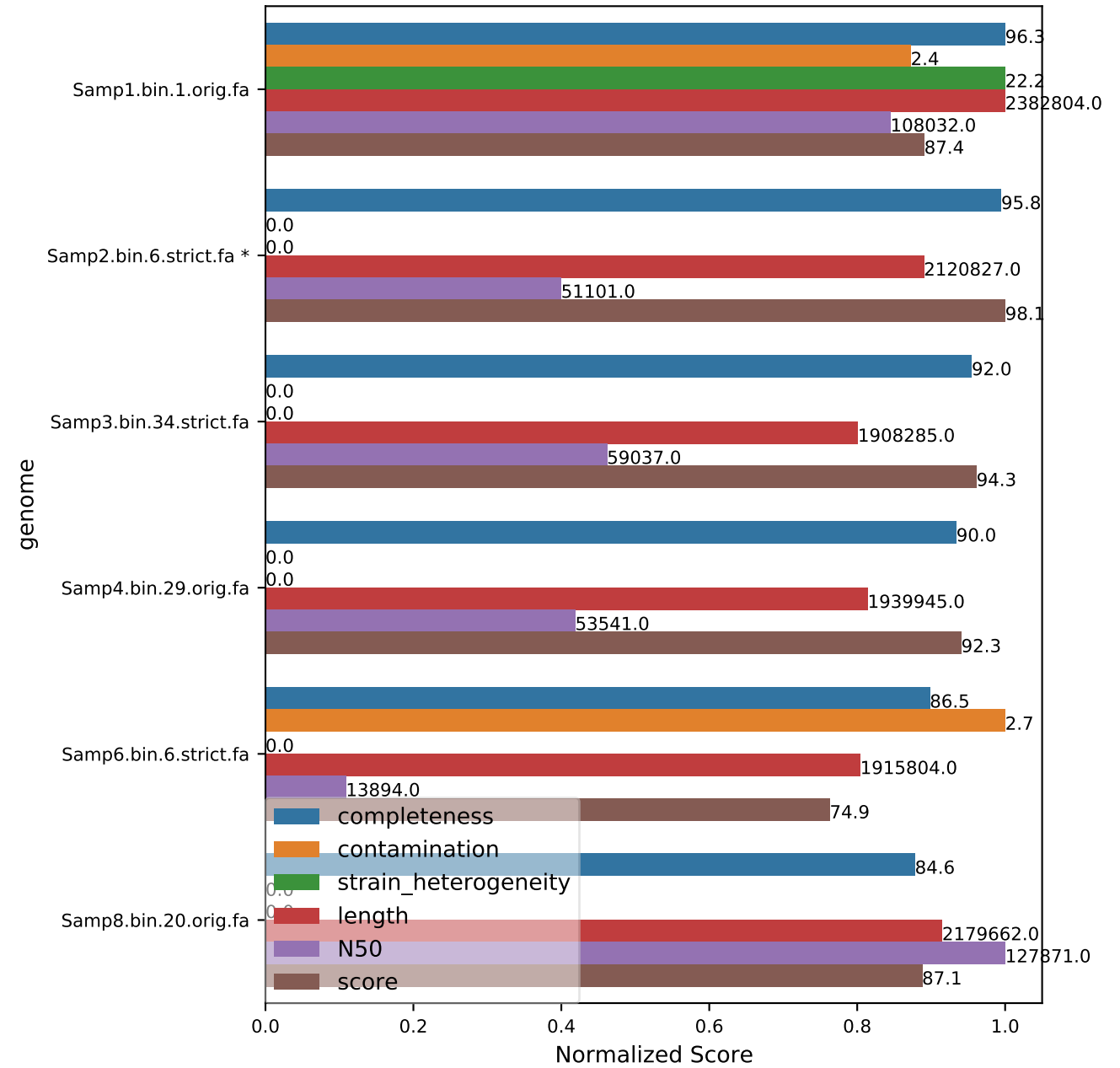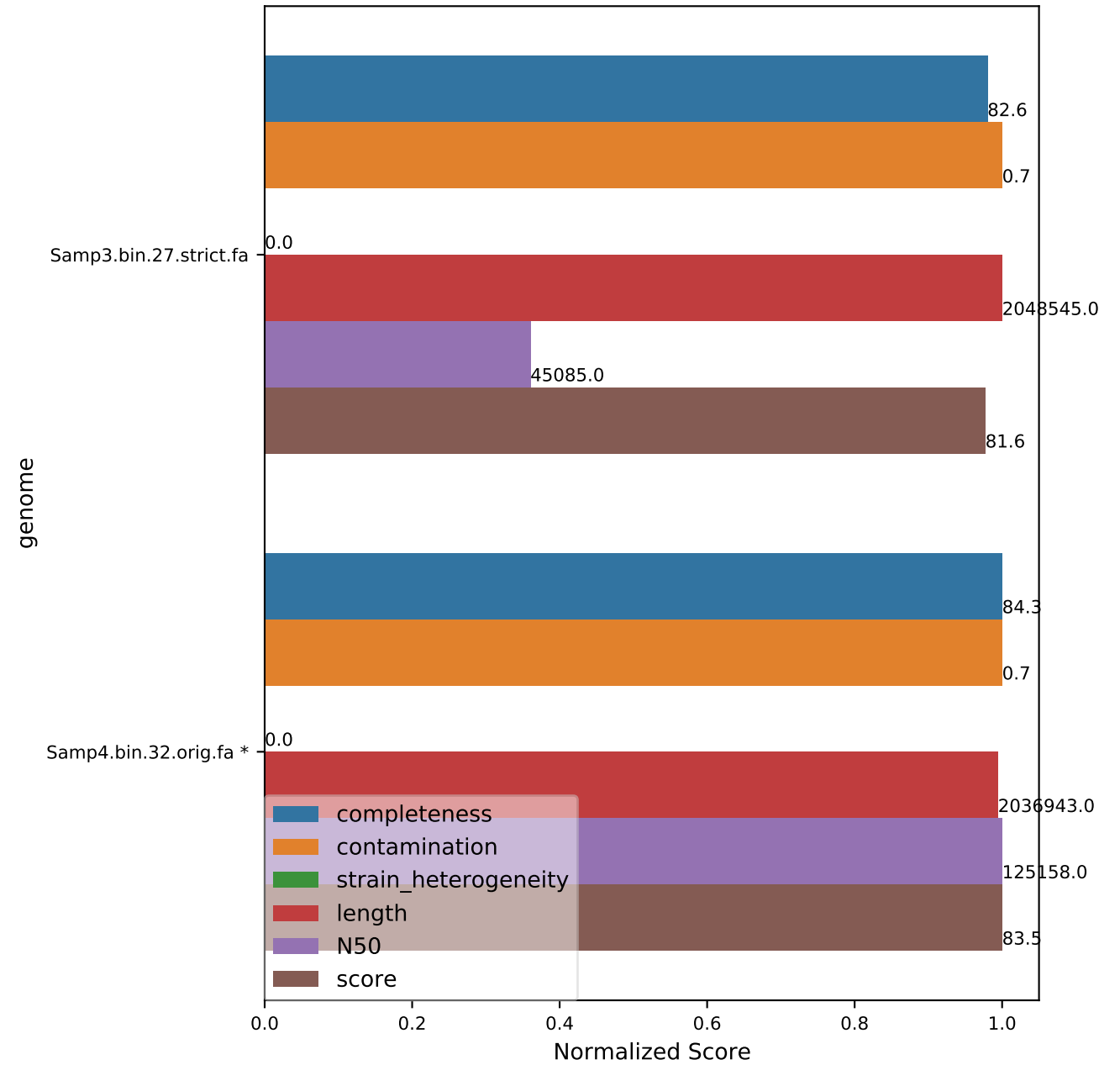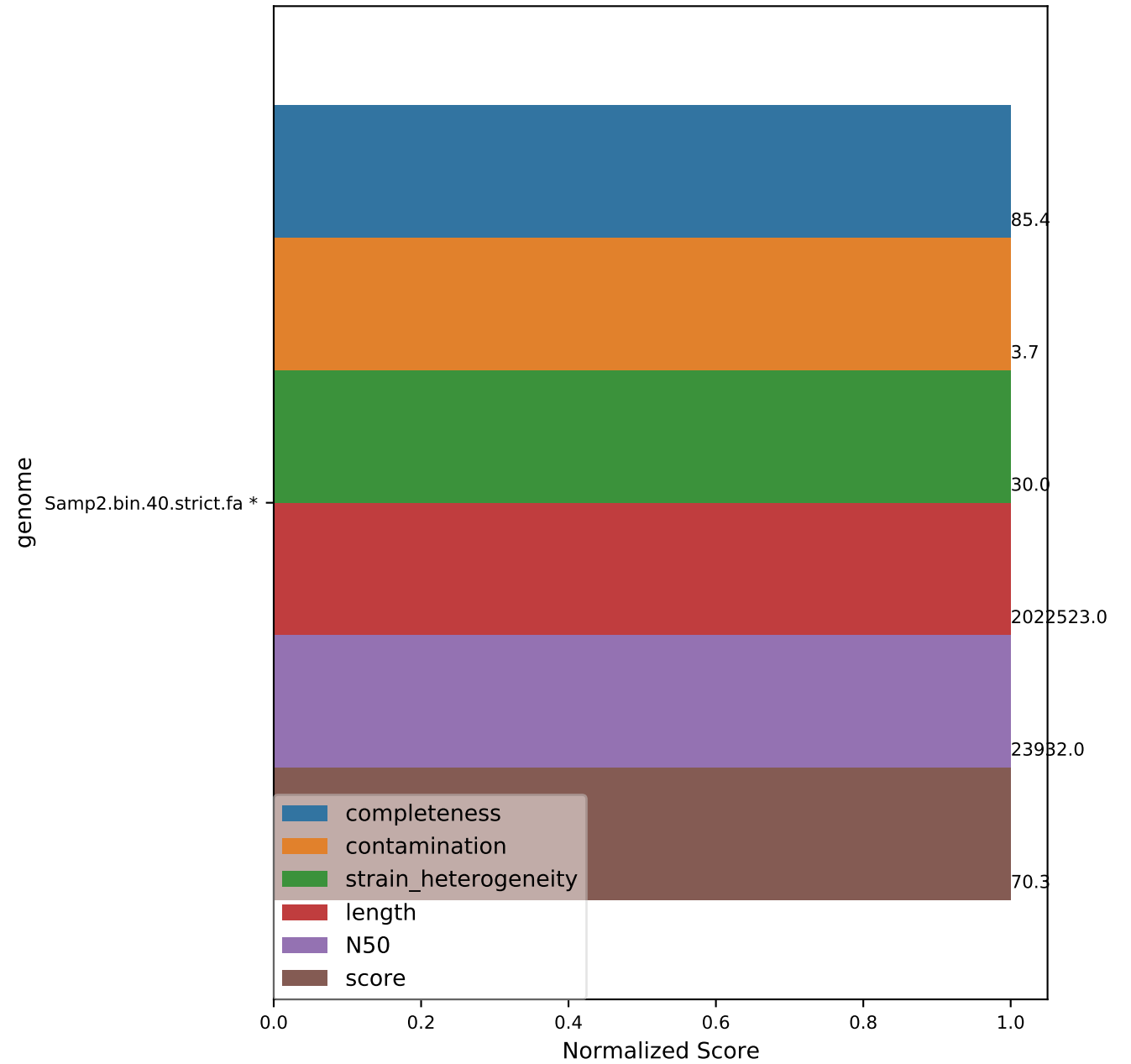
Scoring of cluster 44_1
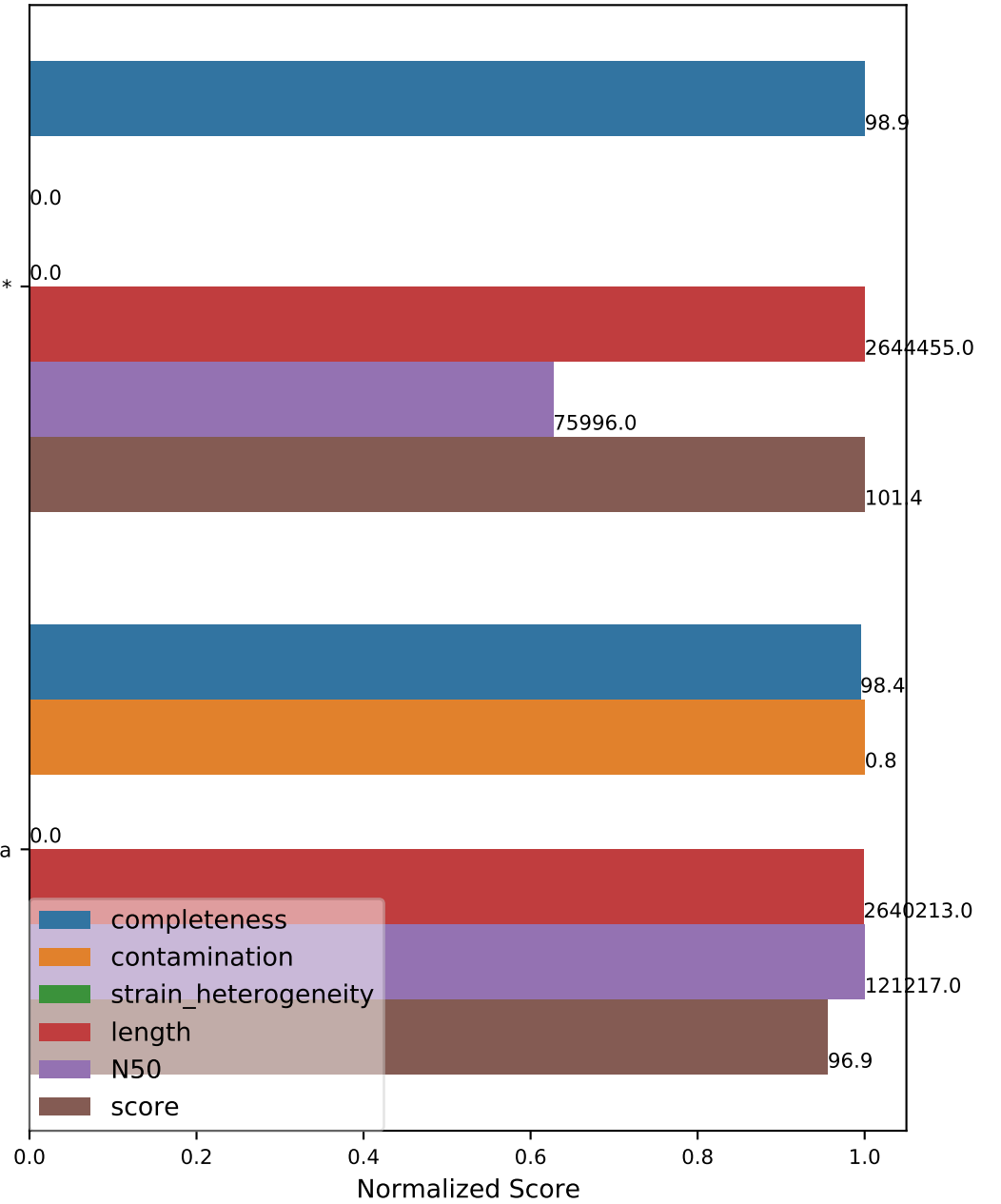
Scoring of cluster 45_1
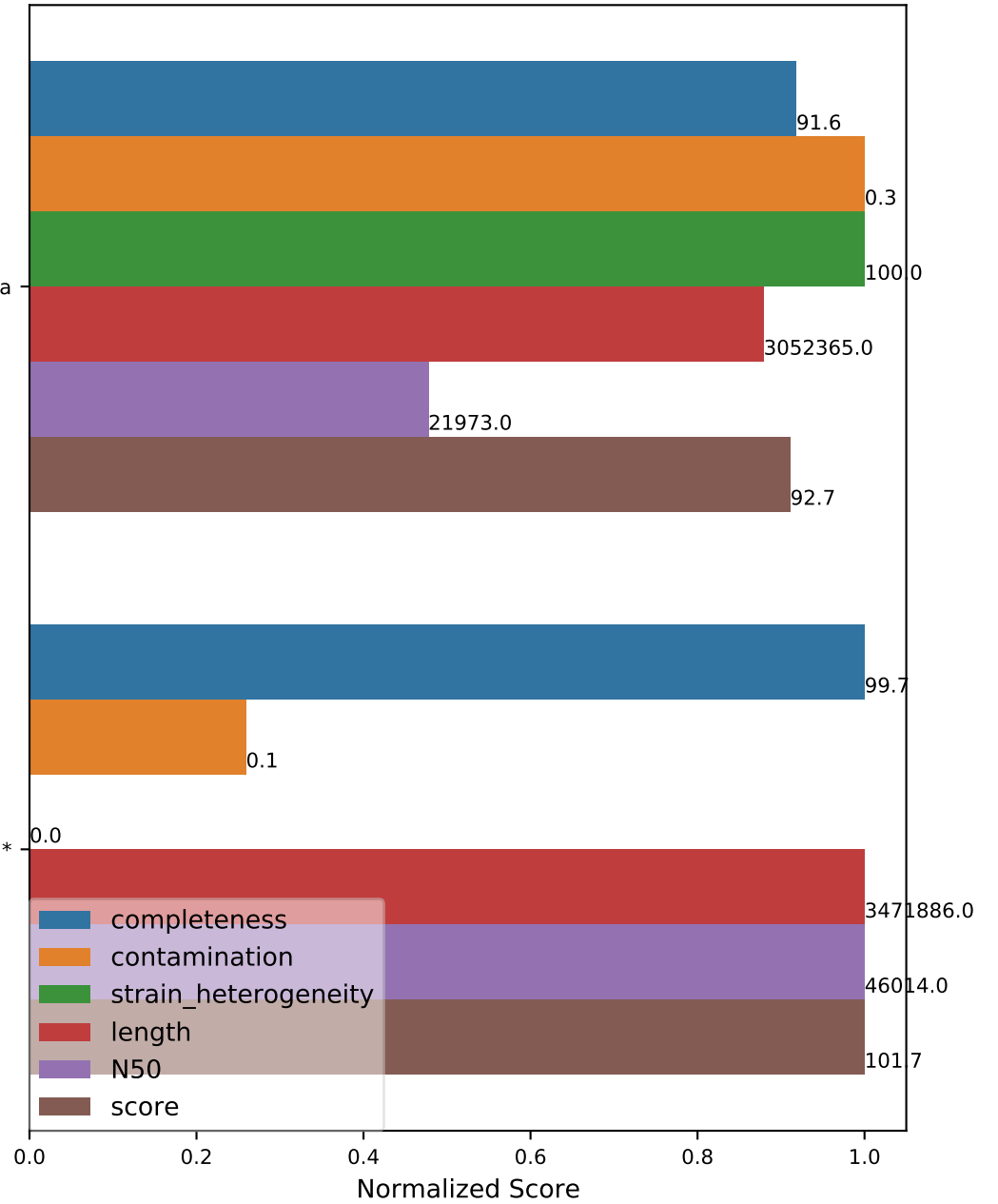
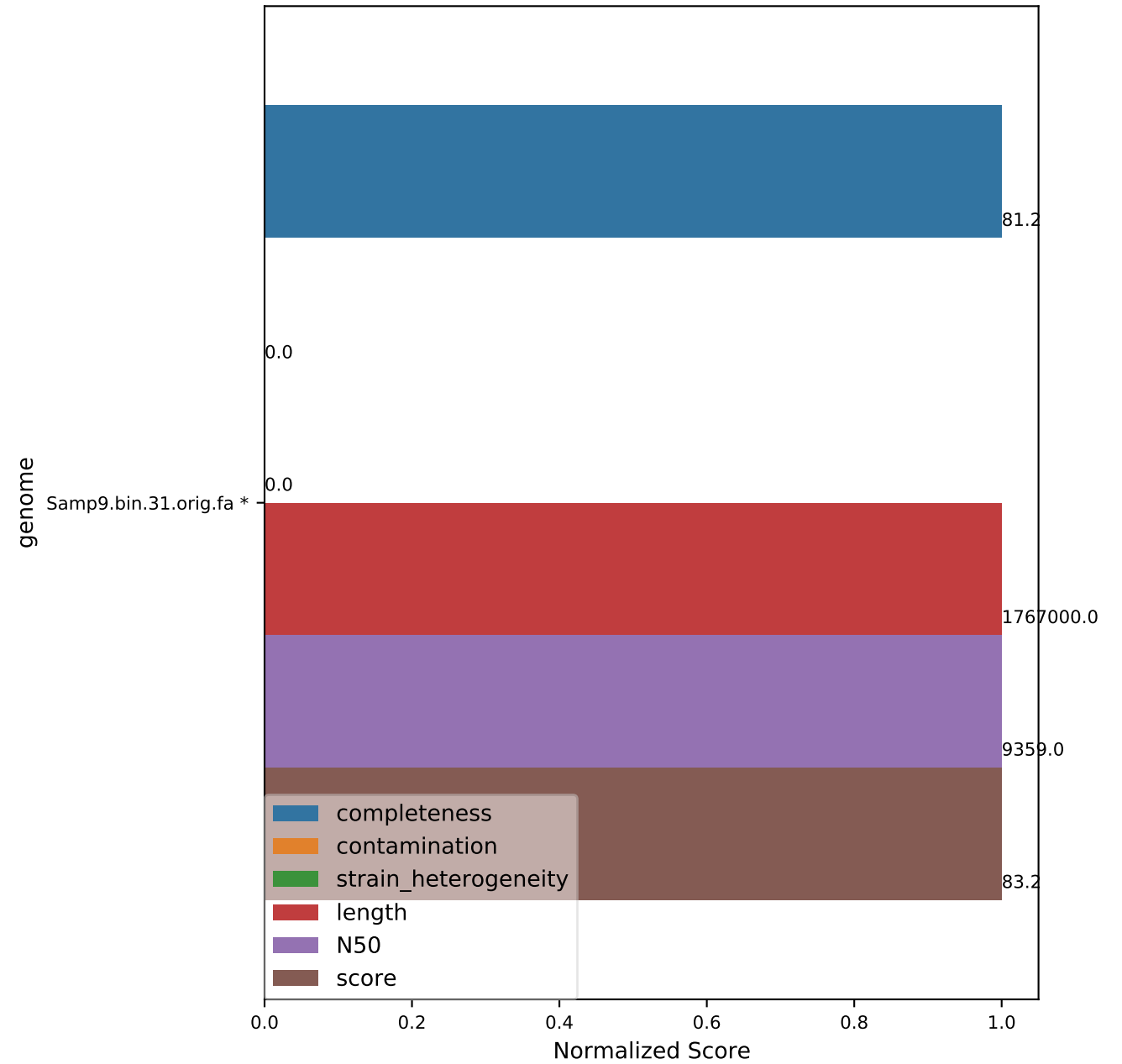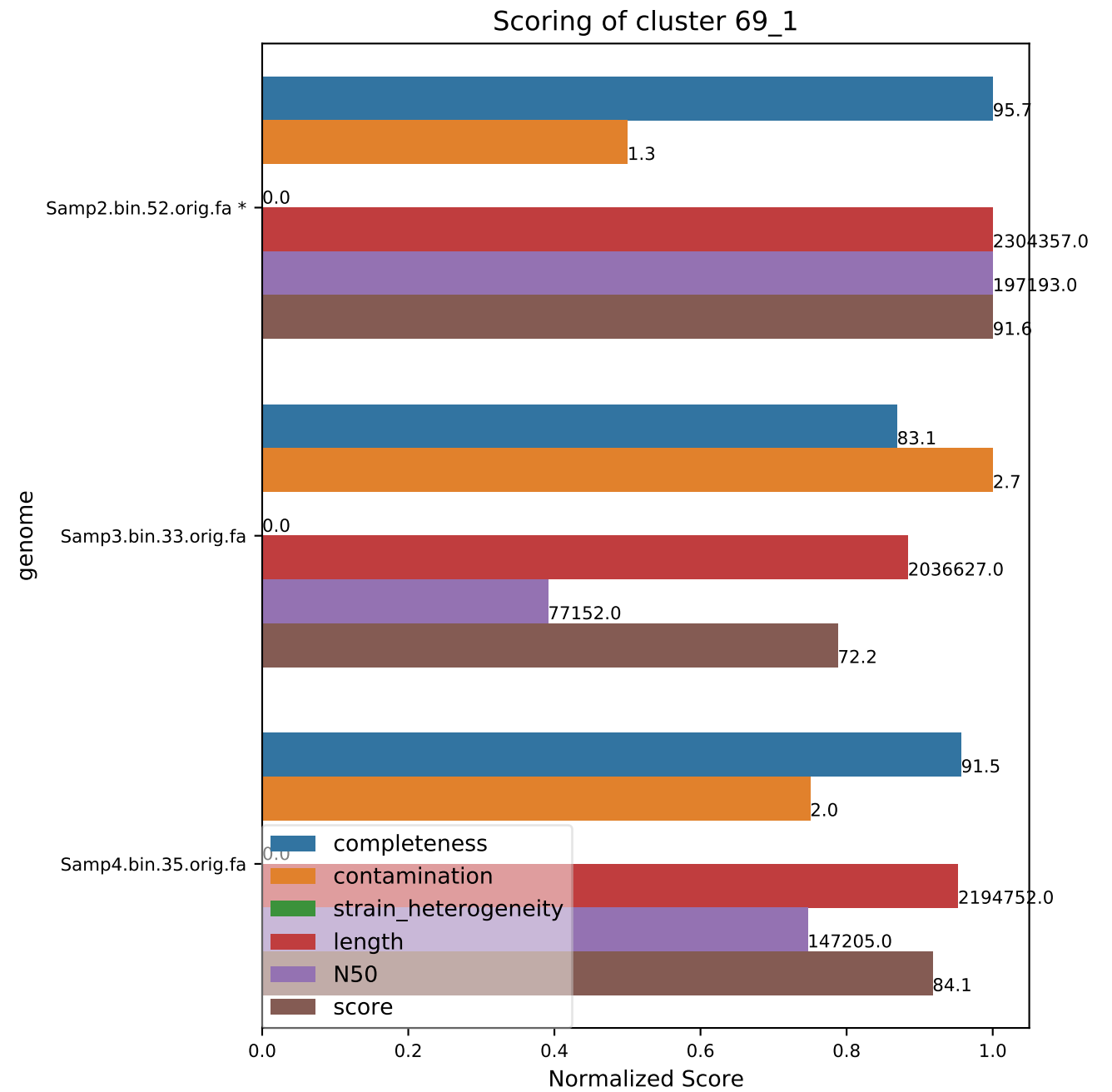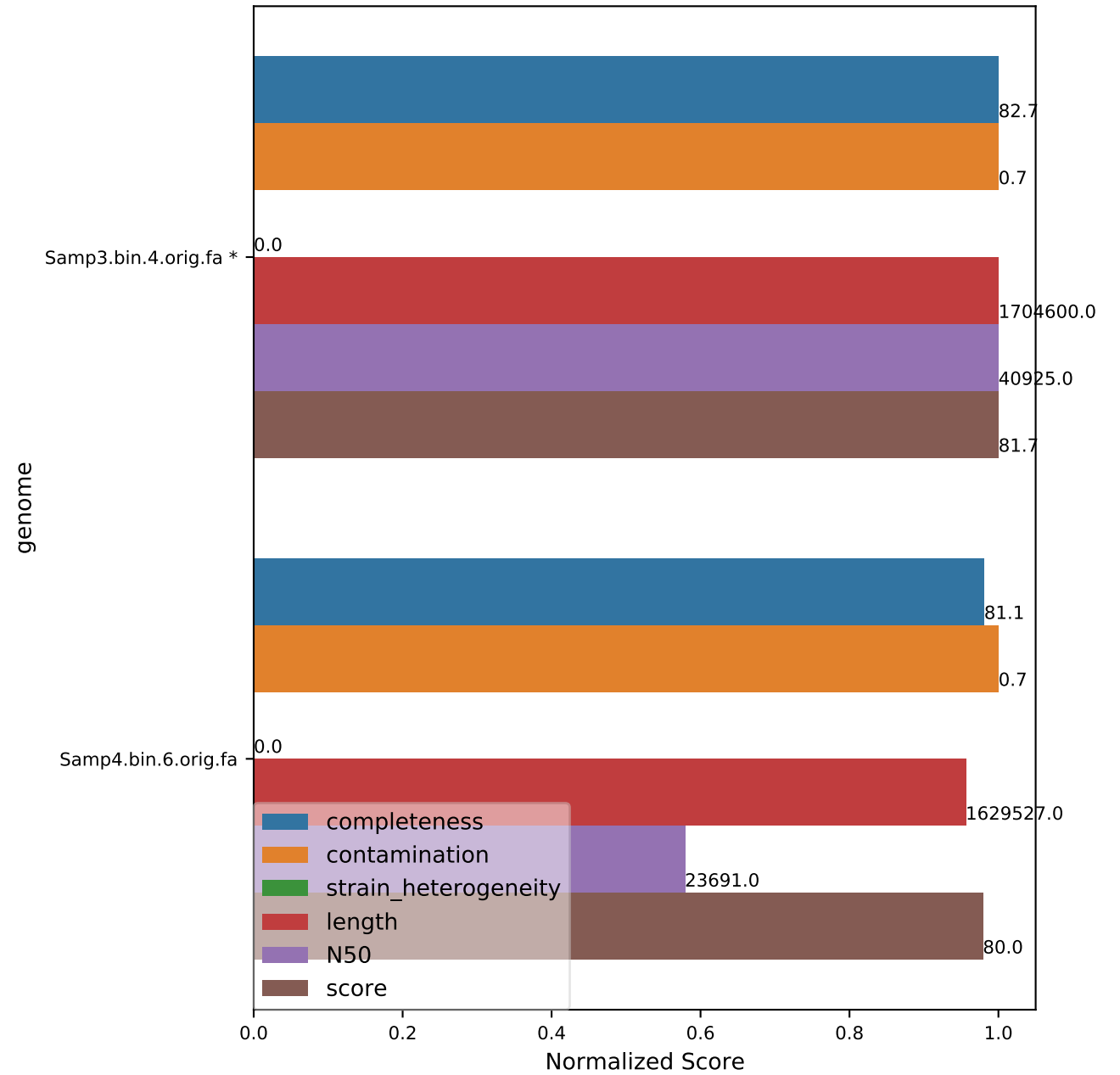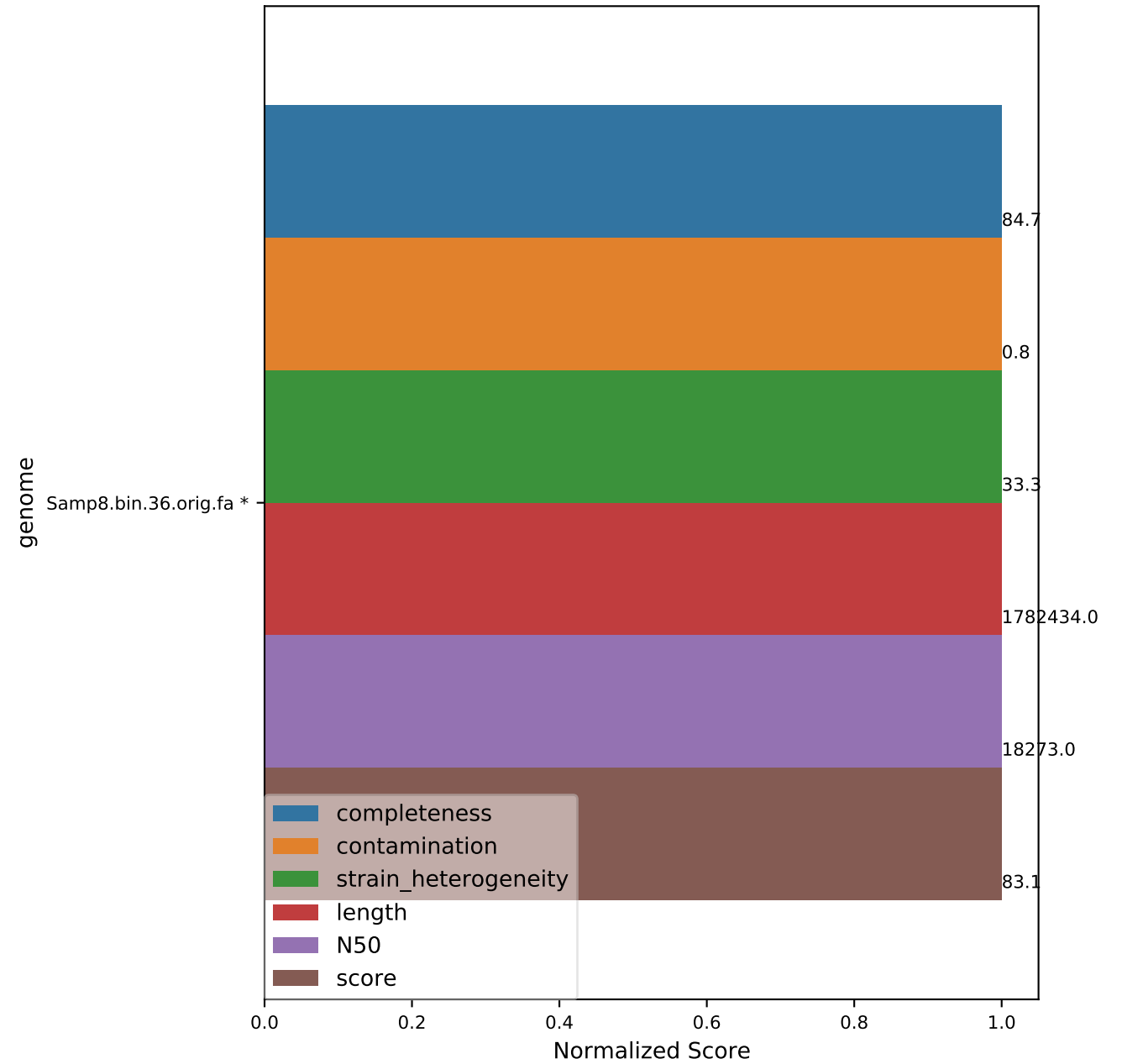Scoring of cluster 46_0
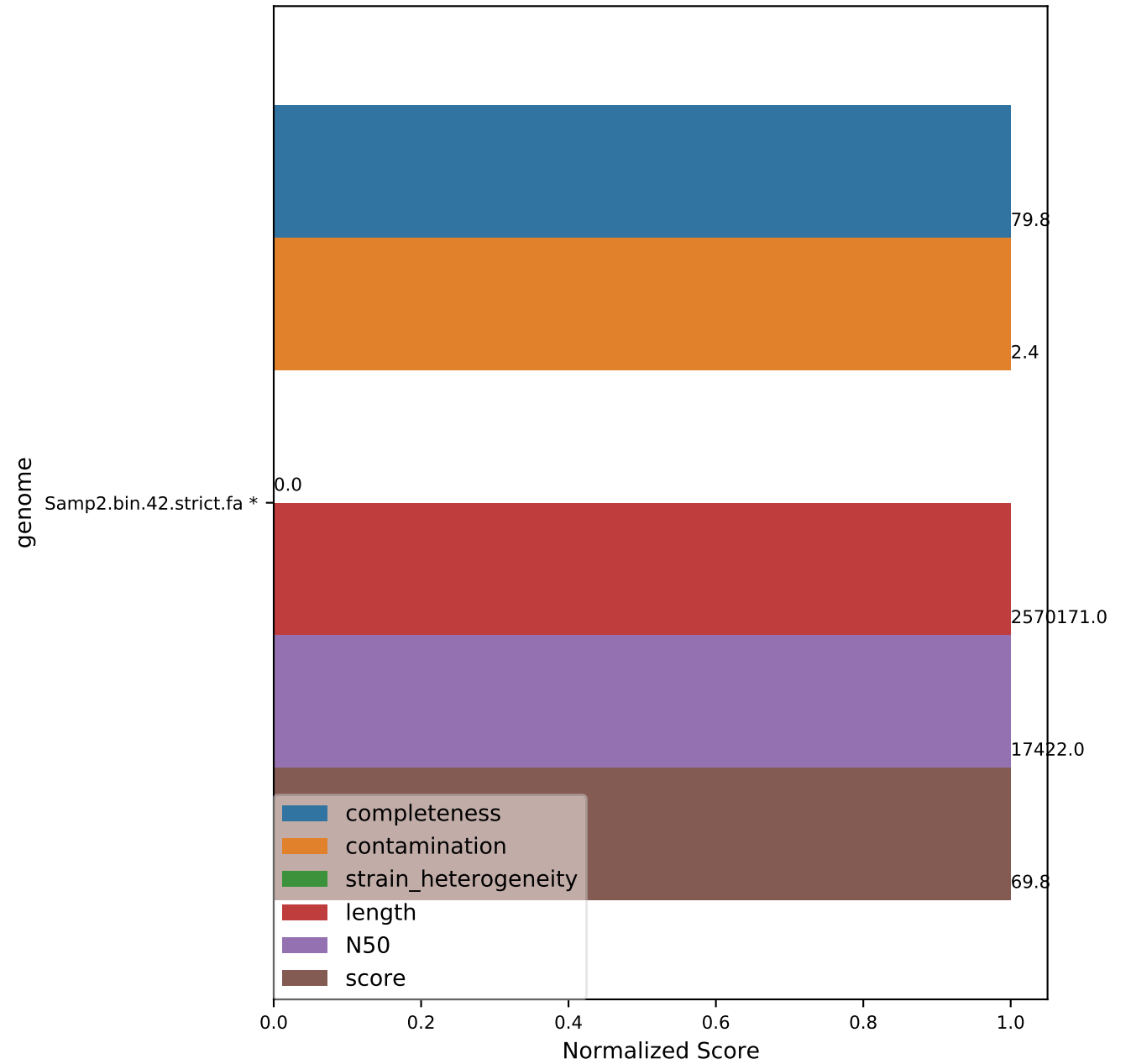
Scoring of cluster 47_0
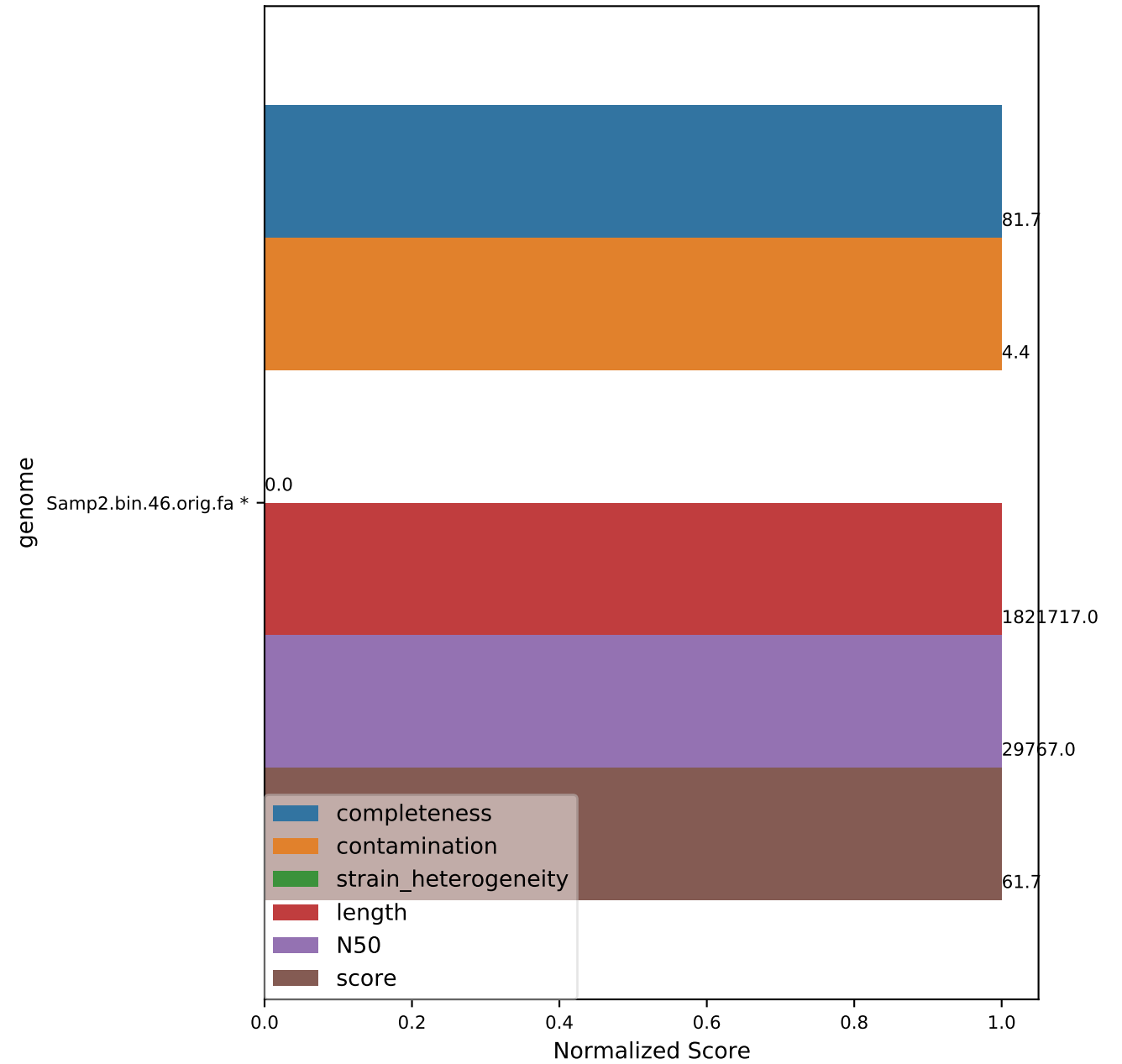
Scoring of cluster 48_1
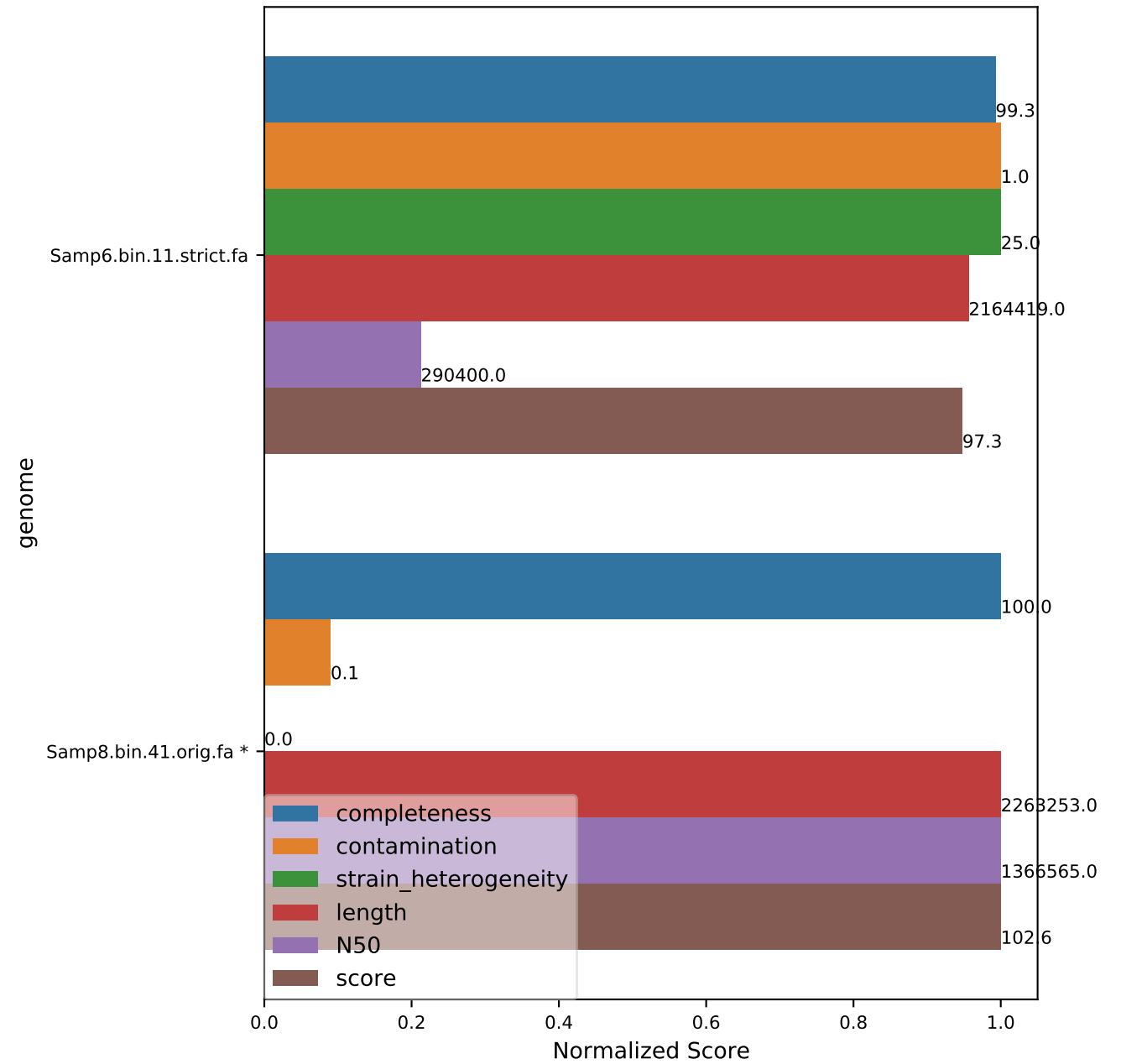
Scoring of cluster 49_1

Scoring of cluster 50_1
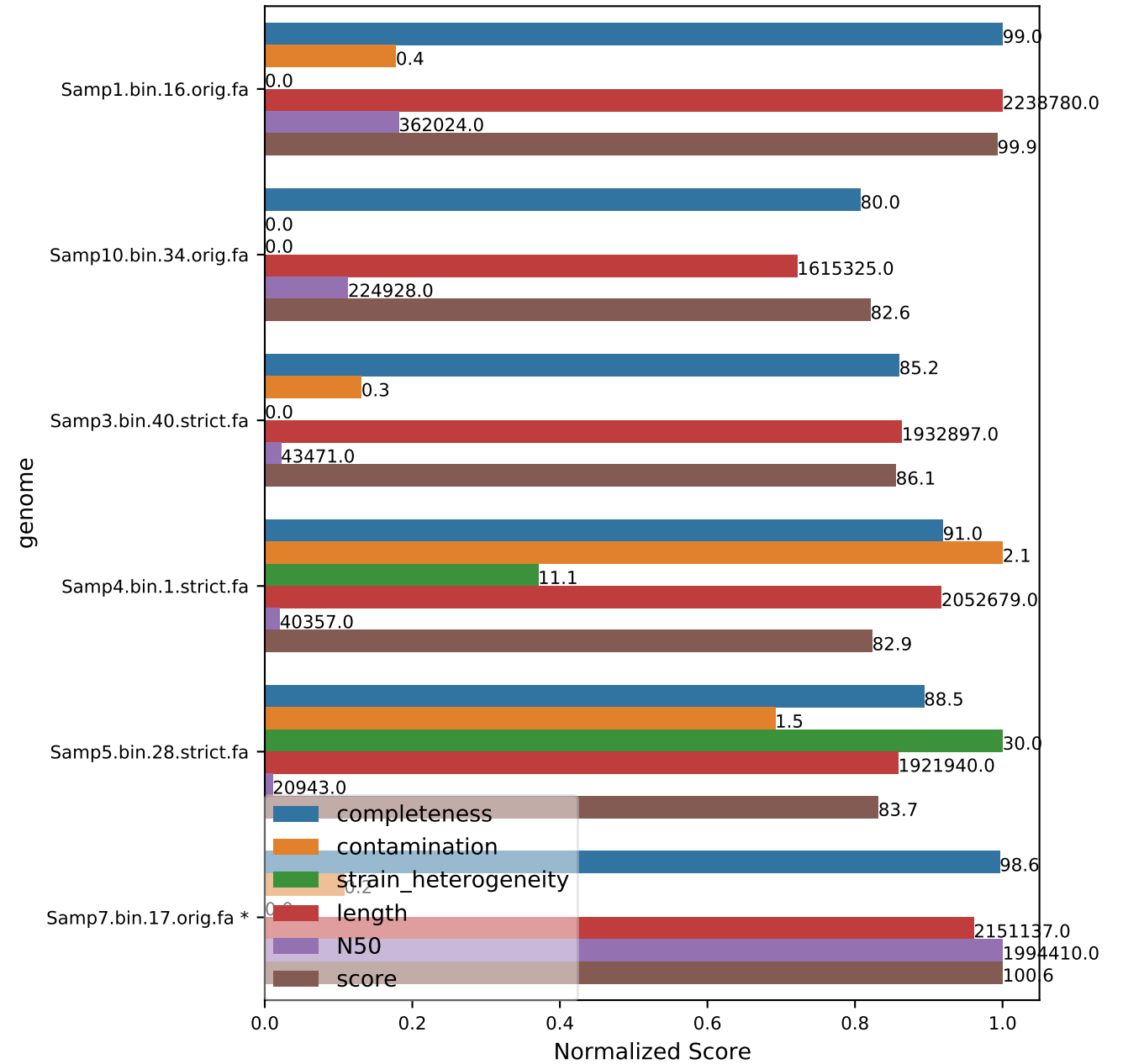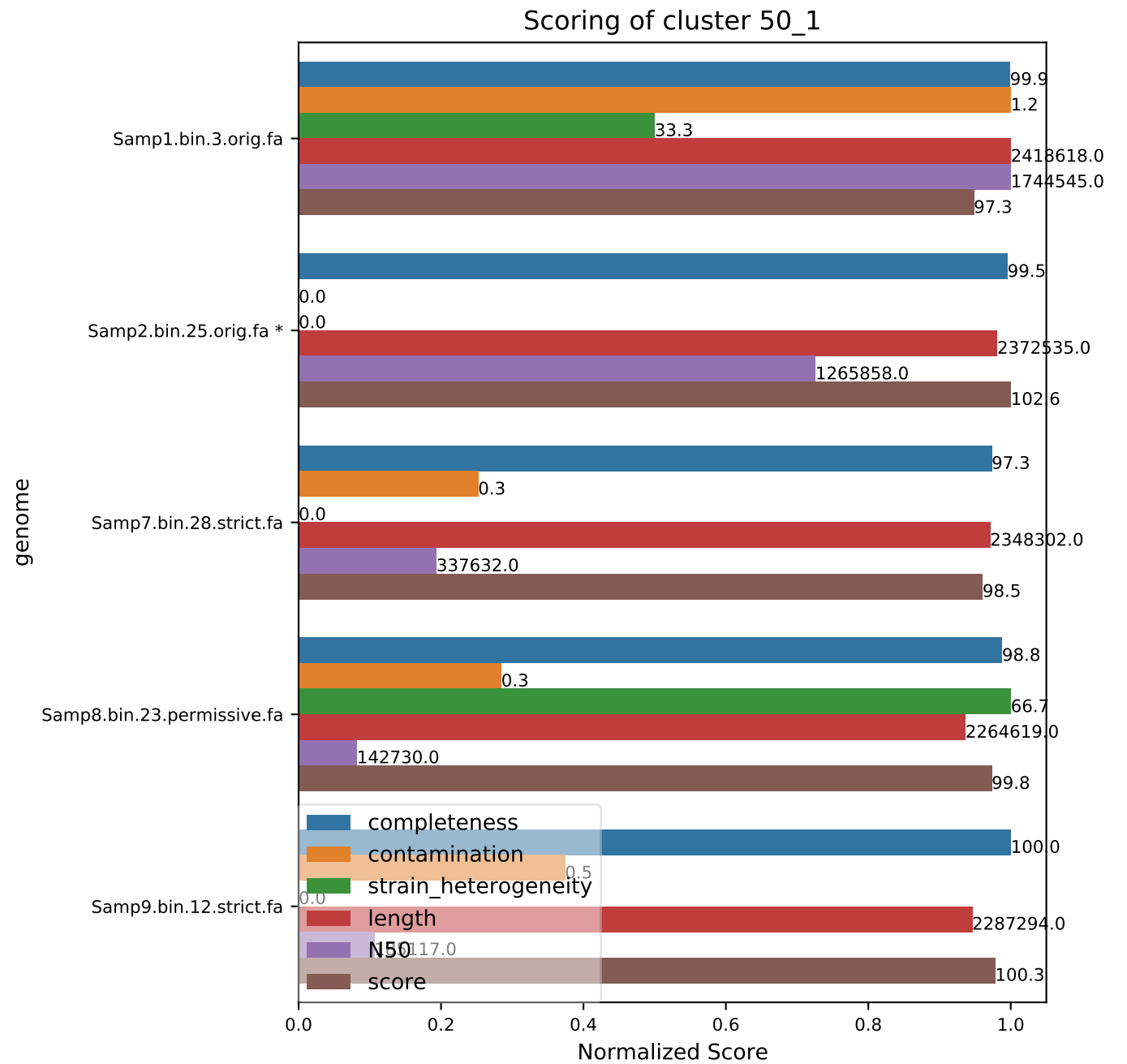
Scoring of cluster 51_1

Scoring of cluster 52_0

Scoring of cluster 53_0

Scoring of cluster 54_1

Scoring of cluster 55_1

Scoring of cluster 56_1

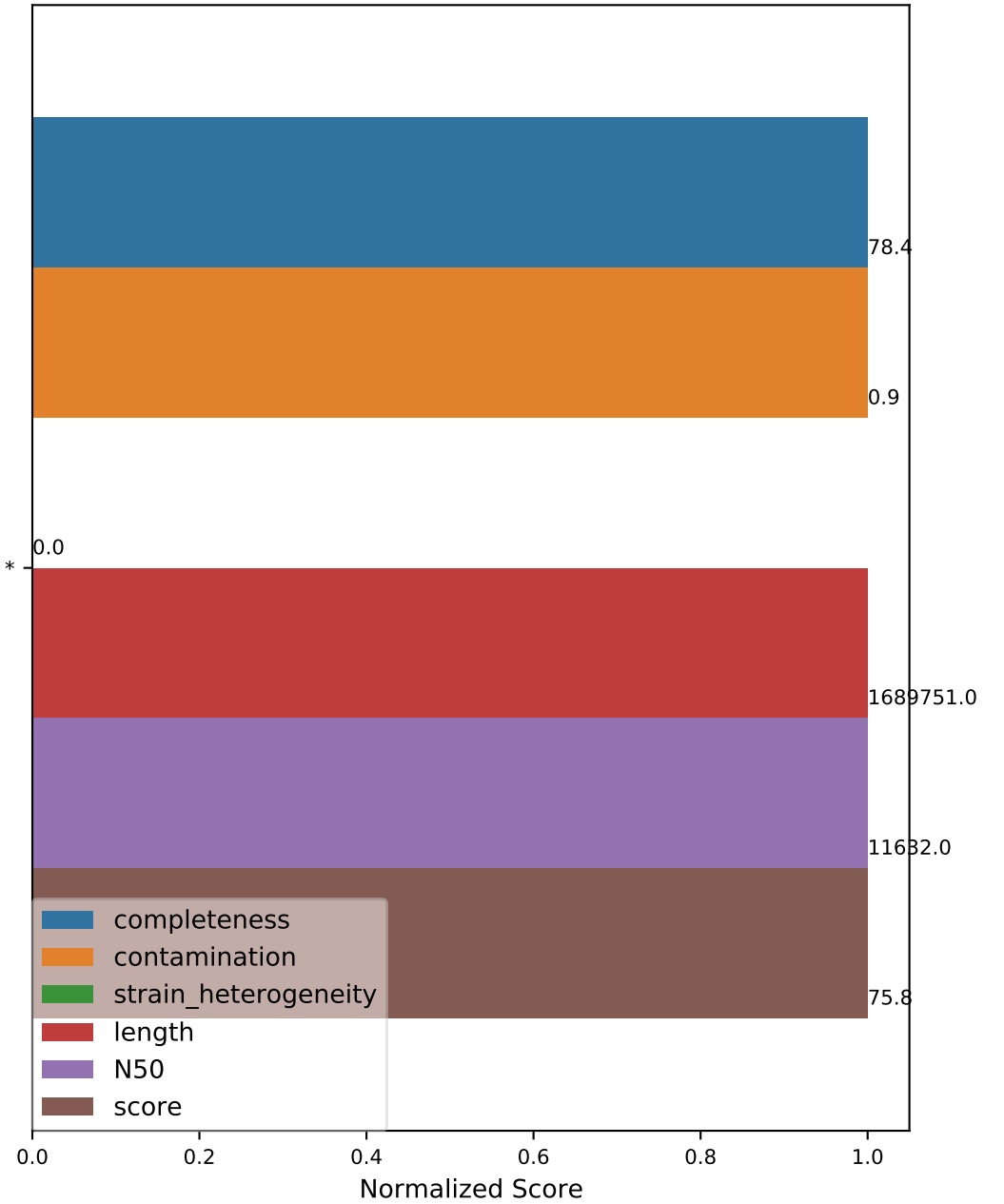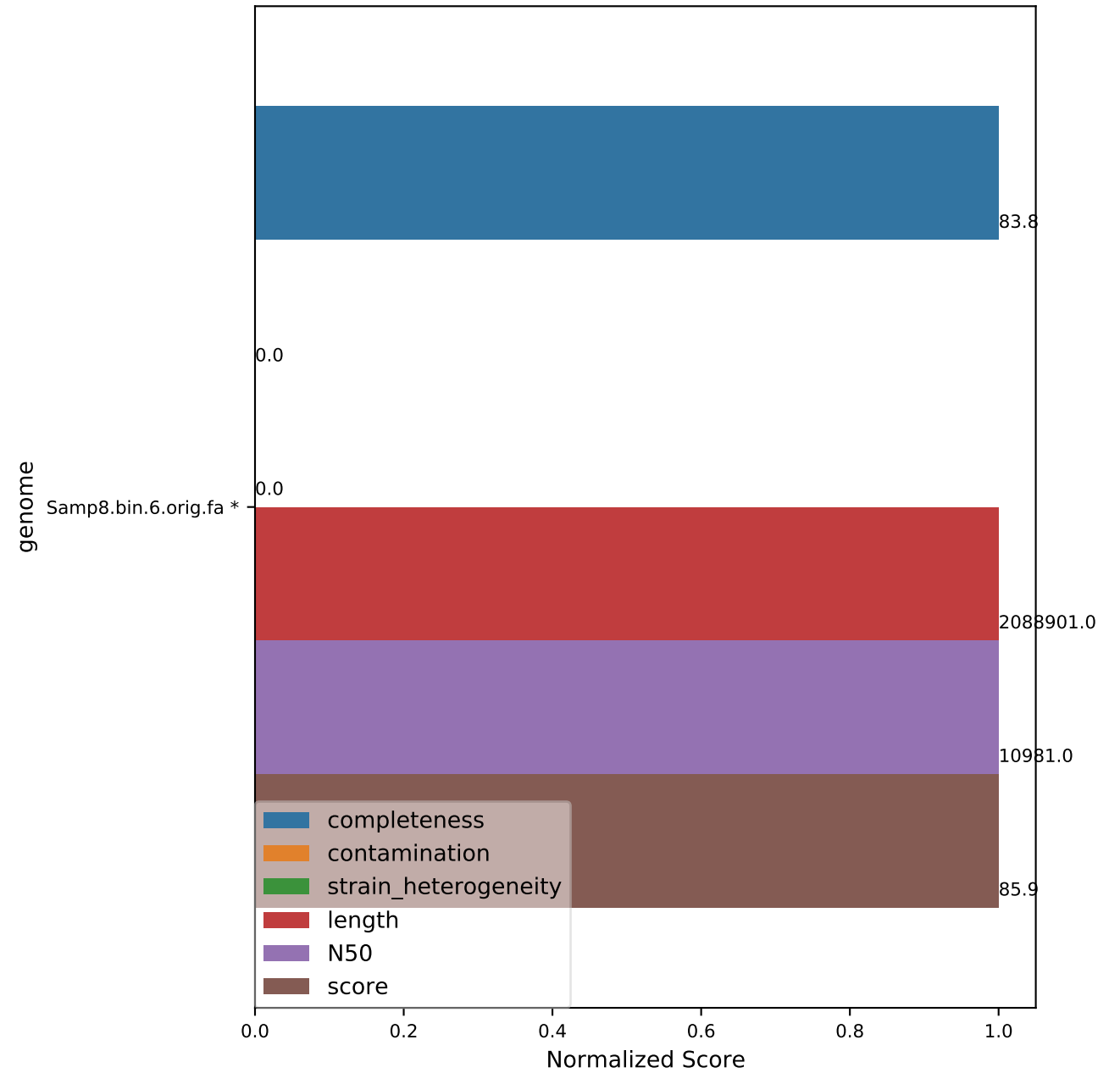Scoring of cluster 57_0

Scoring of cluster 58_0

Scoring of cluster 59_0

Scoring of cluster 60_1

Scoring of cluster 60_2

Scoring of cluster 61_1

Scoring of cluster 61_2

Scoring of cluster 62_0
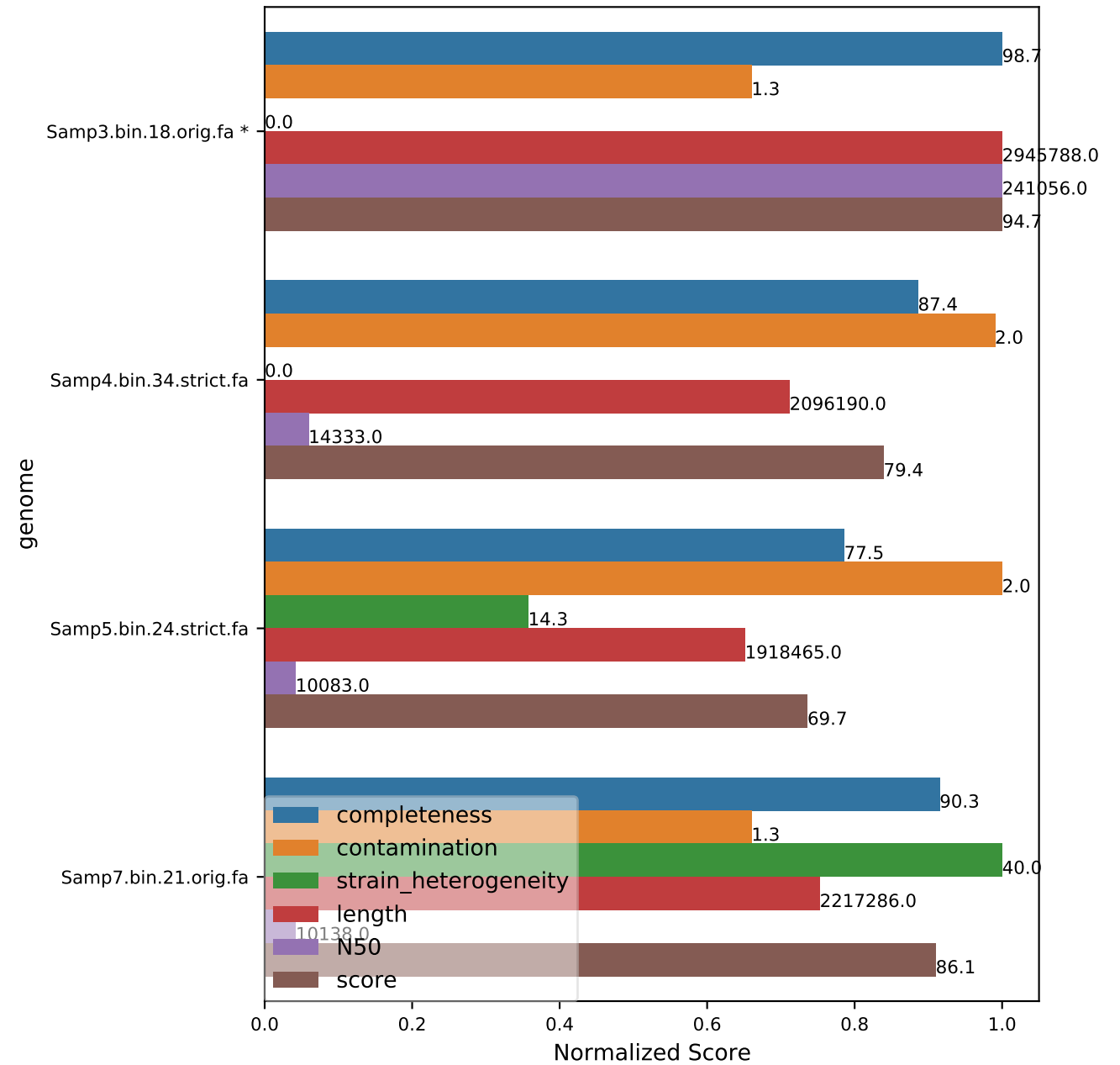
Scoring of cluster 63_1

Scoring of cluster 64_0

Scoring of cluster 65_1
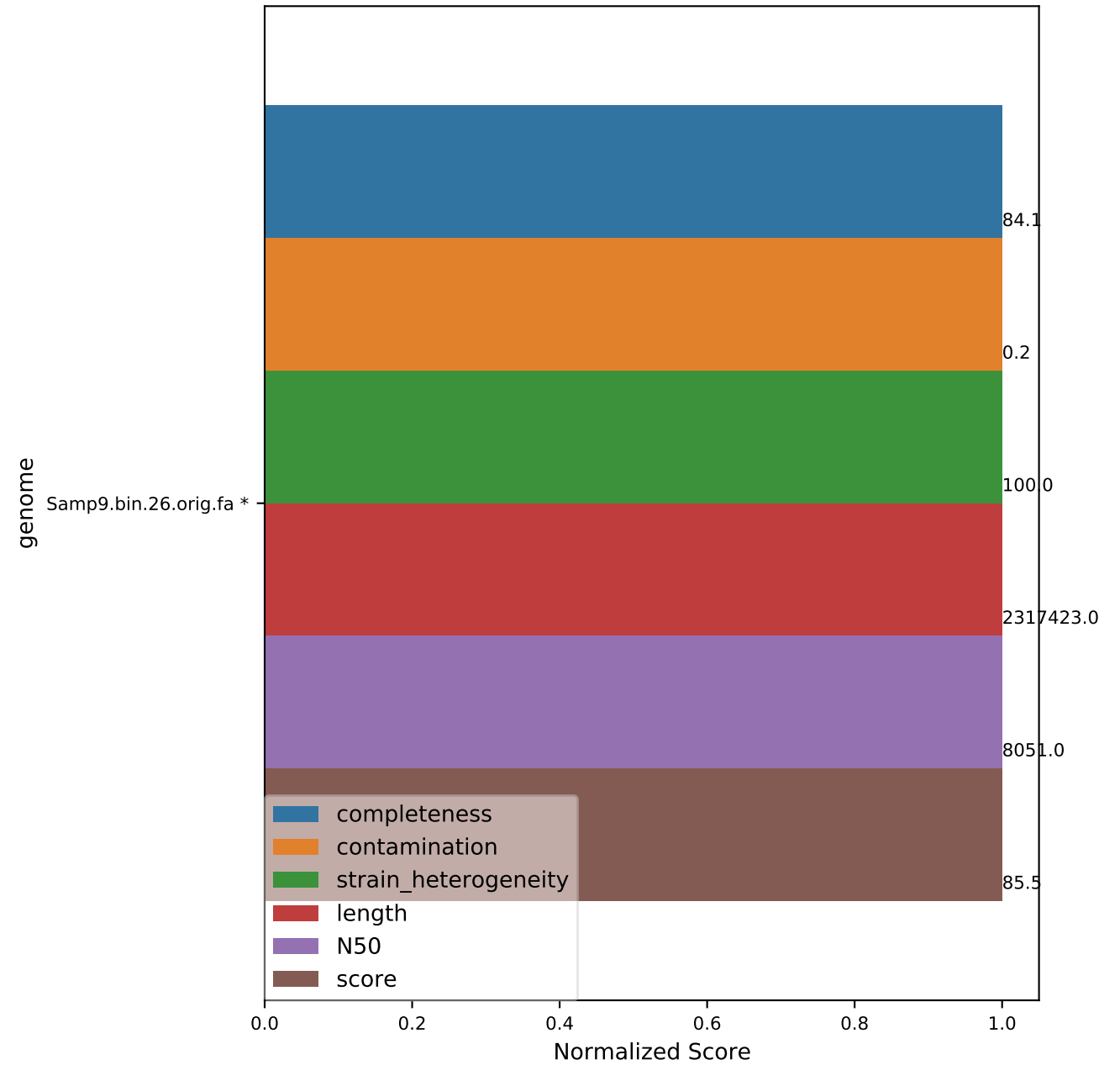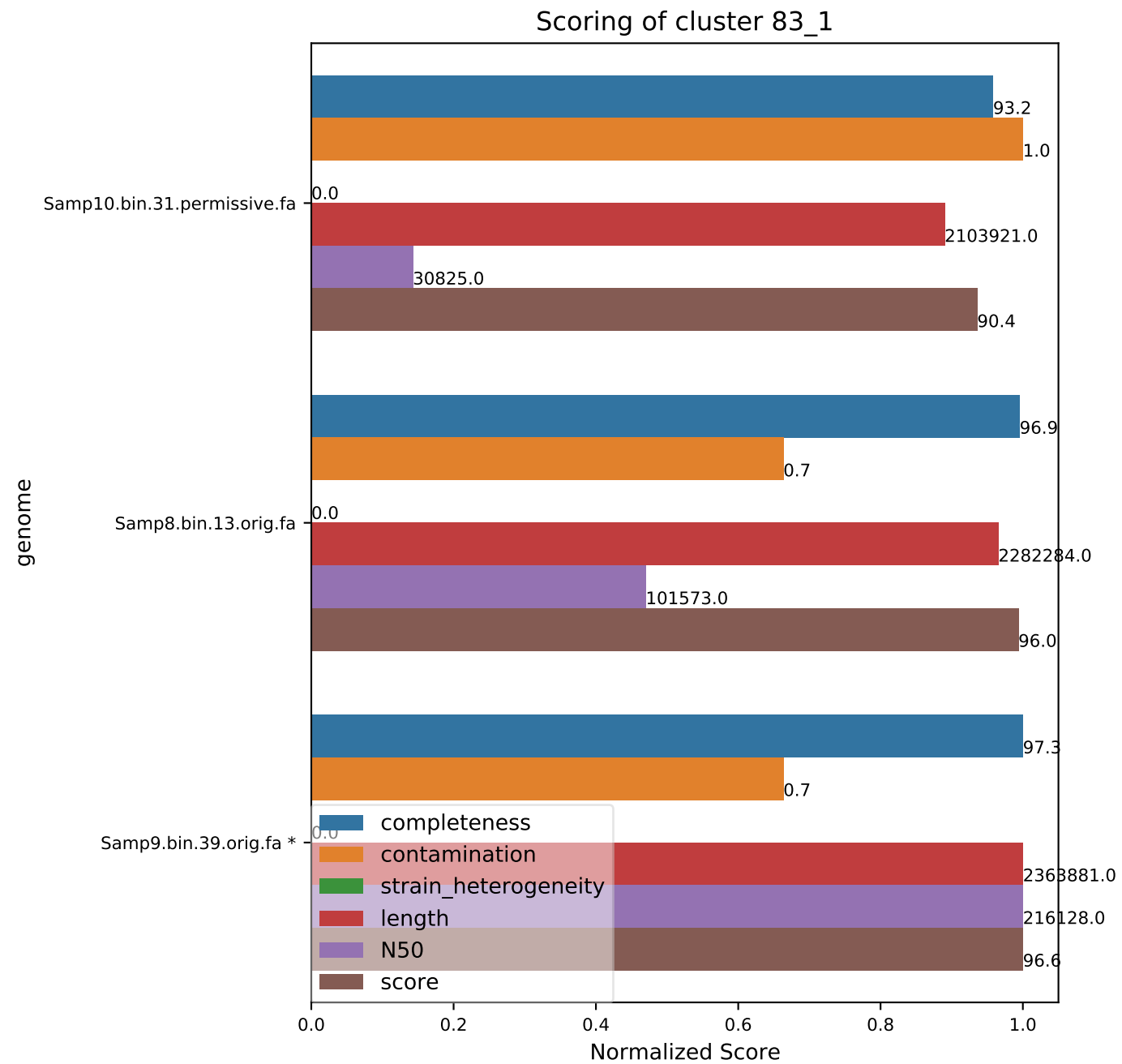
Samp1.bin.1.orig.fa
- completeness: 96.3
- contamination: 2.4
- strain_heterogeneity: 22.2
- length: 2382804.0
- N50: 108032.0
- score: 87.4

Samp2.bin.6.strict.fa *
- completeness: 95.8
- contamination: 0.0
- strain_heterogeneity: 0.0
- length: 2120827.0
- N50: 51101.0
- score: 98.1

Samp3.bin.34.strict.fa
- completeness: 92.0
- contamination: 0.0
- strain_heterogeneity: 0.0
- length: 1908285.0
- N50: 59037.0
- score: 94.3

Samp4.bin.29.orig.fa
- completeness: 90.0
- contamination: 0.0
- strain_heterogeneity: 0.0
- length: 1939945.0
- N50: 53541.0
- score: 92.3

Samp6.bin.6.strict.fa
- completeness: 86.5
- contamination: 2.7
- strain_heterogeneity: 0.0
- length: 1915804.0
- N50: 13894.0
- score: 74.9

Samp8.bin.20.orig.fa
- completeness: 84.6
- length: 2179662.0
- N50: 127871.0
- score: 87.1

Legend: completeness, contamination, strain_heterogeneity, length, N50, score
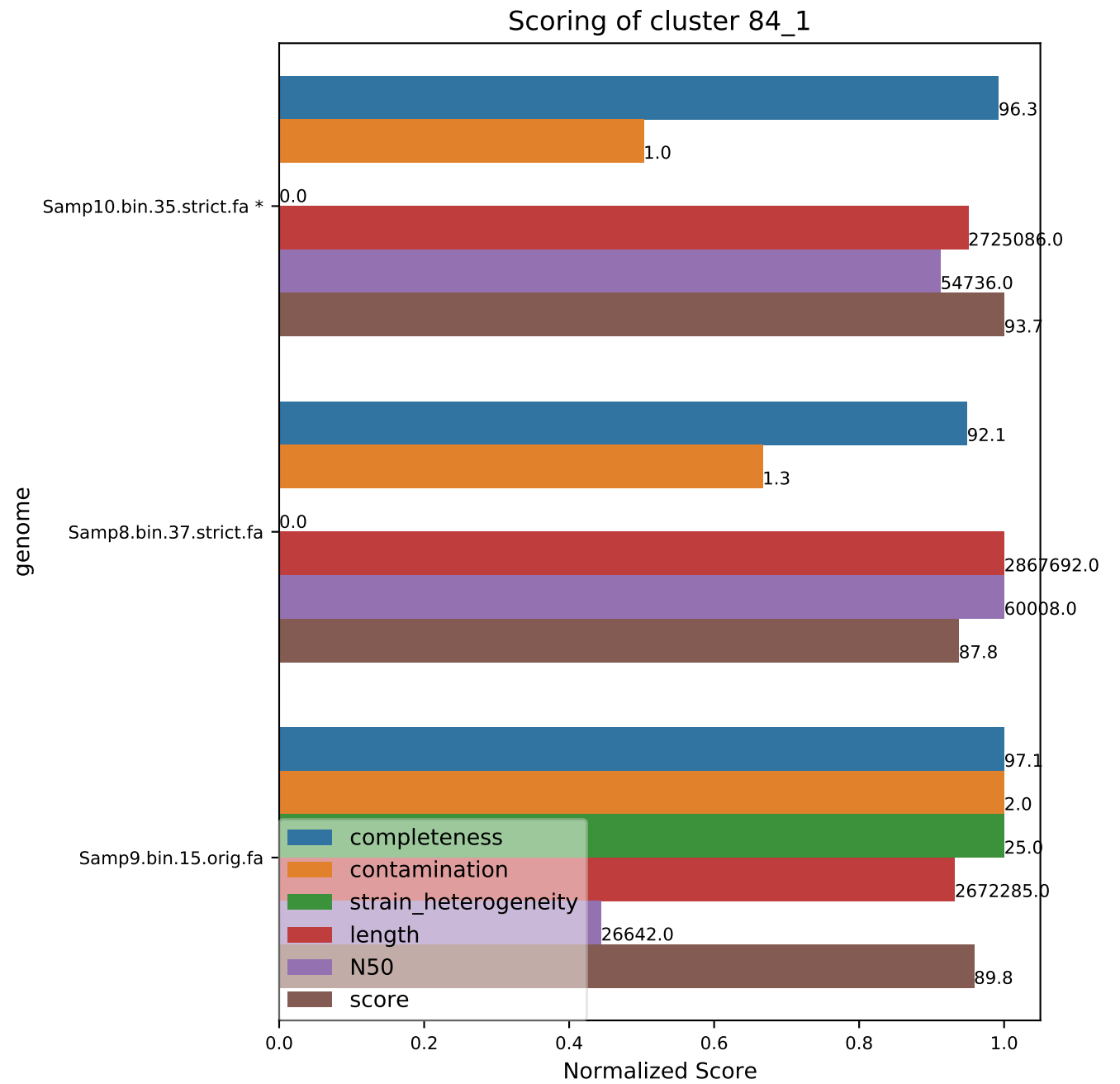
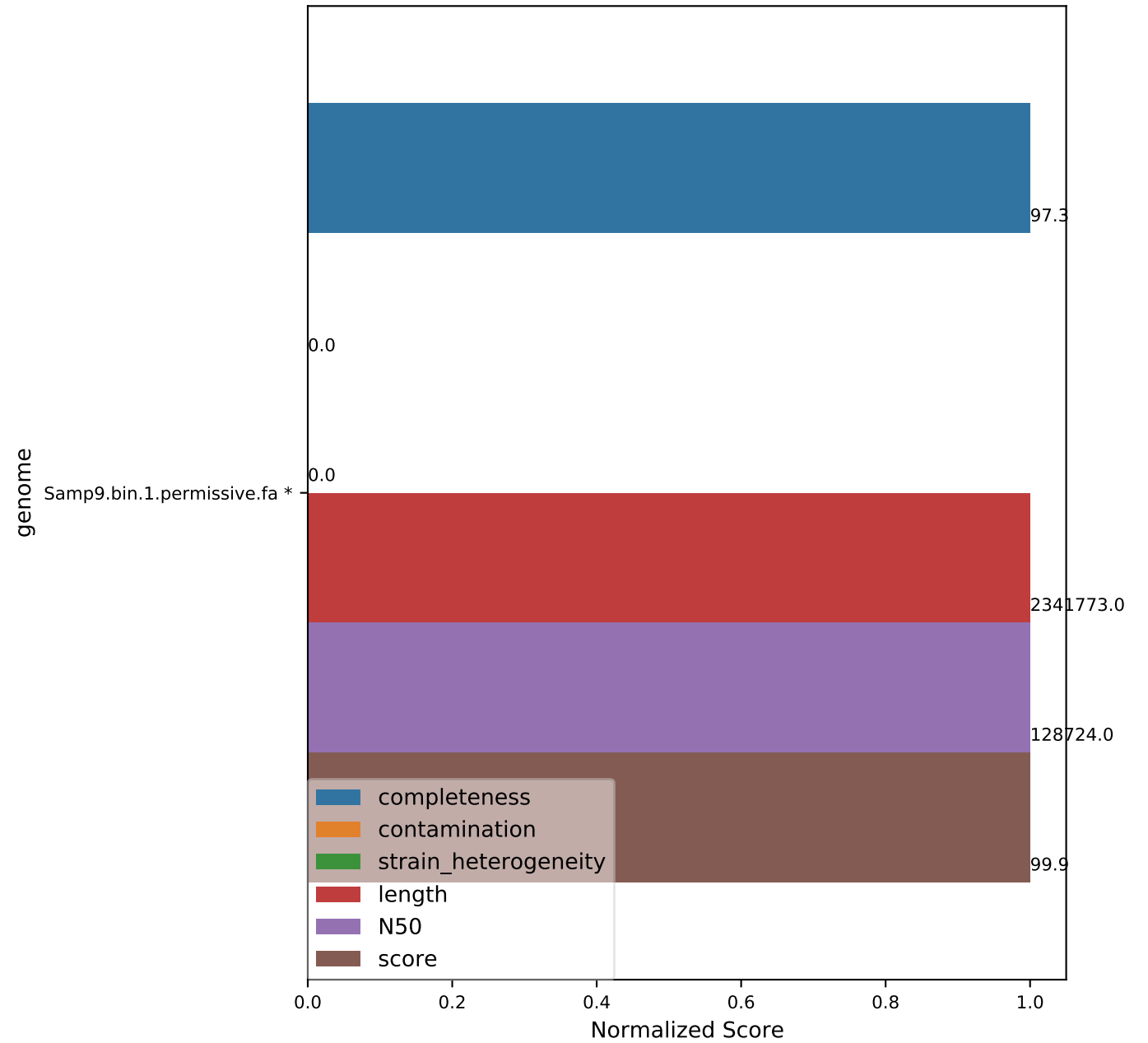genome (y-axis) / Normalized Score (x-axis)

