

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:32:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124785.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_SRR3124785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:32:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	181,669
Mapped reads	175,614 / 96.67%
Unmapped reads	6,055 / 3.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,177 / 3.95%
Read min/max/mean length	30 / 151 / 152.83
Duplicated reads (estimated)	54,826 / 30.18%
Duplication rate	1.16%
Clipped reads	133,218 / 73.33%

2.2. ACGT Content

Number/percentage of A's	6,905,263 / 29.41%
Number/percentage of C's	4,474,224 / 19.05%
Number/percentage of T's	6,509,946 / 27.72%
Number/percentage of G's	5,591,655 / 23.81%
Number/percentage of N's	0 / 0%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0076

Standard Deviation	7.1124
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2.4. Mapping Quality

Mean Mapping Quality	50.85
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2.5. Mismatches and indels

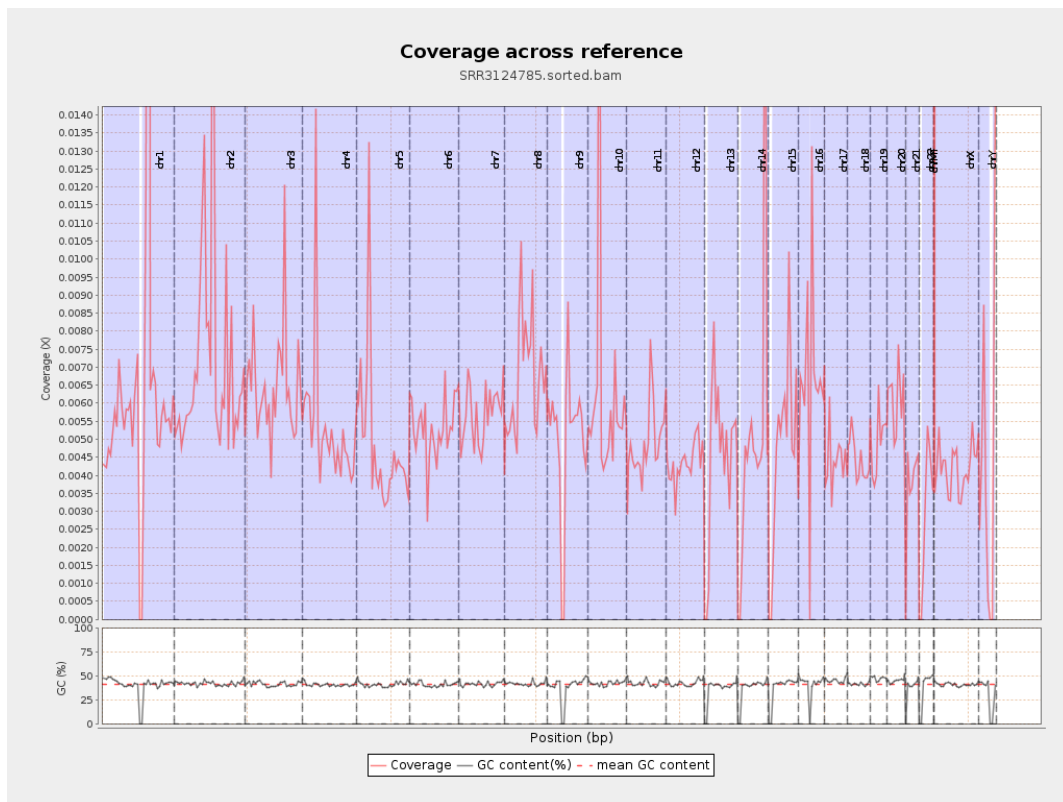
General error rate	1.31%
Mismatches	295,164
Insertions	3,826
Mapped reads with at least one insertion	2%
Deletions	8,921
Mapped reads with at least one deletion	4.9%
Homopolymer indels	46.57%

