Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:33:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068187.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_SRR6068187 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:33:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,624,252
Mapped reads	1,479,852 / 91.11%
Unmapped reads	144,400 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,794 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	56,765 / 3.49%
Duplication rate	2.81%
Clipped reads	551,296 / 33.94%

2.2. ACGT Content

Number/percentage of A's	29,750,714 / 29.33%
Number/percentage of C's	18,819,280 / 18.55%
Number/percentage of T's	31,659,065 / 31.21%
Number/percentage of G's	21,084,010 / 20.79%
Number/percentage of N's	116,097 / 0.11%
GC Percentage	39.34%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.3802

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

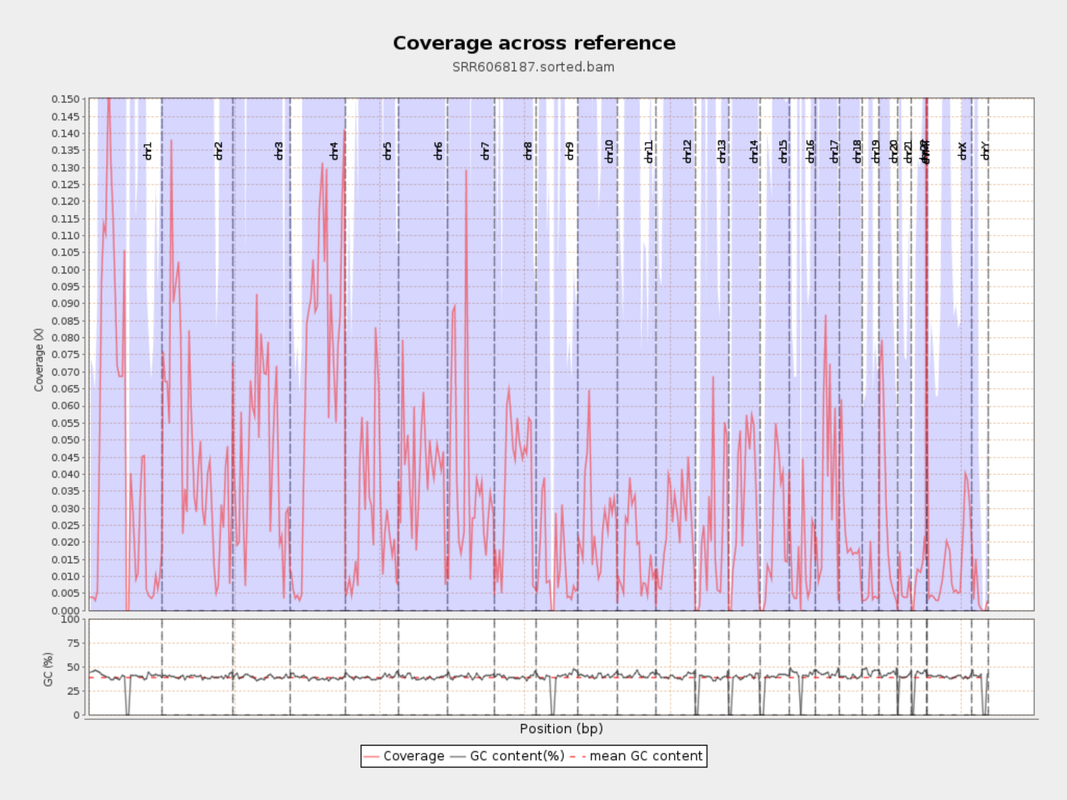
General error rate	0.86%
Mismatches	862,009
Insertions	6,964
Mapped reads with at least one insertion	0.47%
Deletions	25,054
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.68%

2.6. Chromosome stats

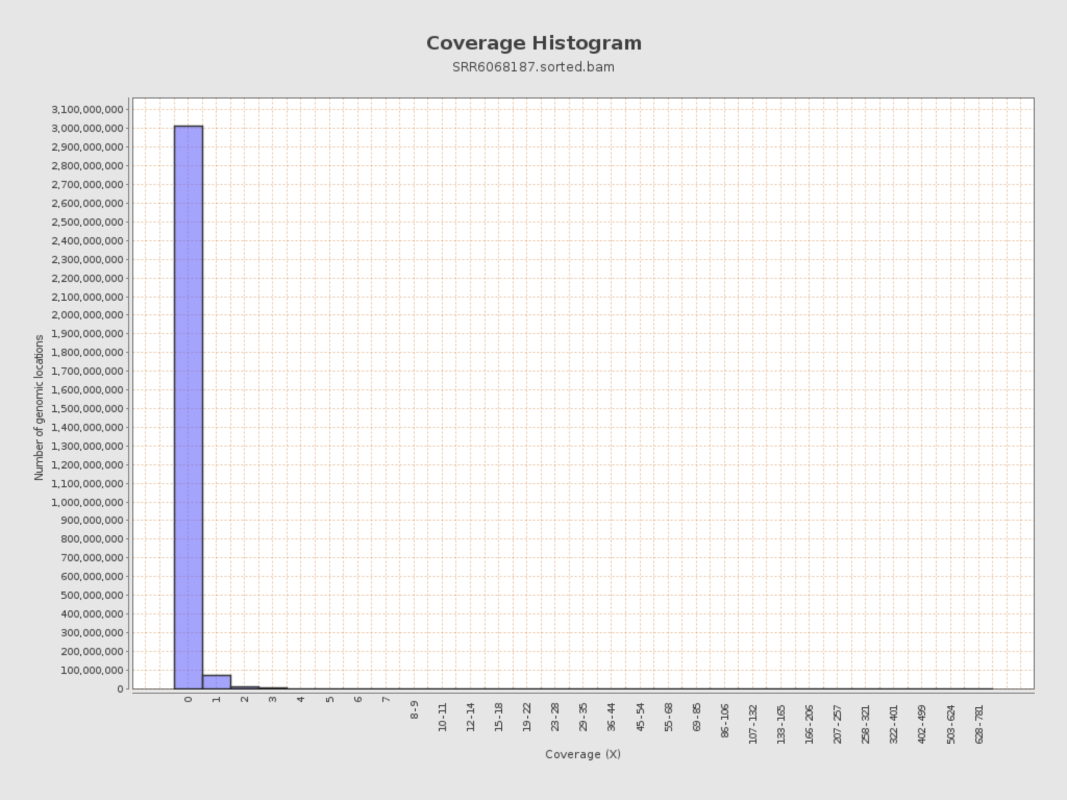
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11314556	0.0454	0.6178
chr2	243199373	11658166	0.0479	0.3448
chr3	198022430	9035824	0.0456	0.2532
chr4	191154276	13883407	0.0726	0.3192
chr5	180915260	4904876	0.0271	0.1885
chr6	171115067	7105327	0.0415	0.2593
chr7	159138663	6349861	0.0399	0.9229

chr8	146364022	5535807	0.0378	0.5077
chr9	141213431	1855399	0.0131	0.2591
chr10	135534747	3582121	0.0264	0.4086
chr11	135006516	2189030	0.0162	0.2261
chr12	133851895	3449618	0.0258	0.2015
chr13	115169878	2612306	0.0227	0.1717
chr14	107349540	3507495	0.0327	0.2306
chr15	102531392	2276400	0.0222	0.1688
chr16	90354753	1245318	0.0138	0.1672
chr17	81195210	3171900	0.0391	0.2662
chr18	78077248	1906380	0.0244	0.4306
chr19	59128983	343047	0.0058	0.4134
chr20	63025520	1975293	0.0313	0.223
chr21	48129895	319819	0.0066	0.1158
chr22	51304566	546726	0.0107	0.115
chrMT	16571	16495	0.9954	1.2245
chrX	155270560	2427905	0.0156	0.164
chrY	59373566	259777	0.0044	0.1407

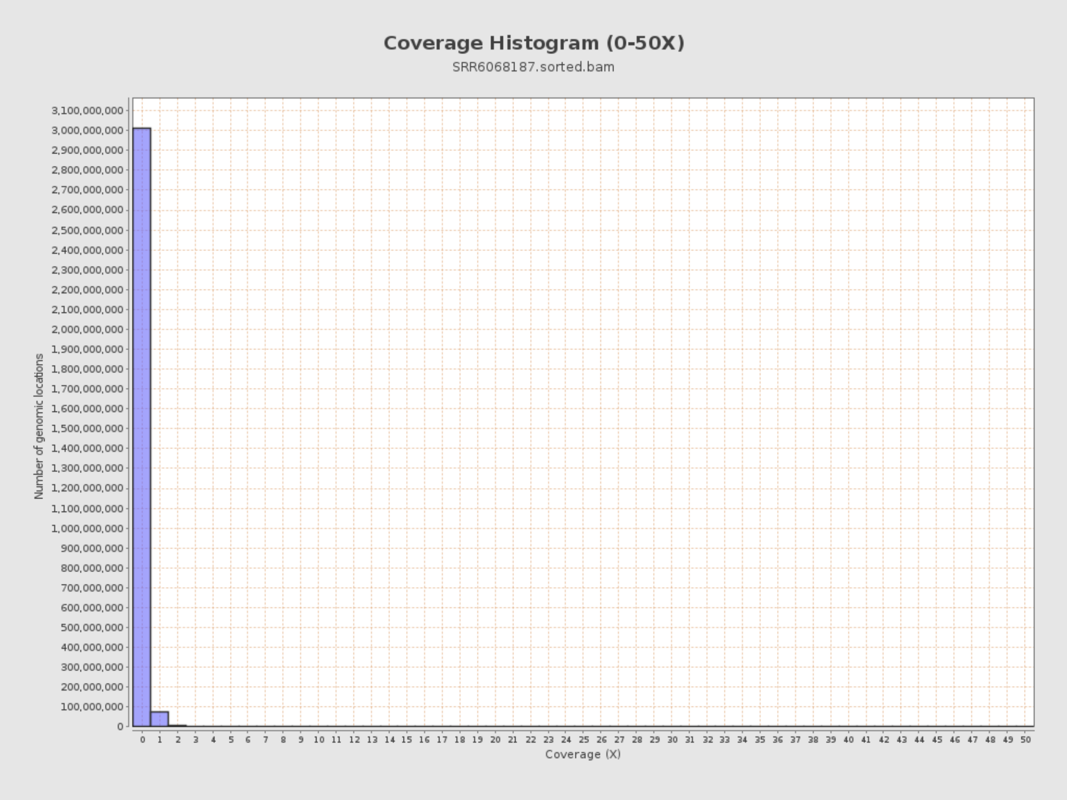
3. Results : Coverage across reference



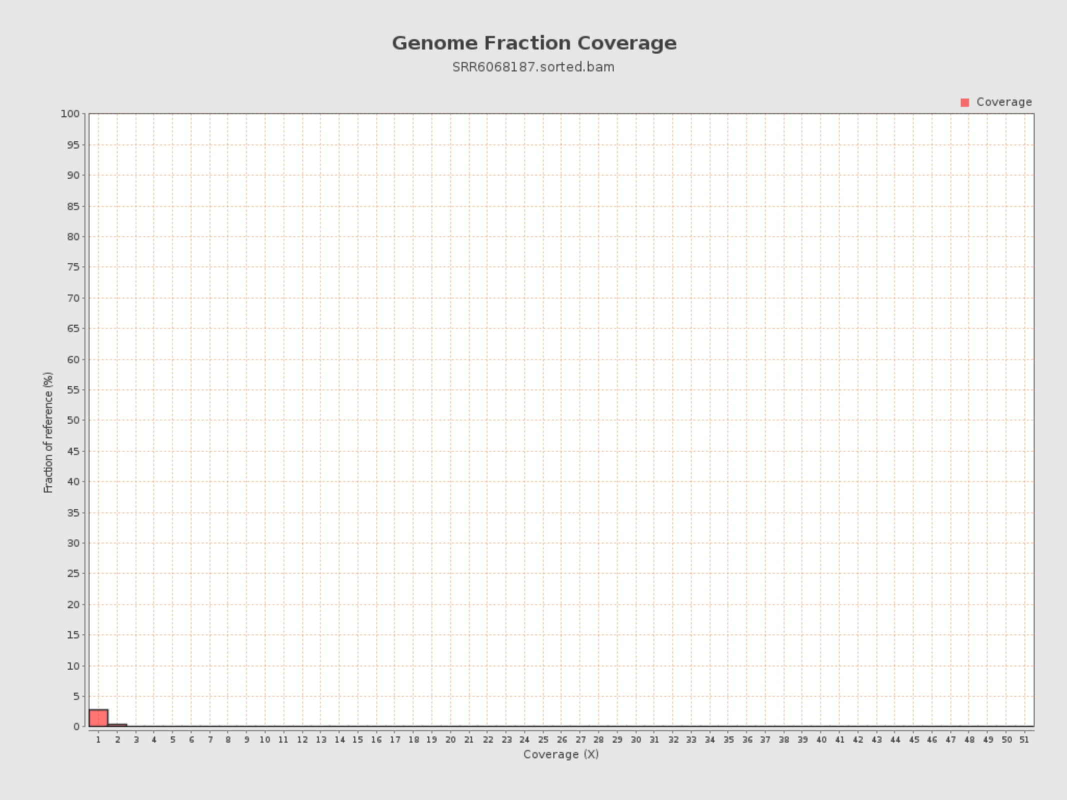
4. Results : Coverage Histogram



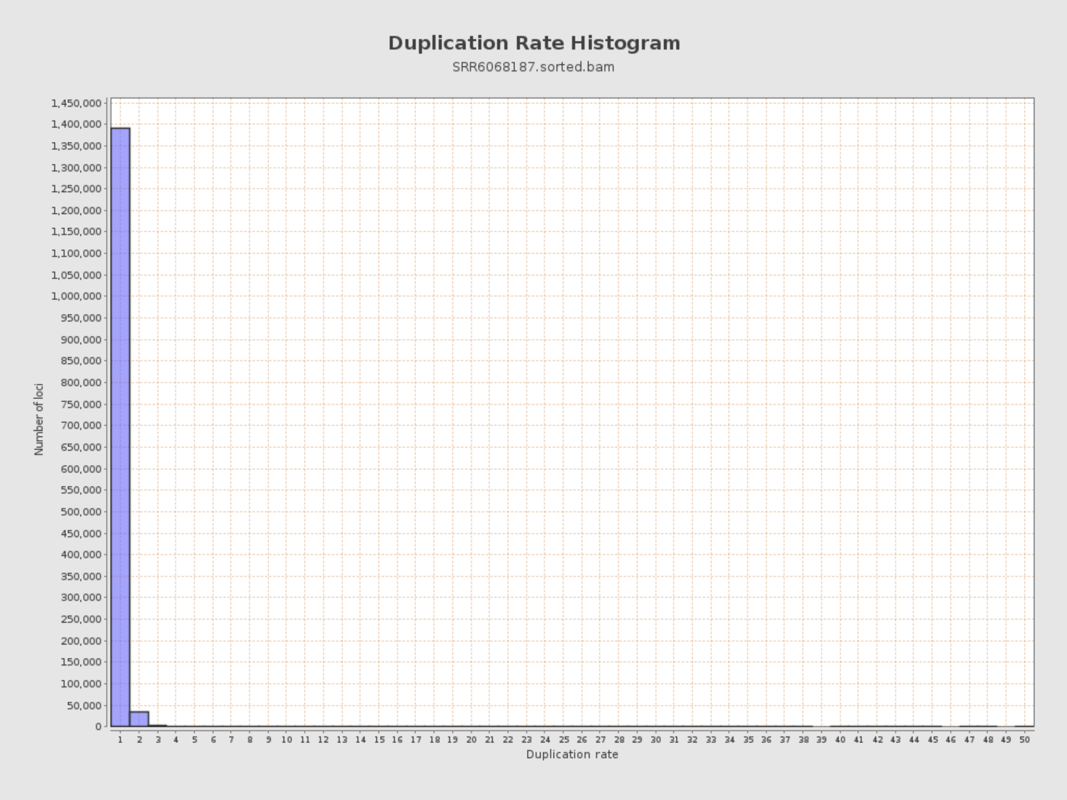
5. Results : Coverage Histogram (0-50X)



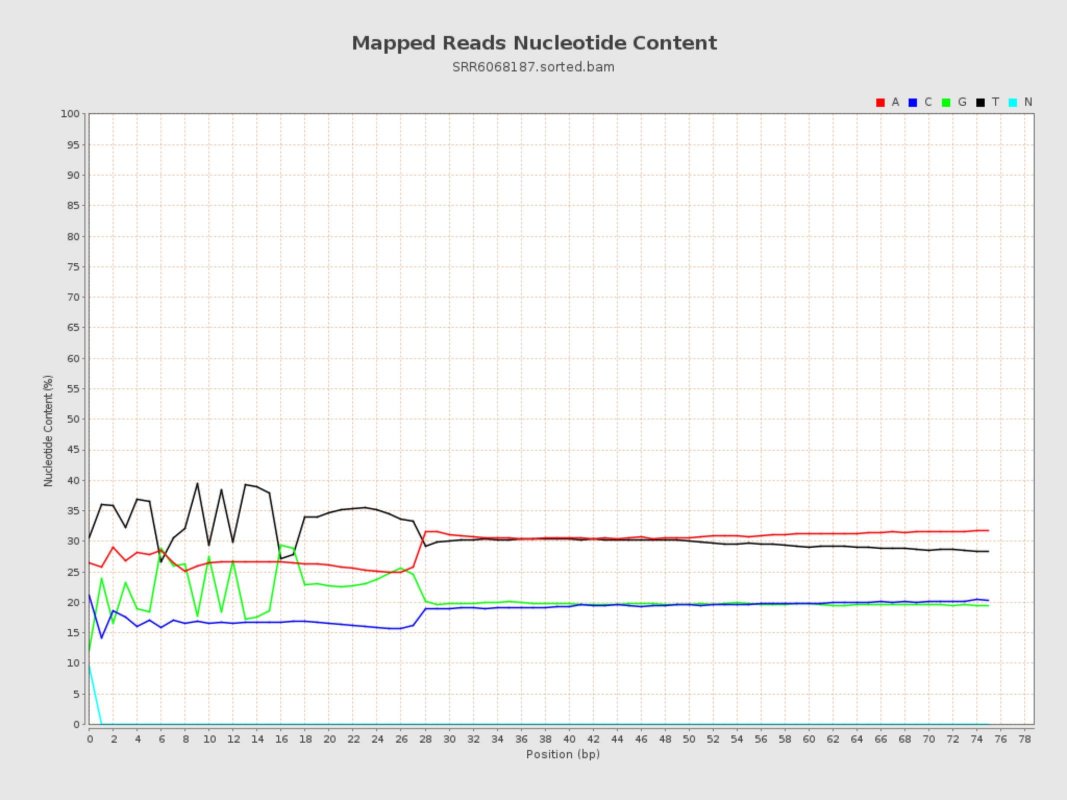
6. Results : Genome Fraction Coverage



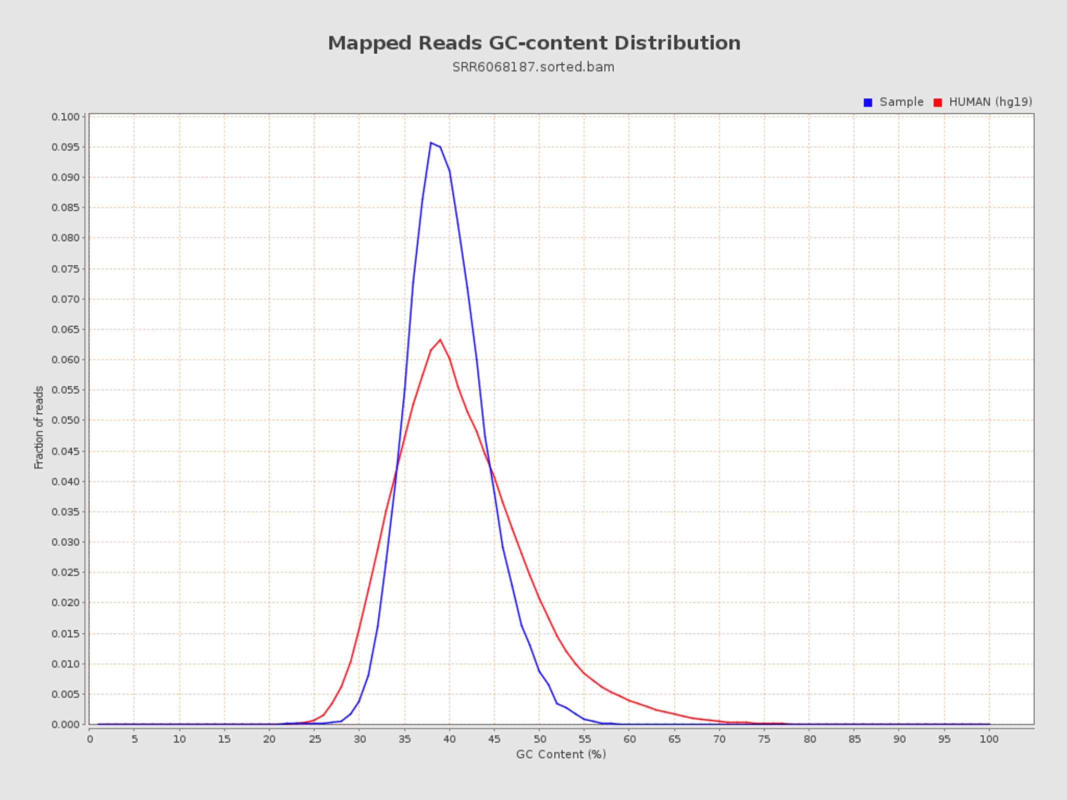
7. Results : Duplication Rate Histogram



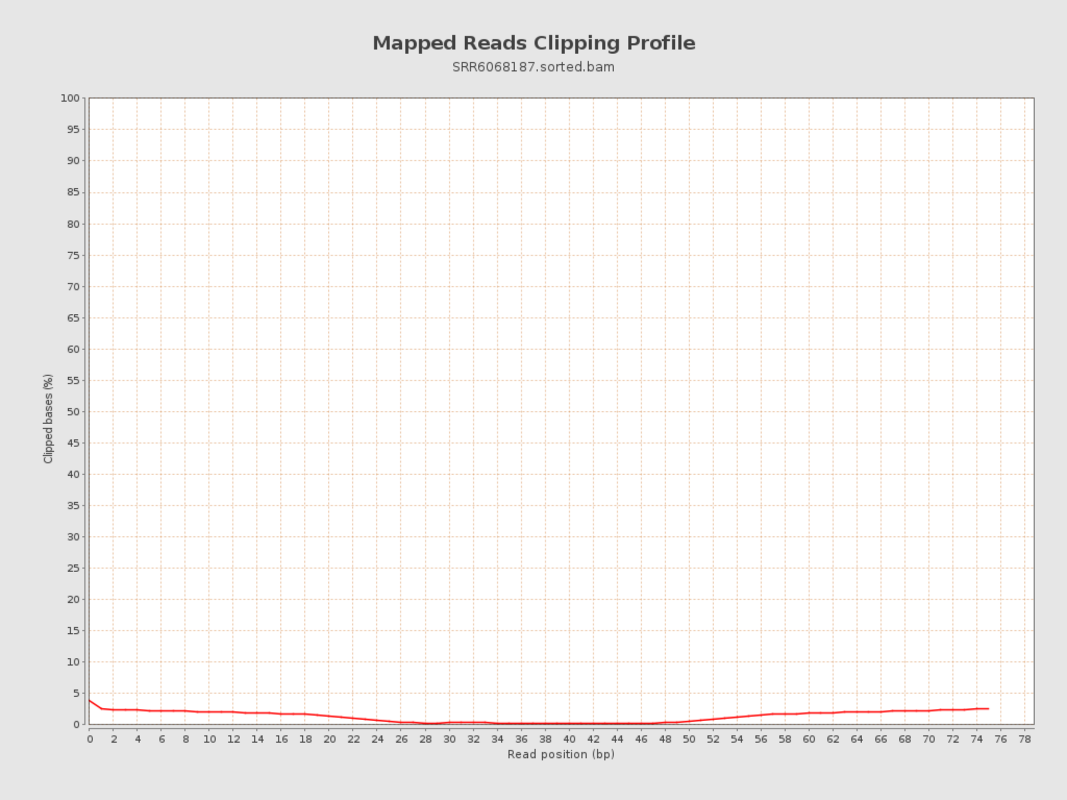
8. Results : Mapped Reads Nucleotide Content



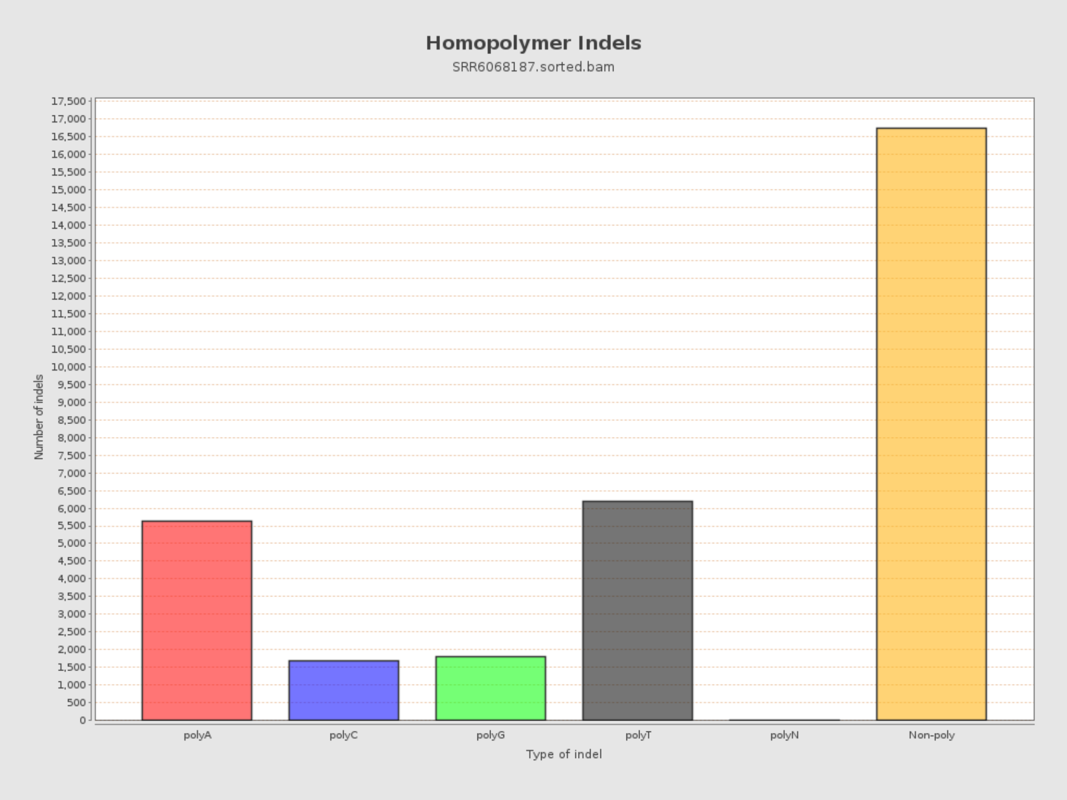
9. Results : Mapped Reads GC-content Distribution



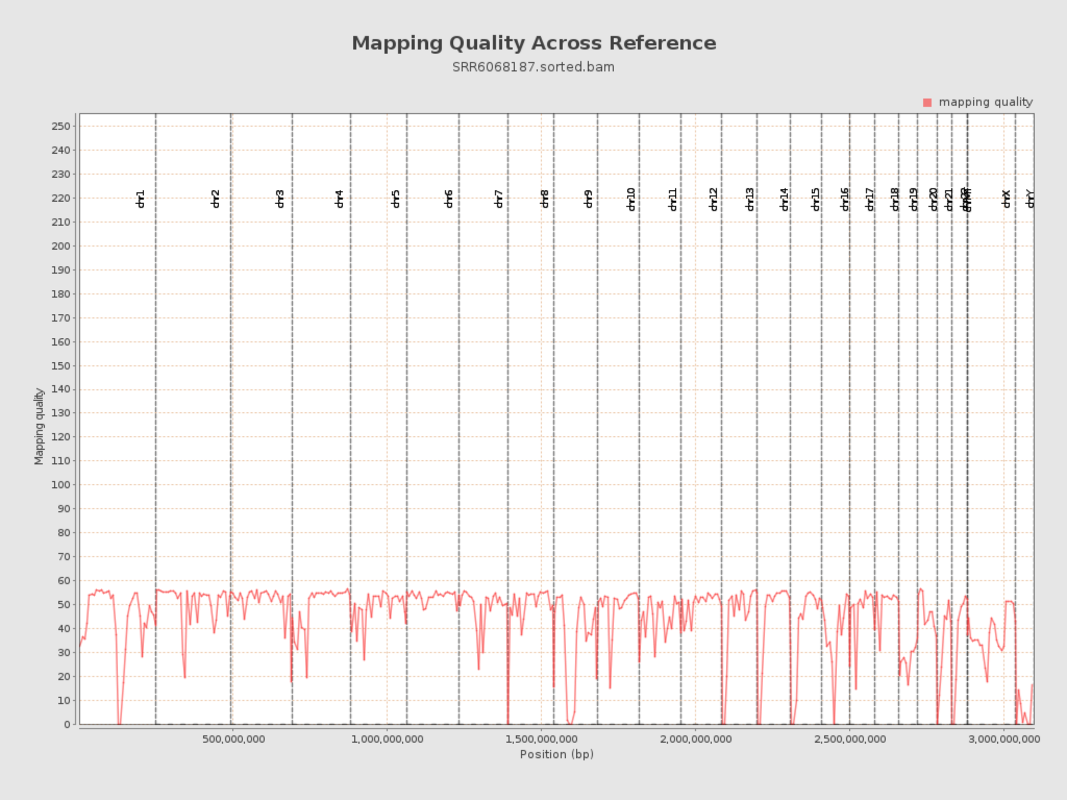
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram