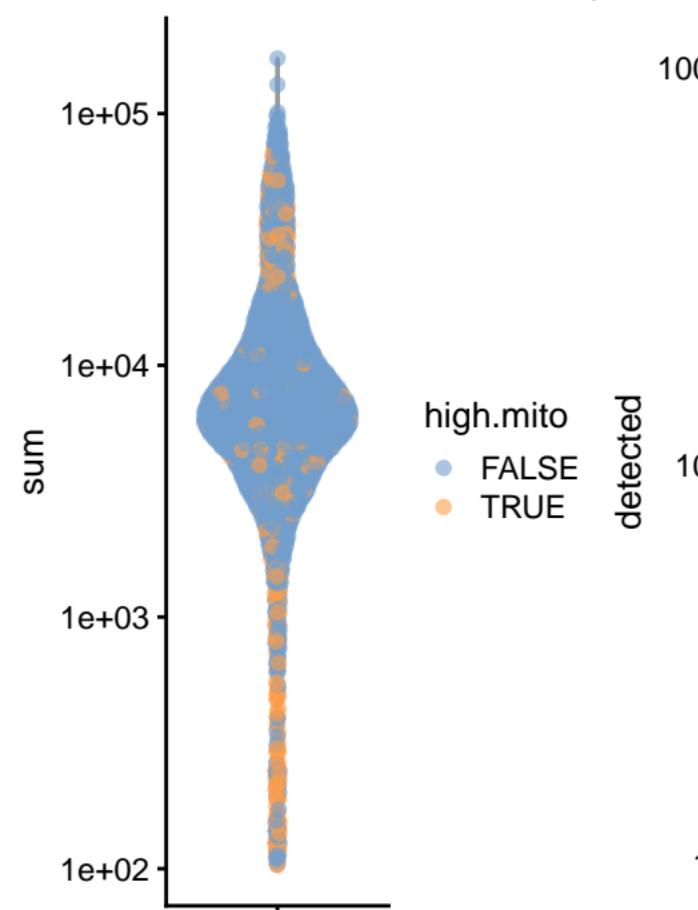
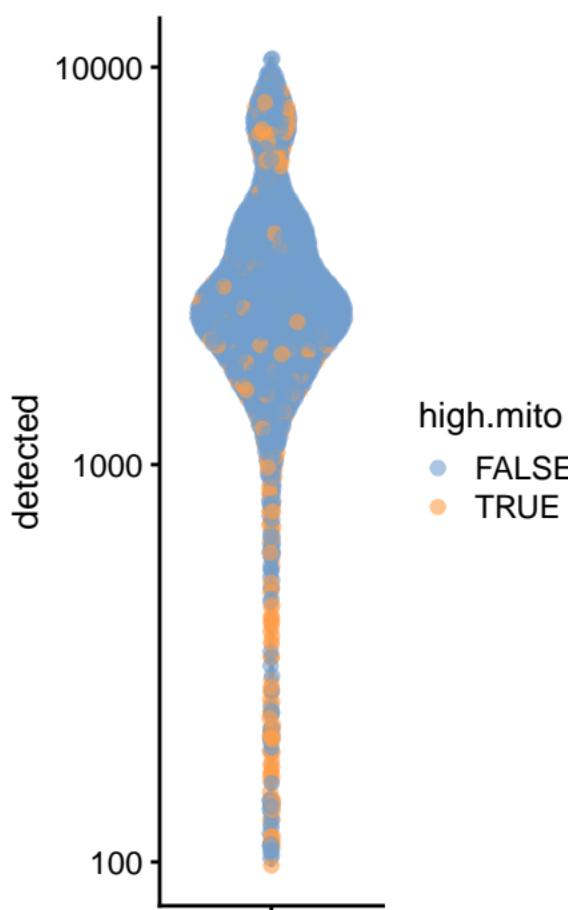


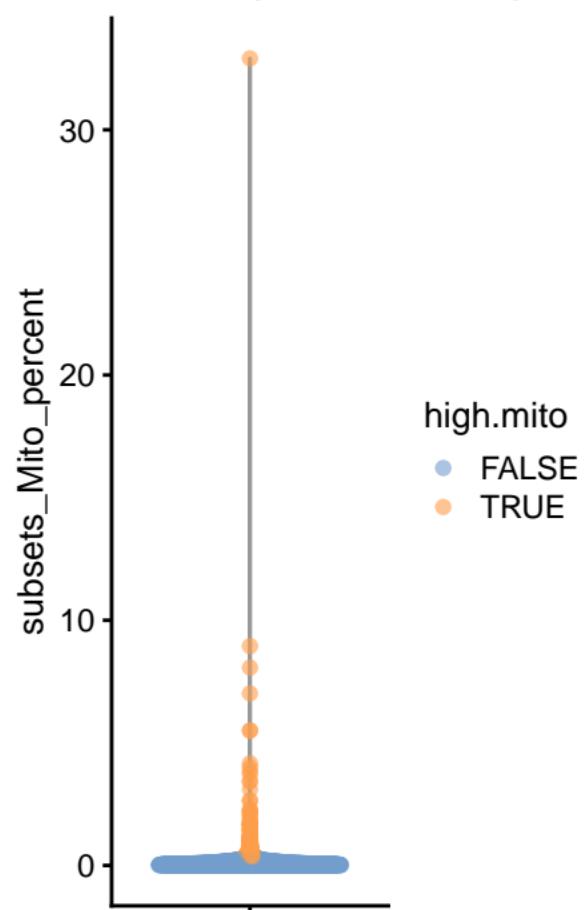
**Total count: br5161.amy**



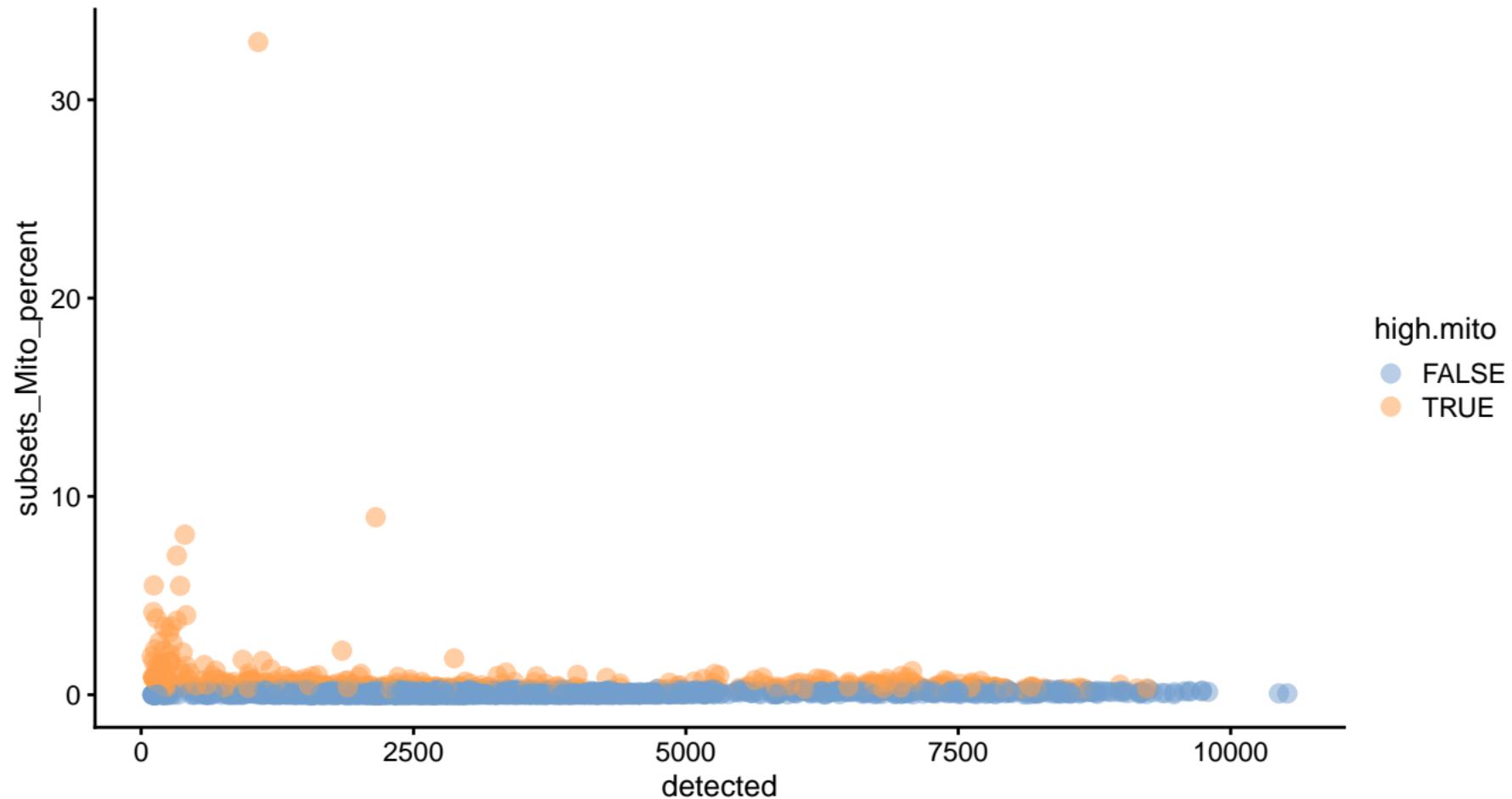
**Detected features**



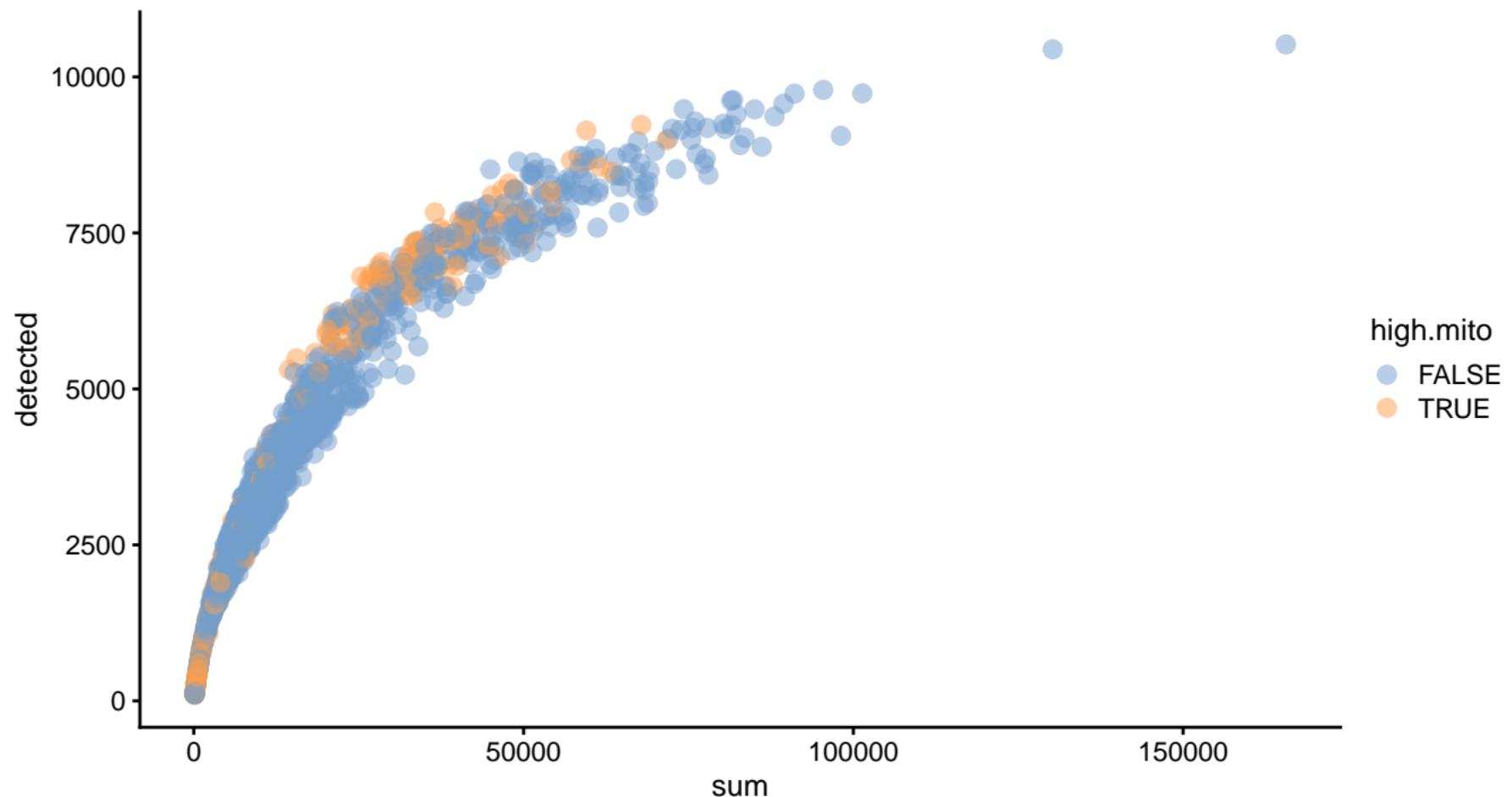
**Mito % (cutoff = 0.284)**



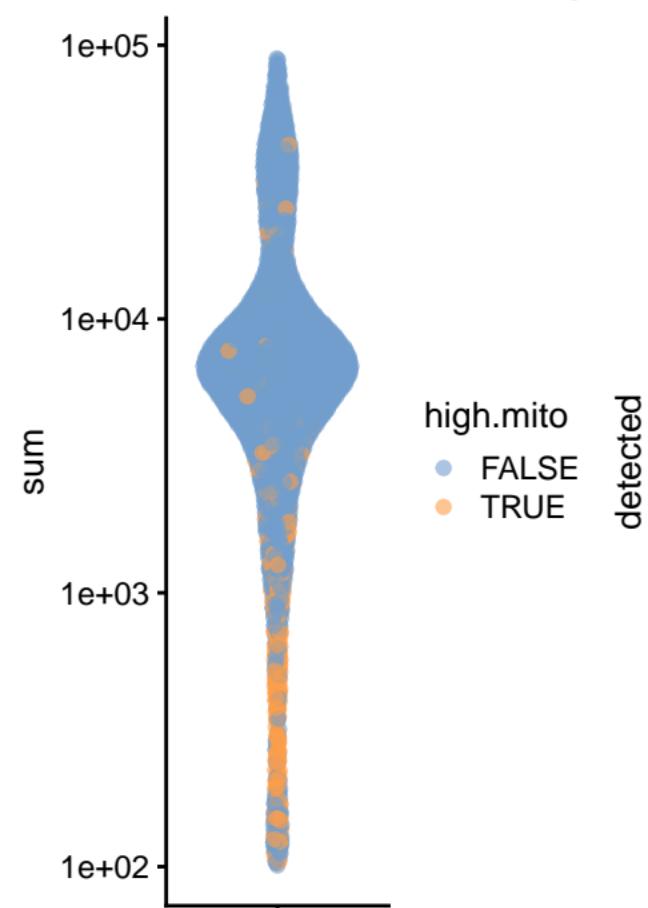
Sample: br5161.amy; pre-QC nNuclei: 3687; nNuclei kept: 3291 (0.89%)



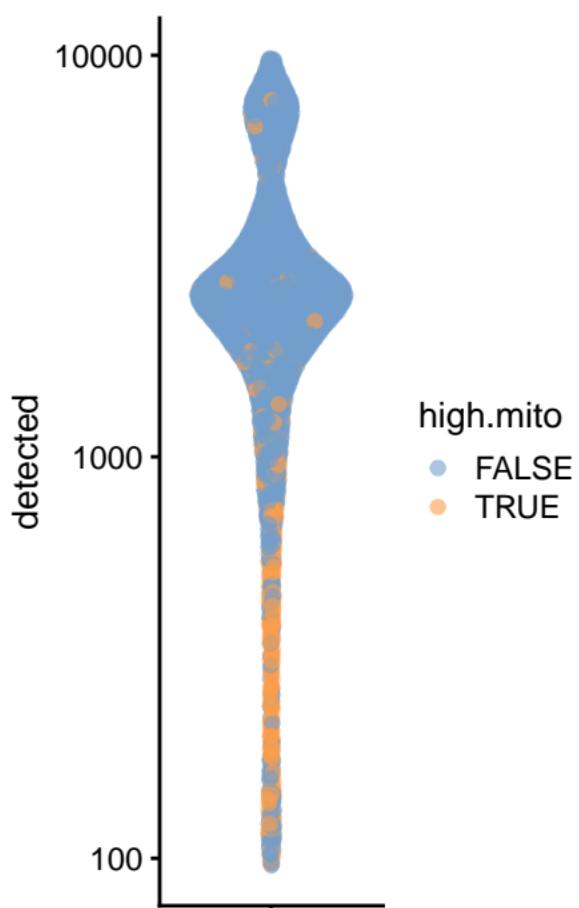
Sample: br5161.amy; pre-QC nNuclei: 3687; nNuclei kept: 3291 (0.89%)



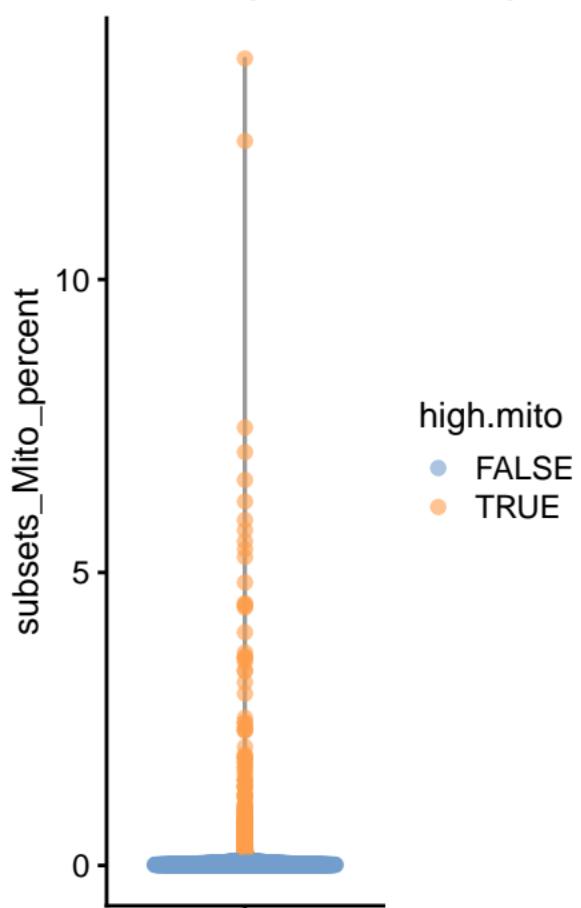
Total count: br5161.dlpfc



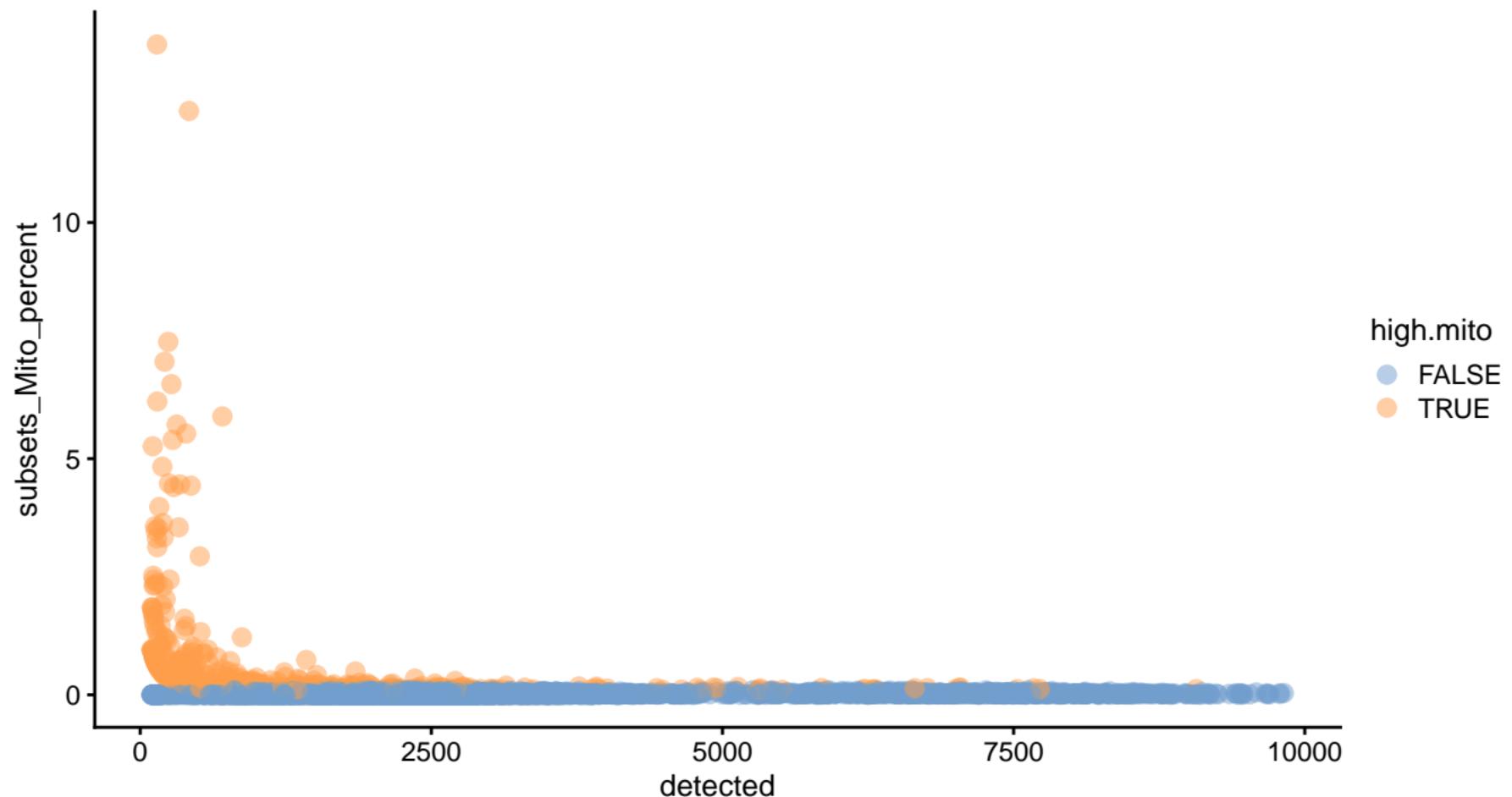
Detected features



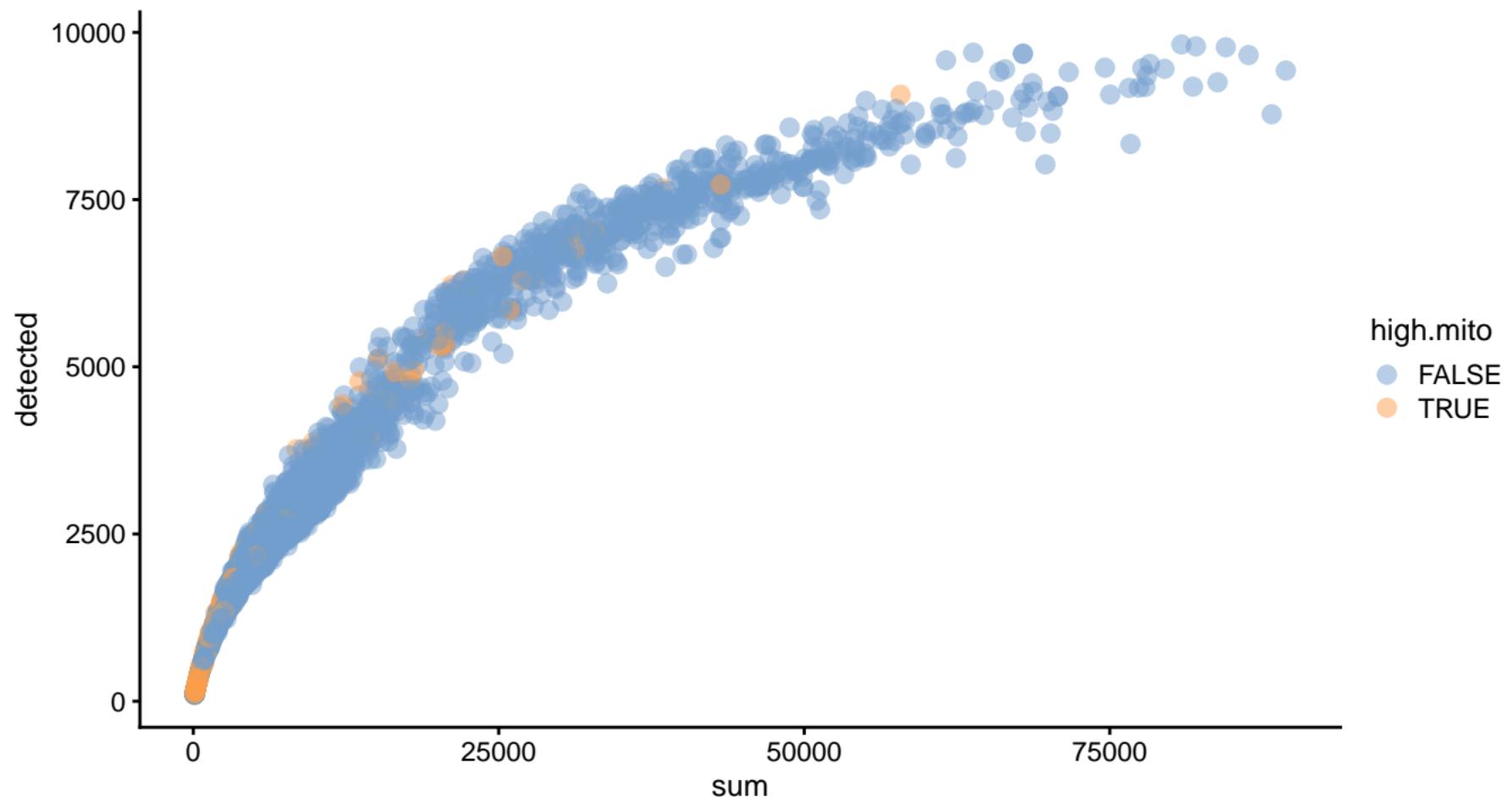
Mito % (cutoff = 0.097)



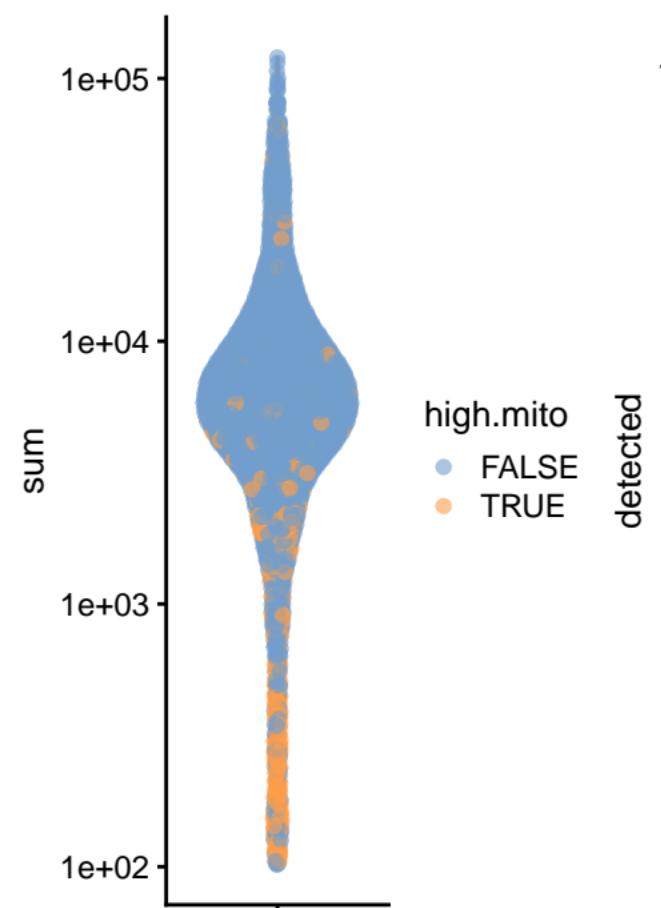
Sample: br5161.dlpfc; pre-QC nNuclei: 4788; nNuclei kept: 4394 (0.92%)



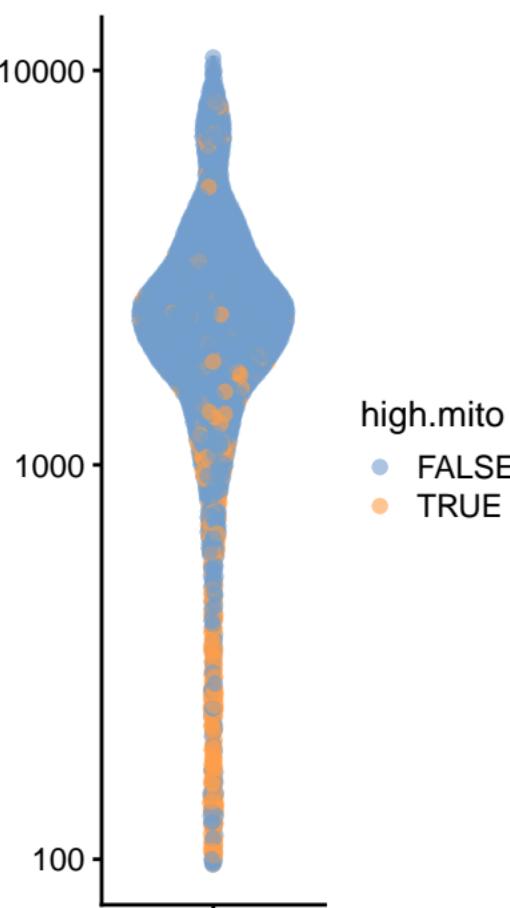
Sample: br5161.dlpfc; pre-QC nNuclei: 4788; nNuclei kept: 4394 (0.92%)



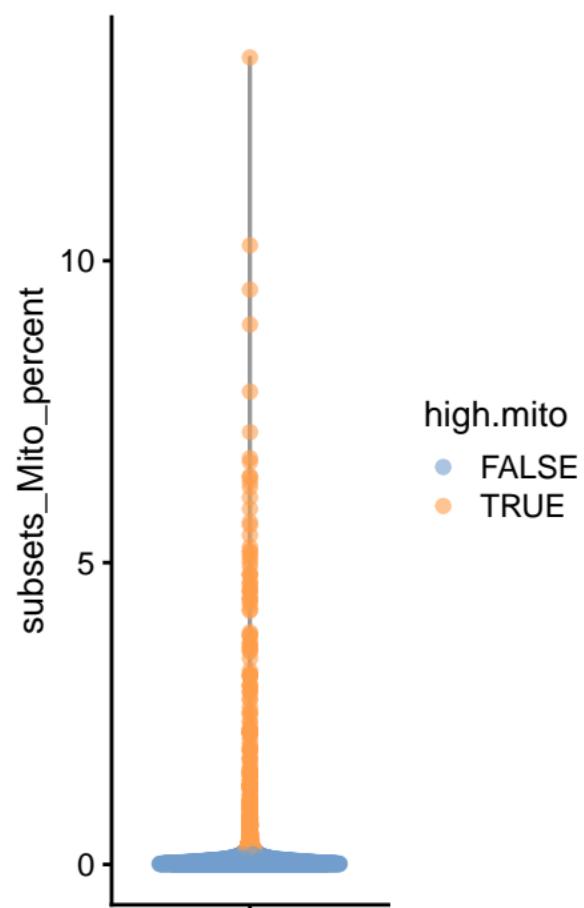
**Total count: br5161.hpc**



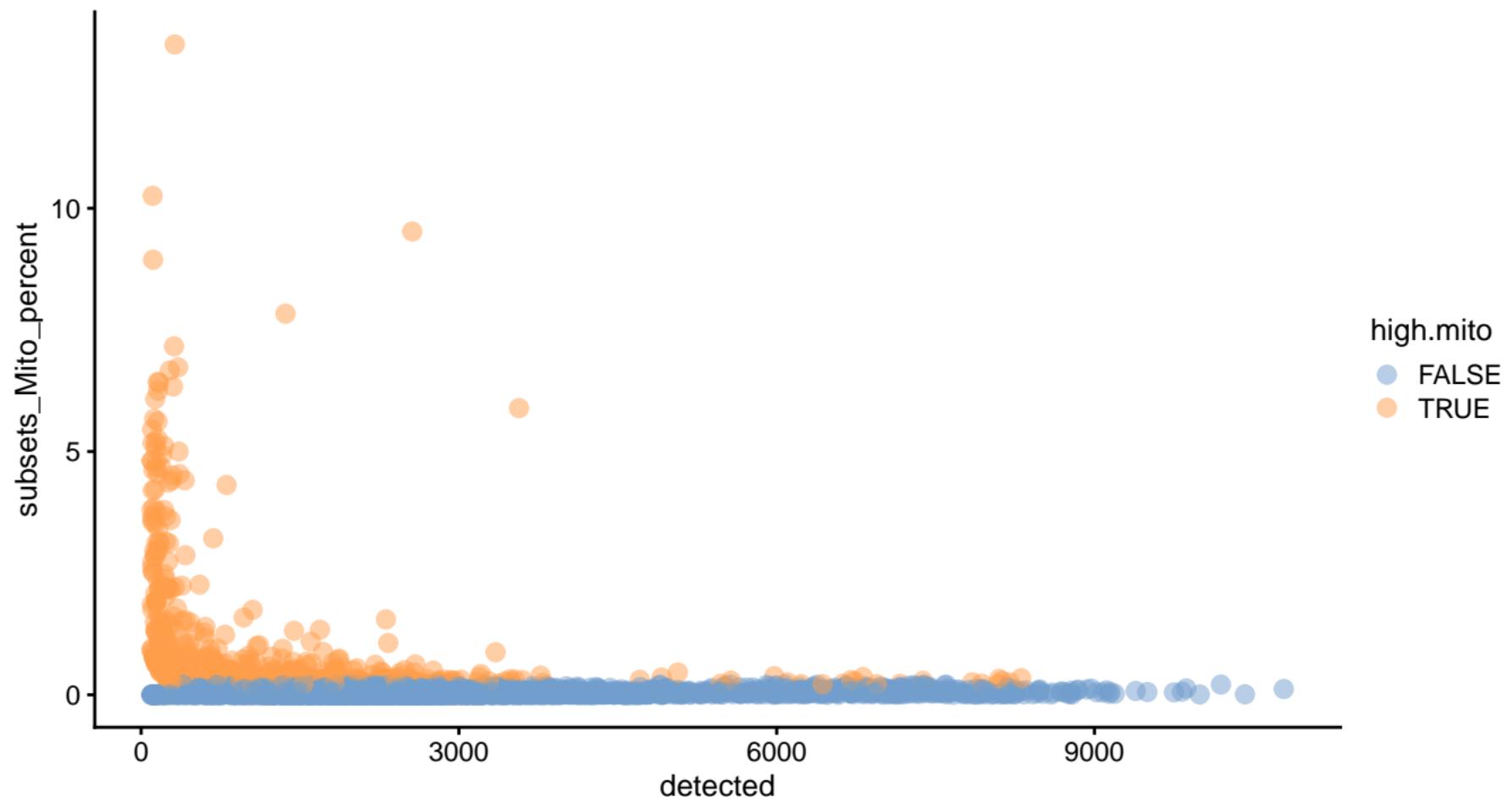
**Detected features**



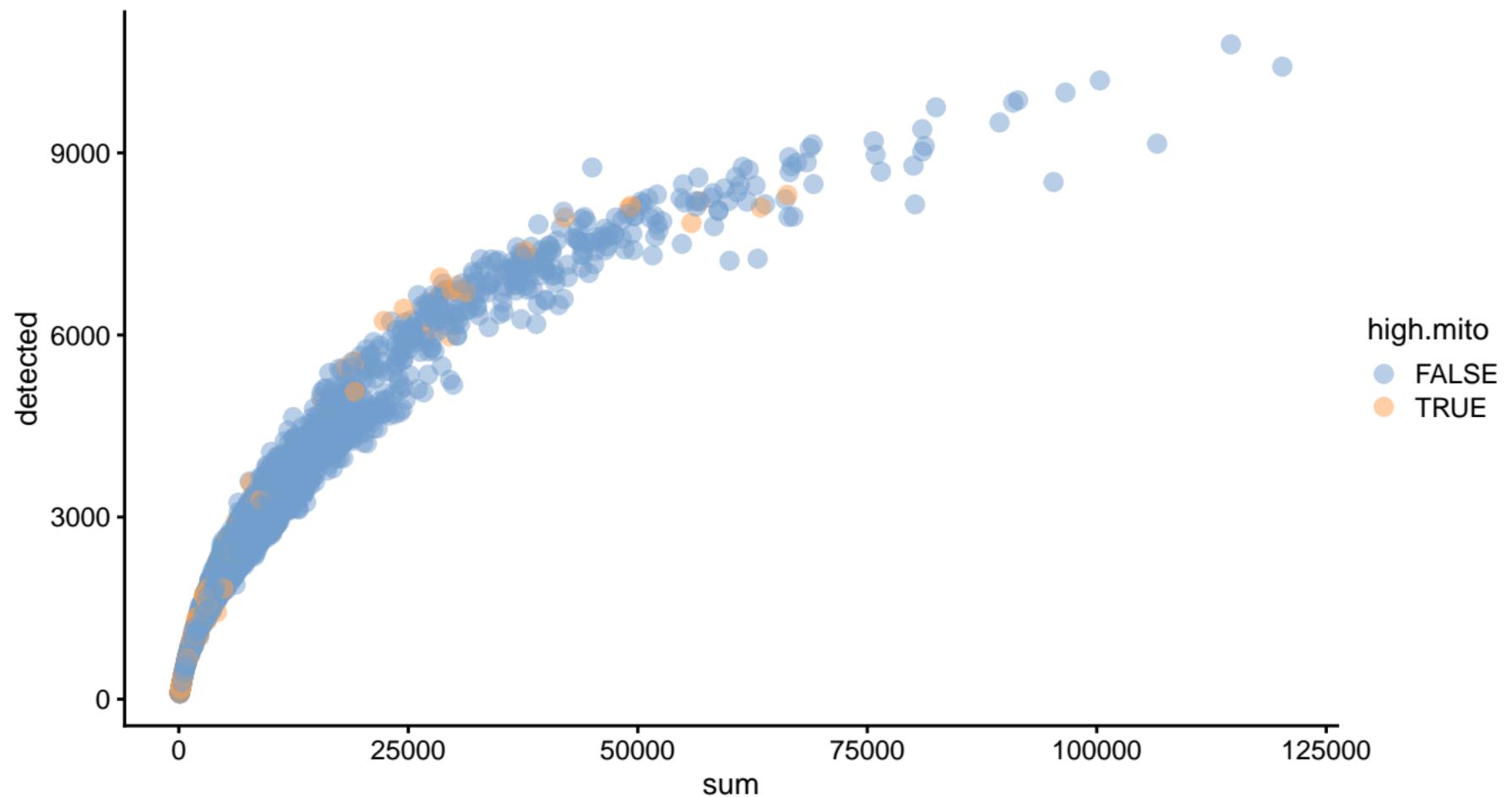
**Mito % (cutoff = 0.212)**



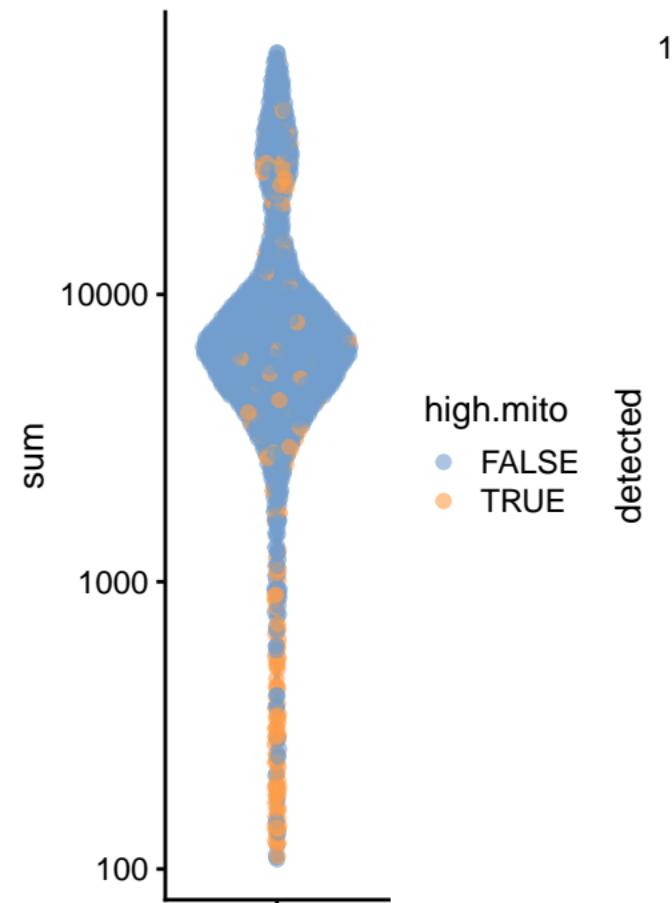
Sample: br5161.hpc; pre-QC nNuclei: 5042; nNuclei kept: 4518 (0.9%)



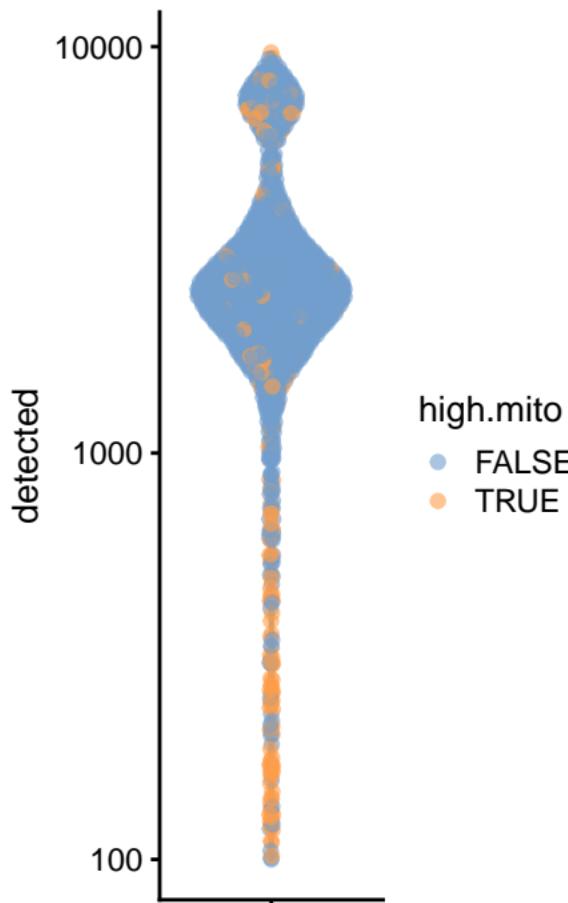
Sample: br5161.hpc; pre-QC nNuclei: 5042; nNuclei kept: 4518 (0.9%)



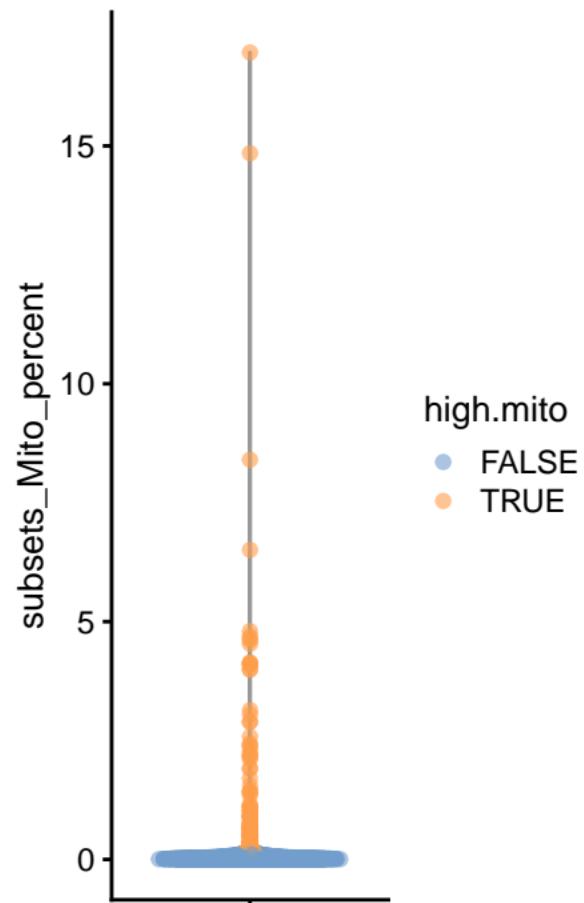
Total count: br5161.nac



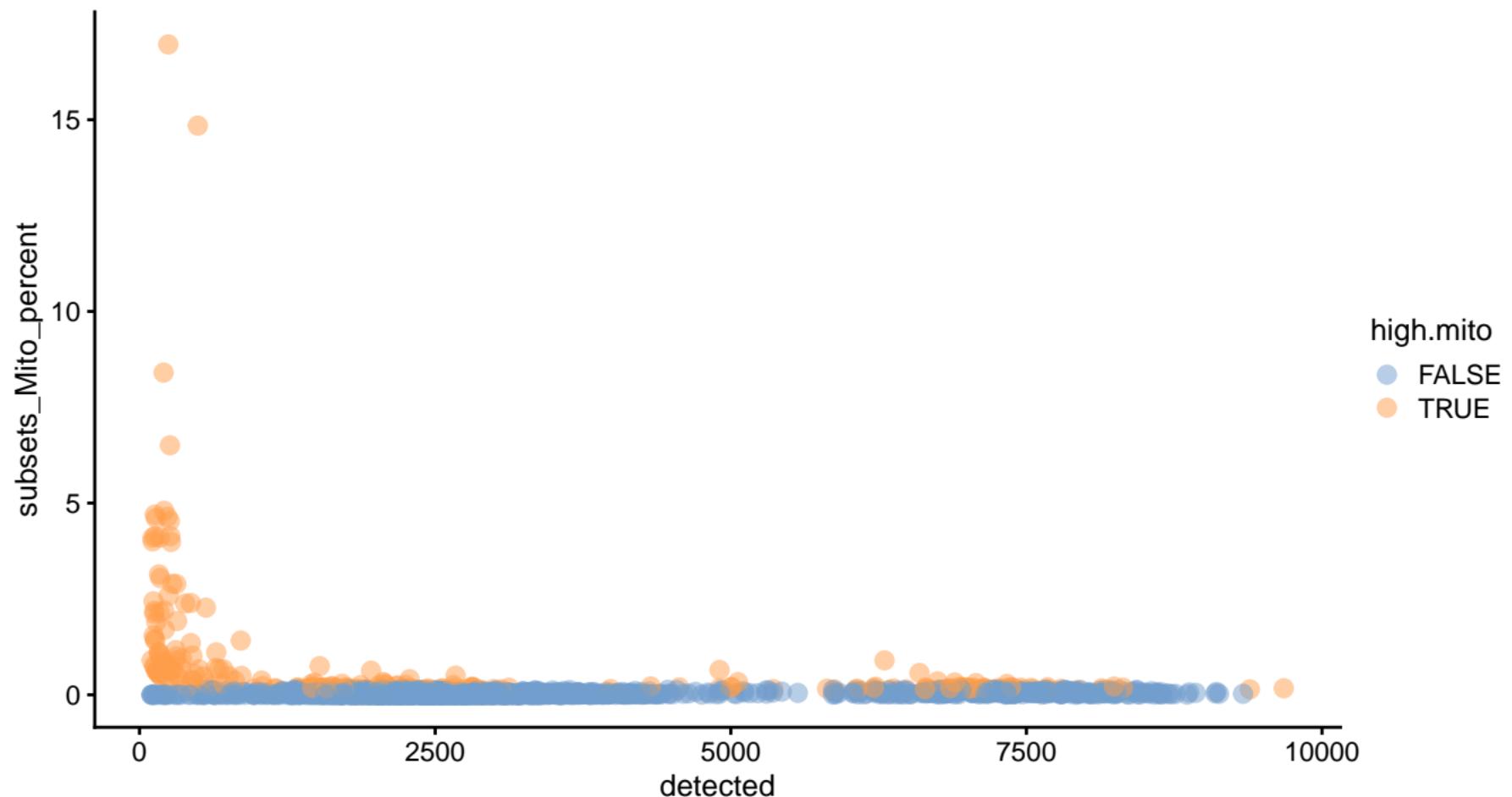
Detected features



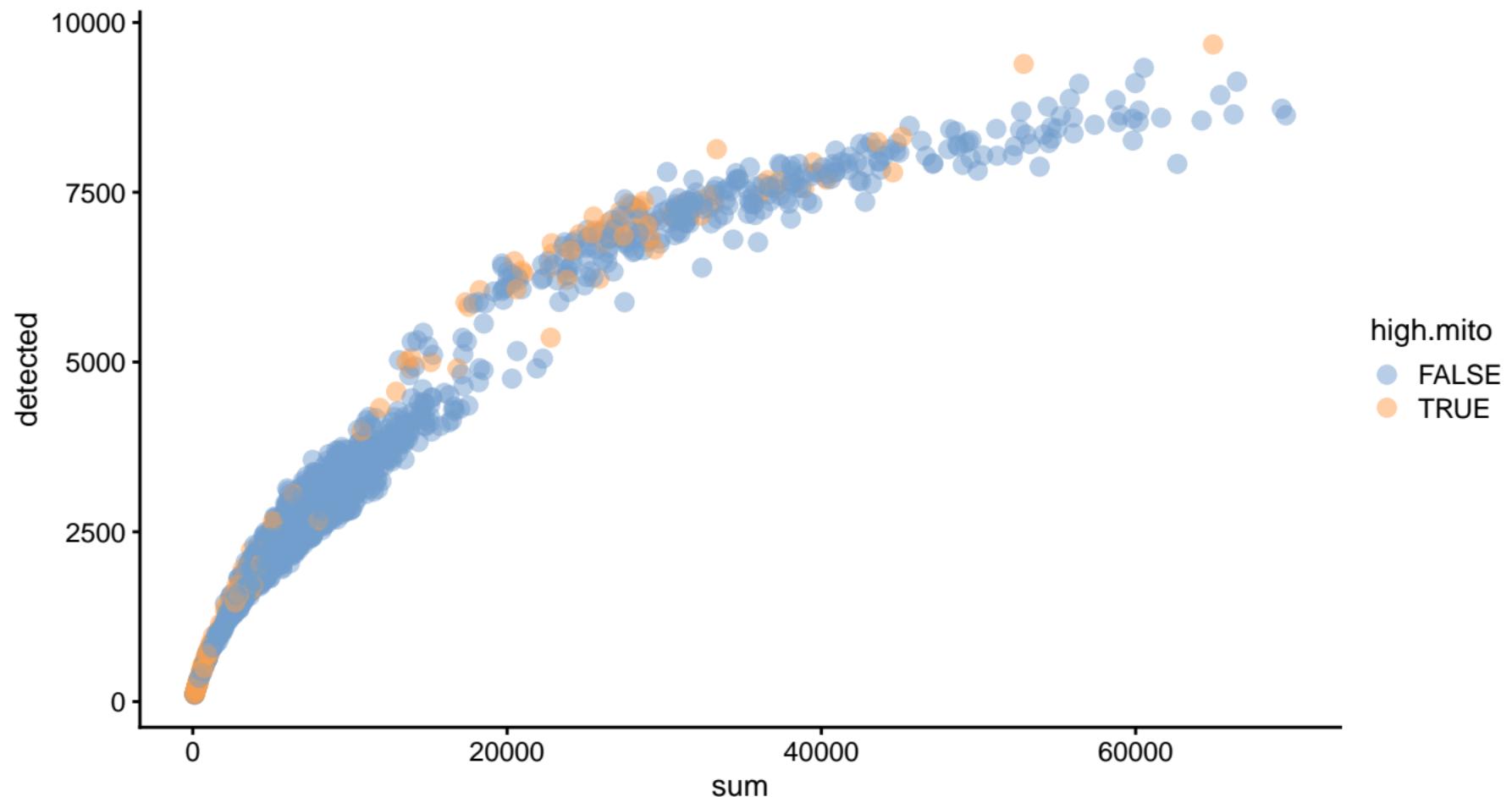
Mito % (cutoff = 0.131)

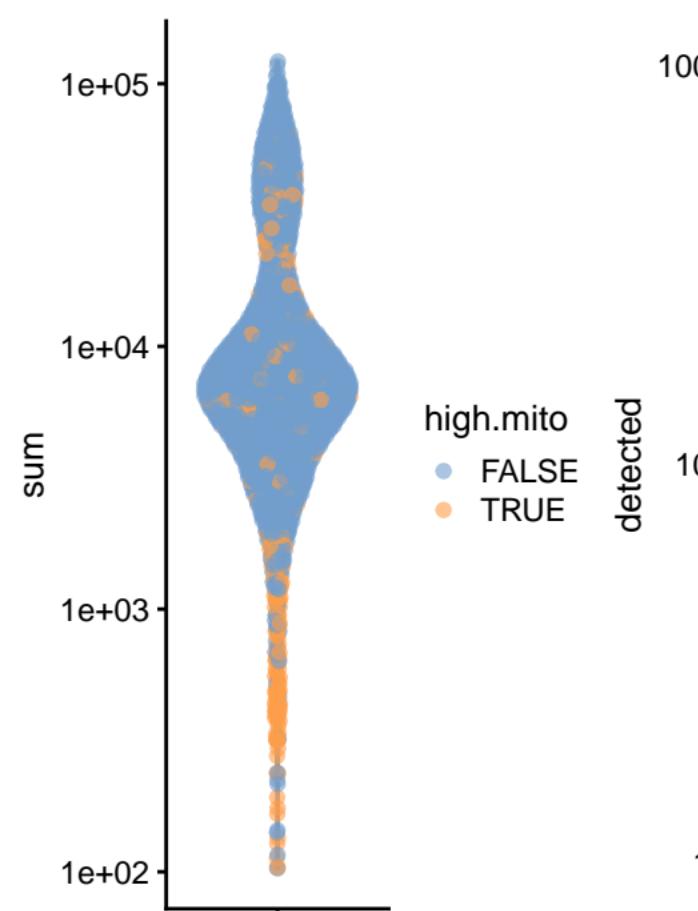
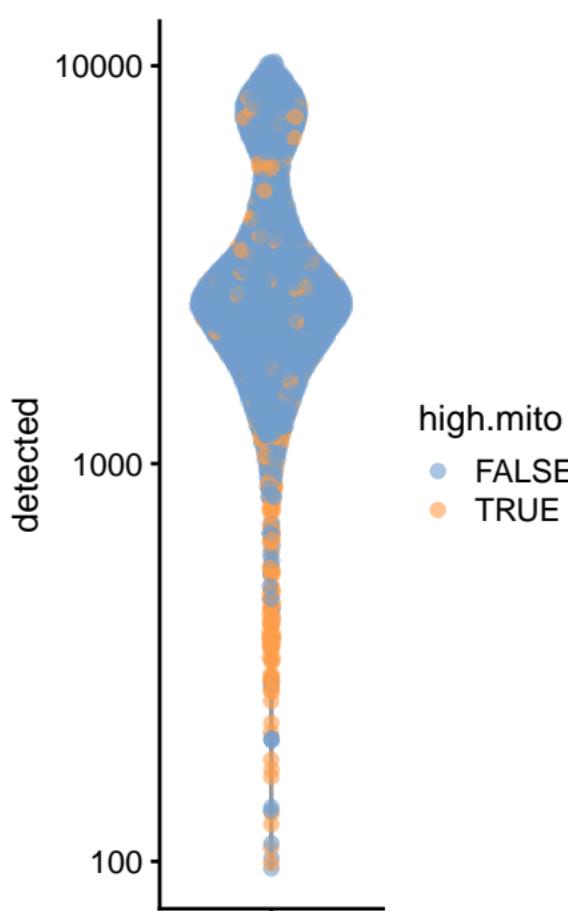
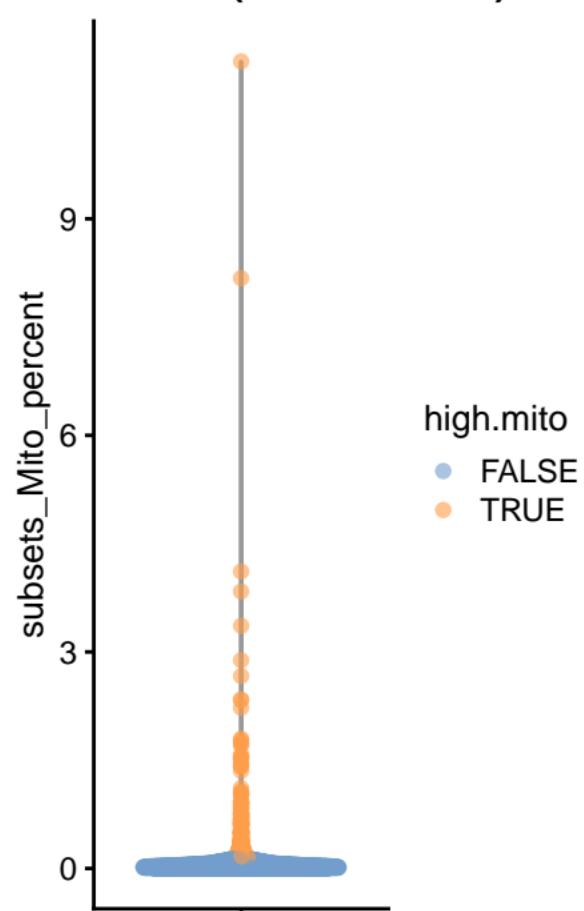


**Sample: br5161.nac; pre-QC nNuclei: 2294; nNuclei kept: 2067 (0.9%)**

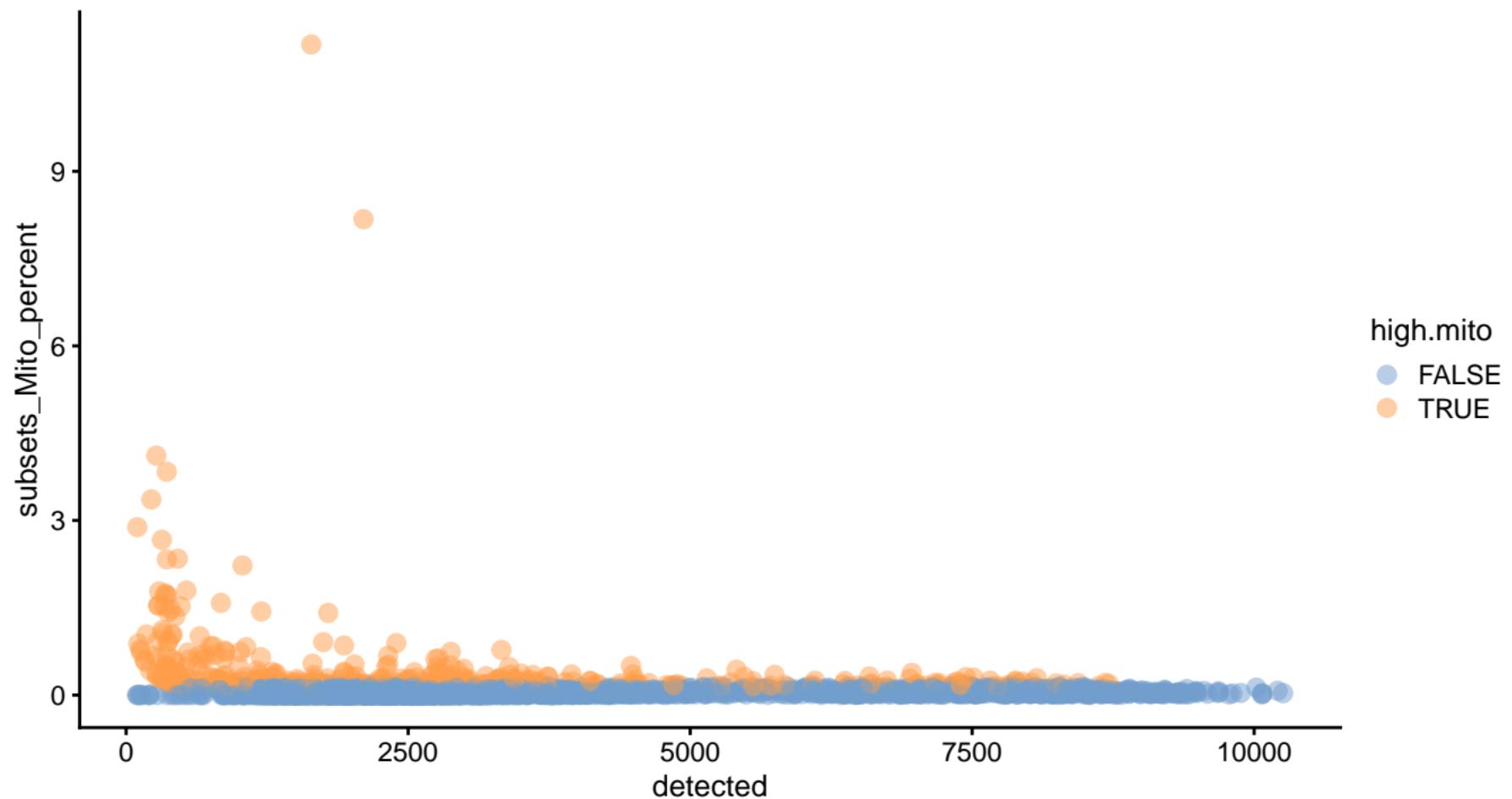


Sample: br5161.nac; pre-QC nNuclei: 2294; nNuclei kept: 2067 (0.9%)

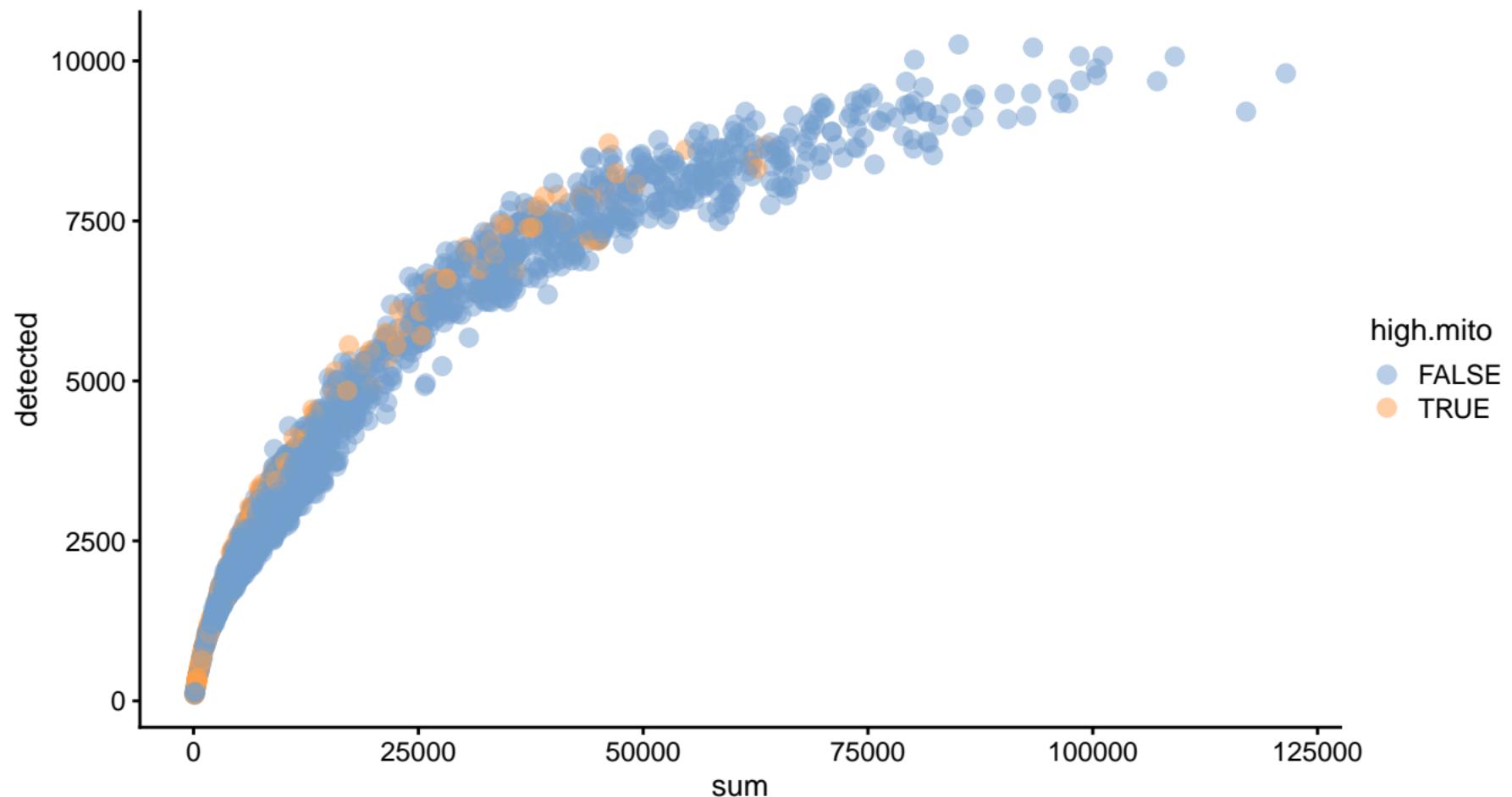


**Total count: br5161.sacc****Detected features****Mito % (cutoff = 0.145)**

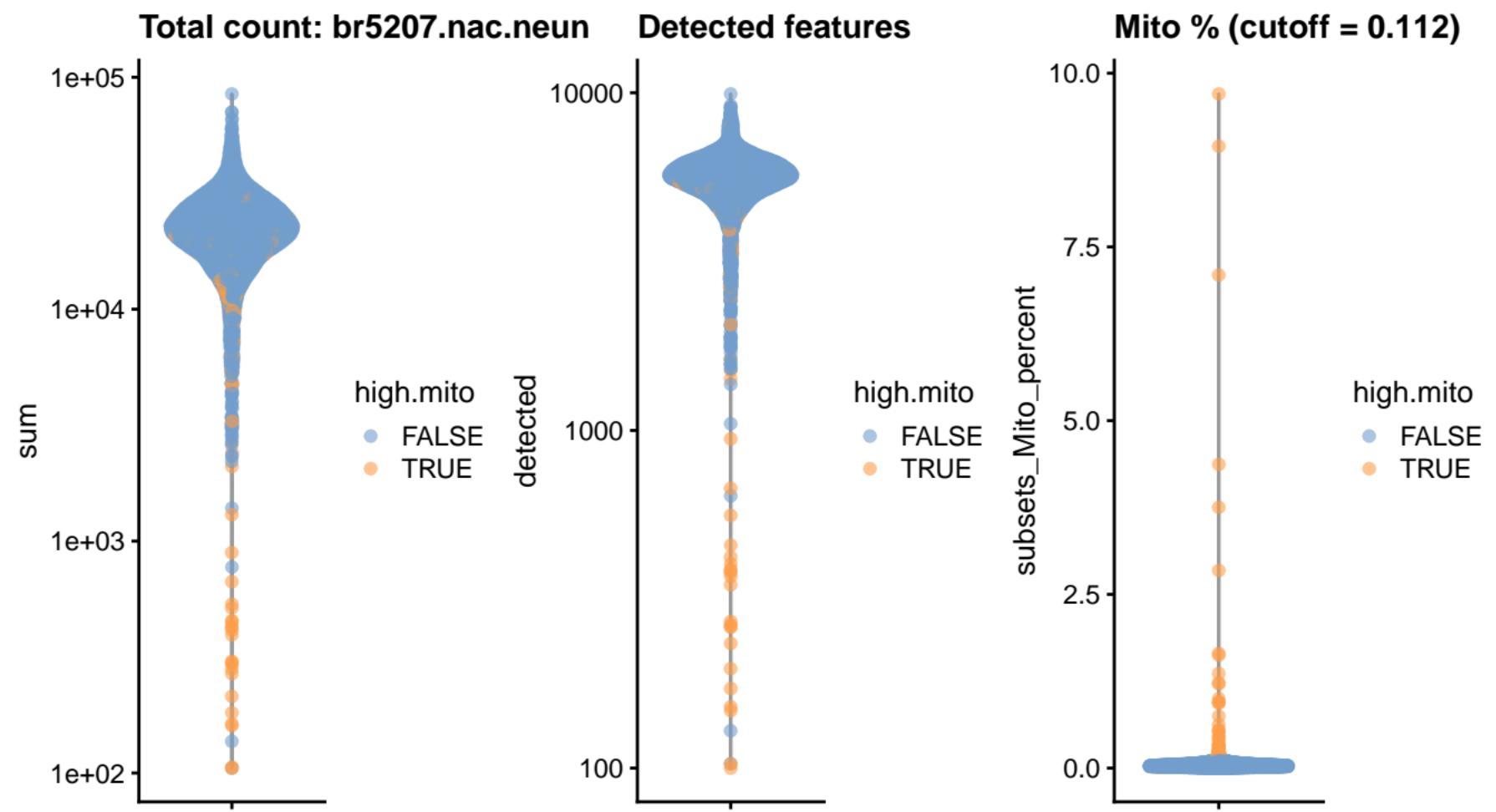
Sample: br5161.sacc; pre-QC nNuclei: 3547; nNuclei kept: 3187 (0.9%)



Sample: br5161.sacc; pre-QC nNuclei: 3547; nNuclei kept: 3187 (0.9%)



Total count: br5207.nac.neun



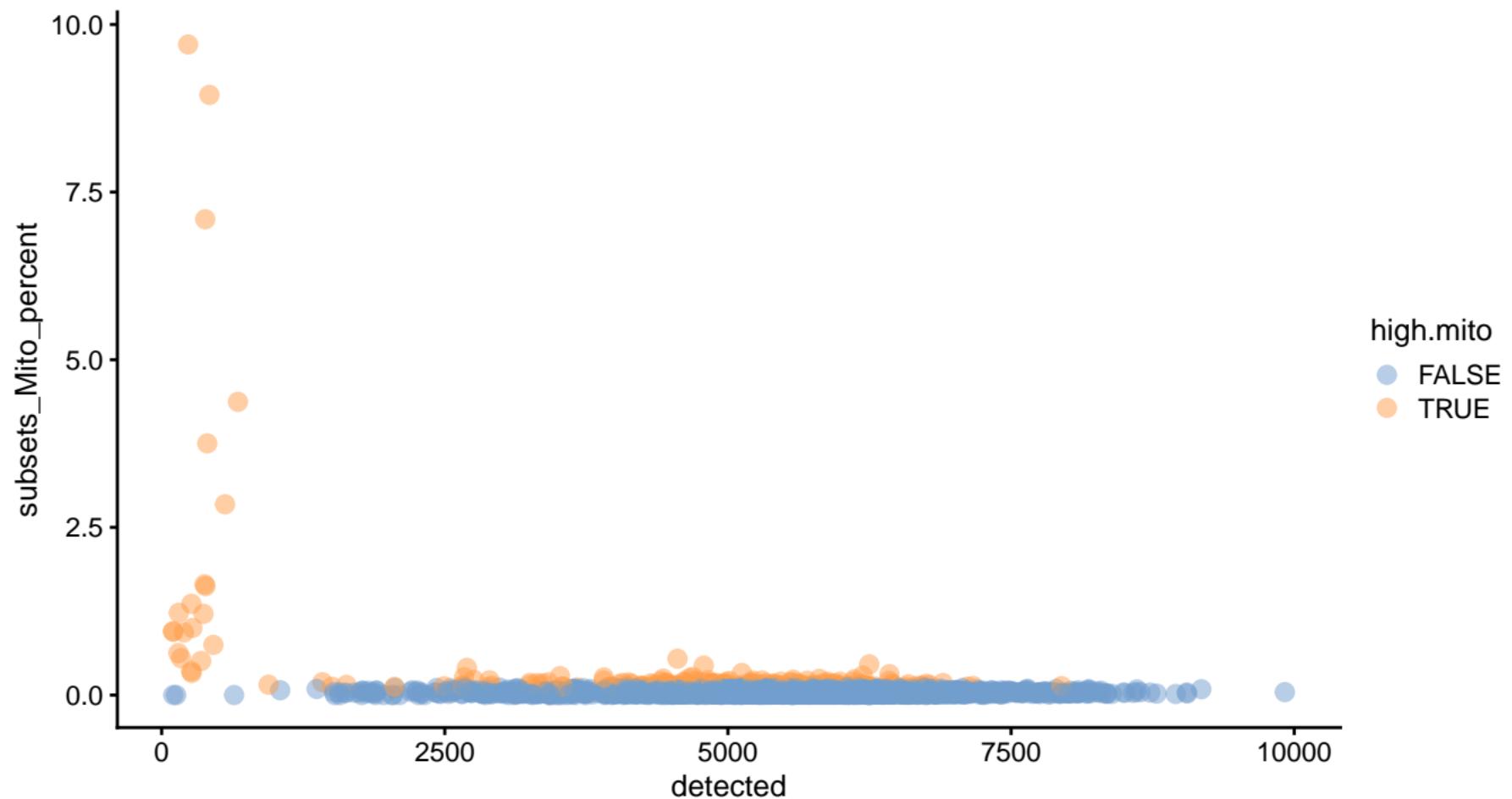
Detected features

high.mito  
• FALSE  
• TRUE

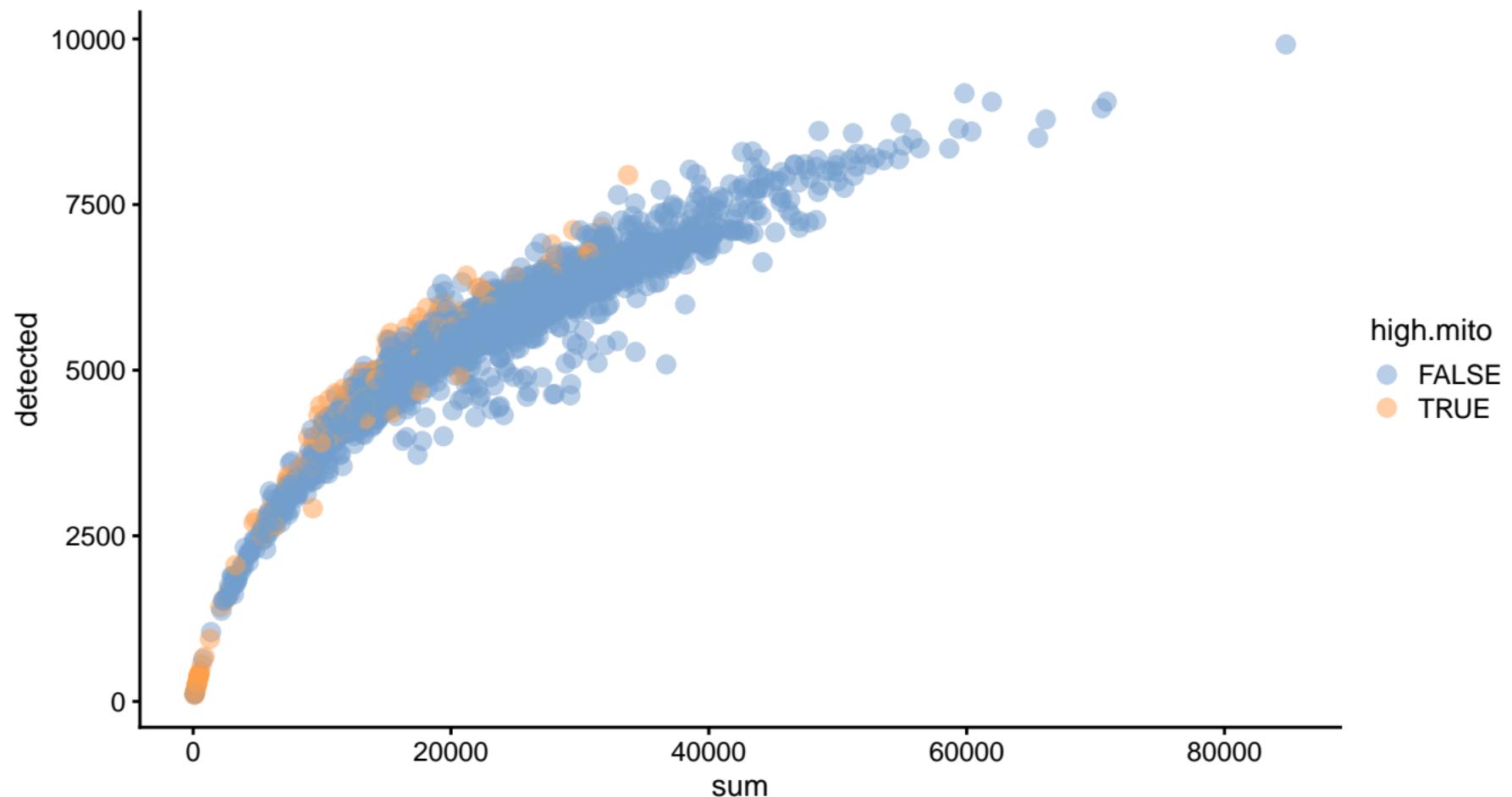
Mito % (cutoff = 0.112)

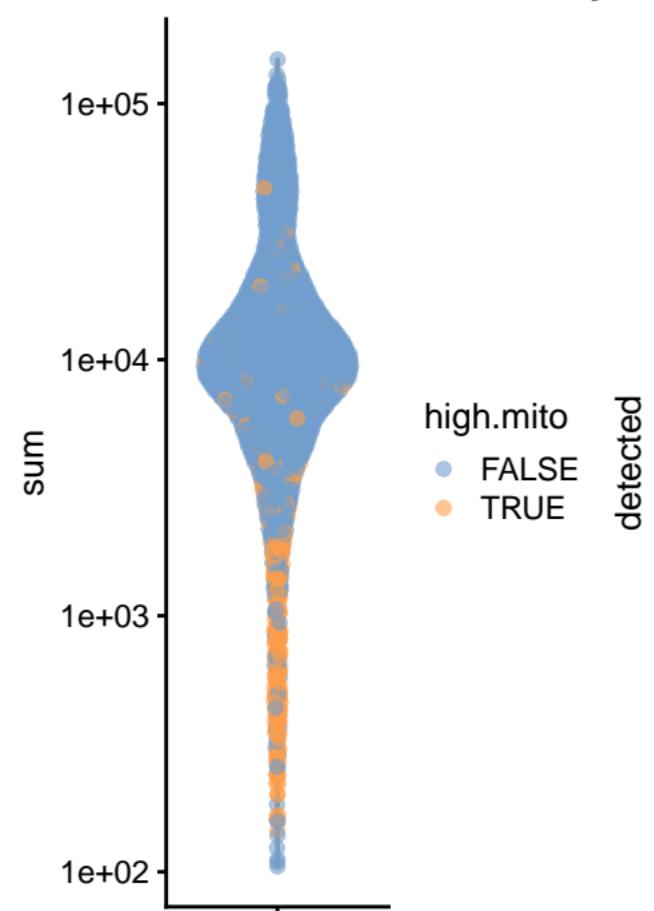
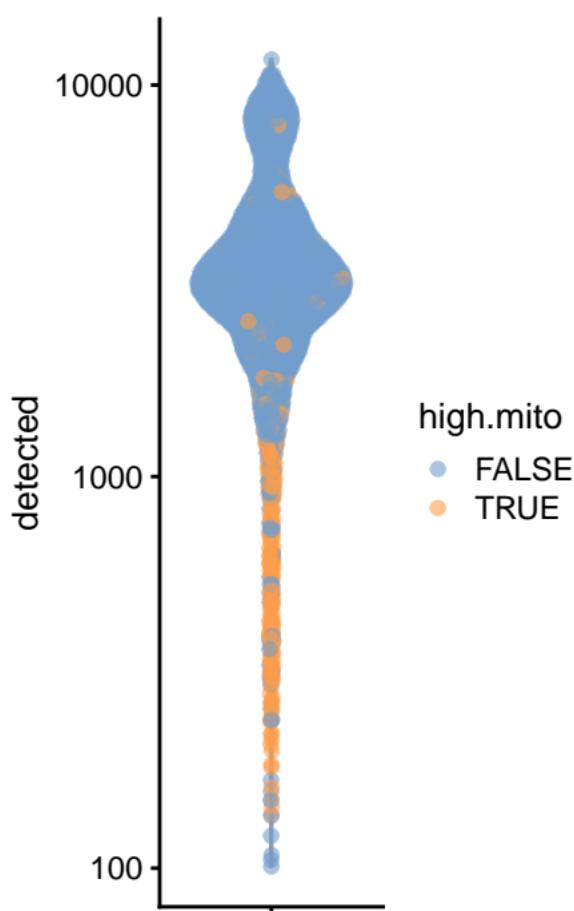
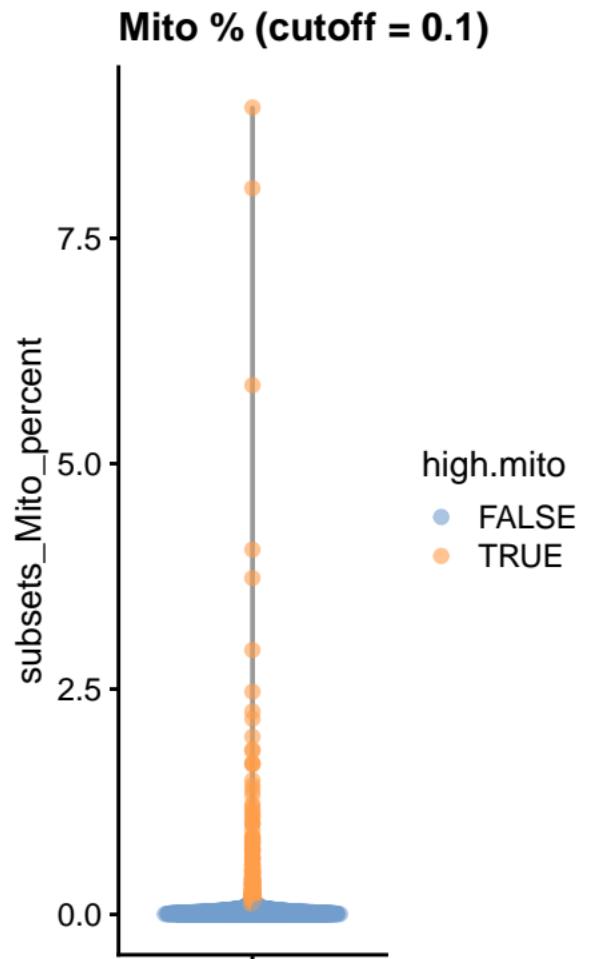
high.mito  
• FALSE  
• TRUE

Sample: br5207.nac.neun; pre-QC nNuclei: 4682; nNuclei kept: 4426 (0.95%)

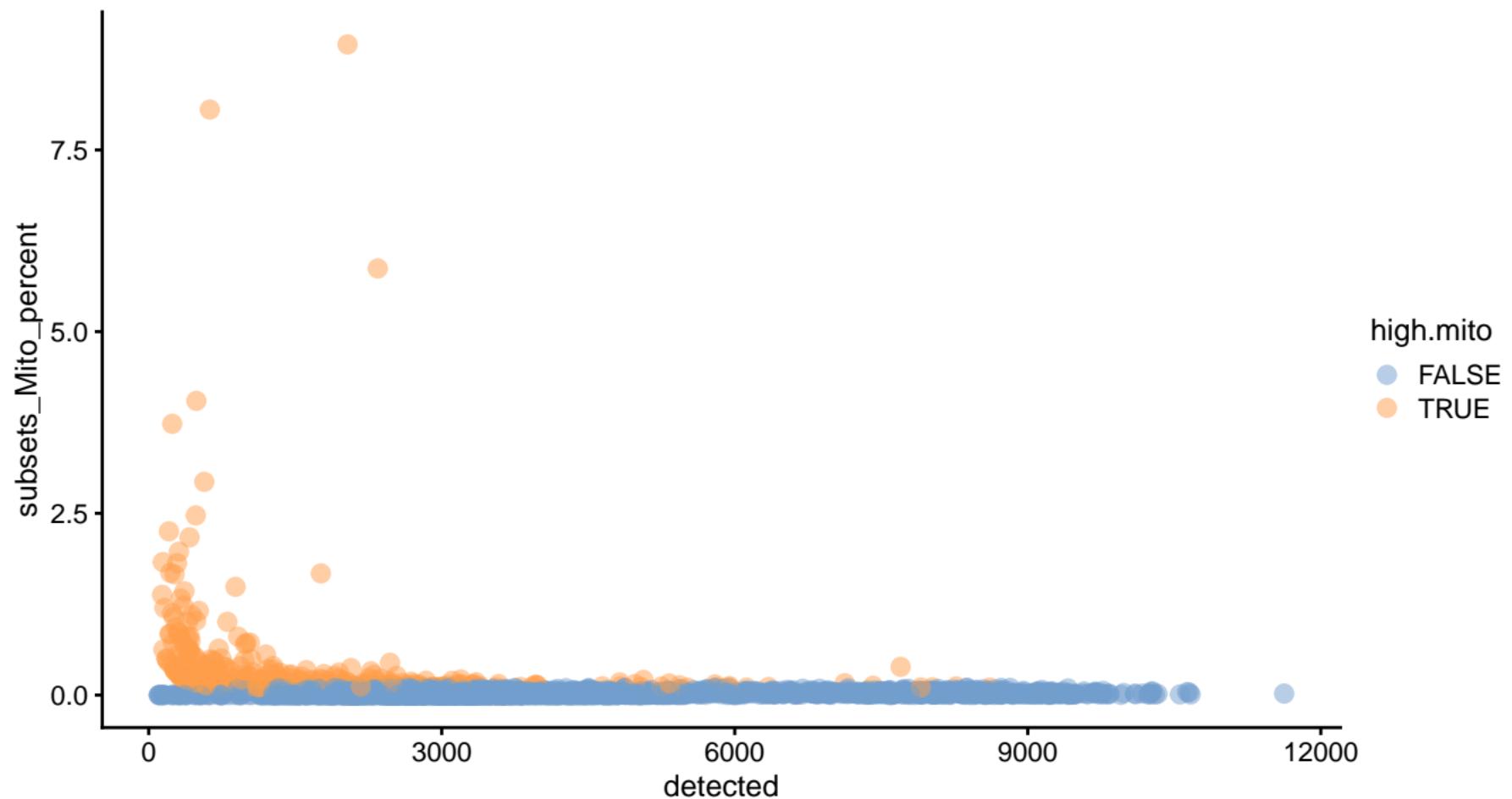


Sample: br5207.nac.neun; pre-QC nNuclei: 4682; nNuclei kept: 4426 (0.95%)

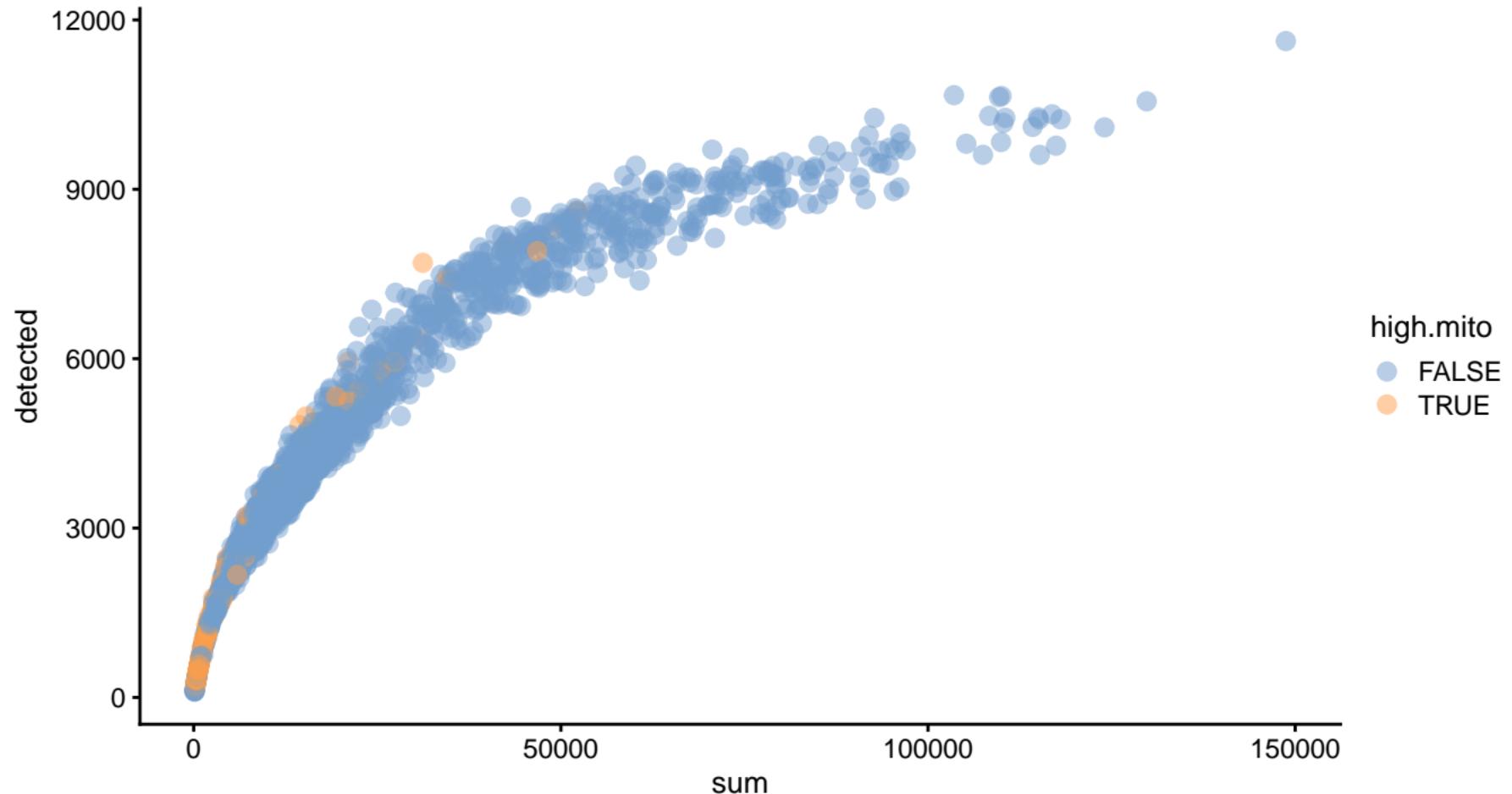


**Total count: br5212.amy****Detected features****Mito % (cutoff = 0.1)**

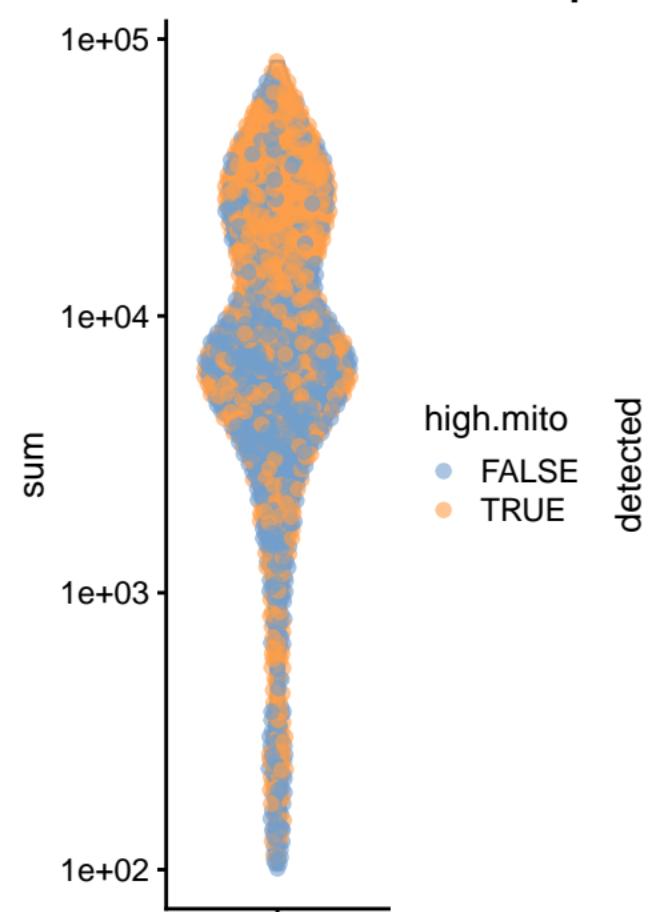
Sample: br5212.amy; pre-QC nNuclei: 3661; nNuclei kept: 3342 (0.91%)



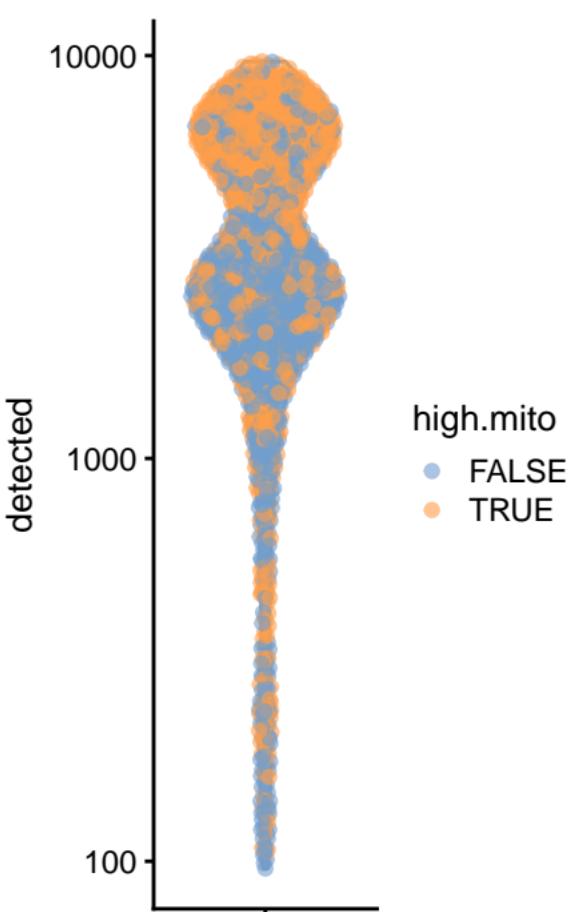
Sample: br5212.amy; pre-QC nNuclei: 3661; nNuclei kept: 3342 (0.91%)



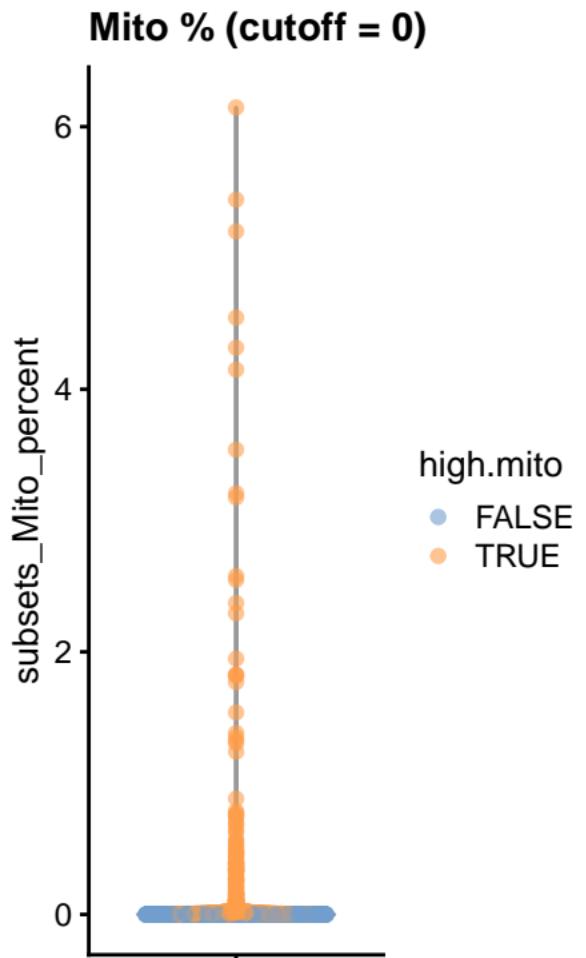
Total count: br5212.dlpfc



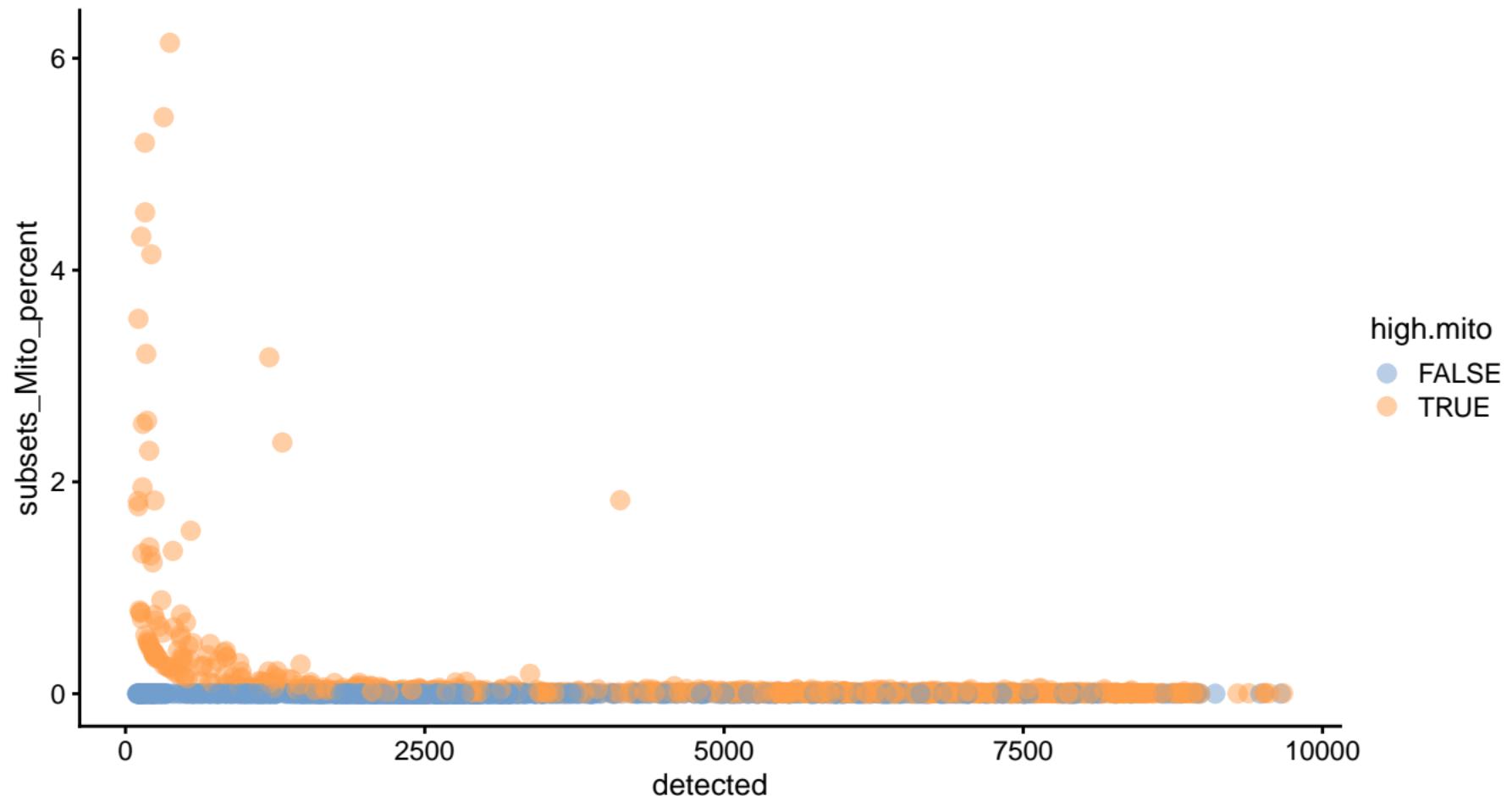
Detected features



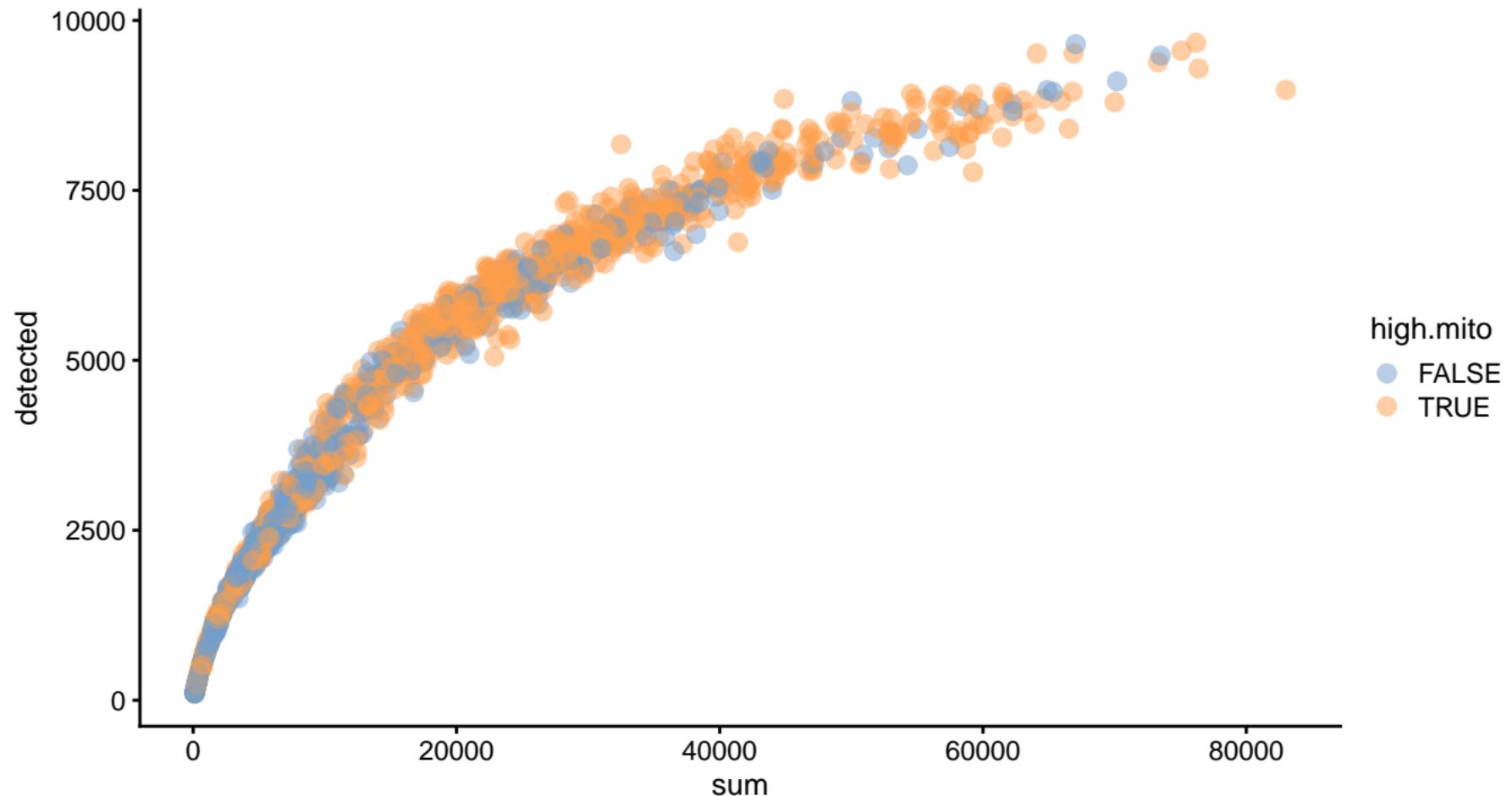
Mito % (cutoff = 0)



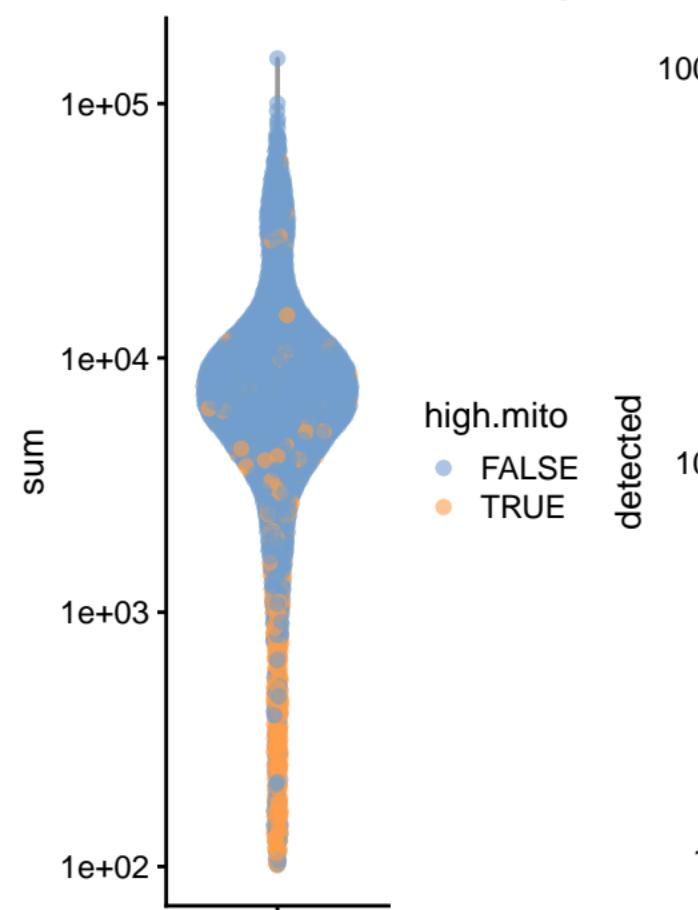
Sample: br5212.dlpfc; pre-QC nNuclei: 2006; nNuclei kept: 1005 (0.5%)



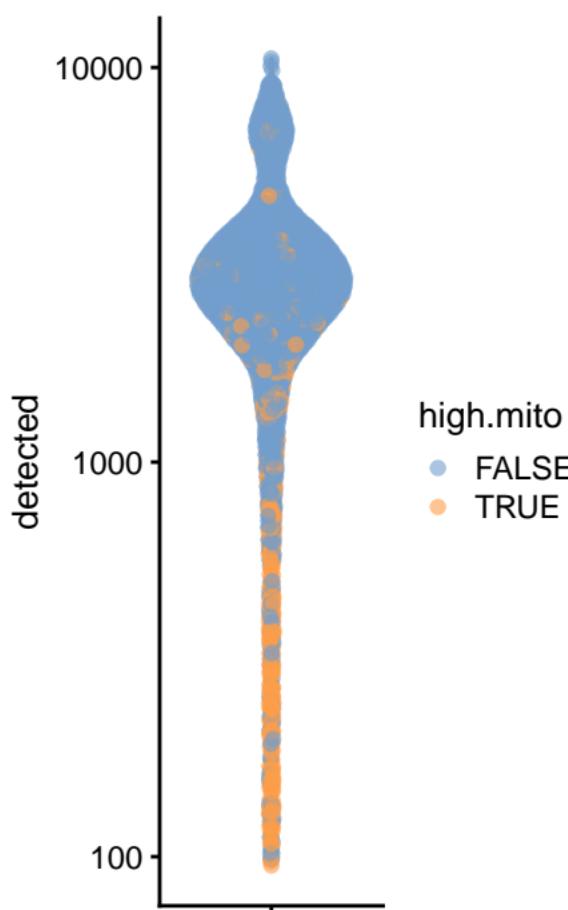
Sample: br5212.dlpfc; pre-QC nNuclei: 2006; nNuclei kept: 1005 (0.5%)



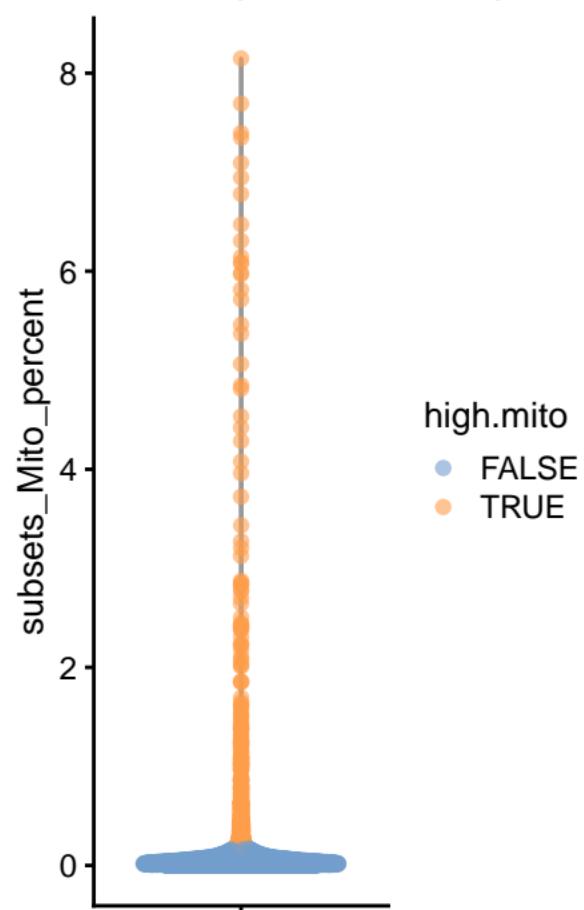
Total count: br5212.hpc



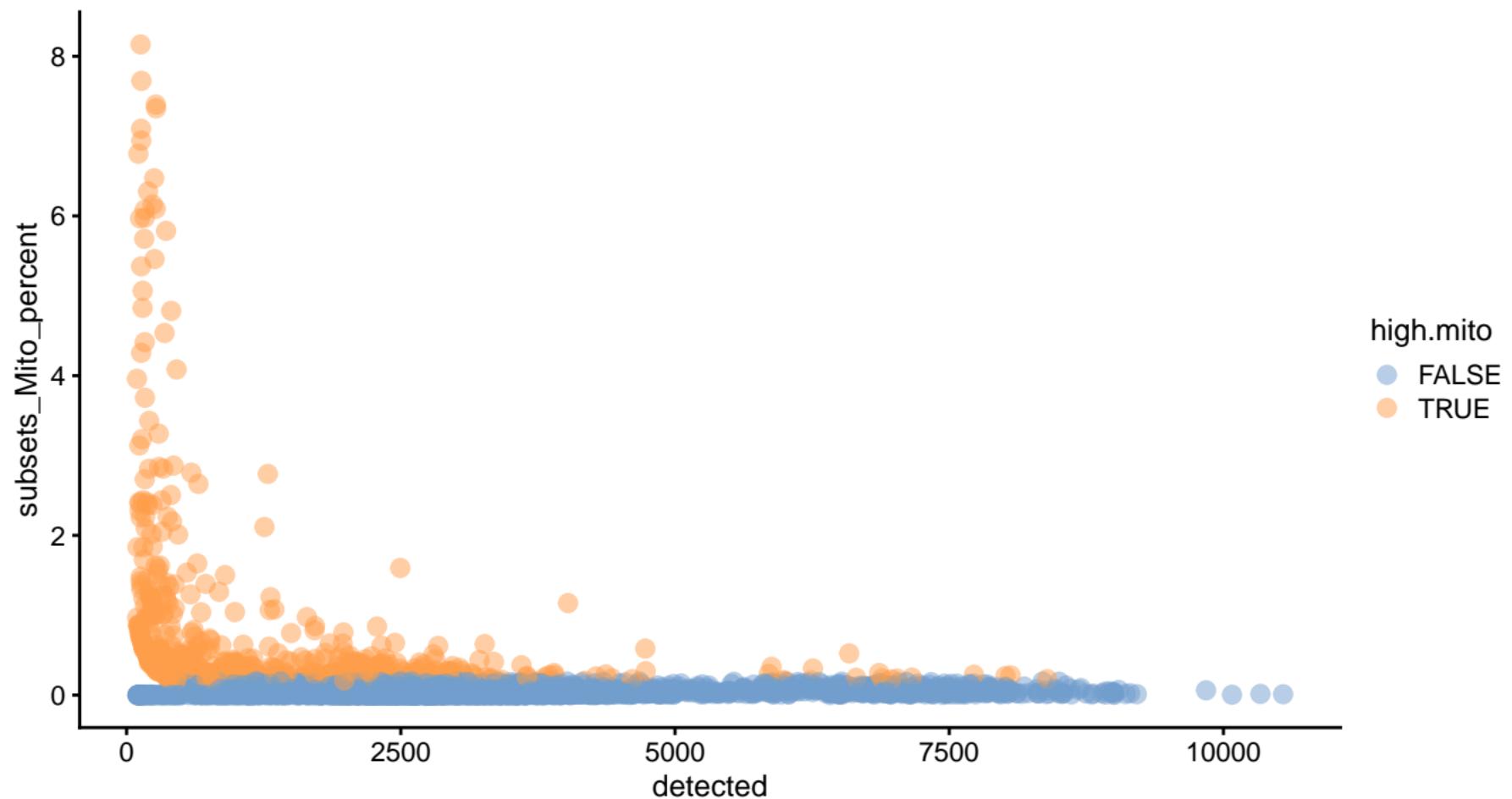
Detected features



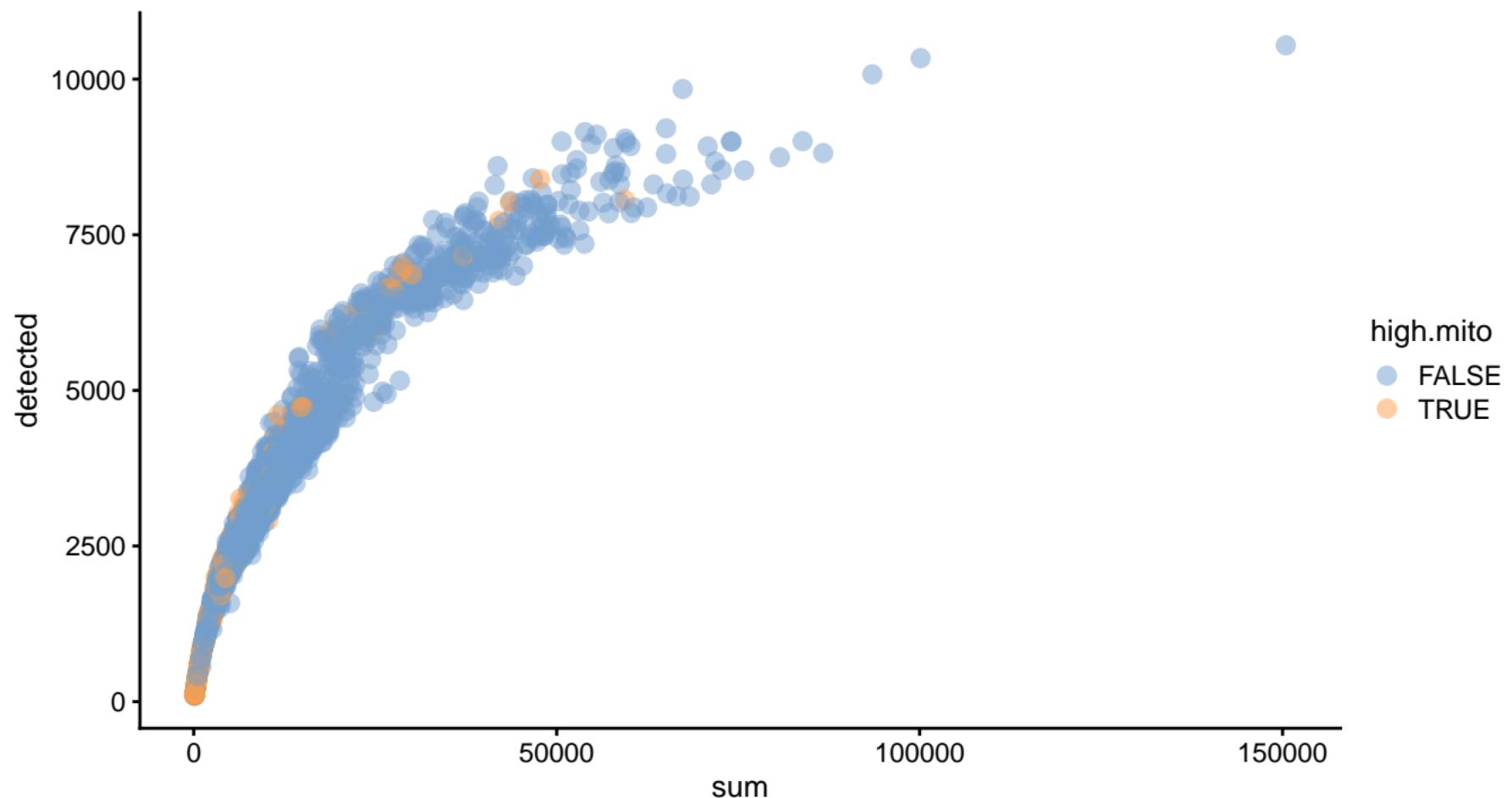
Mito % (cutoff = 0.175)



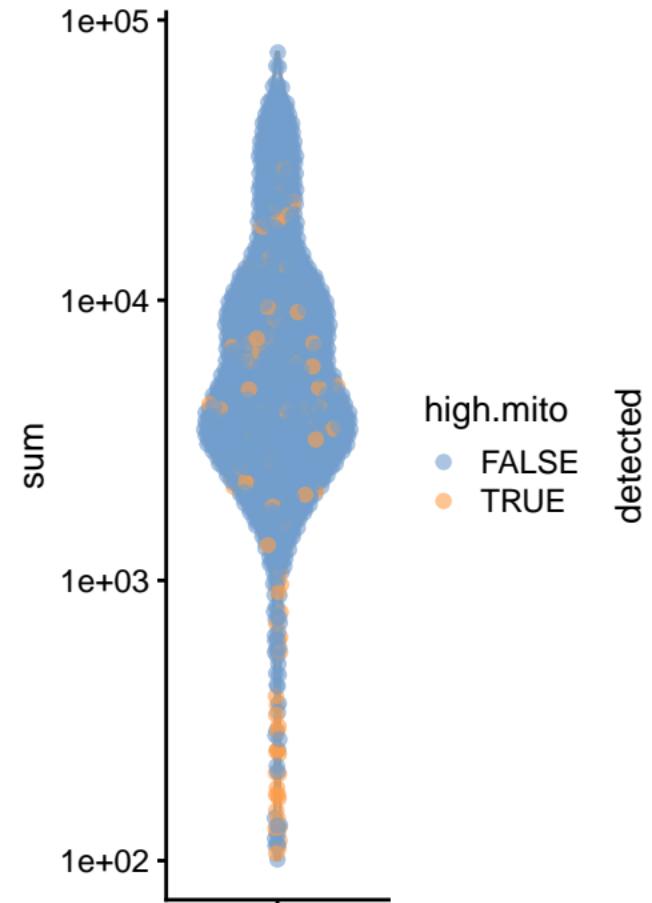
Sample: br5212.hpc; pre-QC nNuclei: 4538; nNuclei kept: 4039 (0.89%)



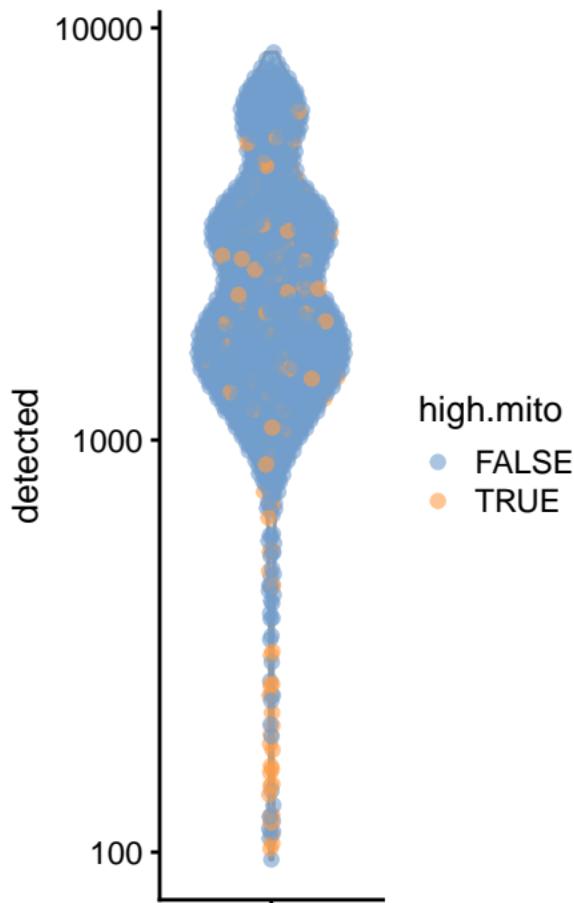
Sample: br5212.hpc; pre-QC nNuclei: 4538; nNuclei kept: 4039 (0.89%)



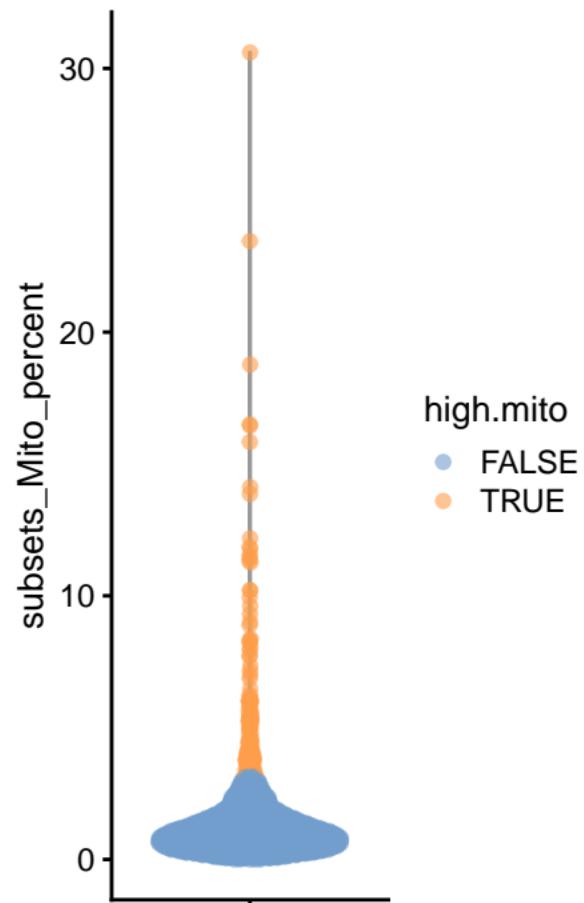
Total count: br5212.nac



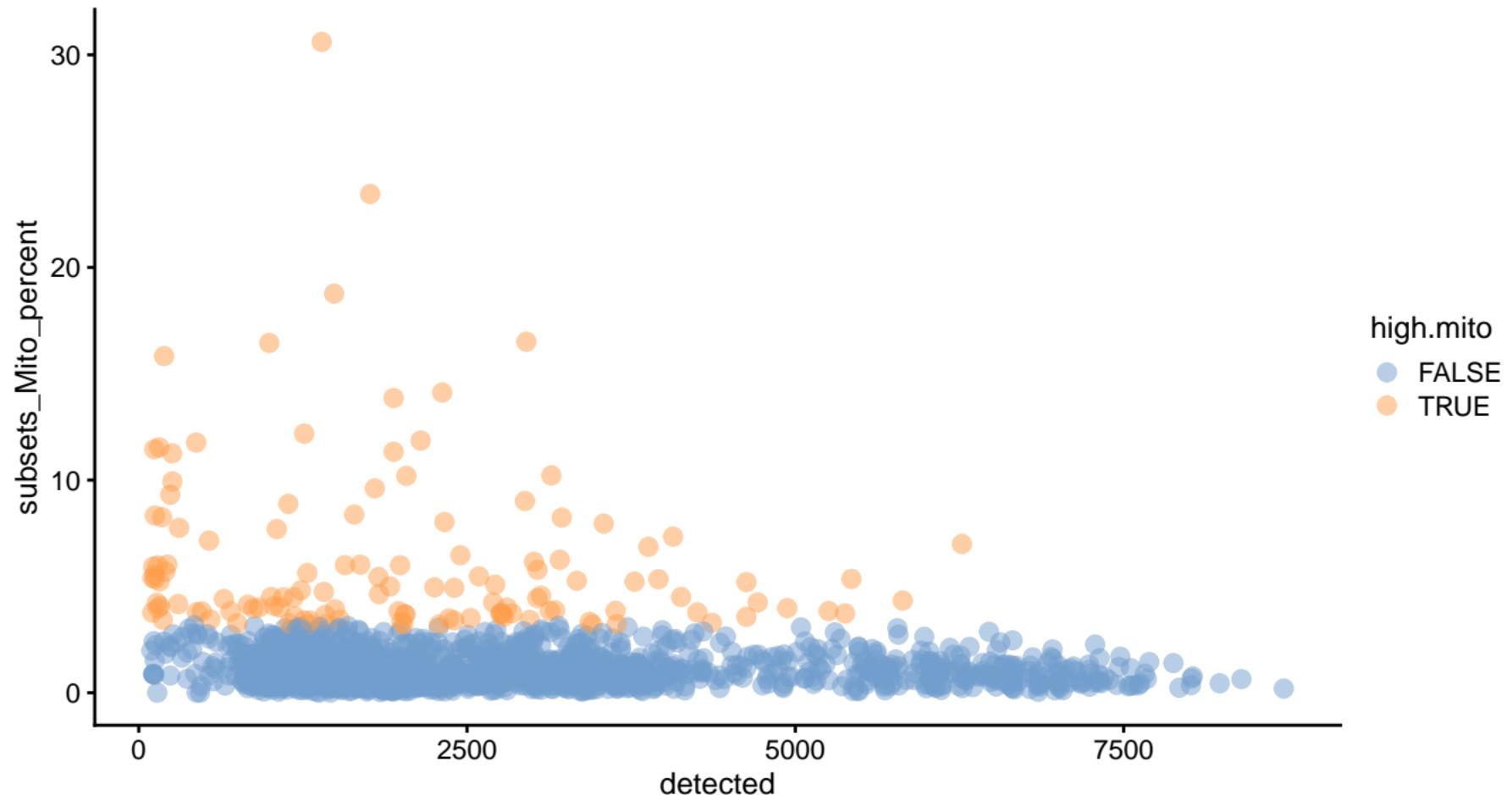
Detected features



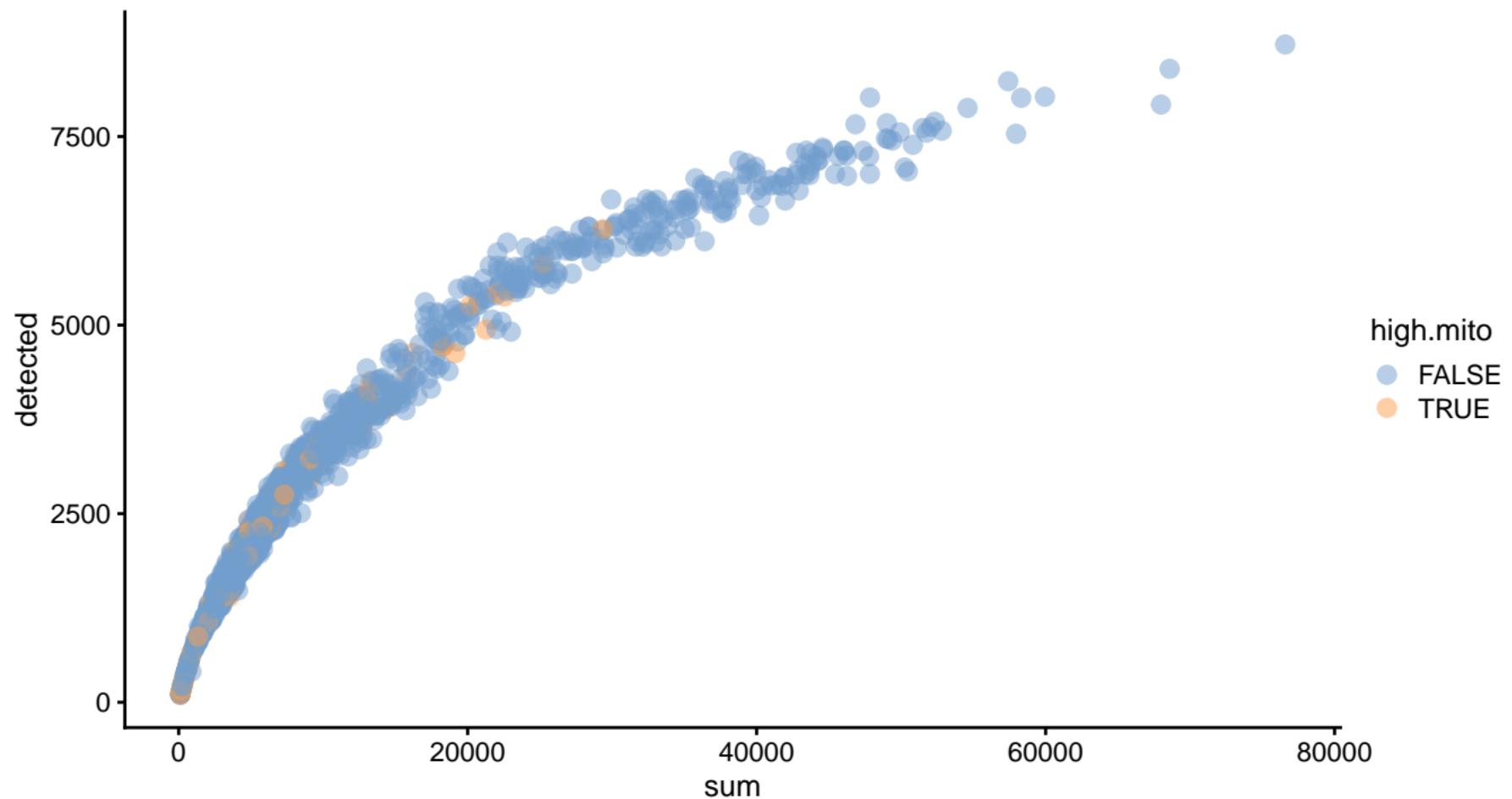
Mito % (cutoff = 3.178)

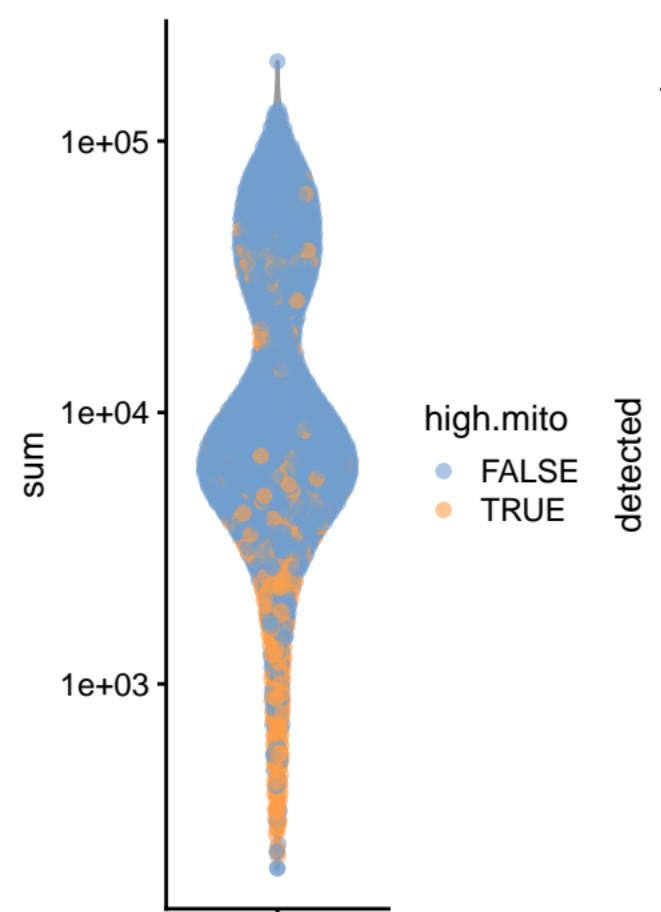
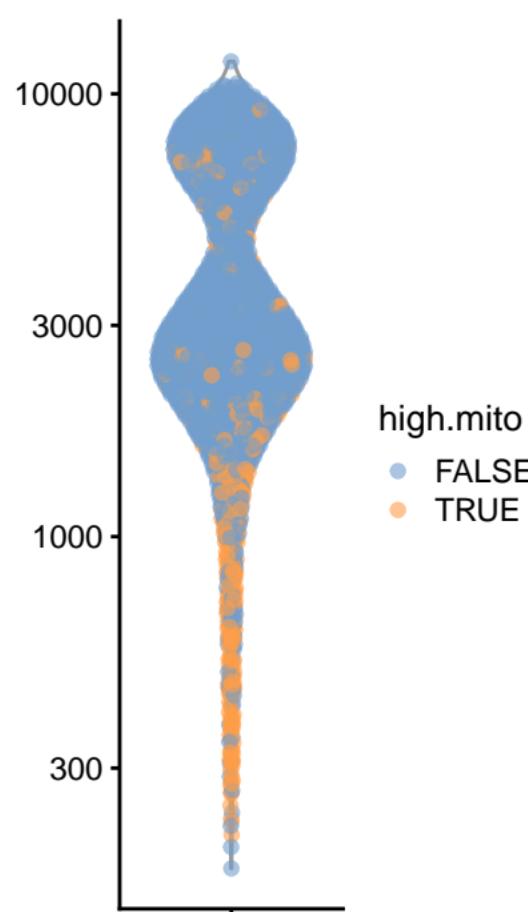
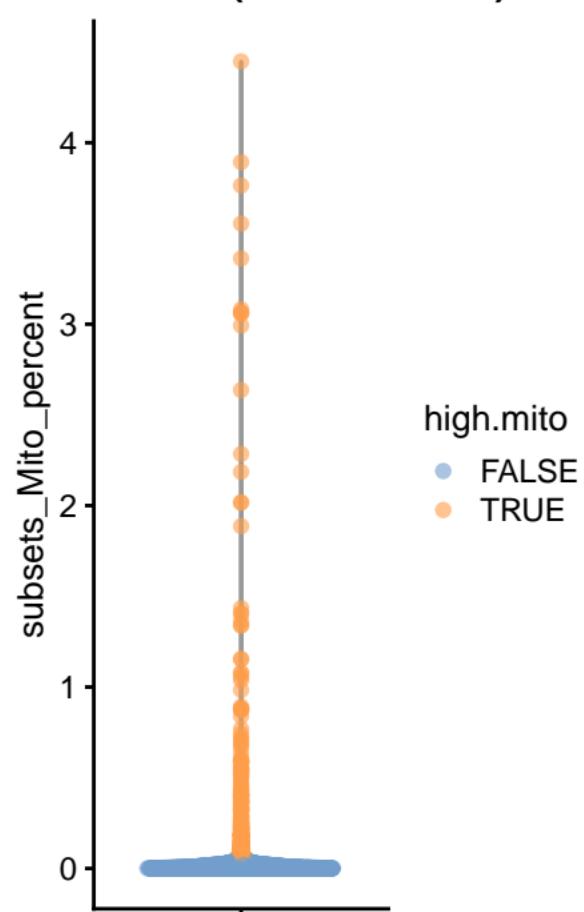


Sample: br5212.nac; pre-QC nNuclei: 1901; nNuclei kept: 1774 (0.93%)

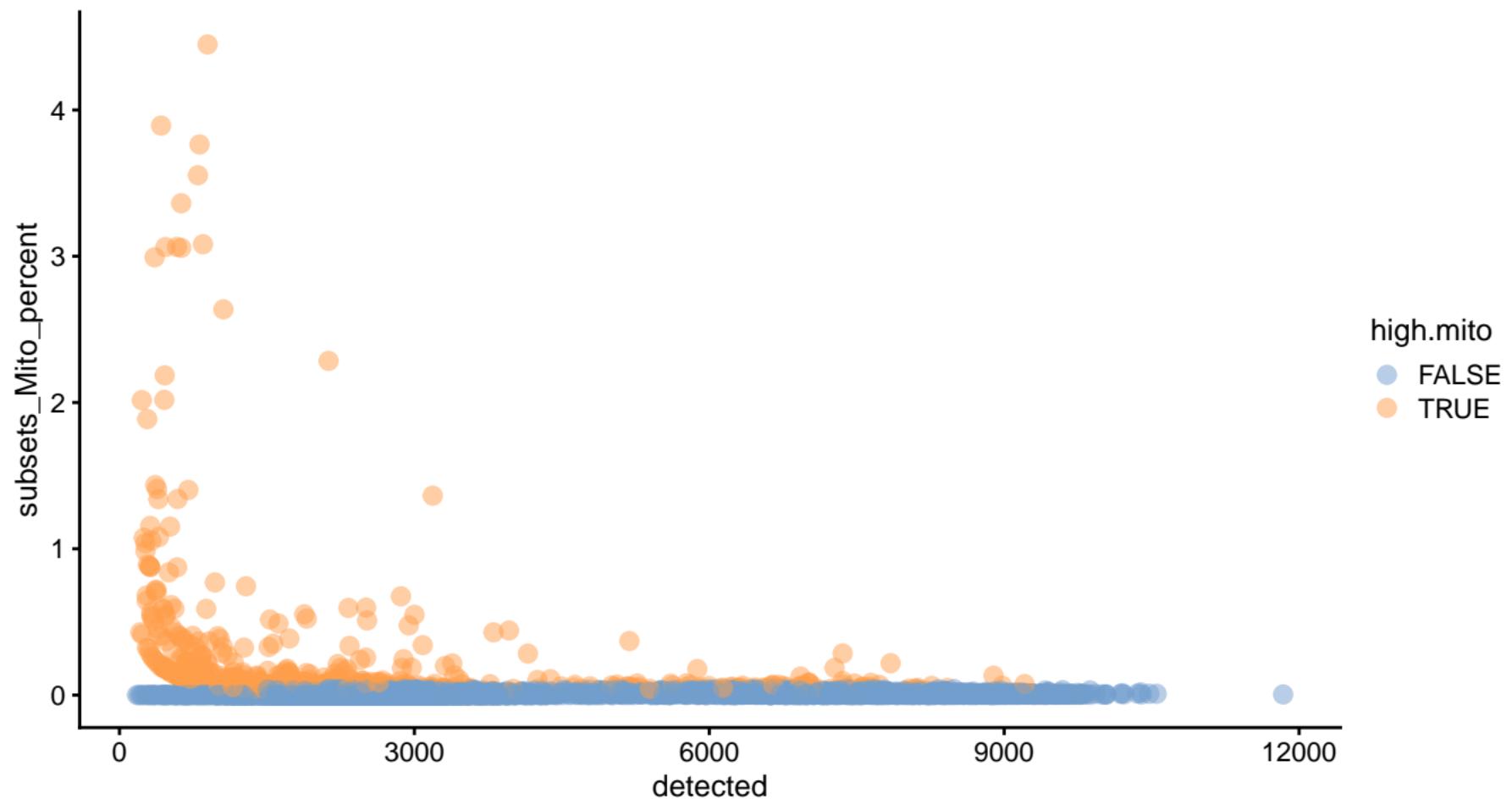


Sample: br5212.nac; pre-QC nNuclei: 1901; nNuclei kept: 1774 (0.93%)

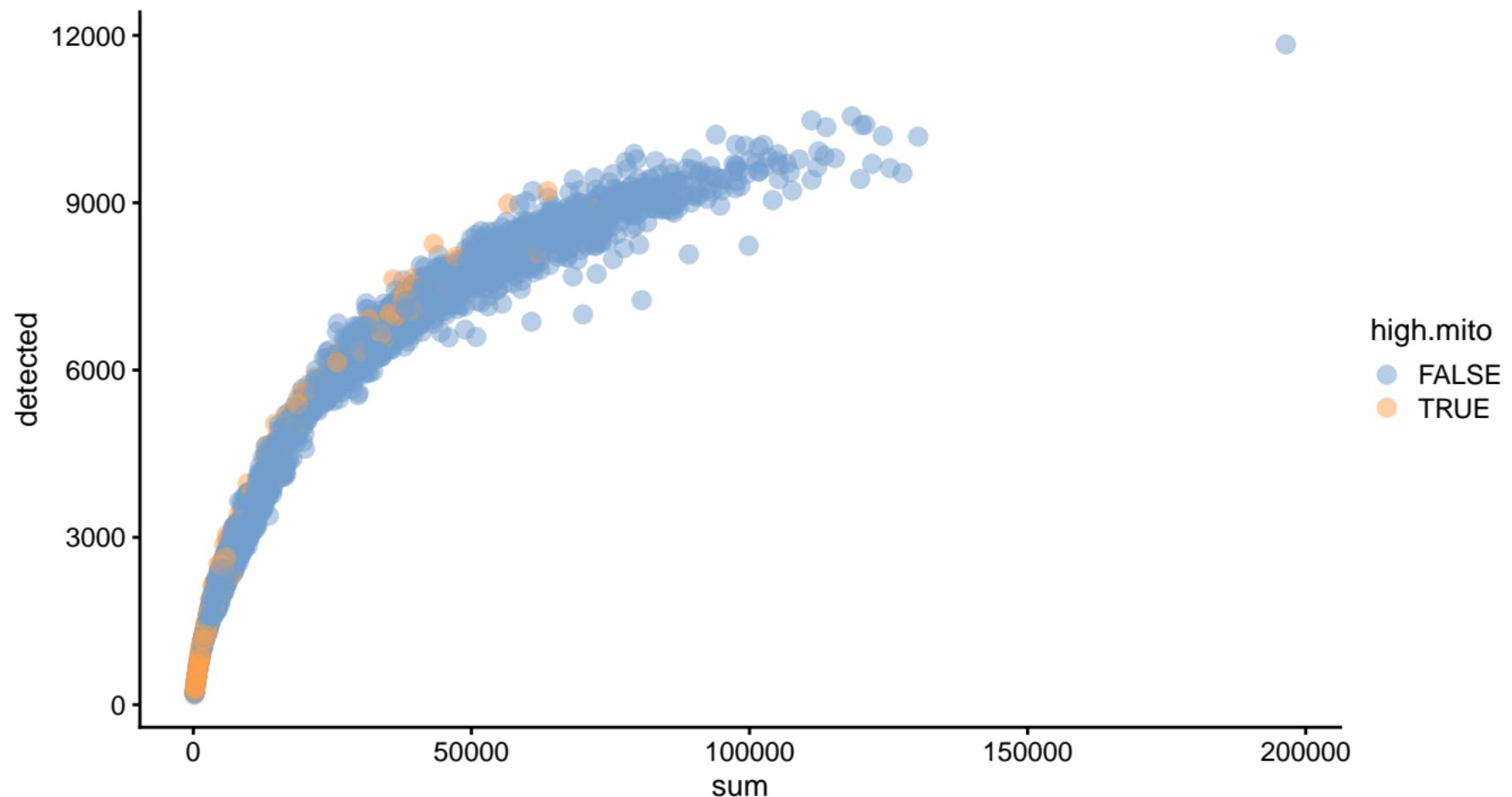


**Total count: br5212.sacc****Detected features****Mito % (cutoff = 0.041)**

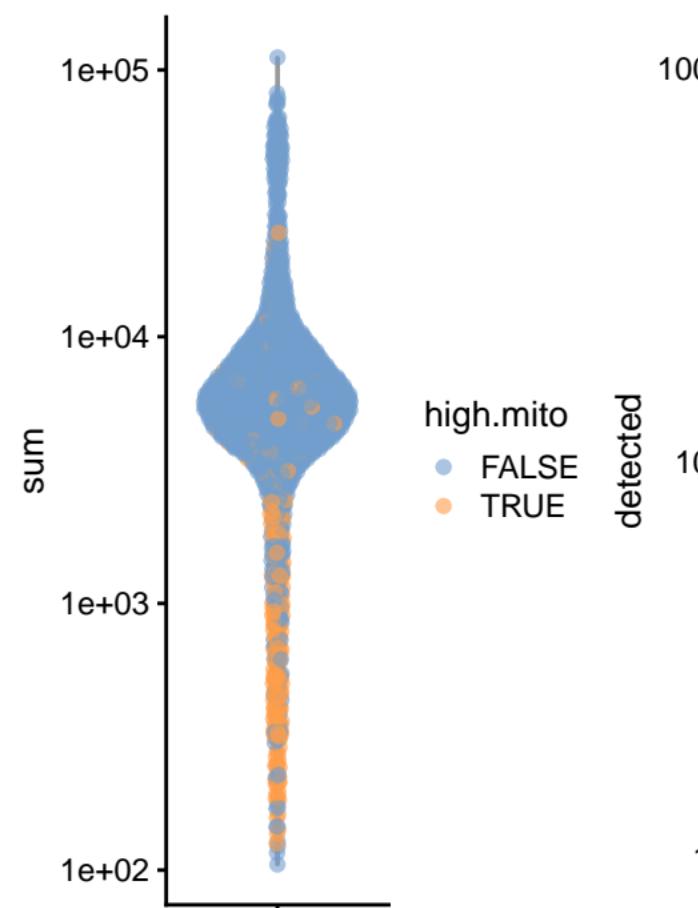
Sample: br5212.sacc; pre-QC nNuclei: 4398; nNuclei kept: 3860 (0.88%)



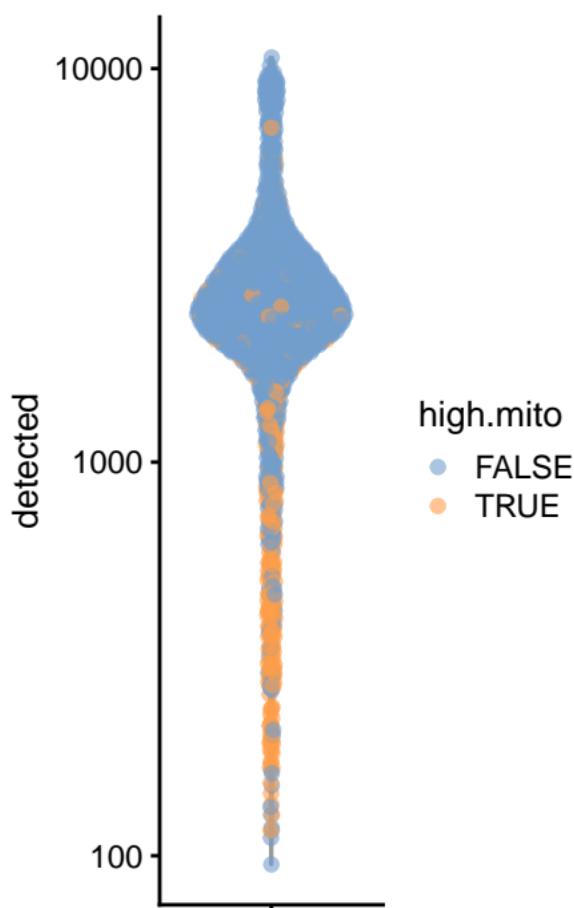
Sample: br5212.sacc; pre-QC nNuclei: 4398; nNuclei kept: 3860 (0.88%)



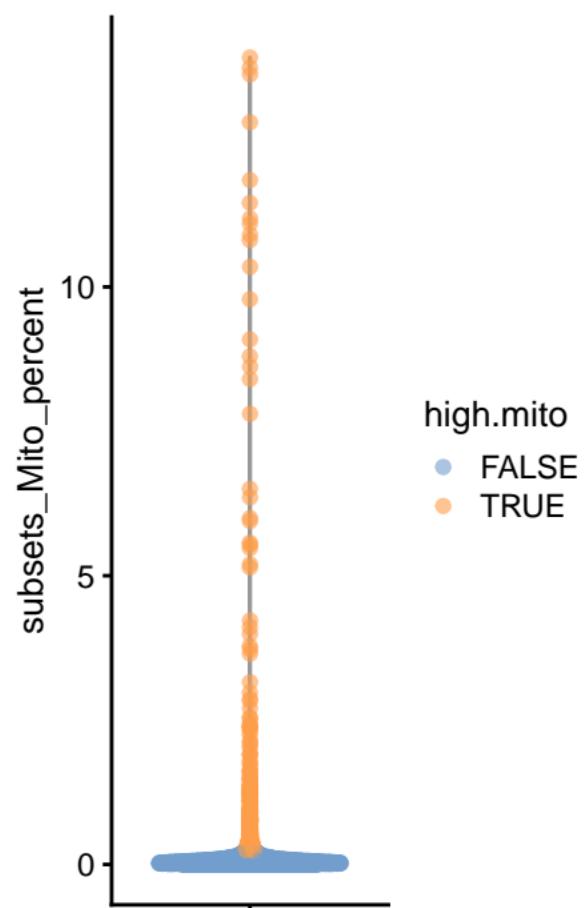
**Total count: br5287.hpc**



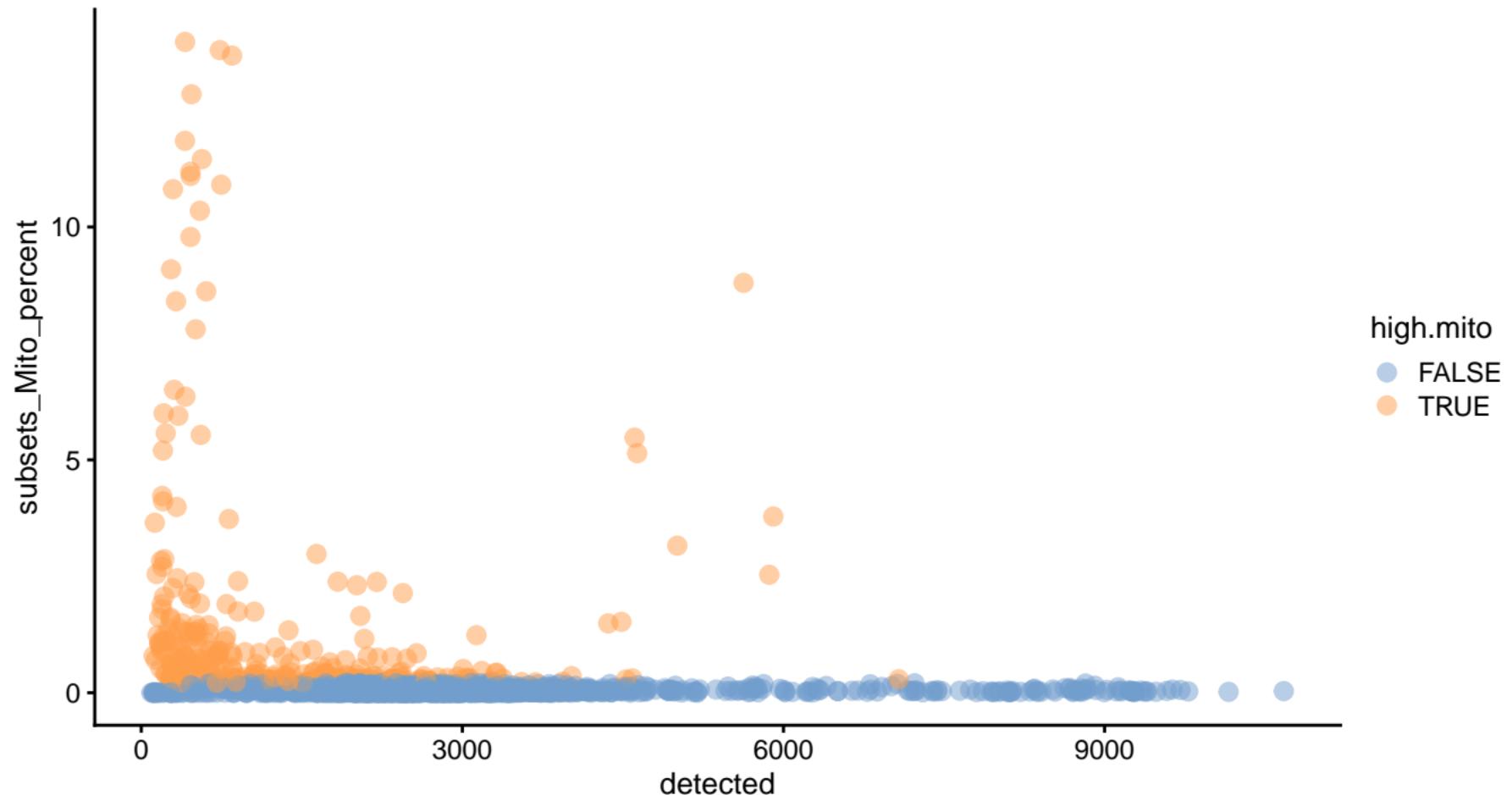
**Detected features**



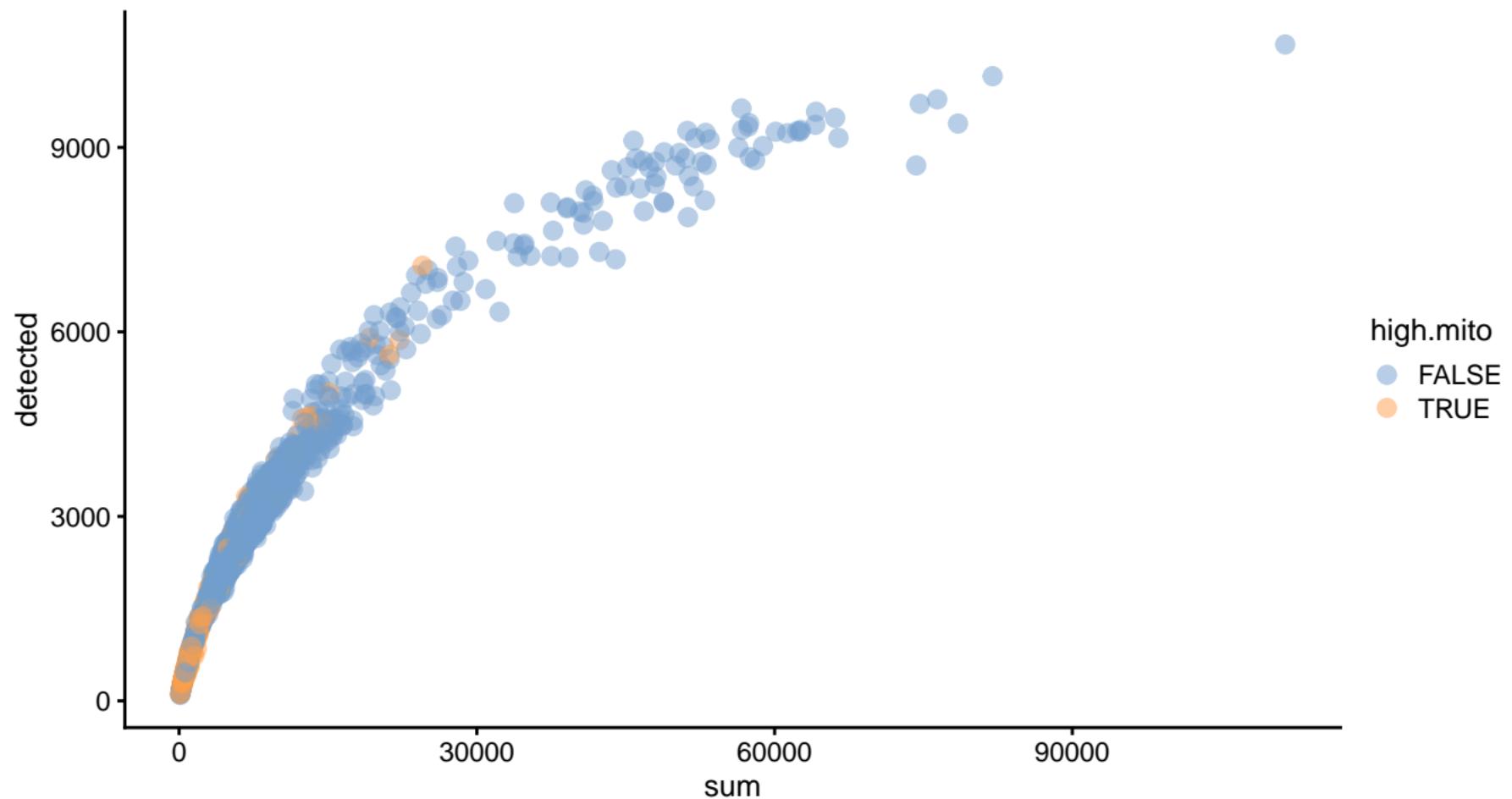
**Mito % (cutoff = 0.211)**



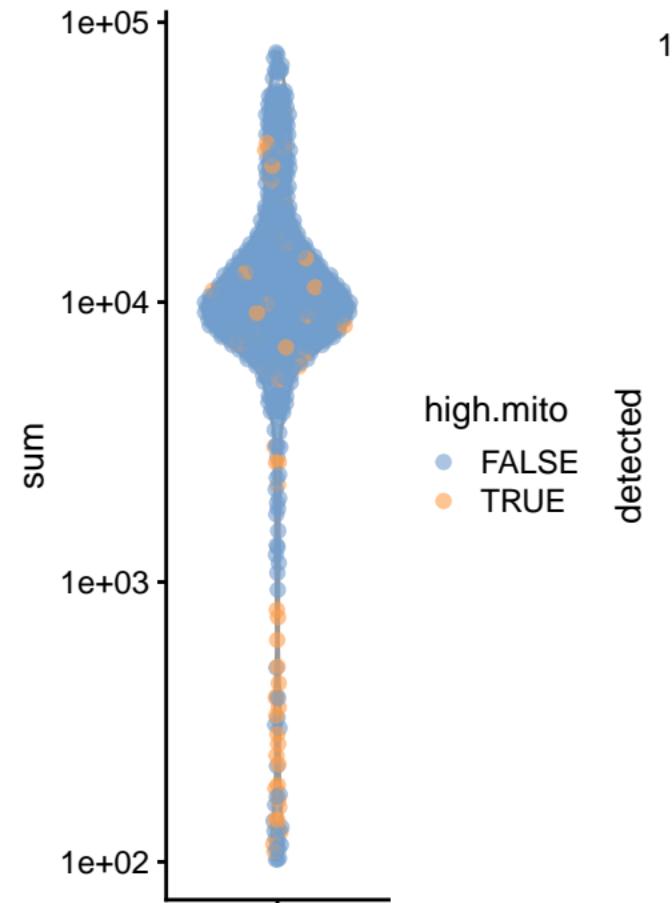
Sample: br5287.hpc; pre-QC nNuclei: 2189; nNuclei kept: 1887 (0.86%)



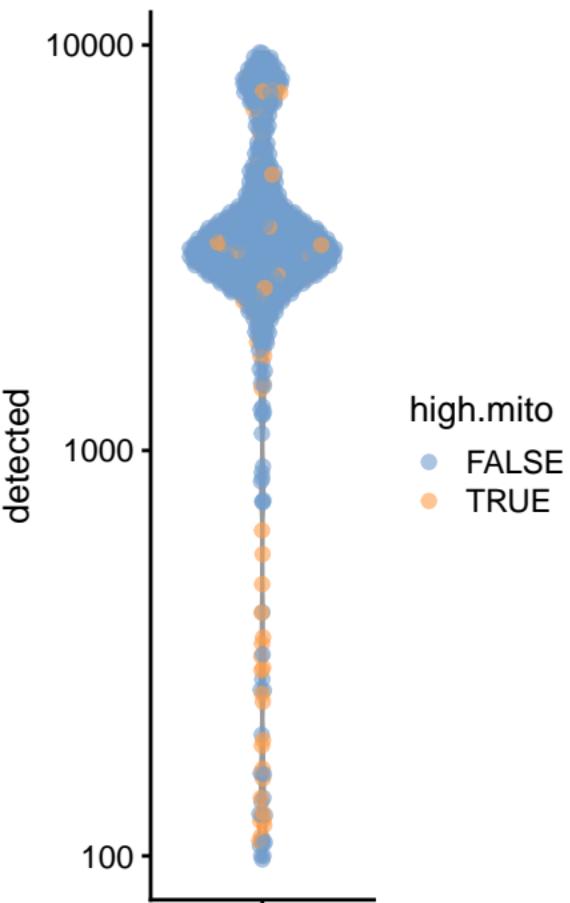
Sample: br5287.hpc; pre-QC nNuclei: 2189; nNuclei kept: 1887 (0.86%)



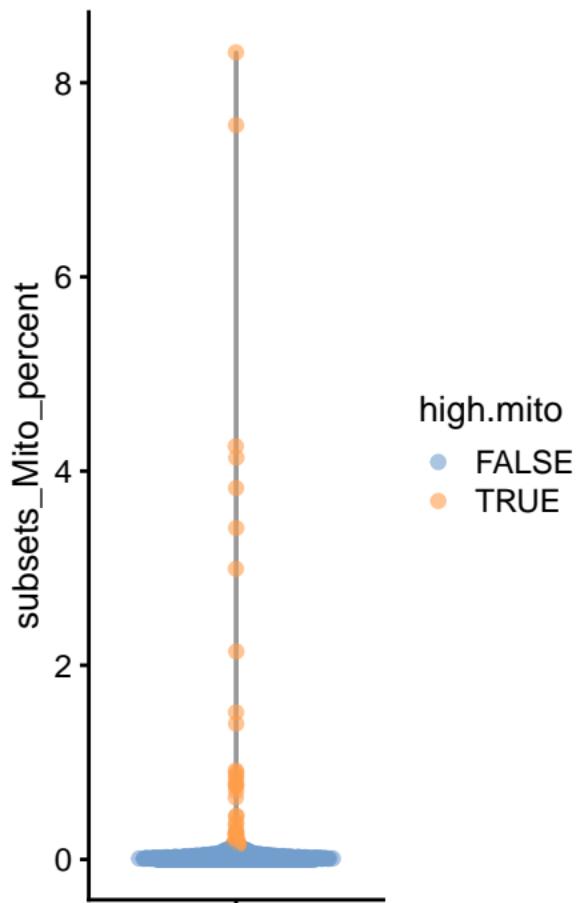
Total count: br5287.nac



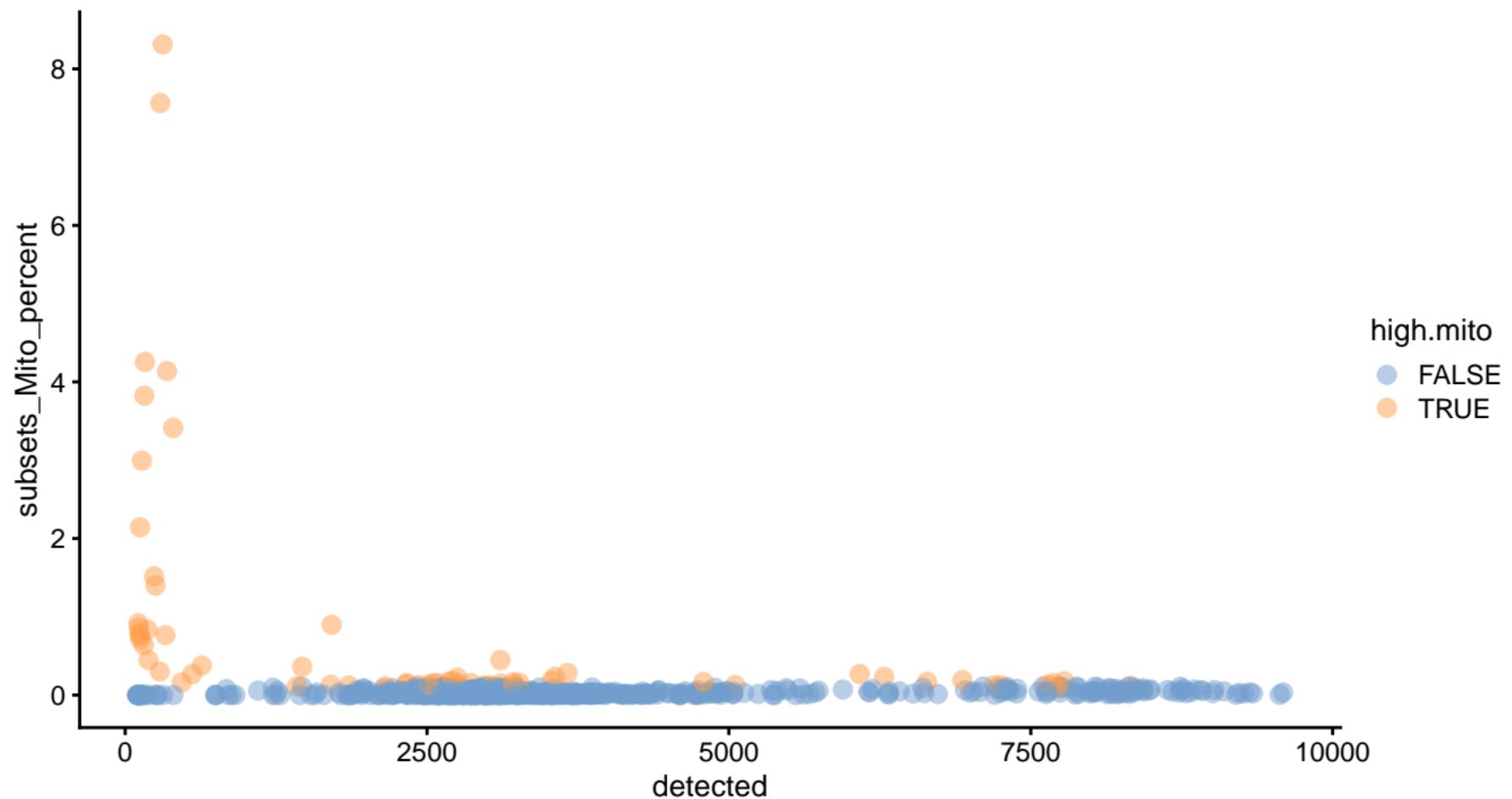
Detected features



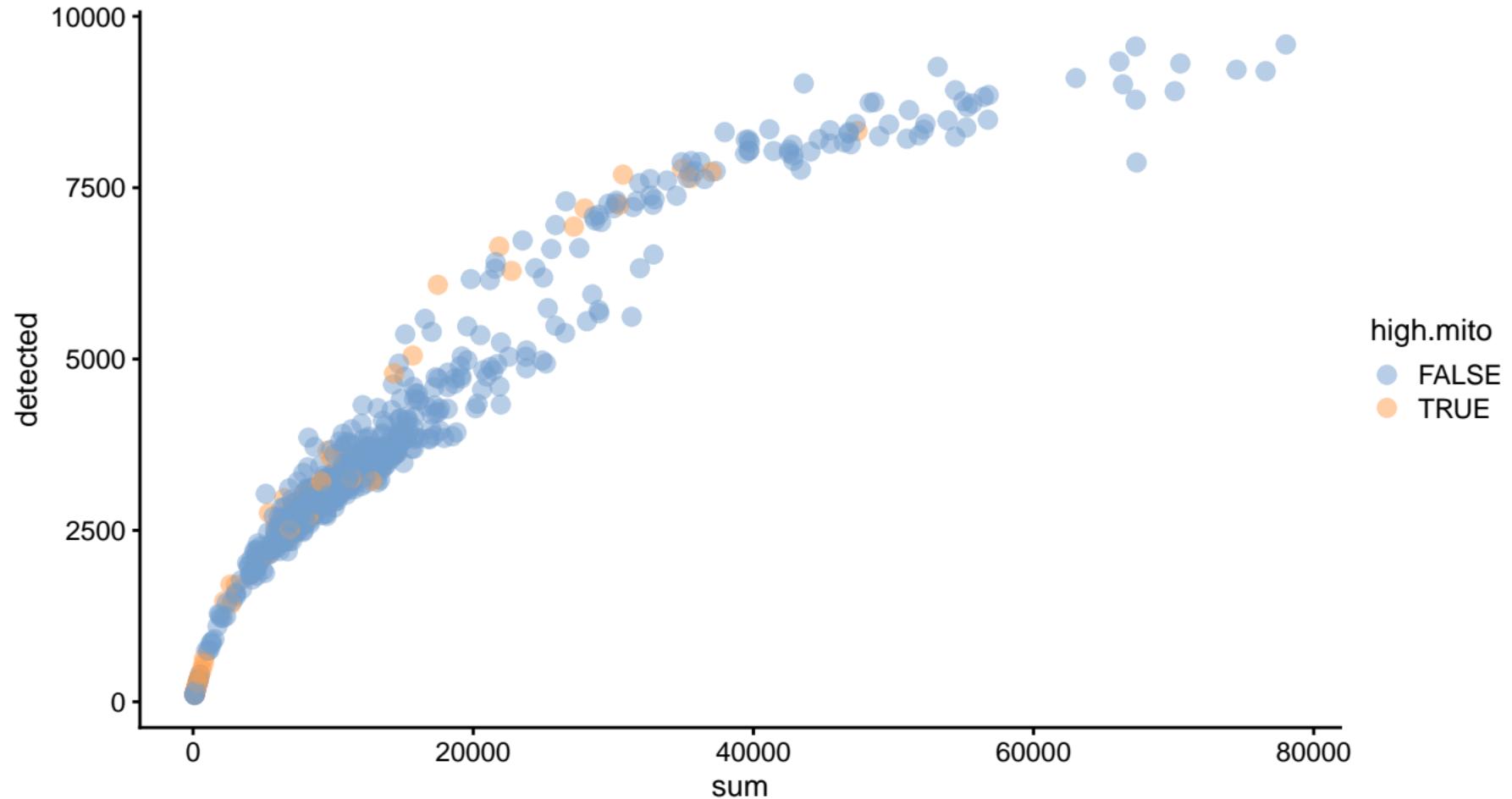
Mito % (cutoff = 0.11)



Sample: br5287.nac; pre-QC nNuclei: 770; nNuclei kept: 707 (0.92%)



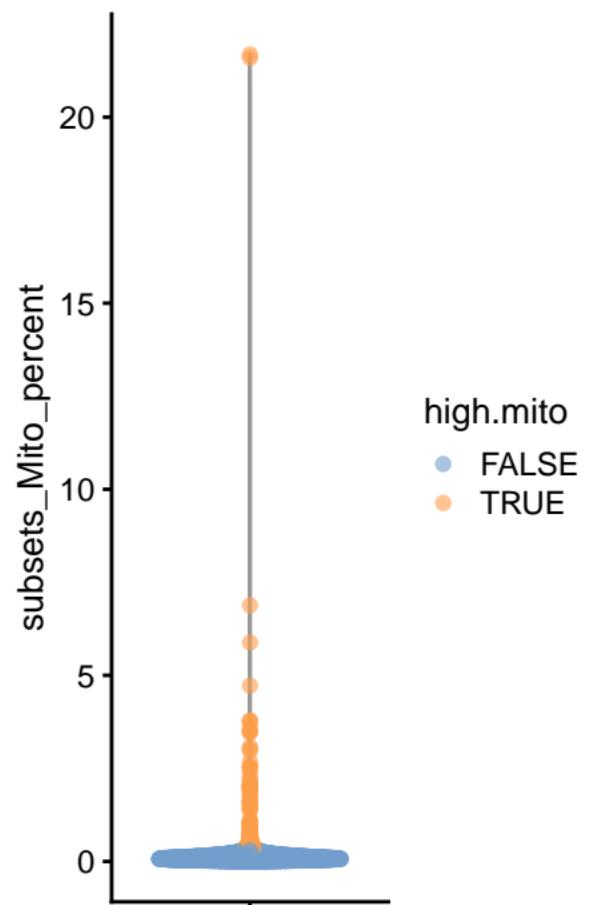
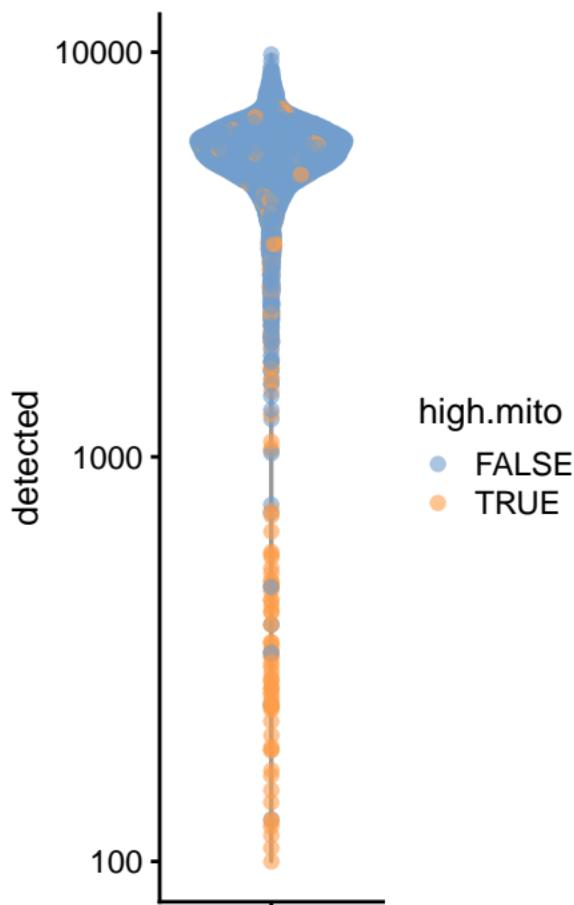
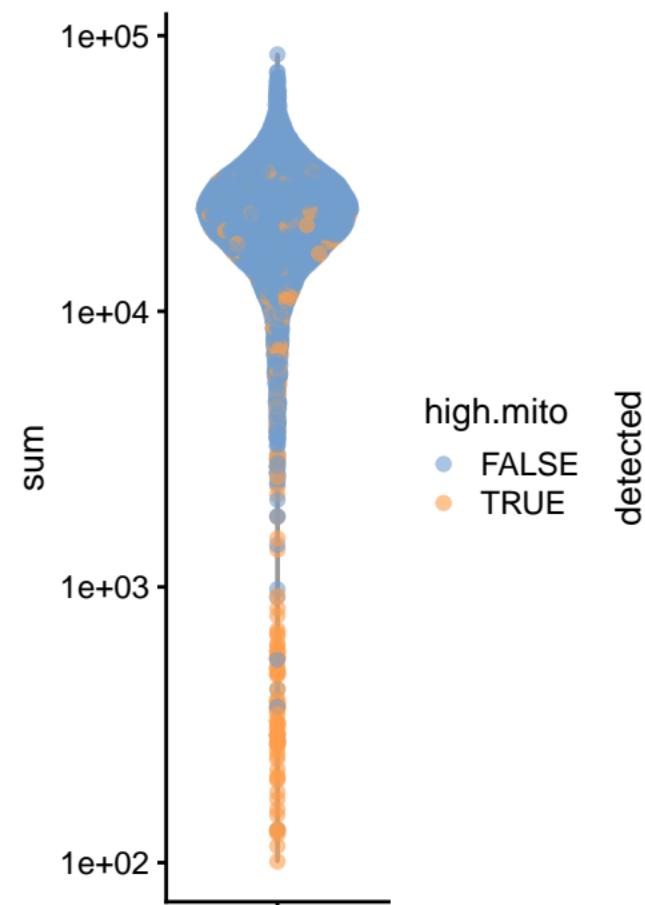
Sample: br5287.nac; pre-QC nNuclei: 770; nNuclei kept: 707 (0.92%)



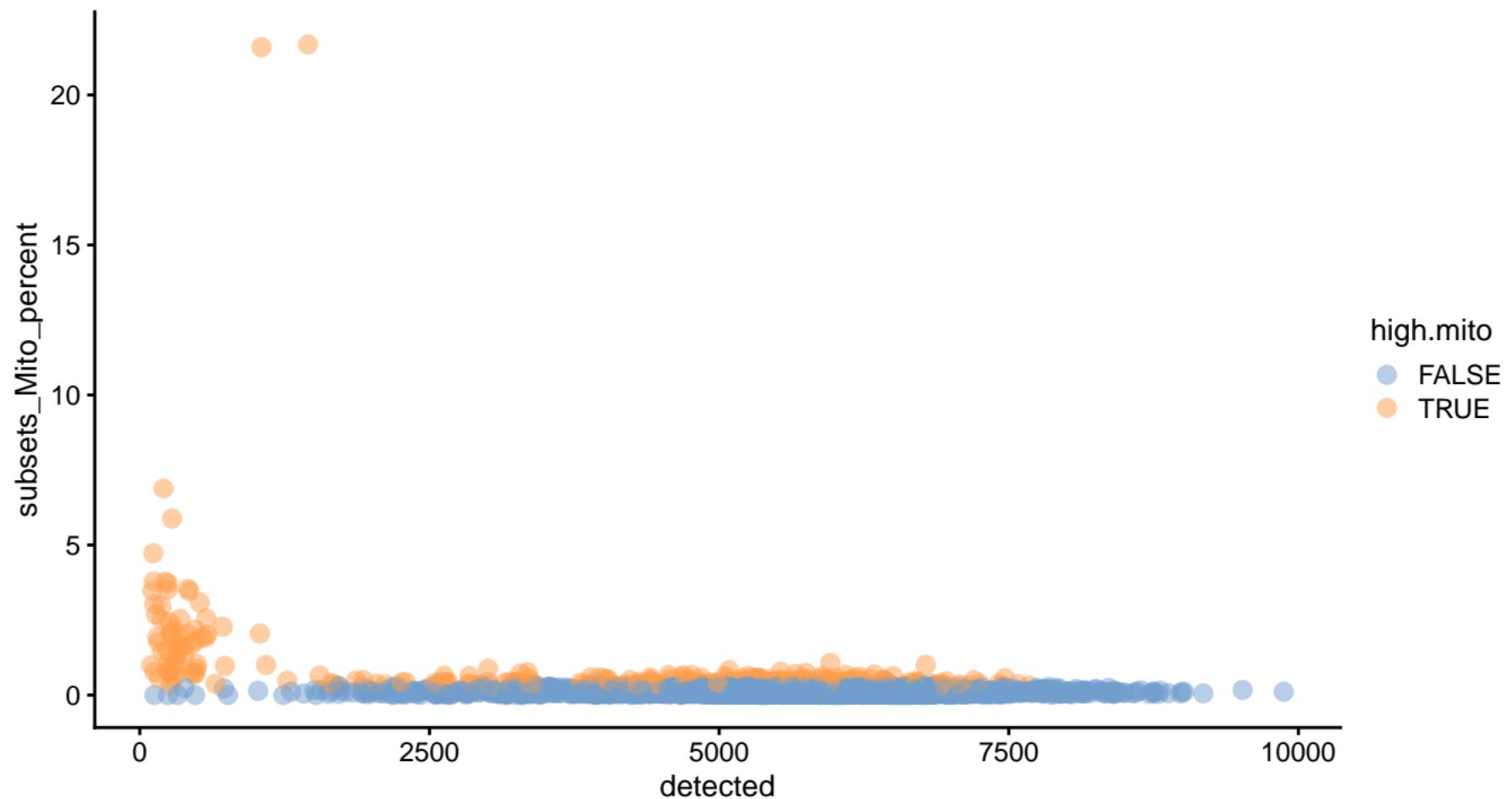
Total count: br5182.nac.neun

Detected features

Mito % (cutoff = 0.309)



Sample: br5182.nac.neun; pre-QC nNuclei: 4602; nNuclei kept: 4267 (0.93%)



Sample: br5182.nac.neun; pre-QC nNuclei: 4602; nNuclei kept: 4267 (0.93%)