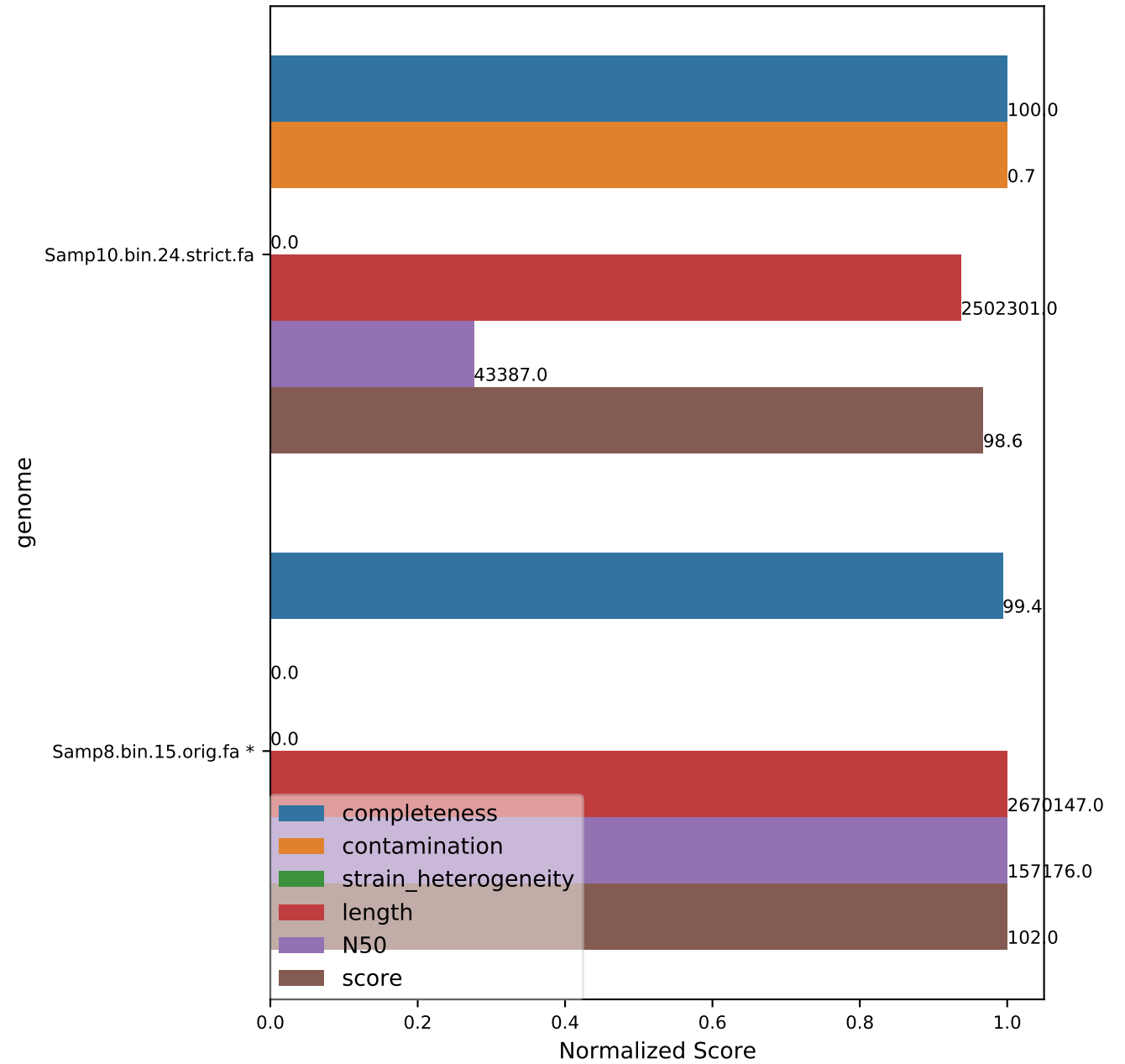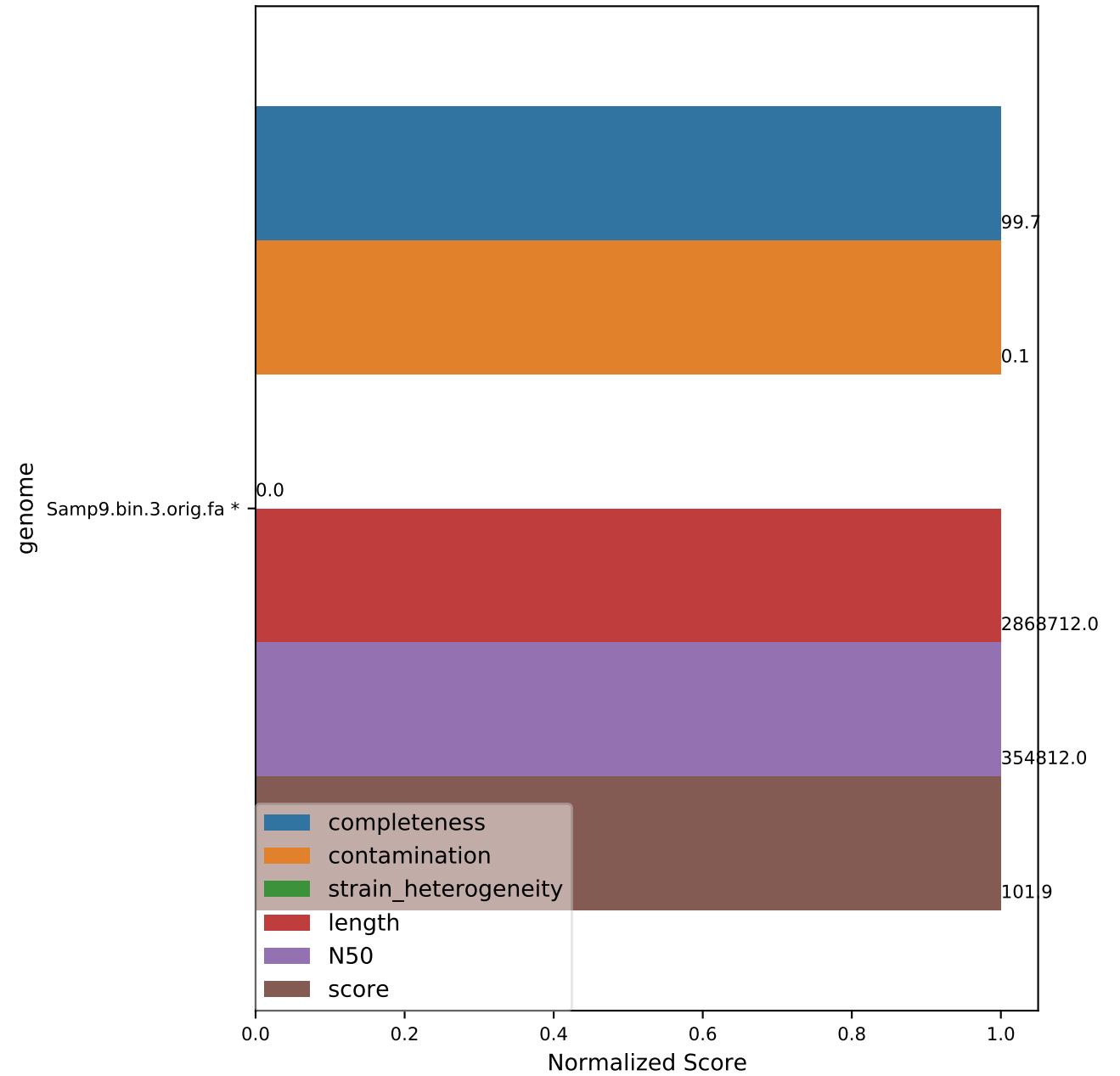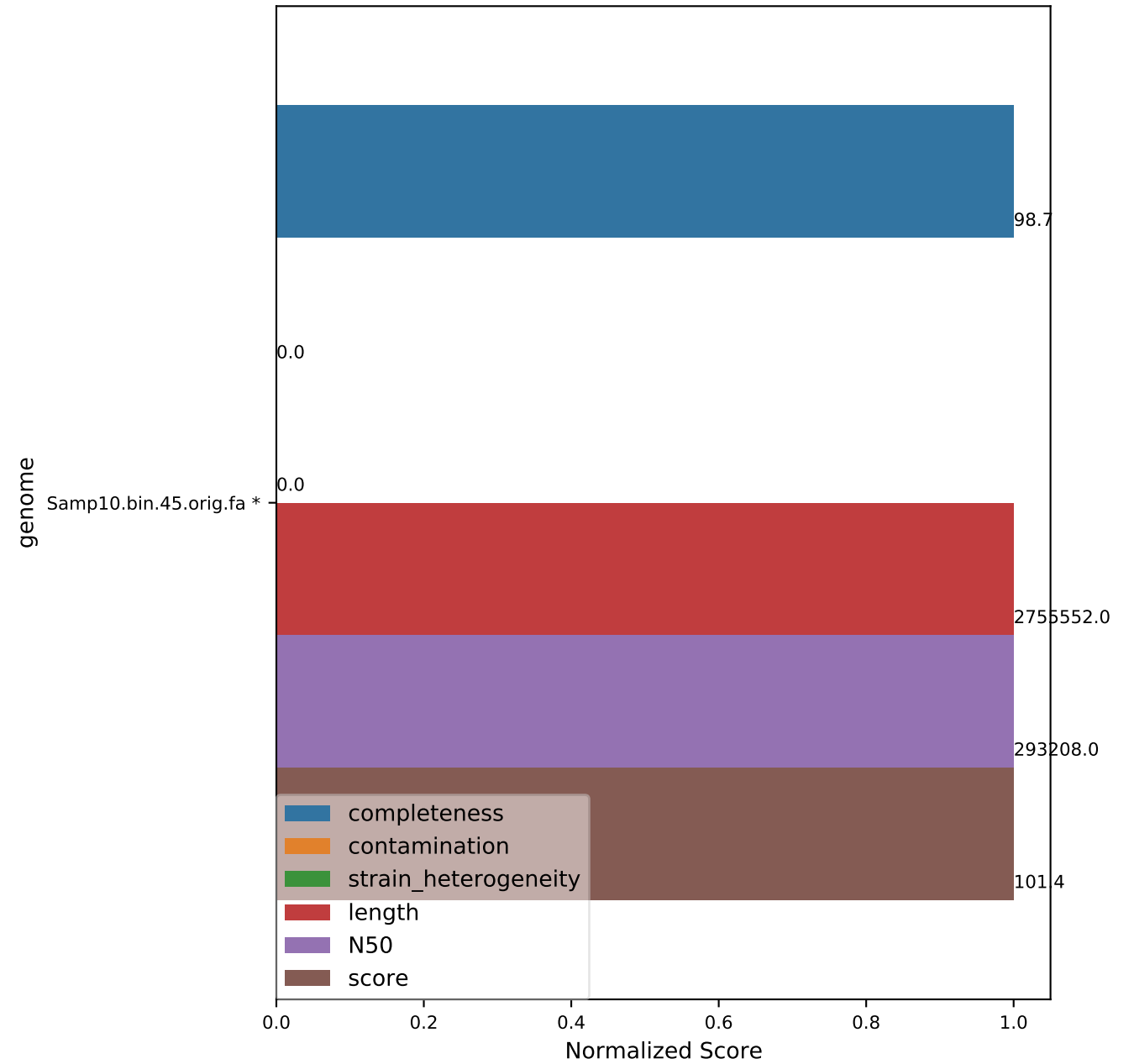Scoring of cluster 66_1

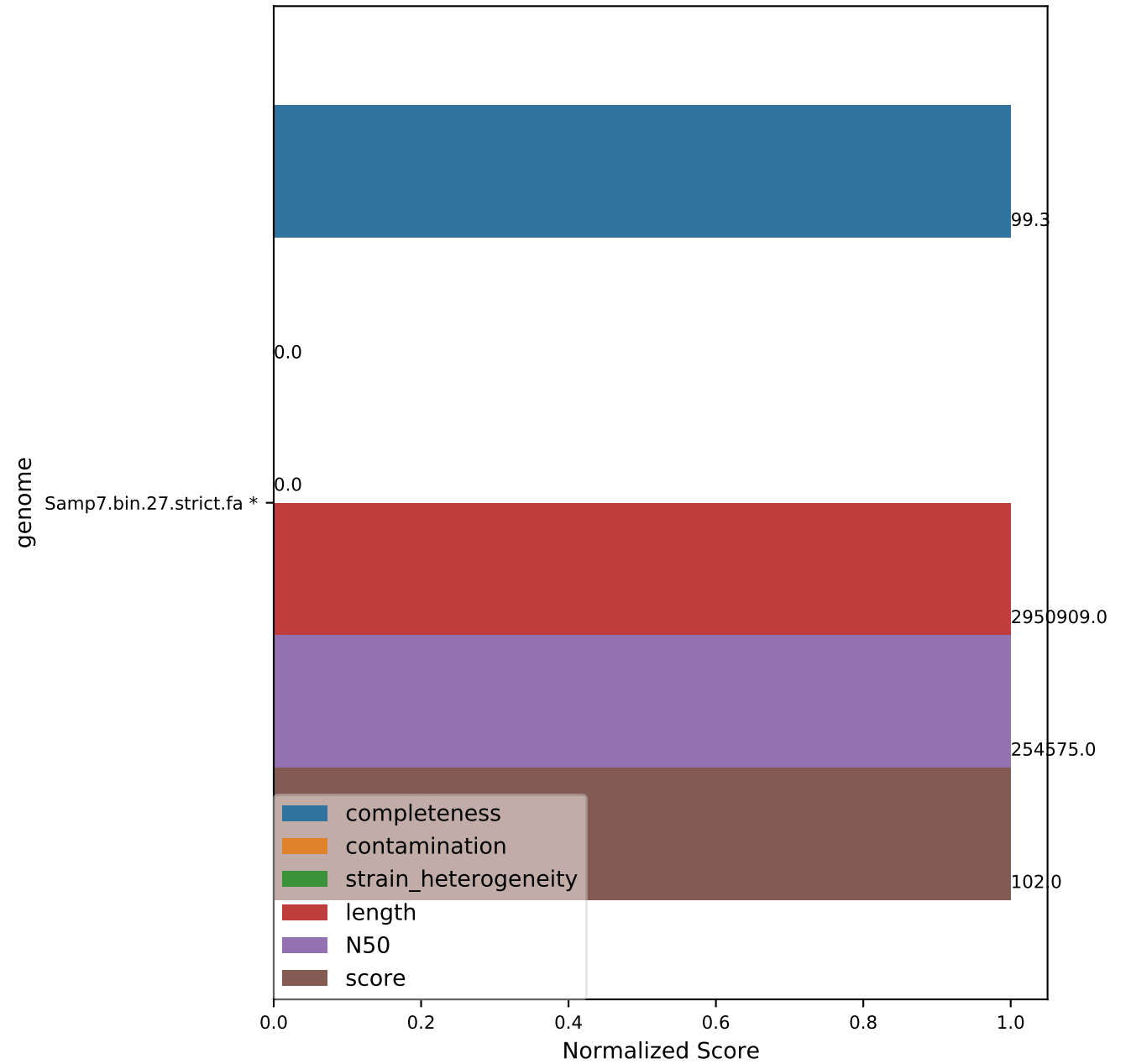Scoring of cluster 67_0

Scoring of cluster 68_0

Scoring of cluster 69_1

Scoring of cluster 70_1

Scoring of cluster 71_0

Scoring of cluster 72_0

Scoring of cluster 73_0

Scoring of cluster 74_0
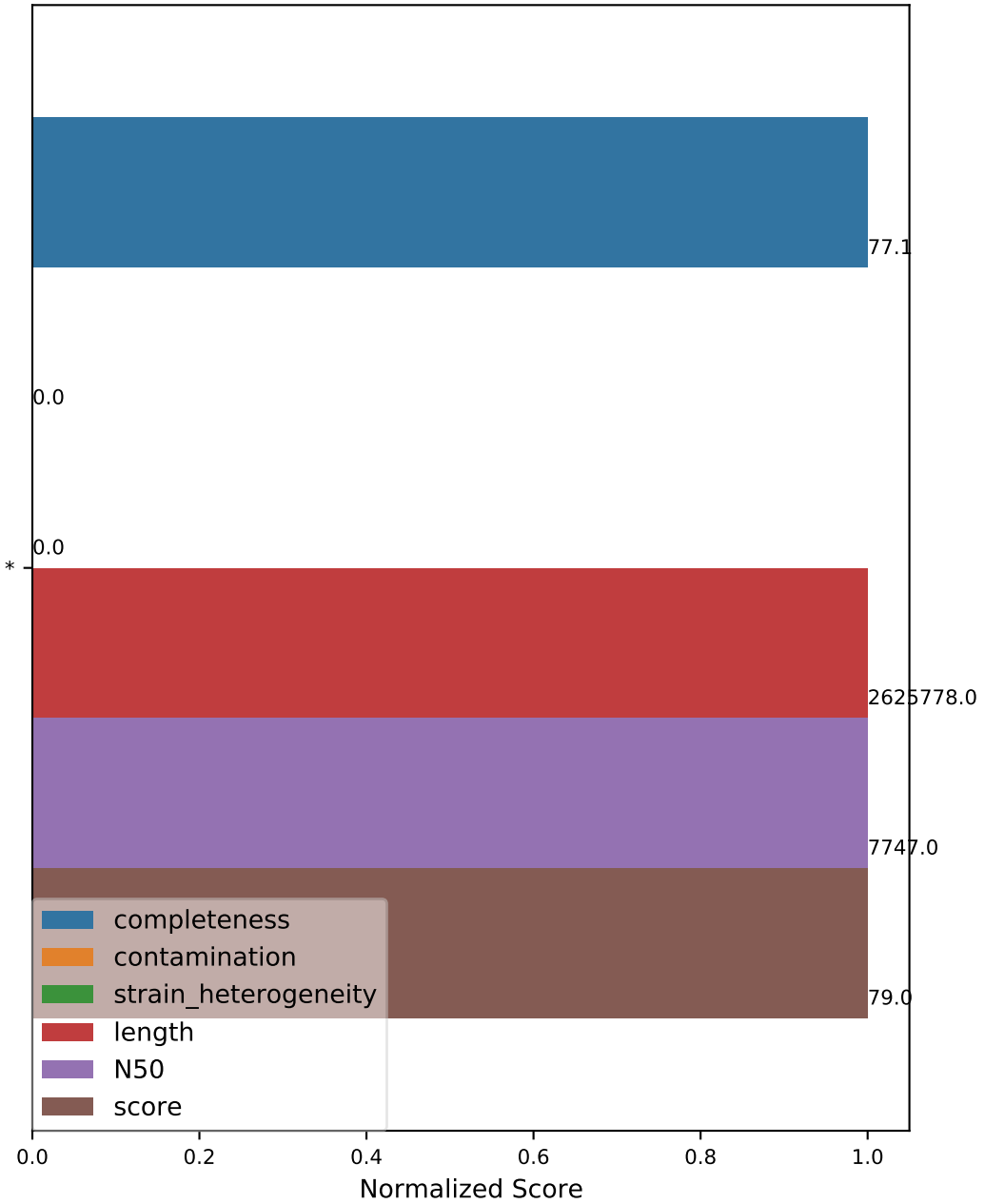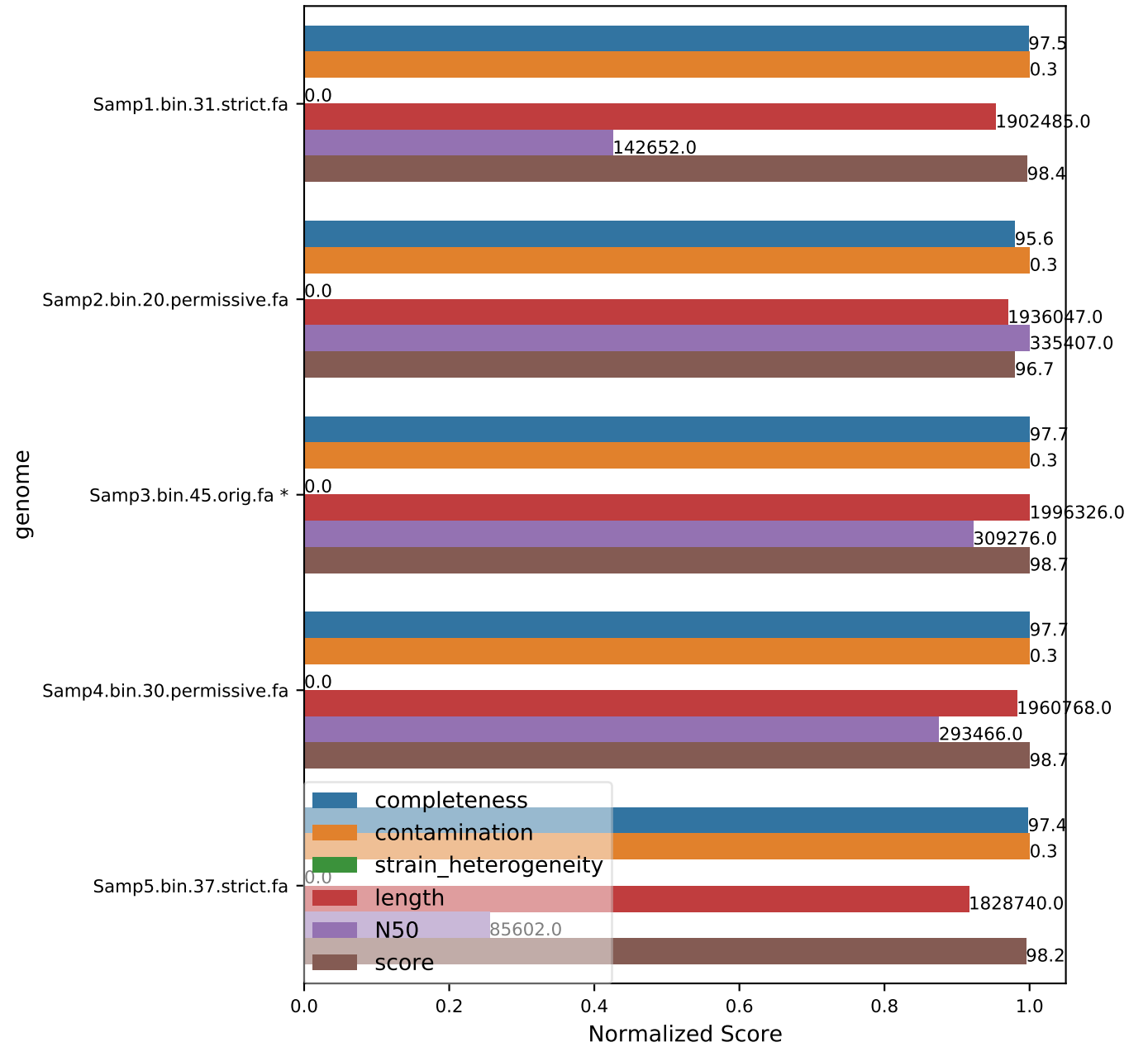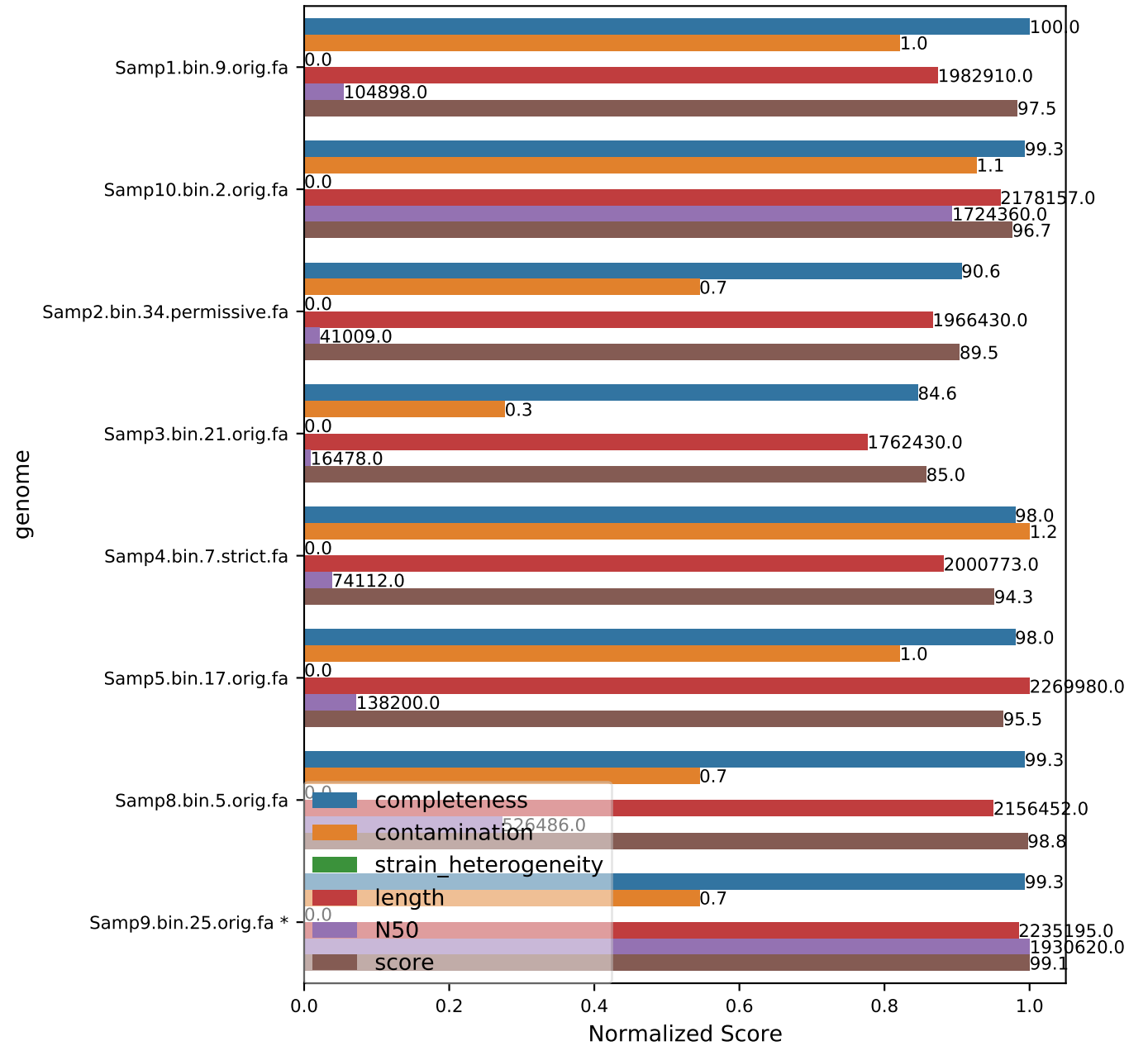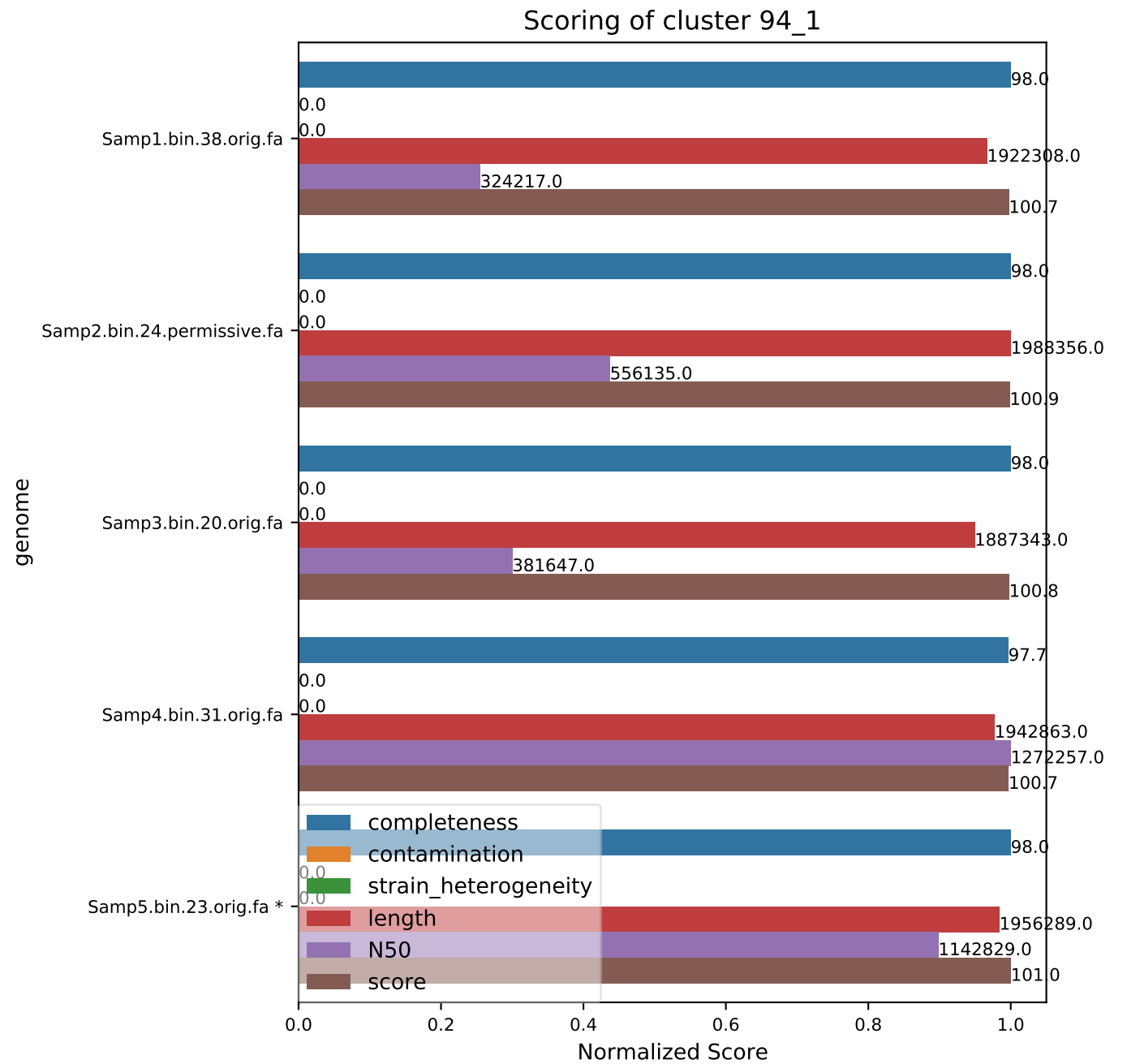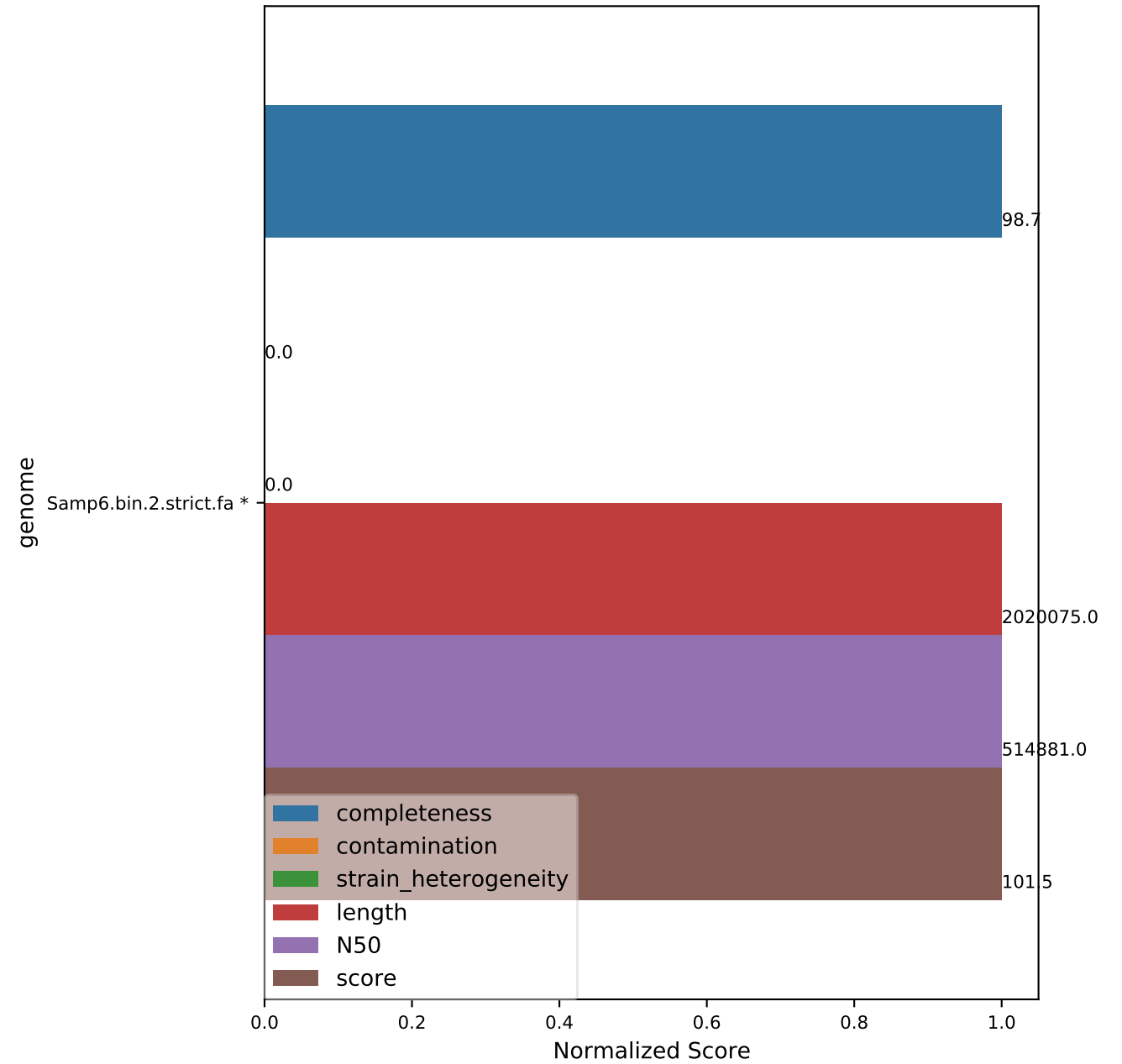
Scoring of cluster 75_1
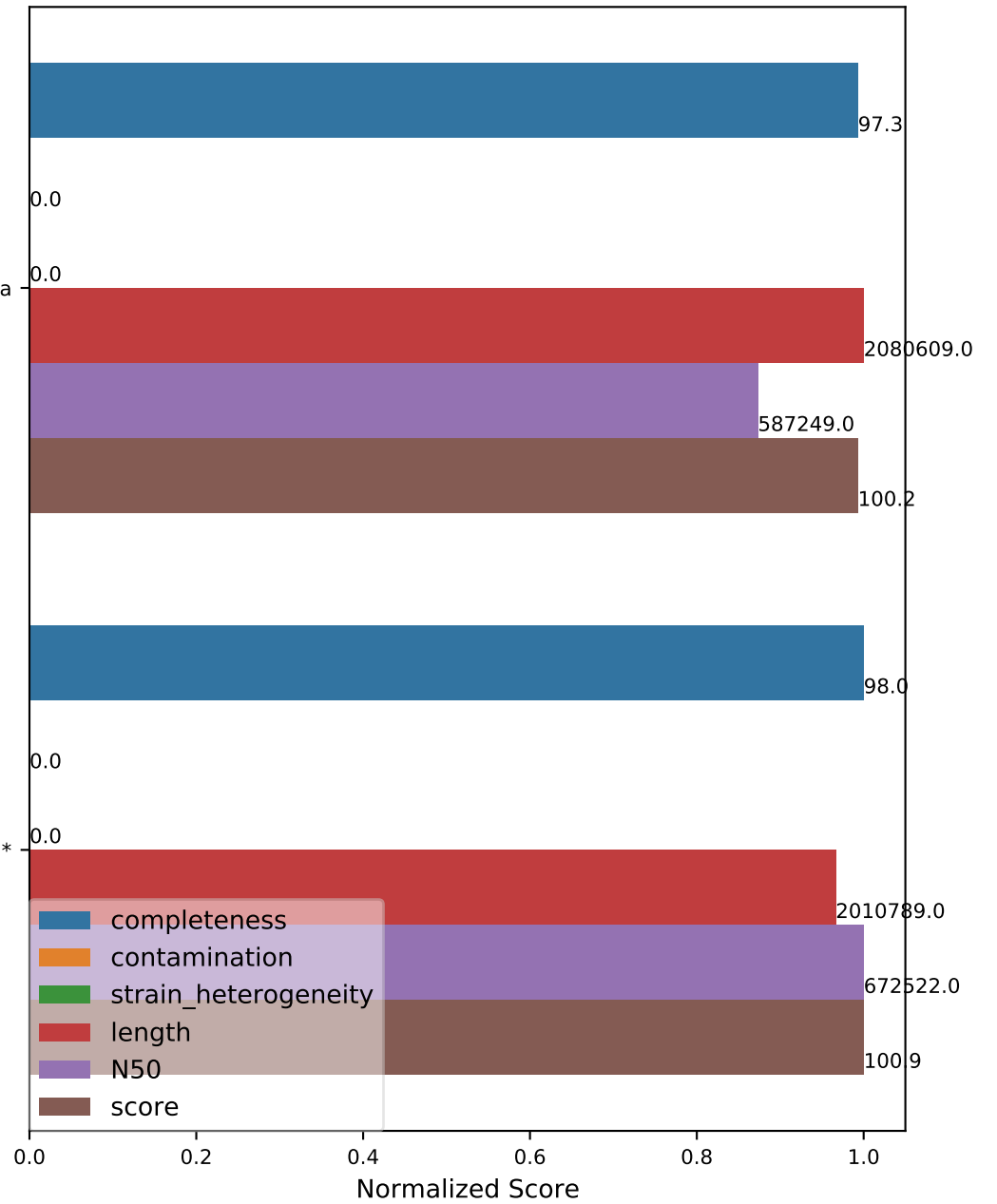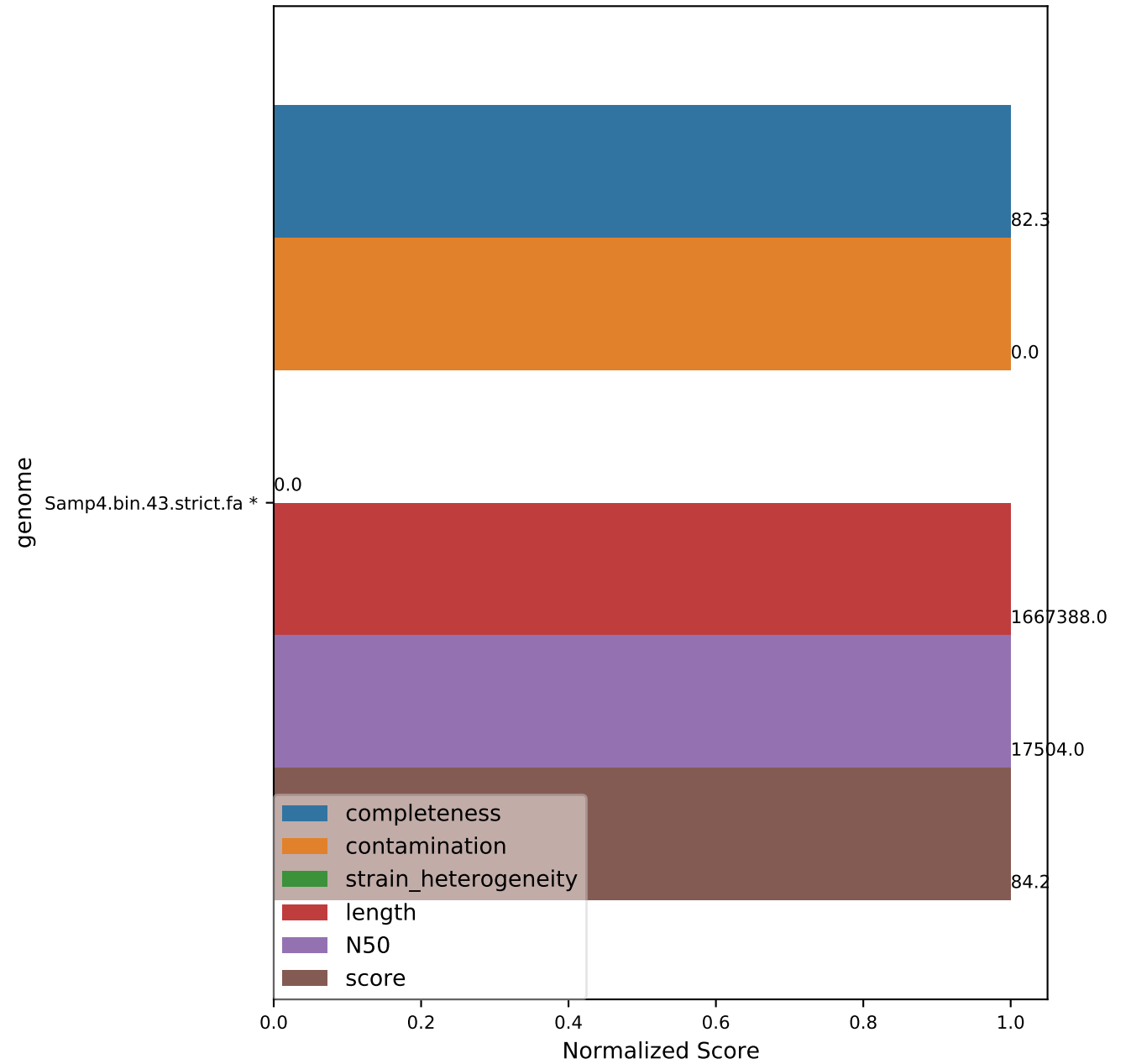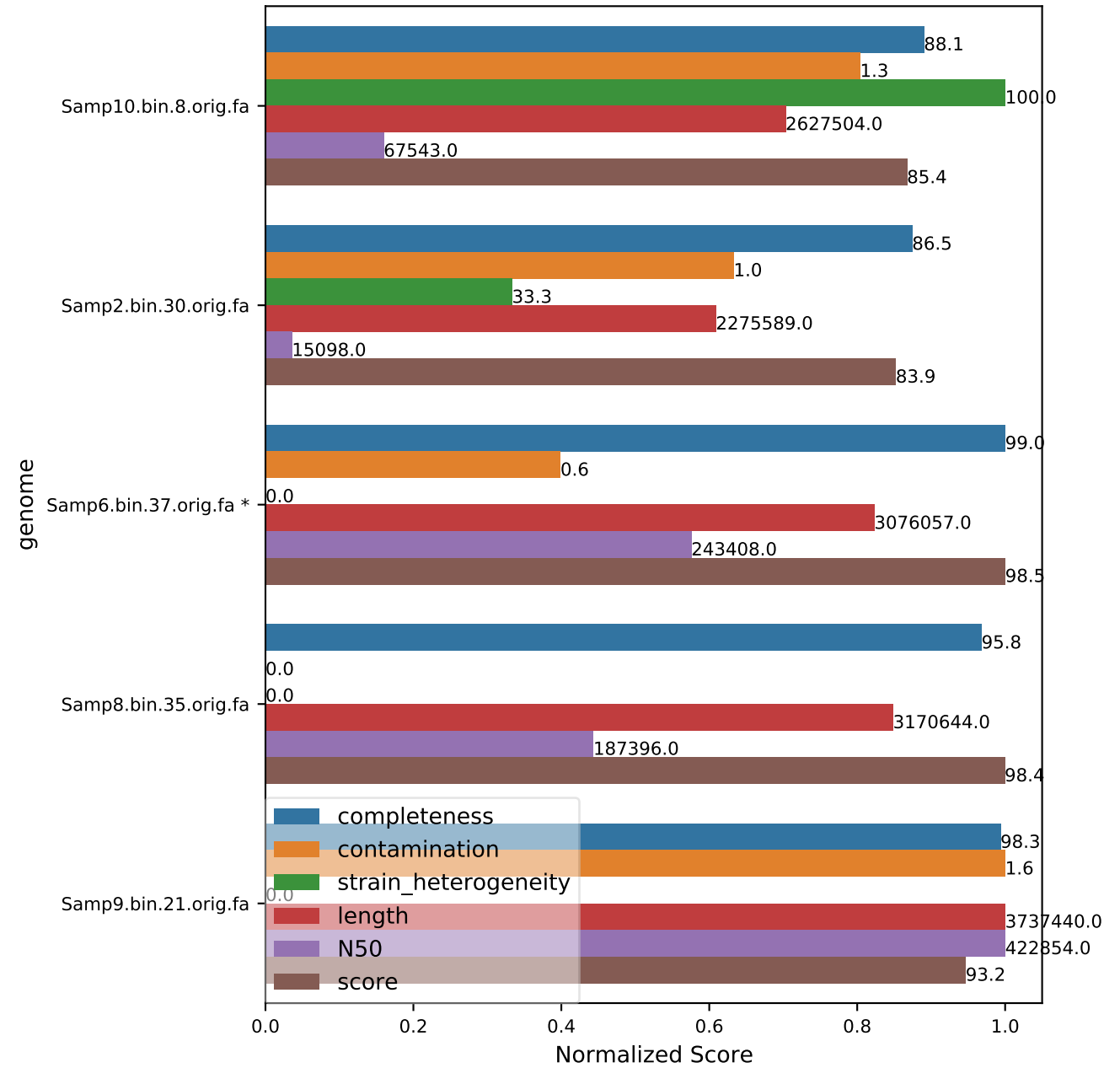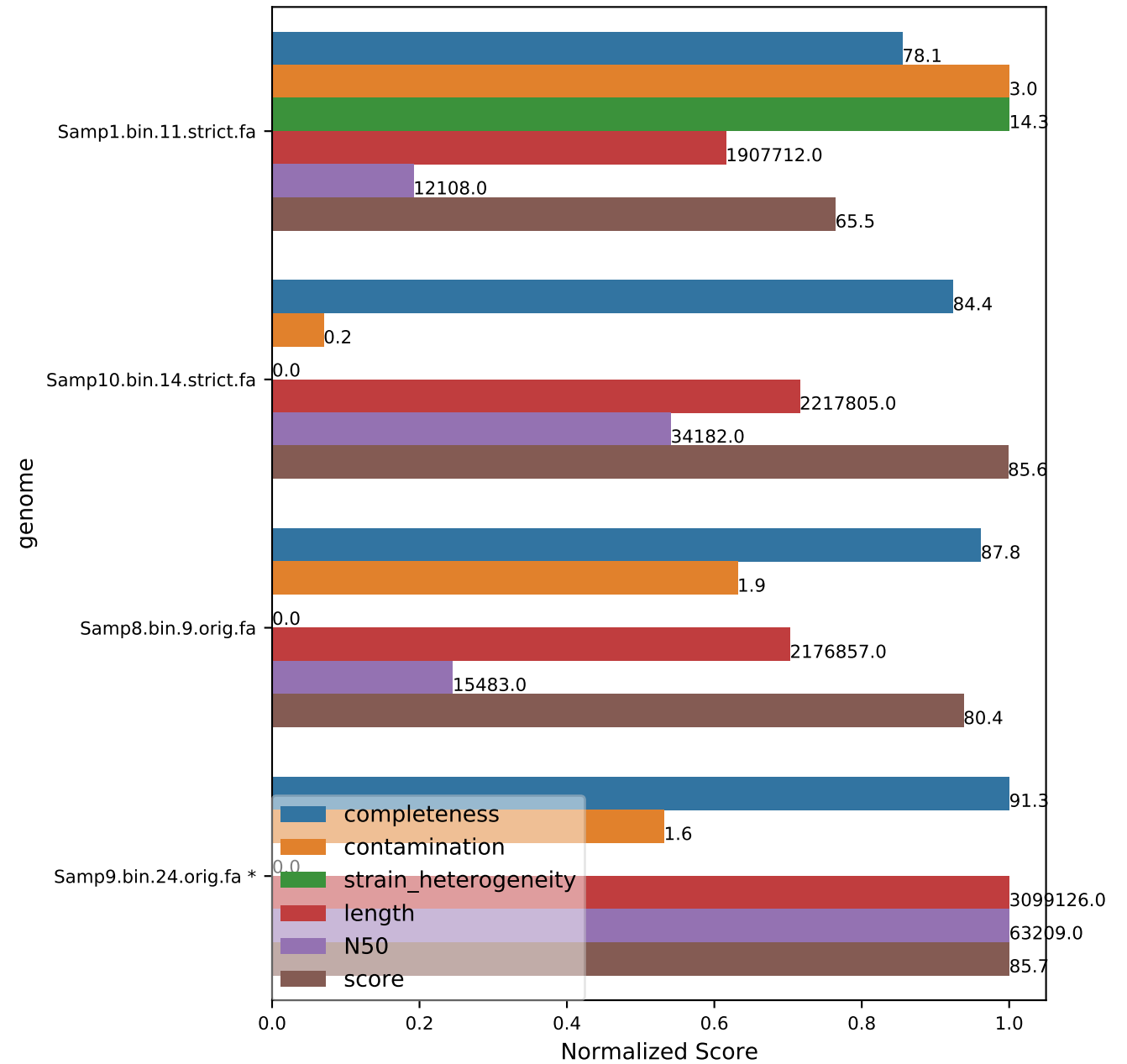
Scoring of cluster 76_1

genome (y-axis), **Normalized Score** (x-axis)

Samp1.bin.28.orig.fa *
- 98.0
- 0.0
- 0.0
- 2647536.0
- 528163.0
- 100.9

Samp10.bin.40.permissive.fa
- 80.7
- 0.0
- 0.0
- 1607915.0
- 10463.0
- 82.7

Samp2.bin.43.permissive.fa
- 94.6
- 1.1
- 33.3
- 2231679.0
- 40293.0
- 92.0

Samp5.bin.15.orig.fa
- 86.4
- 0.0
- 0.0
- 1834164.0
- 19434.0
- 88.6

Samp6.bin.31.permissive.fa
- 97.0
- 3.7
- 6.7
- 2587410.0
- 45771.0
- 81.0

Samp8.bin.47.orig.fa
- 98.0
- 0.0
- 0.0
- 2470601.0
- 301302.0
- 100.7

Samp9.bin.8.orig.fa
- 97.3
- 0.0
- 0.0
- 2515939.0
- 323717.0
- 100.1

Legend:
- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

Scoring of cluster 77_1

Scoring of cluster 78_1
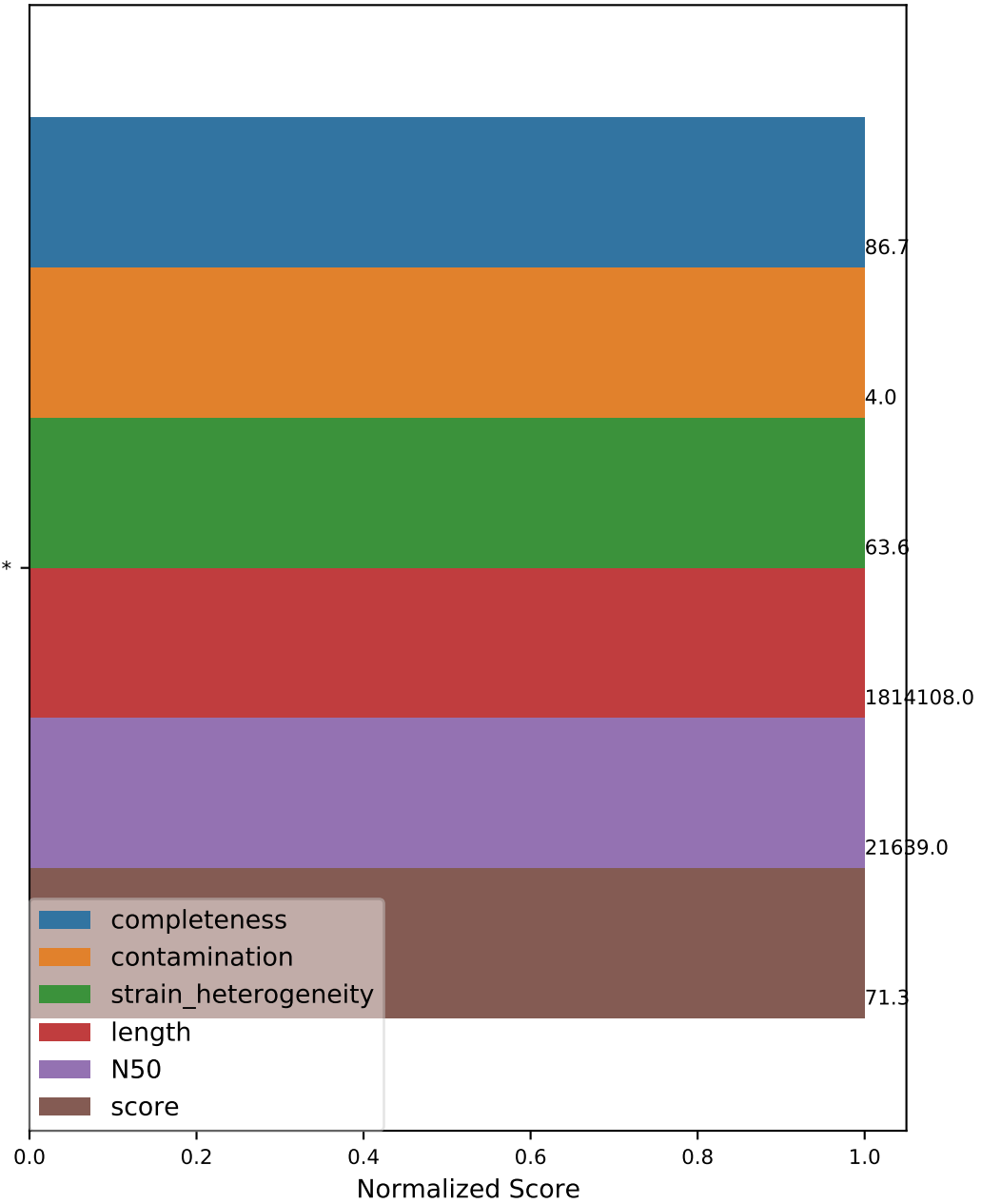
Scoring of cluster 78_2
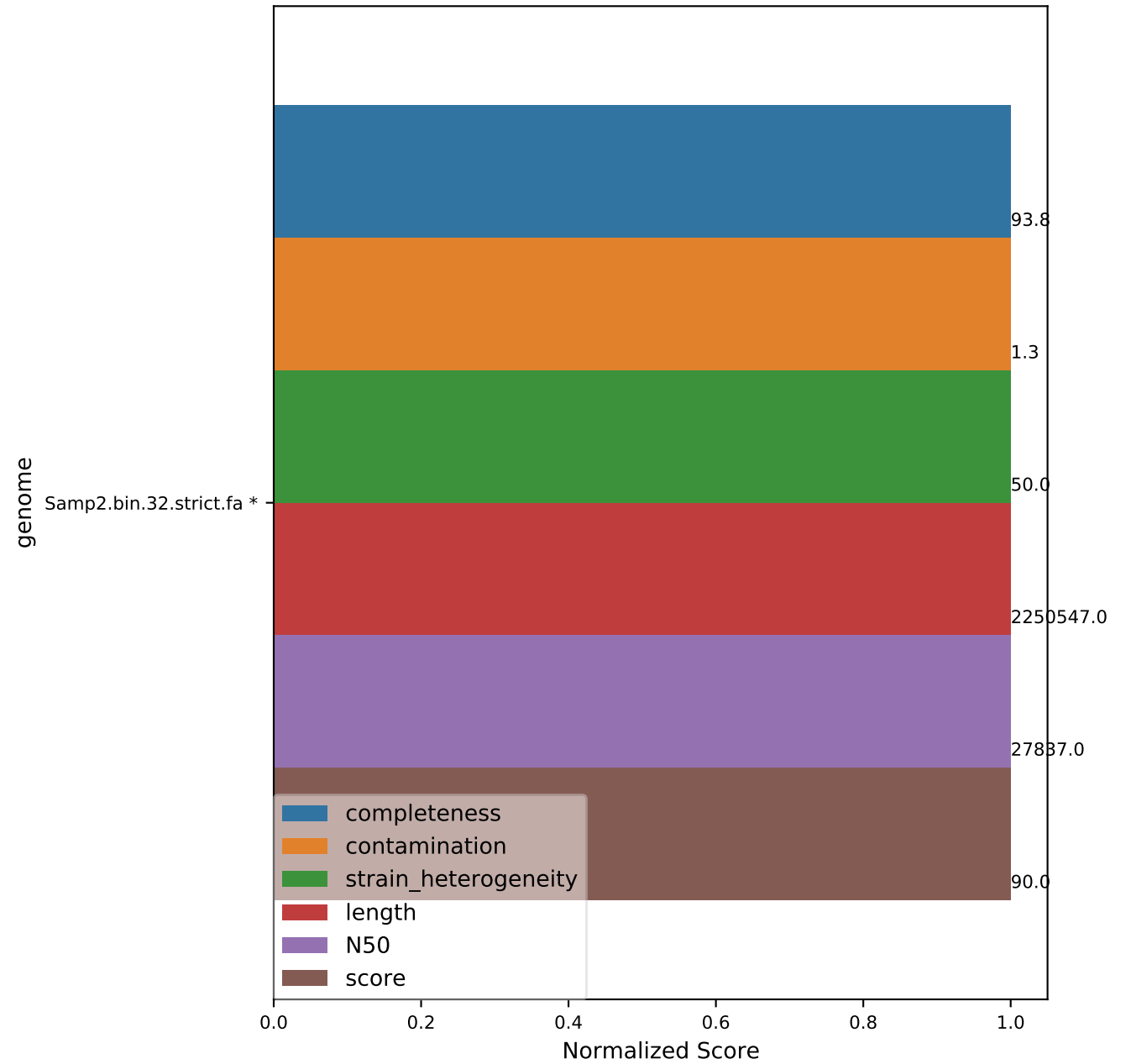
Scoring of cluster 79_0
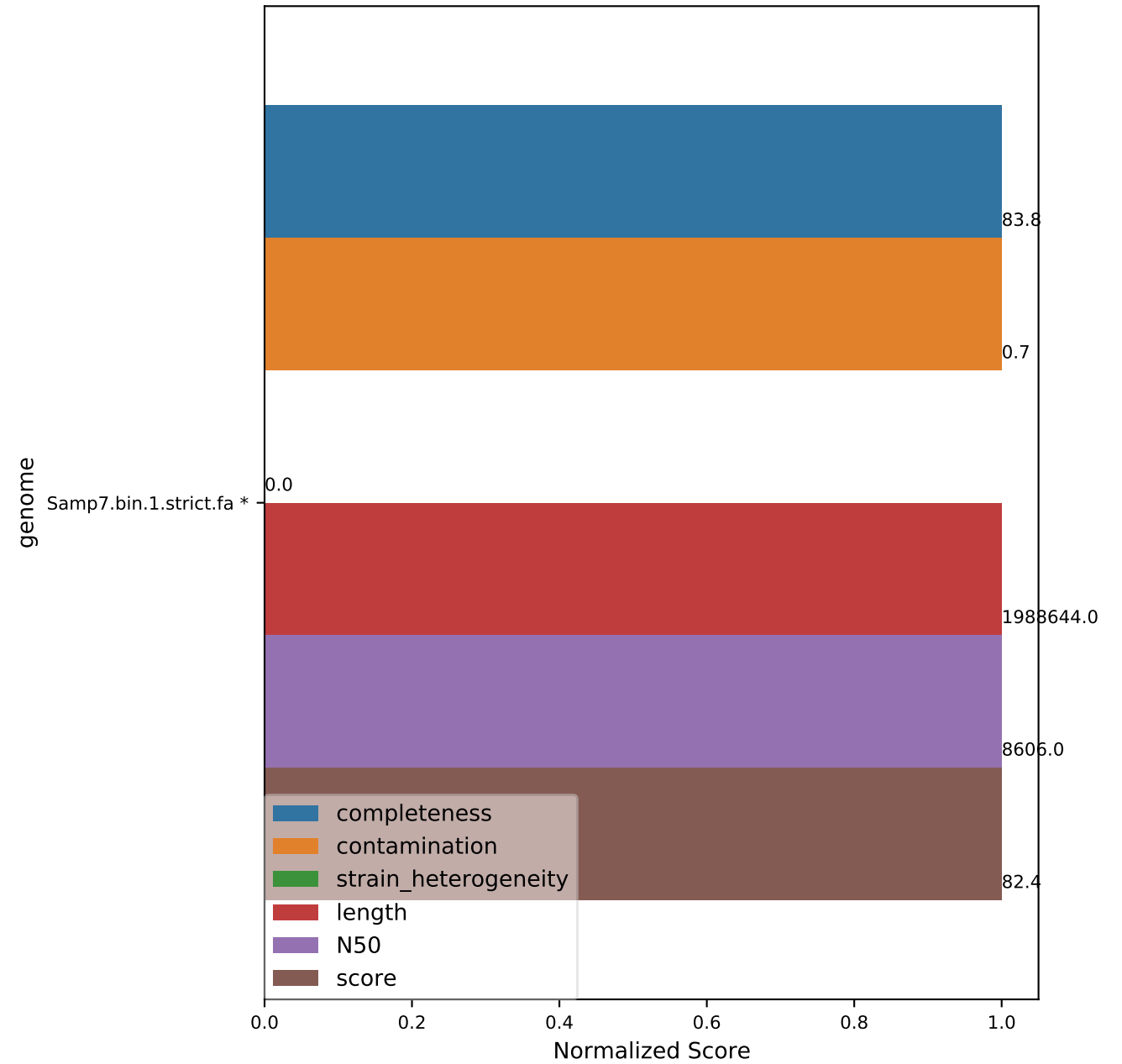
Scoring of cluster 80_1

Scoring of cluster 81_1
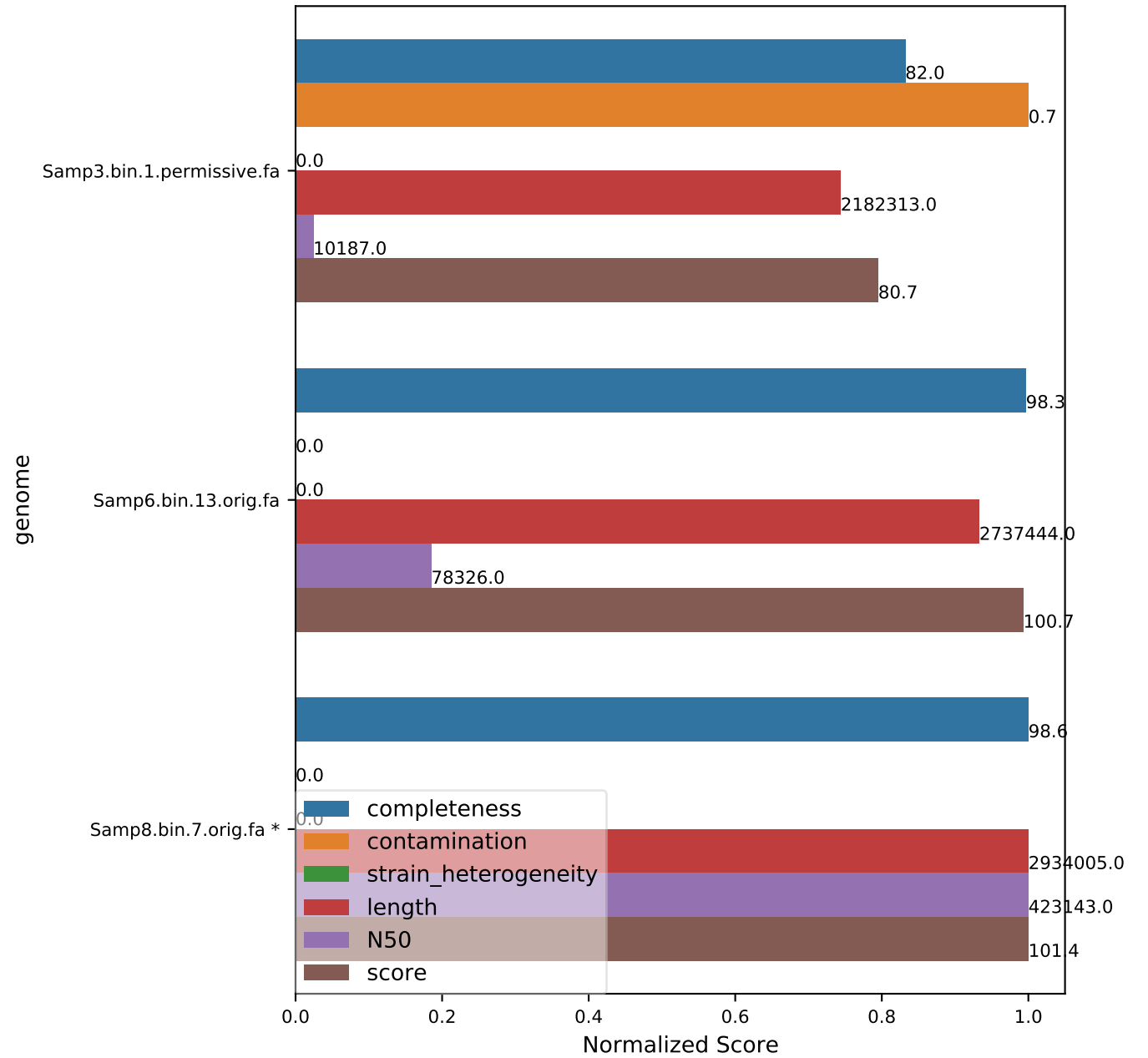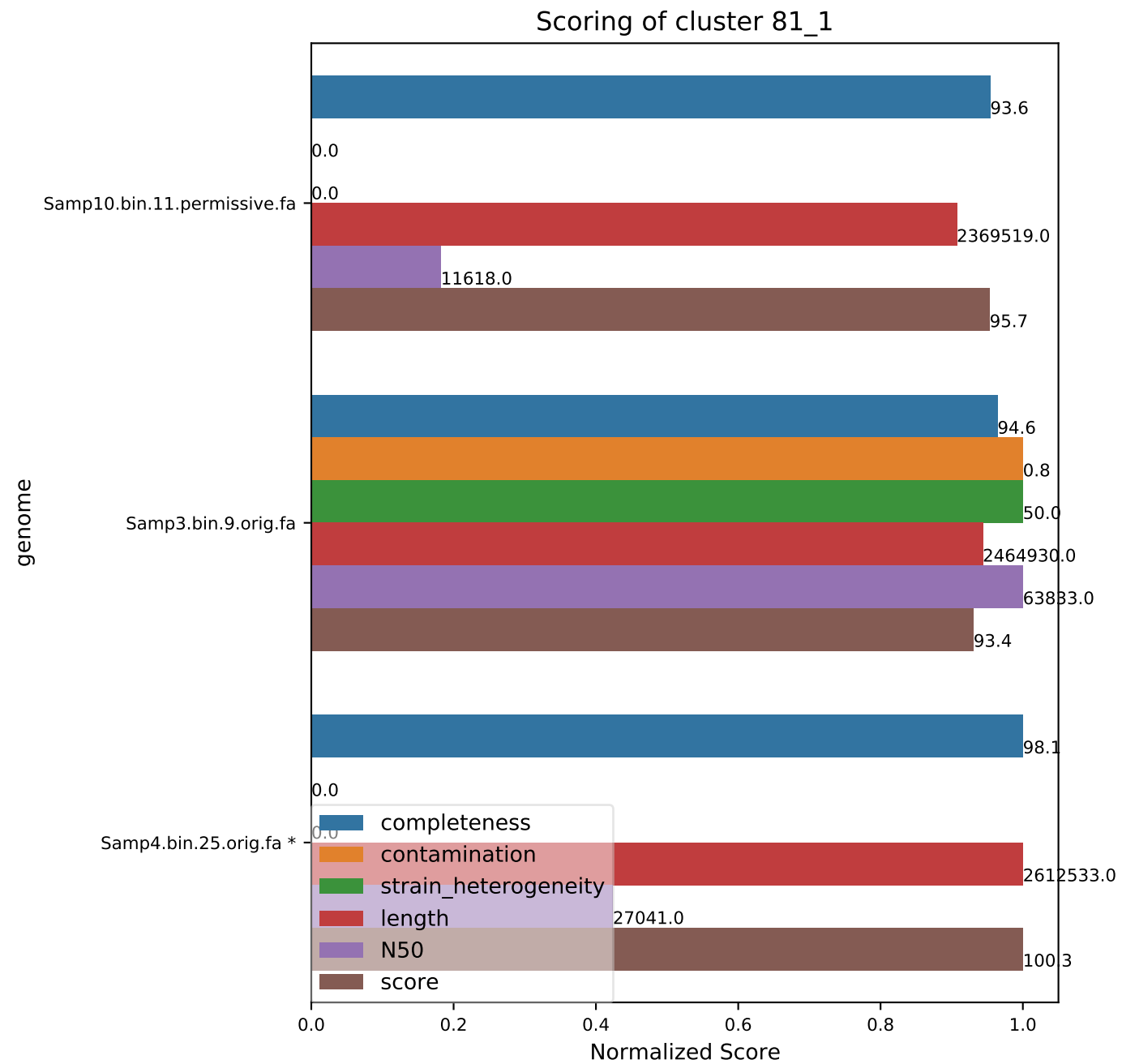
Scoring of cluster 82_0
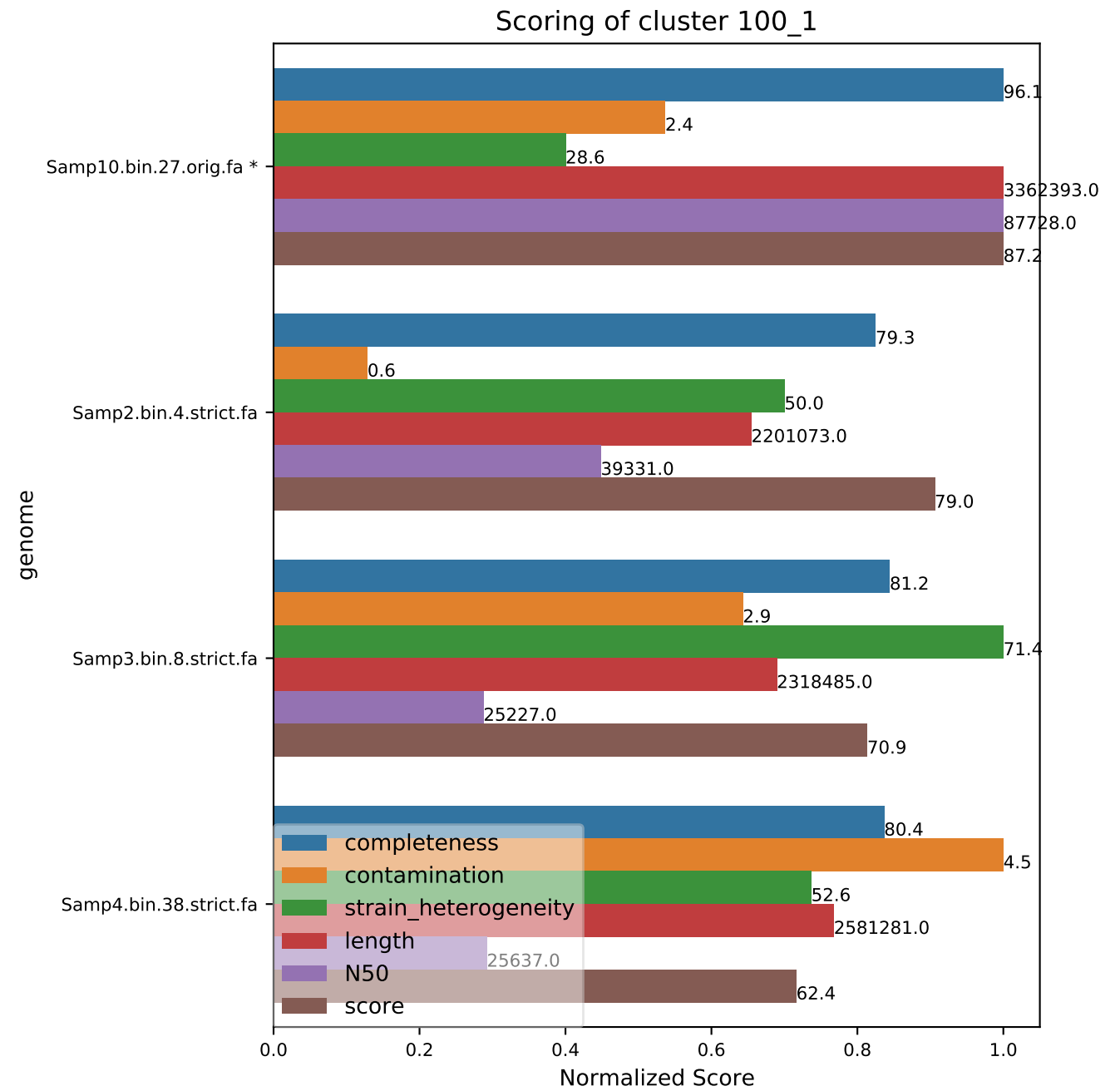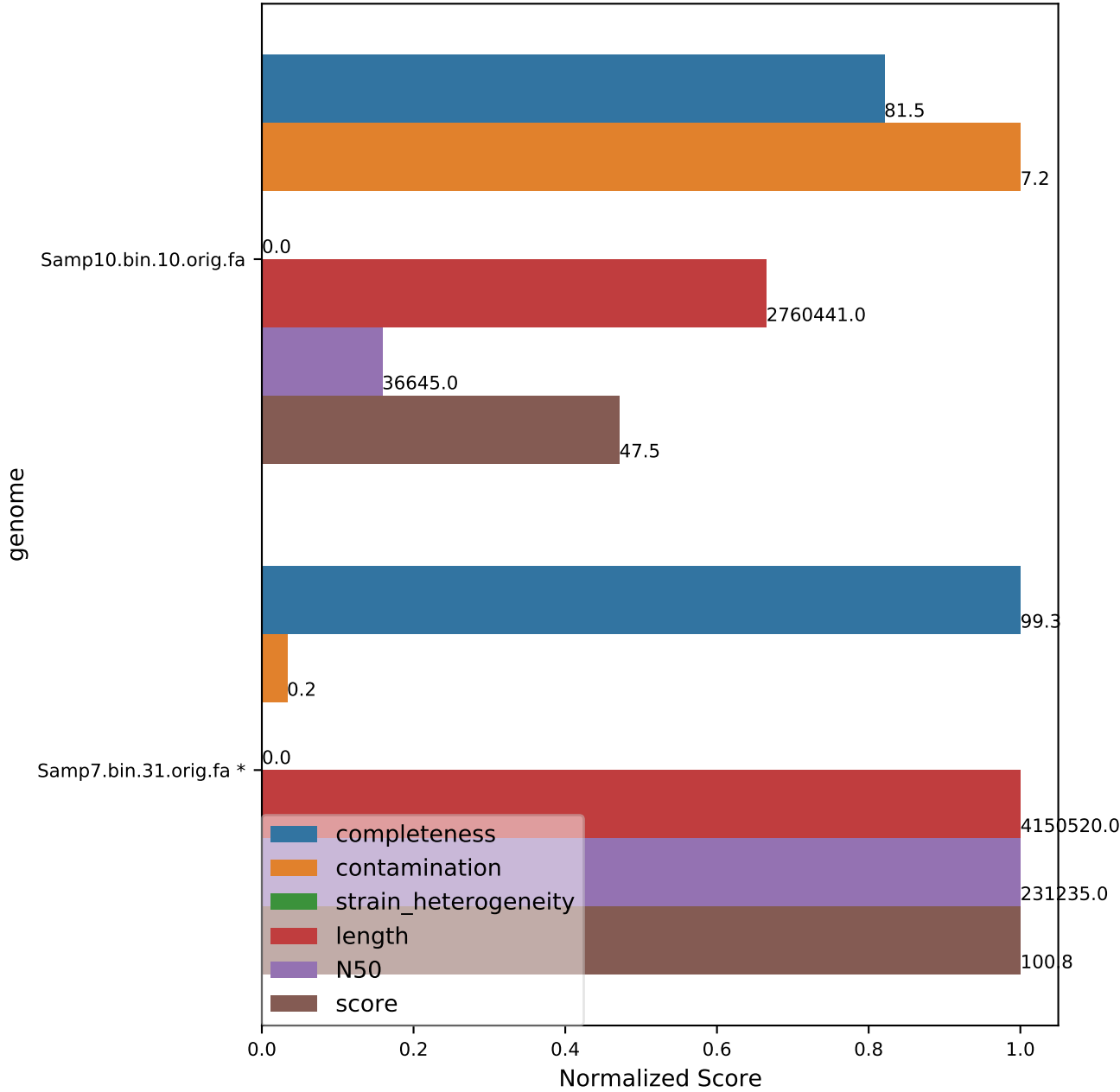
Scoring of cluster 83_1
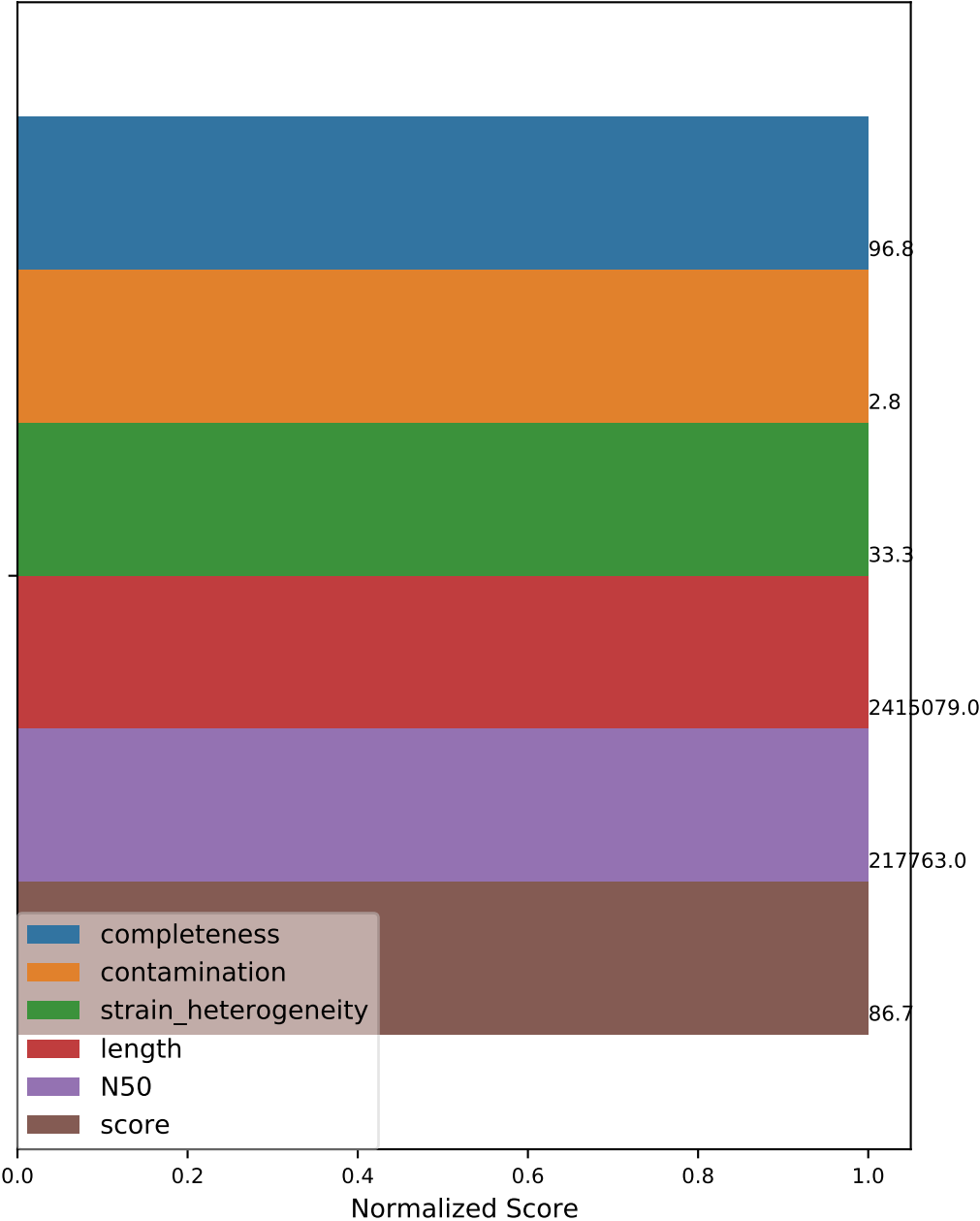
Scoring of cluster 84_1

Scoring of cluster 85_0

Scoring of cluster 86_1

Scoring of cluster 86_2

genome

Samp9.bin.3.orig.fa *

99.7
0.1
0.0
2868712.0
354812.0
1019

completeness
contamination
strain_heterogeneity
length
N50
score

Normalized Score

Scoring of cluster 87_0

Scoring of cluster 88_0

Scoring of cluster 89_0

genome

Samp5.bin.31.permissive.fa *

81.8

0.0

0.0

1706608.0

17631.0

83.9

- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

Normalized Score
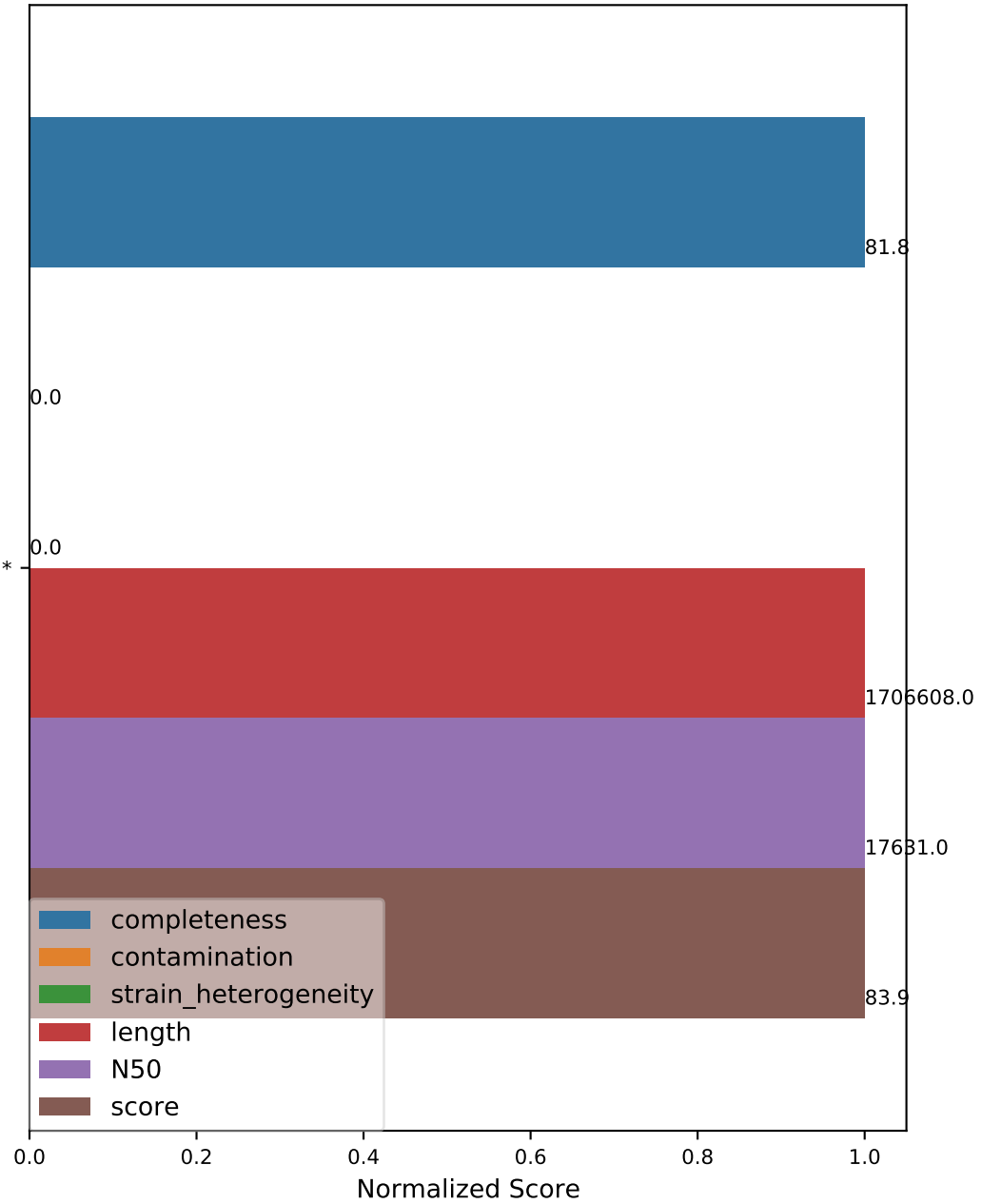
Scoring of cluster 90_0
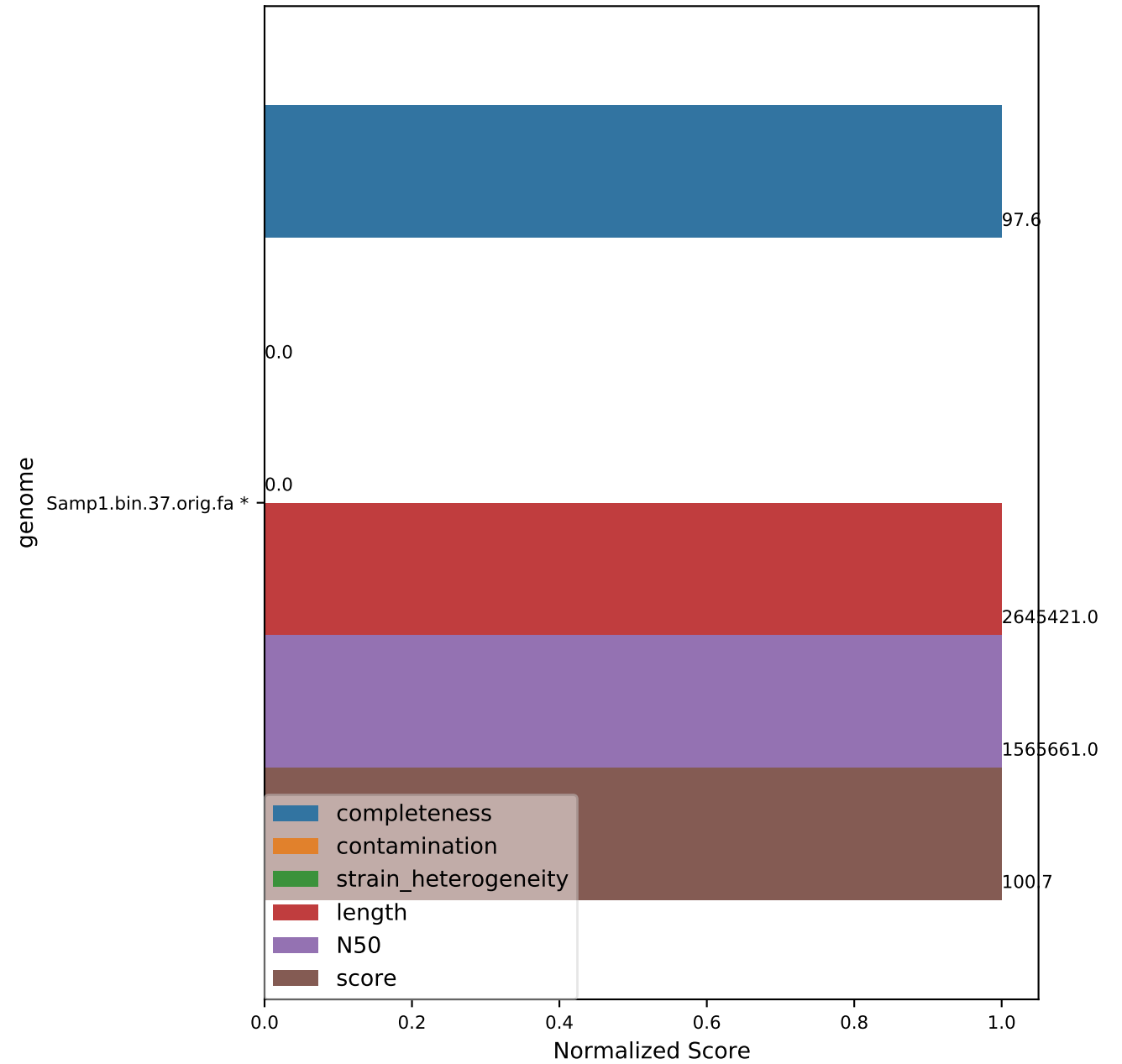
Scoring of cluster 91_0
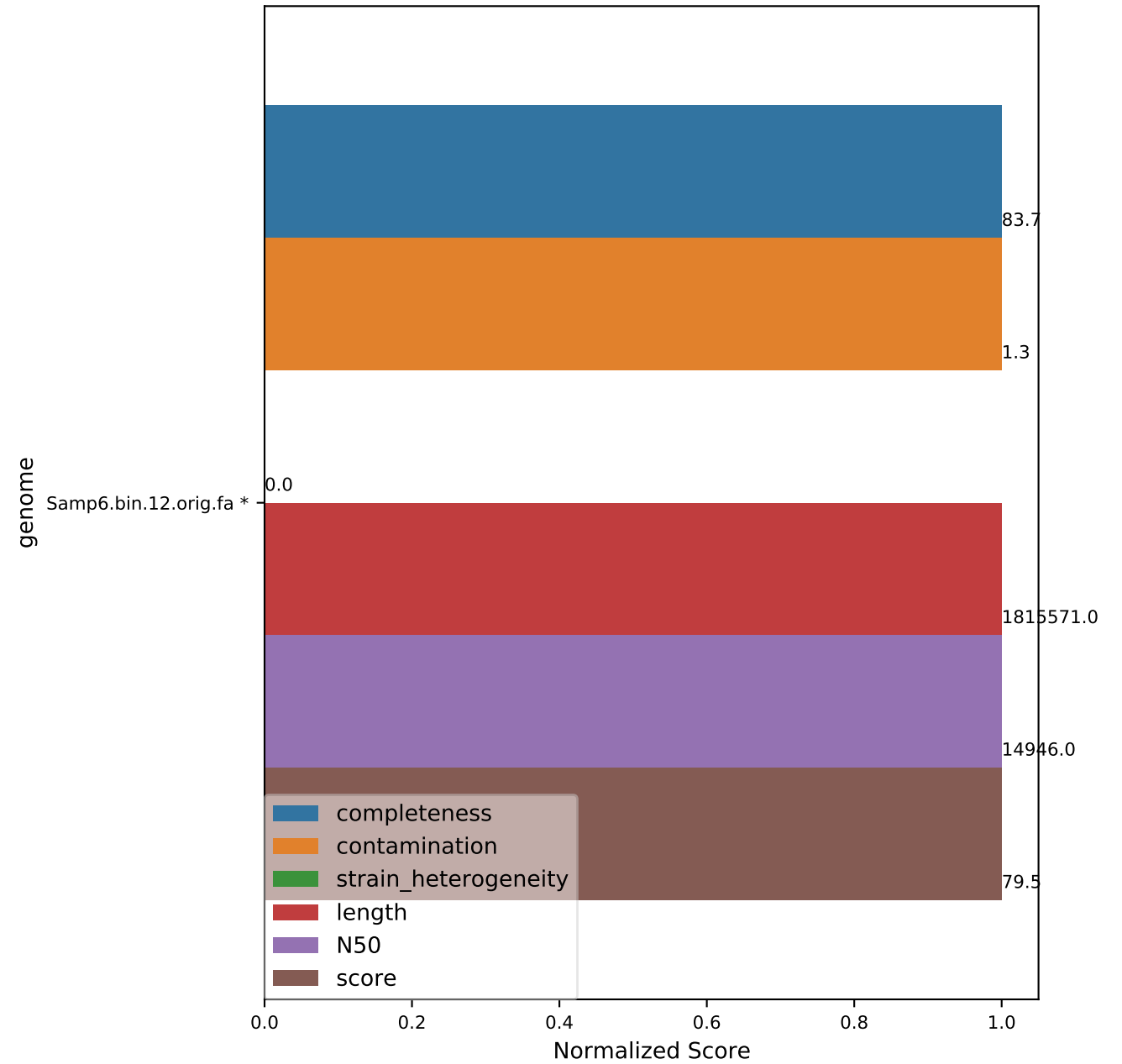
Scoring of cluster 92_1

Scoring of cluster 93_1

Scoring of cluster 94_1

Scoring of cluster 95_0

Scoring of cluster 96_1

Scoring of cluster 97_0

Scoring of cluster 98_1

Scoring of cluster 99_1

Scoring of cluster 100_1

Scoring of cluster 100_2
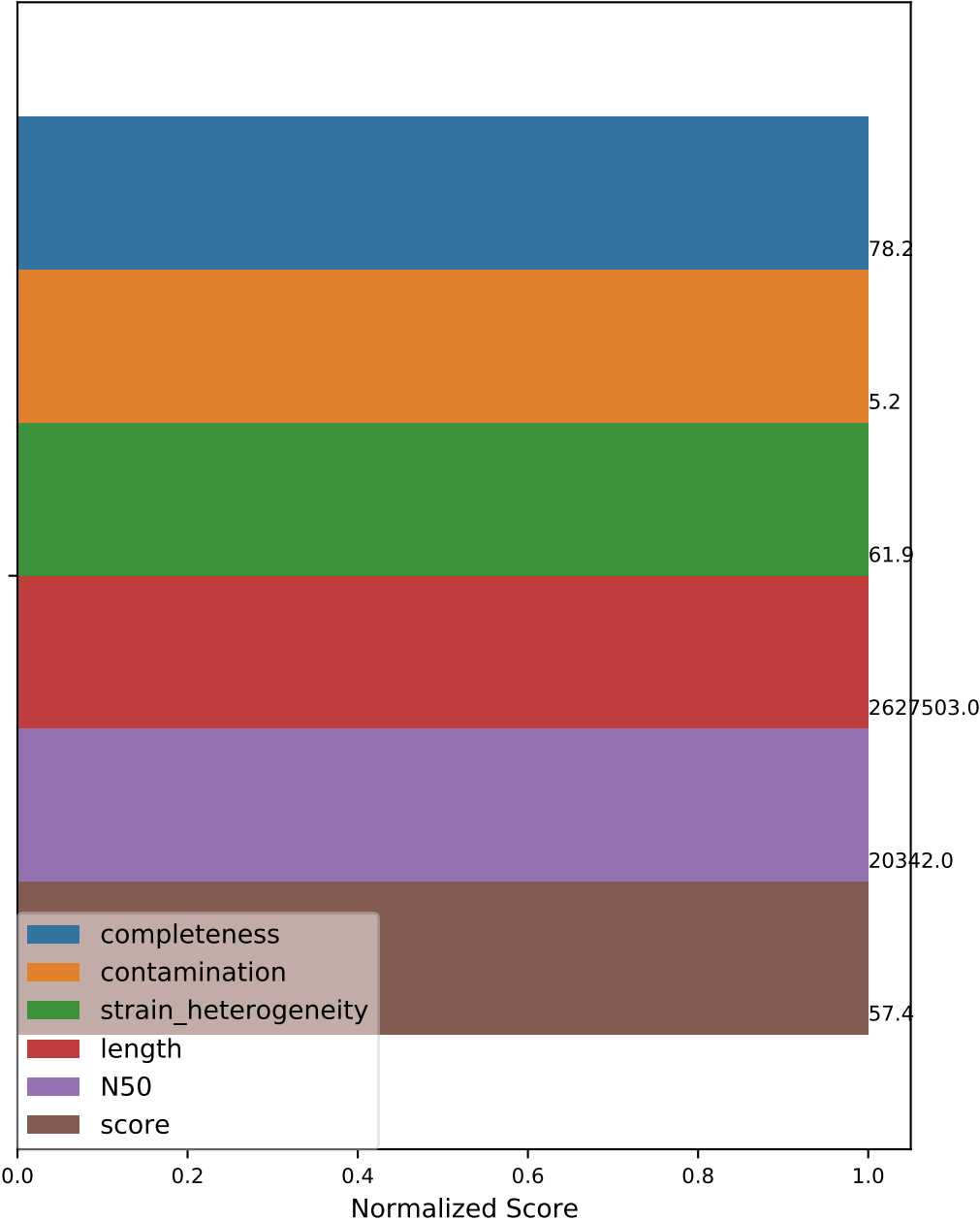
Scoring of cluster 101_1

Scoring of cluster 102_0

Scoring of cluster 103_1
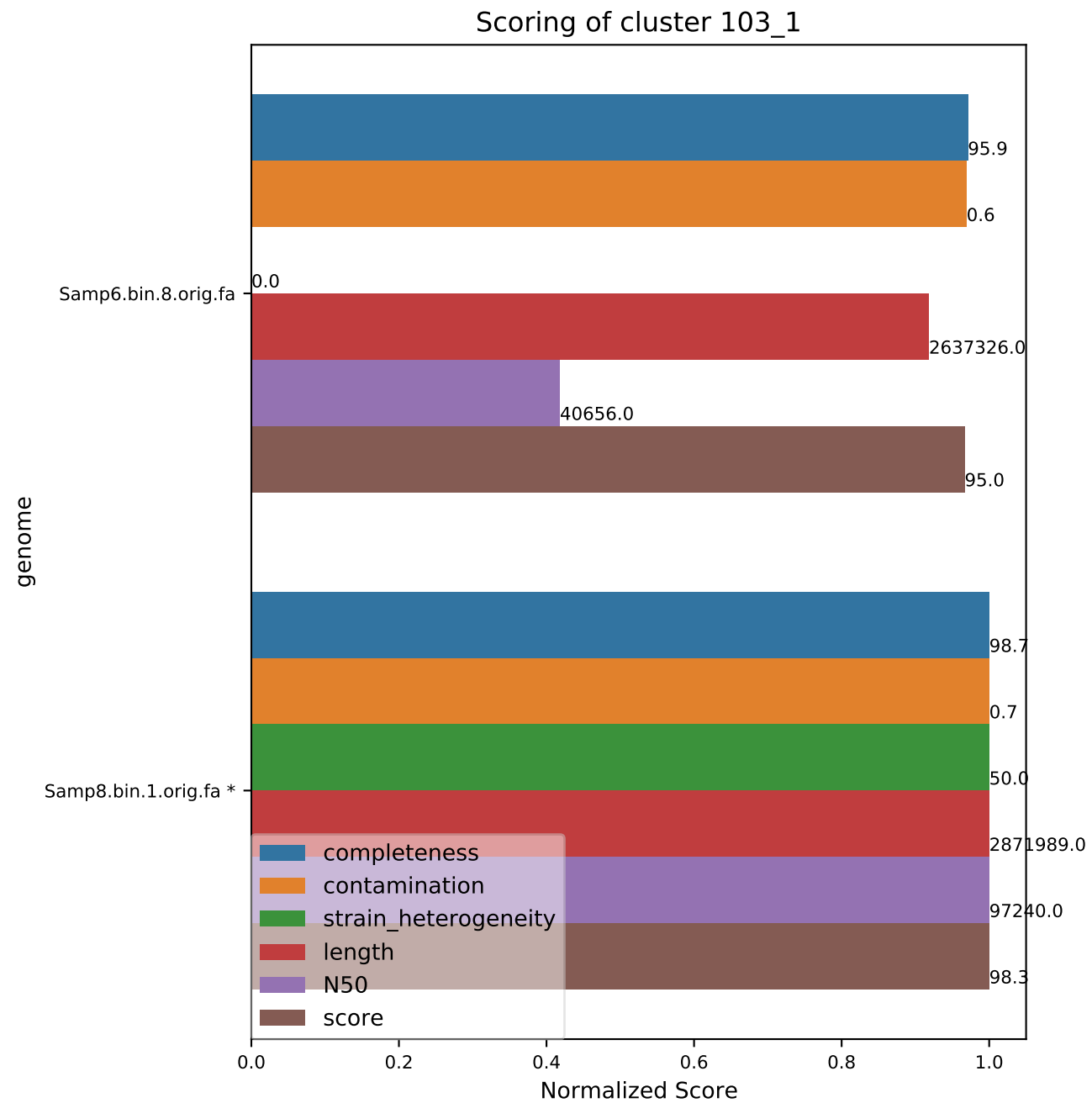
Scoring of cluster 104_0
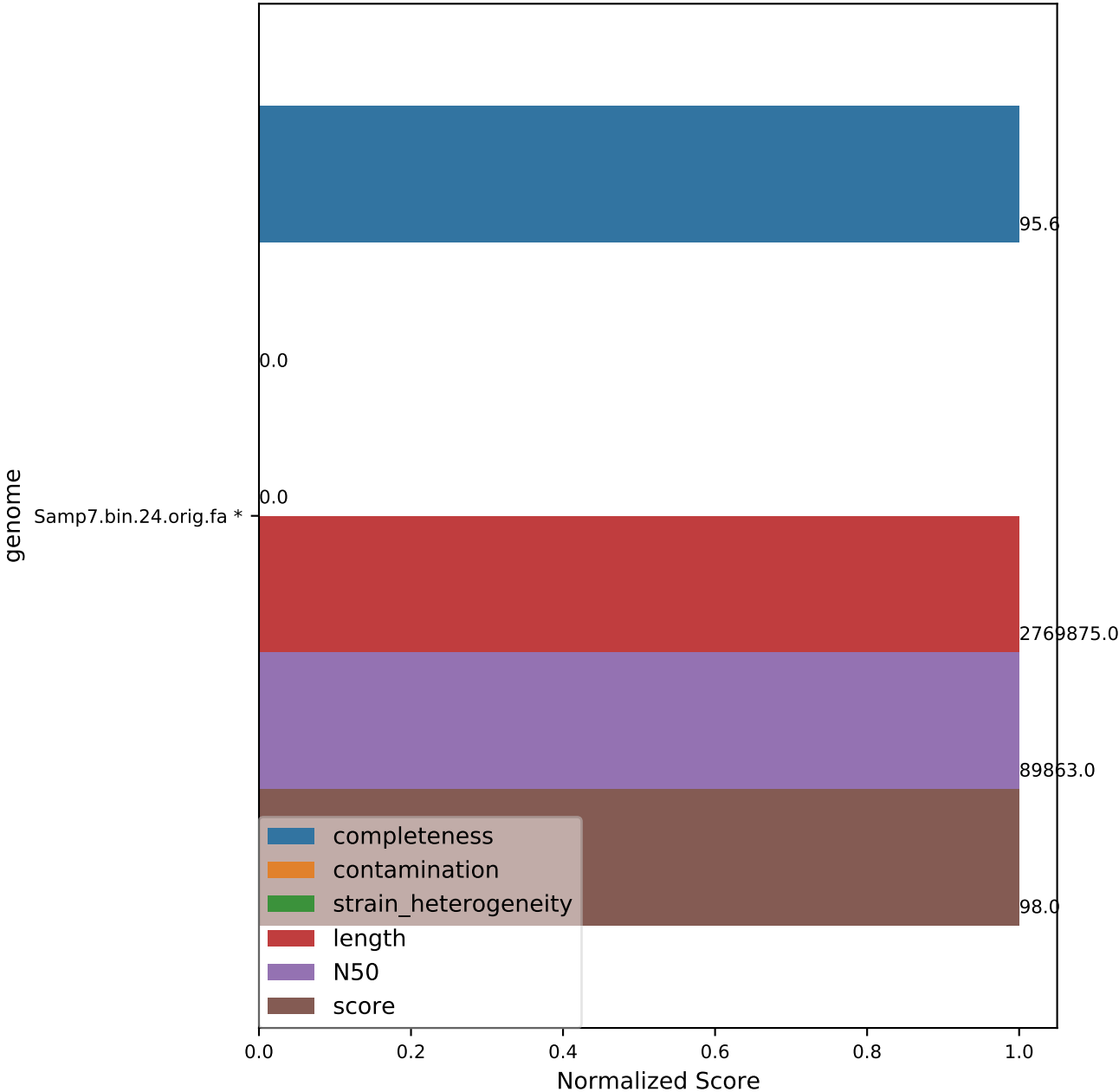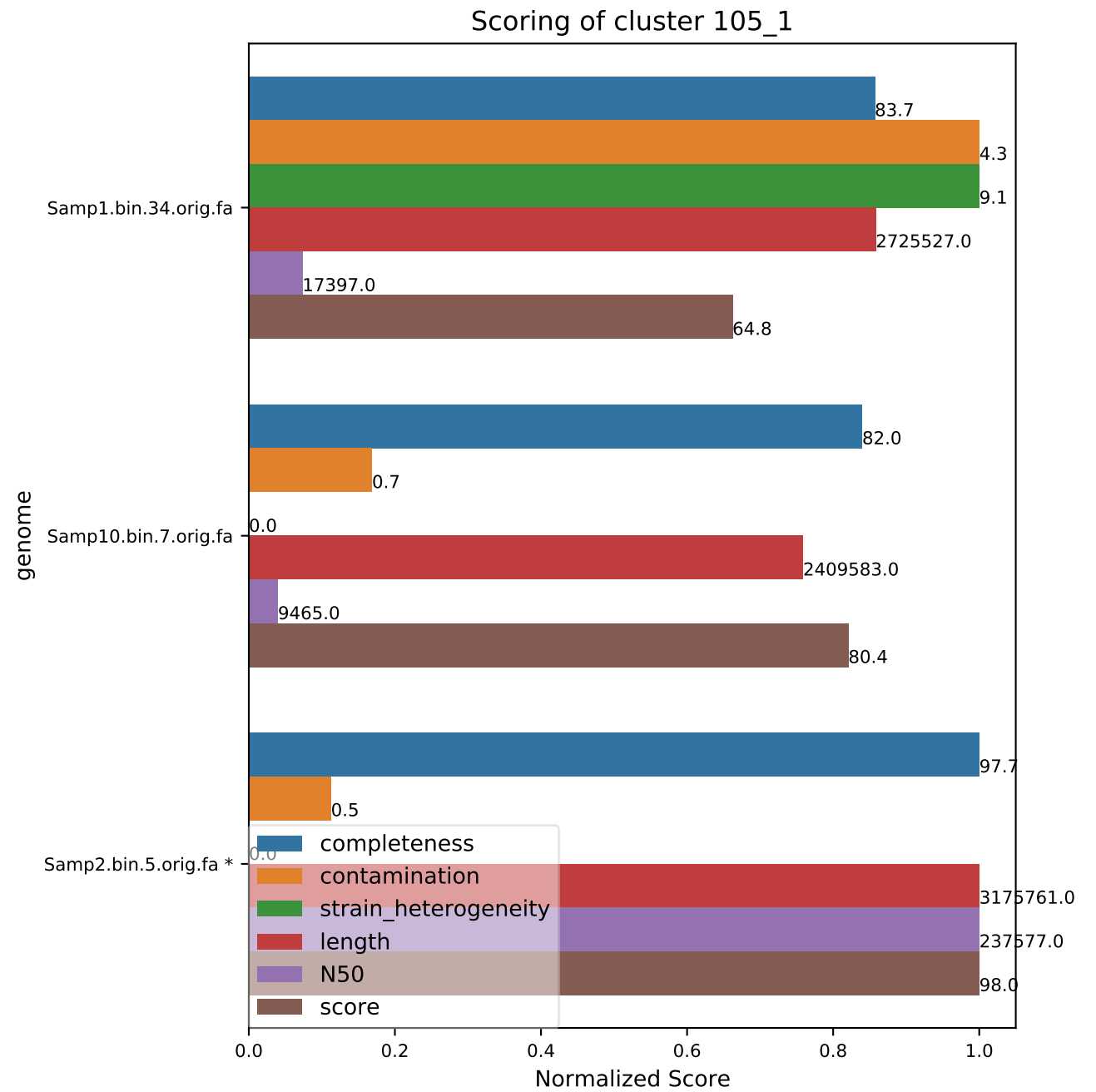
Scoring of cluster 105_1

Scoring of cluster 106_0
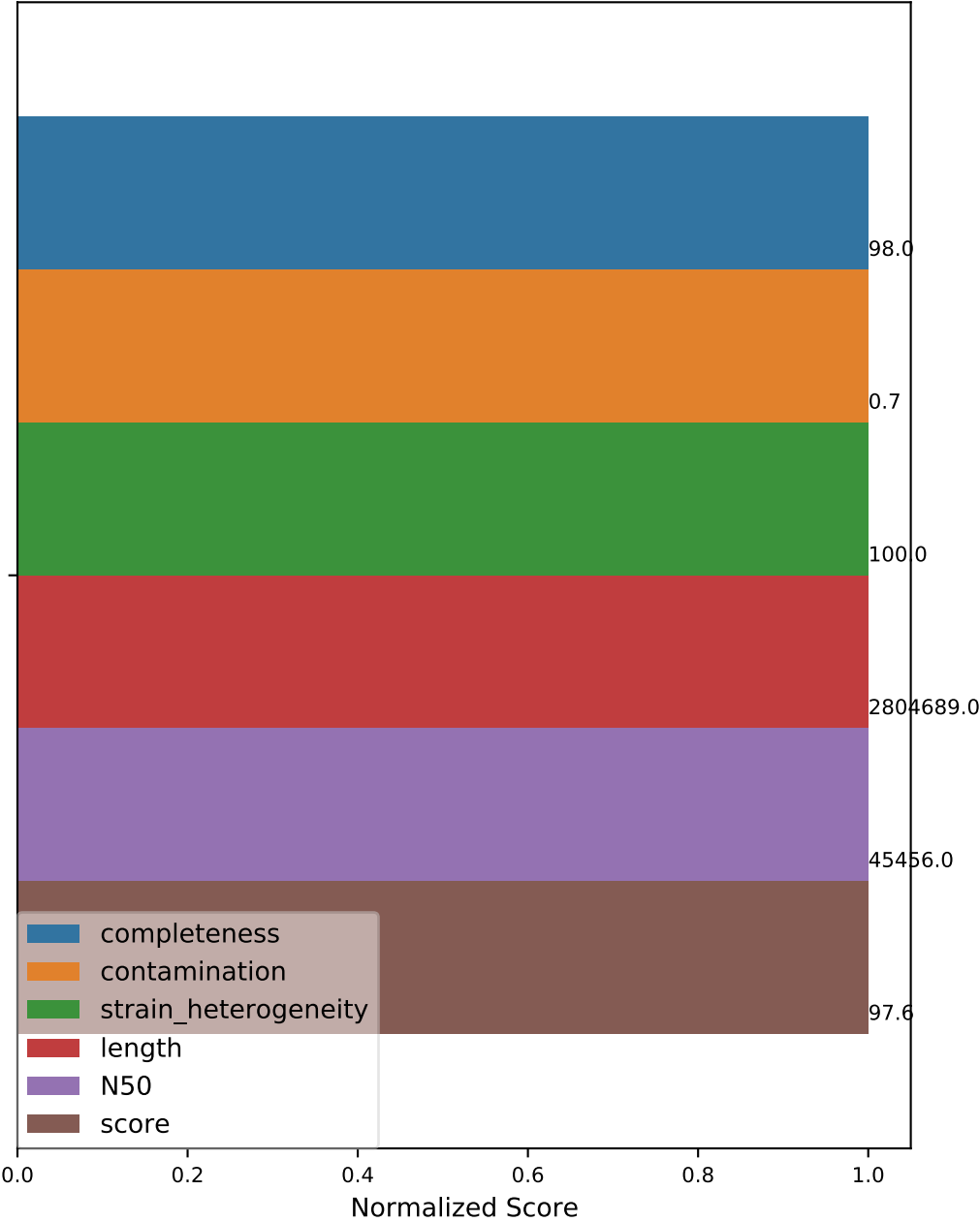
Scoring of cluster 107_0
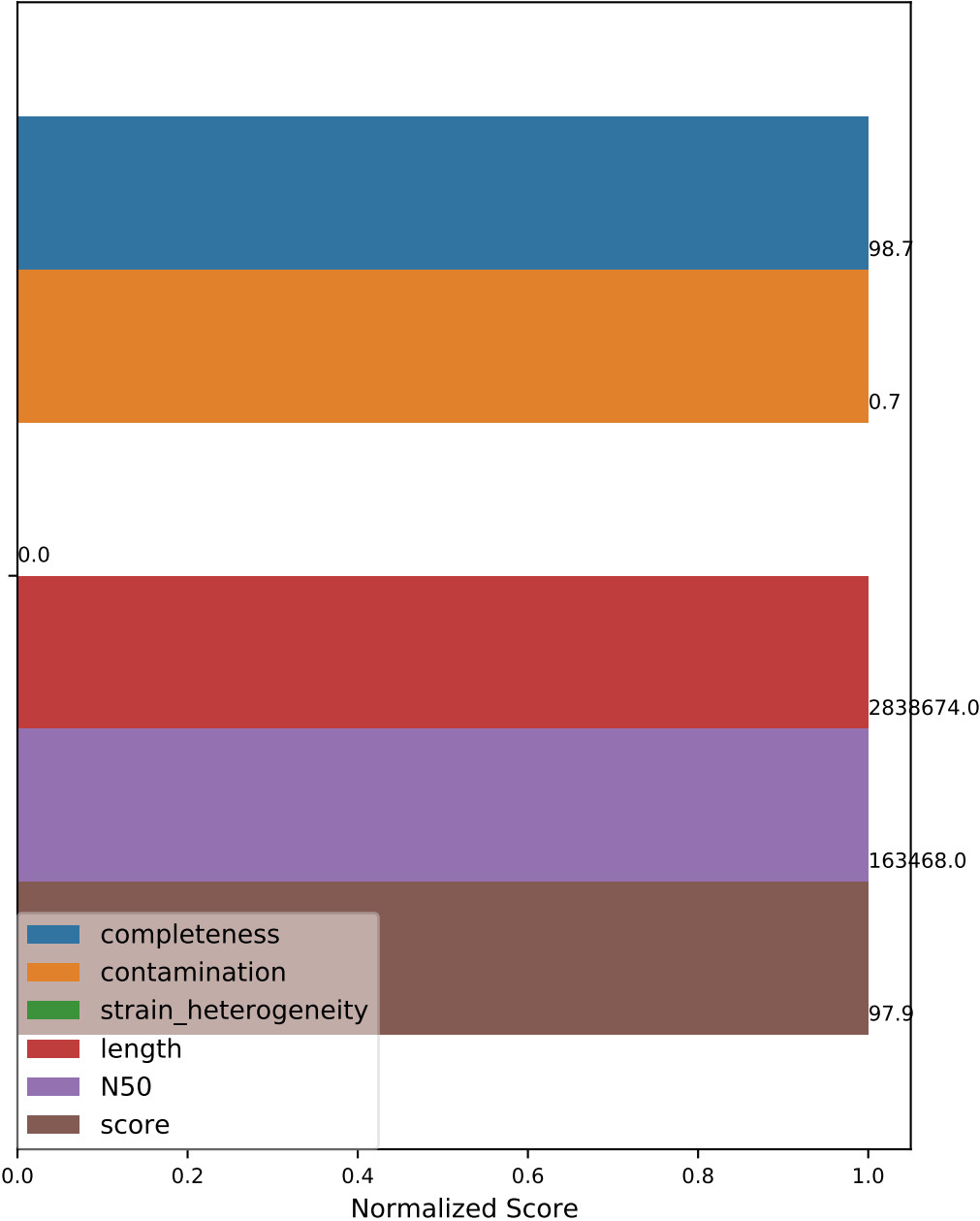
Scoring of cluster 108_0
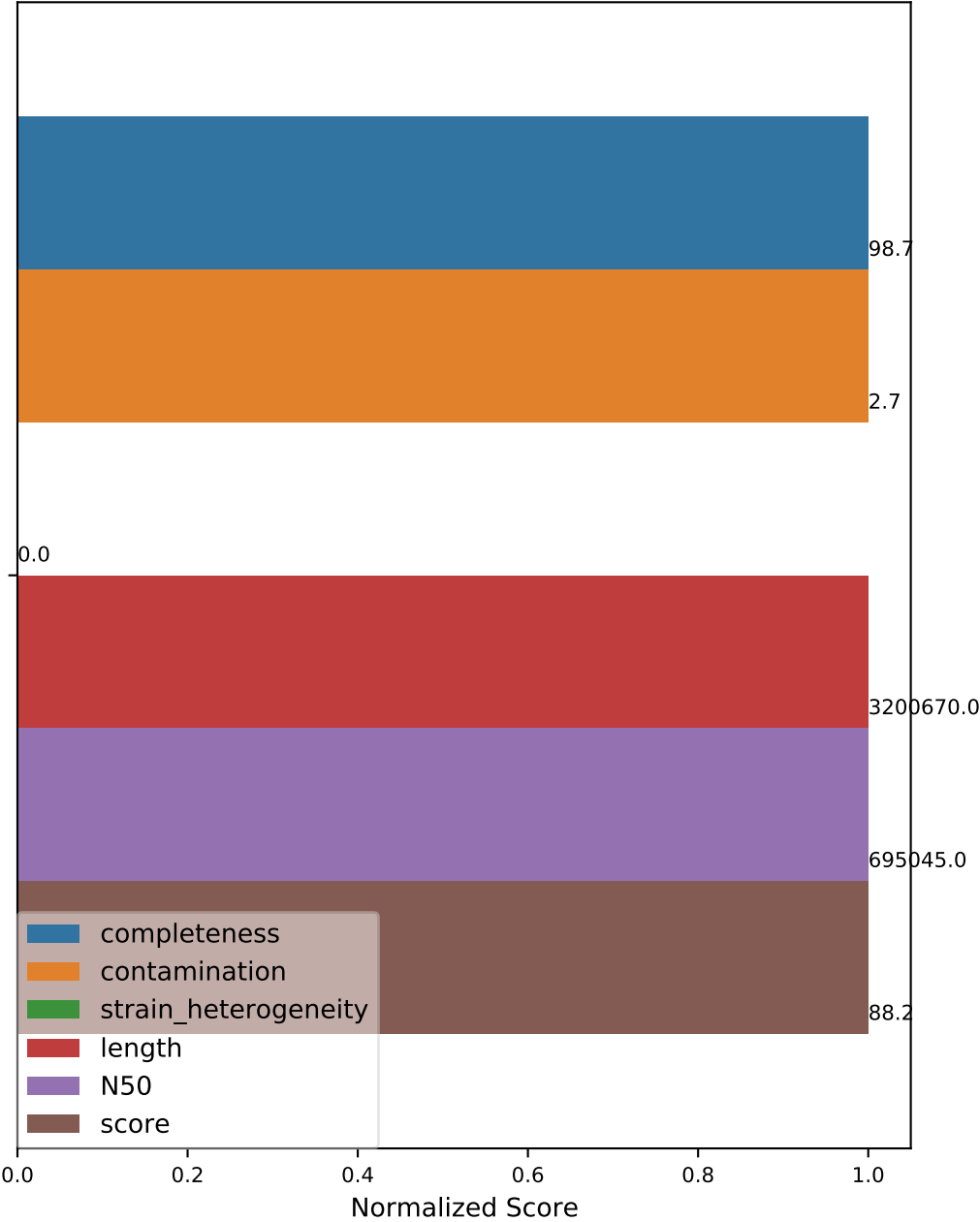
Scoring of cluster 109_0
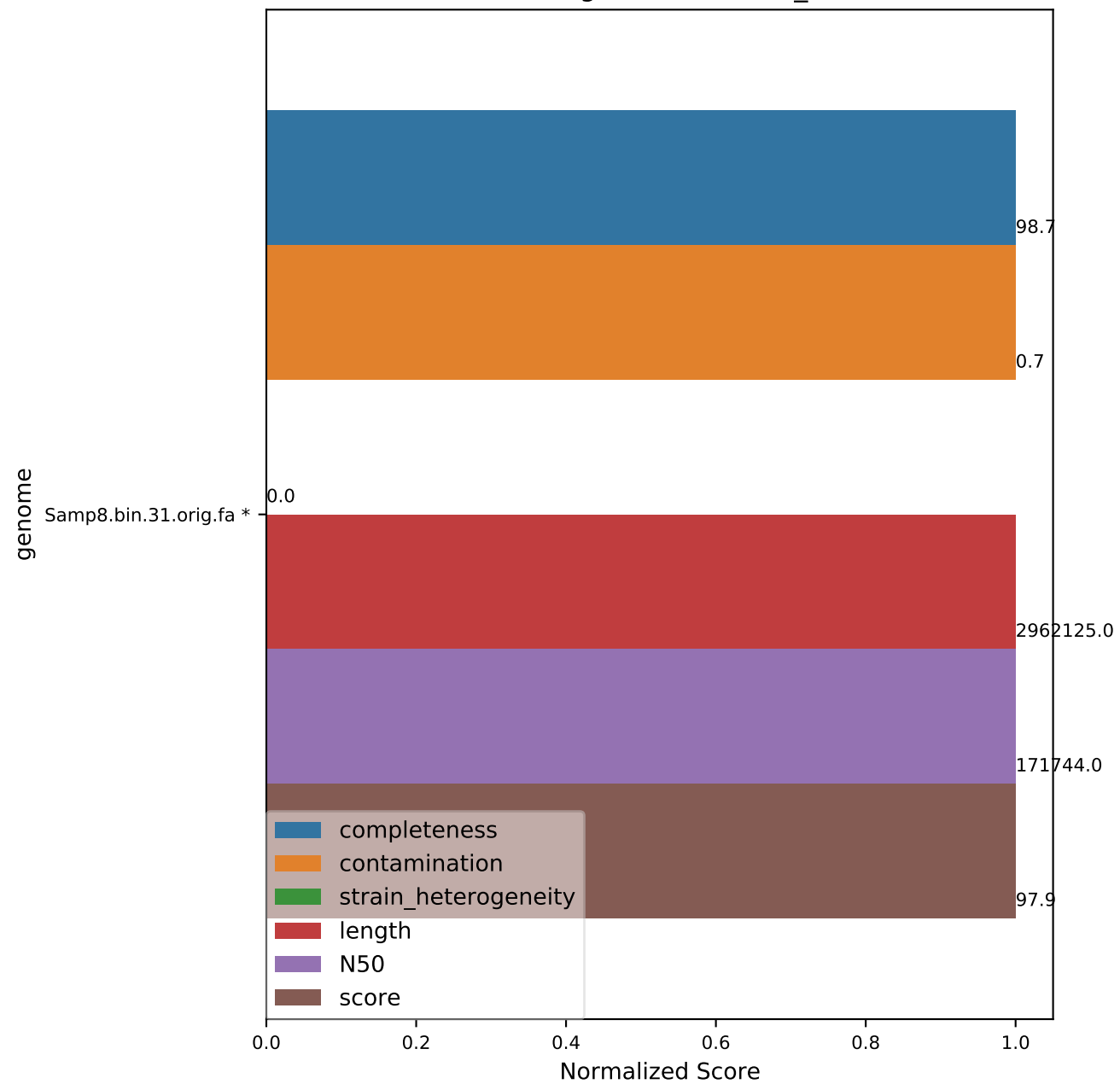
Scoring of cluster 110_1
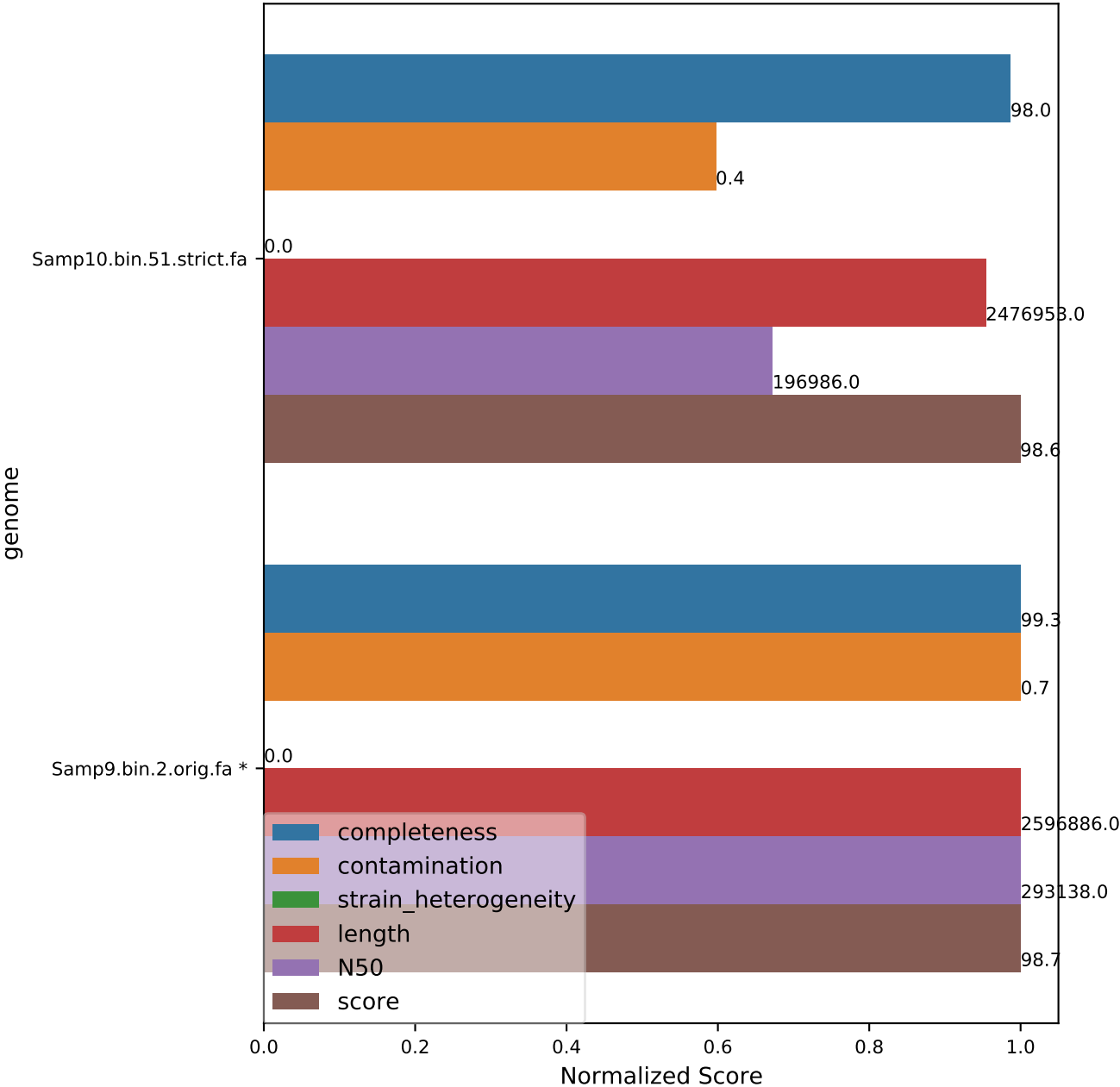
Scoring of cluster 111_1
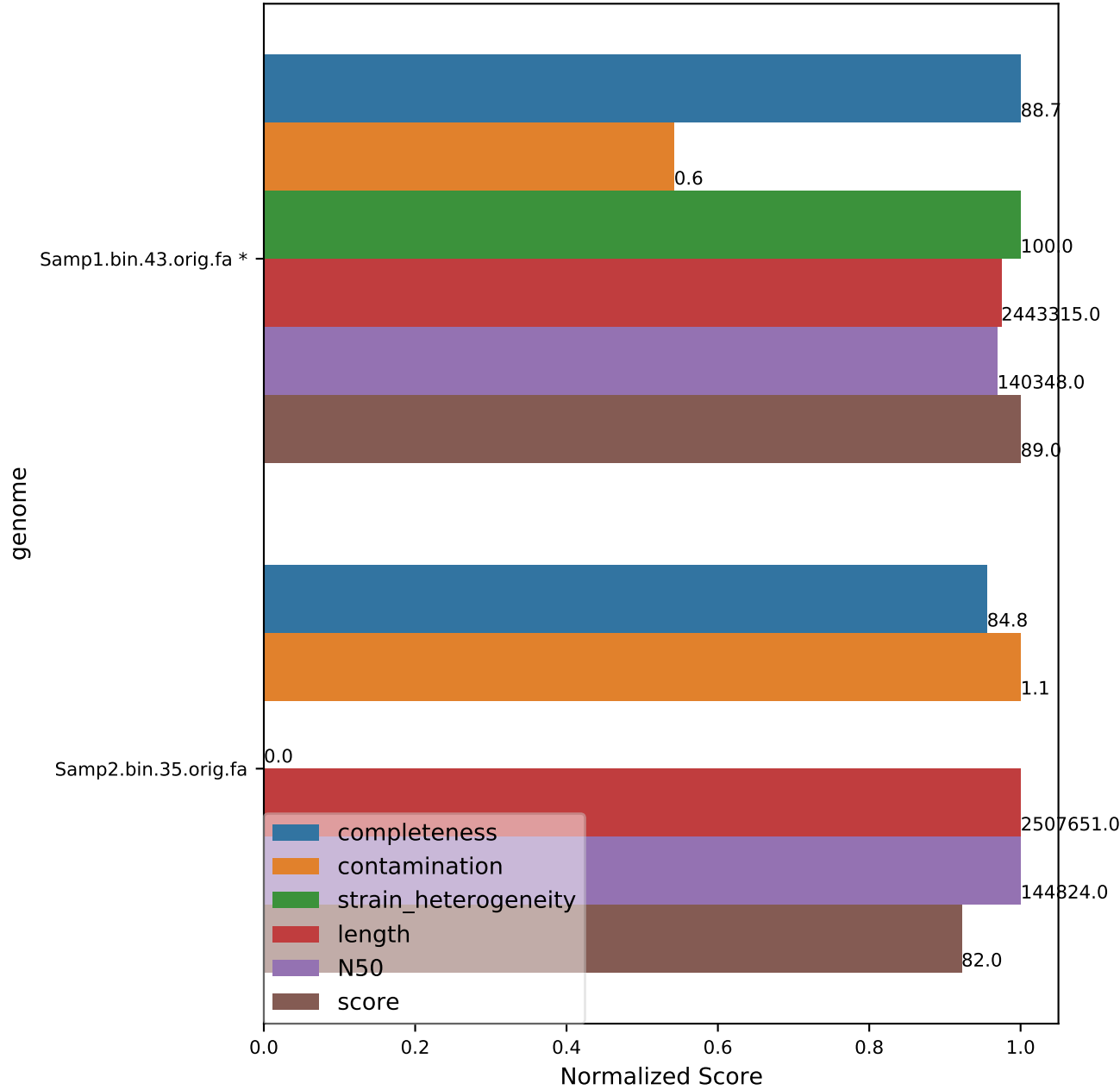
Scoring of cluster 111_2

Scoring of cluster 112_1
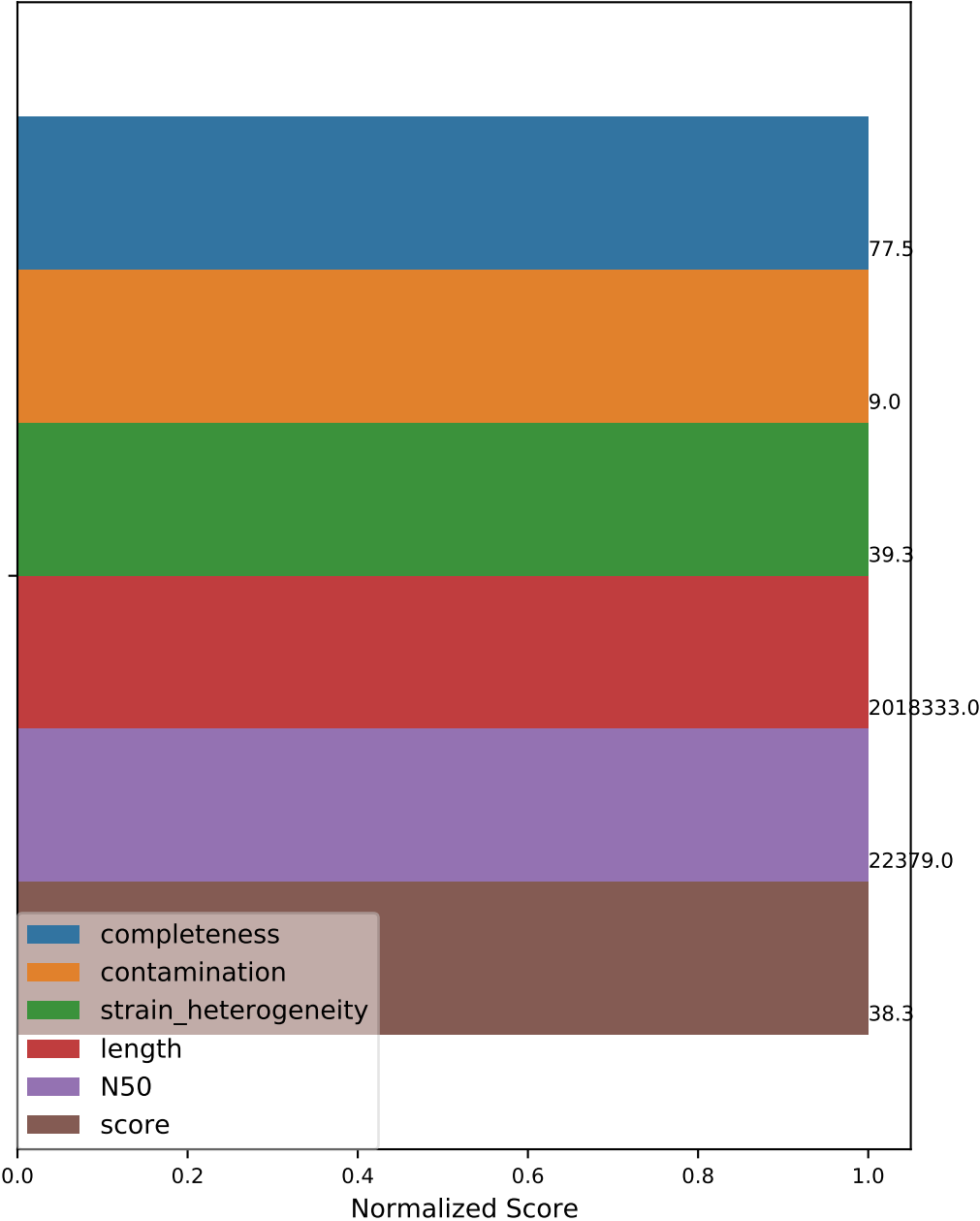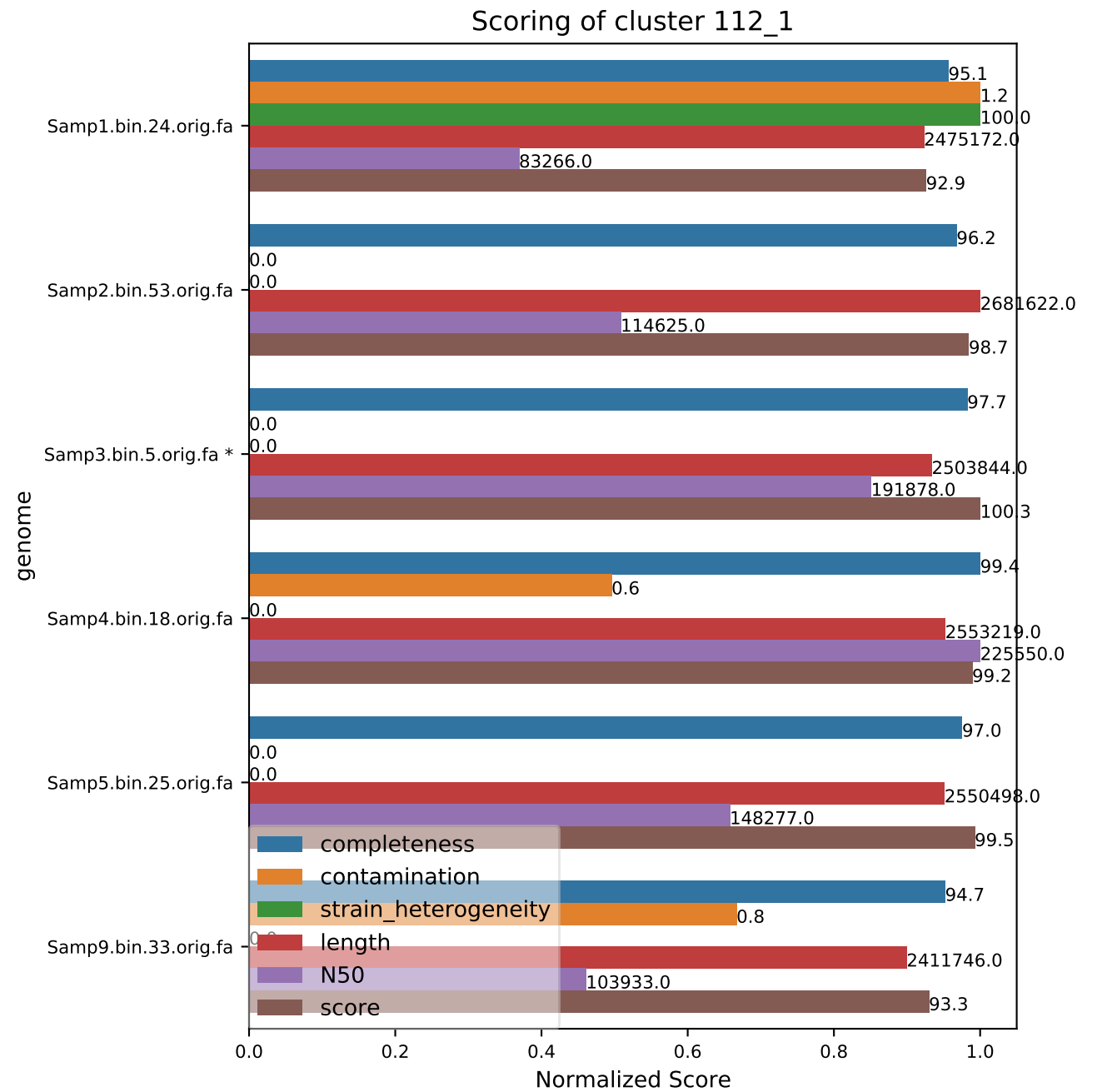
Scoring of cluster 113_1
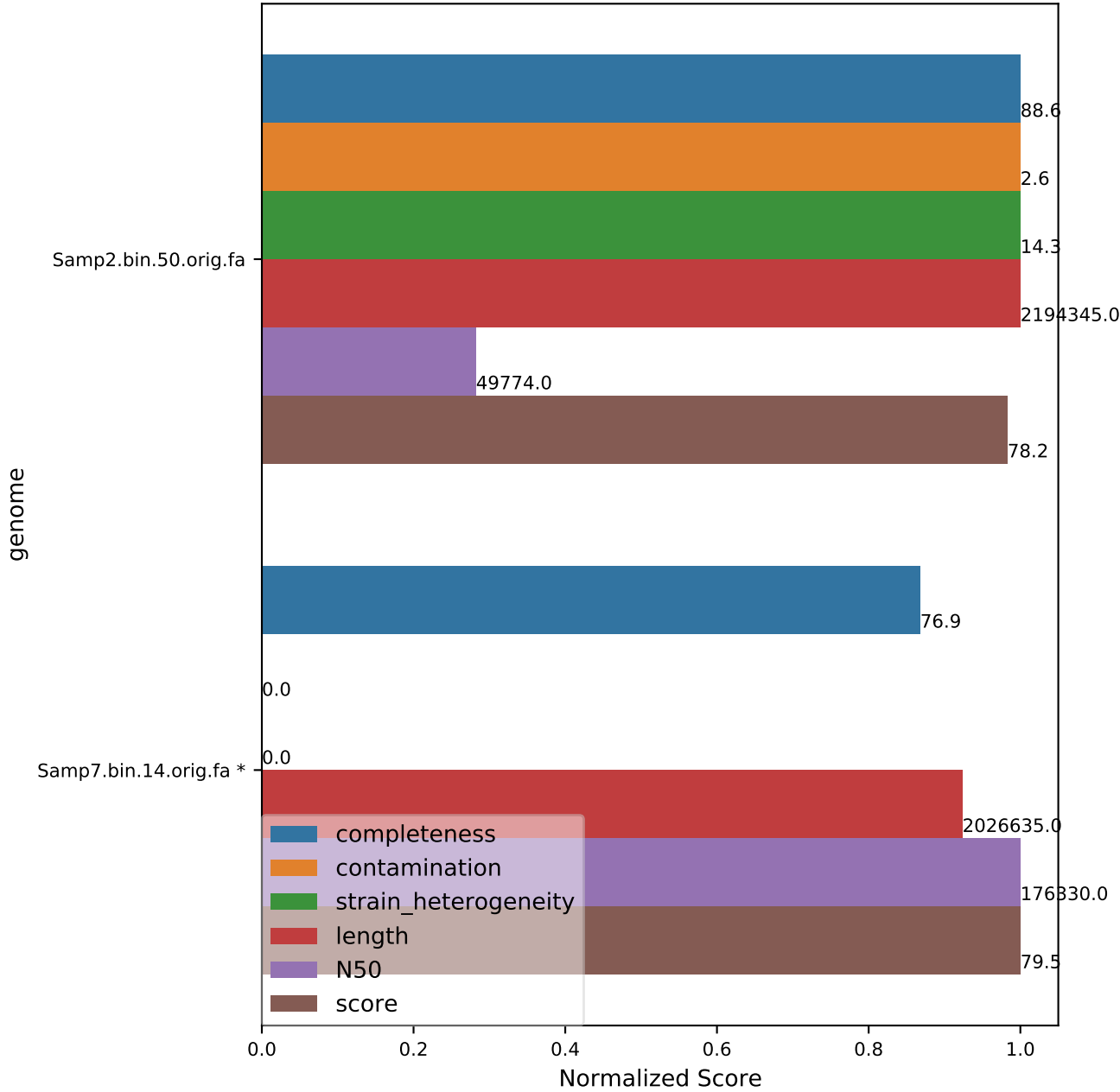
Scoring of cluster 114_0
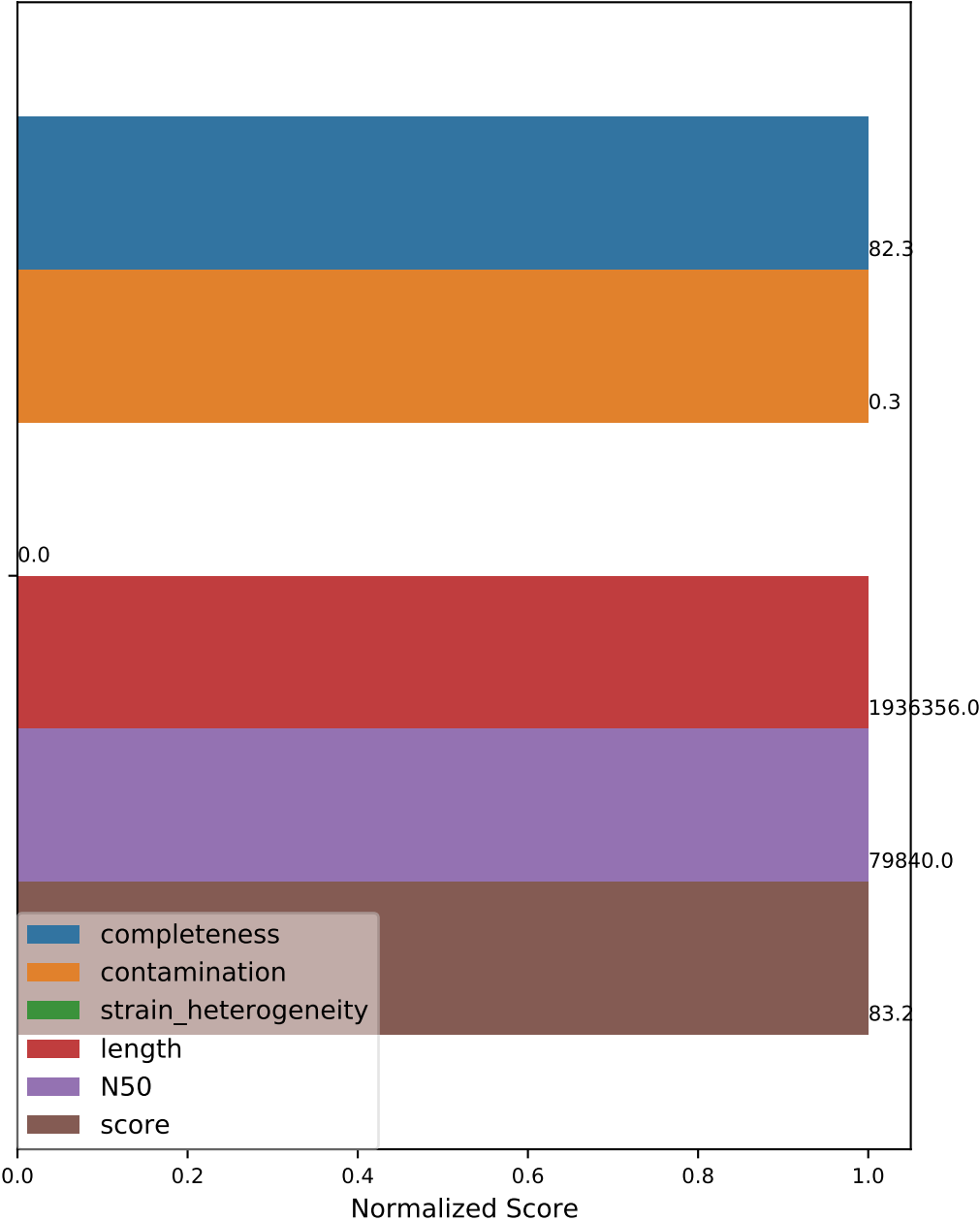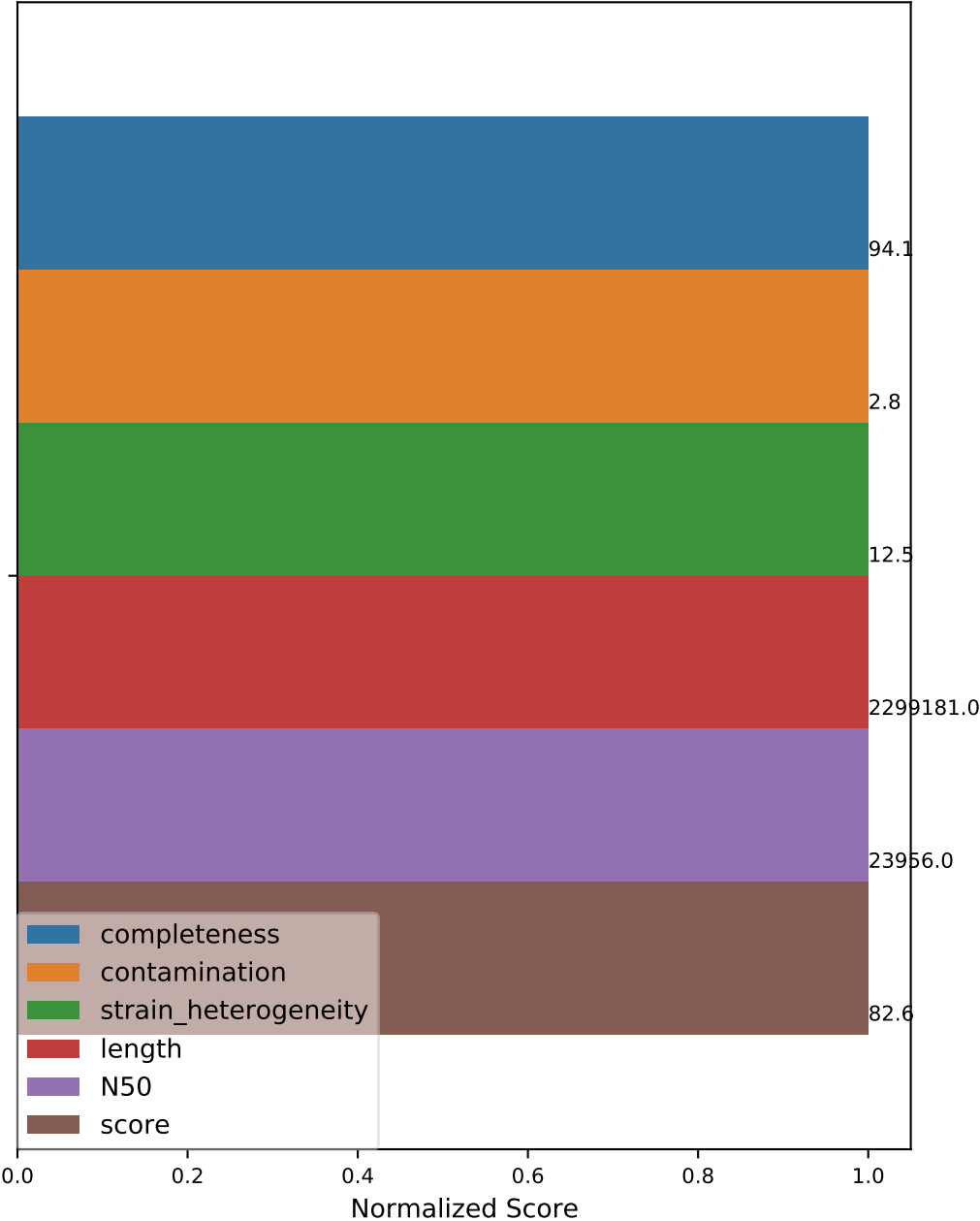
Scoring of cluster 115_0
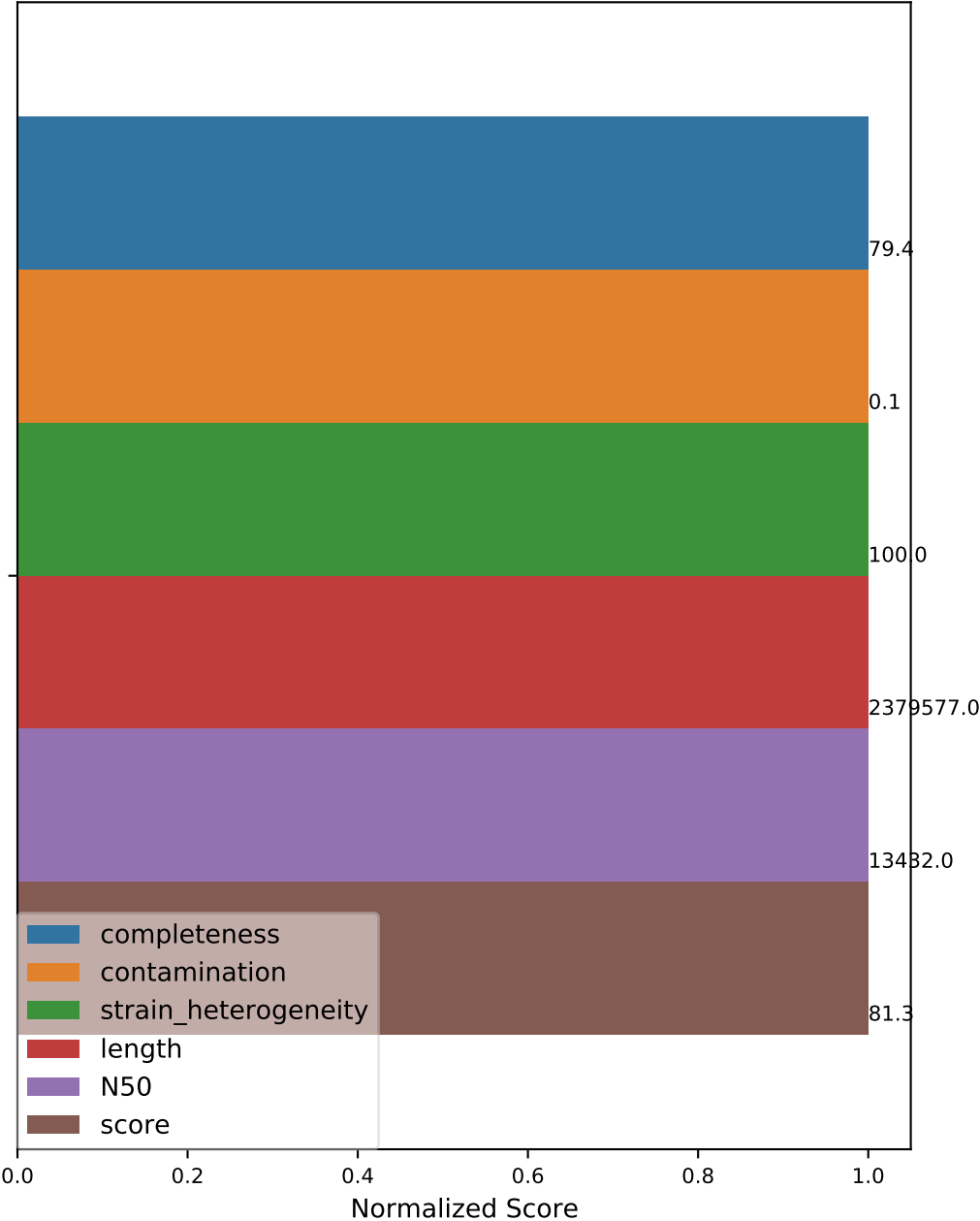
Scoring of cluster 116_0

Scoring of cluster 117_1
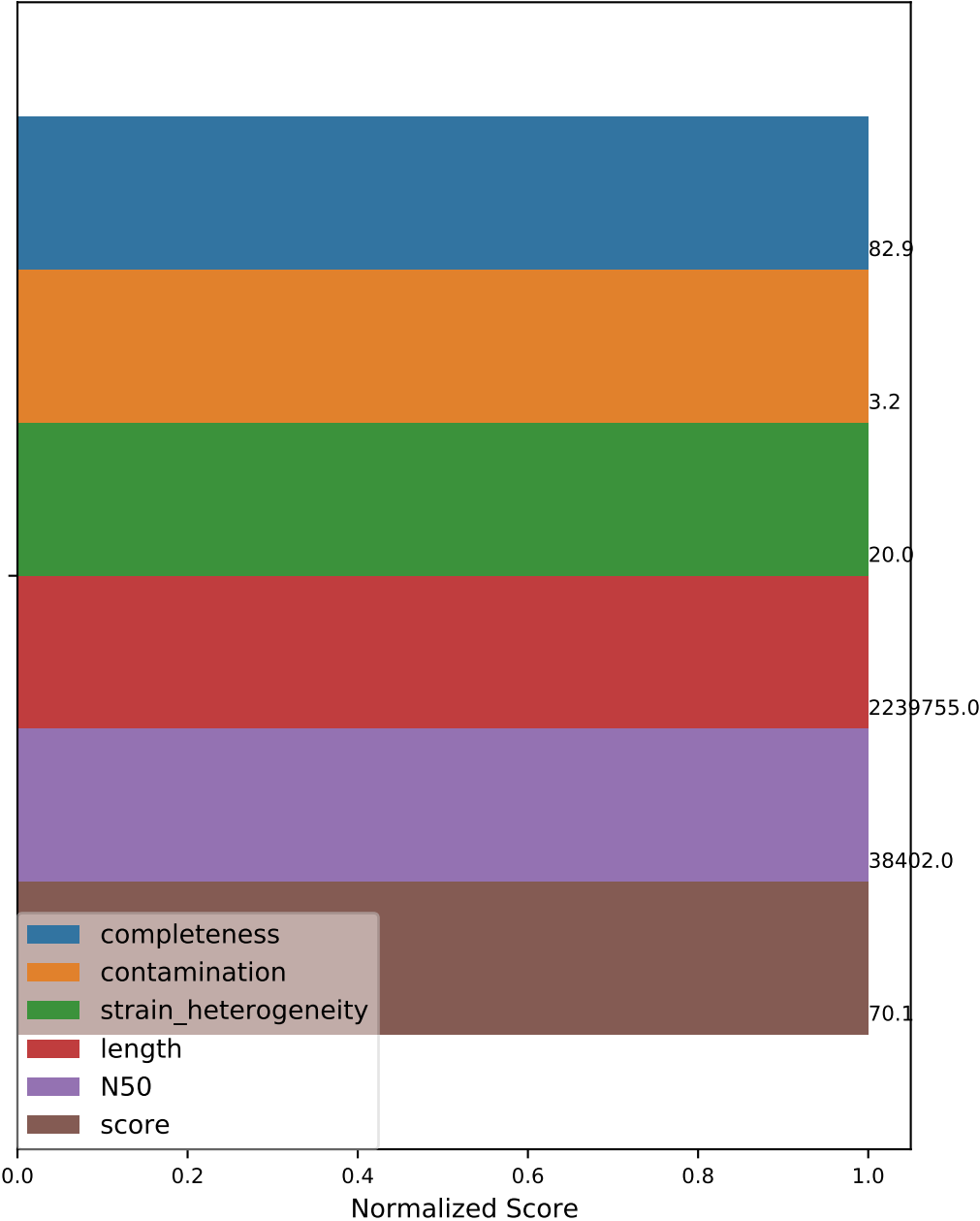
Scoring of cluster 117_2

Scoring of cluster 118_1
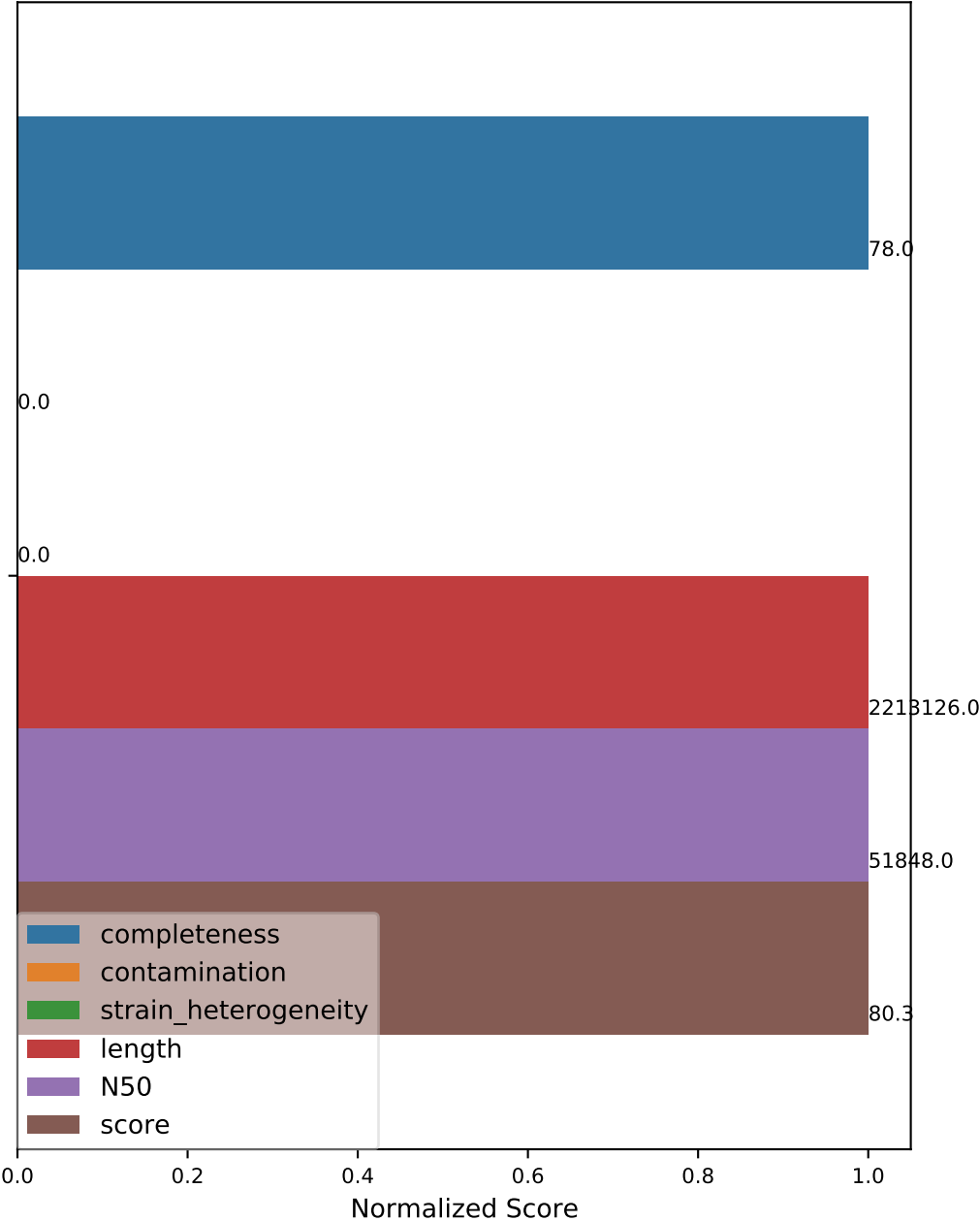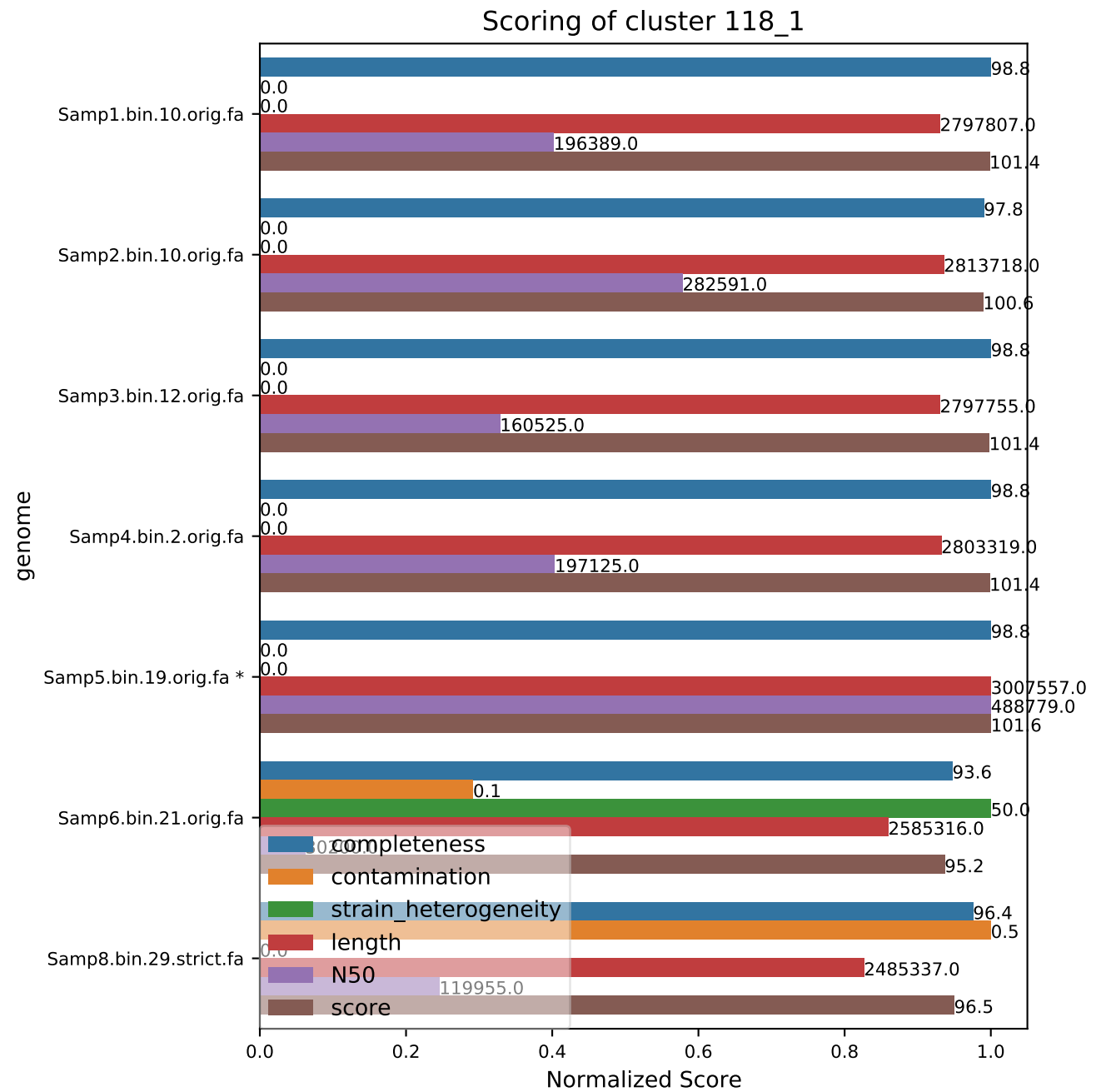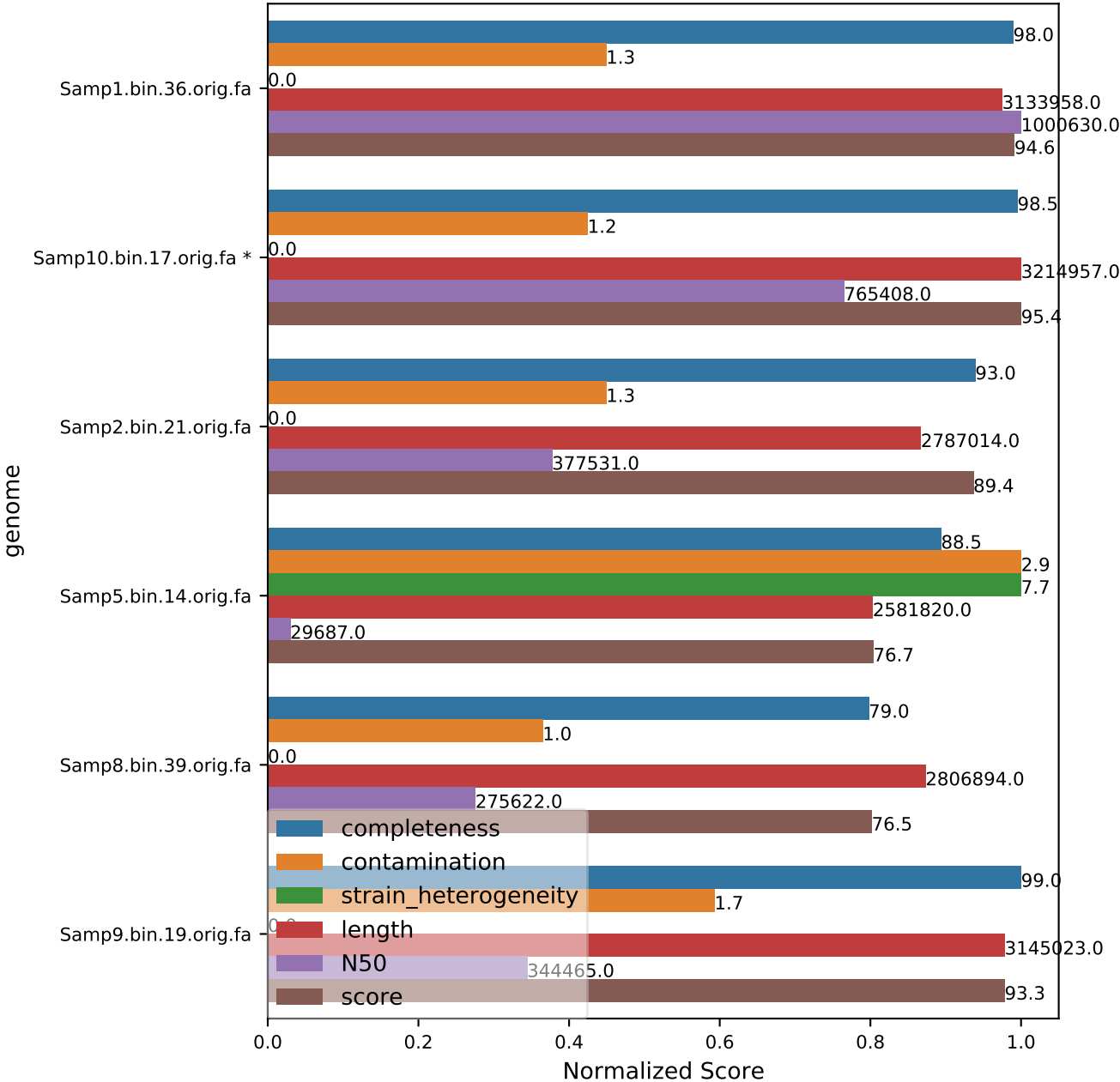
Scoring of cluster 119_1

Scoring of cluster 120_0
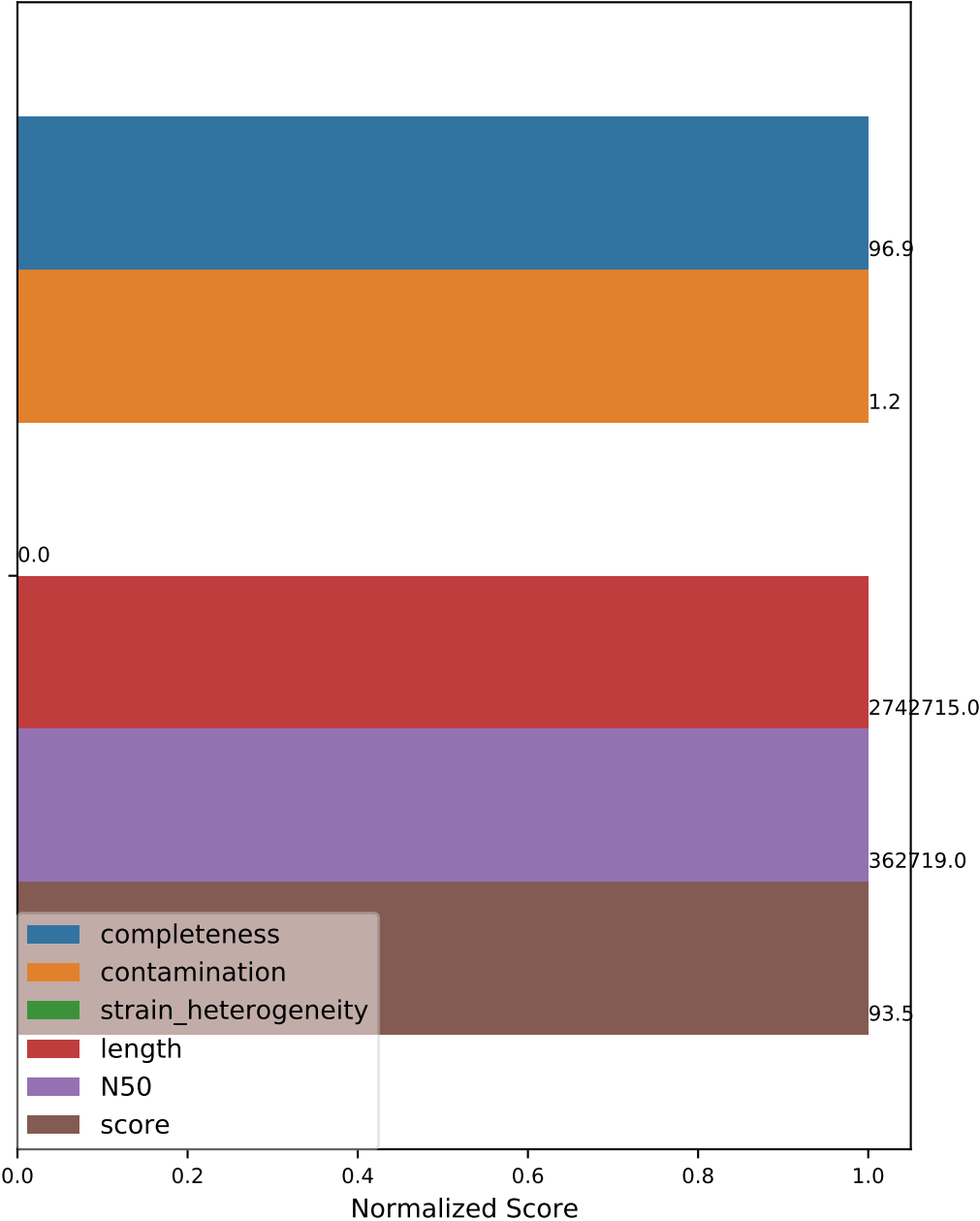
Scoring of cluster 121_1
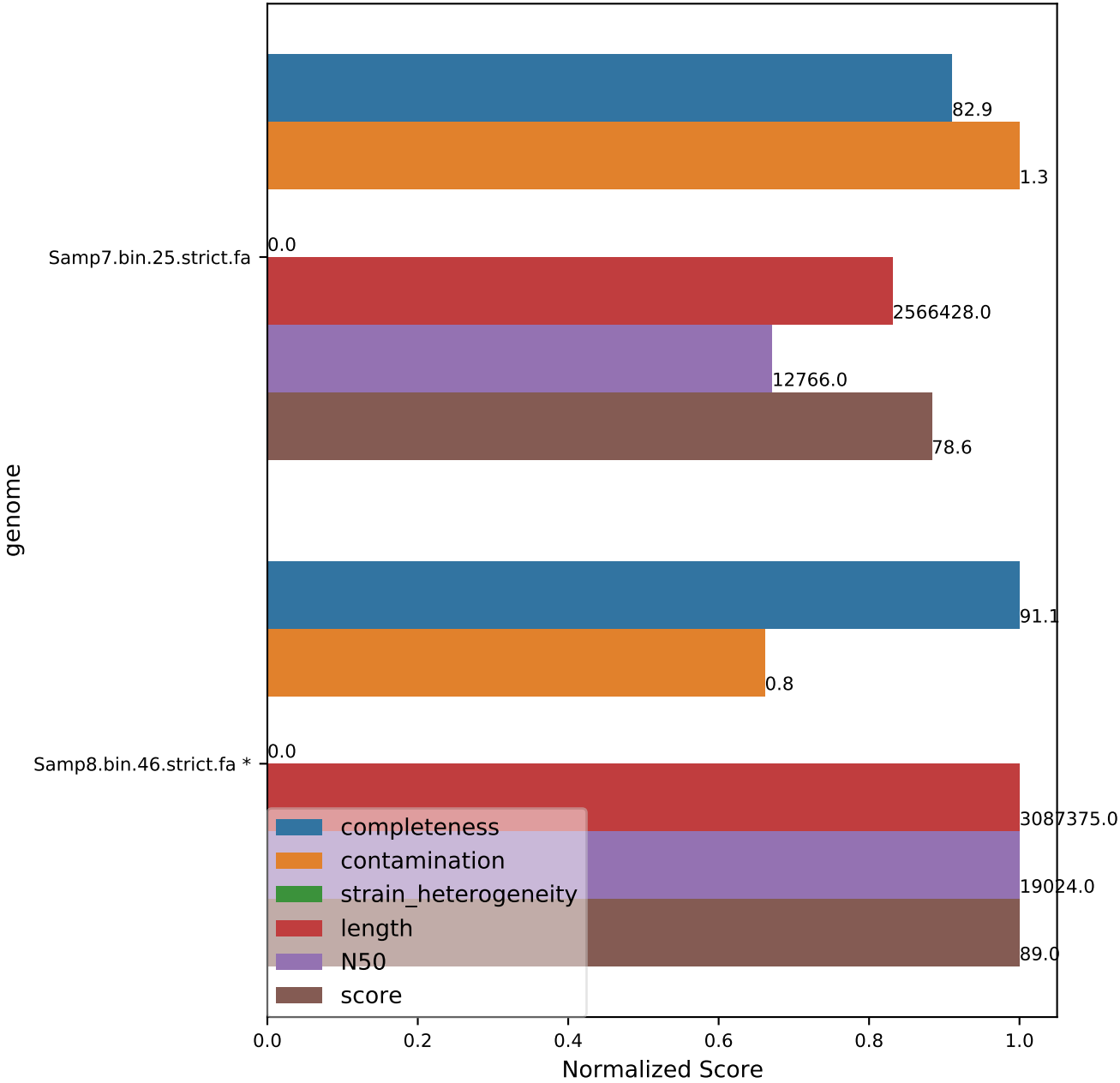
Scoring of cluster 122_0

