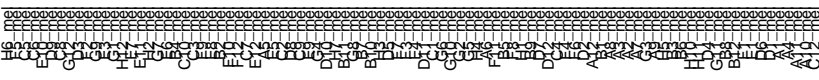
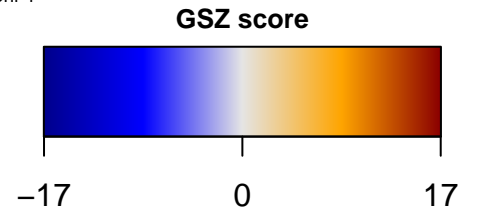
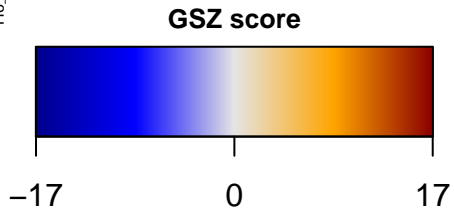
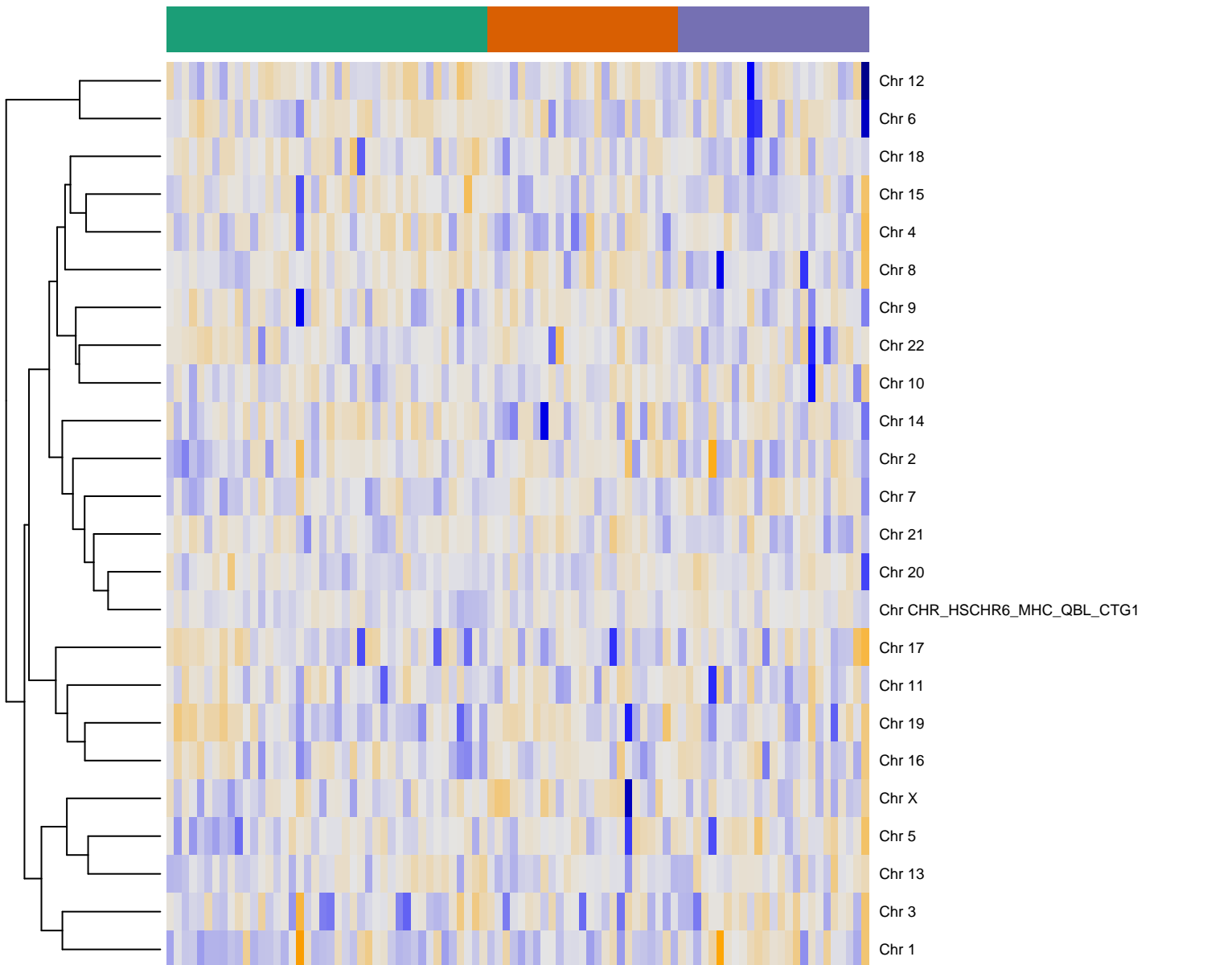
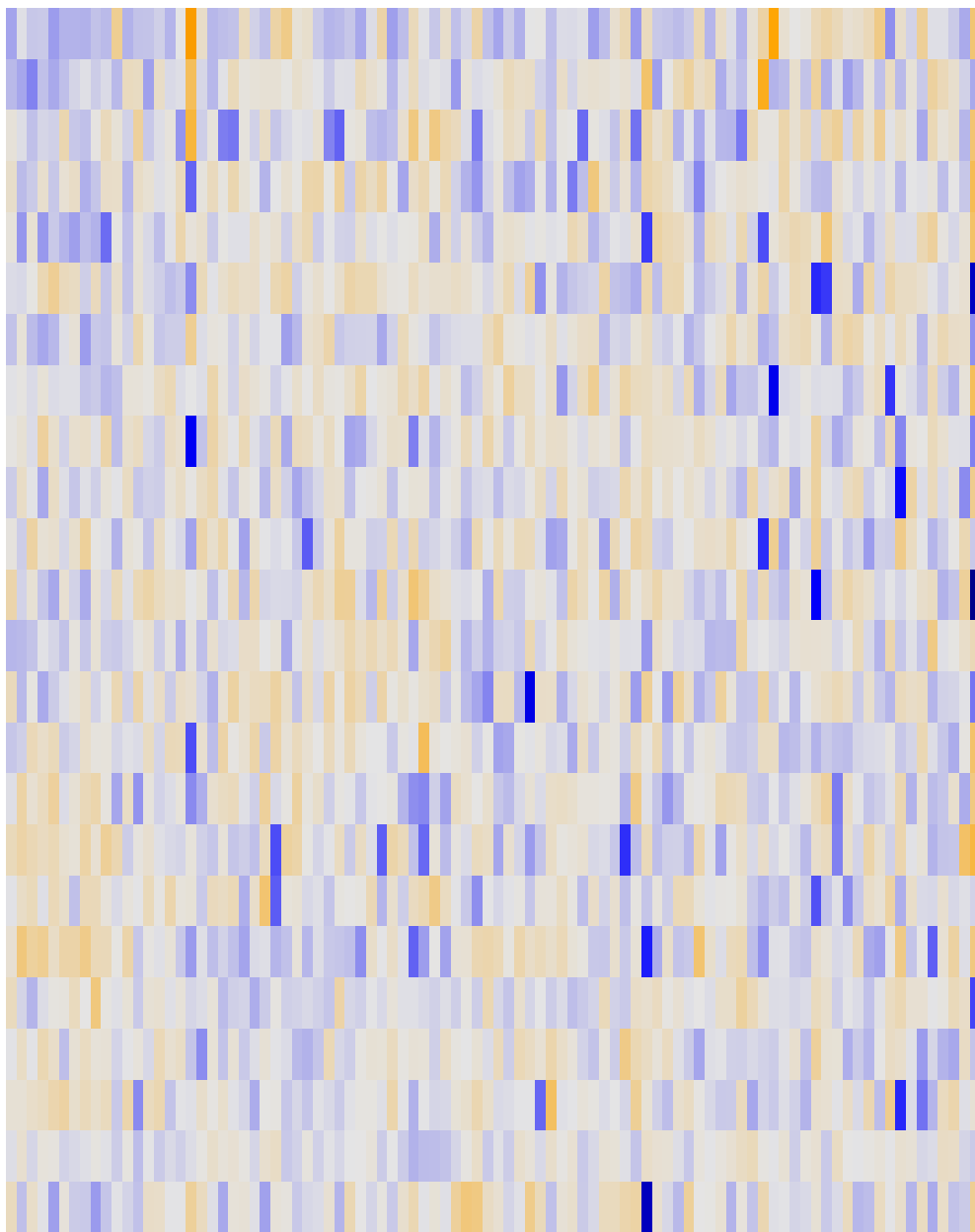


Chr 12
Chr 6
Chr 18
Chr 15
Chr 4
Chr 8
Chr 9
Chr 22
Chr 10
Chr 14
Chr 2
Chr 7
