

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:33:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008787.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_SRR6008787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:33:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,533,859
Mapped reads	1,303,325 / 84.97%
Unmapped reads	230,534 / 15.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,497 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	47,348 / 3.09%
Duplication rate	2.4%
Clipped reads	689,018 / 44.92%

2.2. ACGT Content

Number/percentage of A's	22,879,657 / 27.29%
Number/percentage of C's	15,118,023 / 18.03%
Number/percentage of T's	26,008,136 / 31.02%
Number/percentage of G's	19,829,791 / 23.65%
Number/percentage of N's	13,849 / 0.02%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.3121
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2.4. Mapping Quality

Mean Mapping Quality	43.17
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2.5. Mismatches and indels

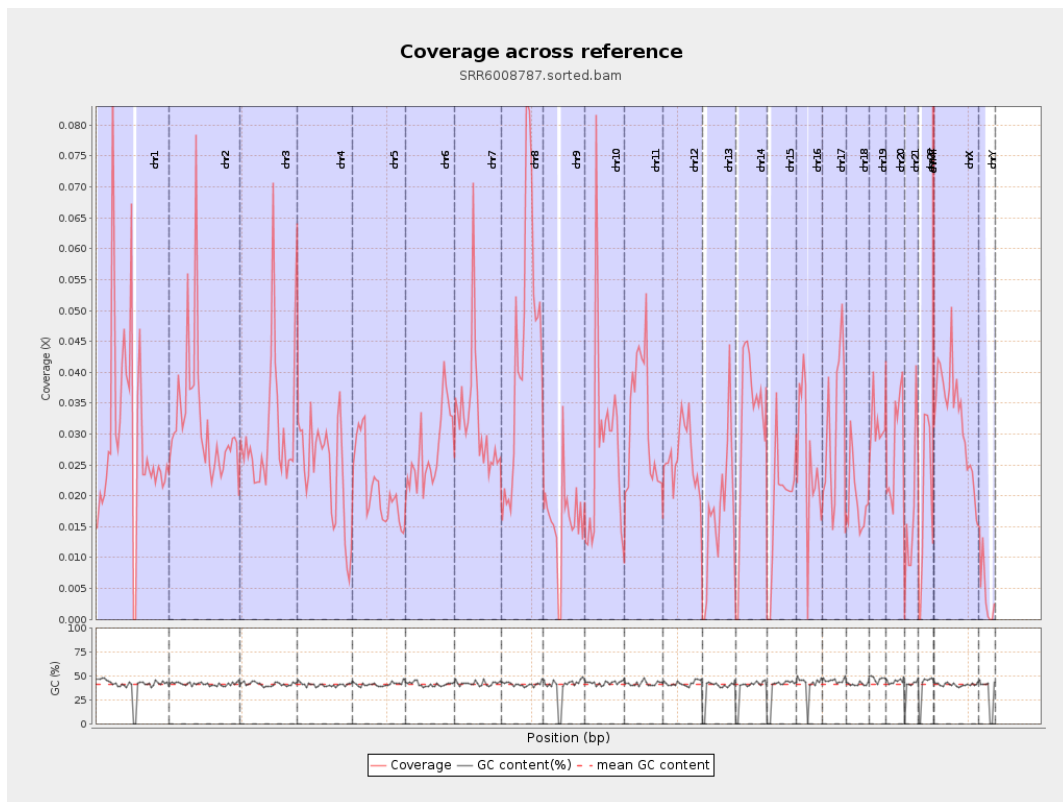
General error rate	0.83%
Mismatches	682,569
Insertions	7,627
Mapped reads with at least one insertion	0.58%
Deletions	25,659
Mapped reads with at least one deletion	1.95%
Homopolymer indels	46.94%

2.6. Chromosome stats

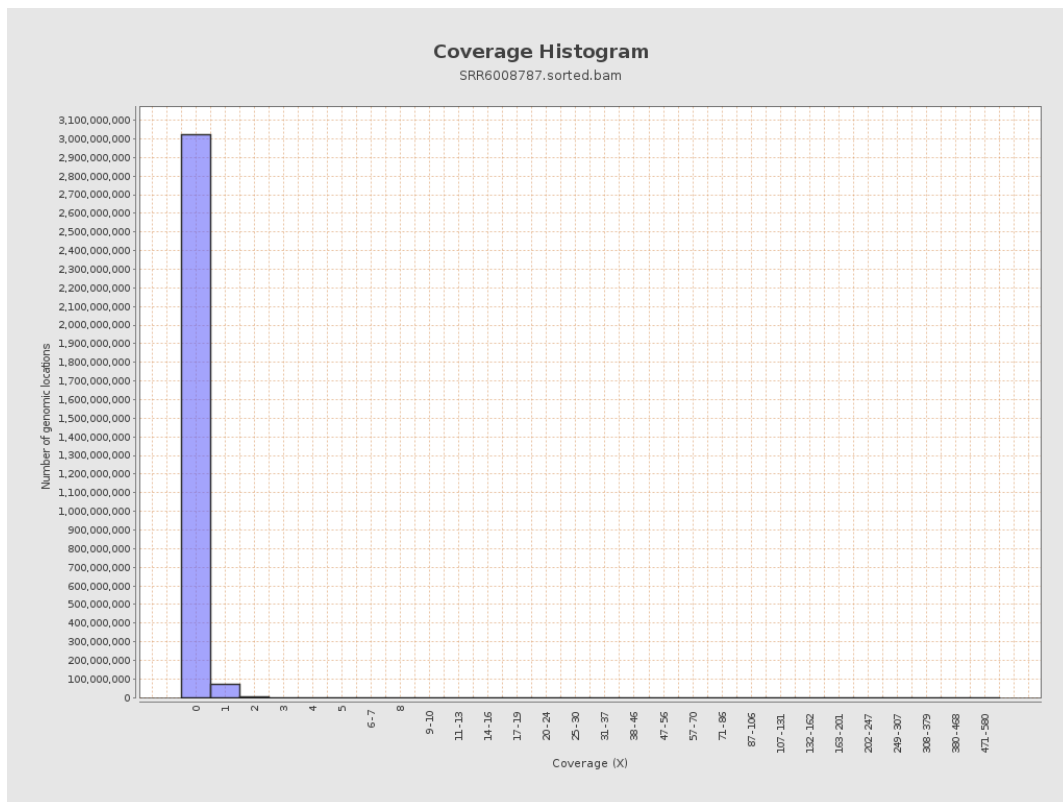
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7222689	0.029	0.5255
chr2	243199373	7785612	0.032	0.3643
chr3	198022430	6021149	0.0304	0.2011
chr4	191154276	4573795	0.0239	0.1773
chr5	180915260	3890123	0.0215	0.1581
chr6	171115067	4662914	0.0273	0.2099
chr7	159138663	5185450	0.0326	0.4666

