

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:59:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237795.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_SRR6237795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237795.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:59:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,120,776
Mapped reads	3,597,888 / 87.31%
Unmapped reads	522,888 / 12.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,214 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	427,888 / 10.38%
Duplication rate	9.87%
Clipped reads	1,350,786 / 32.78%

2.2. ACGT Content

Number/percentage of A's	76,070,603 / 30.16%
Number/percentage of C's	50,233,264 / 19.92%
Number/percentage of T's	73,940,312 / 29.31%
Number/percentage of G's	51,564,682 / 20.44%
Number/percentage of N's	425,262 / 0.17%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0815

Standard Deviation	1.2851
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2.4. Mapping Quality

Mean Mapping Quality	47.66
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2.5. Mismatches and indels

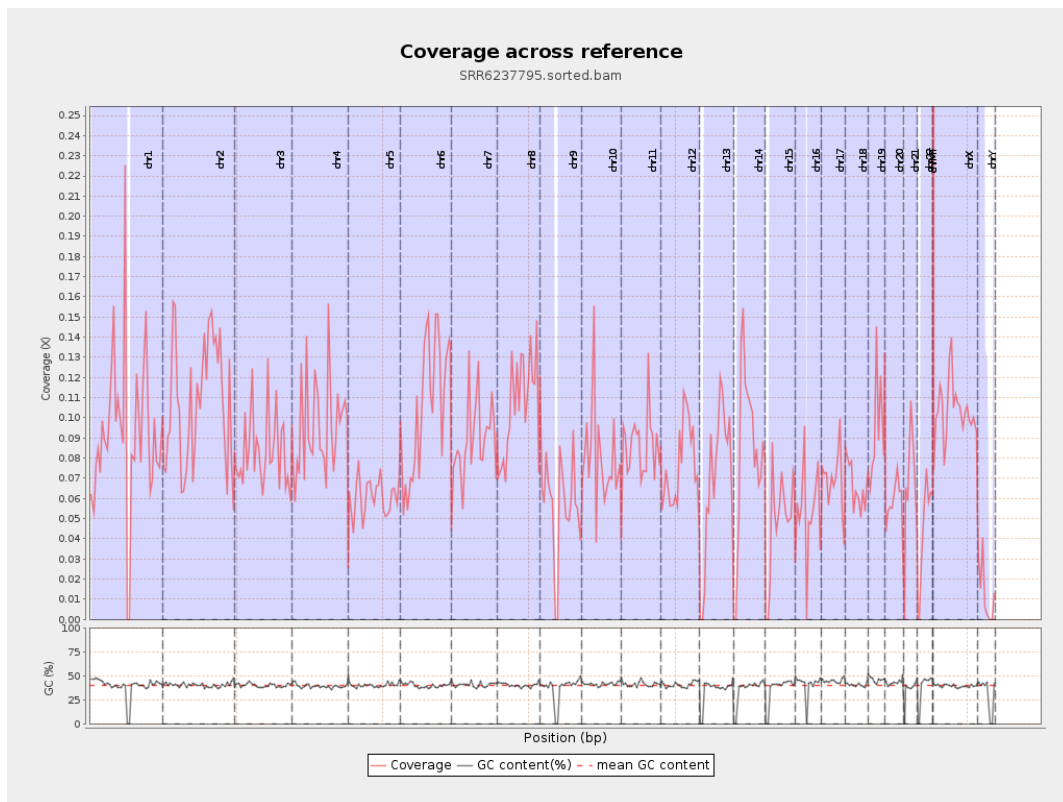
General error rate	0.9%
Mismatches	2,223,988
Insertions	18,320
Mapped reads with at least one insertion	0.5%
Deletions	75,260
Mapped reads with at least one deletion	2.07%
Homopolymer indels	43.73%

2.6. Chromosome stats

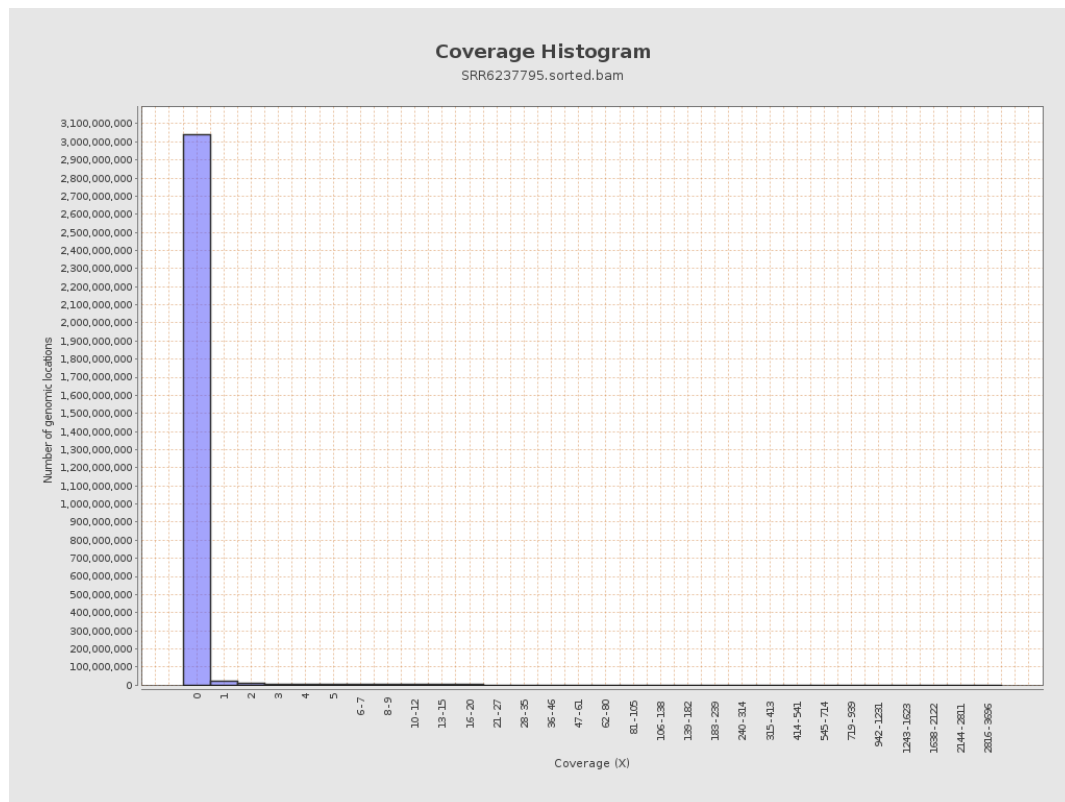
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22895099	0.0919	2.8356
chr2	243199373	26138711	0.1075	1.1801
chr3	198022430	16498594	0.0833	0.988
chr4	191154276	18068725	0.0945	1.0579
chr5	180915260	11062565	0.0611	0.846
chr6	171115067	18035595	0.1054	1.1561
chr7	159138663	14145348	0.0889	1.2577

chr8	146364022	15577338	0.1064	1.2104
chr9	141213431	8115062	0.0575	0.909
chr10	135534747	10809847	0.0798	1.1463
chr11	135006516	11620605	0.0861	1.0775
chr12	133851895	10180003	0.0761	0.9497
chr13	115169878	8012317	0.0696	0.897
chr14	107349540	9120350	0.085	0.9988
chr15	102531392	5012315	0.0489	0.7696
chr16	90354753	4660213	0.0516	0.8
chr17	81195210	5707820	0.0703	0.9223
chr18	78077248	5138771	0.0658	1.2657
chr19	59128983	5586187	0.0945	1.6254
chr20	63025520	3702338	0.0587	0.8456
chr21	48129895	3225630	0.067	0.9024
chr22	51304566	2307008	0.045	0.7441
chrMT	16571	63811	3.8508	5.618
chrX	155270560	15935740	0.1026	1.0582
chrY	59373566	749212	0.0126	0.3742