Chr 21
Chr 20
Chr CHR_HSCHR6_MHC_QBL_CTG1
Chr 17
Chr 11
Chr 19
Chr 16
Chr X
Chr 5
Chr 13
Chr 3
Chr 1



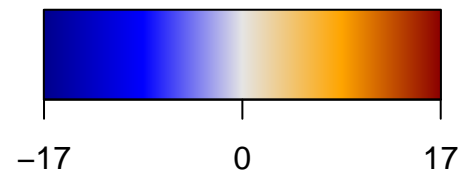


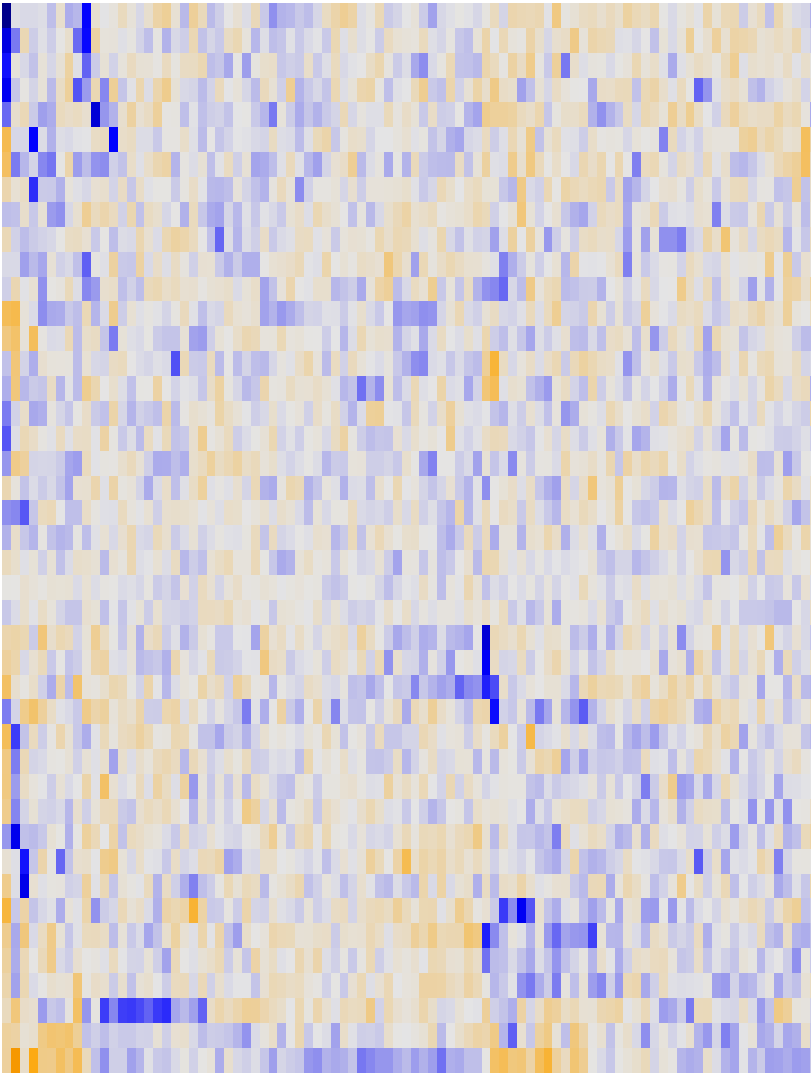
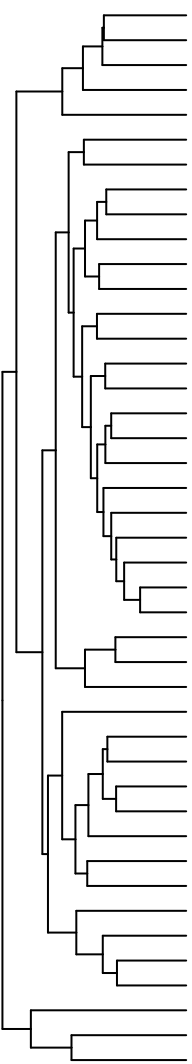
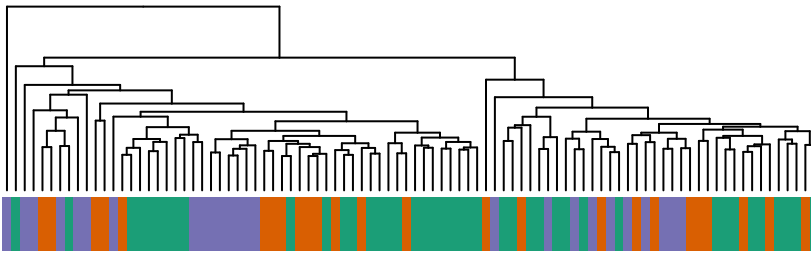


11 12 13 14 15 16 17 18 19 20 21 22 X
A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

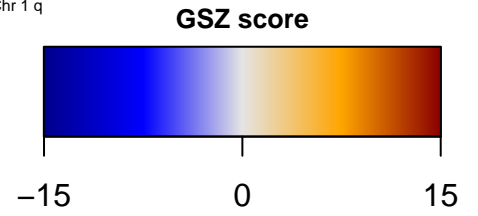
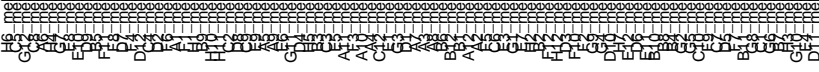
Chr 1
Chr 2
Chr 3
Chr 4
Chr 5
Chr 6
Chr 7
Chr 8
Chr 9
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Chr 12
Chr 13
Chr 14
Chr 15
Chr 16
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Chr 21
Chr 22
Chr CHR_HSCHR6_MHC_QBL_CTG1
Chr X

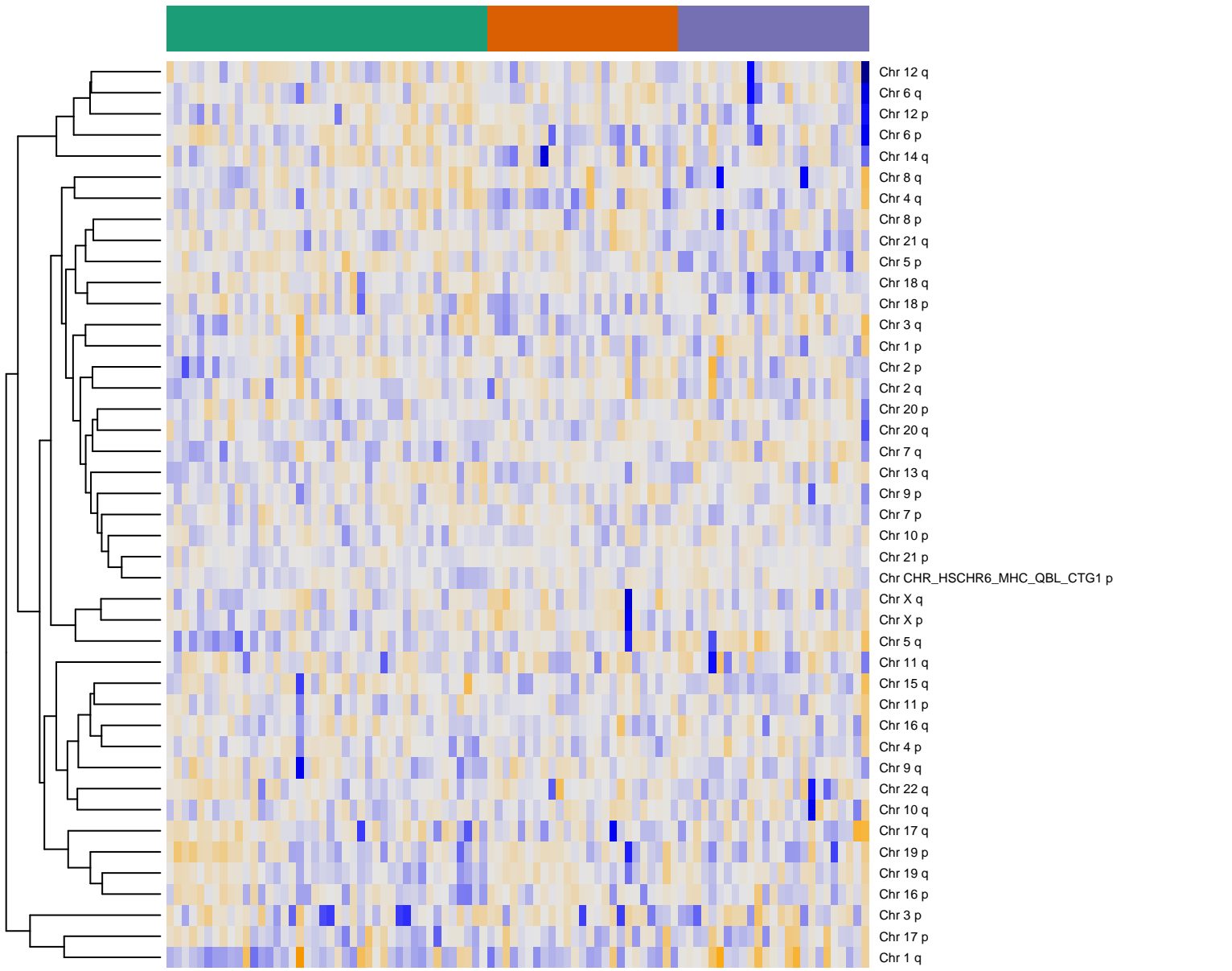
GSZ score





Chr 12 q
Chr 6 q
Chr 12 p
Chr 6 p
Chr 14 q
Chr 8 q
Chr 4 q
Chr 8 p
Chr 21 q
Chr 5 p
Chr 18 q
Chr 18 p
Chr 3 q
Chr 1 p
Chr 2 p
Chr 2 q
Chr 20 p
Chr 20 q
Chr 7 q
Chr 13 q
Chr 9 p
Chr 7 p
Chr 10 p
Chr 21 p
Chr CHR_HSCHR6_MHC_QBL_CTG1 p
Chr X q
Chr X p
Chr 5 q
Chr 11 q
Chr 15 q
Chr 11 p
Chr 16 q
Chr 4 p
Chr 9 q
Chr 22 q
Chr 10 q
Chr 17 q
Chr 19 p
Chr 19 q
Chr 16 p
Chr 3 p
Chr 17 p
Chr 1 q





GSZ score

