

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 00:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548919.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_SRR1548919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 00:42:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,436,716
Mapped reads	6,465,474 / 86.94%
Unmapped reads	971,242 / 13.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	220,859 / 2.97%
Duplication rate	2.48%
Clipped reads	499,133 / 6.71%

2.2. ACGT Content

Number/percentage of A's	74,261,984 / 29.03%
Number/percentage of C's	53,338,300 / 20.85%
Number/percentage of T's	74,954,839 / 29.3%
Number/percentage of G's	53,288,013 / 20.83%
Number/percentage of N's	2,700 / 0%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0827
Standard Deviation	0.8906

2.4. Mapping Quality

Mean Mapping Quality	41.6
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2.5. Mismatches and indels

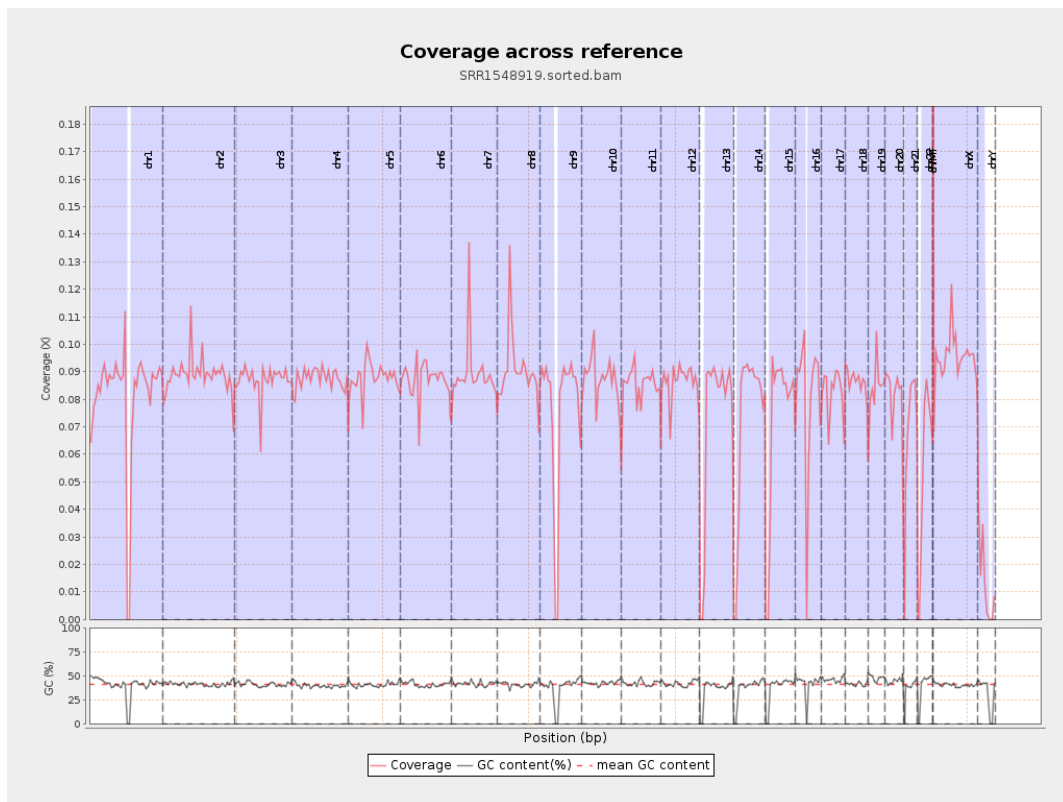
General error rate	0.27%
Mismatches	693,093
Insertions	8,372
Mapped reads with at least one insertion	0.13%
Deletions	20,962
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.24%

2.6. Chromosome stats

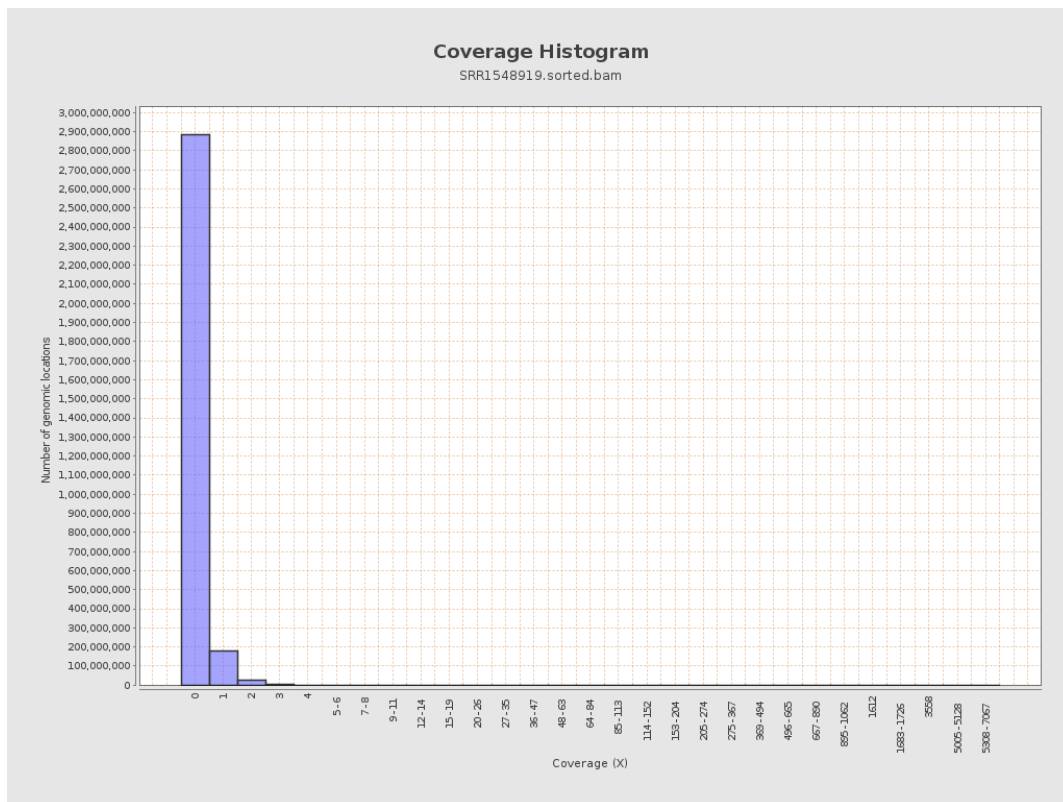
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20229456	0.0812	0.8928
chr2	243199373	21624487	0.0889	0.4752
chr3	198022430	17233128	0.087	0.345
chr4	191154276	16751577	0.0876	0.3563
chr5	180915260	15858283	0.0877	0.3494
chr6	171115067	14932195	0.0873	0.3822
chr7	159138663	14204647	0.0893	0.7269
chr8	146364022	13293412	0.0908	3.4286

chr9	141213431	10749100	0.0761	0.4457
chr10	135534747	11870238	0.0876	0.4456
chr11	135006516	11531440	0.0854	0.5161
chr12	133851895	11612637	0.0868	0.3559
chr13	115169878	8363029	0.0726	0.3113
chr14	107349540	7881293	0.0734	0.3675
chr15	102531392	7313652	0.0713	0.3097
chr16	90354753	7098335	0.0786	0.3553
chr17	81195210	6743853	0.0831	0.362
chr18	78077248	6782873	0.0869	0.8116
chr19	59128983	5016647	0.0848	0.7853
chr20	63025520	5151223	0.0817	0.3406
chr21	48129895	3250180	0.0675	0.339
chr22	51304566	2809171	0.0548	0.322
chrMT	16571	11038	0.6661	0.9974
chrX	155270560	14782149	0.0952	0.4262
chrY	59373566	779608	0.0131	0.1831

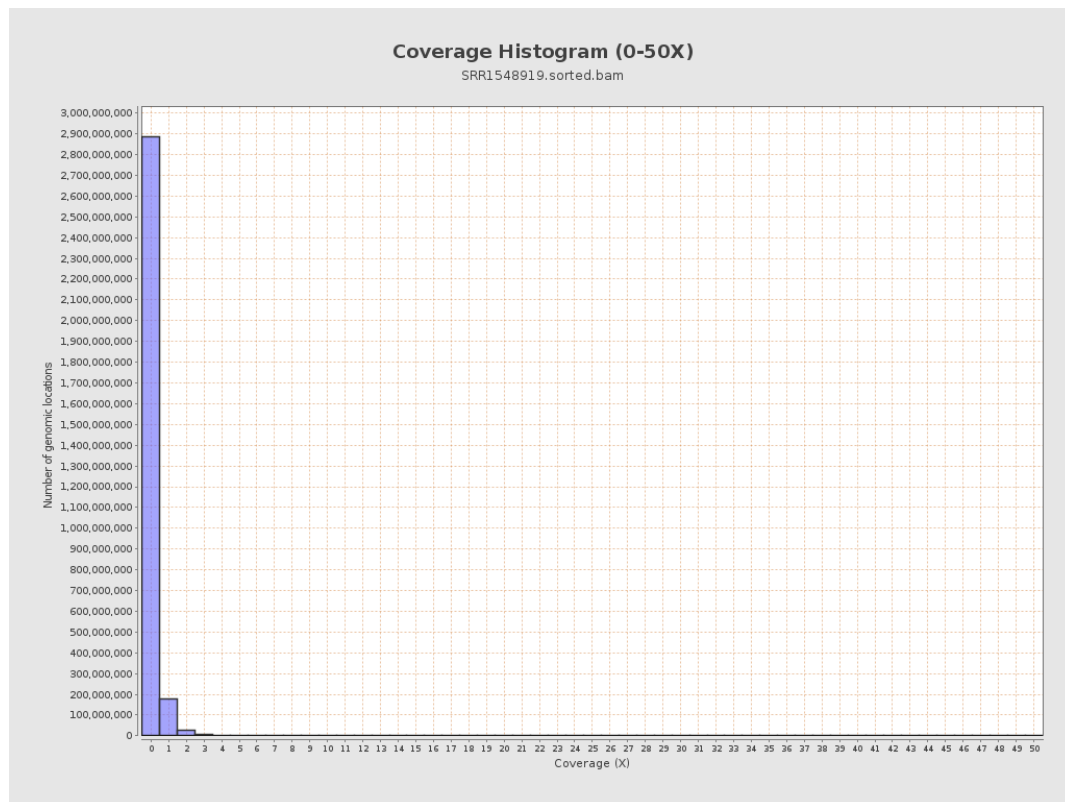
3. Results : Coverage across reference



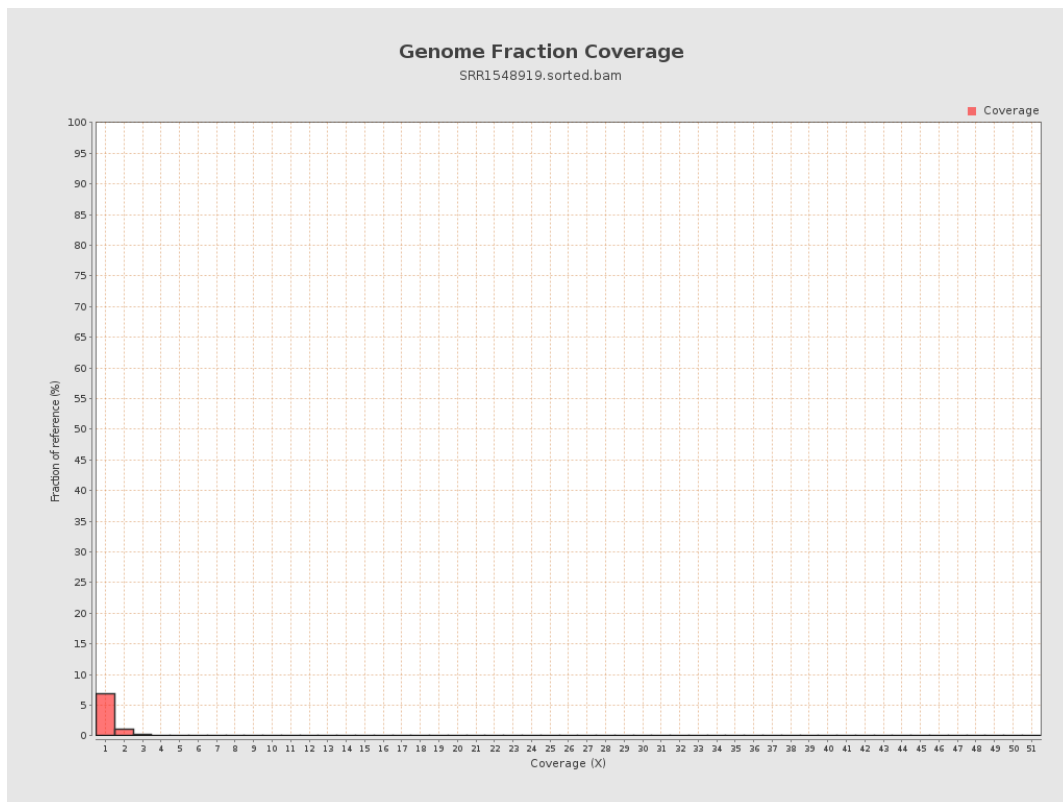
4. Results : Coverage Histogram



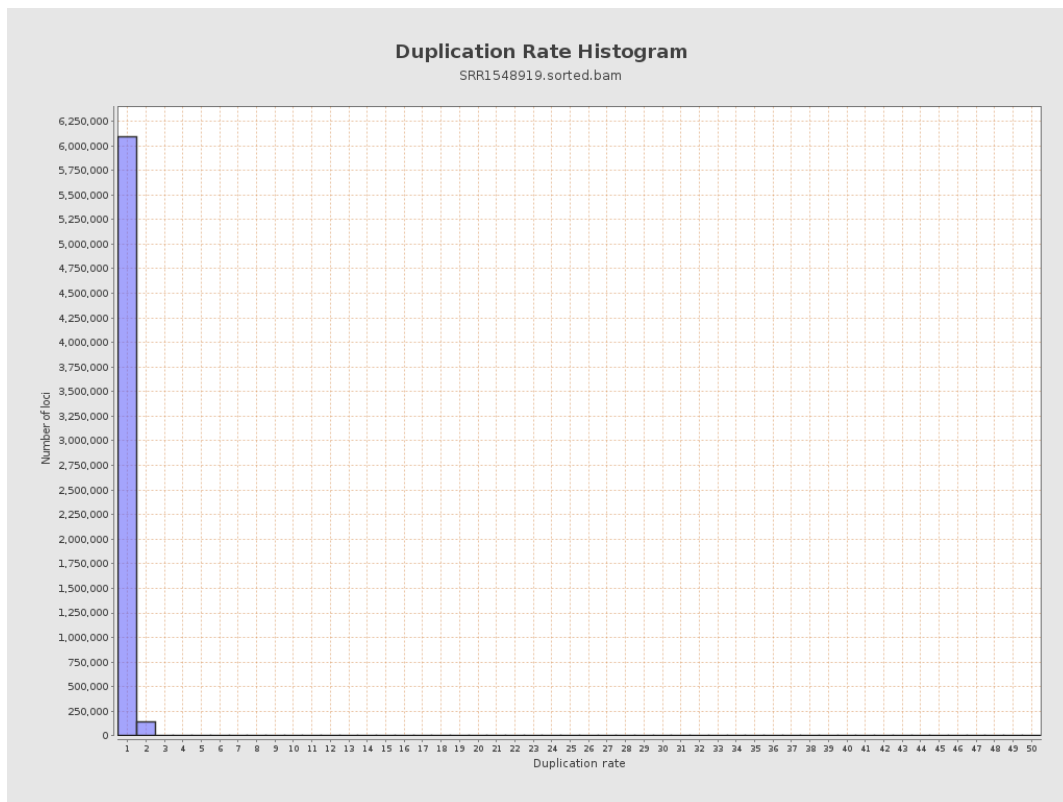
5. Results : Coverage Histogram (0-50X)



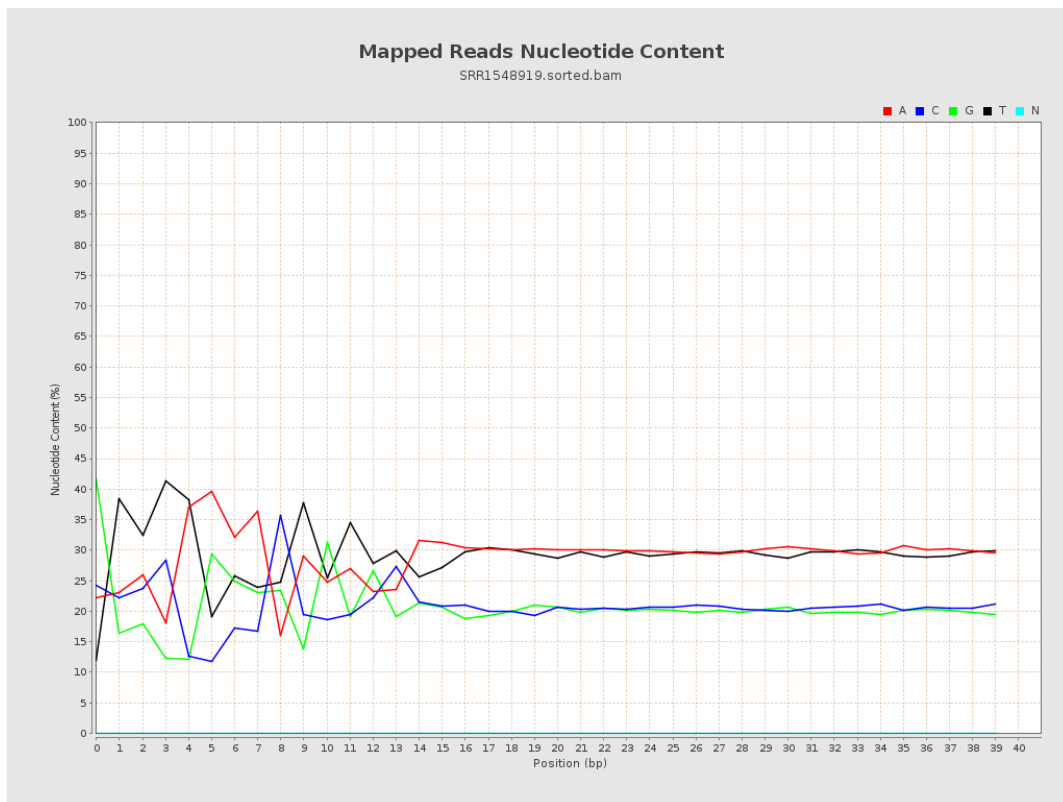
6. Results : Genome Fraction Coverage



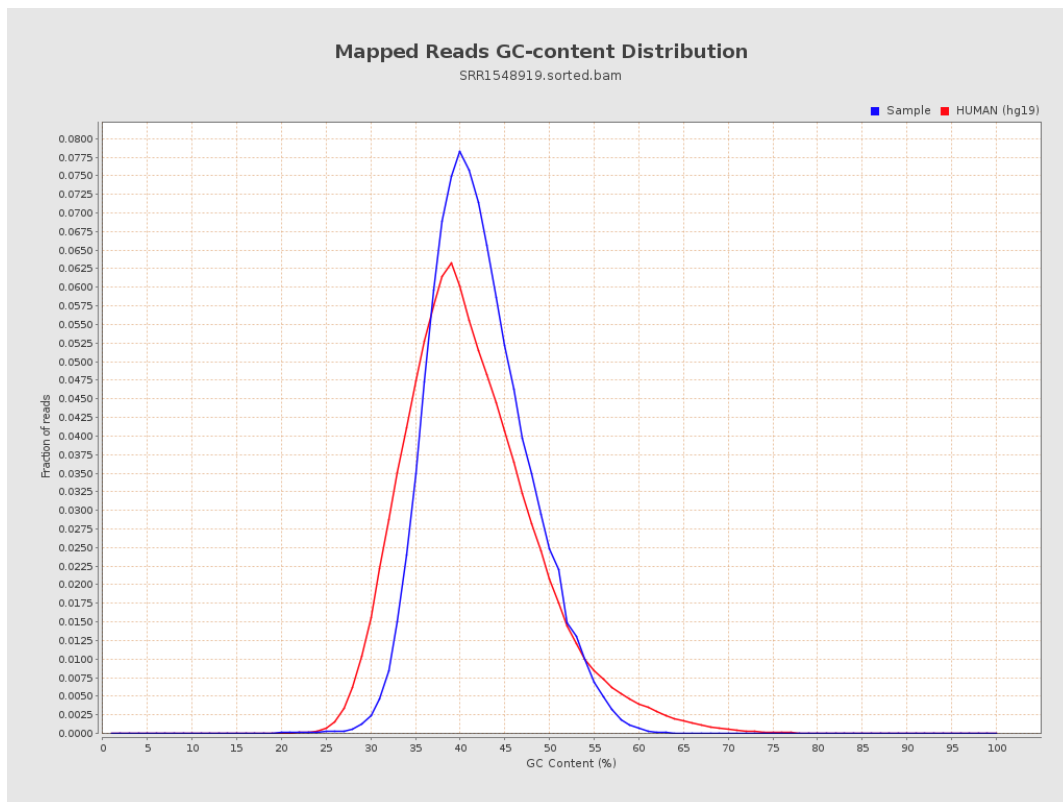
7. Results : Duplication Rate Histogram



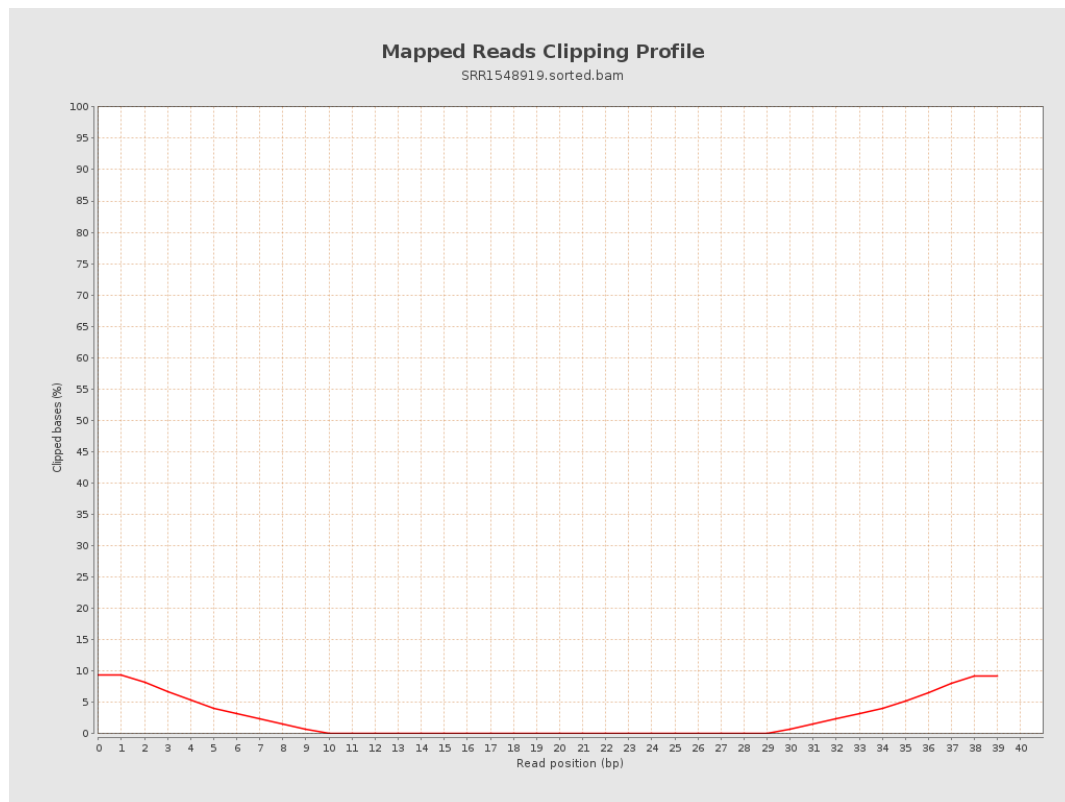
8. Results : Mapped Reads Nucleotide Content



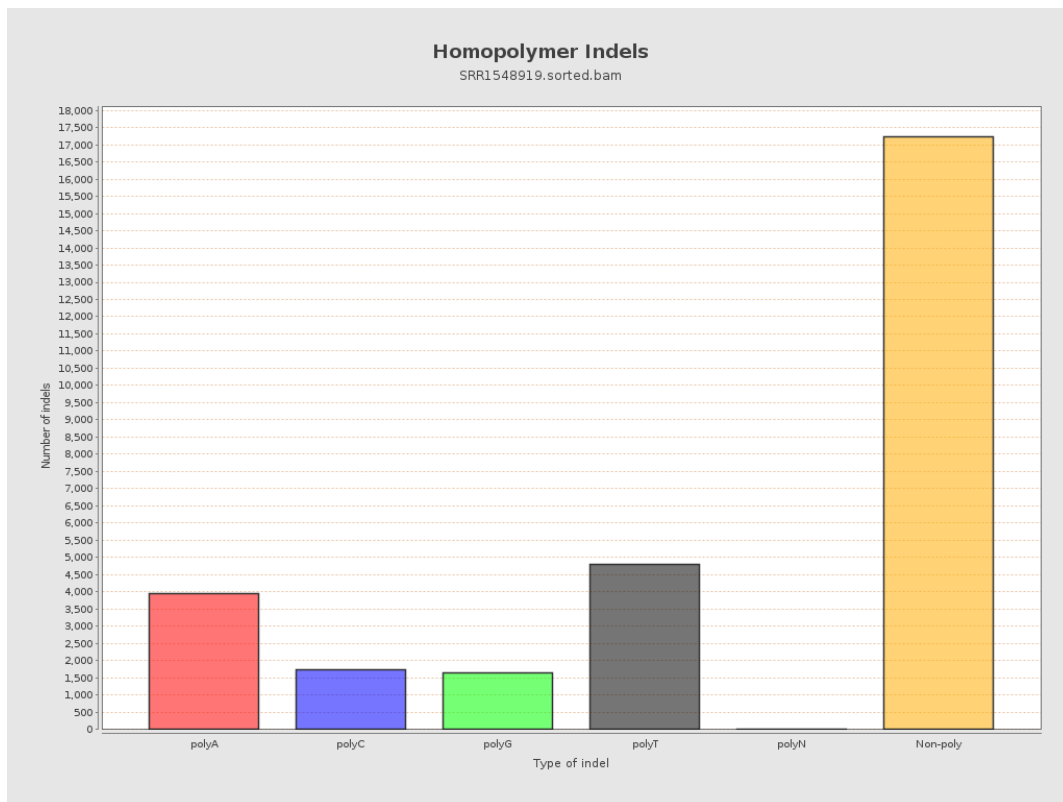
9. Results : Mapped Reads GC-content Distribution



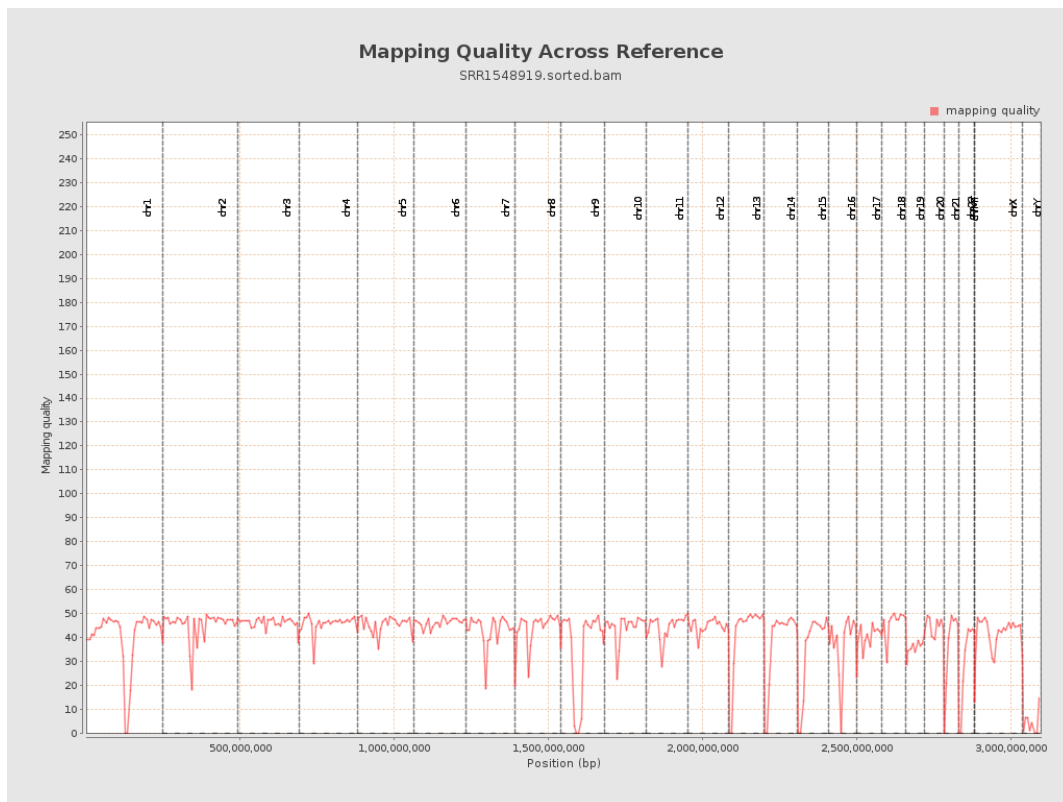
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

