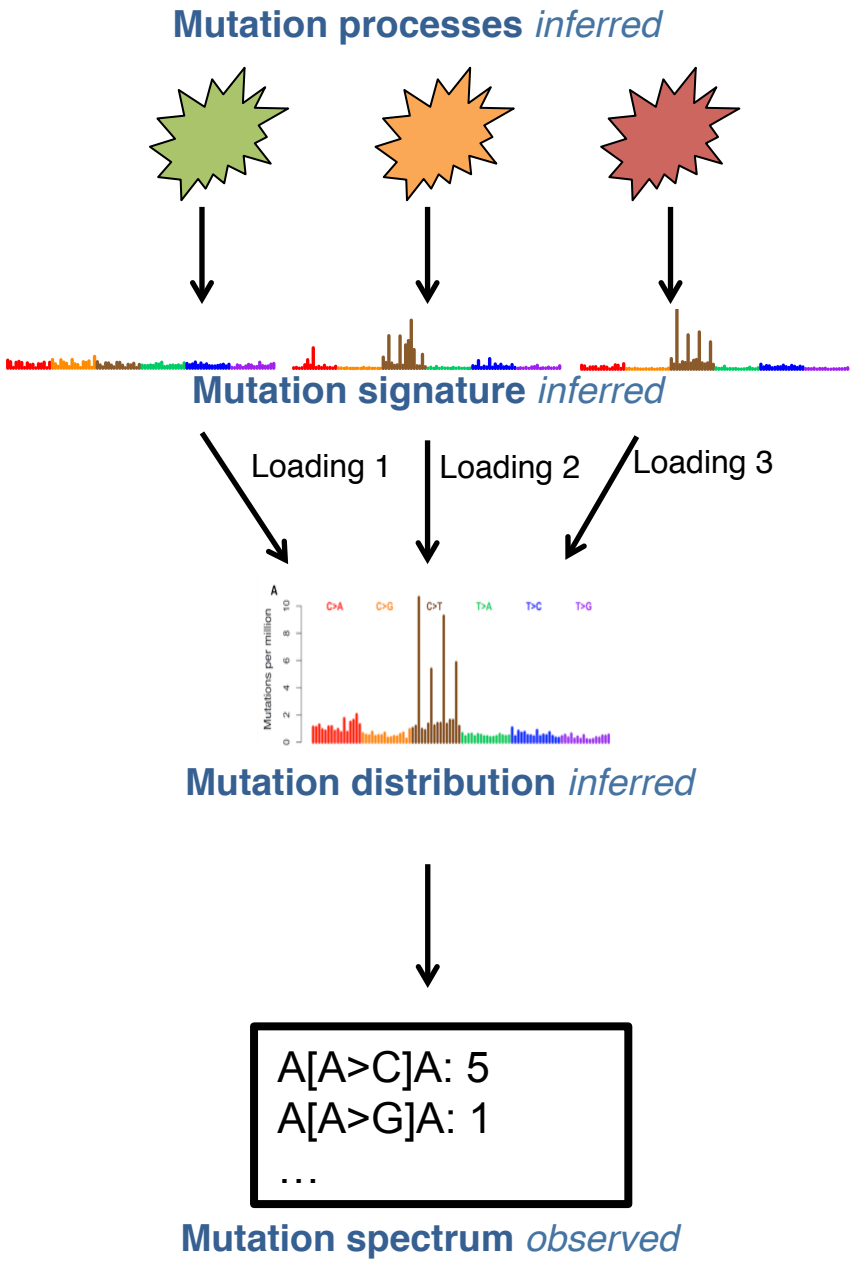
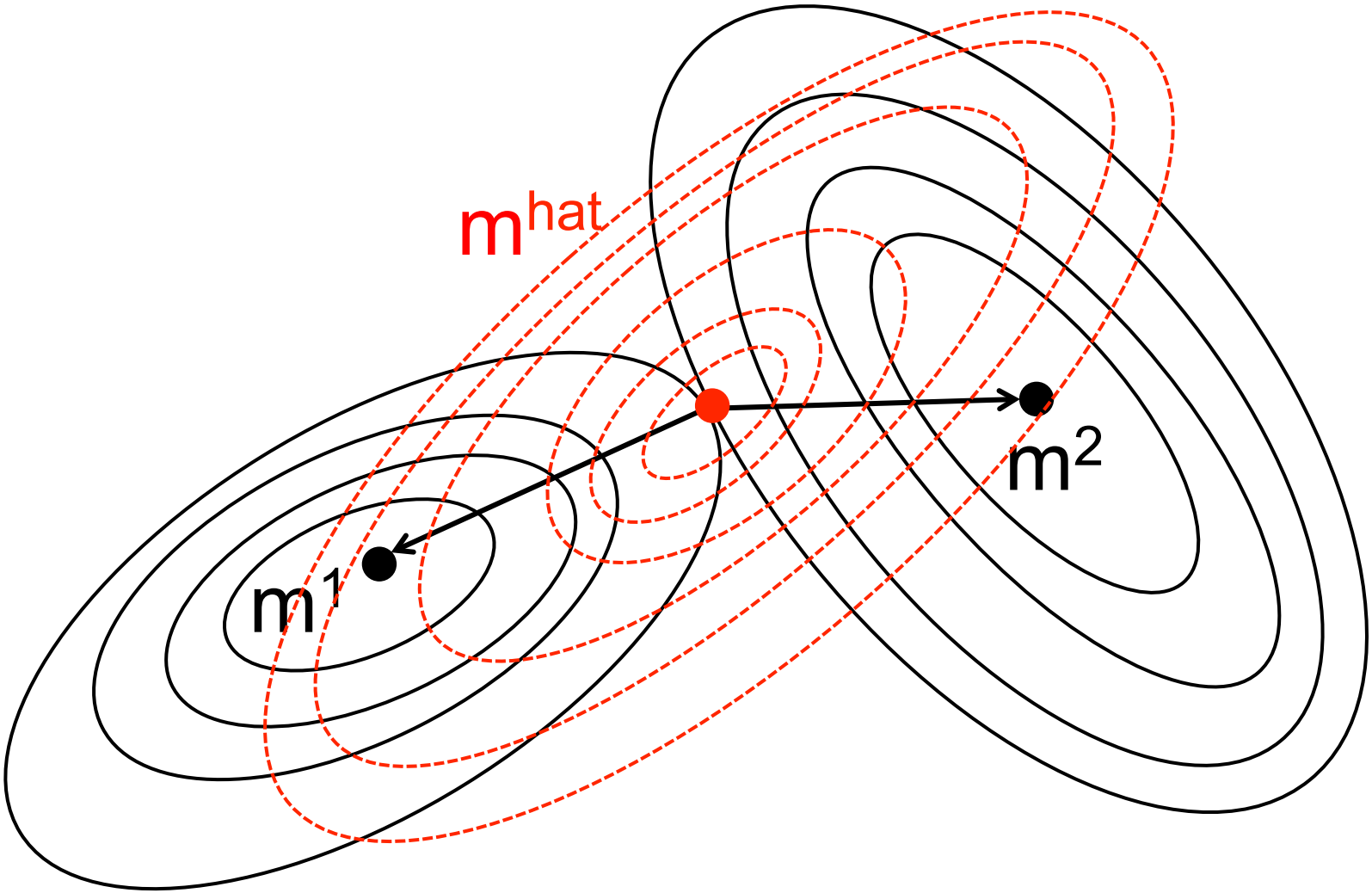

Mutation processes inferred
Mutation signature inferred
Loading 1
Loading 2
Loading 3
A
C>A
C>G
C>T
T>A
T>C
T>G
Mutations per million
0
2
4
6
8
10
Mutation distribution inferred
A[A>C]A: 5
A[A>G]A: 1
…
Mutation spectrum observed

Figure 1


m^hat
m^1
m^2

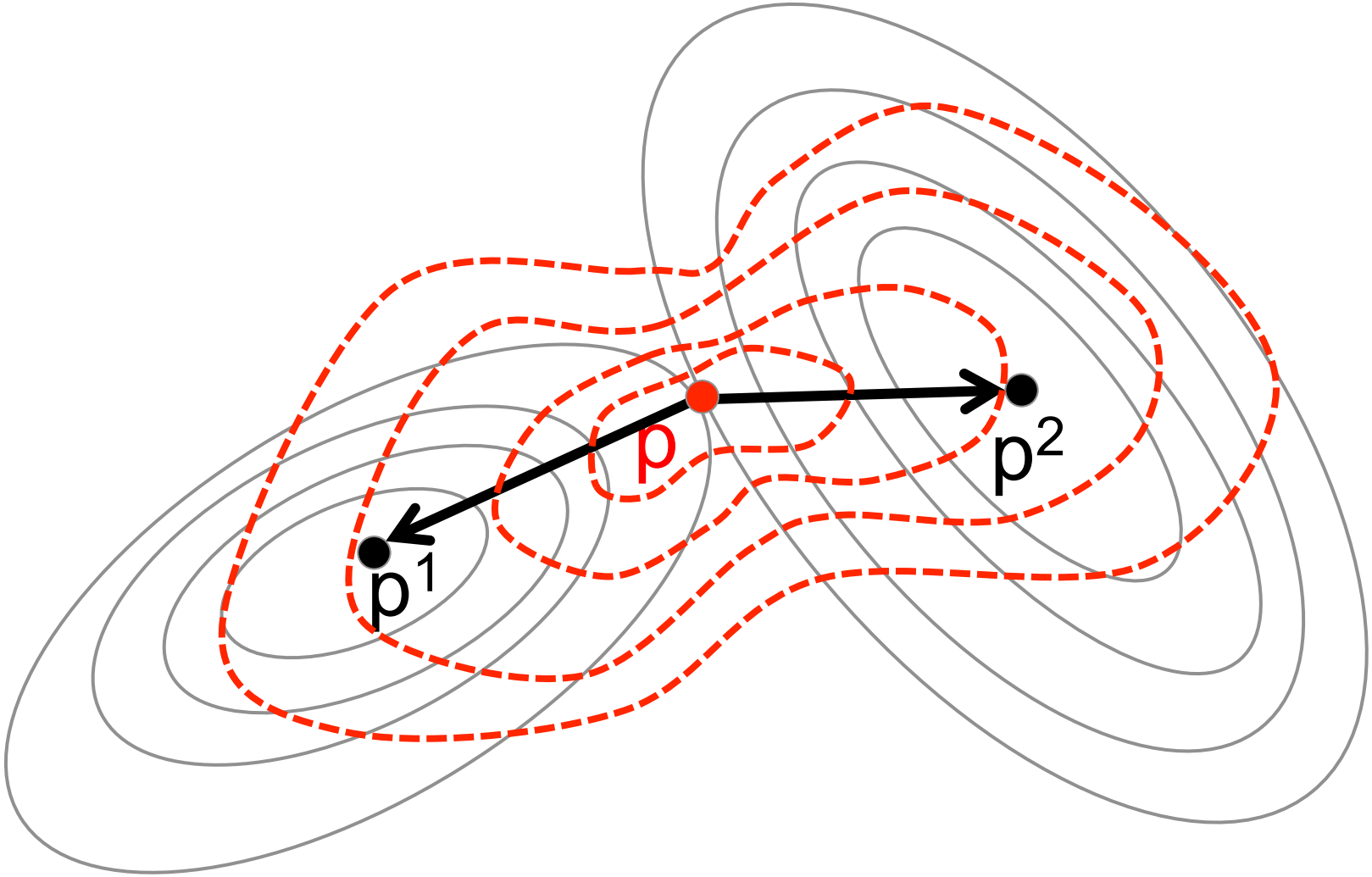


Figure 2A

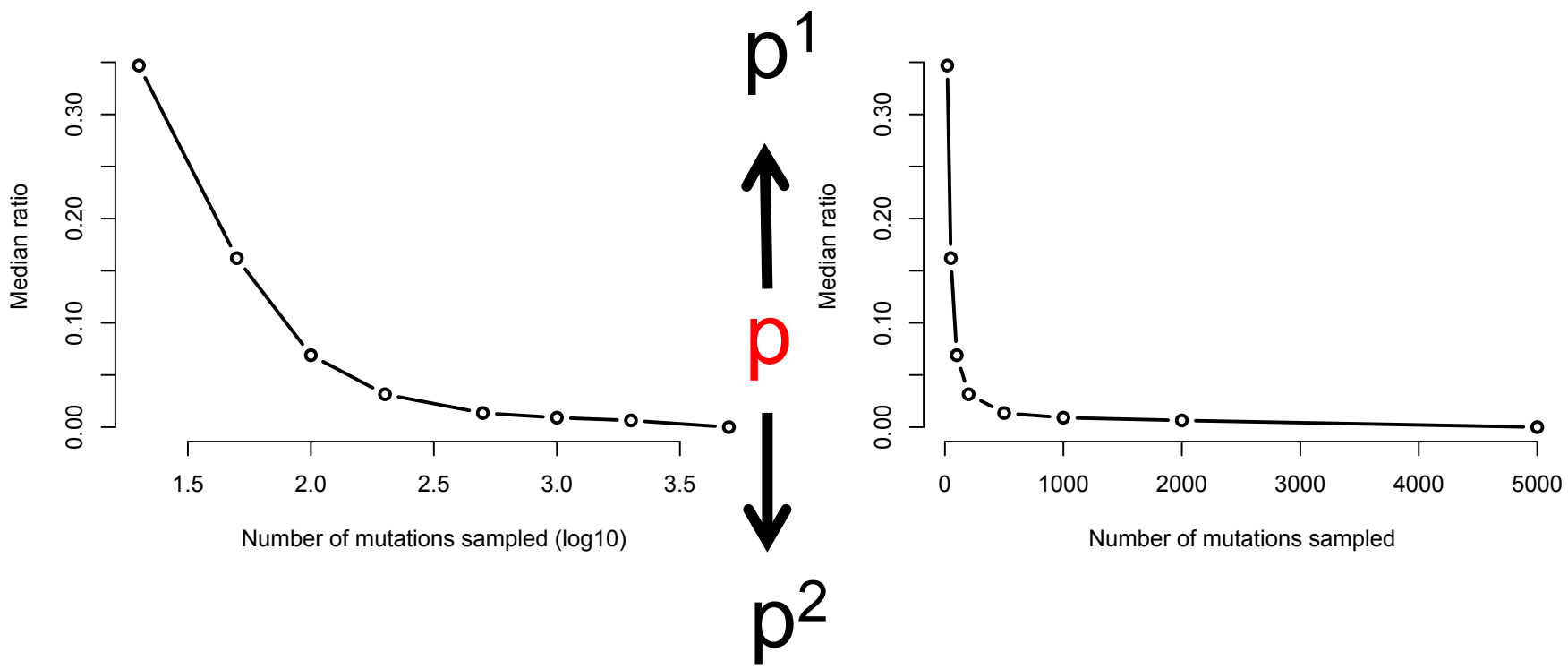

p1
p
p2
Median ratio
0.00
0.10
0.20
0.30
1.5
2.0
2.5
3.0
3.5
Number of mutations sampled (log10)
Median ratio
0.00
0.10
0.20
0.30
0
1000
2000
3000
4000
5000
Number of mutations sampled

Figure 2B

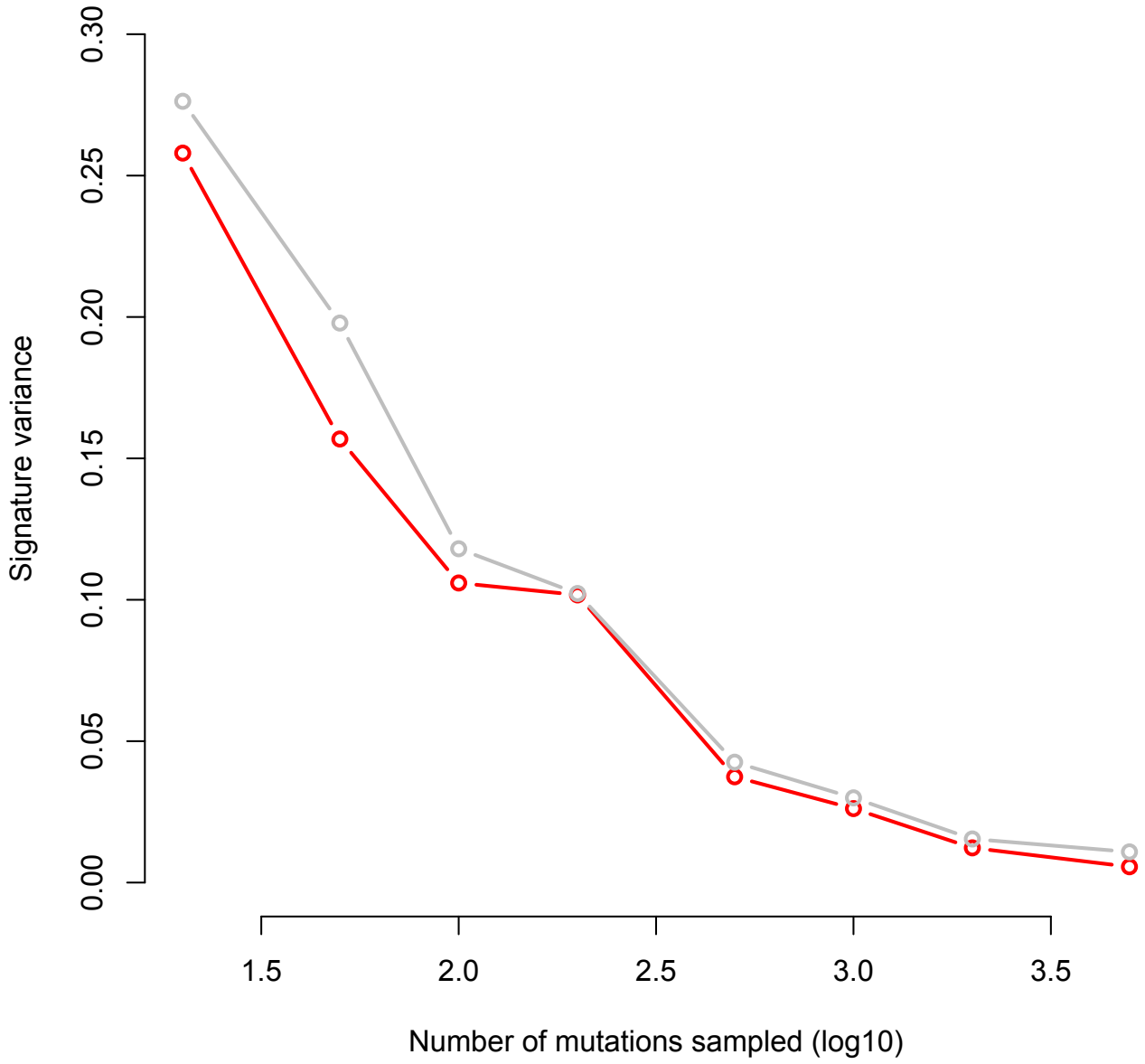

Signature variance
0.00
0.05
0.10
0.15
0.20
0.25
0.30
1.5
2.0
2.5
3.0
3.5
Number of mutations sampled (log10)

Figure 2C?

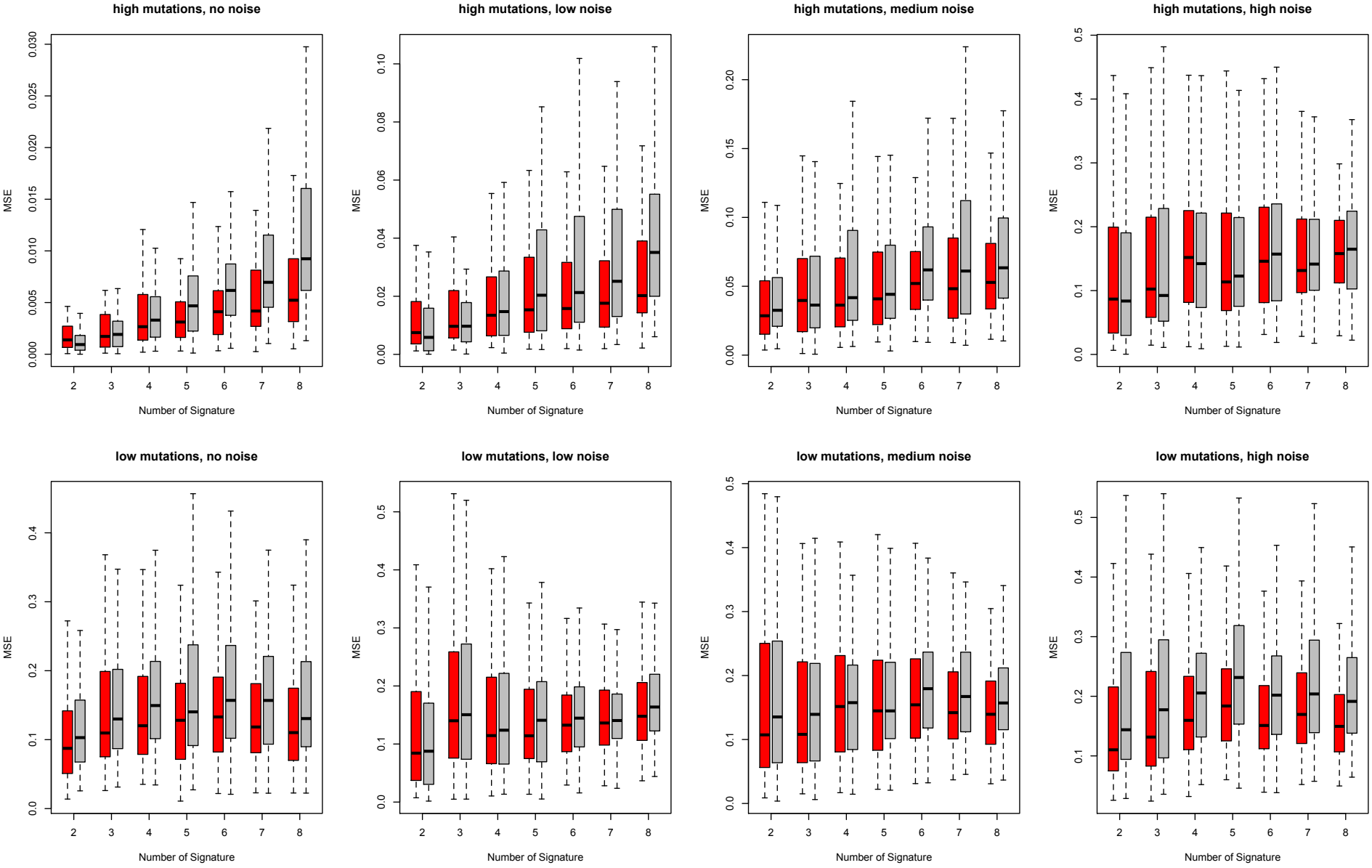
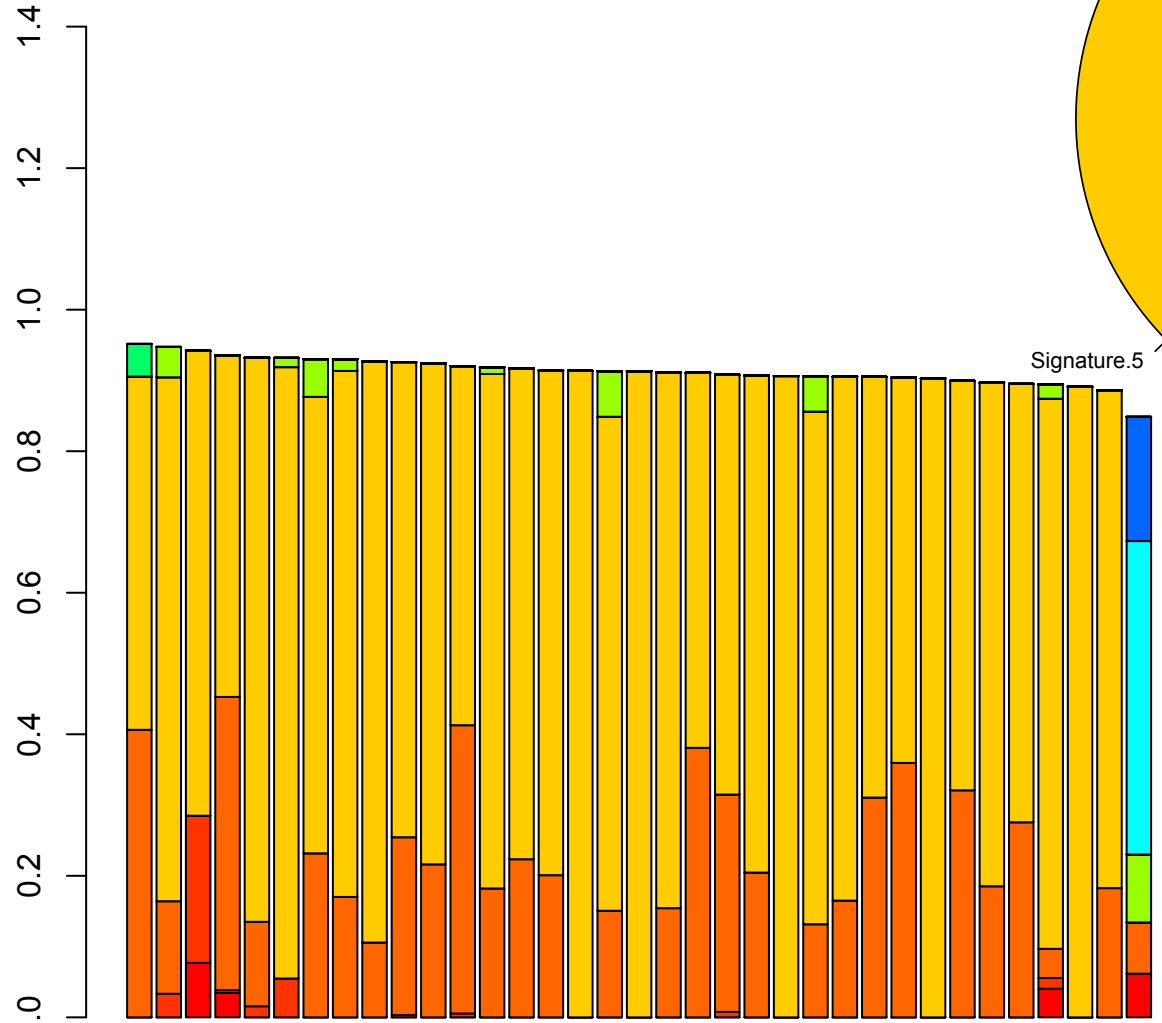

high mutations, no noise
high mutations, low noise
high mutations, medium noise
high mutations, high noise
low mutations, no noise
low mutations, low noise
low mutations, medium noise
low mutations, high noise
MSE
Number of Signature

Figure 3



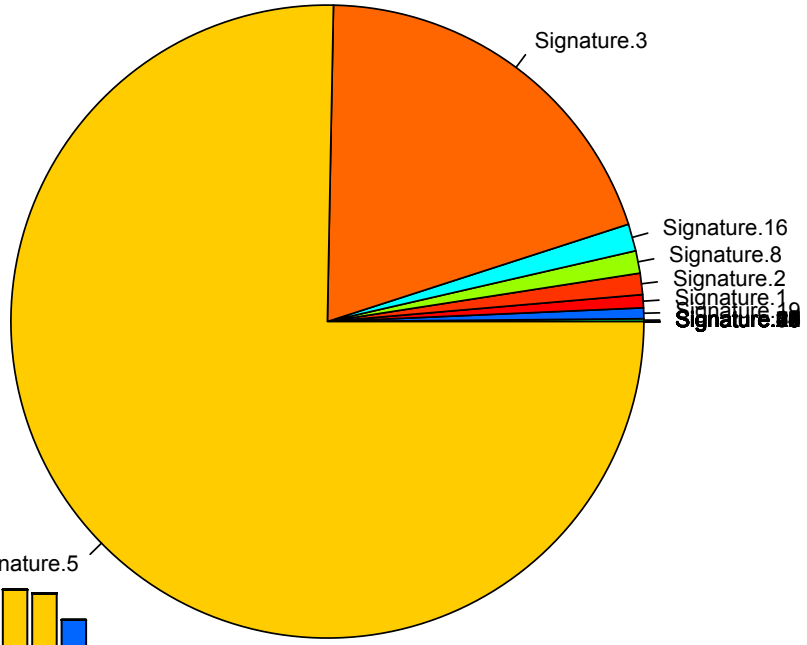


Figure 4A

Kidney-RCC Sampels

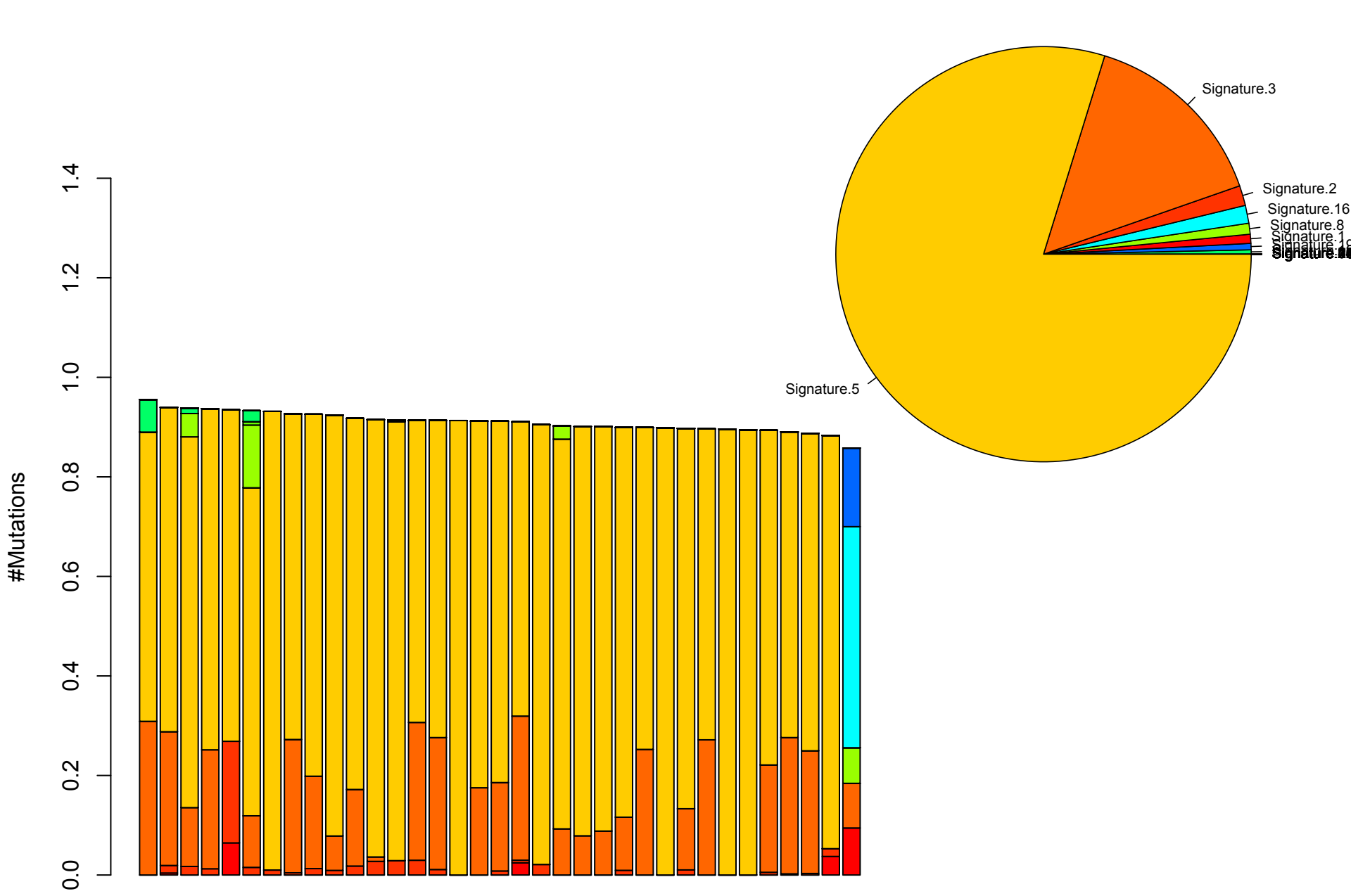
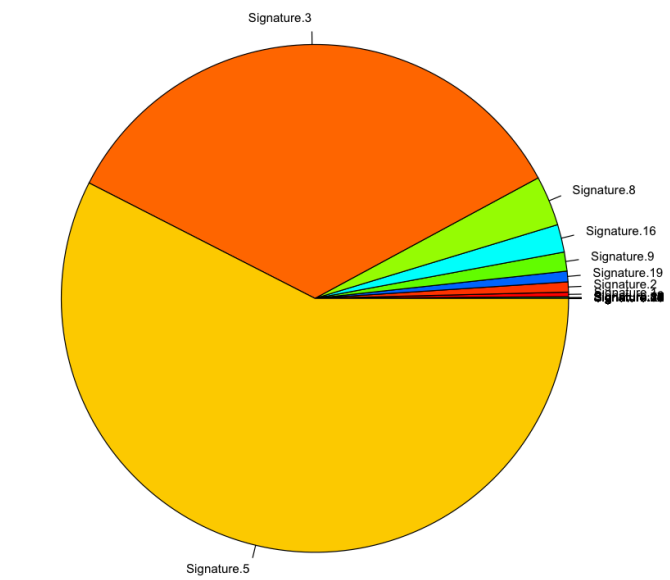
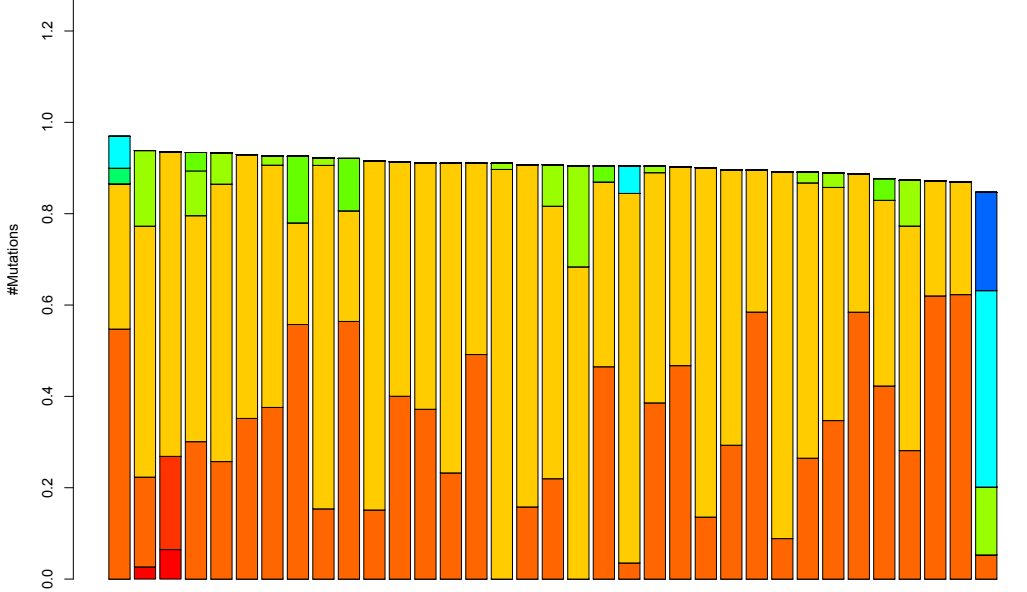
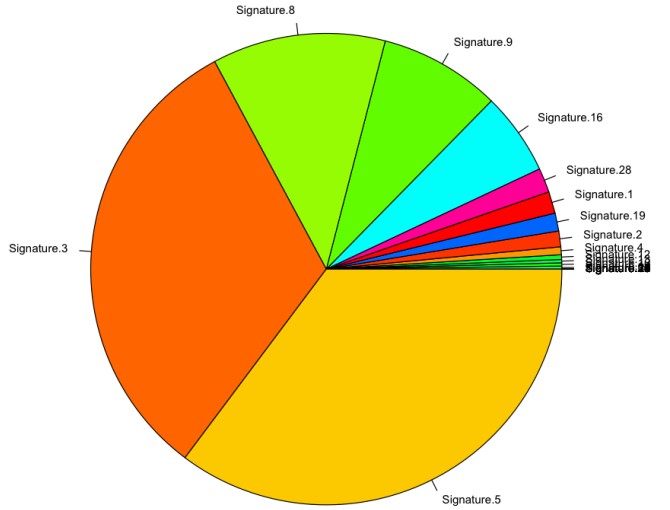


Figure 4A_2

Kidney-RCC Sampels


Signature.3
Signature.8
Signature.16
Signature.9
Signature.19
Signature.2
Signature.5


#Mutations
0.0
0.2
0.4
0.6
0.8
1.0
1.2
Kidney-RCC Samples


Signature.8
Signature.9
Signature.16
Signature.28
Signature.1
Signature.19
Signature.2
Signature.3
Signature.5

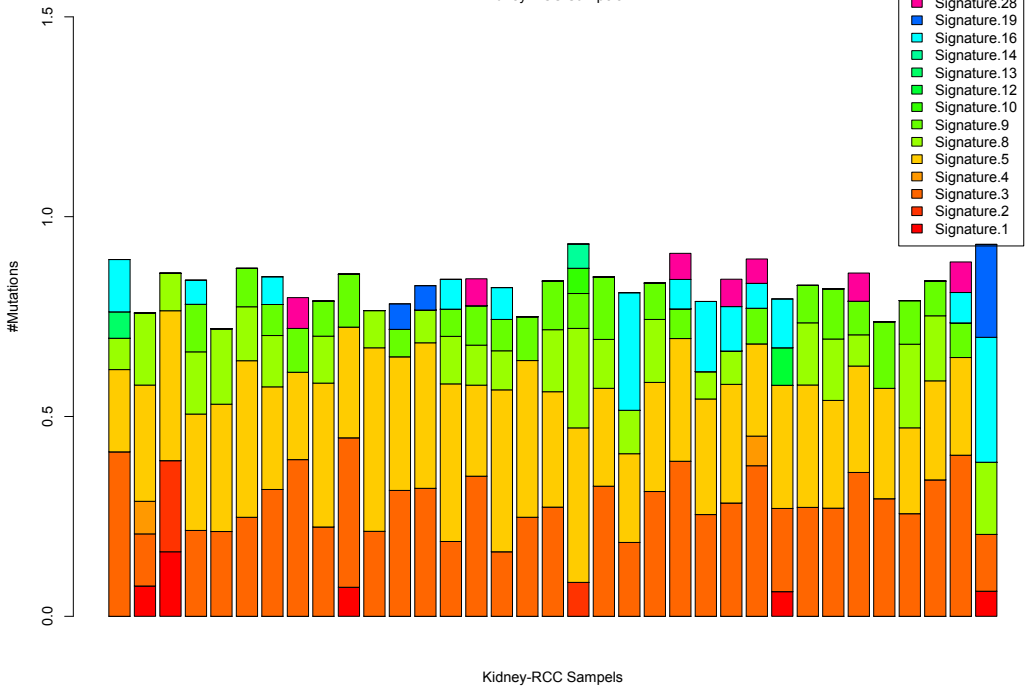

#Mutations
0.0
0.5
1.0
1.5
Kidney-RCC Samples
Signature.28
Signature.19
Signature.16
Signature.14
Signature.13
Signature.12
Signature.10
Signature.9
Signature.8
Signature.5
Signature.4
Signature.3
Signature.2
Signature.1

Figure 4A