2.6. Chromosome stats

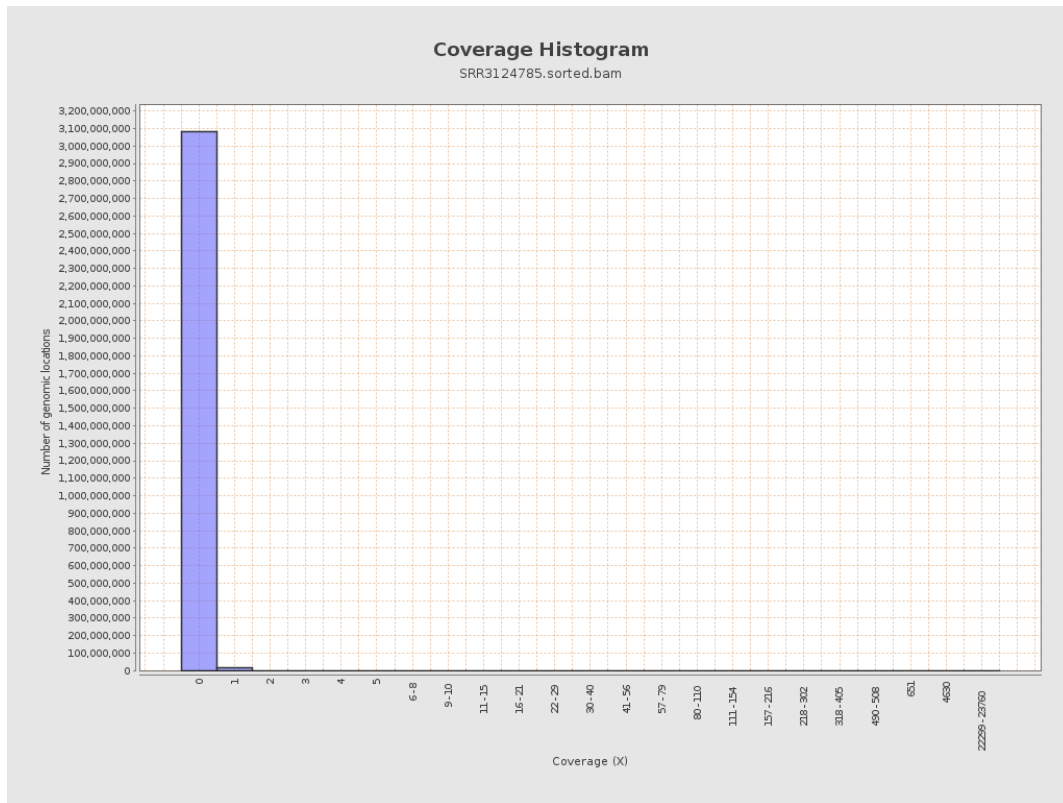
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8068223	0.0324	25.0524
chr2	243199373	1748604	0.0072	0.3776
chr3	198022430	1287263	0.0065	0.2542
chr4	191154276	1010949	0.0053	0.0881
chr5	180915260	869584	0.0048	0.242
chr6	171115067	907838	0.0053	0.124
chr7	159138663	908382	0.0057	0.0837

chr8	146364022	990433	0.0068	0.1857
chr9	141213431	714592	0.0051	0.1529
chr10	135534747	870081	0.0064	0.196
chr11	135006516	655682	0.0049	0.0914
chr12	133851895	580280	0.0043	0.0759
chr13	115169878	513158	0.0045	0.1753
chr14	107349540	558975	0.0052	0.8068
chr15	102531392	486262	0.0047	0.2474
chr16	90354753	591943	0.0066	0.1144
chr17	81195210	354622	0.0044	0.0842
chr18	78077248	343569	0.0044	0.0882
chr19	59128983	288541	0.0049	0.1137
chr20	63025520	381666	0.0061	0.0875
chr21	48129895	180836	0.0038	0.0712
chr22	51304566	151798	0.003	0.0581
chrMT	16571	124805	7.5315	5.0399
chrX	155270560	654659	0.0042	0.067
chrY	59373566	255460	0.0043	0.1374

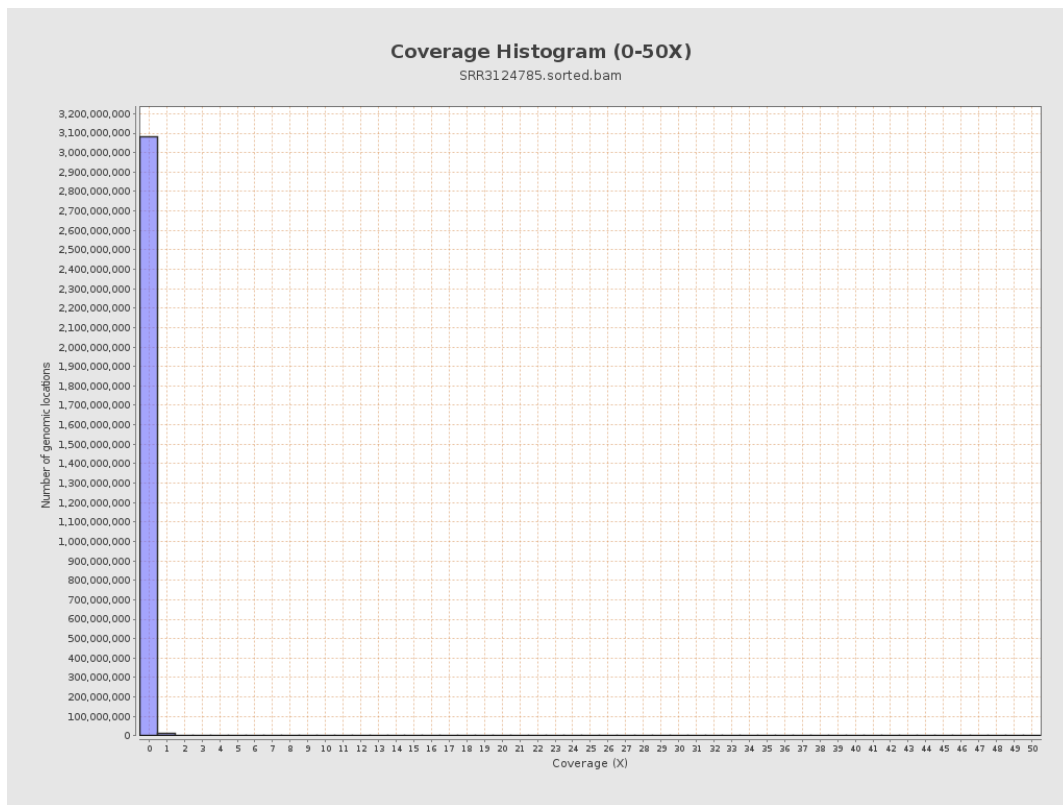
3. Results : Coverage across reference



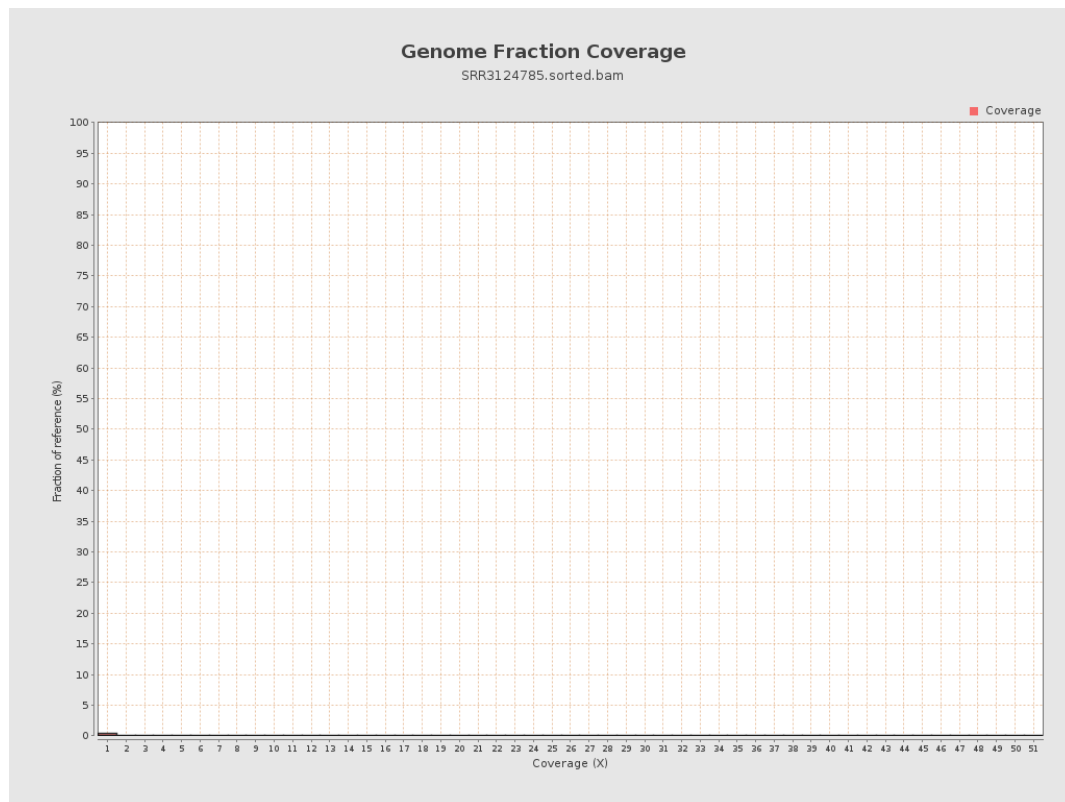
4. Results : Coverage Histogram



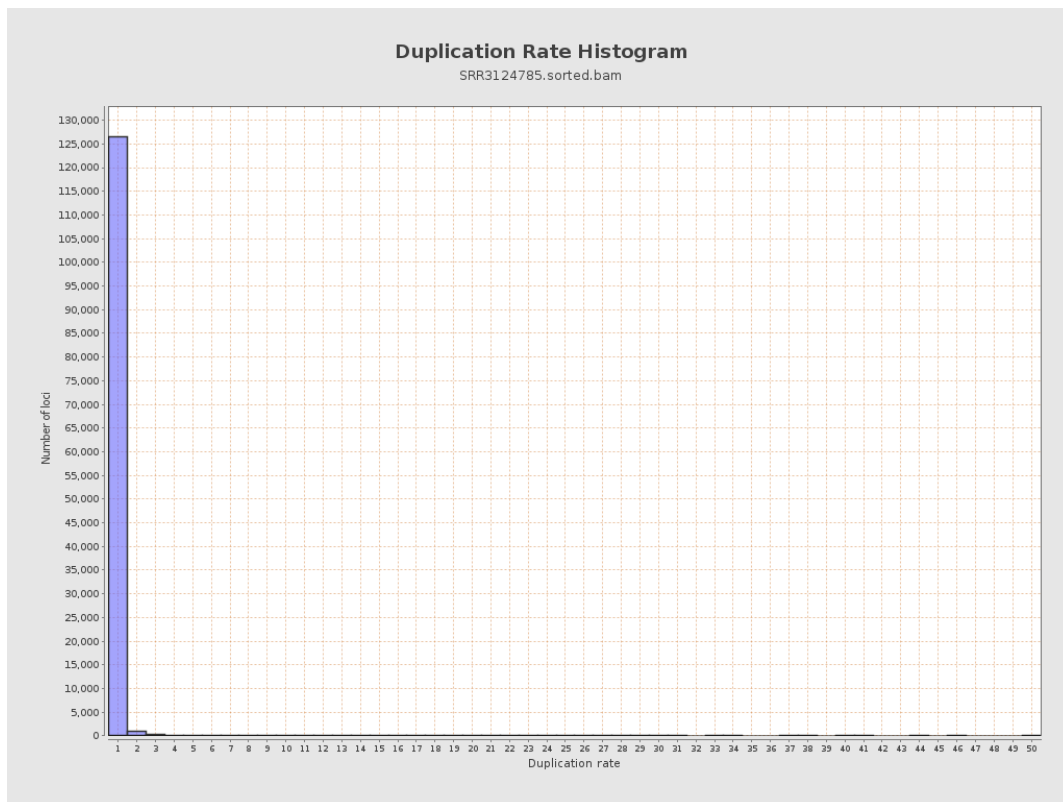
5. Results : Coverage Histogram (0-50X)



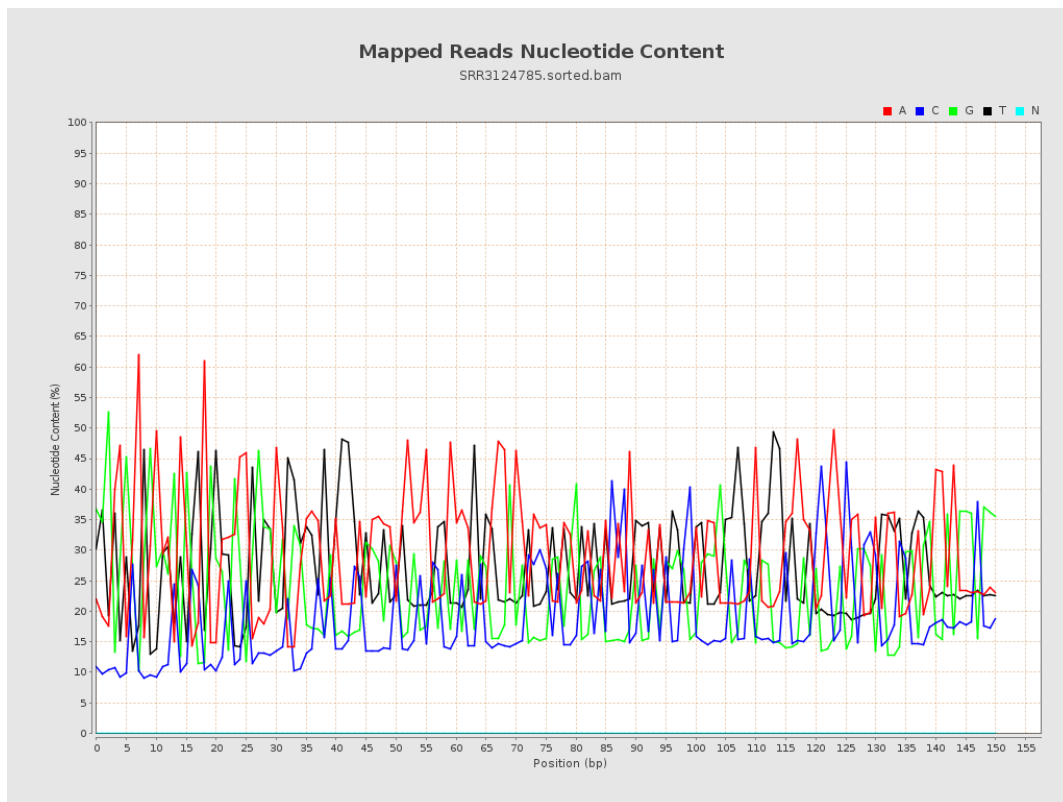
6. Results : Genome Fraction Coverage



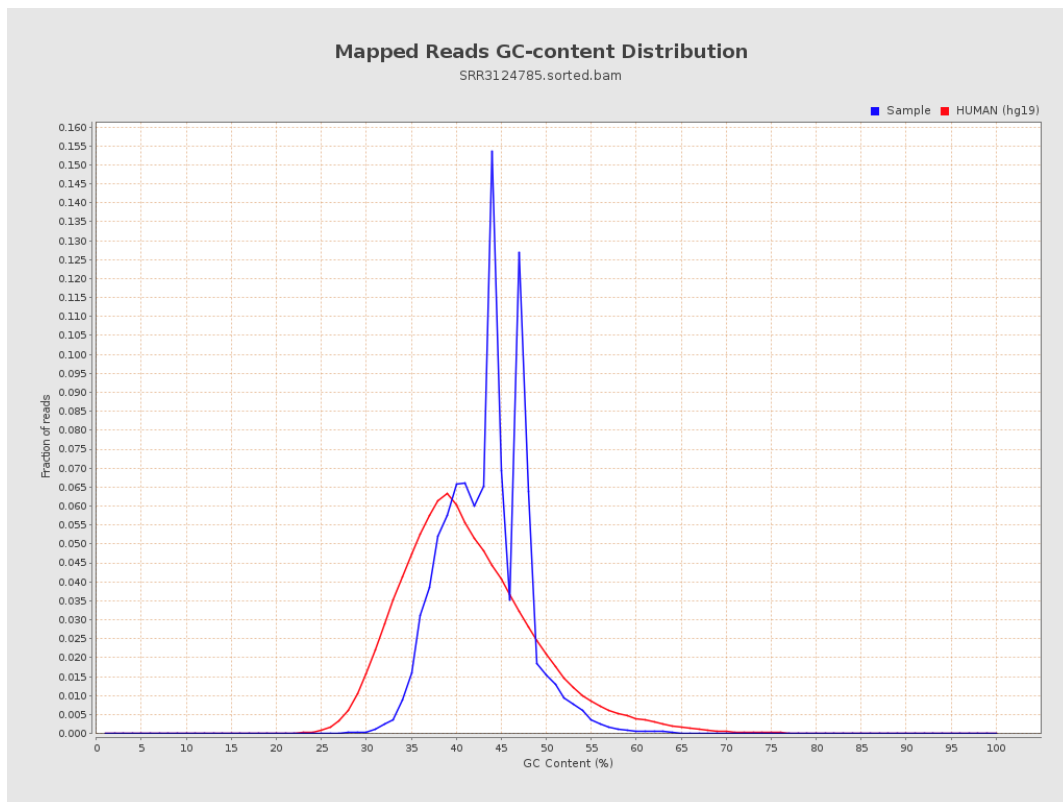
7. Results : Duplication Rate Histogram



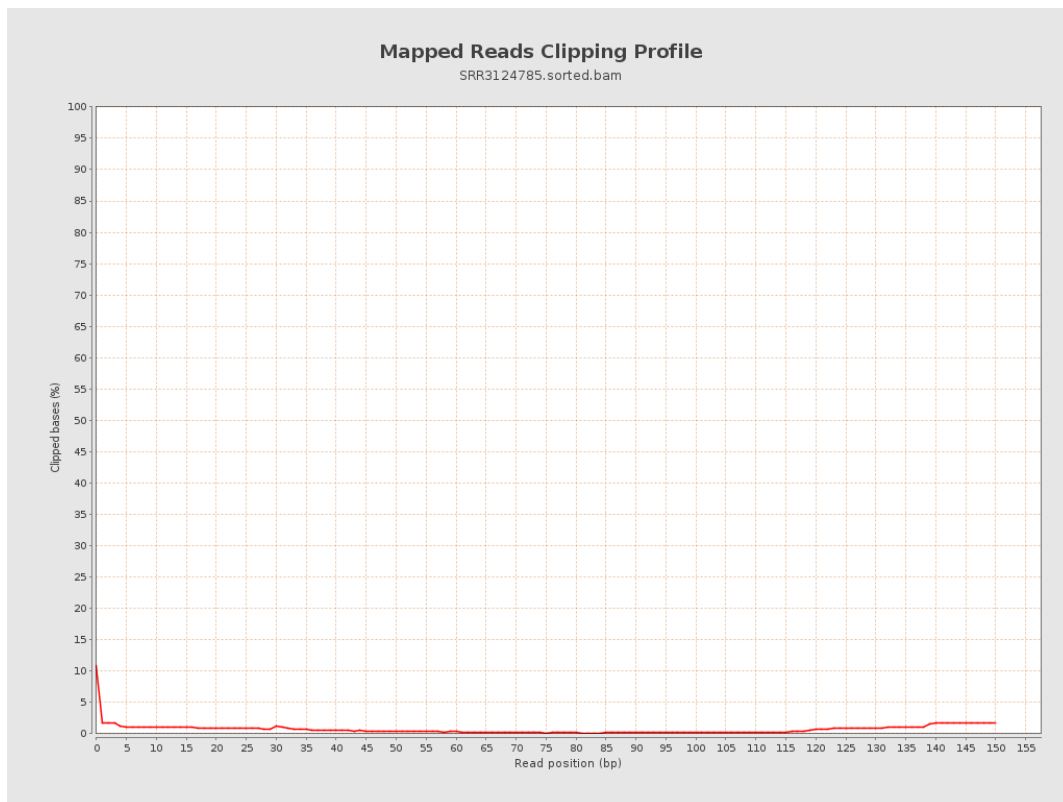
8. Results : Mapped Reads Nucleotide Content



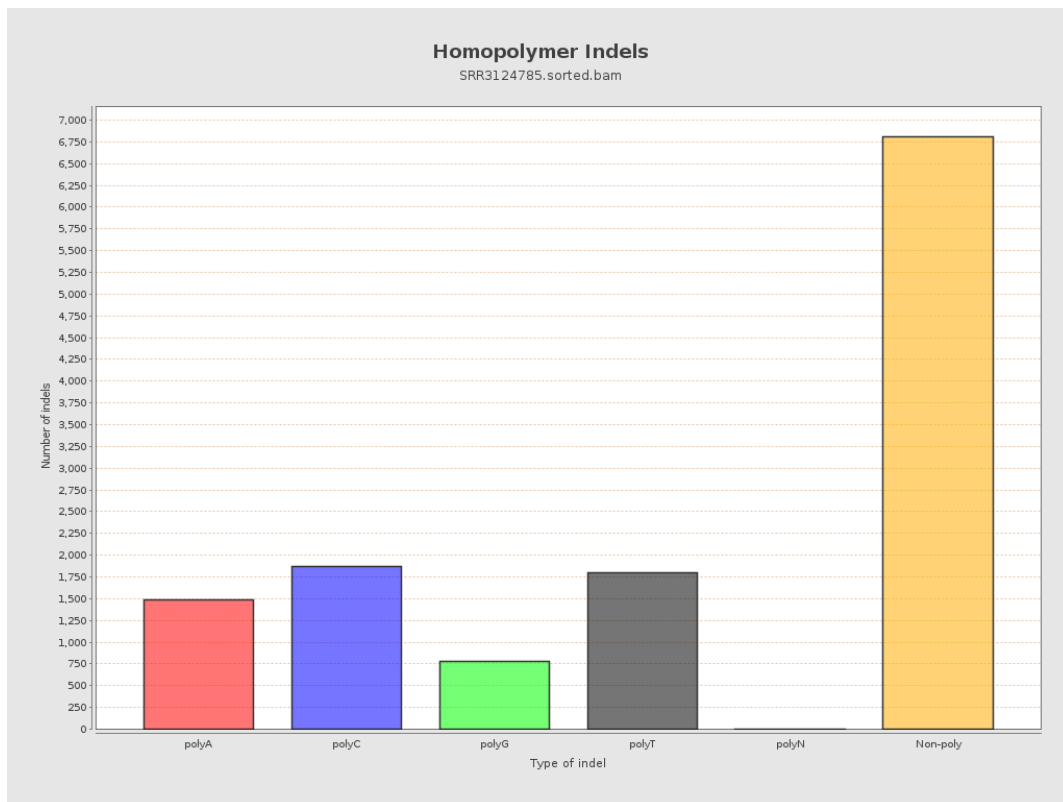
9. Results : Mapped Reads GC-content Distribution



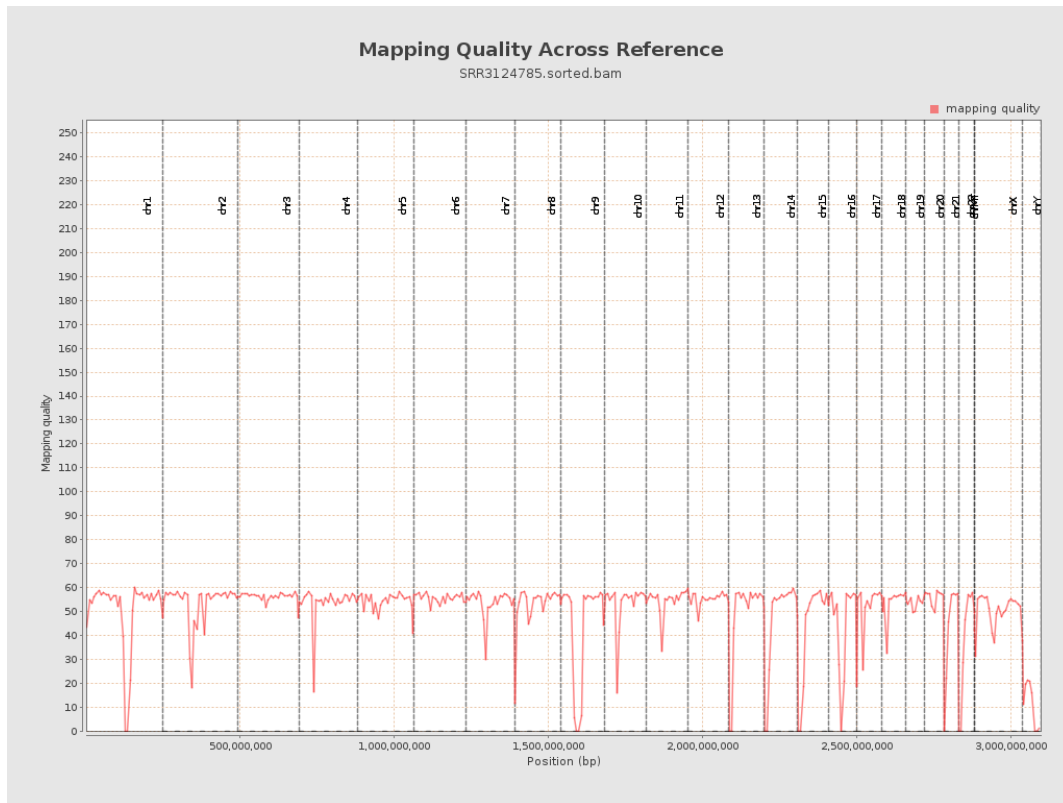
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

