

## **Frequency plots to support inferred genotypes**

KE4-1-C02  
inferred genotype: homozygous, deletion (delta/delta)

R1+R2, sequences with >20% representation among reads:

Allele 1: [82/144] mutant, likely deletion, 84 bp

query

ACTTAAACTGGAGCTCTGACTTATGTTCCTTACTGCCCTAGAGCAATTTTGTTT-----

|||||

reference

ACTTAAACTGGAGCTCTGACTTATGTTCCTTACTGCCCTAGAGCAATTTGTTTGAAGAGCACAGAACCCCTGTTCTGAATGTGGCTGGCACATGAA

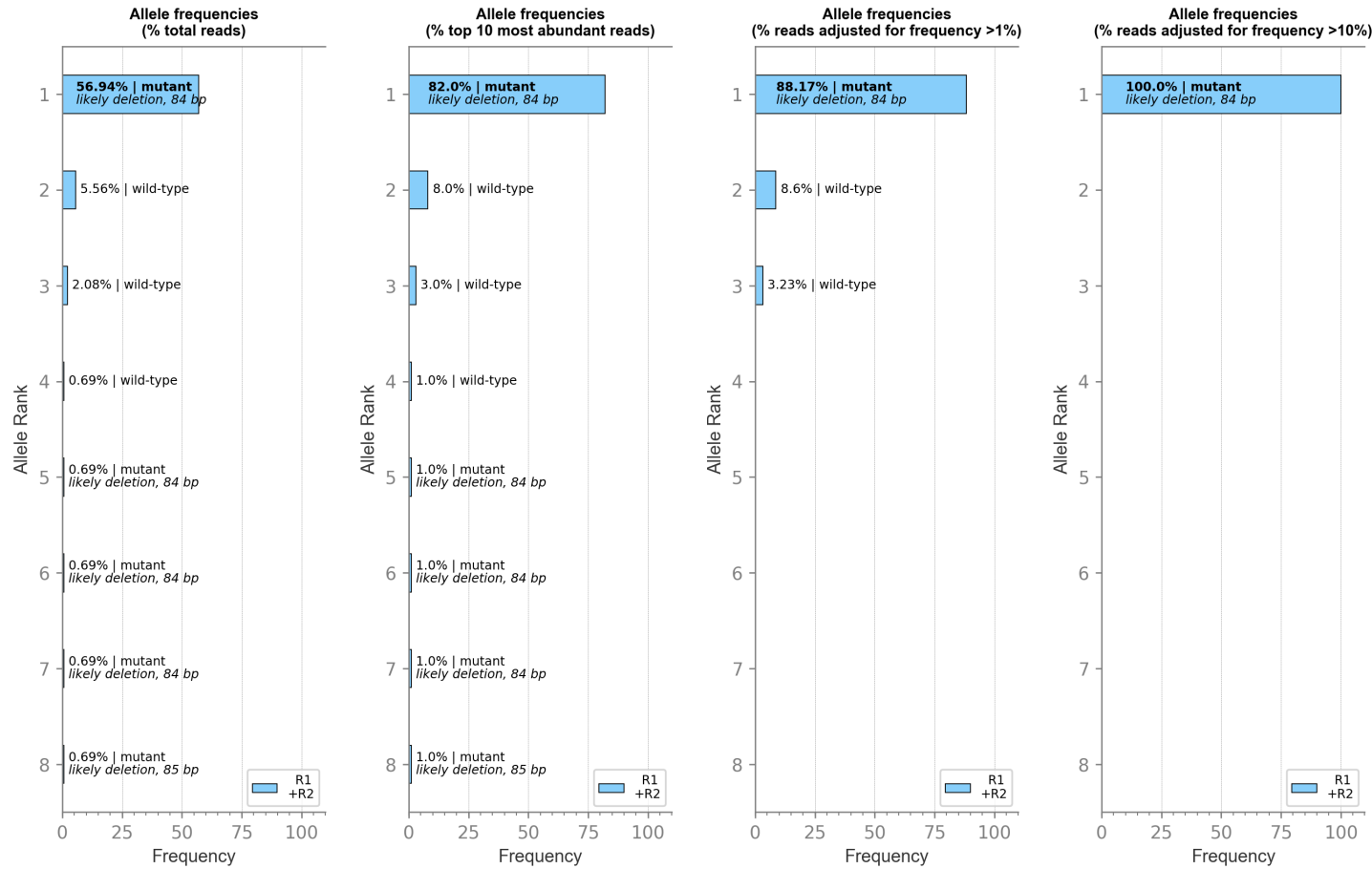
query

-----GGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

|||||

reference

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA



KE4-2-A01

inferred genotype: heterozygous, deletion + wild-type (delta/wt)

R1+R2, sequences with >20% representation among reads:

Allele 1: [195/435] wild-type

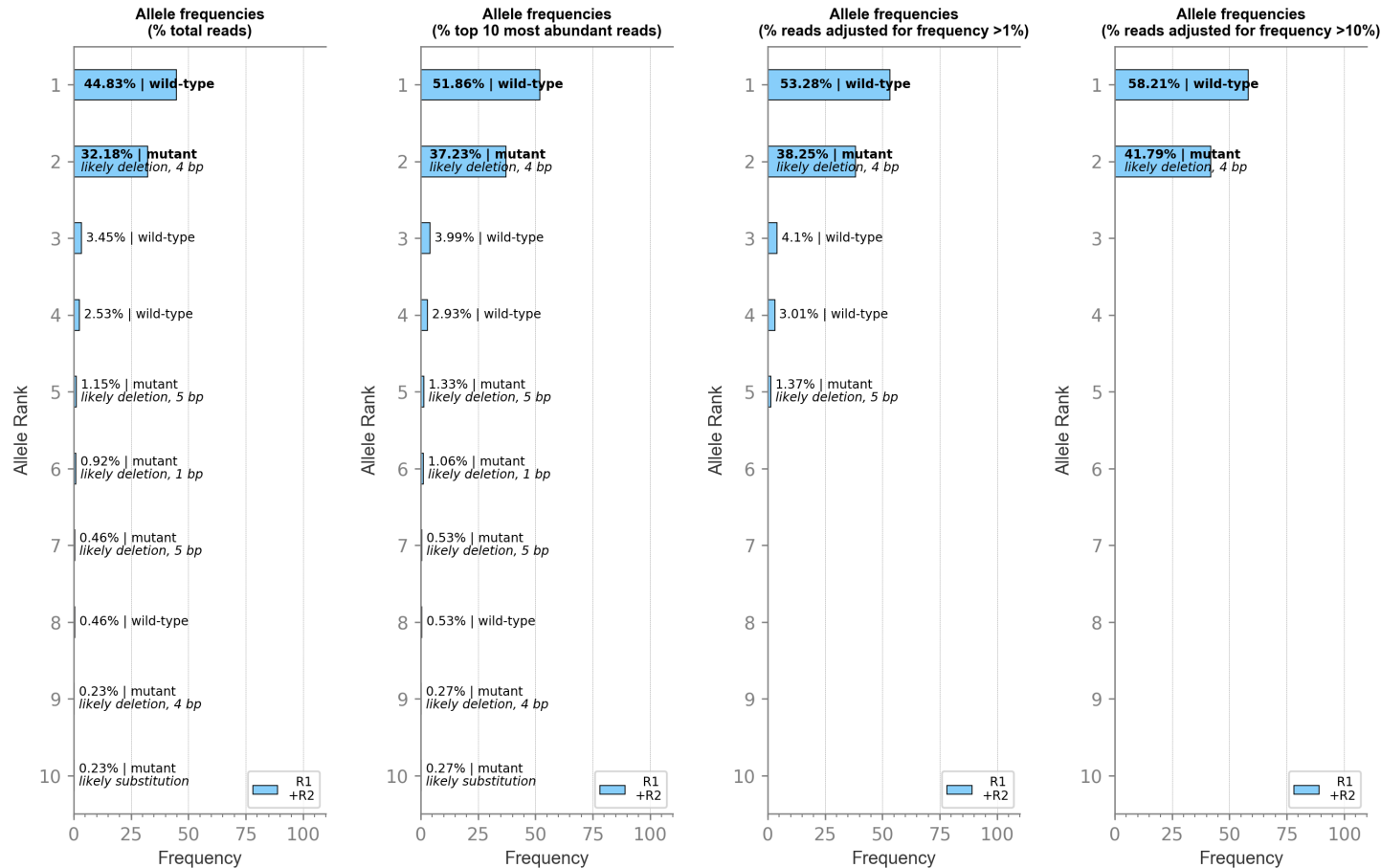
query    ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA  
          |||||  
reference ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query    CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
          |||||  
reference CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

Allele 2: [140/435] mutant, likely deletion, 4 bp

query    ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTT-T---TGTGGCTGGCACATGAA  
          |||||  
reference ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query    CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
          |||||  
reference CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA



KE4-4-G02  
inferred genotype: heterozygous, deletion1 + deletion2 (del1/del2)

R1+R2, sequences with >20% representation among reads:

Allele 1: [443/996] mutant, likely deletion, 4 bp

query

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTT----ATGTGGCTGGCACATGAA

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

reference

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

Allele 2: [364/996] mutant, likely deletion, 2 bp

query

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTG--CTGAATGTGGCTGGCACATGAA

reference

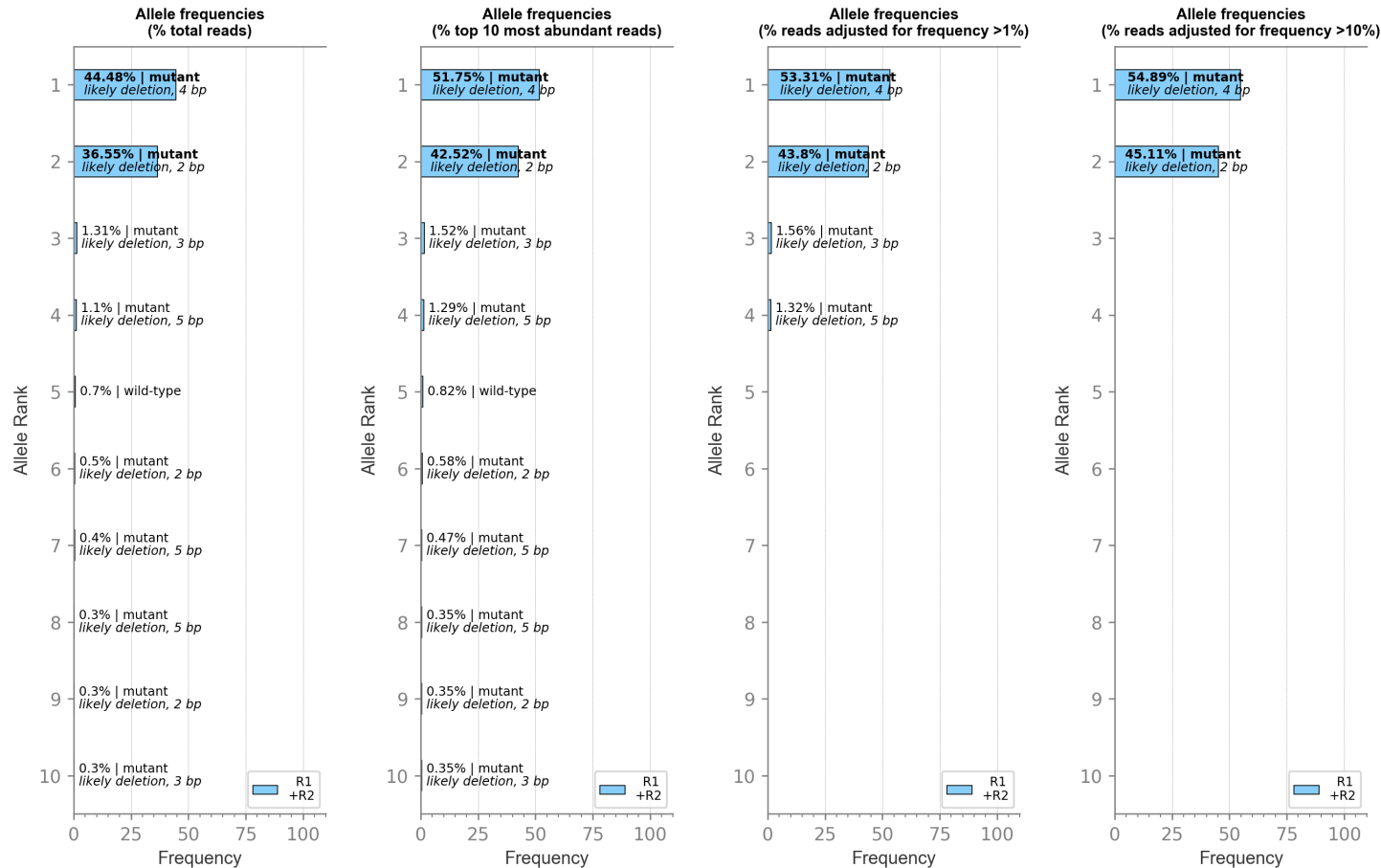
ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

reference

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA



**KE4-4-G10**  
inferred genotype: heterozygous, deletion1 + deletion2 (del1/del2)

R1+R2, sequences with >20% representation among reads:

Allele 1: [347/806] mutant, likely deletion, 4 bp

query

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTT----ATGTGGCTGGCACATGAA

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

reference

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

Allele 2: [314/806] mutant, likely deletion, 2 bp

query

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTG--CTGAATGTGGCTGGCACATGAA

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGAA

query

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

reference

CTCGATGTGCTGACAGCAATTTGTACTCCGATTAAAAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

