Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 20:34:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536751.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_SRR536751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 20:34:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,013,773
Mapped reads	23,167,785 / 96.48%
Unmapped reads	845,988 / 3.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	516 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	213,507 / 0.89%
Duplication rate	0.91%
Clipped reads	371,770 / 1.55%

2.2. ACGT Content

Number/percentage of A's	361,140,662 / 31.26%
Number/percentage of C's	215,257,695 / 18.63%
Number/percentage of T's	359,308,759 / 31.1%
Number/percentage of G's	219,055,320 / 18.96%
Number/percentage of N's	459,780 / 0.04%
GC Percentage	37.6%

2.3. Coverage

Mean	0.3732

Standard Deviation	0.6829

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

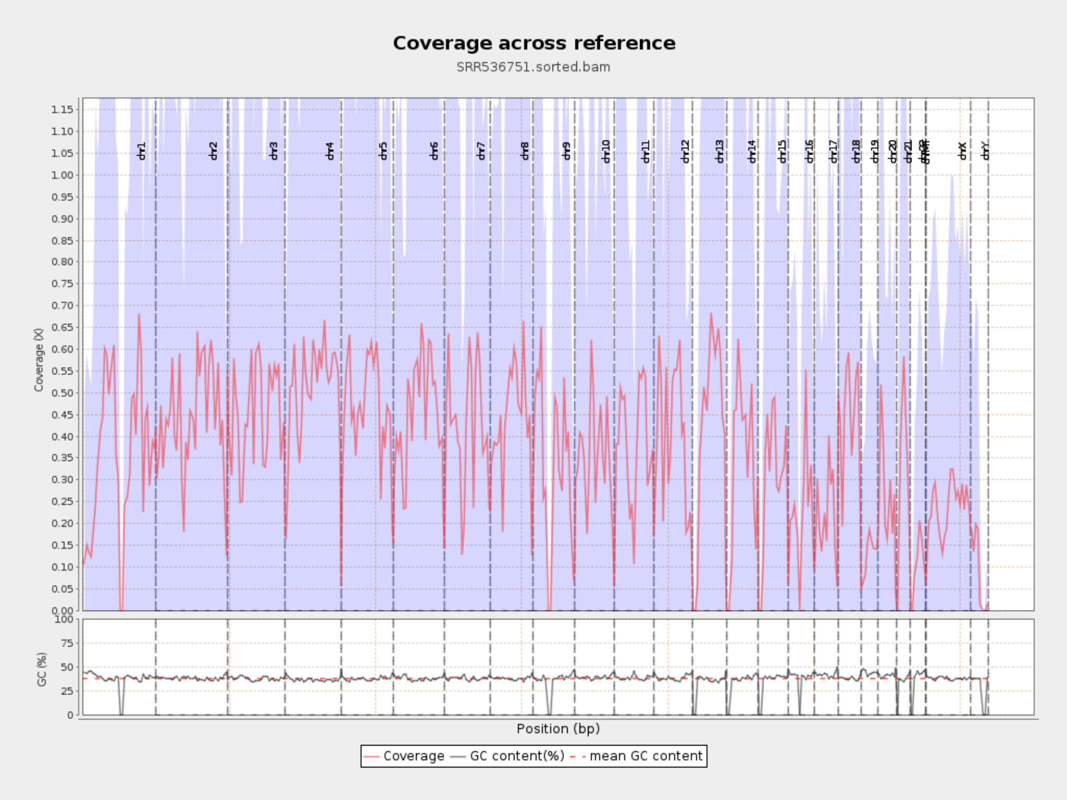
General error rate	0.35%
Mismatches	3,985,945
Insertions	64,159
Mapped reads with at least one insertion	0.28%
Deletions	61,438
Mapped reads with at least one deletion	0.26%
Homopolymer indels	48.26%

2.6. Chromosome stats

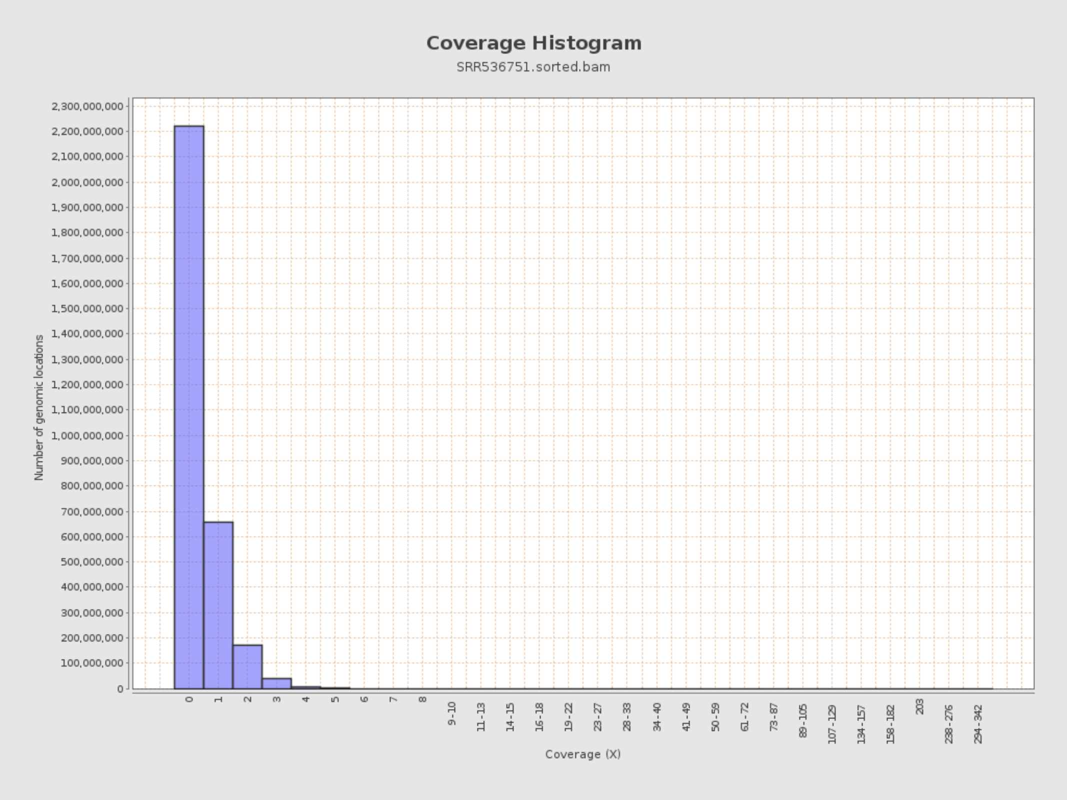
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88140052	0.3536	0.6811
chr2	243199373	107030651	0.4401	0.7258
chr3	198022430	89885860	0.4539	0.7322
chr4	191154276	97913339	0.5122	0.7763
chr5	180915260	83311641	0.4605	0.739
chr6	171115067	78775225	0.4604	0.7425
chr7	159138663	66443201	0.4175	0.7185

chr8	146364022	64603723	0.4414	0.7261
chr9	141213431	47949699	0.3396	0.6587
chr10	135534747	48941686	0.3611	0.6564
chr11	135006516	51319349	0.3801	0.6916
chr12	133851895	53430239	0.3992	0.7023
chr13	115169878	49471554	0.4296	0.7347
chr14	107349540	36797944	0.3428	0.6617
chr15	102531392	30642675	0.2989	0.6209
chr16	90354753	20266170	0.2243	0.5299
chr17	81195210	17934045	0.2209	0.5345
chr18	78077248	35139742	0.4501	0.7339
chr19	59128983	7701294	0.1302	0.3936
chr20	63025520	17137643	0.2719	0.5842
chr21	48129895	14994905	0.3116	0.6538
chr22	51304566	5536870	0.1079	0.3648
chrMT	16571	977	0.059	0.2436
chrX	155270560	36734395	0.2366	0.5129
chrY	59373566	5221240	0.0879	0.3338

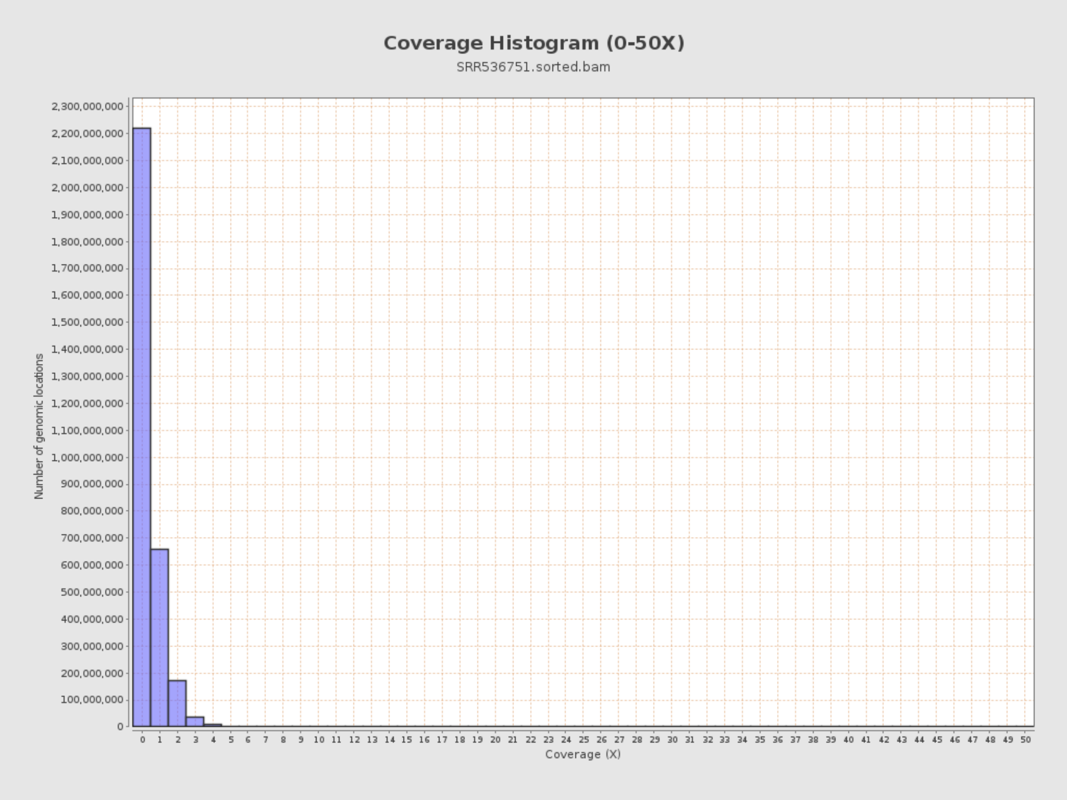
3. Results : Coverage across reference



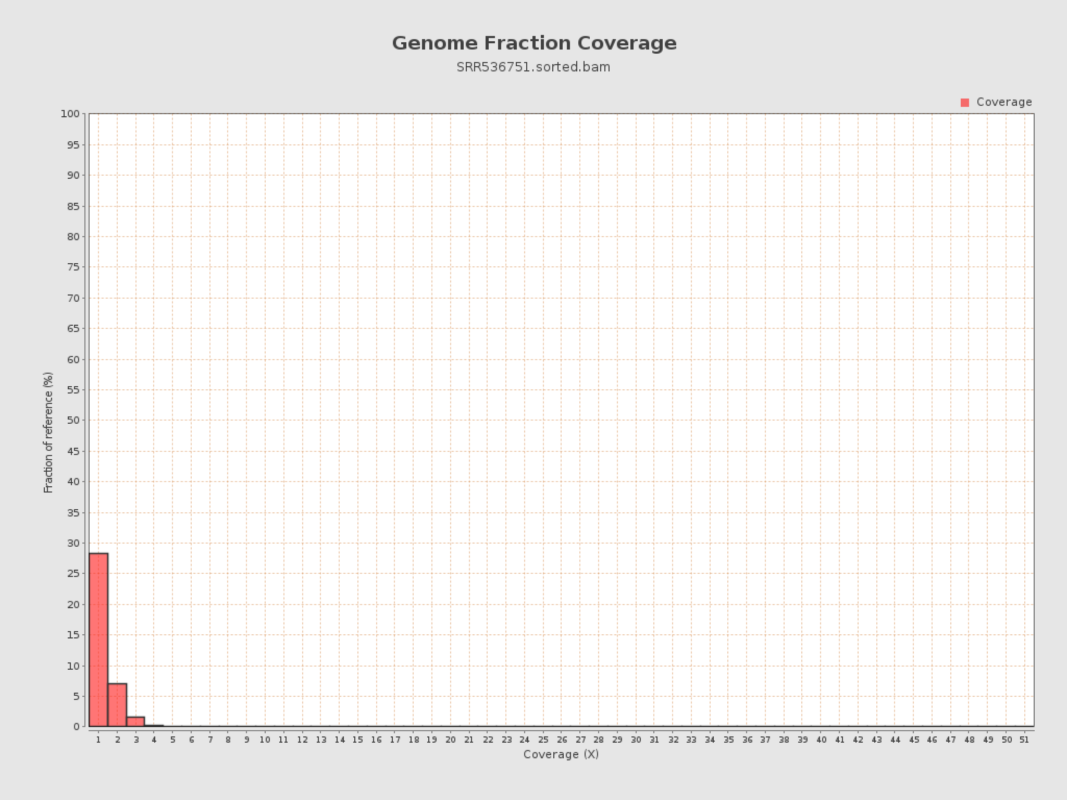
4. Results : Coverage Histogram



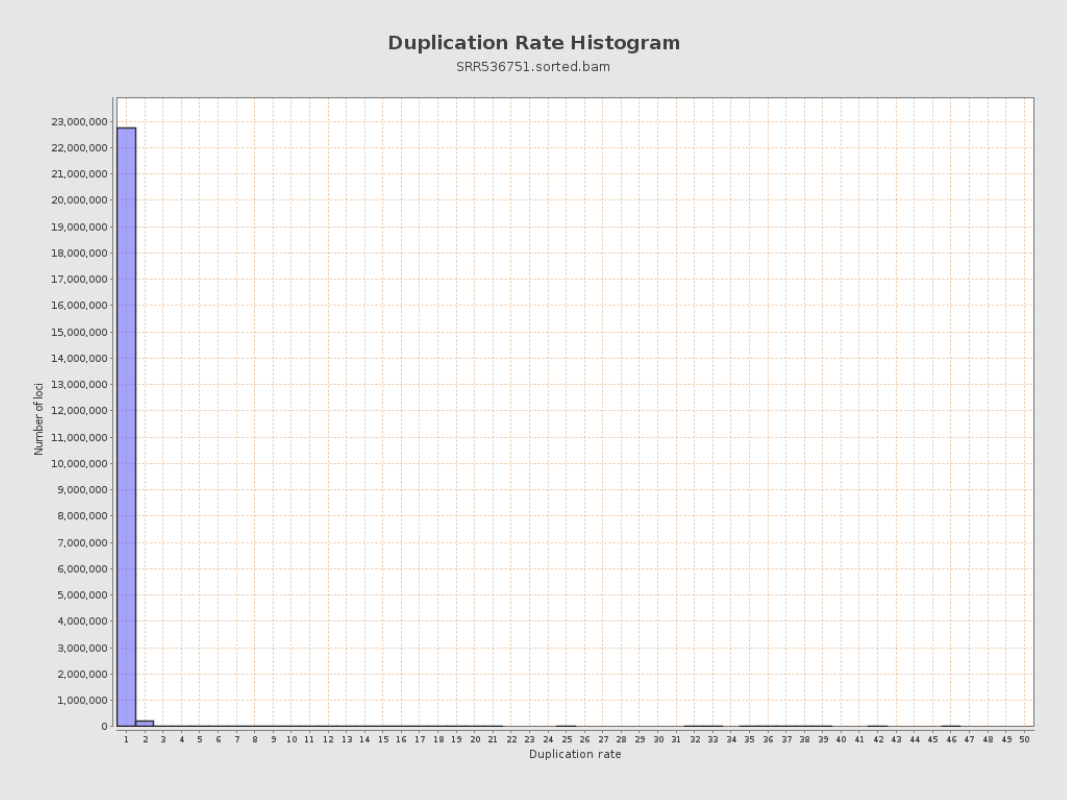
5. Results : Coverage Histogram (0-50X)



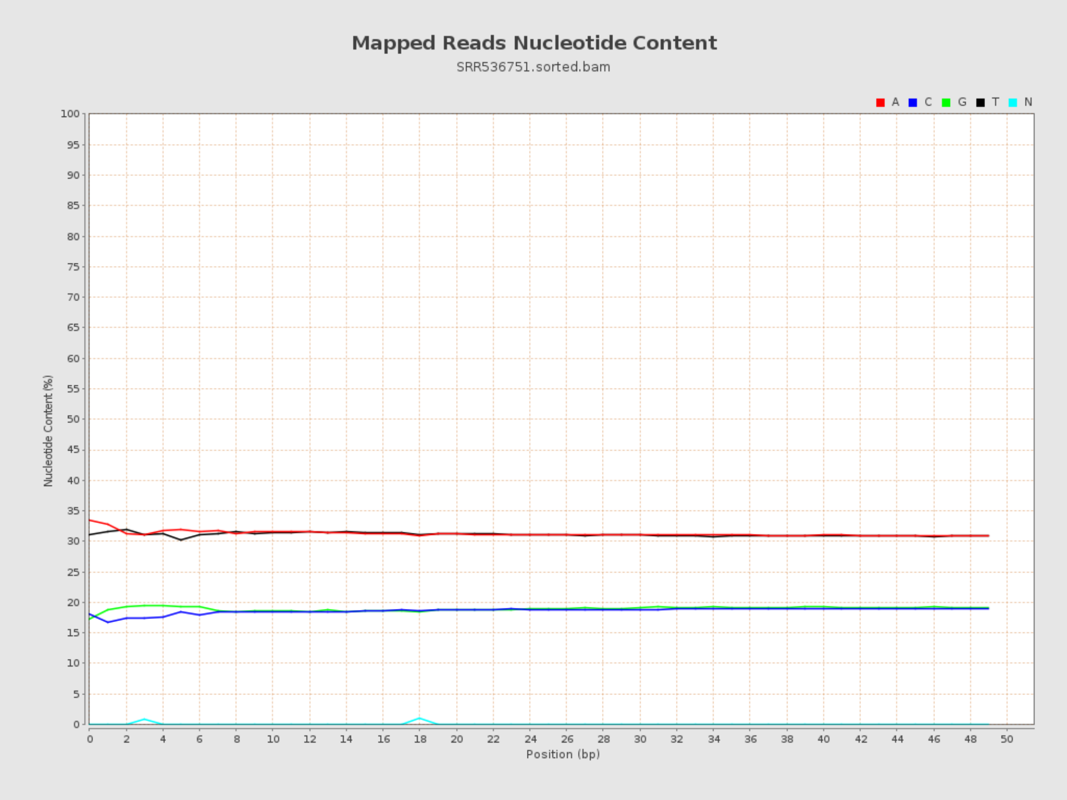
6. Results : Genome Fraction Coverage



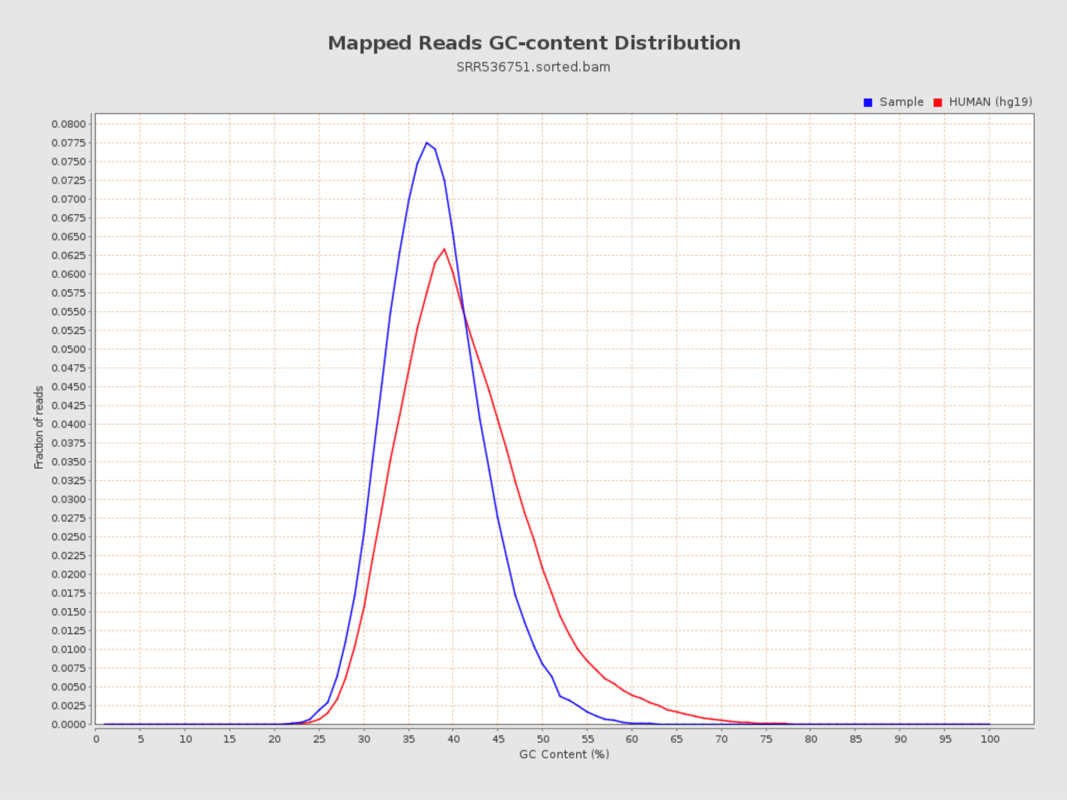
