

## **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

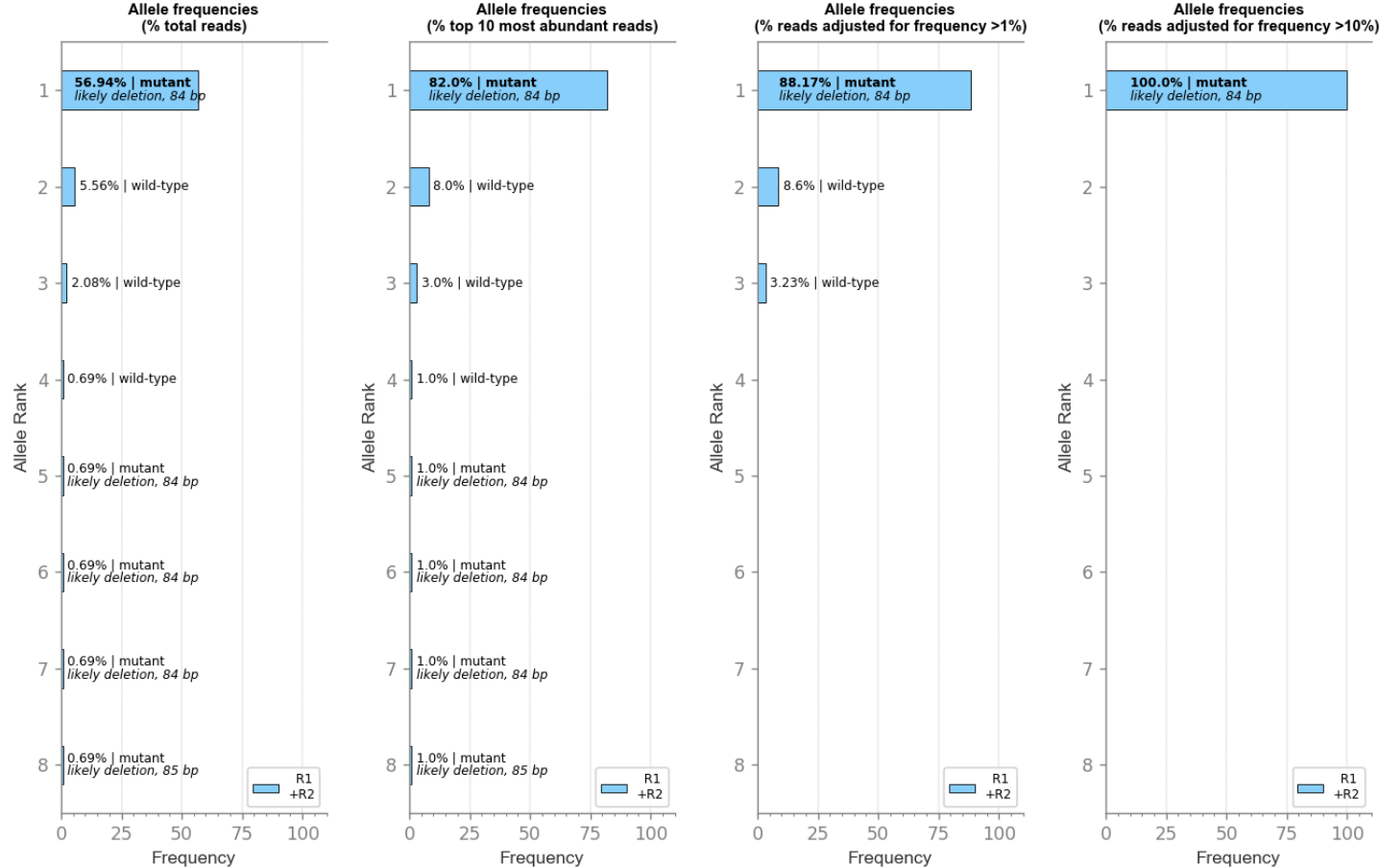
reference

ACTTAAACTGGAGCTCTGACTTATGTTCCTTACTGCCCTAGAGCAATTTGT

ACTTAAACTGGAGCTCTGACTTATGTTCCTTACTGCCCTAGAGCAATTTGT

GGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

GGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA



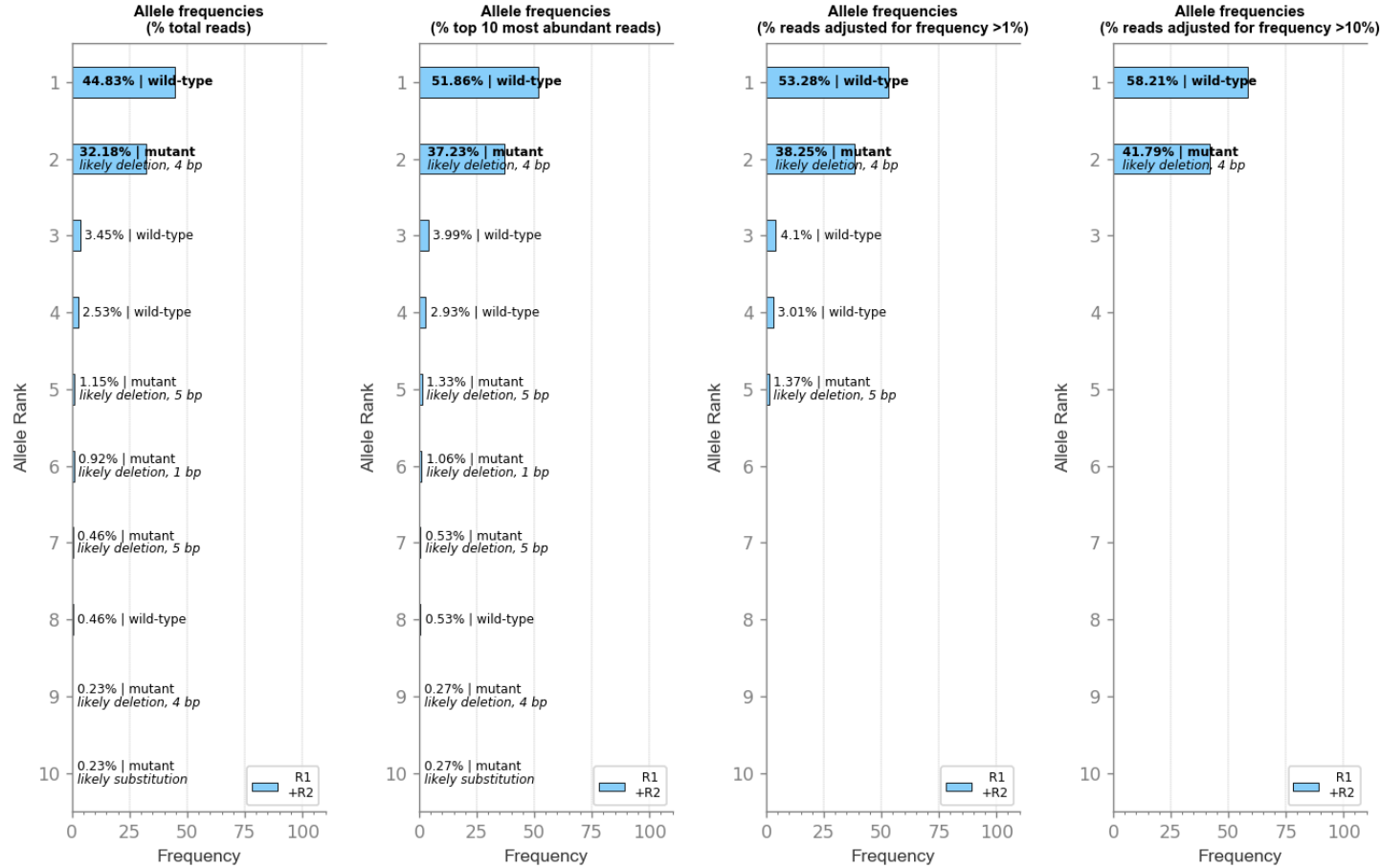
**KE4-2-A01**  
inferred genotype: heterozygous, deletion + wild-type (delta/wt)  
R1+R2, sequences with >20% representation among reads:

Allele 1: [195/435] wild-type

query	ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA
reference	ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA
query	ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAAGGGGGGAAAAAGGAAAGAGAGTGCACAGCAGTAA
reference	ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAAGGGGGGAAAAAGGAAAGAGAGTGCACAGCAGTAA

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

query	ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTT-T---TGTGGCTGGCACATGA
reference	ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA
query	ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAAGGGGGGAAAAAGGAAAGAGAGTGCACAGCAGTAA
reference	ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAAGGGGGGAAAAAGGAAAGAGAGTGCACAGCAGTAA



**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

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTT---ATGTGGCTGGCACATGA  
|||||  
ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA

ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
|||||  
ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

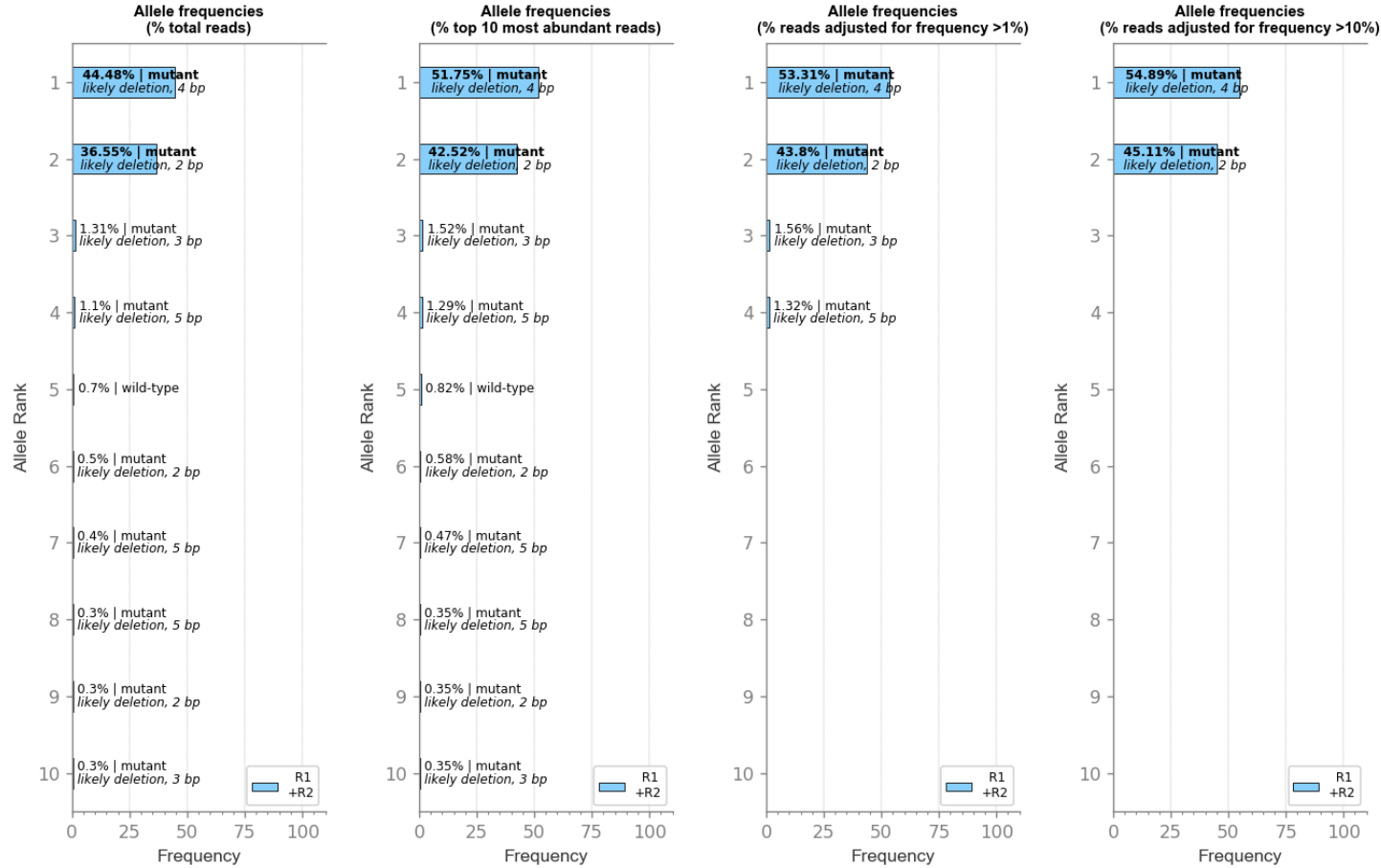
Allele 2: [364/996] mutant, likely deletion, 2 bp

query

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTG--CTGAATGTGGCTGGCACATGA  
|||||  
ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA

ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
|||||  
ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA



**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

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTT---ATGTGGCTGGCACATGA  
|||||  
ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA

ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
|||||  
ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

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

query

reference

ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTG--CTGAATGTGGCTGGCACATGA  
|||||  
ACTTAAACTGGAGCTCTGACTTATTGTTCTCTTACTGCCCTAGAGCAATTTTGTTTGAAGAGCACAGAACACCCTGTTCTGAATGTGGCTGGCACATGA

ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA  
|||||  
ACTCGATGTGCTGACAGCAATTTGTACTCCGATTAATAATAGGGGGGAAAAAAGGAAAGAGAGTGCACAGCAGTAA