Scoring of cluster 123_1
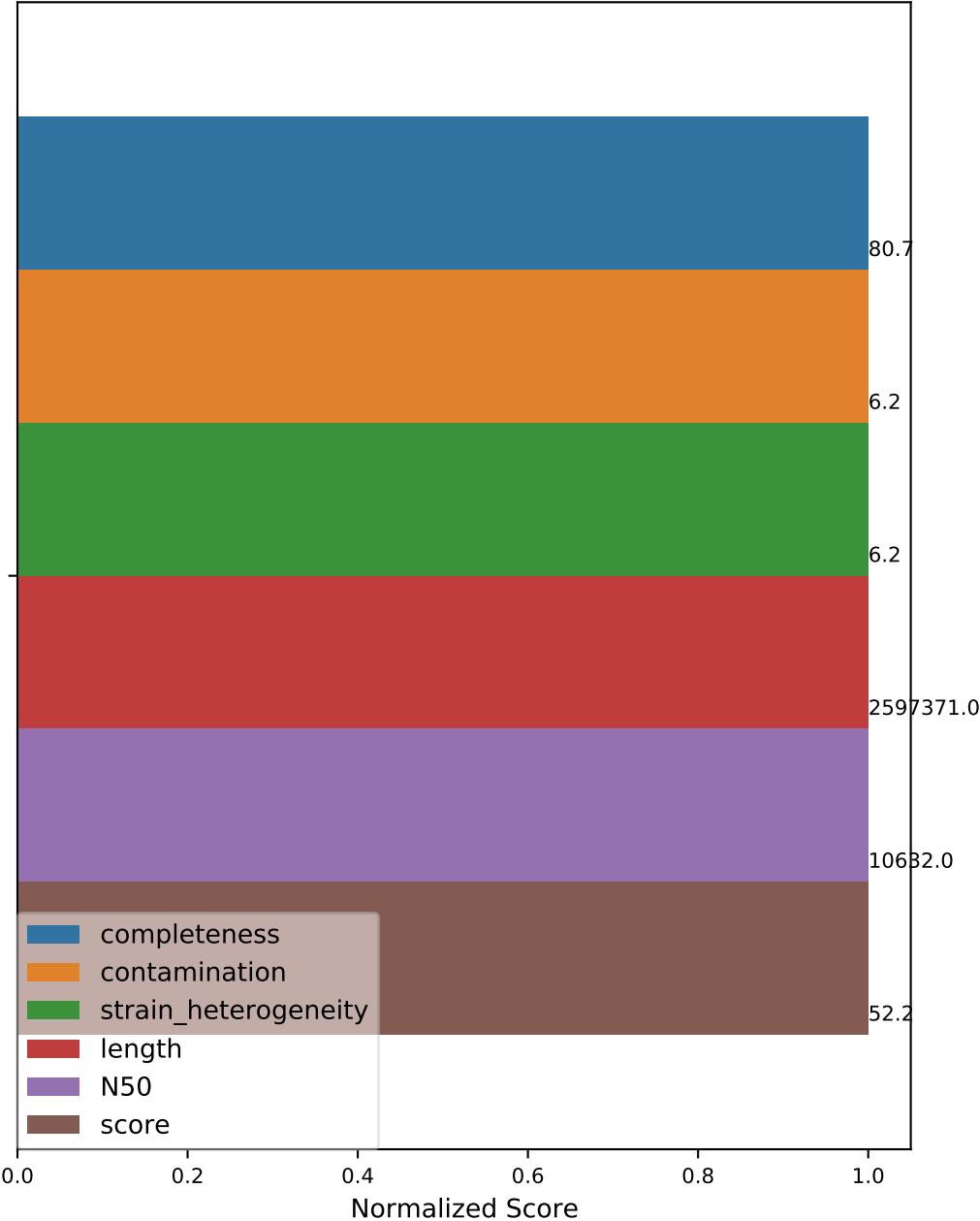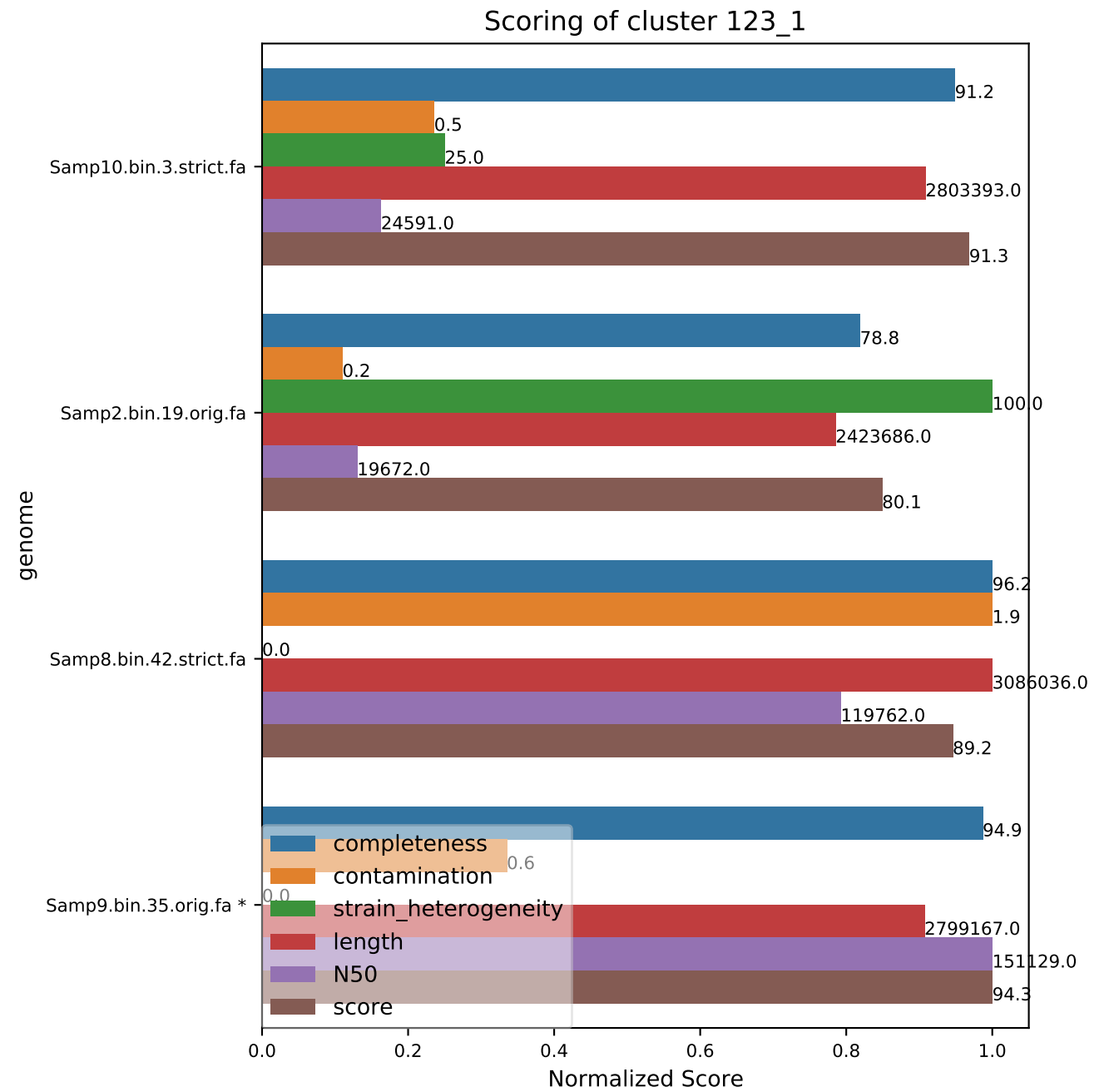
Scoring of cluster 124_1
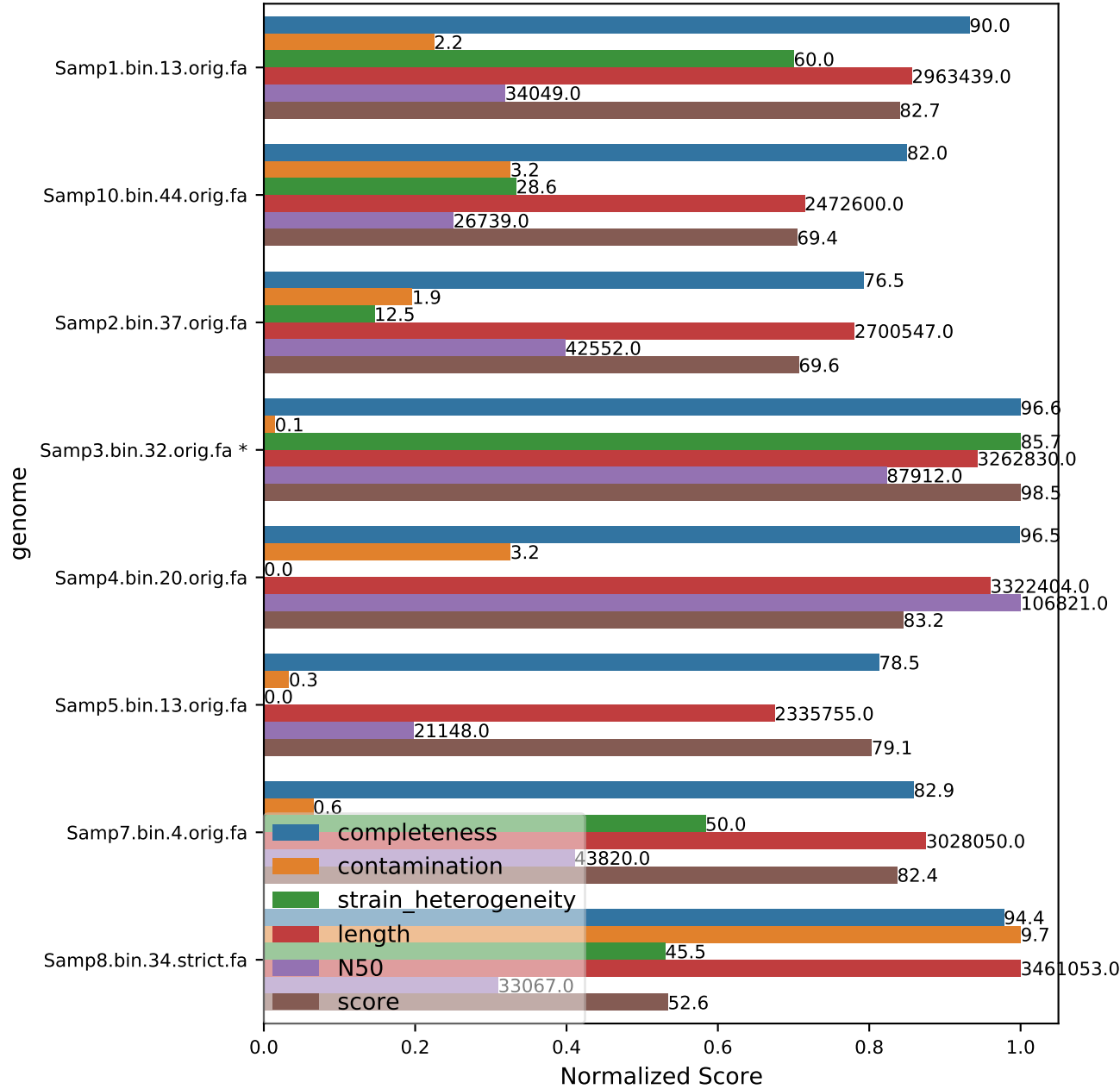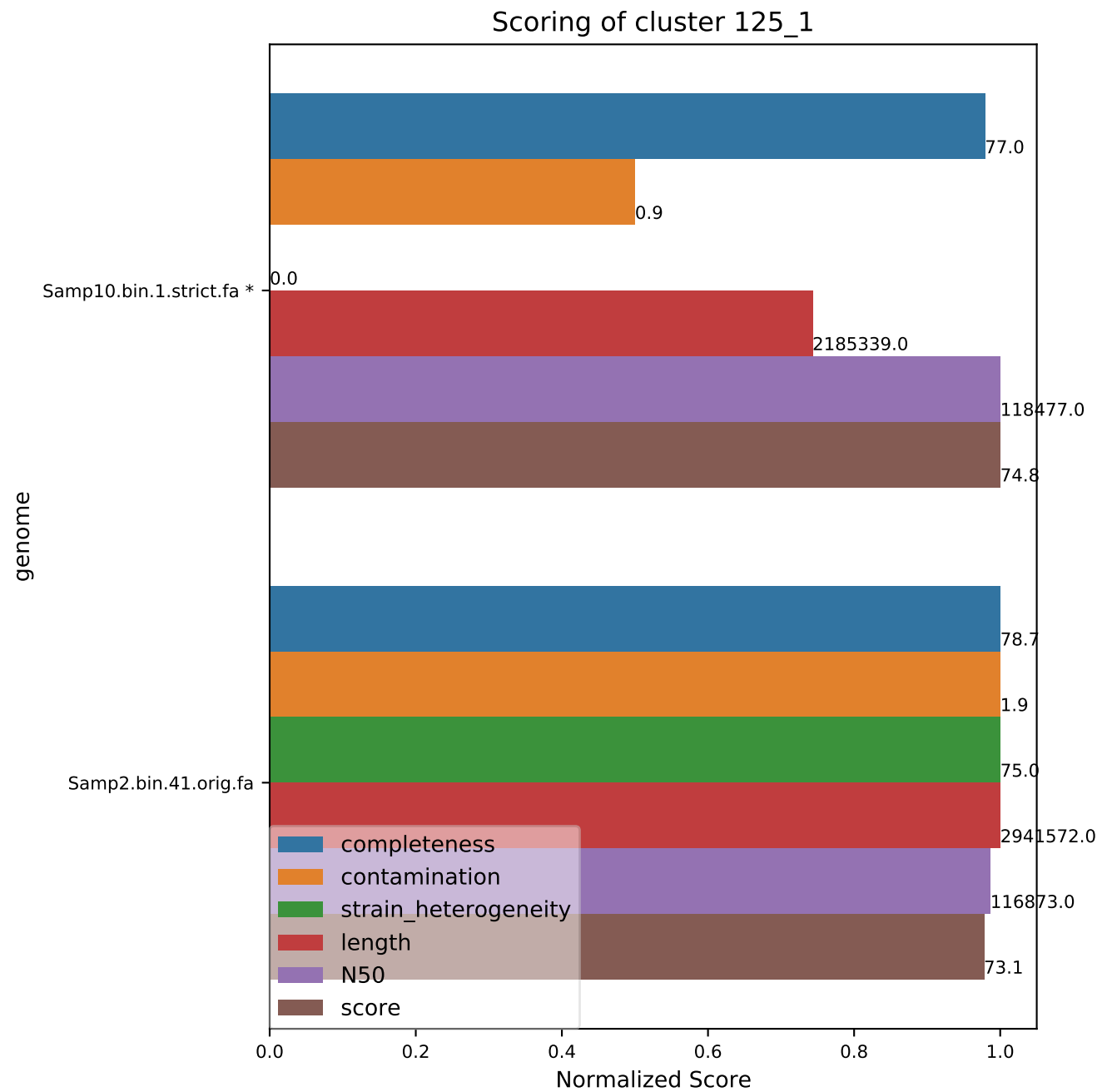
Scoring of cluster 125_1

Scoring of cluster 125_2
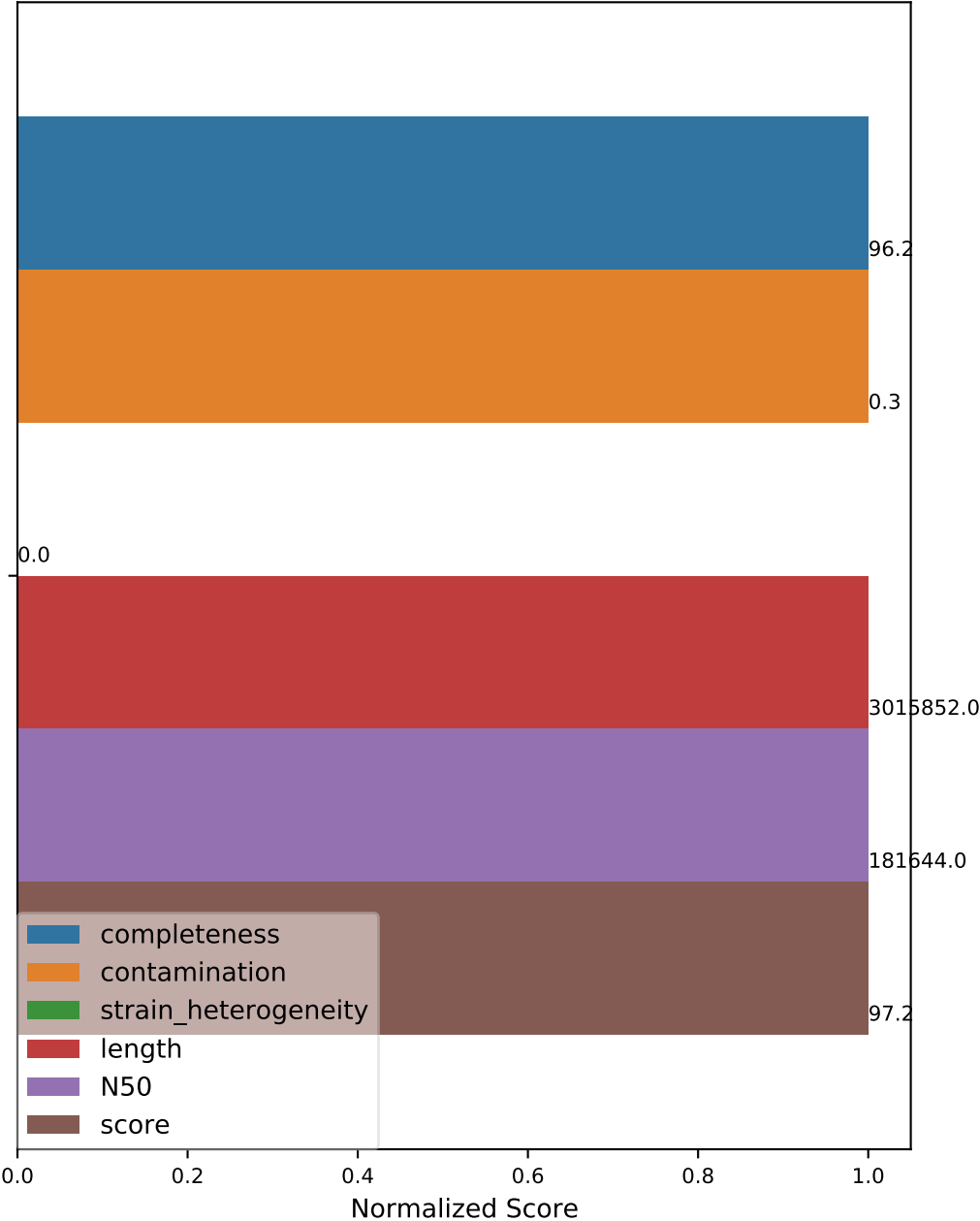
Scoring of cluster 126_0
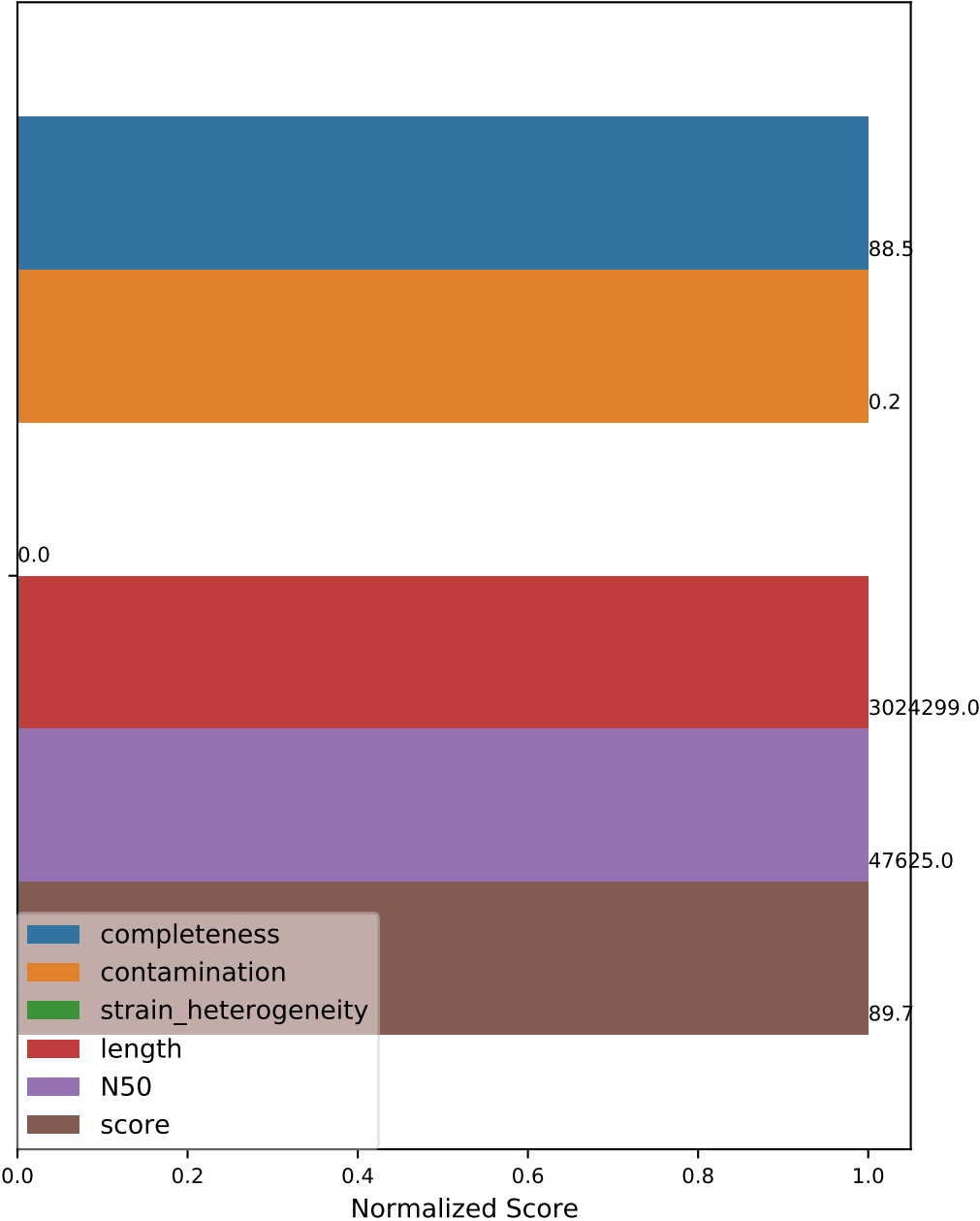
Scoring of cluster 127_0

Scoring of cluster 128_1
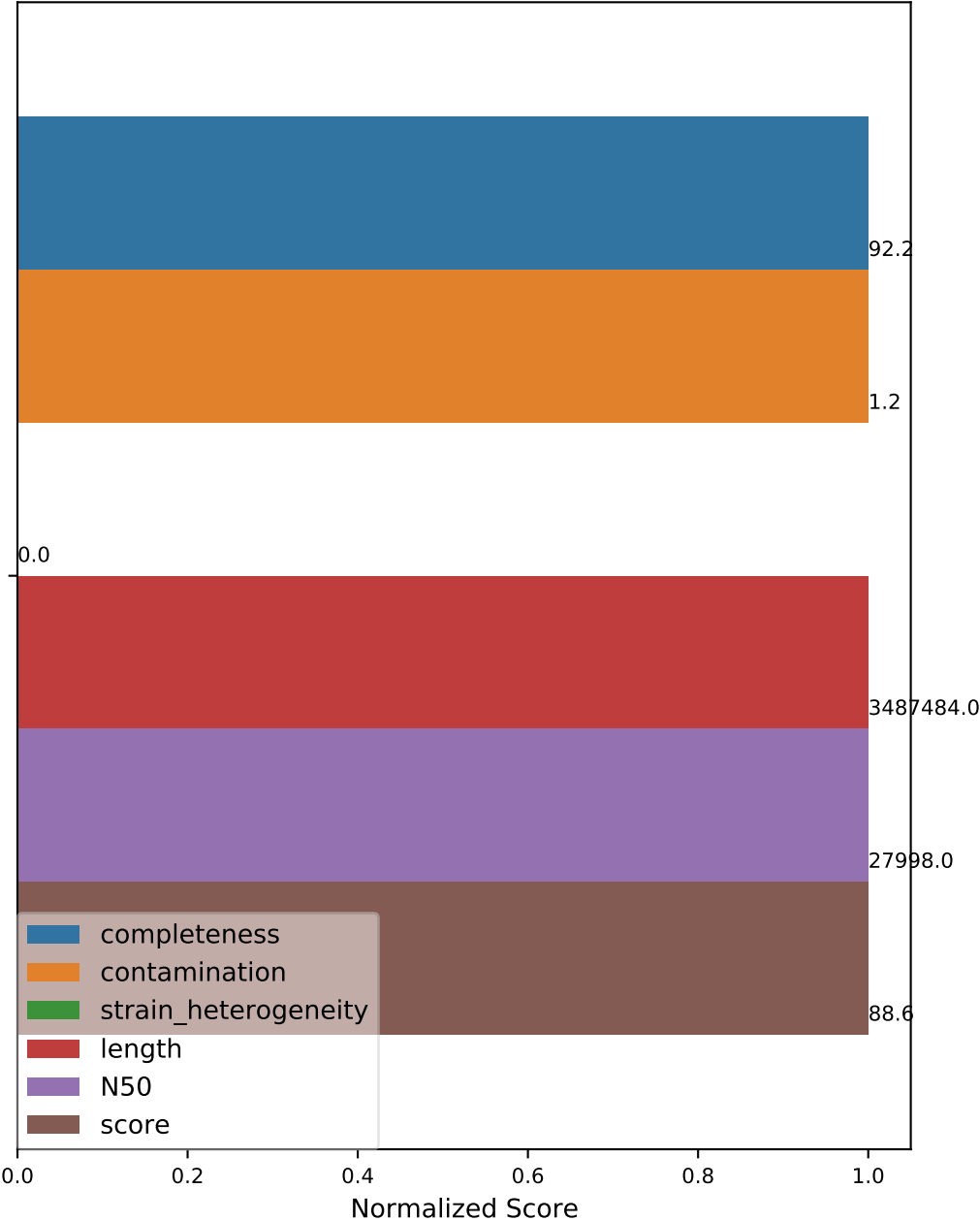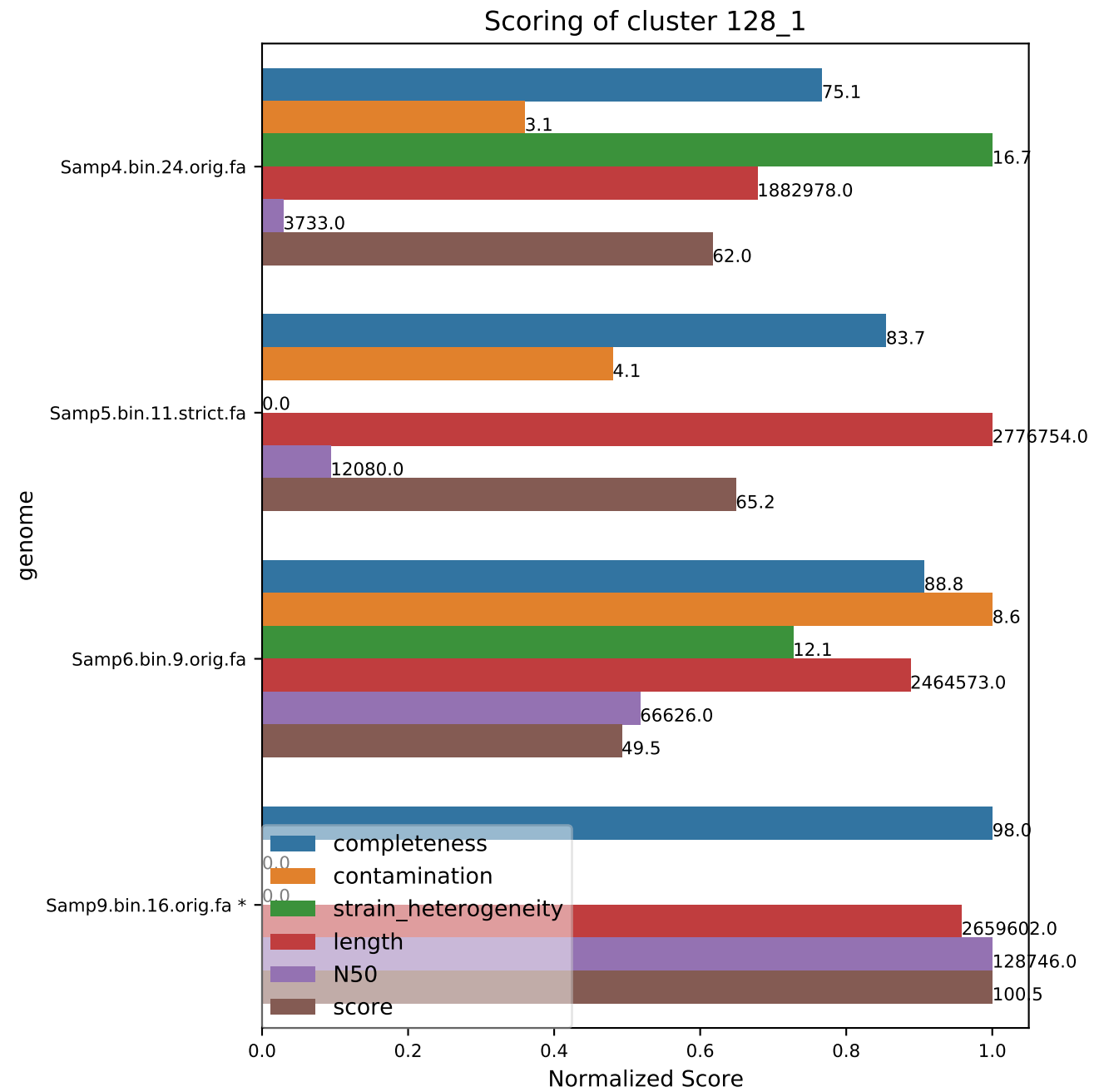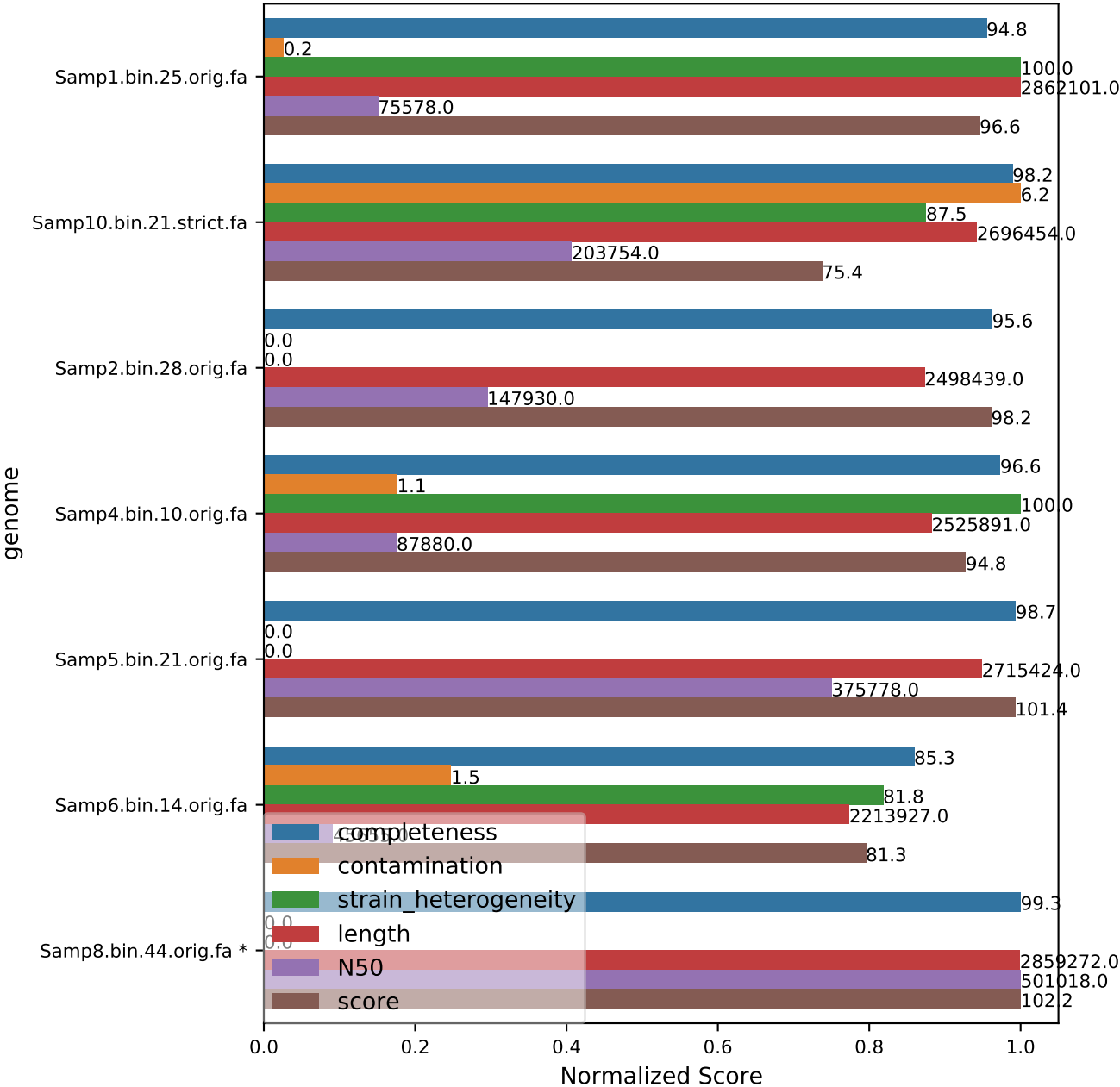
Scoring of cluster 129_1

Scoring of cluster 130_0
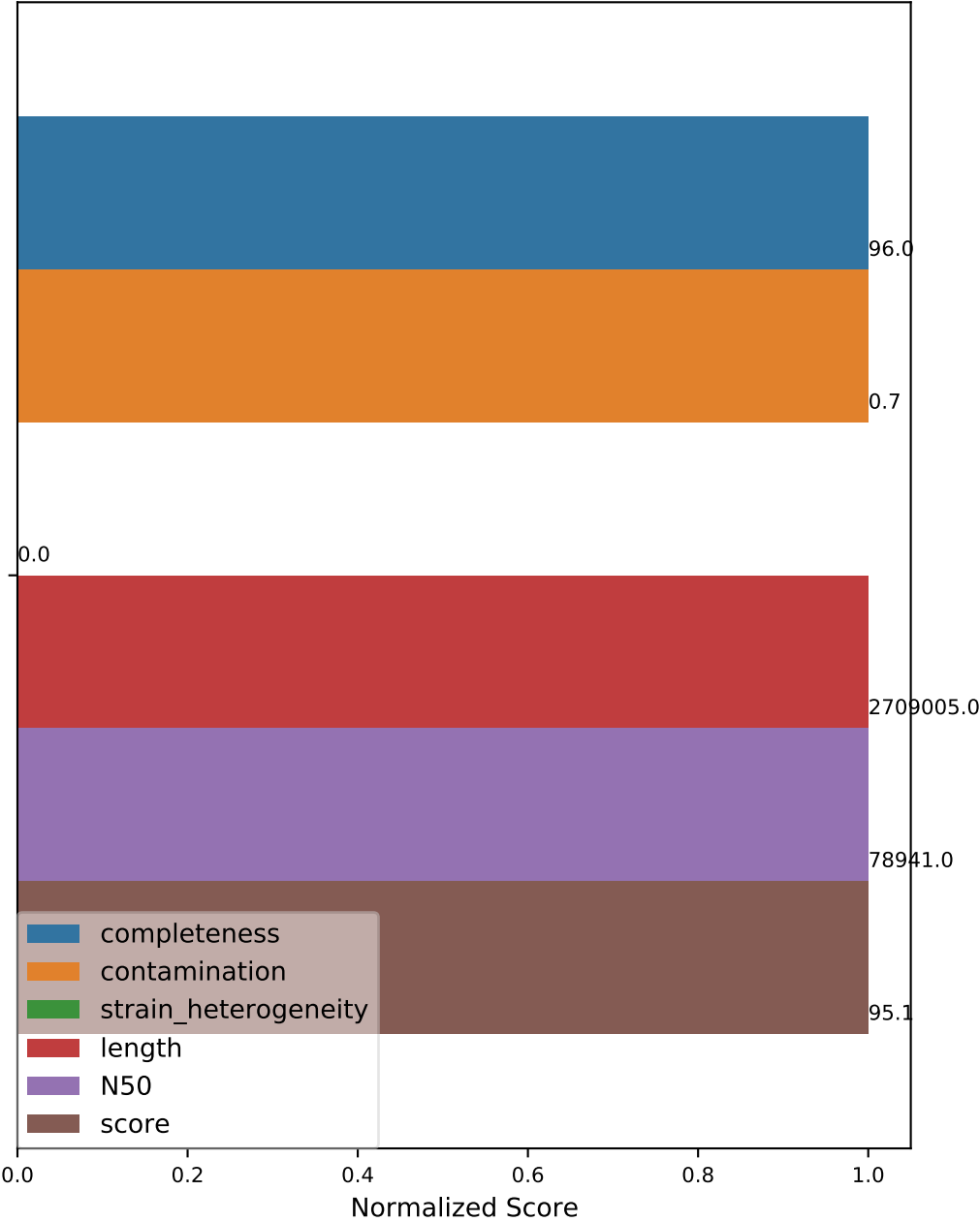
Scoring of cluster 131_1
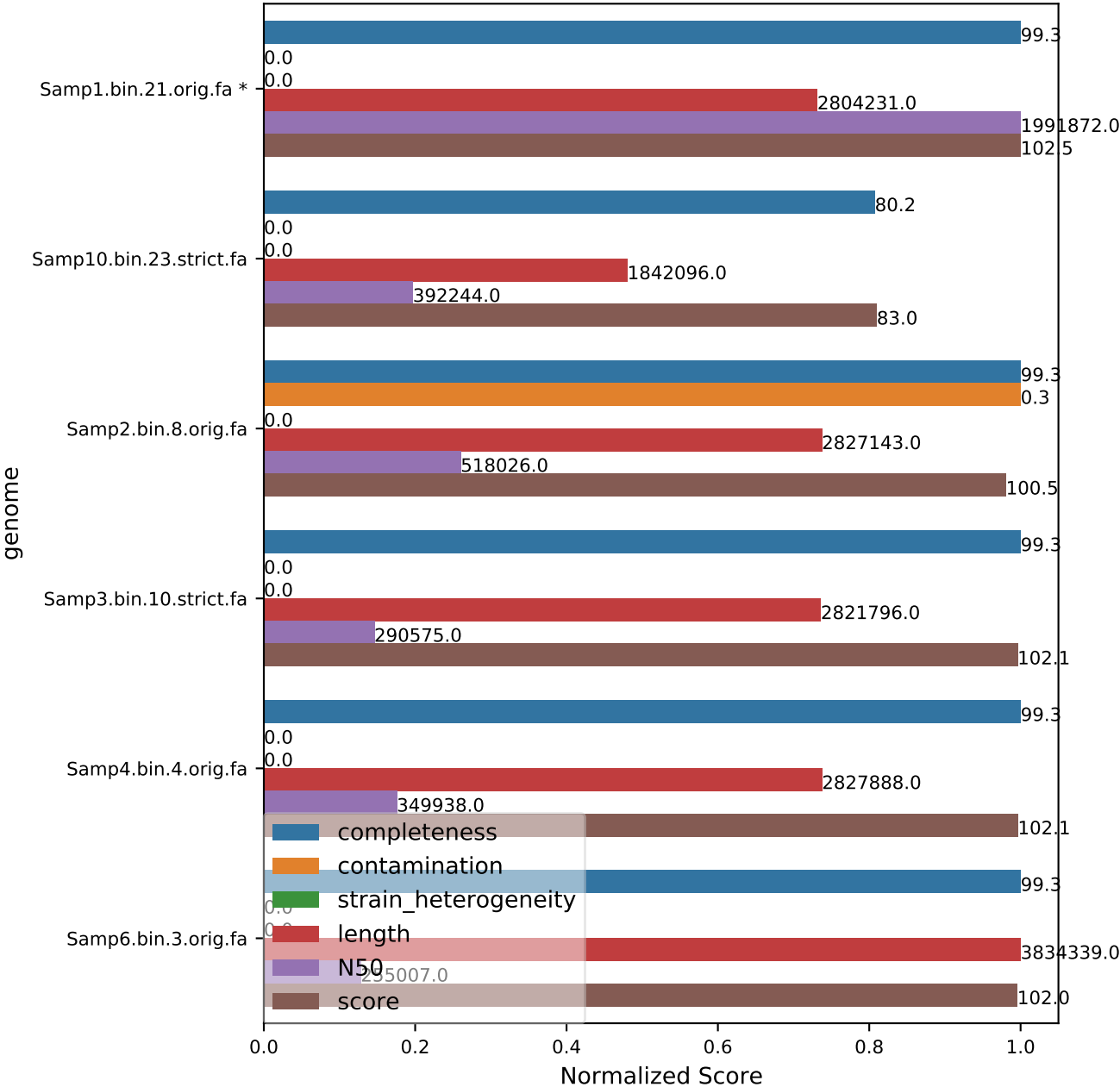
Scoring of cluster 132_1
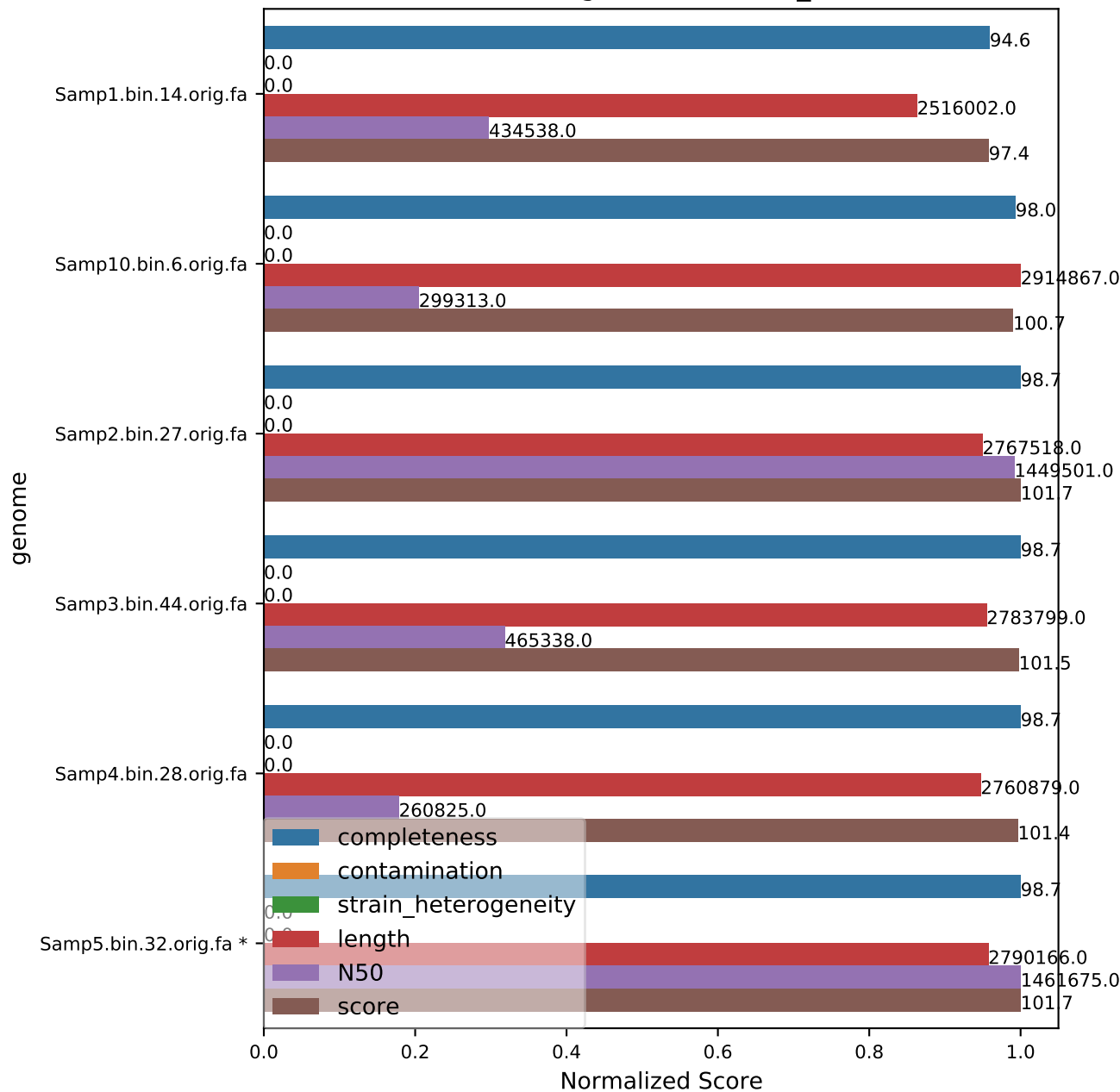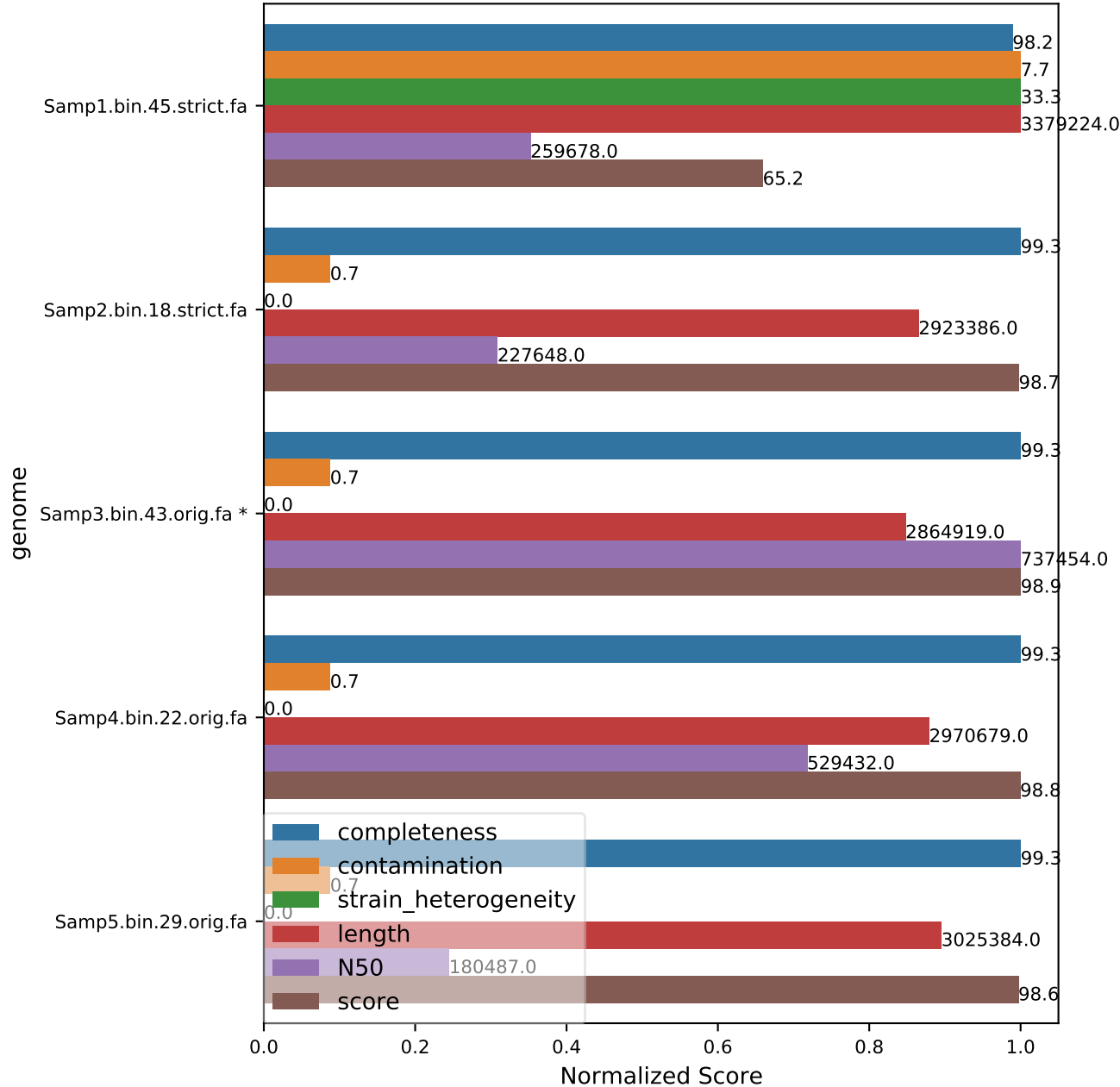
Scoring of cluster 133_1

Scoring of cluster 133_2
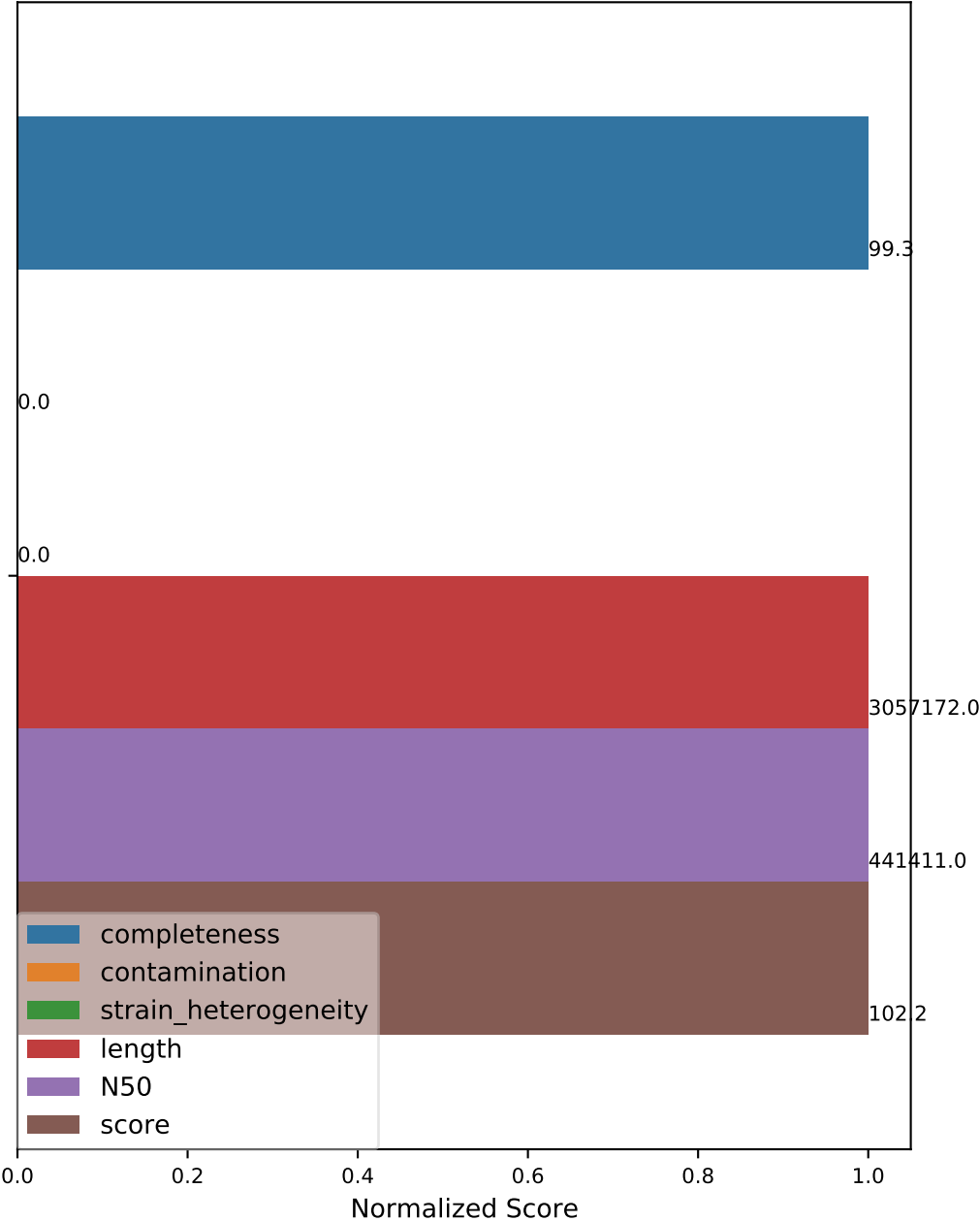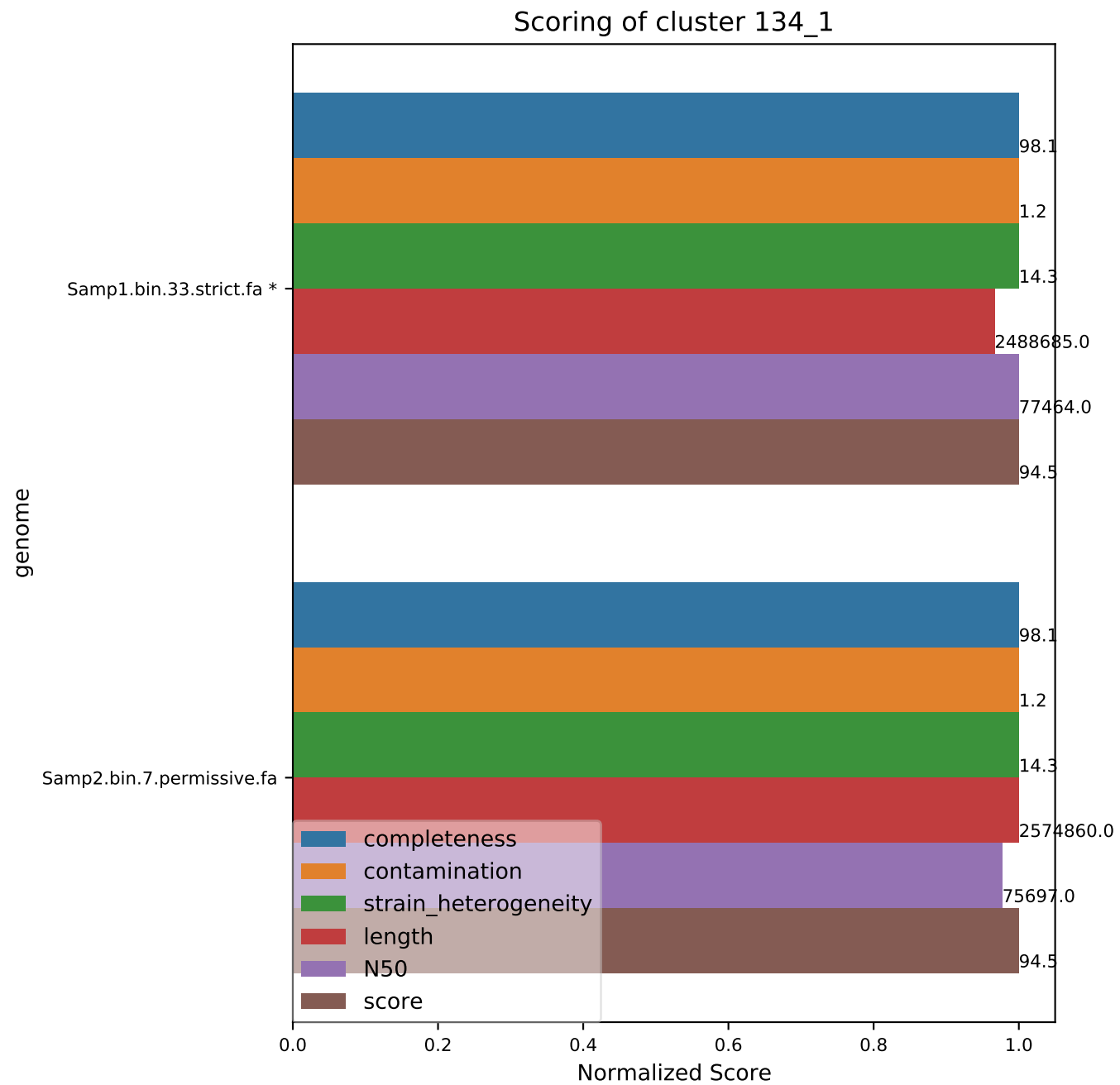
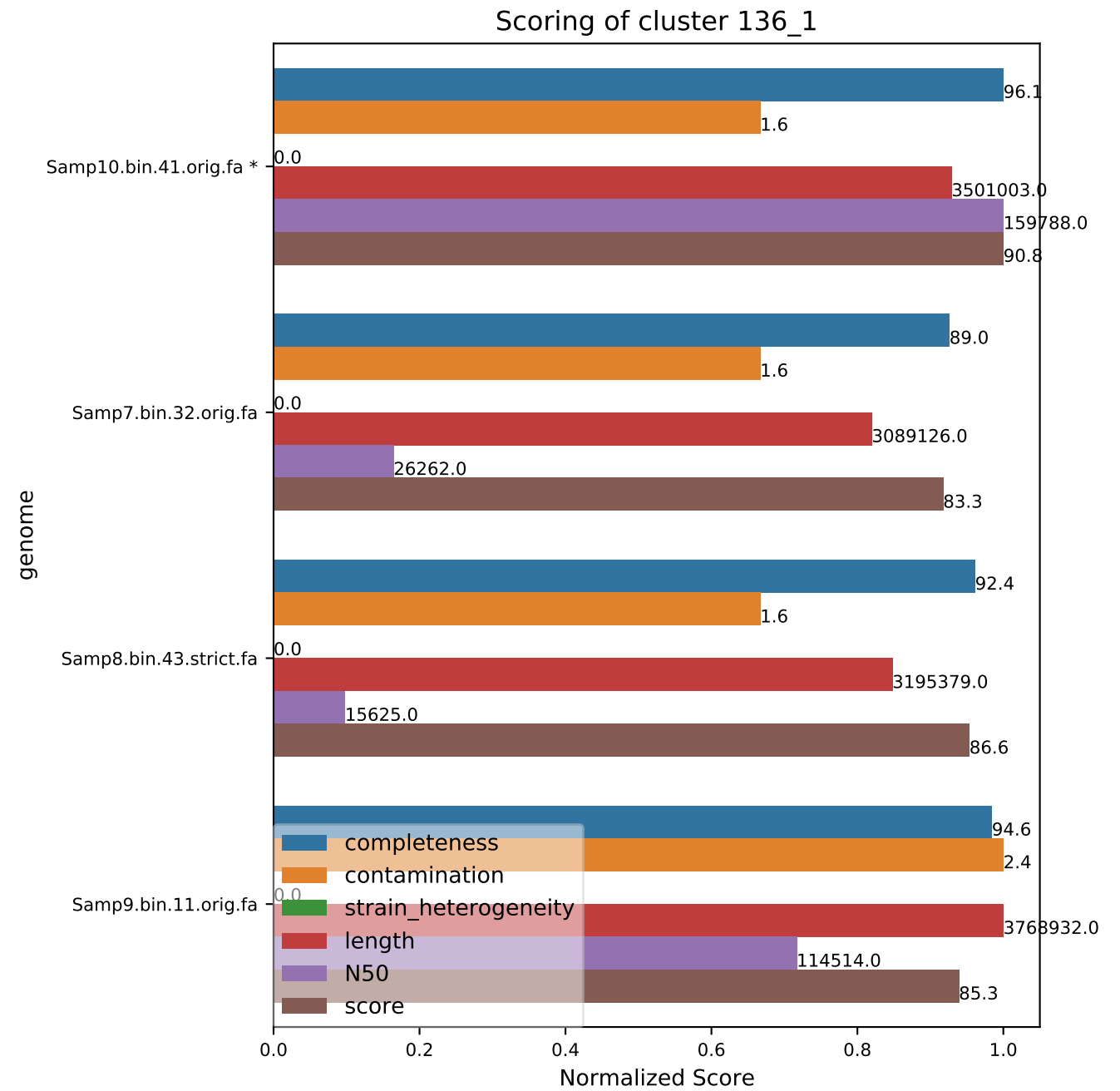Scoring of cluster 134_1

Scoring of cluster 135_1

genome

Samp6.bin.19.orig.fa *

- 99.0
- 0.3
- 0.0
- 2318461.0
- 564877.0
- 100.2

Samp7.bin.30.orig.fa

- 99.3
- 0.3
- 0.0
- 2435262.0
- 49135.0
- 100.0

Legend:
- completeness
- contamination
- strain_heterogeneity
- length
- N50
- score

Normalized Score
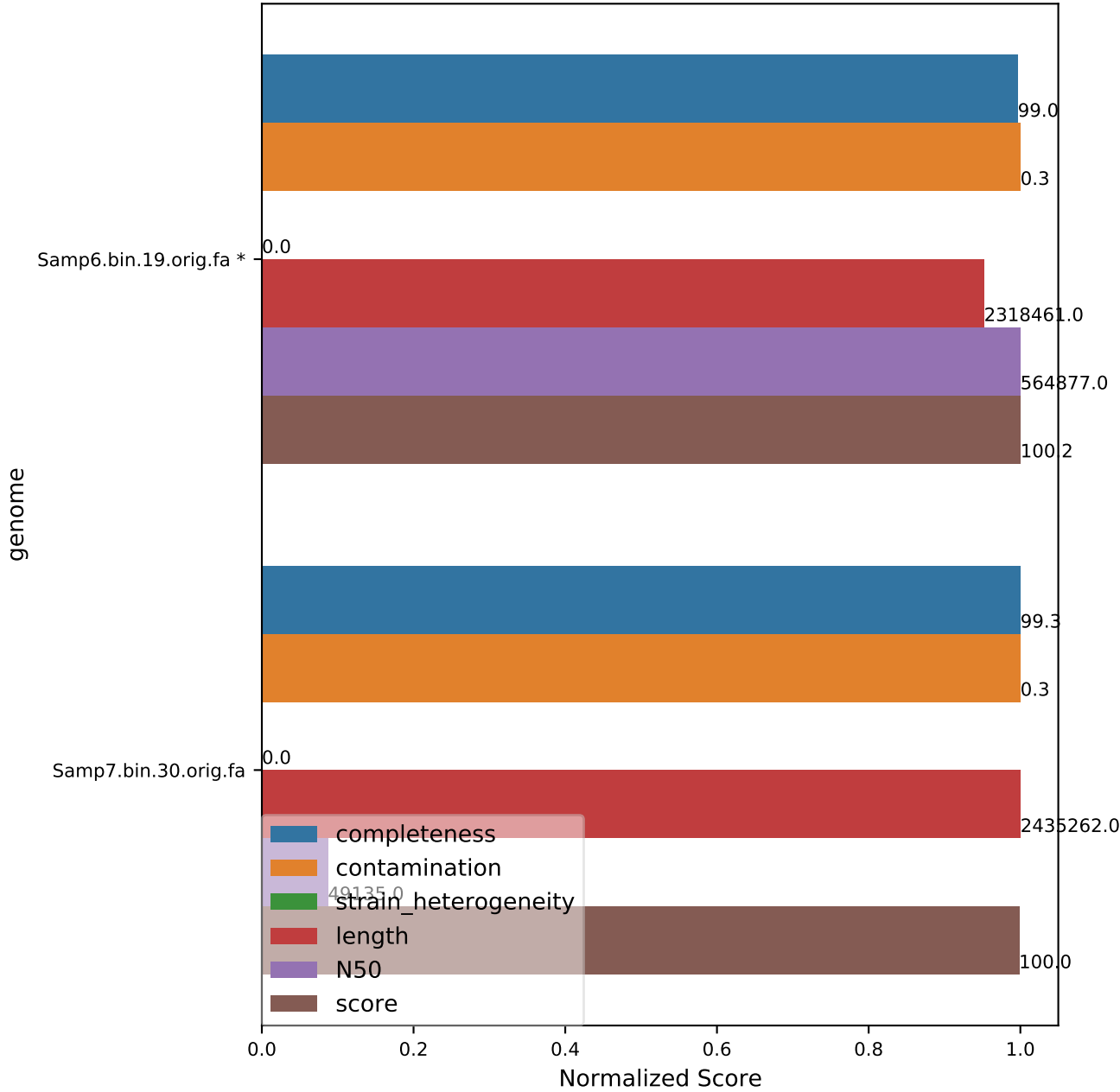
Scoring of cluster 136_1

Scoring of cluster 137_0
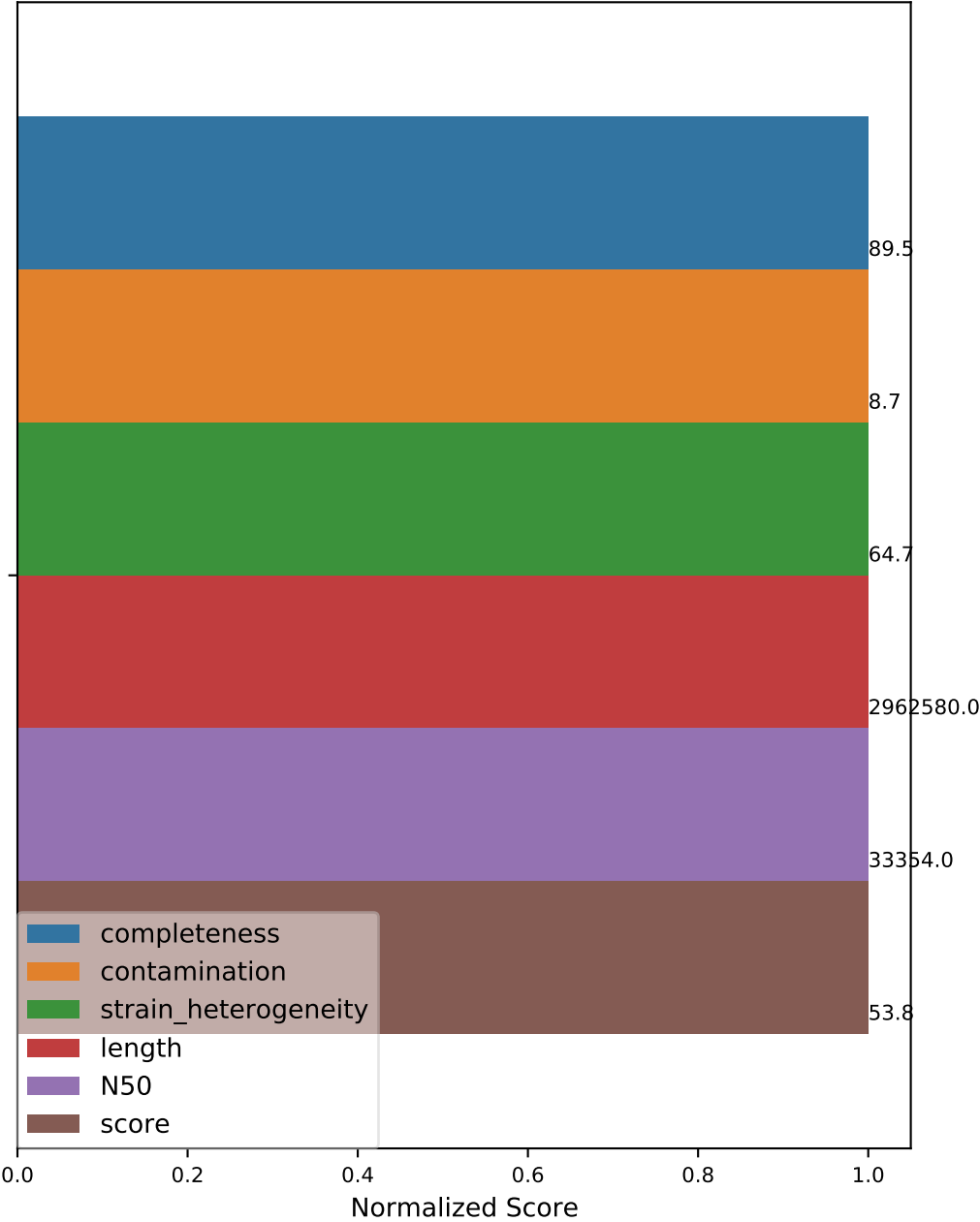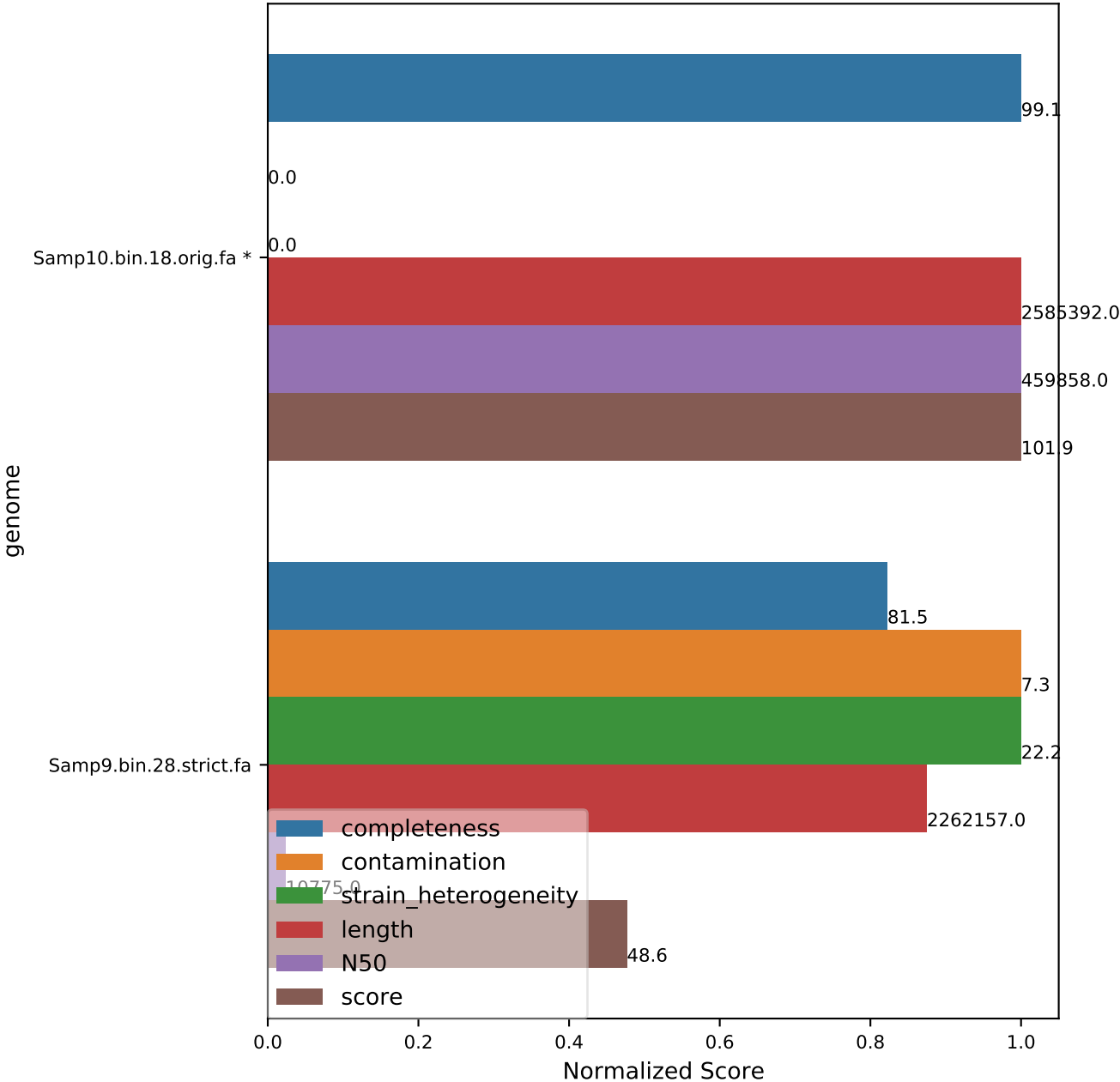
Scoring of cluster 138_1
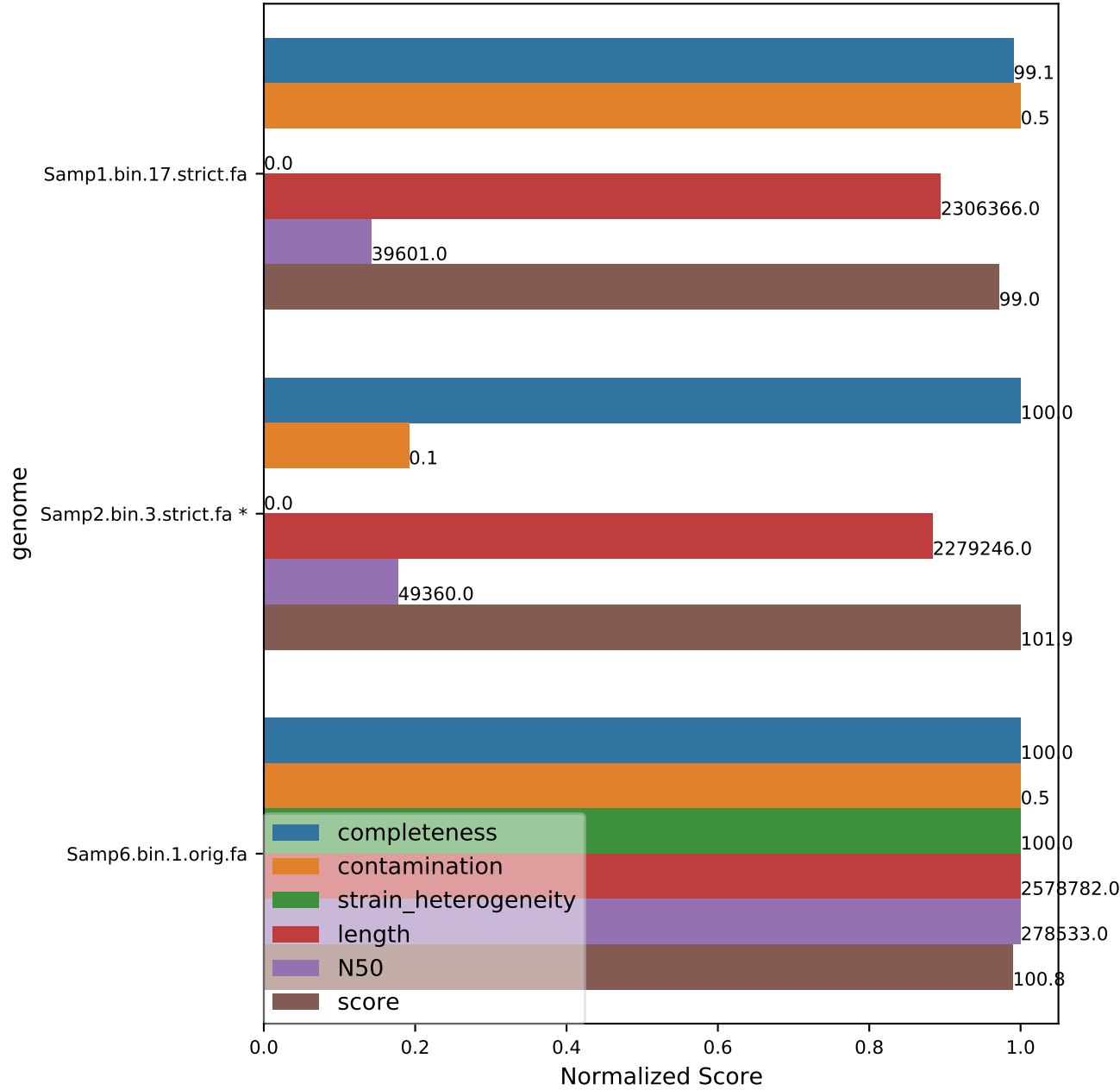
Scoring of cluster 139_1

Scoring of cluster 139_2

Scoring of cluster 140_1
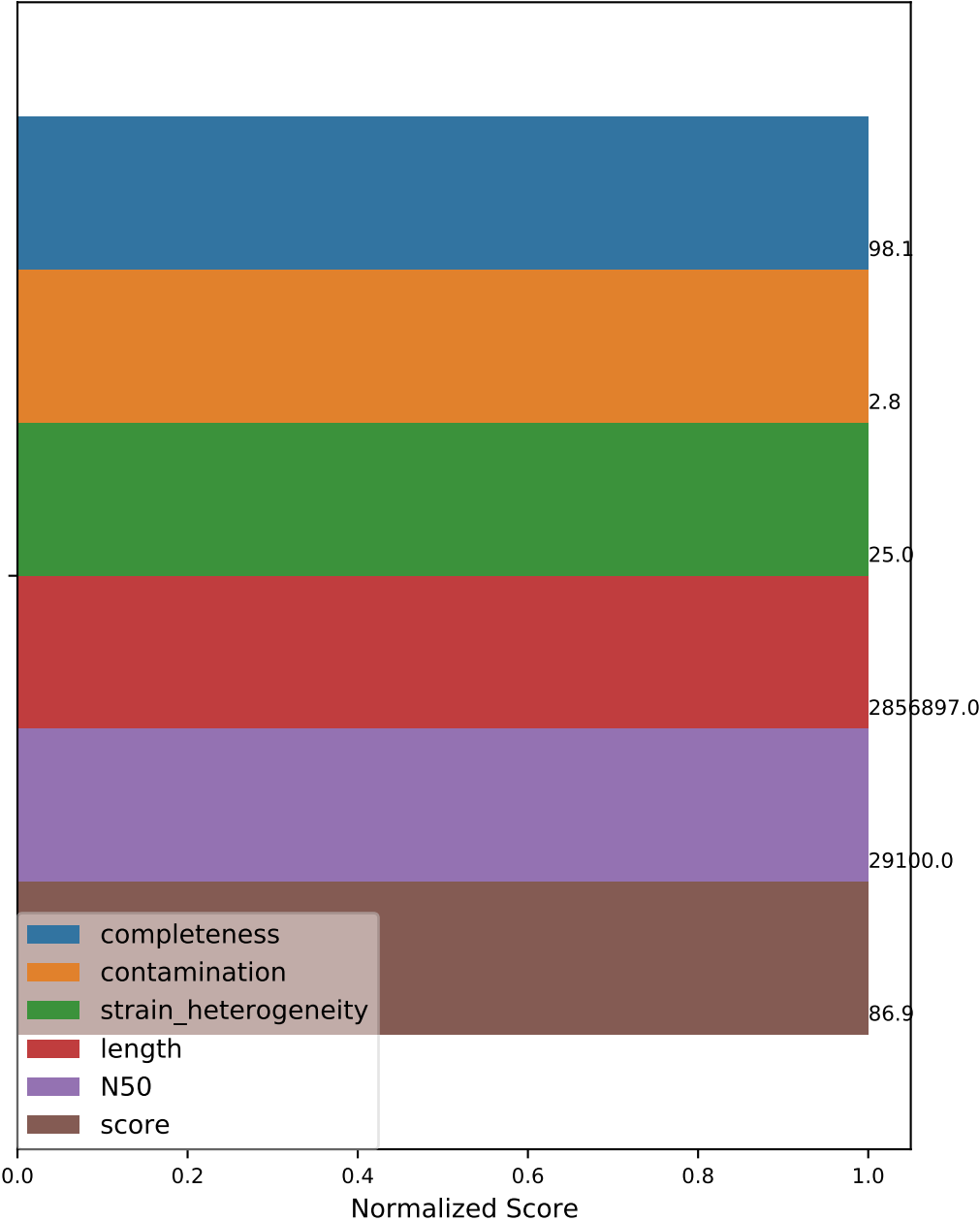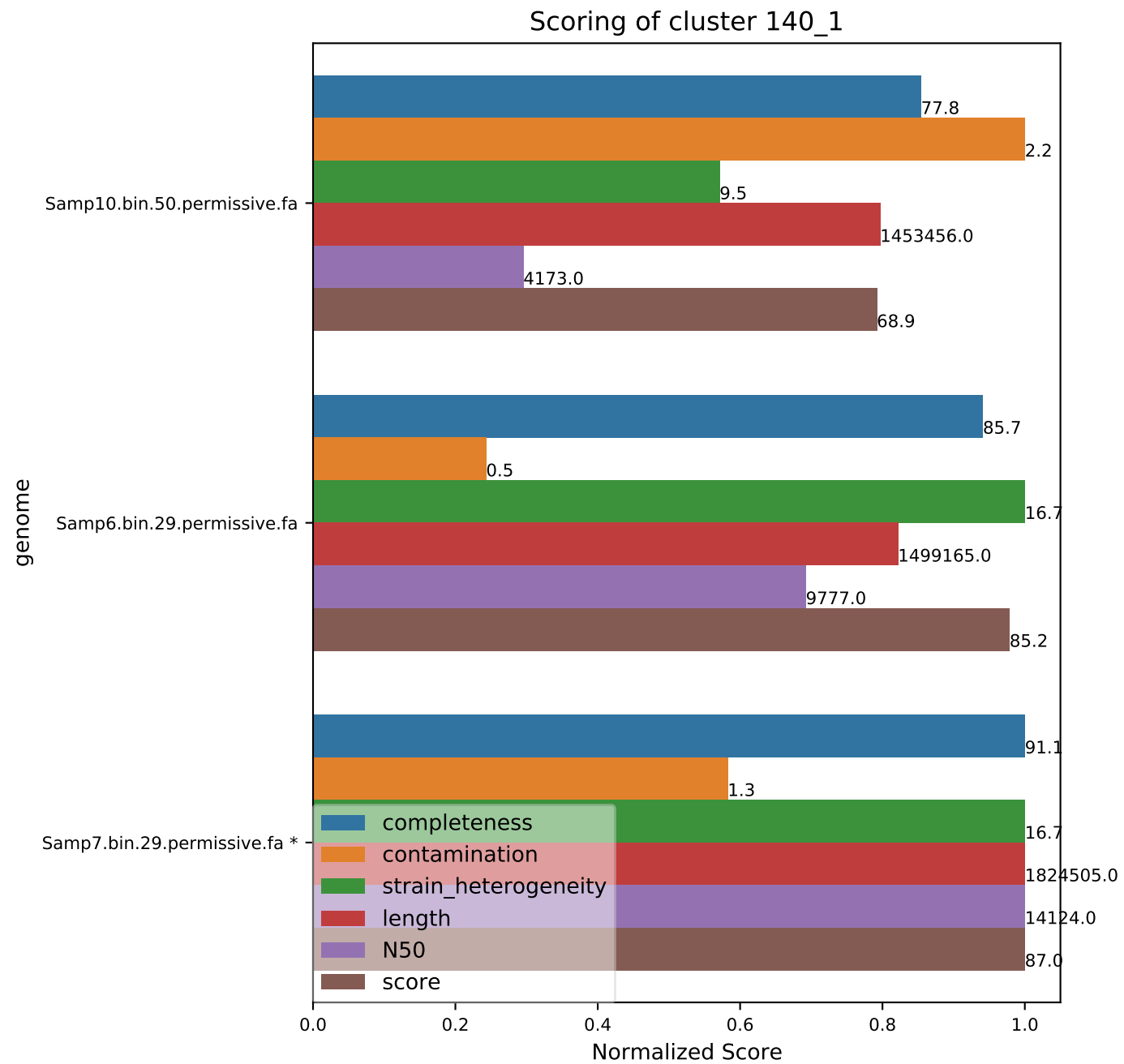
Scoring of cluster 141_1
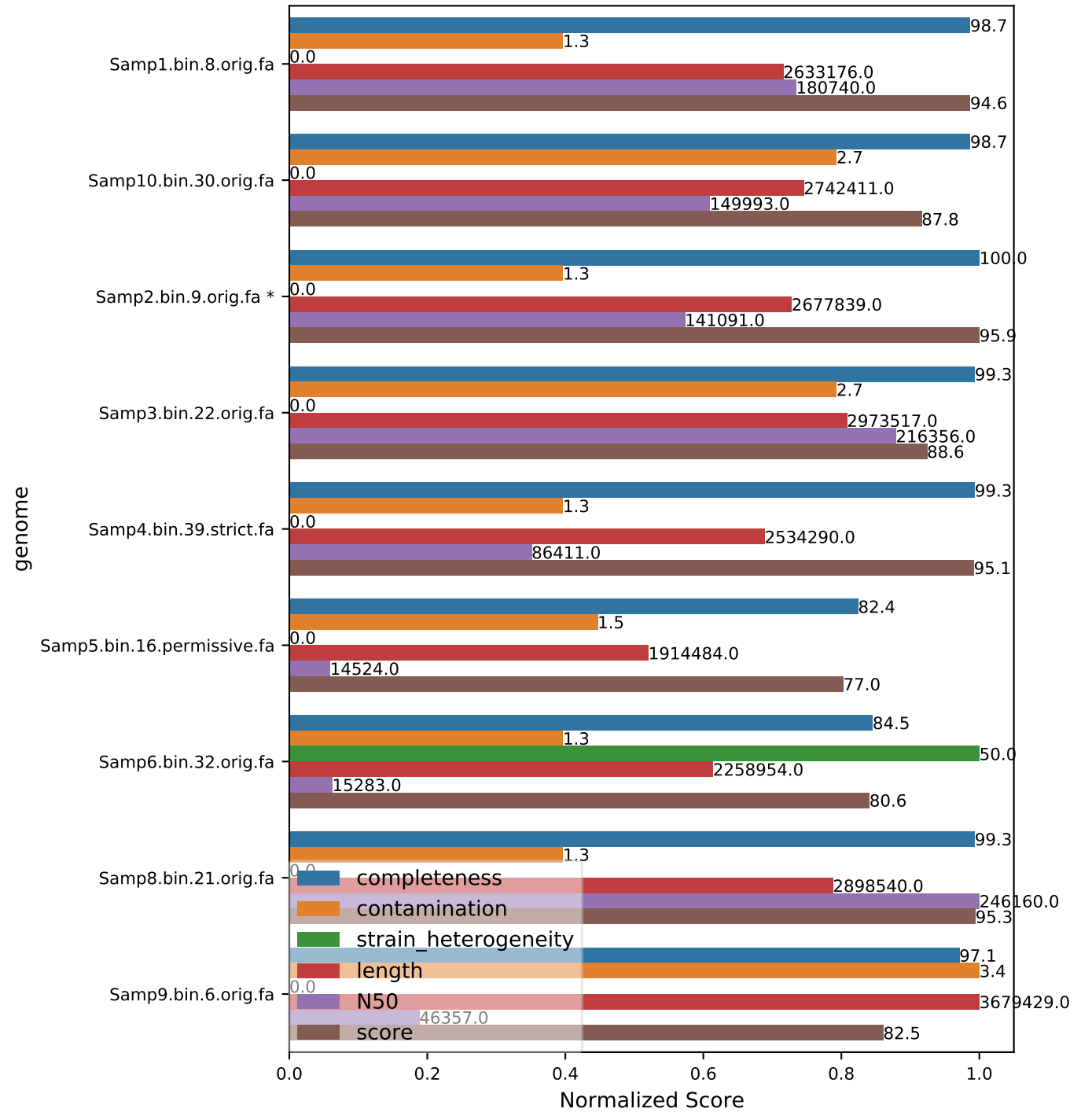
Scoring of cluster 142_1

Scoring of cluster 143_0