7. Results : Duplication Rate Histogram



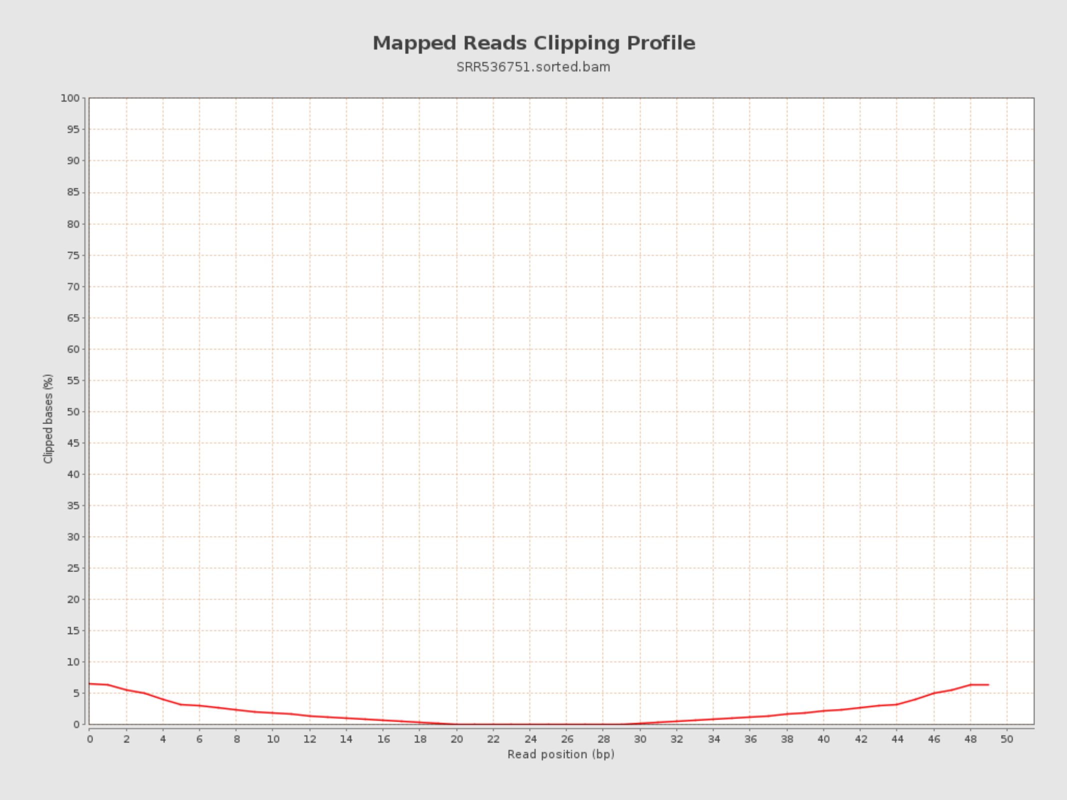
8. Results : Mapped Reads Nucleotide Content



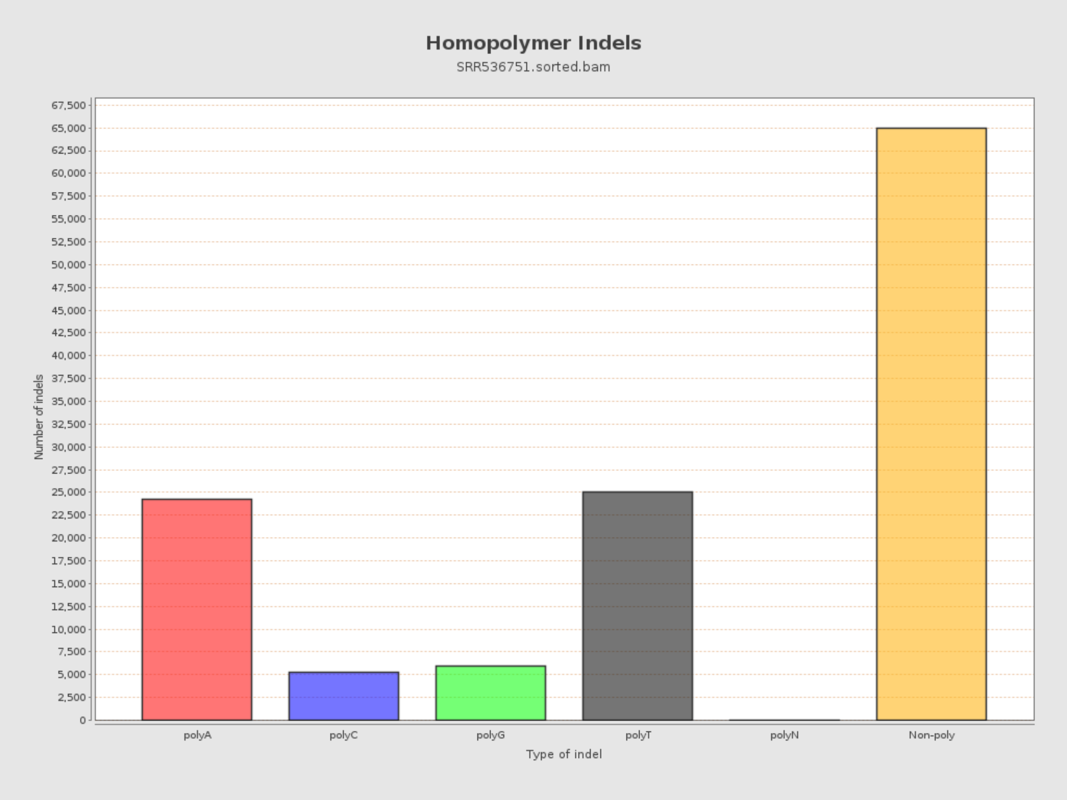
9. Results : Mapped Reads GC-content Distribution



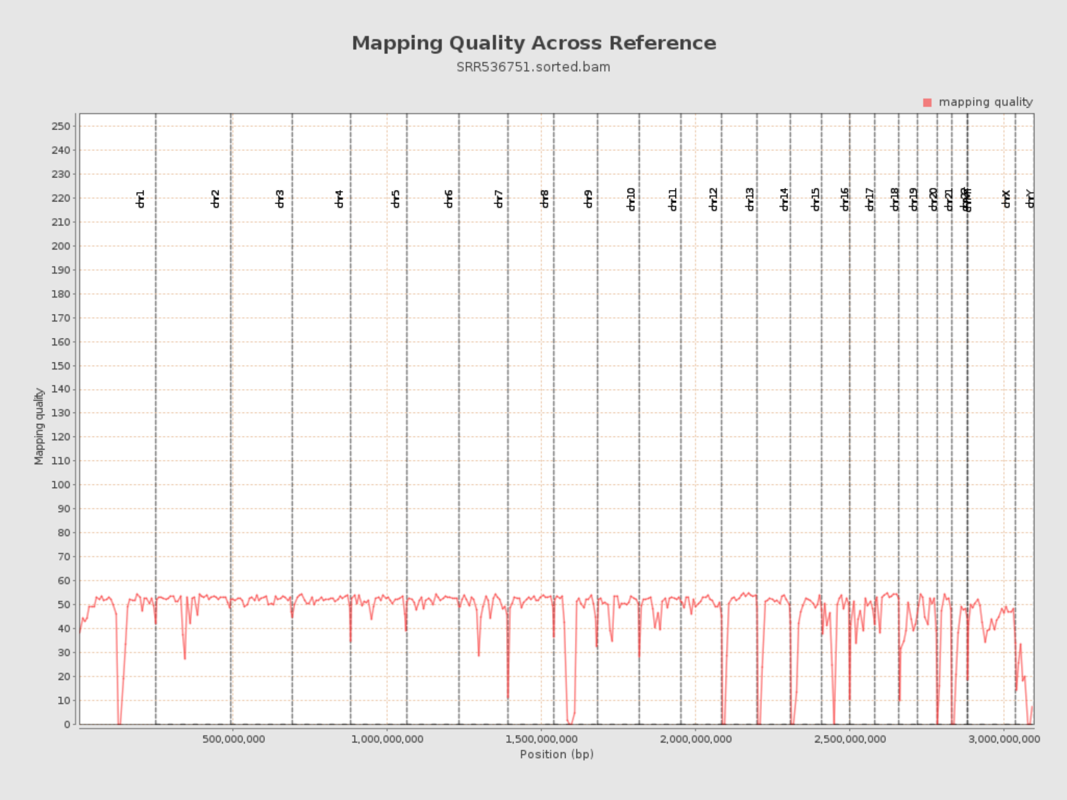
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram