

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 00:24:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548917.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_SRR1548917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 00:24:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,651,772
Mapped reads	4,981,173 / 88.13%
Unmapped reads	670,599 / 11.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	147,438 / 2.61%
Duplication rate	1.99%
Clipped reads	277,268 / 4.91%

2.2. ACGT Content

Number/percentage of A's	58,259,641 / 29.48%
Number/percentage of C's	40,118,918 / 20.3%
Number/percentage of T's	58,896,134 / 29.8%
Number/percentage of G's	40,331,494 / 20.41%
Number/percentage of N's	2,003 / 0%
GC Percentage	40.71%

2.3. Coverage

Mean	0.0638
Standard Deviation	0.5377

2.4. Mapping Quality

Mean Mapping Quality	42.68
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2.5. Mismatches and indels

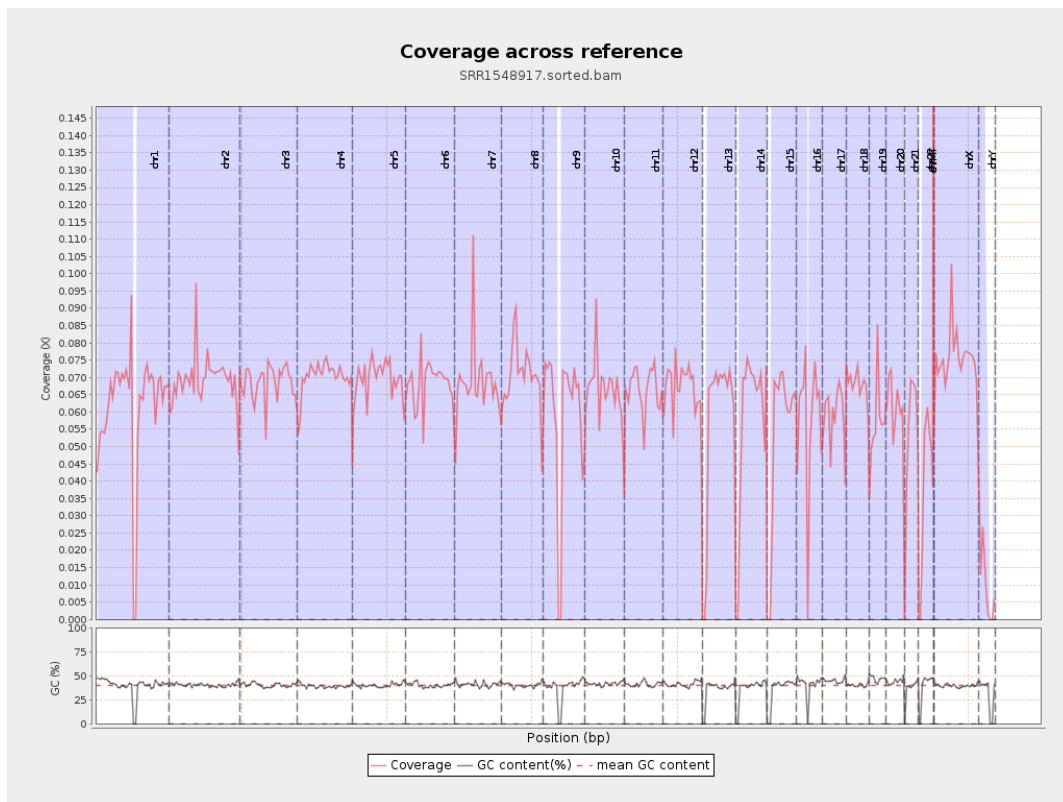
General error rate	0.25%
Mismatches	489,406
Insertions	5,106
Mapped reads with at least one insertion	0.1%
Deletions	14,455
Mapped reads with at least one deletion	0.29%
Homopolymer indels	43.65%

2.6. Chromosome stats

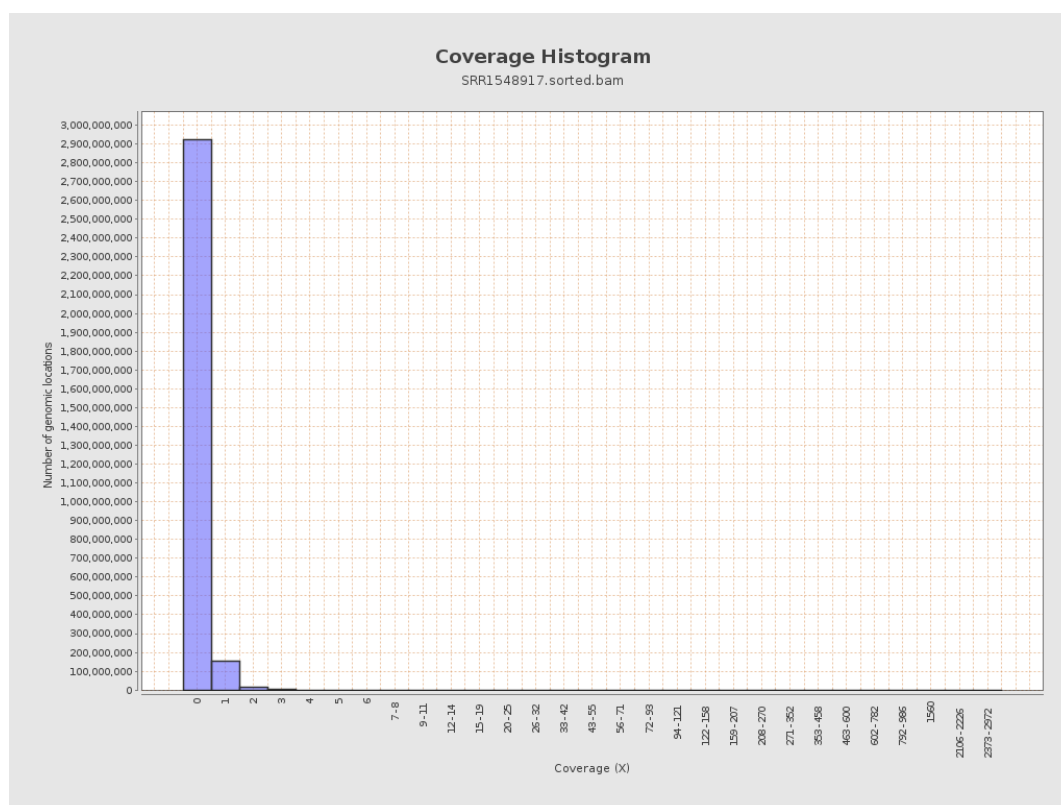
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15373252	0.0617	0.7719
chr2	243199373	16893648	0.0695	0.4312
chr3	198022430	13611920	0.0687	0.2927
chr4	191154276	13429149	0.0703	0.3038
chr5	180915260	12601603	0.0697	0.2982
chr6	171115067	11672787	0.0682	0.329
chr7	159138663	10998762	0.0691	0.6523
chr8	146364022	10288457	0.0703	1.4793

chr9	141213431	8344364	0.0591	0.4333
chr10	135534747	9066377	0.0669	0.3989
chr11	135006516	8934818	0.0662	0.4459
chr12	133851895	8978036	0.0671	0.2993
chr13	115169878	6546210	0.0568	0.262
chr14	107349540	6082193	0.0567	0.3156
chr15	102531392	5487838	0.0535	0.2567
chr16	90354753	5221169	0.0578	0.3073
chr17	81195210	4754898	0.0586	0.2953
chr18	78077248	5323597	0.0682	0.8166
chr19	59128983	3423517	0.0579	0.705
chr20	63025520	3851258	0.0611	0.283
chr21	48129895	2554675	0.0531	0.303
chr22	51304566	1922506	0.0375	0.2132
chrMT	16571	5562	0.3356	0.6582
chrX	155270560	11666970	0.0751	0.3711
chrY	59373566	593741	0.01	0.1428

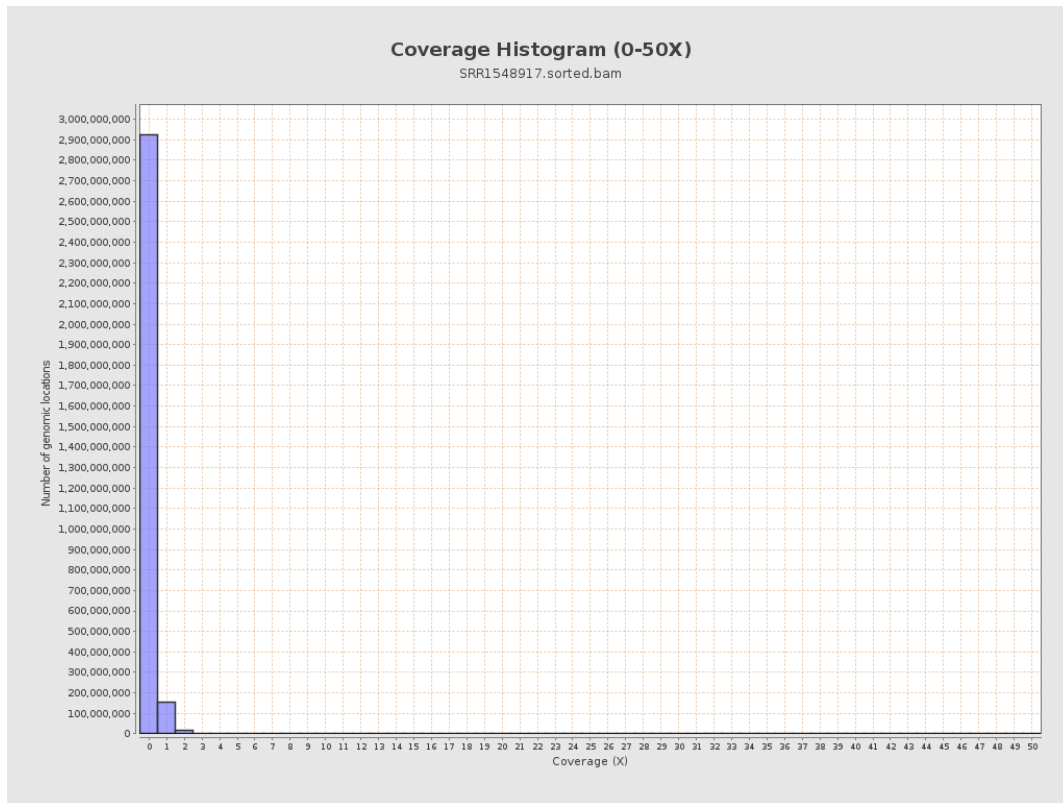
3. Results : Coverage across reference



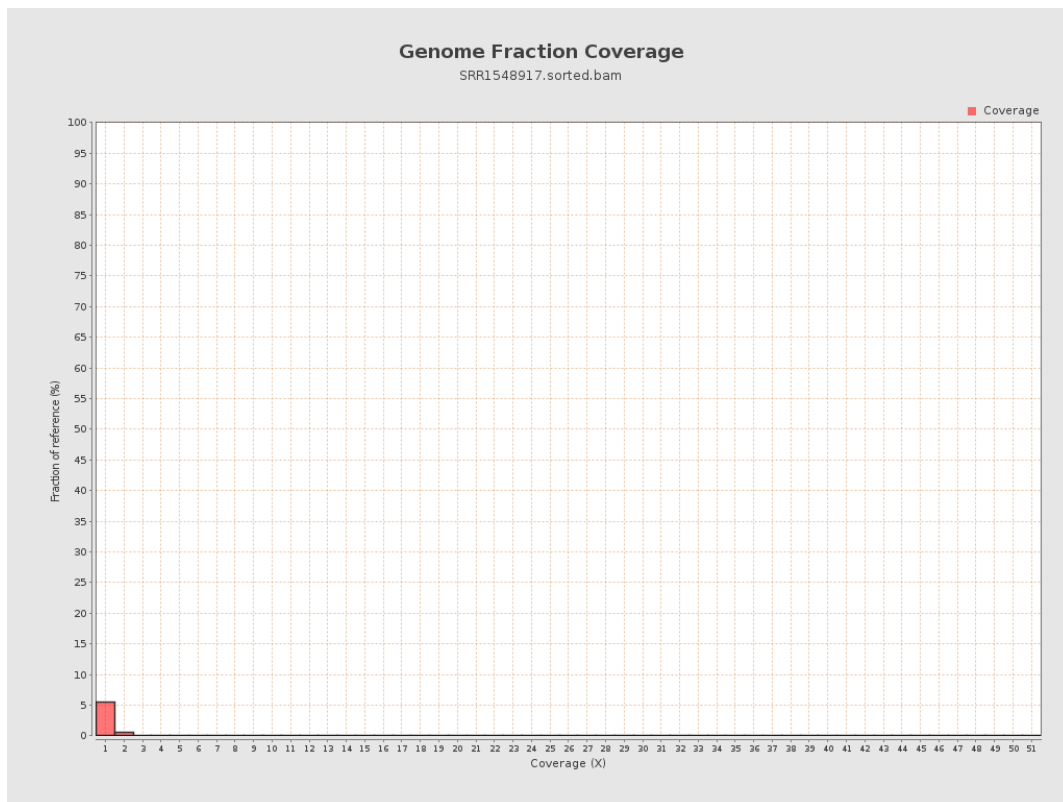
4. Results : Coverage Histogram



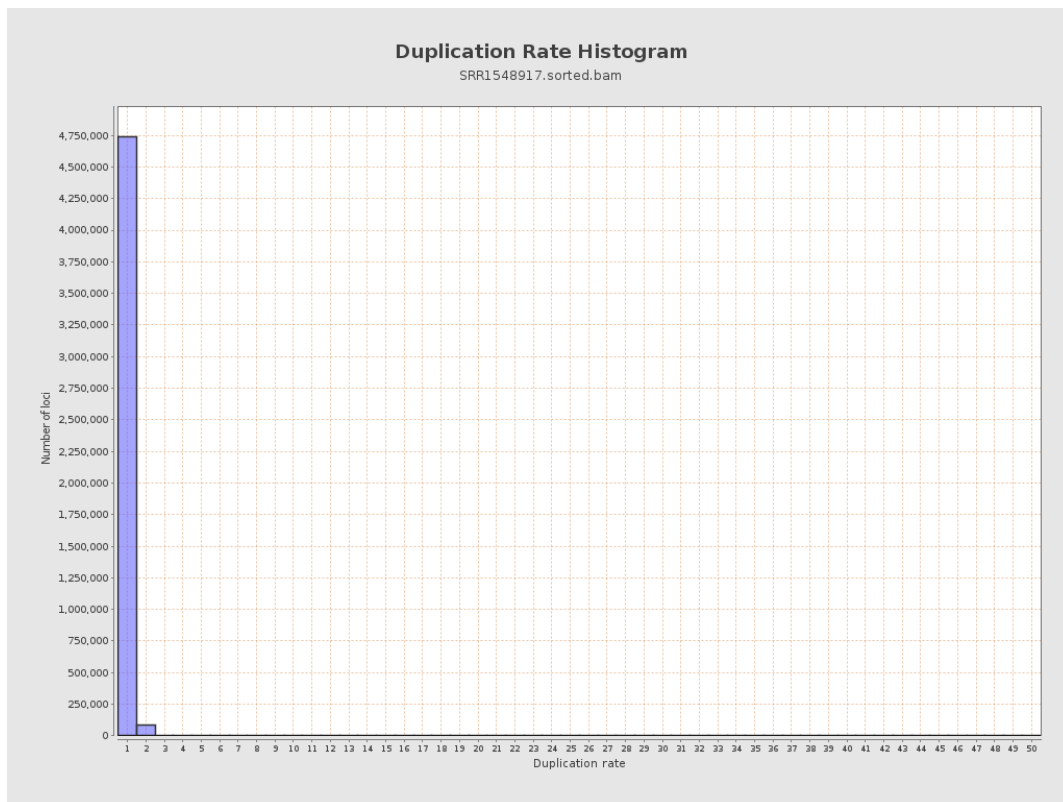
5. Results : Coverage Histogram (0-50X)



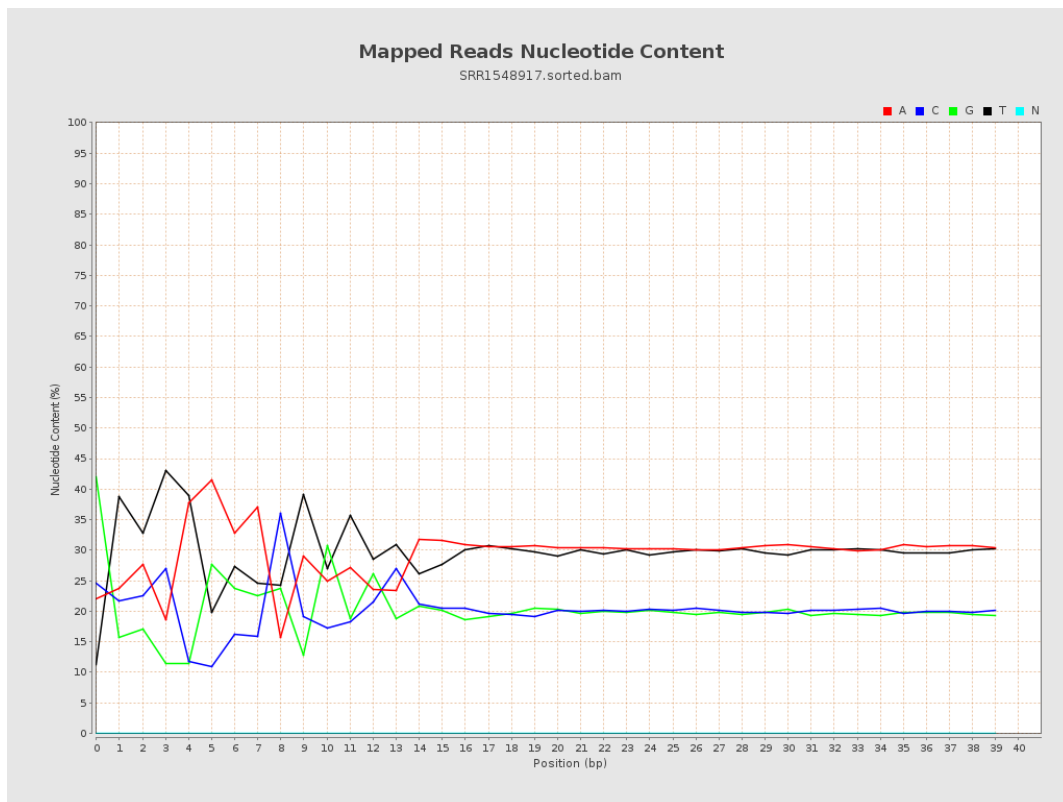
6. Results : Genome Fraction Coverage



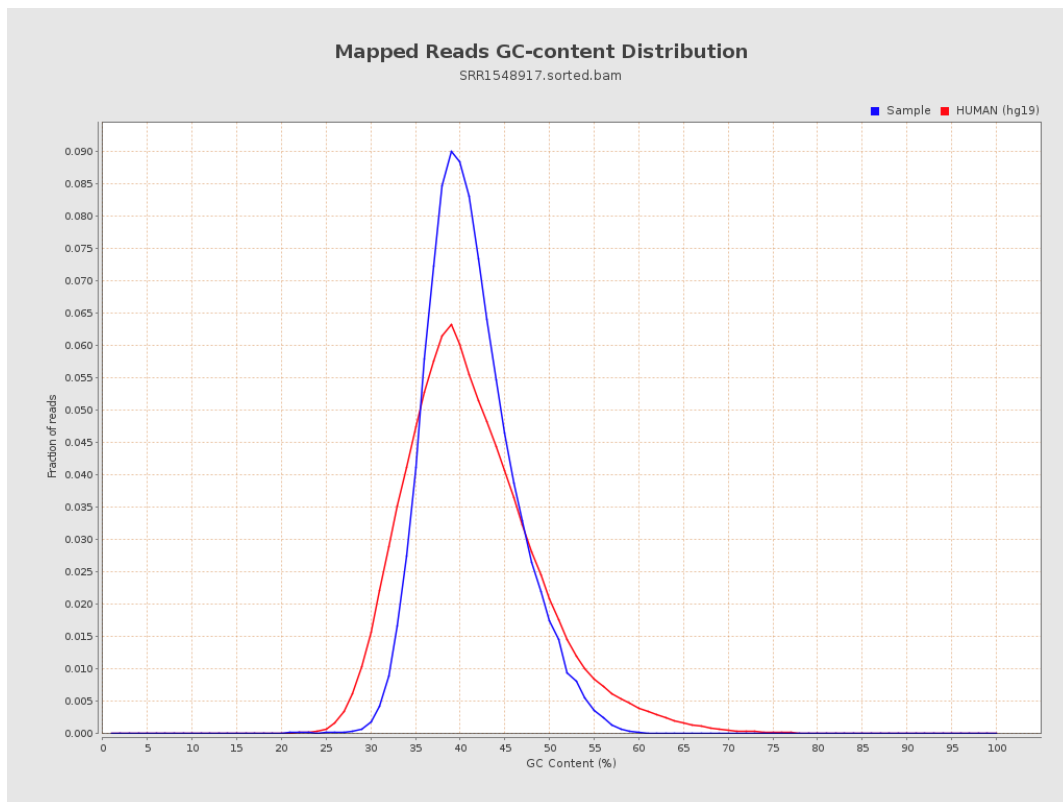
7. Results : Duplication Rate Histogram



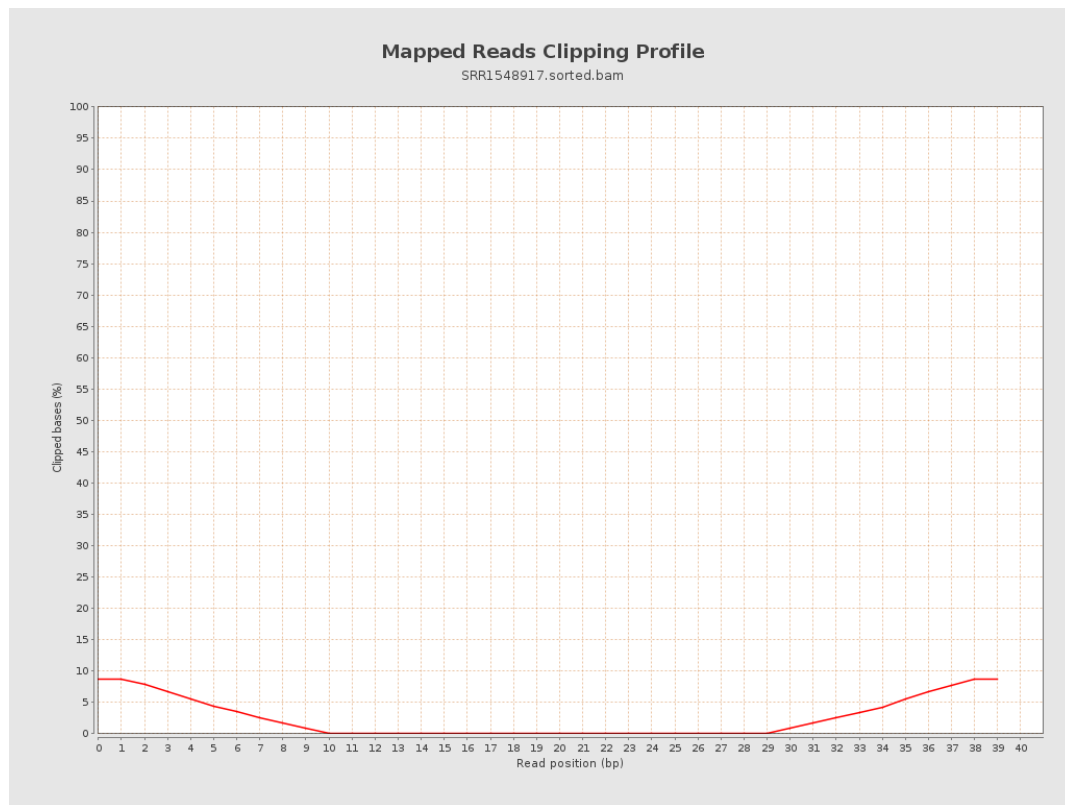
8. Results : Mapped Reads Nucleotide Content



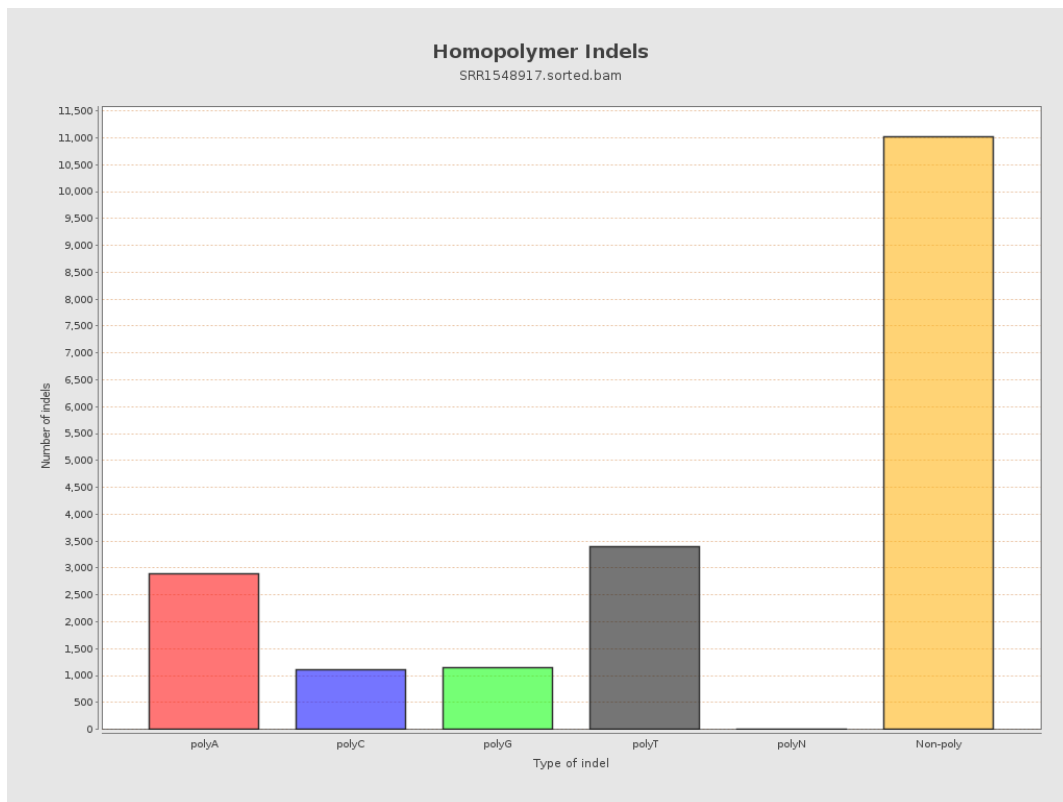
9. Results : Mapped Reads GC-content Distribution



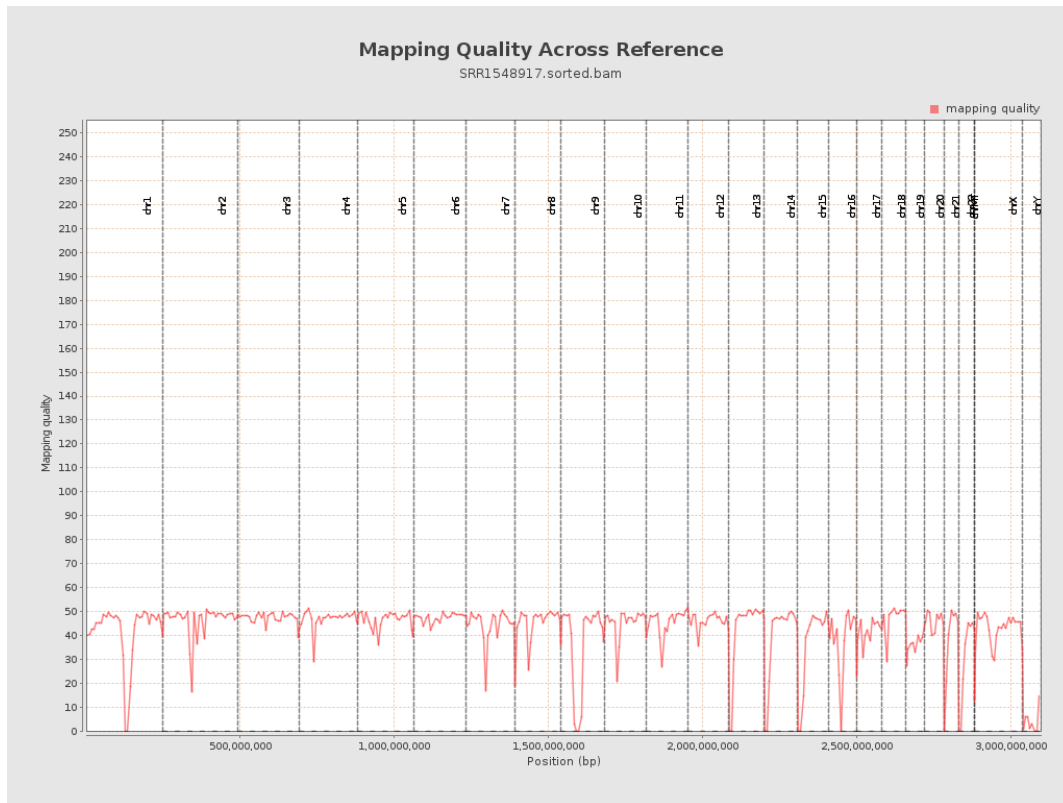
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

