

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 00:30:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548918.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_SRR1548918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548918.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 00:29:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,389,125
Mapped reads	4,666,376 / 86.59%
Unmapped reads	722,749 / 13.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	160,328 / 2.98%
Duplication rate	2.71%
Clipped reads	370,120 / 6.87%

2.2. ACGT Content

Number/percentage of A's	53,685,536 / 29.08%
Number/percentage of C's	37,972,079 / 20.57%
Number/percentage of T's	54,546,422 / 29.54%
Number/percentage of G's	38,416,115 / 20.81%
Number/percentage of N's	1,865 / 0%
GC Percentage	41.38%

2.3. Coverage

Mean	0.0596
Standard Deviation	0.3912

2.4. Mapping Quality

Mean Mapping Quality	41.63
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2.5. Mismatches and indels

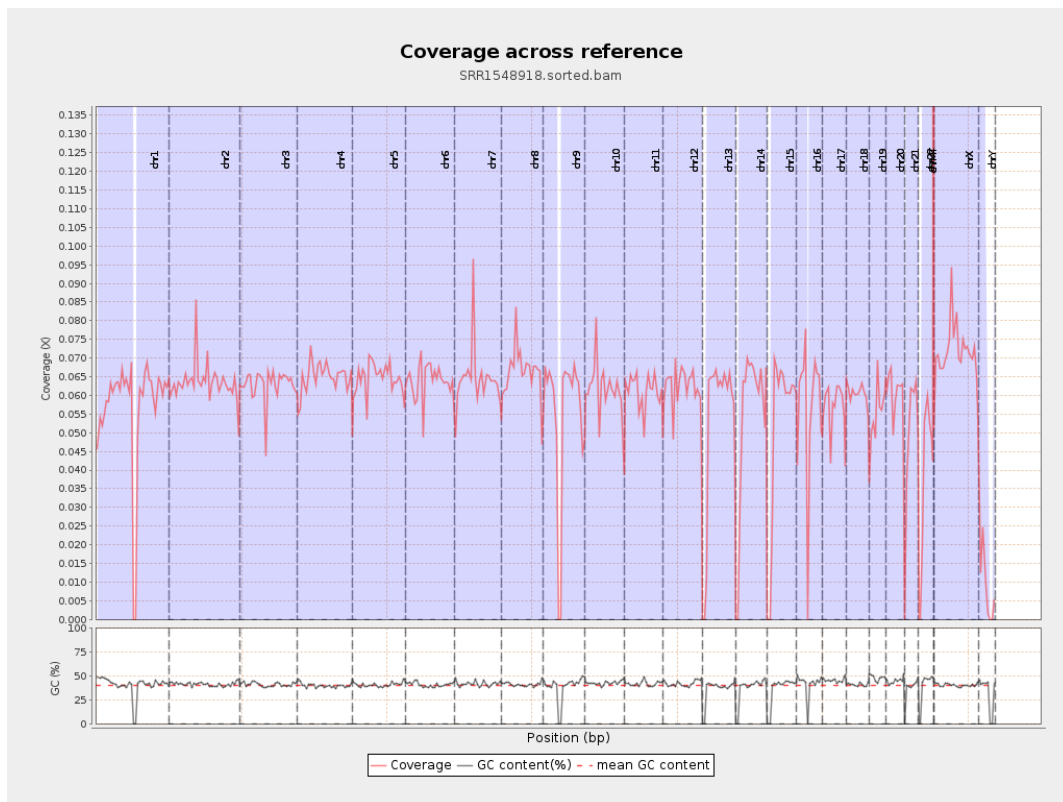
General error rate	0.29%
Mismatches	520,528
Insertions	6,298
Mapped reads with at least one insertion	0.13%
Deletions	16,019
Mapped reads with at least one deletion	0.34%
Homopolymer indels	42.67%

2.6. Chromosome stats

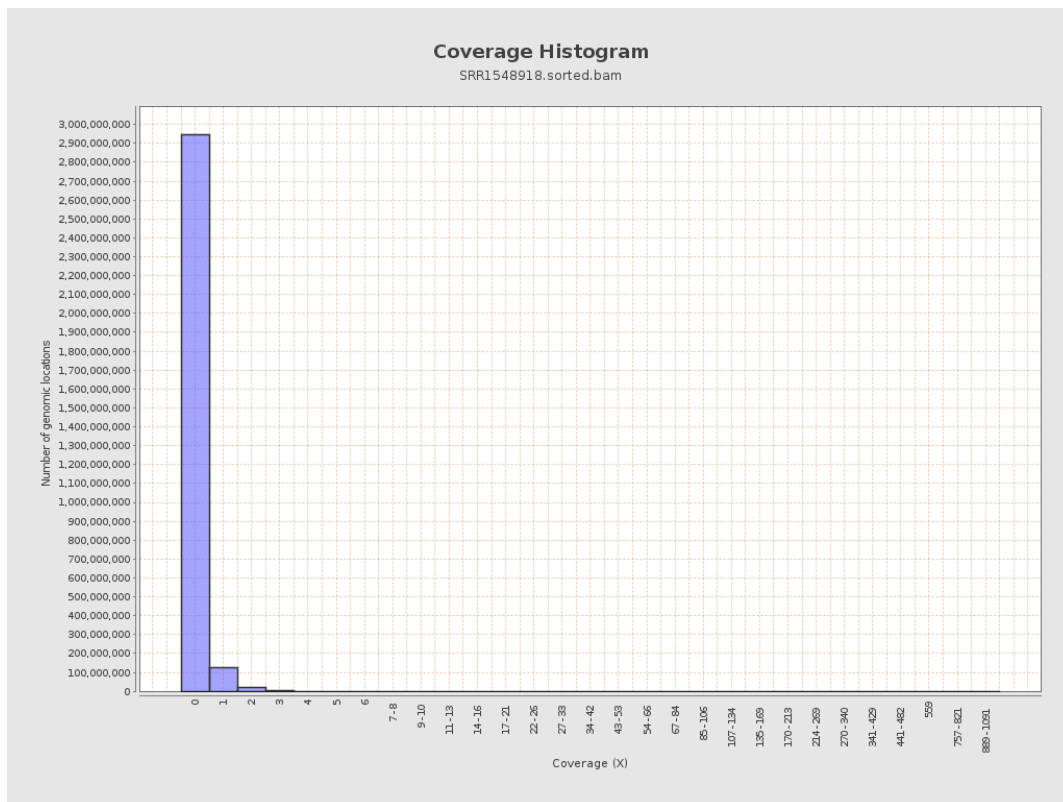
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14220069	0.0571	0.419
chr2	243199373	15454971	0.0635	0.4063
chr3	198022430	12466237	0.063	0.3056
chr4	191154276	12418402	0.065	0.3154
chr5	180915260	11692541	0.0646	0.3092
chr6	171115067	10930131	0.0639	0.3302
chr7	159138663	10315126	0.0648	0.589
chr8	146364022	9709906	0.0663	0.6336

chr9	141213431	7814684	0.0553	0.4142
chr10	135534747	8388760	0.0619	0.3623
chr11	135006516	8219698	0.0609	0.4176
chr12	133851895	8324408	0.0622	0.3071
chr13	115169878	6075263	0.0528	0.2784
chr14	107349540	5750753	0.0536	0.3407
chr15	102531392	5331481	0.052	0.2759
chr16	90354753	5149519	0.057	0.318
chr17	81195210	4594883	0.0566	0.3063
chr18	78077248	4737501	0.0607	0.6249
chr19	59128983	3293786	0.0557	0.4489
chr20	63025520	3795641	0.0602	0.3076
chr21	48129895	2360162	0.049	0.303
chr22	51304566	1898994	0.037	0.2625
chrMT	16571	7996	0.4825	0.9438
chrX	155270560	11129081	0.0717	0.3632
chrY	59373566	563151	0.0095	0.1414

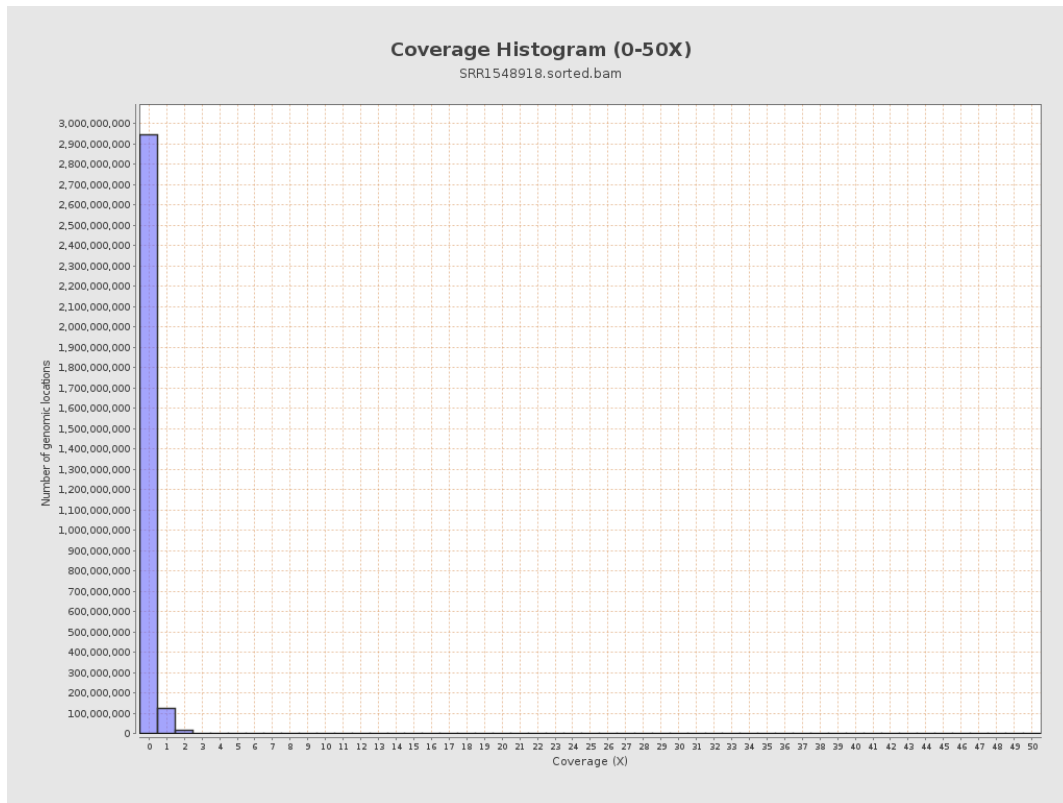
3. Results : Coverage across reference



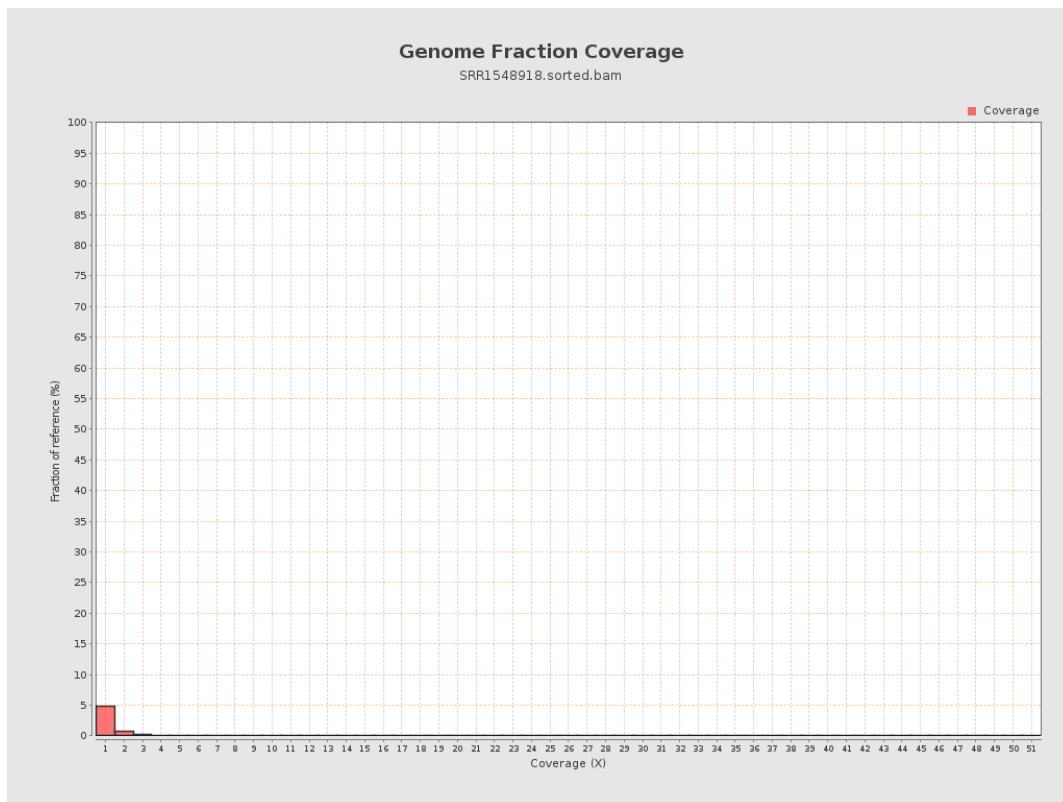
4. Results : Coverage Histogram



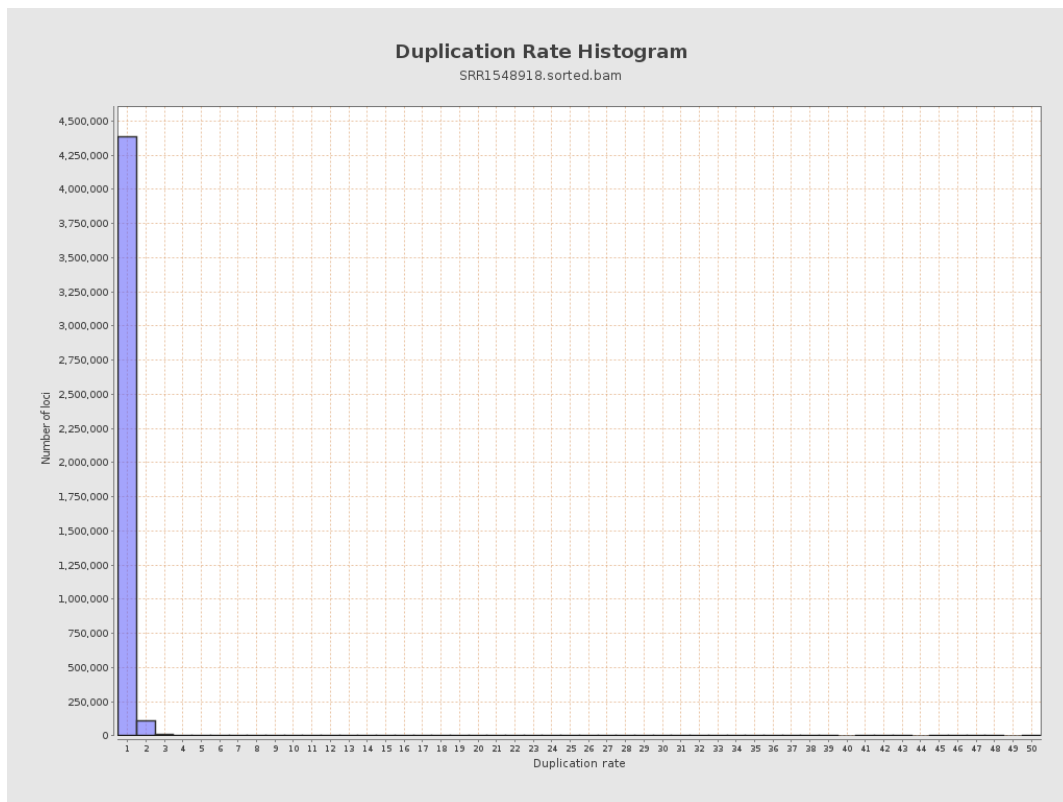
5. Results : Coverage Histogram (0-50X)



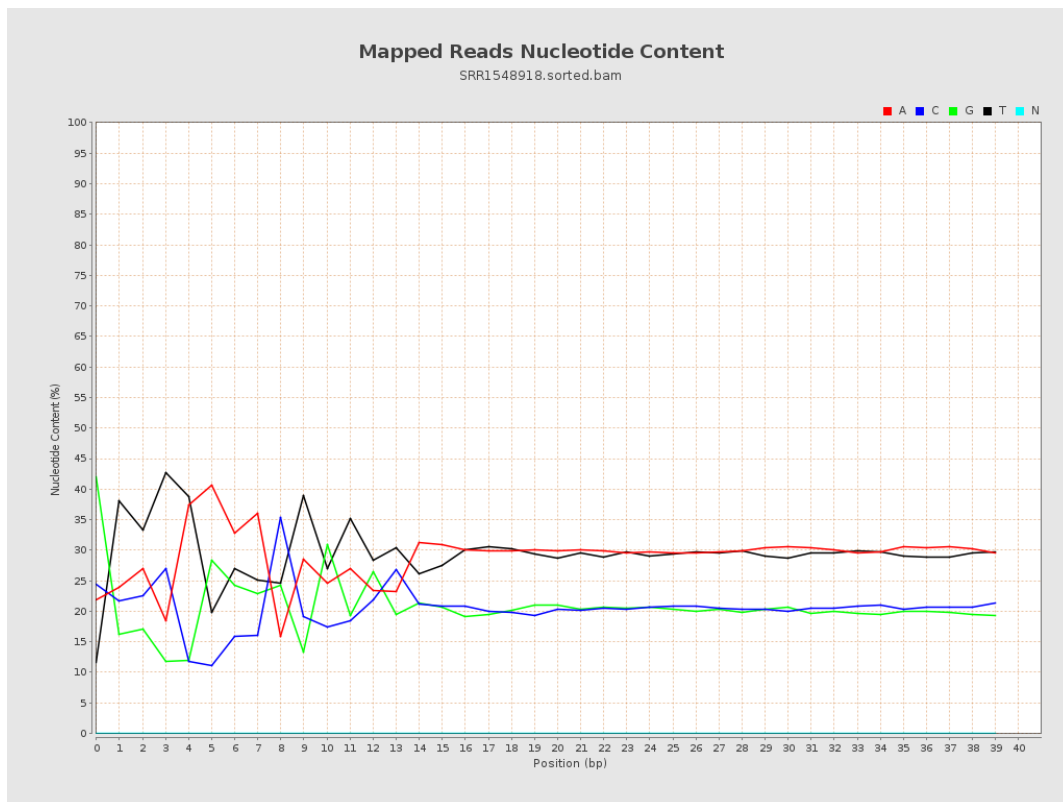
6. Results : Genome Fraction Coverage



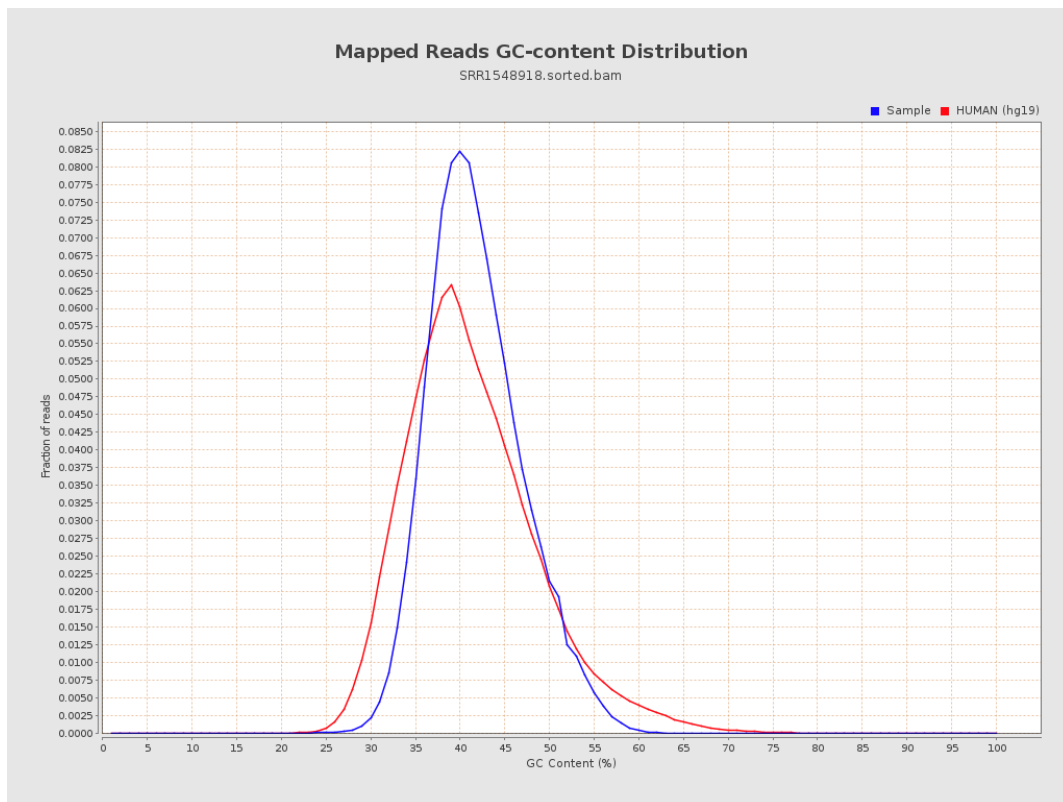
7. Results : Duplication Rate Histogram



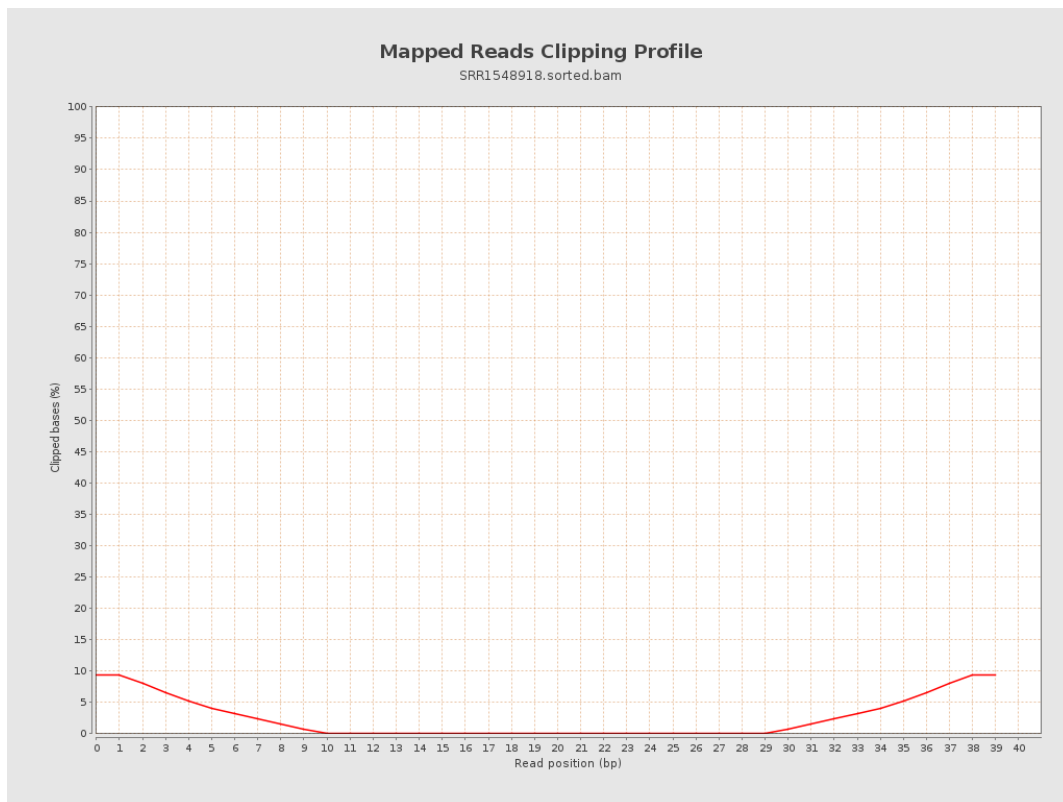
8. Results : Mapped Reads Nucleotide Content



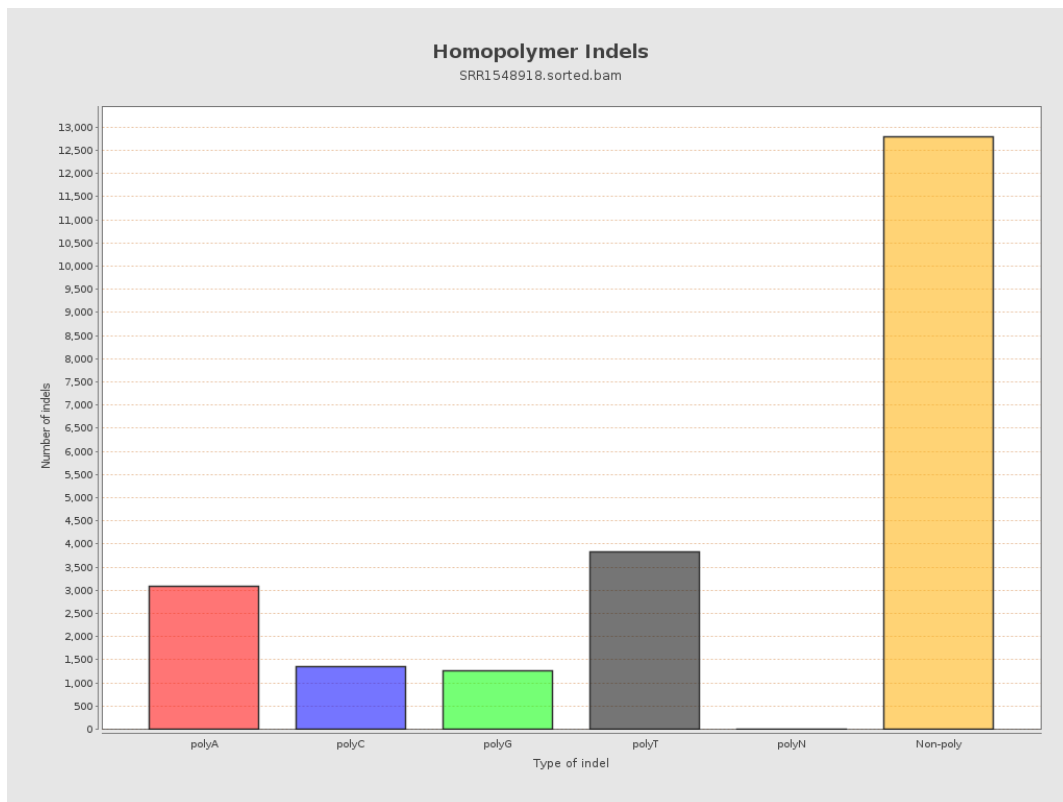
9. Results : Mapped Reads GC-content Distribution



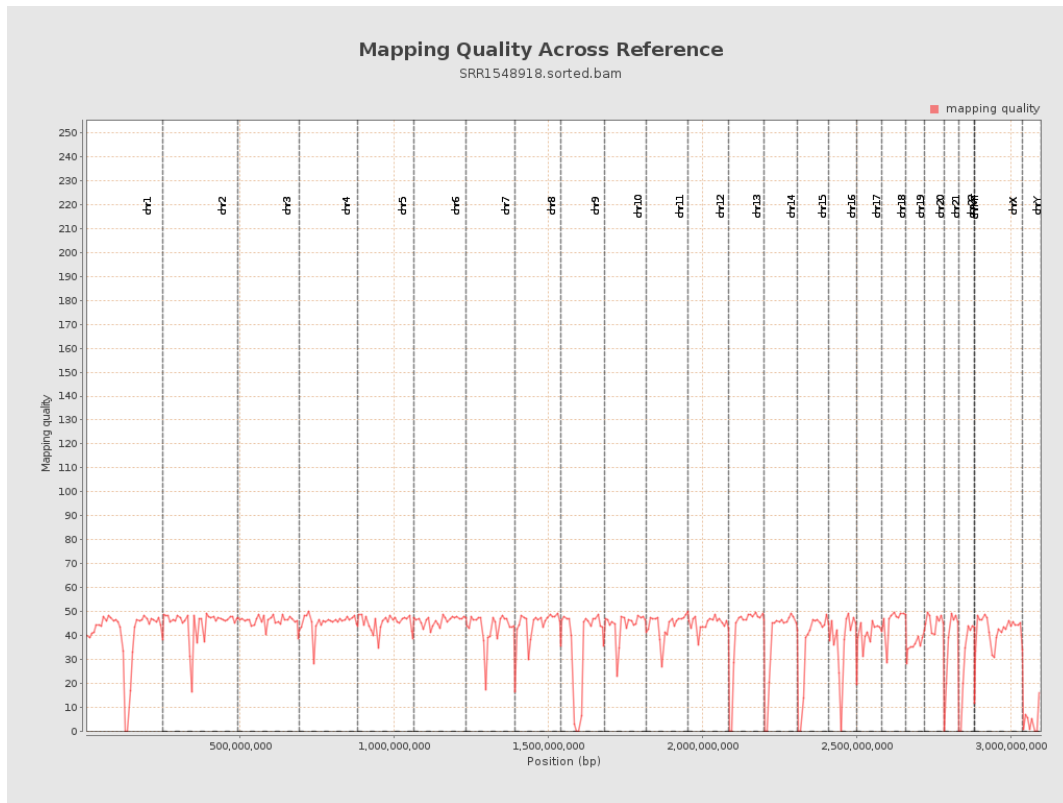
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

