

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:10:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505917.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1505917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:10:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,683,568
Mapped reads	5,248,577 / 68.31%
Unmapped reads	2,434,991 / 31.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	315 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	304,512 / 3.96%
Duplication rate	4.52%
Clipped reads	1,153,387 / 15.01%

2.2. ACGT Content

Number/percentage of A's	69,865,837 / 29.06%
Number/percentage of C's	50,868,320 / 21.16%
Number/percentage of T's	68,295,893 / 28.41%
Number/percentage of G's	51,392,888 / 21.38%
Number/percentage of N's	666 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0777

Standard Deviation	0.6253
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2.4. Mapping Quality

Mean Mapping Quality	43.16
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2.5. Mismatches and indels

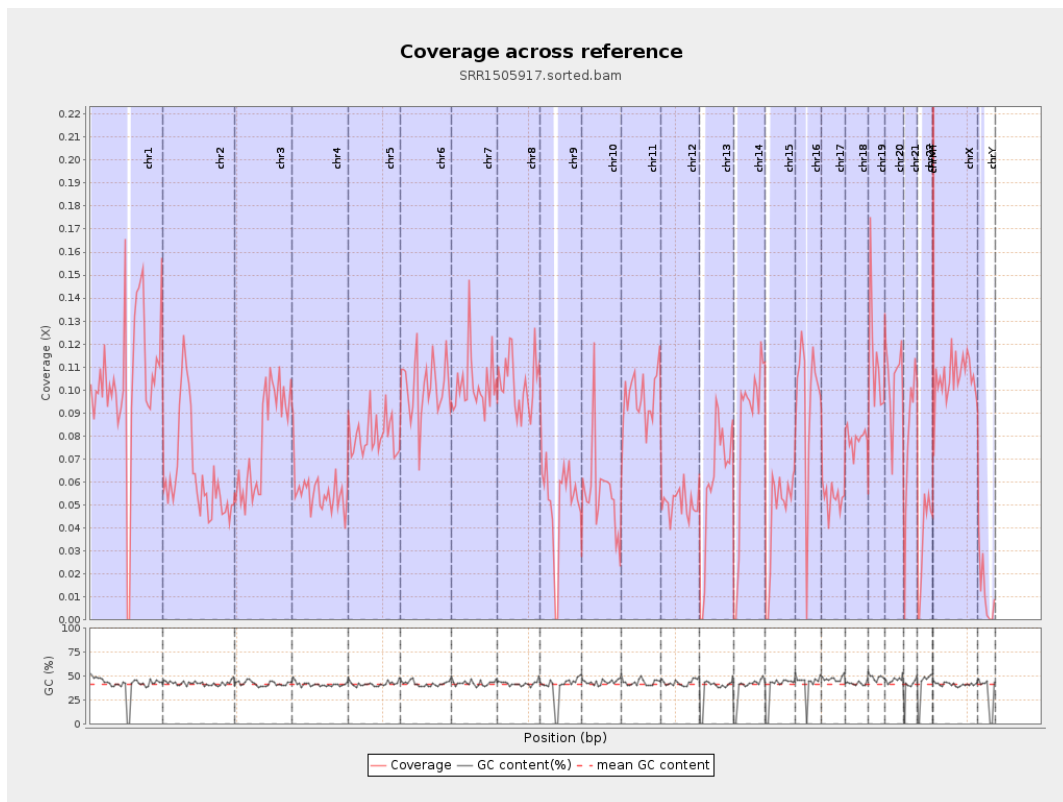
General error rate	0.51%
Mismatches	1,213,485
Insertions	10,691
Mapped reads with at least one insertion	0.2%
Deletions	34,228
Mapped reads with at least one deletion	0.65%
Homopolymer indels	44.18%

2.6. Chromosome stats

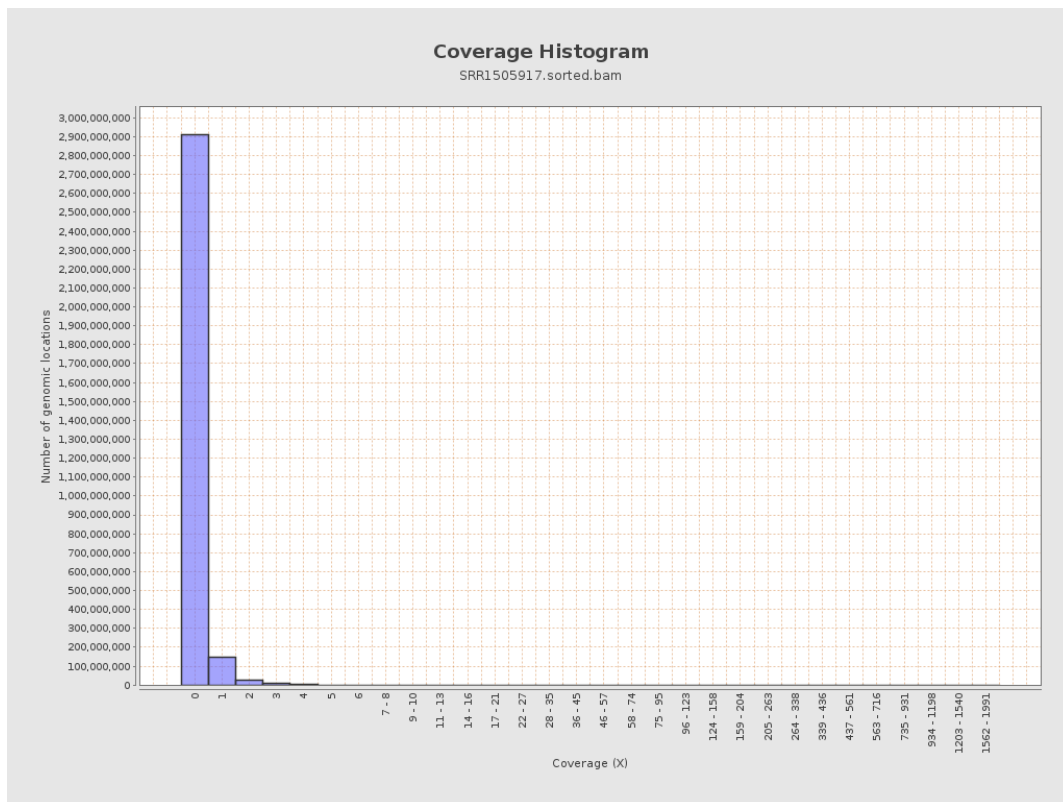
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25938342	0.1041	1.3618
chr2	243199373	15521964	0.0638	0.426
chr3	198022430	15415483	0.0778	0.3513
chr4	191154276	10538560	0.0551	0.2942
chr5	180915260	14471247	0.08	0.3592
chr6	171115067	17300566	0.1011	0.5313
chr7	159138663	16296531	0.1024	0.8869

chr8	146364022	15036274	0.1027	0.925
chr9	141213431	7230733	0.0512	0.3558
chr10	135534747	7497761	0.0553	0.6118
chr11	135006516	12996106	0.0963	0.6078
chr12	133851895	6771166	0.0506	0.2926
chr13	115169878	6985135	0.0607	0.3047
chr14	107349540	8852450	0.0825	0.4537
chr15	102531392	4656450	0.0454	0.2601
chr16	90354753	8613812	0.0953	0.4347
chr17	81195210	4300667	0.053	0.3292
chr18	78077248	6139937	0.0786	0.7256
chr19	59128983	6659317	0.1126	0.9096
chr20	63025520	6543532	0.1038	0.4122
chr21	48129895	3844997	0.0799	0.3729
chr22	51304566	1807196	0.0352	0.2315
chrMT	16571	13703	0.8269	1.1375
chrX	155270560	16351270	0.1053	0.4527
chrY	59373566	687832	0.0116	0.1612

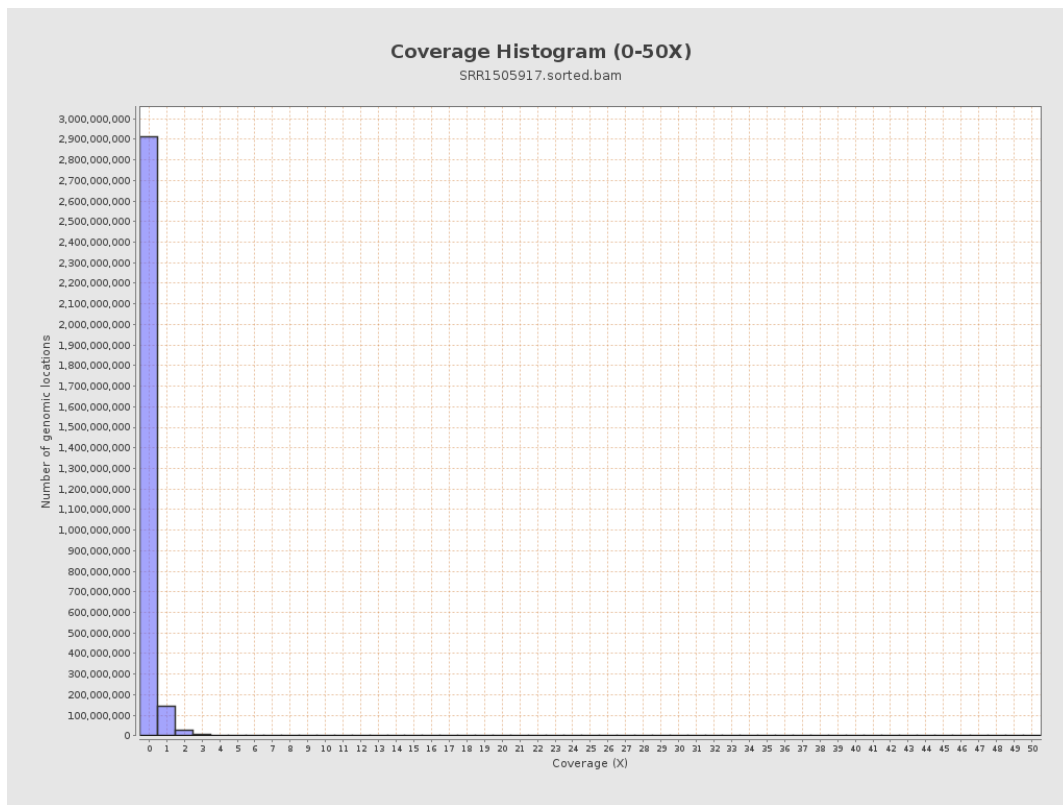
3. Results : Coverage across reference



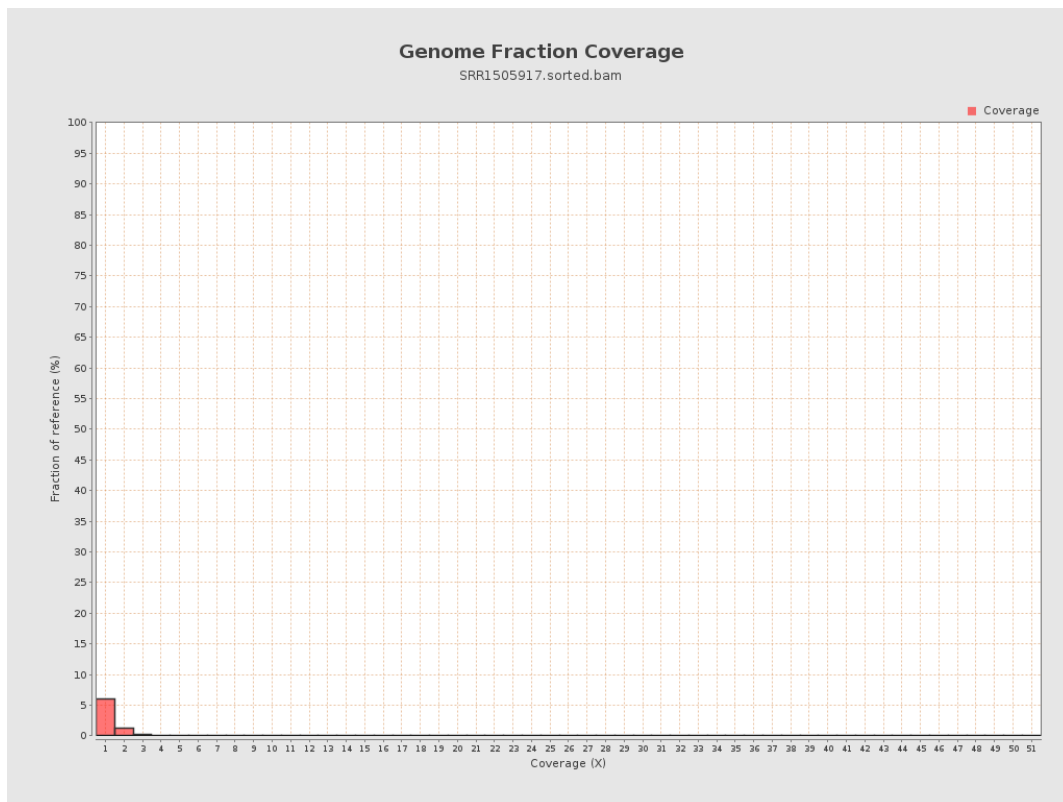
4. Results : Coverage Histogram



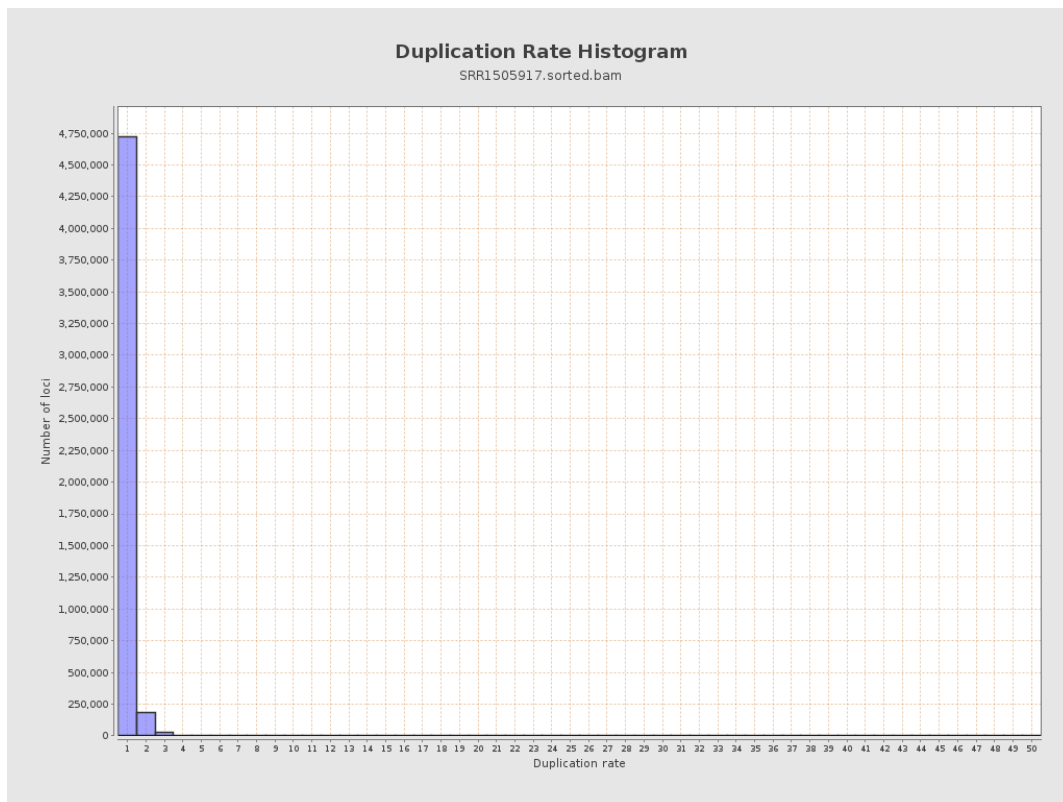
5. Results : Coverage Histogram (0-50X)



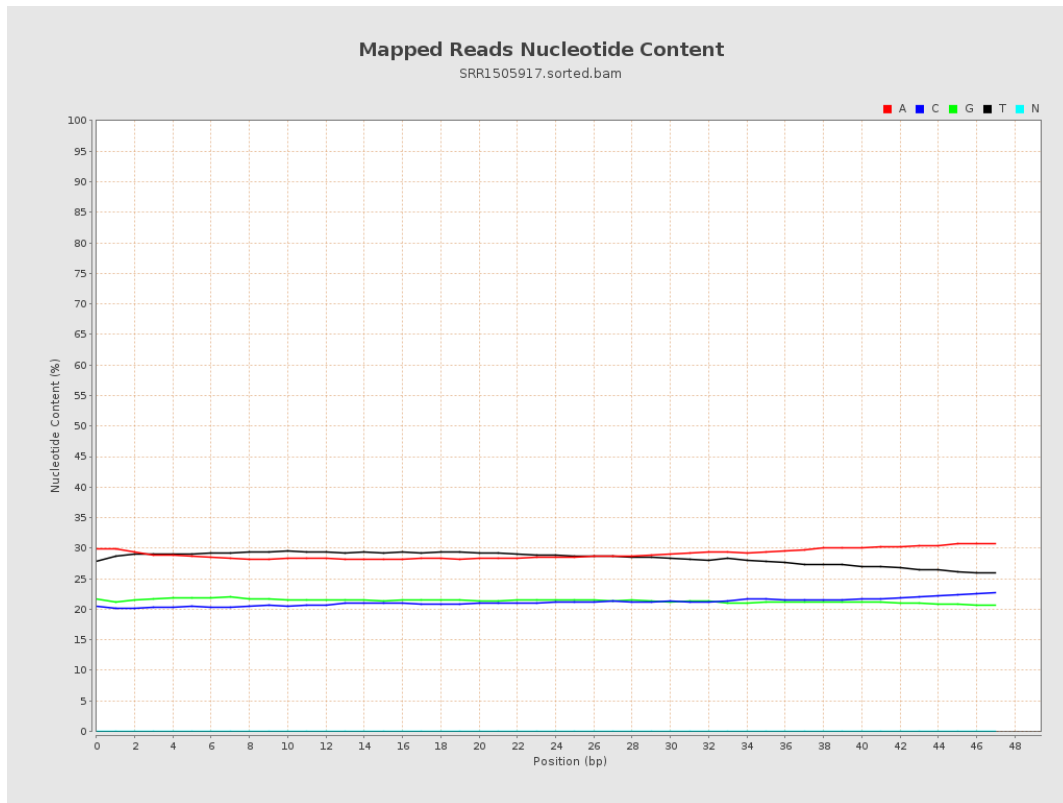
6. Results : Genome Fraction Coverage



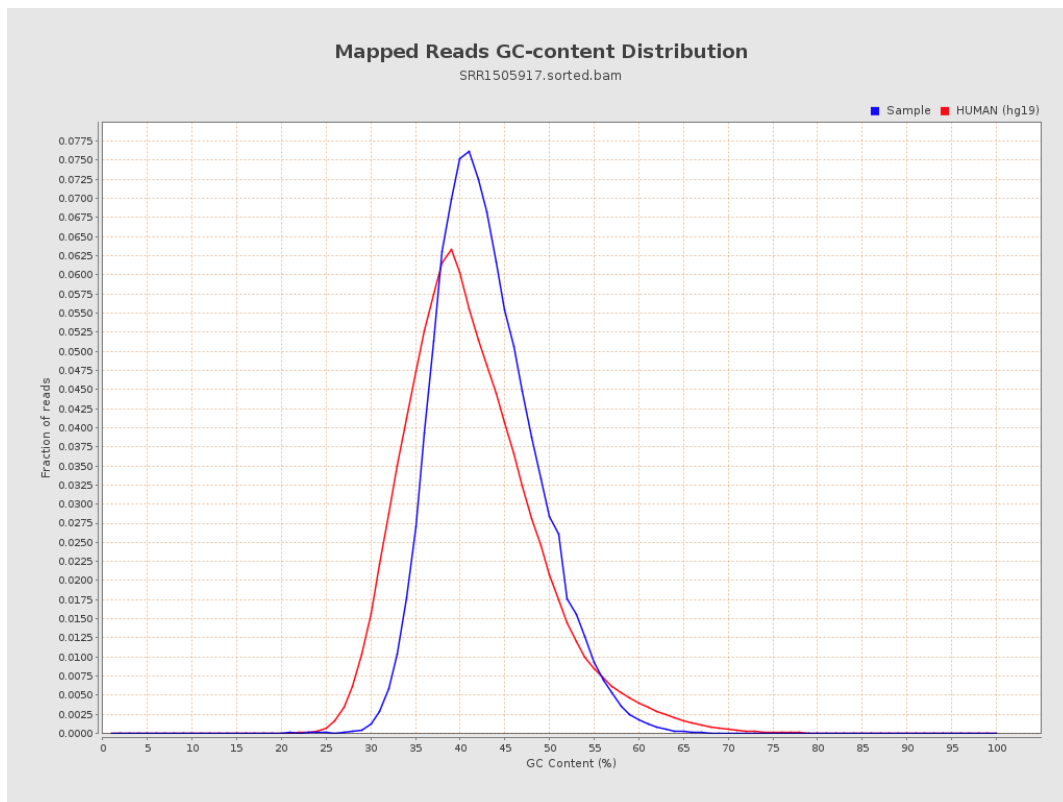
7. Results : Duplication Rate Histogram



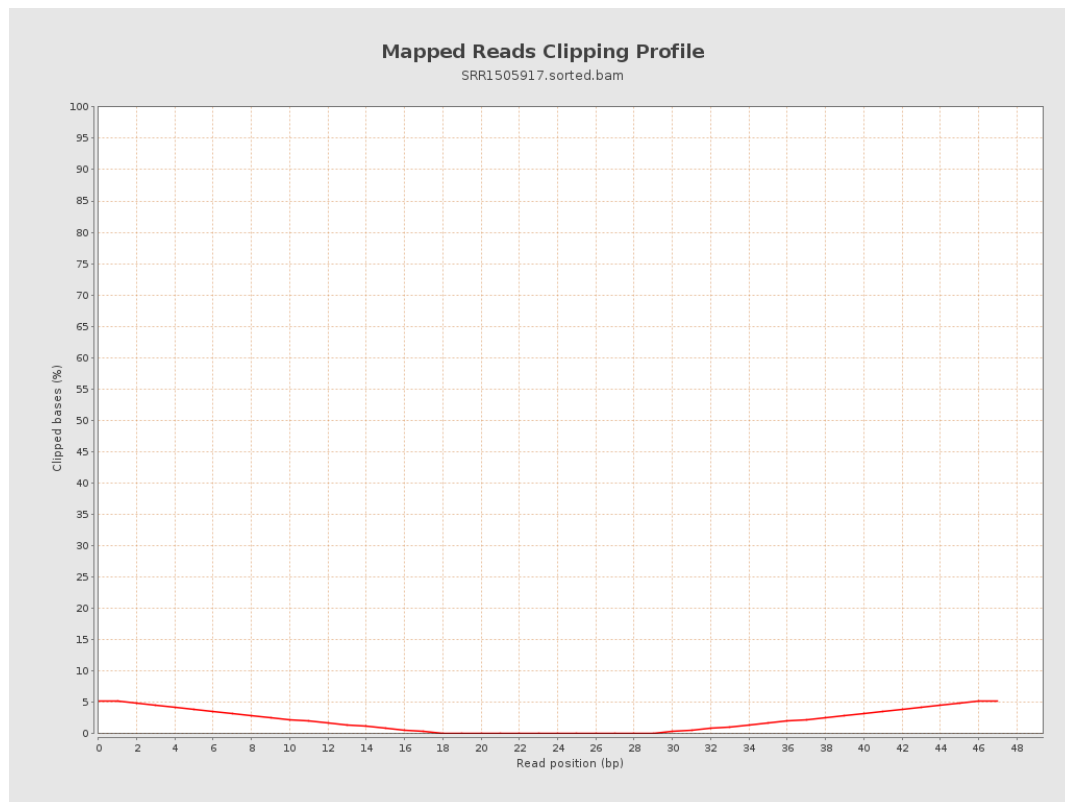
8. Results : Mapped Reads Nucleotide Content



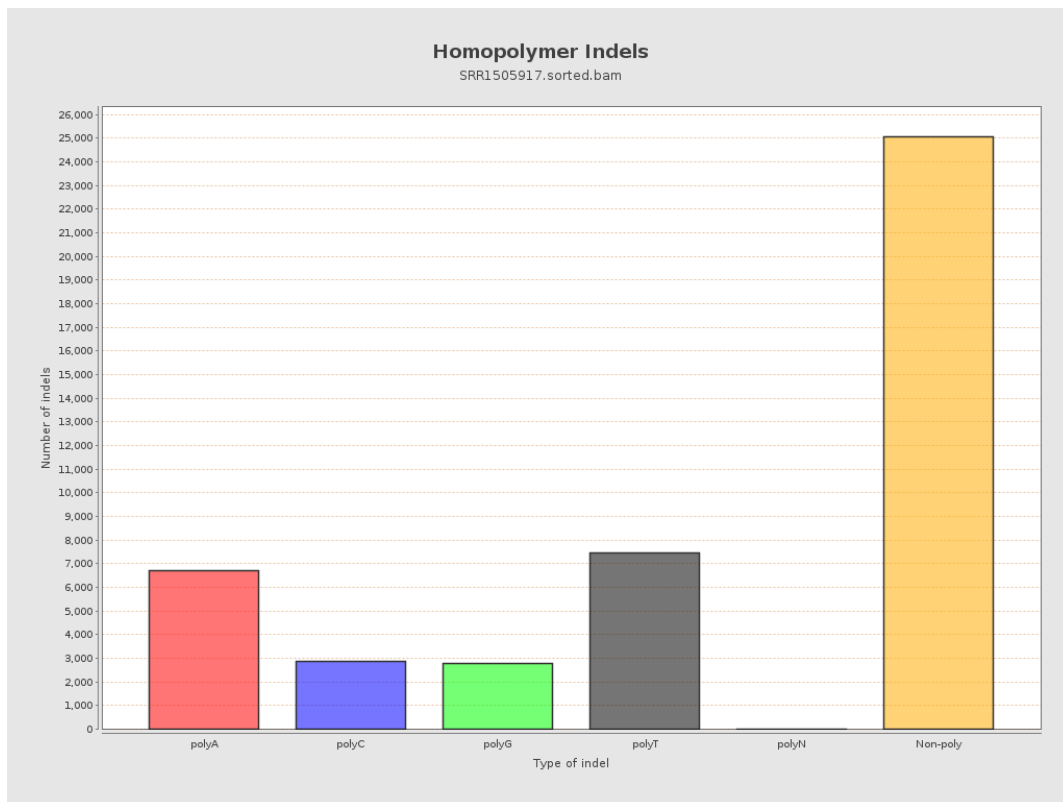
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

