

Samtools: flagstat: percentage of total

11 samples

Total Reads

0%

20%

40%

60%

80%

100%

Total Passed QC

0%

20%

40%

60%

80%

100%

Mapped

0%

20%

40%

60%

80%

100%

Duplicates

0%

20%

40%

60%

80%

100%

Paired in Sequencing

0%

20%

40%

60%

80%

100%

Properly Paired

0%

20%

40%

60%

80%

100%

Self and mate mapped

0%

20%

40%

60%

80%

100%

Singletons

0%

20%

40%

60%

80%

100%

Mate mapped to diff chr

0%

20%

40%

60%

80%

100%

Diff chr (mapQ >= 5)

0%

20%

40%

60%

80%

100%

