## Estimating fitness from reads

- Noncoding DNA Annotated essential gene 14 Non-essential genes Other genamic regions 17 Reads per bp s/bp I Basepair position in chromosome ized reads per bp 0 1 2 2 Λ 5 1e5 Basepair position on chromosome VIII Basepair position in chromosome Noncoding DNA Annotated essential gene Non essential genes Other genomic regi 0.8 0.6 Basepair position in chromosome 0.2
- Divide barplot in multiple ٠ windows (denoted a, b and c)

Normalize each window ٠ individually by average number of reads

Normalize all reads by highest

Not perfect method:

٠

value

- How to define windows?

- What to do with outliers (i.e. few bars with many reads).

Basepair position on chromosome VIII