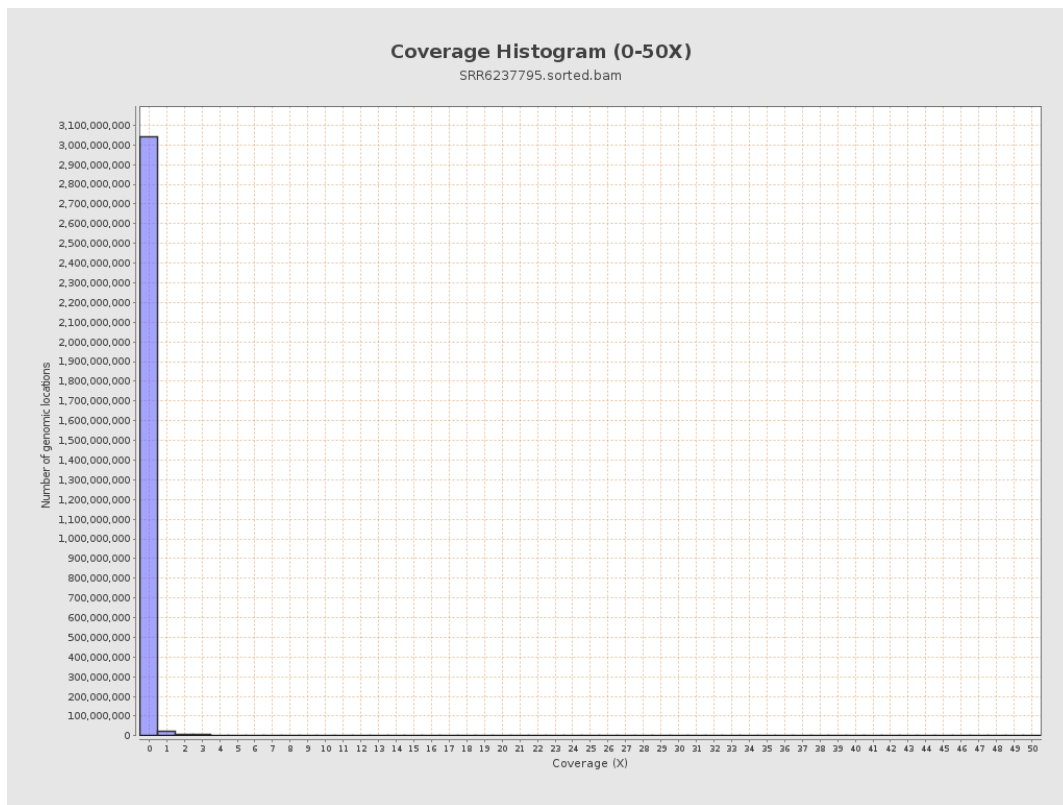
3. Results : Coverage across reference



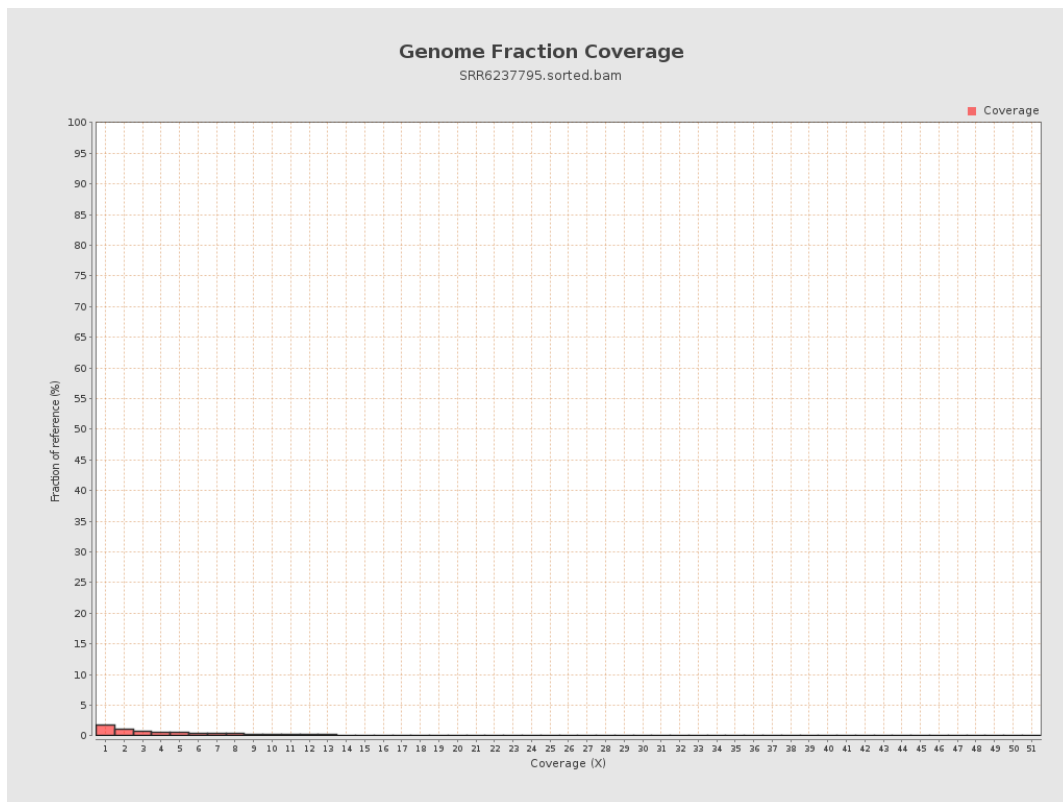
4. Results : Coverage Histogram



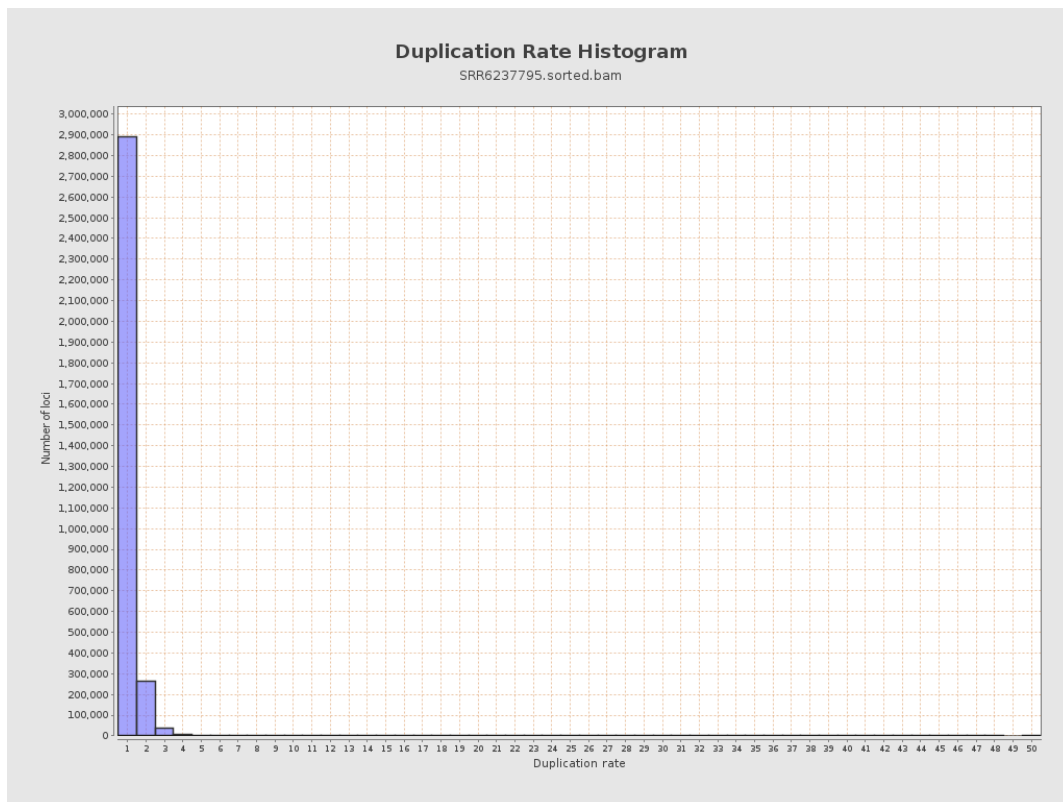
5. Results : Coverage Histogram (0-50X)



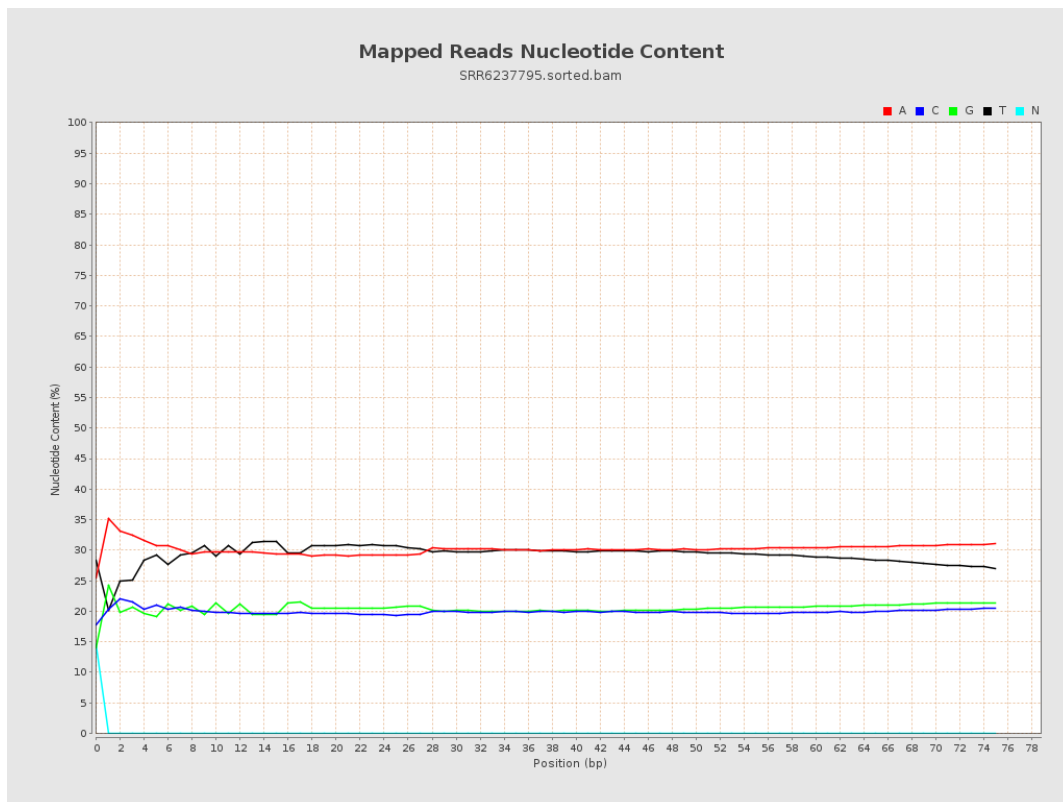
6. Results : Genome Fraction Coverage



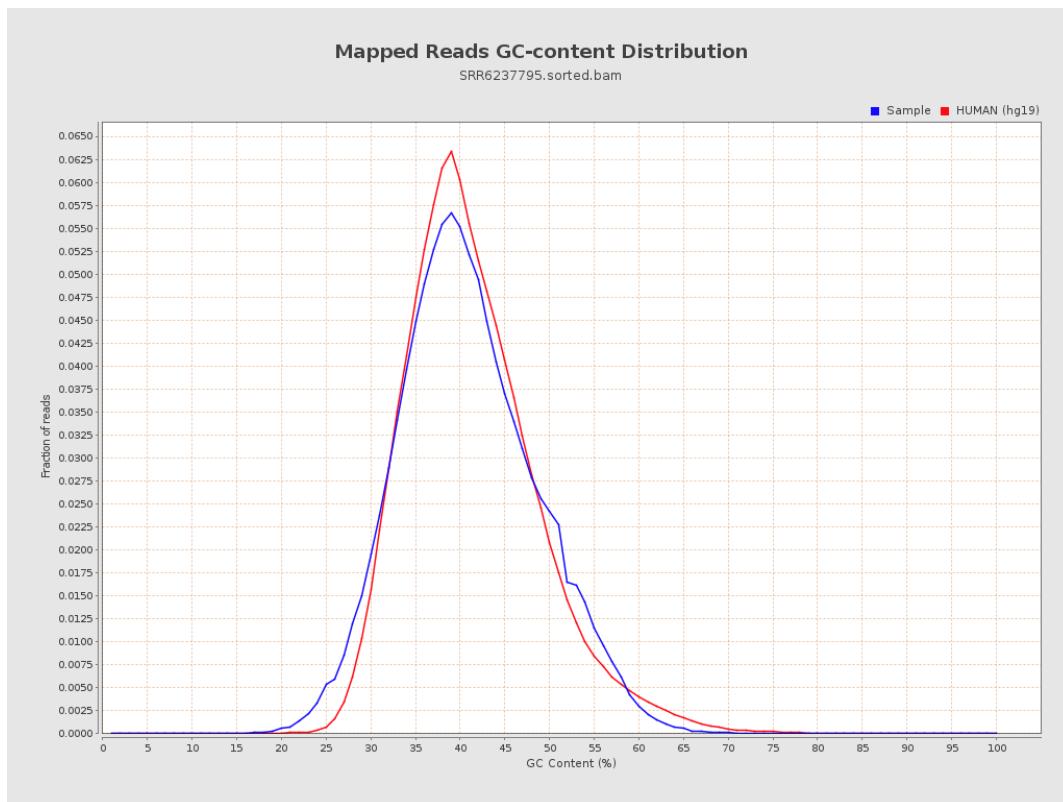
7. Results : Duplication Rate Histogram



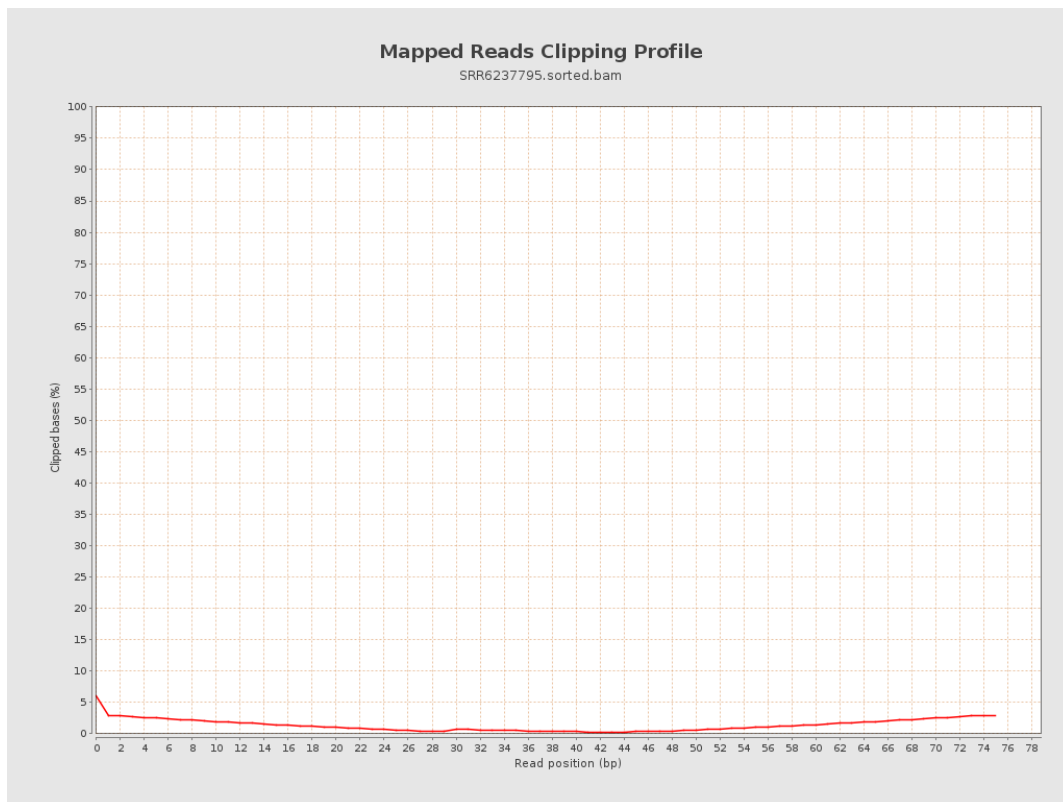
8. Results : Mapped Reads Nucleotide Content



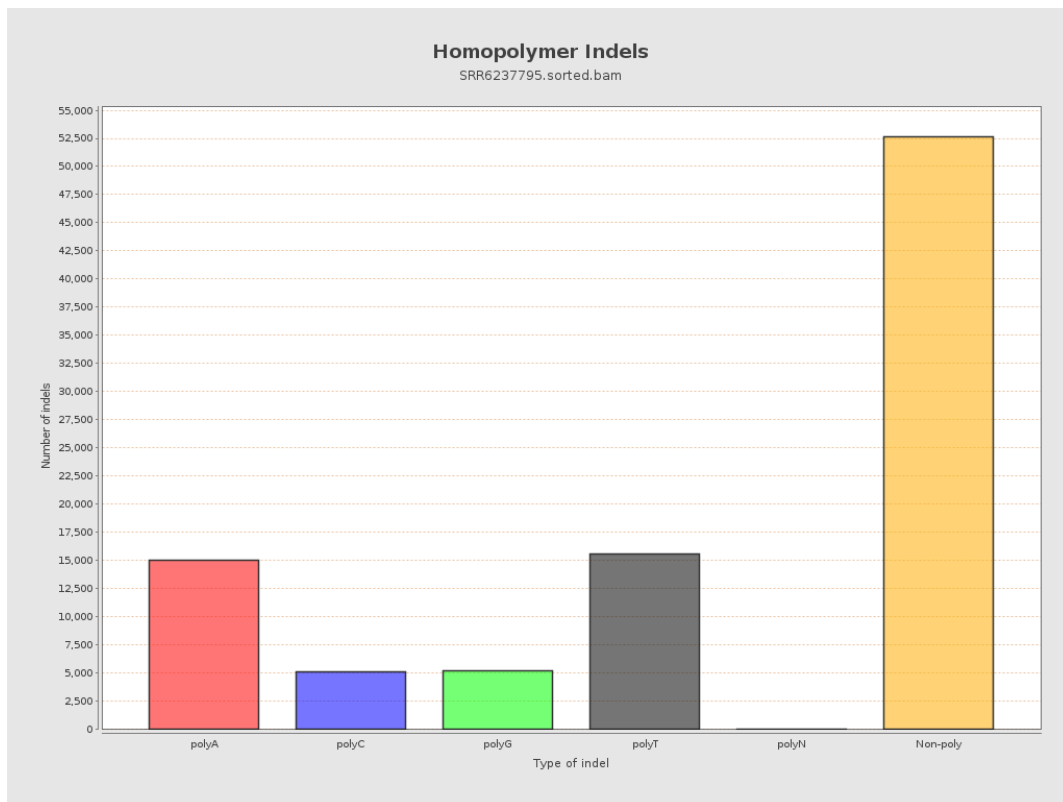
9. Results : Mapped Reads GC-content Distribution



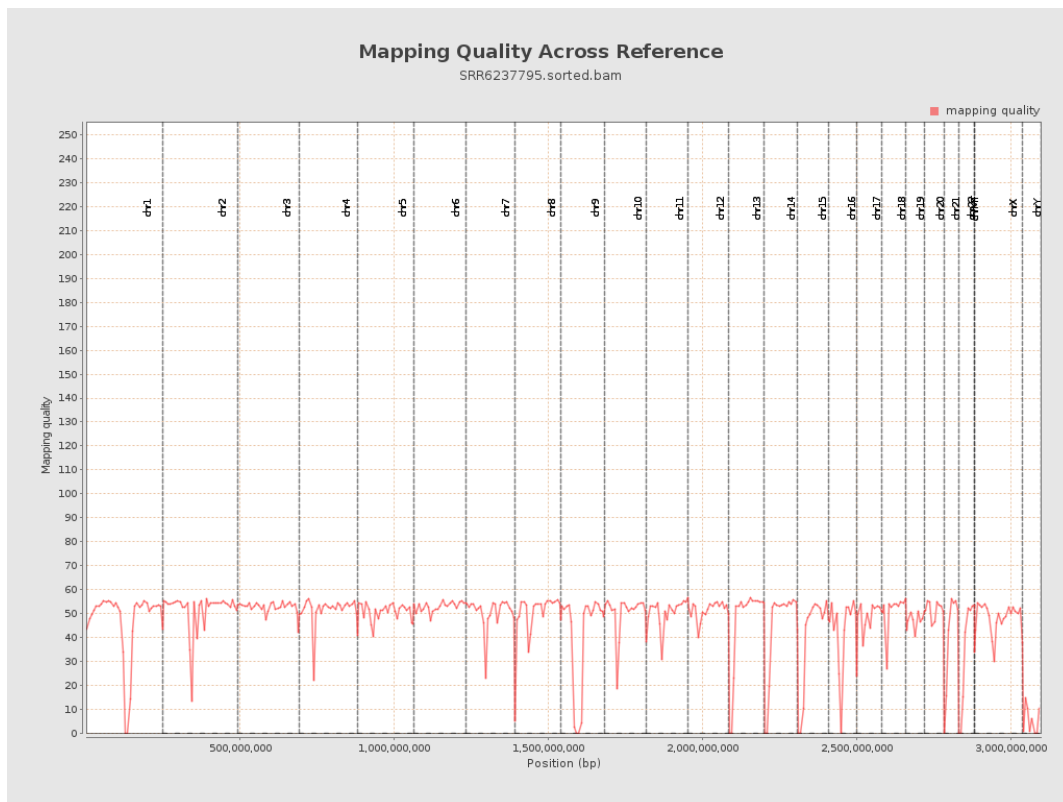
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

