Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 19:03:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620539.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR620539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 19:03:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,747,486
Mapped reads	5,945,531 / 50.61%
Unmapped reads	5,801,955 / 49.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	176 / 0%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	622,242 / 5.3%
Duplication rate	5.65%
Clipped reads	2,382,095 / 20.28%

2.2. ACGT Content

Number/percentage of A's	67,150,358 / 25.78%
Number/percentage of C's	47,201,485 / 18.12%
Number/percentage of T's	80,464,563 / 30.89%
Number/percentage of G's	65,668,555 / 25.21%
Number/percentage of N's	3,321 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0842

Standard Deviation	0.9681

2.4. Mapping Quality

Mean Mapping Quality	40.6

2.5. Mismatches and indels

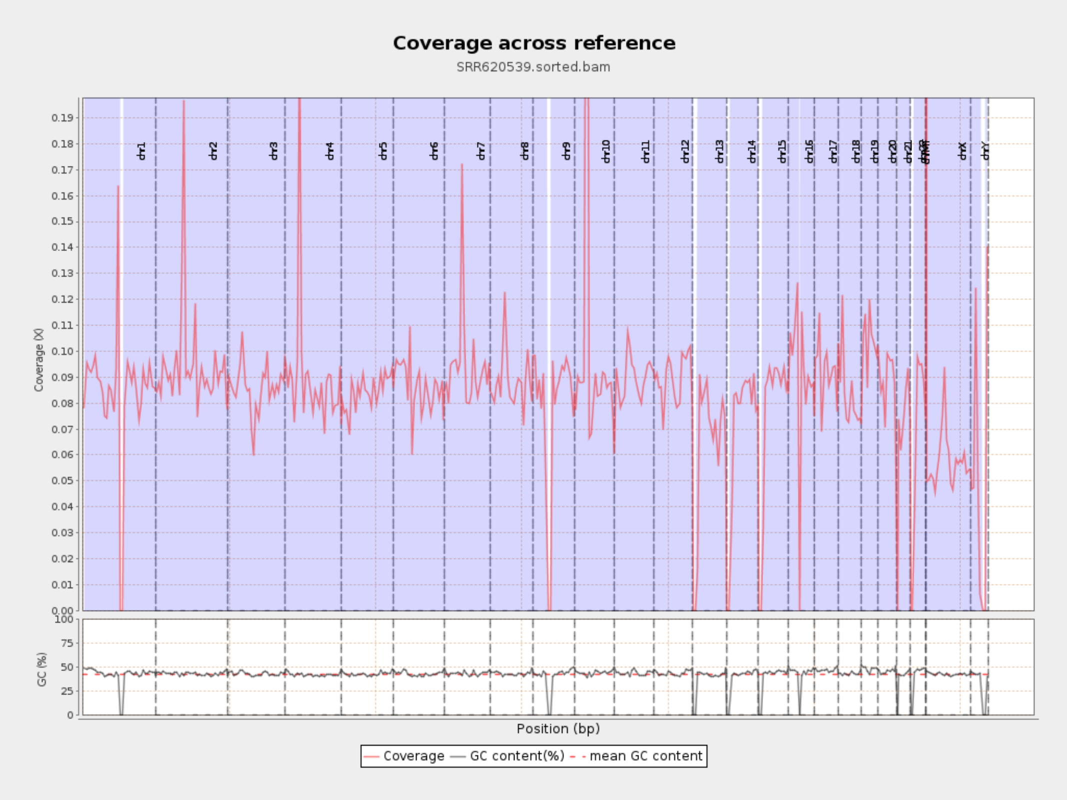
General error rate	0.78%
Mismatches	1,998,045
Insertions	21,850
Mapped reads with at least one insertion	0.37%
Deletions	53,472
Mapped reads with at least one deletion	0.87%
Homopolymer indels	39.71%

