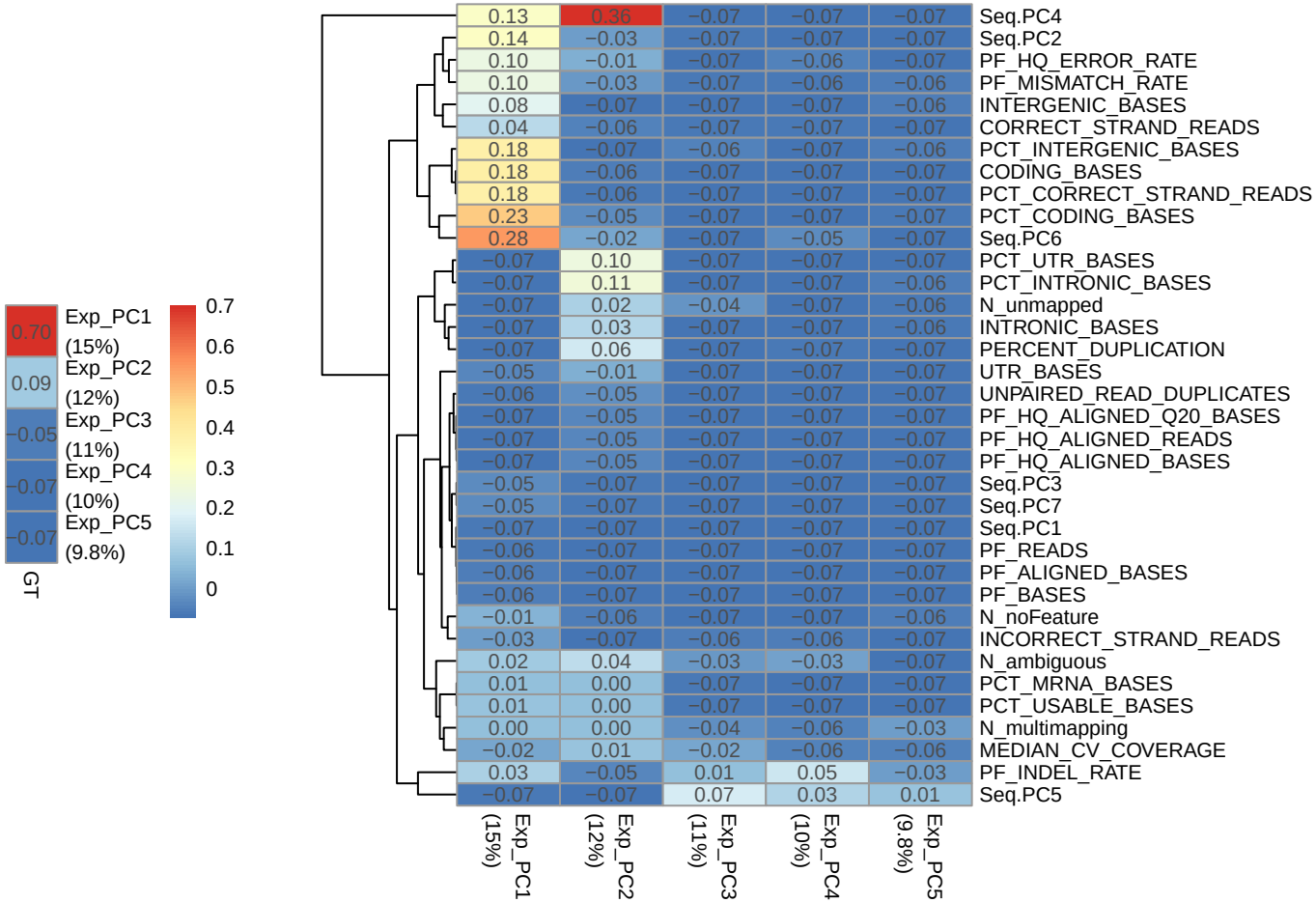
0.70
0.09
−0.05
−0.07
−0.07
Exp_PC1 (15%)
Exp_PC2 (12%)
Exp_PC3 (11%)
Exp_PC4 (10%)
Exp_PC5 (9.8%)
GT
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Seq.PC4
Seq.PC2
PF_HQ_ERROR_RATE
PF_MISMATCH_RATE
INTERGENIC_BASES
CORRECT_STRAND_READS
PCT_INTERGENIC_BASES
CODING_BASES
PCT_CORRECT_STRAND_READS
PCT_CODING_BASES
Seq.PC6
PCT_UTR_BASES
PCT_INTRONIC_BASES
N_unmapped
INTRONIC_BASES
PERCENT_DUPLICATION
UTR_BASES
UNPAIRED_READ_DUPLICATES
PF_HQ_ALIGNED_Q20_BASES
PF_HQ_ALIGNED_READS
PF_HQ_ALIGNED_BASES
Seq.PC3
Seq.PC7
Seq.PC1
PF_READS
PF_ALIGNED_BASES
PF_BASES
N_noFeature
INCORRECT_STRAND_READS
N_ambiguous
PCT_MRNA_BASES
PCT_USABLE_BASES
N_multimapping
MEDIAN_CV_COVERAGE
PF_INDEL_RATE
Seq.PC5
Exp_PC1 (15%)
Exp_PC2 (12%)
Exp_PC3 (11%)
Exp_PC4 (10%)
Exp_PC5 (9.8%)