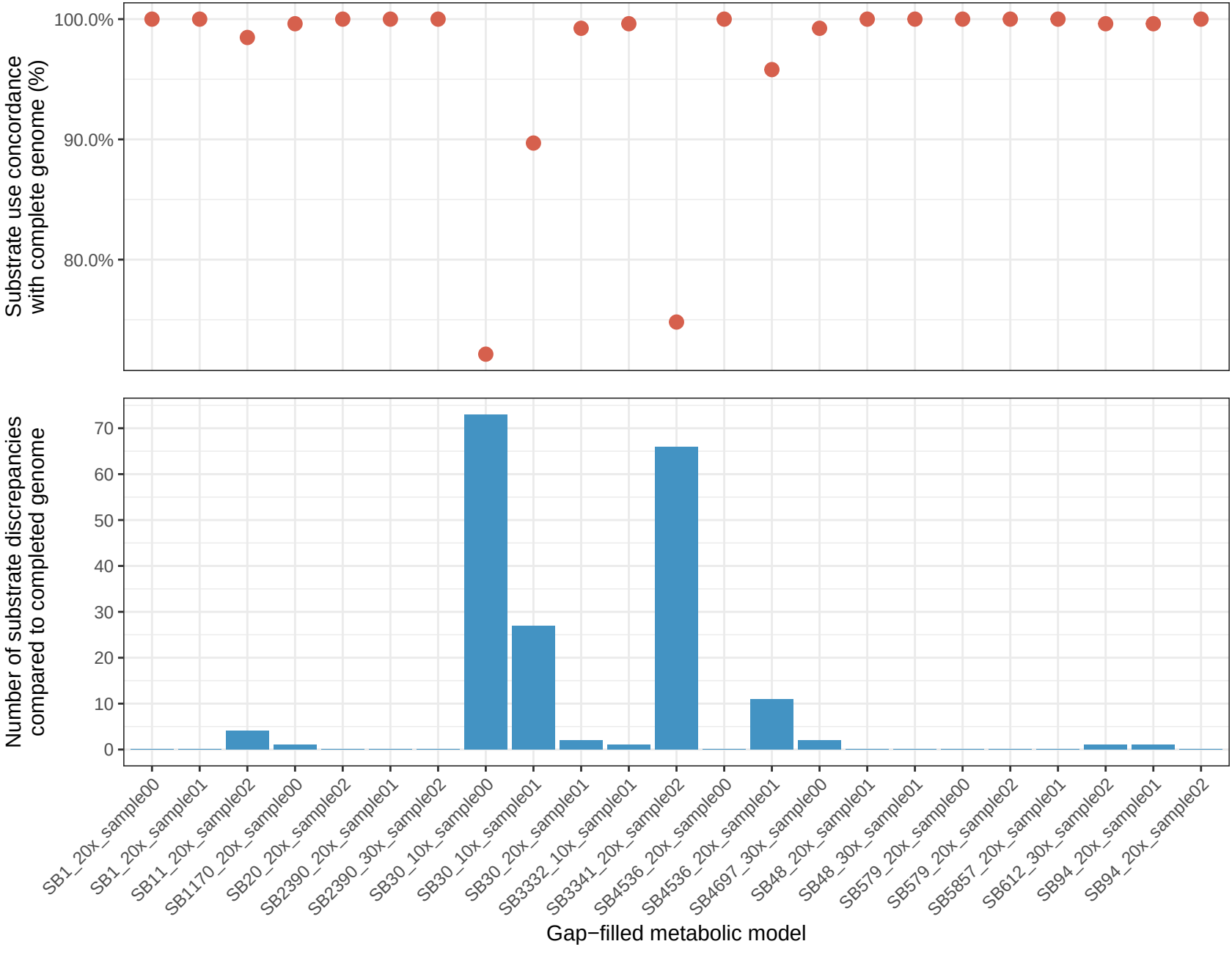
Substrate use concordance with complete genome (%)
100.0%
90.0%
80.0%
Number of substrate discrepancies compared to completed genome
70
60
50
40
30
20
10
0
SB1_20x_sample00
SB1_20x_sample01
SB11_20x_sample02
SB1170_20x_sample00
SB20_20x_sample02
SB2390_20x_sample01
SB2390_30x_sample02
SB30_10x_sample00
SB30_10x_sample01
SB30_20x_sample01
SB3332_10x_sample01
SB3341_20x_sample02
SB4536_20x_sample00
SB4536_20x_sample01
SB4697_30x_sample00
SB48_20x_sample01
SB48_30x_sample01
SB579_20x_sample00
SB579_20x_sample02
SB5857_20x_sample01
SB612_30x_sample02
SB94_20x_sample01
SB94_20x_sample02
Gap−filled metabolic model