2.6. Chromosome stats

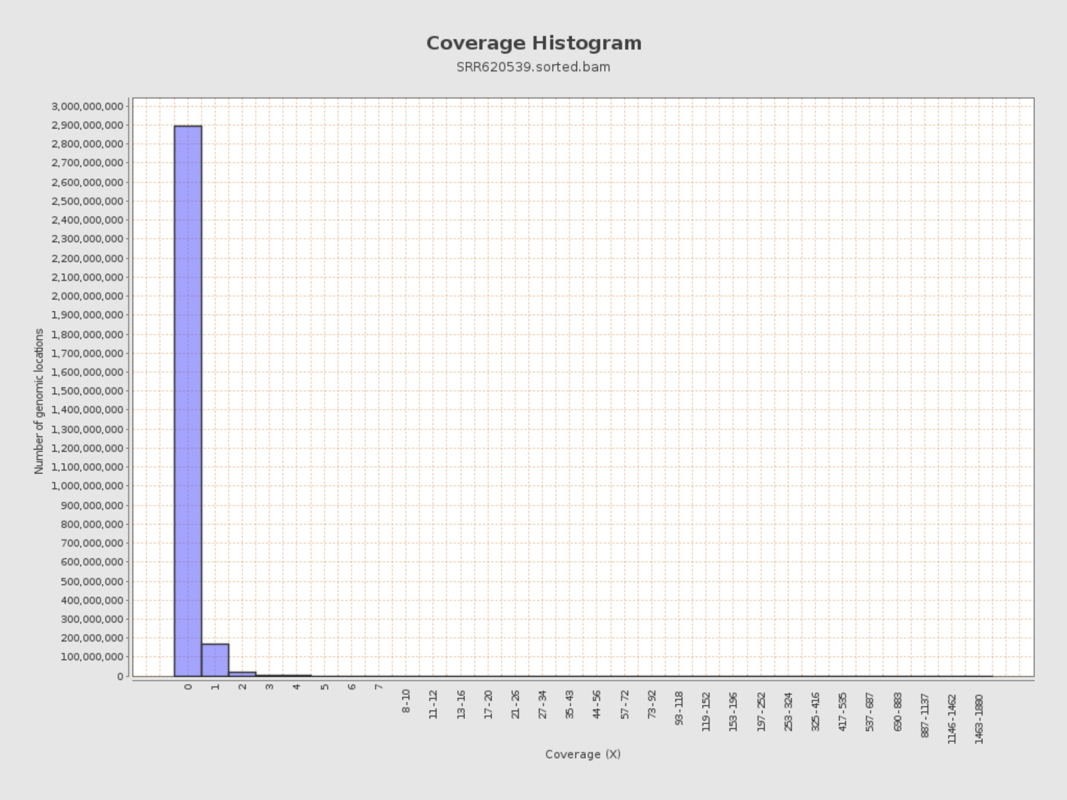
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20967795	0.0841	1.4928
chr2	243199373	23105539	0.095	0.9928
chr3	198022430	16953160	0.0856	0.8347
chr4	191154276	17389704	0.091	0.7538
chr5	180915260	15276898	0.0844	0.4367
chr6	171115067	14793539	0.0865	0.6126
chr7	159138663	15091458	0.0948	1.14

chr8	146364022	12911843	0.0882	0.7288
chr9	141213431	10920888	0.0773	0.6898
chr10	135534747	13877753	0.1024	2.2429
chr11	135006516	12073332	0.0894	0.8978
chr12	133851895	12061042	0.0901	0.4802
chr13	115169878	7318227	0.0635	0.4058
chr14	107349540	7552898	0.0704	0.4723
chr15	102531392	7468910	0.0728	0.3932
chr16	90354753	8108916	0.0897	0.6443
chr17	81195210	7556915	0.0931	0.5985
chr18	78077248	6570185	0.0841	1.8126
chr19	59128983	6108556	0.1033	1.0591
chr20	63025520	5568624	0.0884	0.5994
chr21	48129895	3382783	0.0703	0.5763
chr22	51304566	3320929	0.0647	0.4127
chrMT	16571	93217	5.6253	5.2837
chrX	155270560	8972547	0.0578	0.6032
chrY	59373566	3118891	0.0525	0.7613

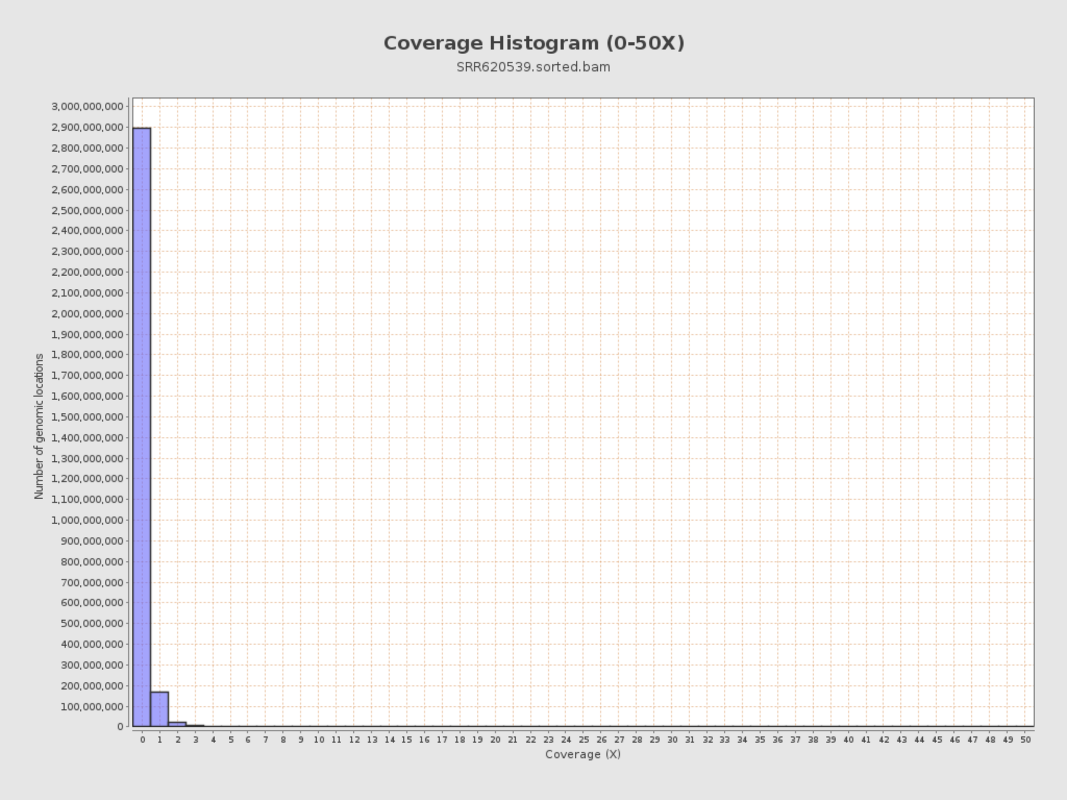
3. Results : Coverage across reference



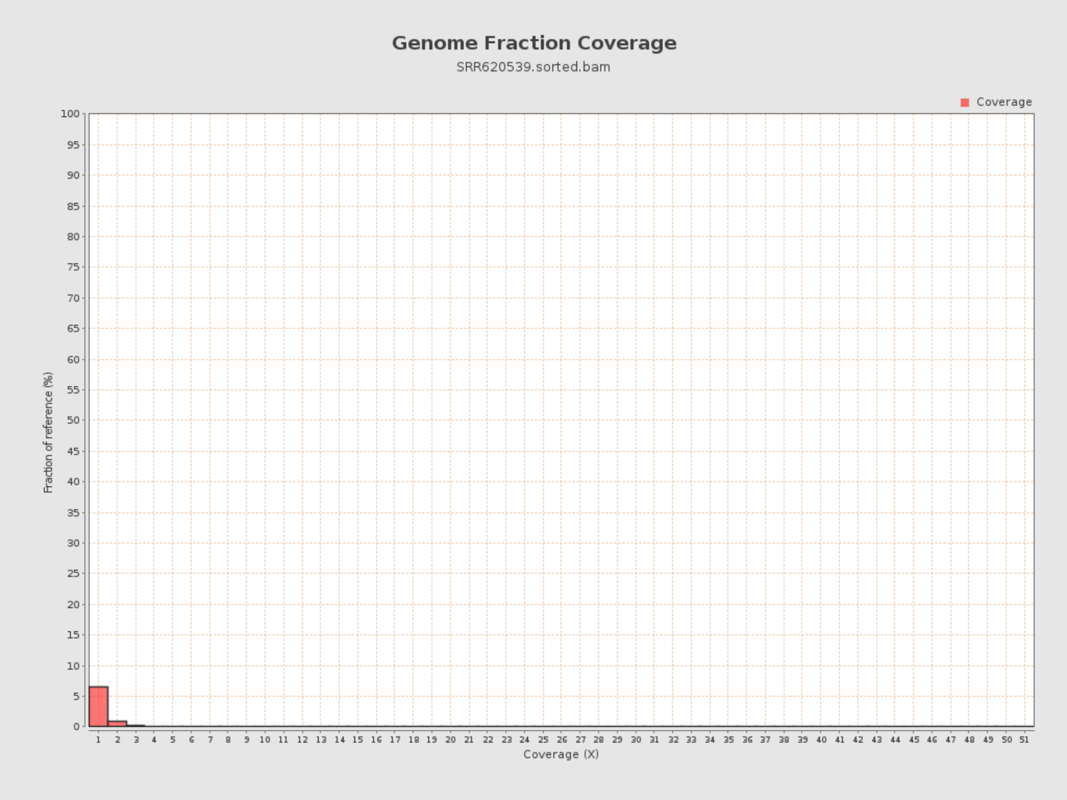
4. Results : Coverage Histogram



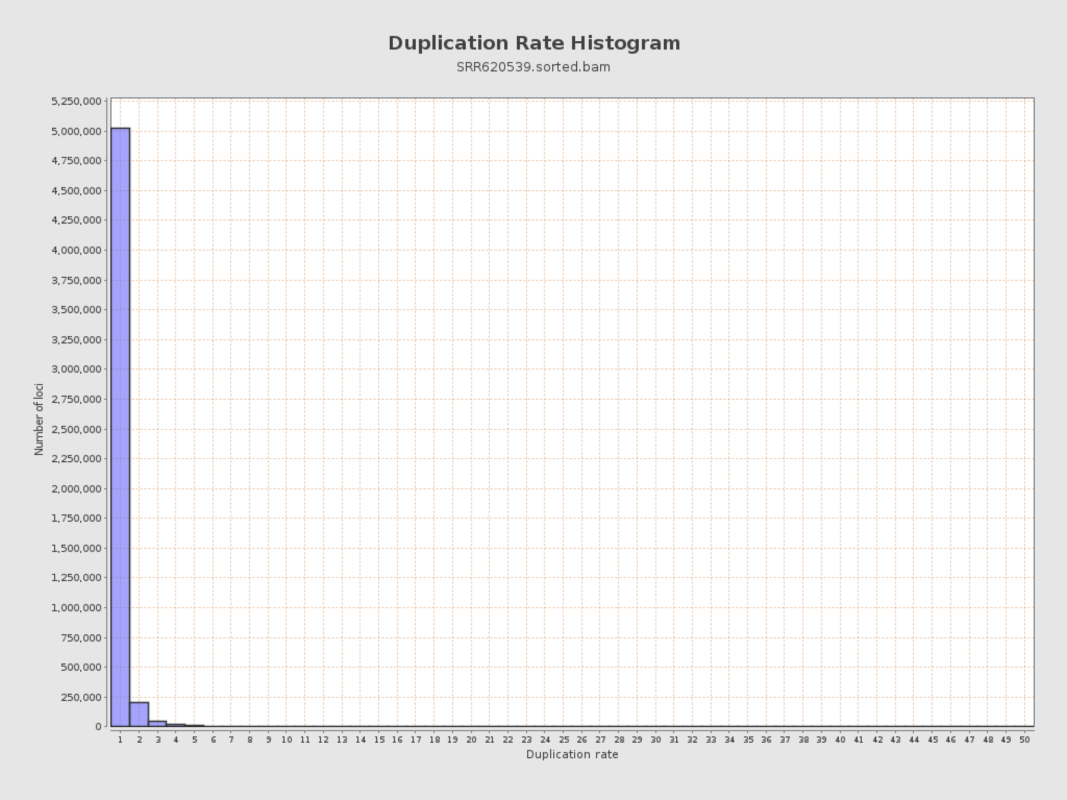
5. Results : Coverage Histogram (0-50X)



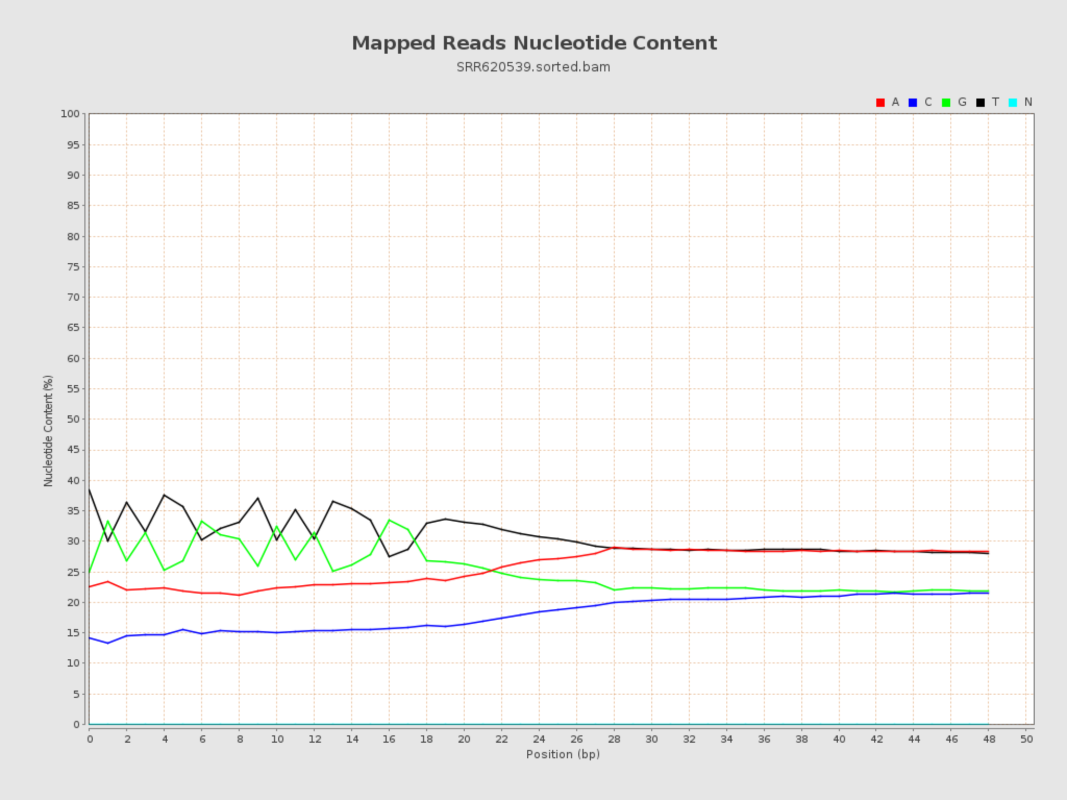
6. Results : Genome Fraction Coverage



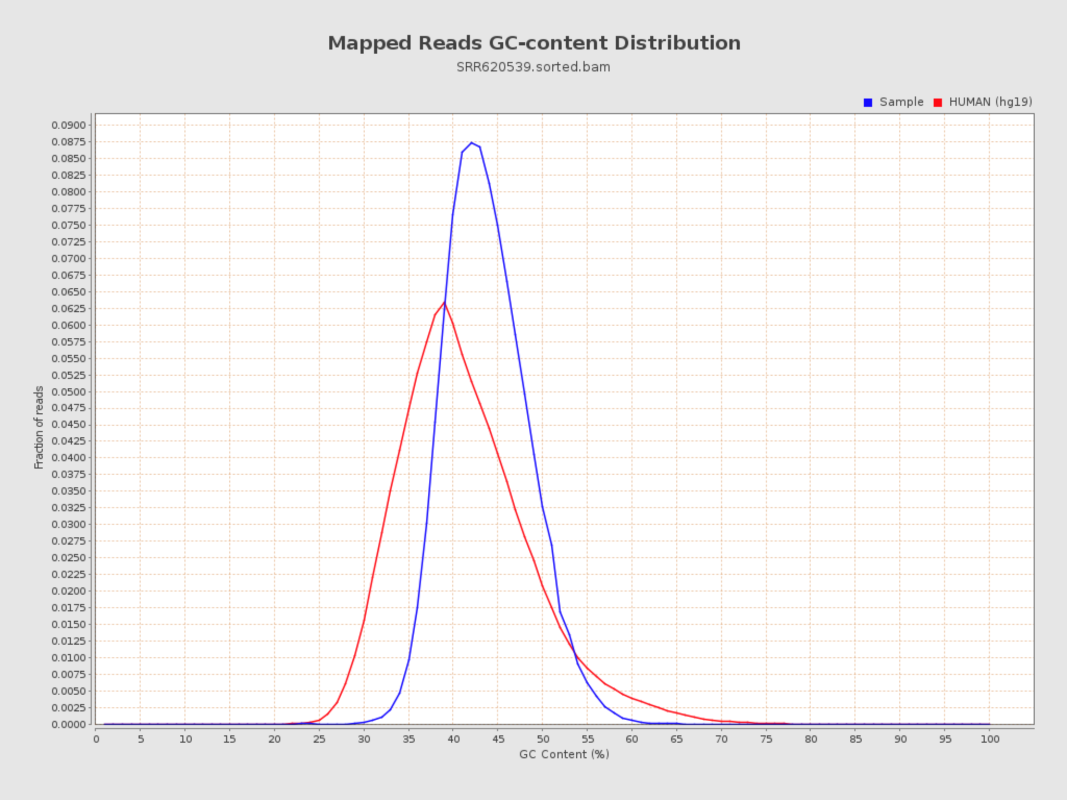
7. Results : Duplication Rate Histogram



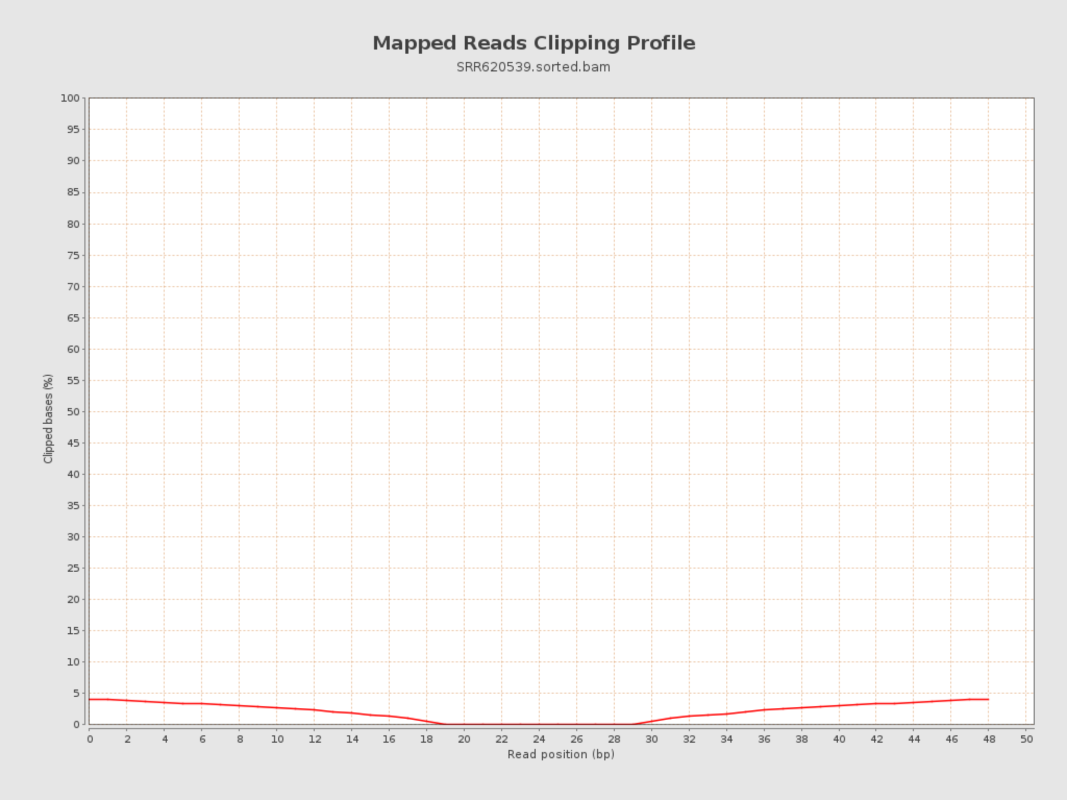
8. Results : Mapped Reads Nucleotide Content



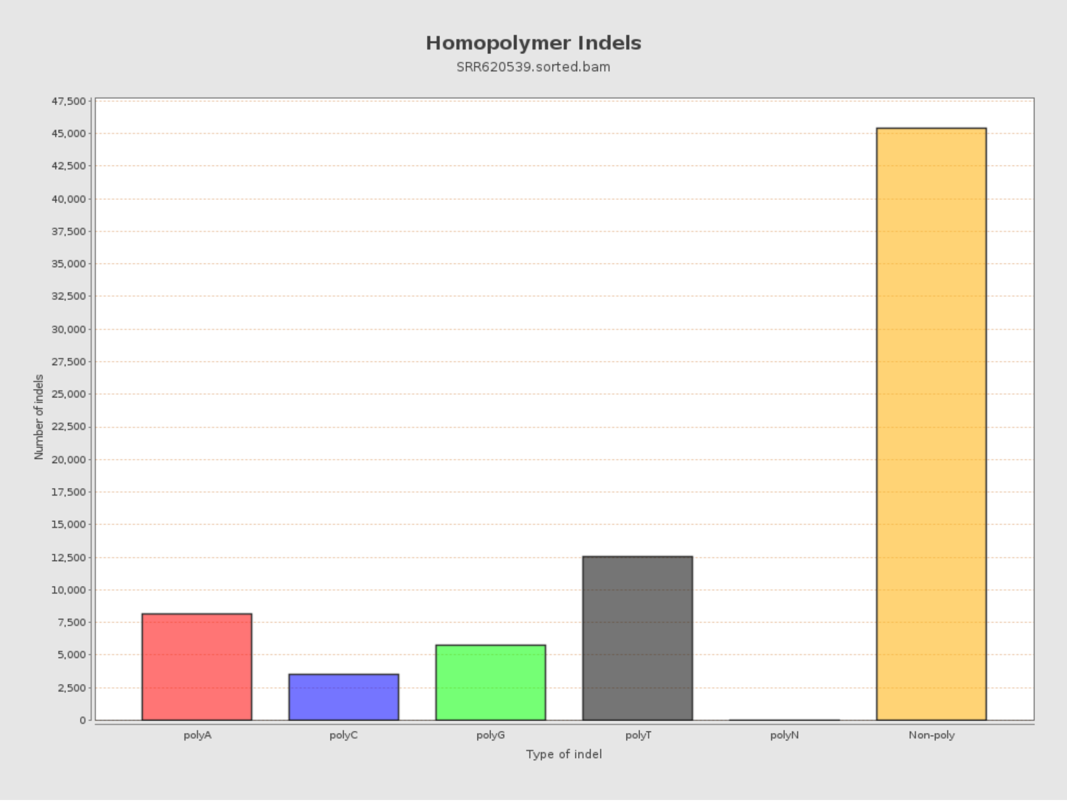
9. Results : Mapped Reads GC-content Distribution



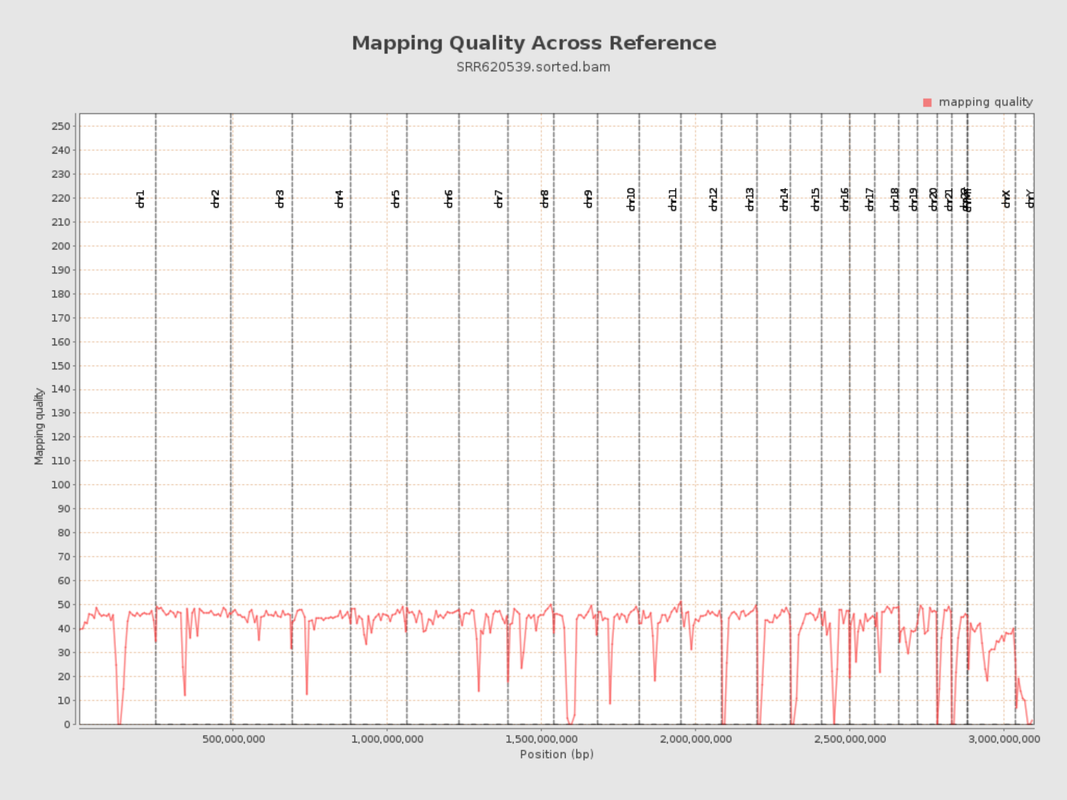
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram