## Header description

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Here is a list of header terms in the fitting result file.

- group: name of the gene set

  - all: all genesboot\_X: bootstrap of random sampling of gene subset
- ullet sample\_d:  $d_{sample}$
- ullet theta:  $heta_{pool}$
- ullet phi:  $\phi_{pool}$
- ullet fbar:  $ar{f}$
- ullet ratio:  $\gamma/\mu$
- rho:  $\gamma \bar{f}$
- ullet sample\_theta:  $heta_{sample}$
- ullet sample\_rho: c