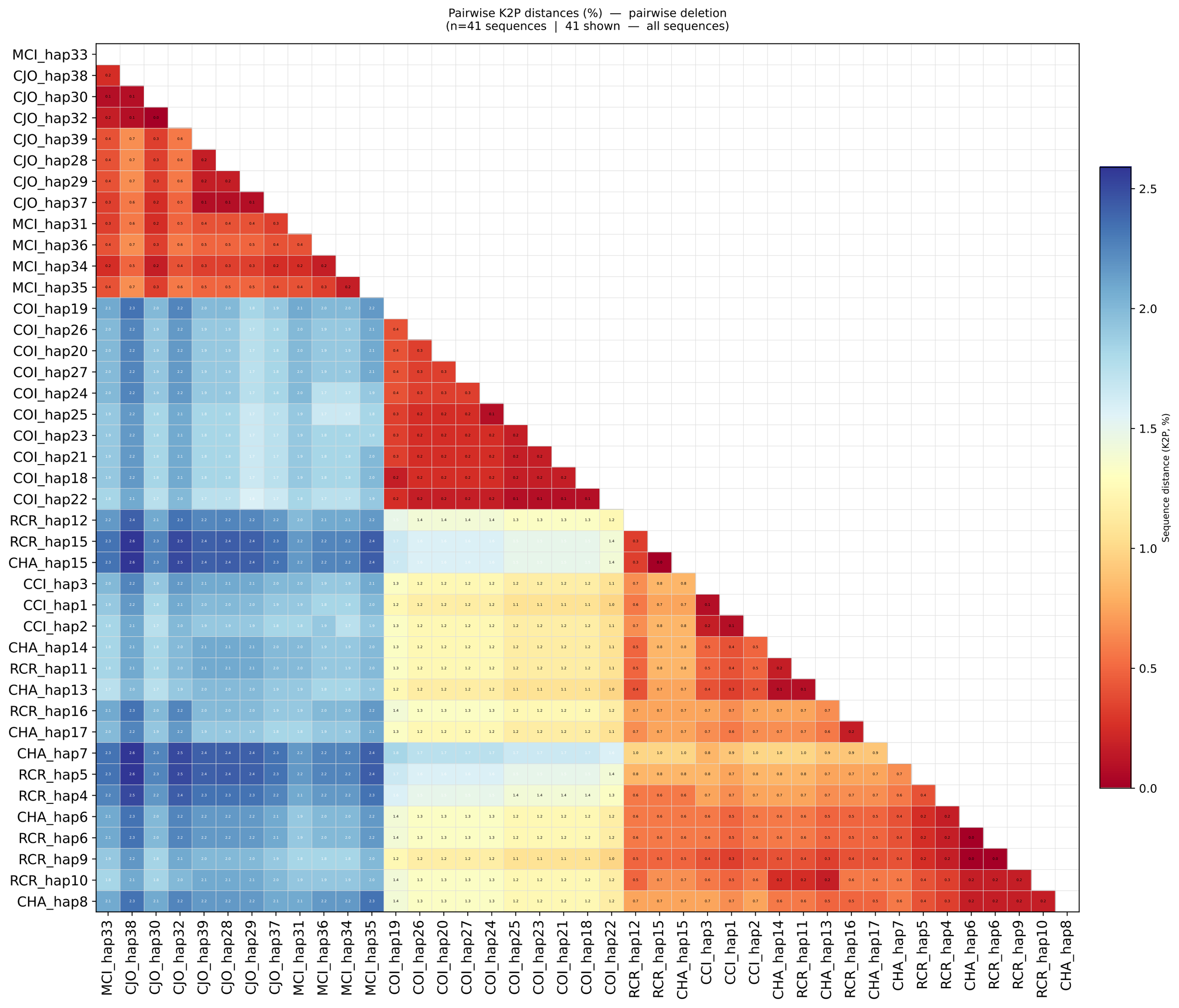
Pairwise K2P distances (%) — pairwise deletion
(n=41 sequences | 41 shown — all sequences)
MCI_hap33
CJO_hap38
CJO_hap30
CJO_hap32
CJO_hap39
CJO_hap28
CJO_hap29
CJO_hap37
MCI_hap31
MCI_hap36
MCI_hap34
MCI_hap35
COI_hap19
COI_hap26
COI_hap20
COI_hap27
COI_hap24
COI_hap25
COI_hap23
COI_hap21
COI_hap18
COI_hap22
RCR_hap12
RCR_hap15
CHA_hap15
CCI_hap3
CCI_hap1
CCI_hap2
CHA_hap14
RCR_hap11
CHA_hap13
RCR_hap16
CHA_hap17
CHA_hap7
RCR_hap5
RCR_hap4
CHA_hap6
RCR_hap6
RCR_hap9
RCR_hap10
CHA_hap8
Sequence distance (K2P, %)
2.5
2.0
1.5
1.0
0.5
0.0