chr8	146364022	6311518	0.0431	0.3206
chr9	141213431	2246437	0.0159	0.2673
chr10	135534747	3684979	0.0272	0.5043
chr11	135006516	4261920	0.0316	0.3299
chr12	133851895	3513857	0.0263	0.178
chr13	115169878	2004648	0.0174	0.1397
chr14	107349540	3414057	0.0318	0.1979
chr15	102531392	1944661	0.019	0.1482
chr16	90354753	2335807	0.0259	0.2245
chr17	81195210	2466134	0.0304	0.2573
chr18	78077248	1526852	0.0196	0.4951
chr19	59128983	1876185	0.0317	0.3697
chr20	63025520	1758267	0.0279	0.1837
chr21	48129895	842285	0.0175	0.1559
chr22	51304566	994945	0.0194	0.1481
chrMT	16571	45206	2.728	2.2437
chrX	155270560	5058387	0.0326	0.2514
chrY	59373566	263890	0.0044	0.1067

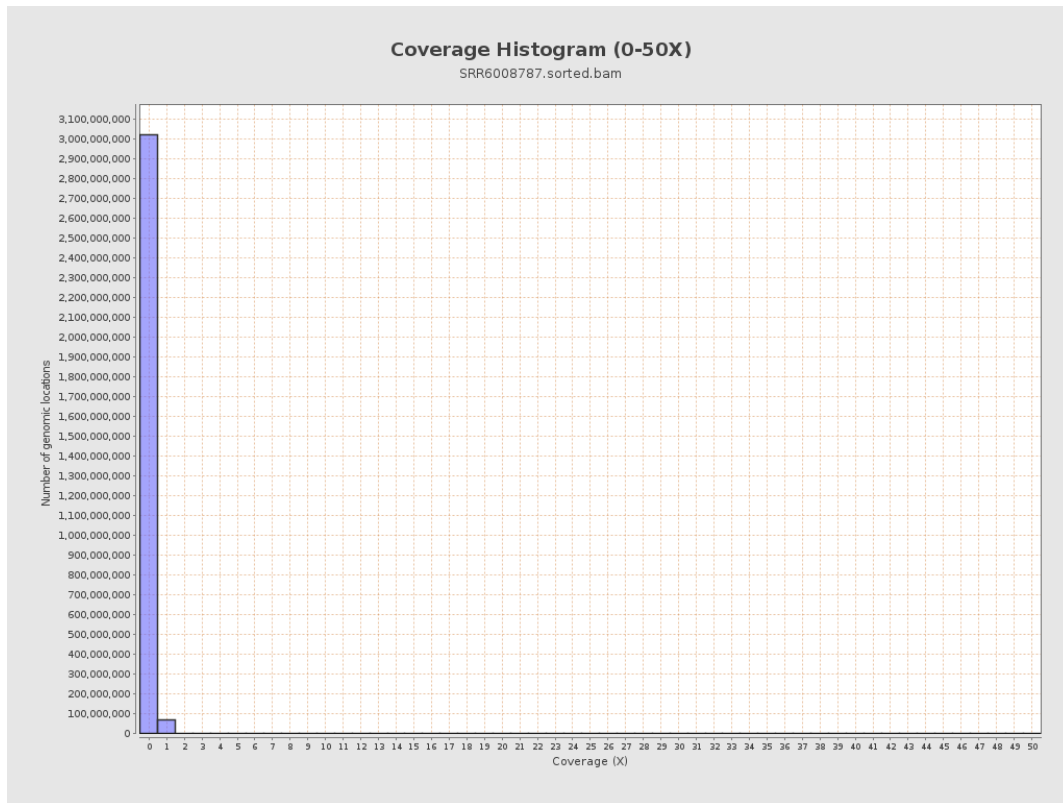
3. Results : Coverage across reference



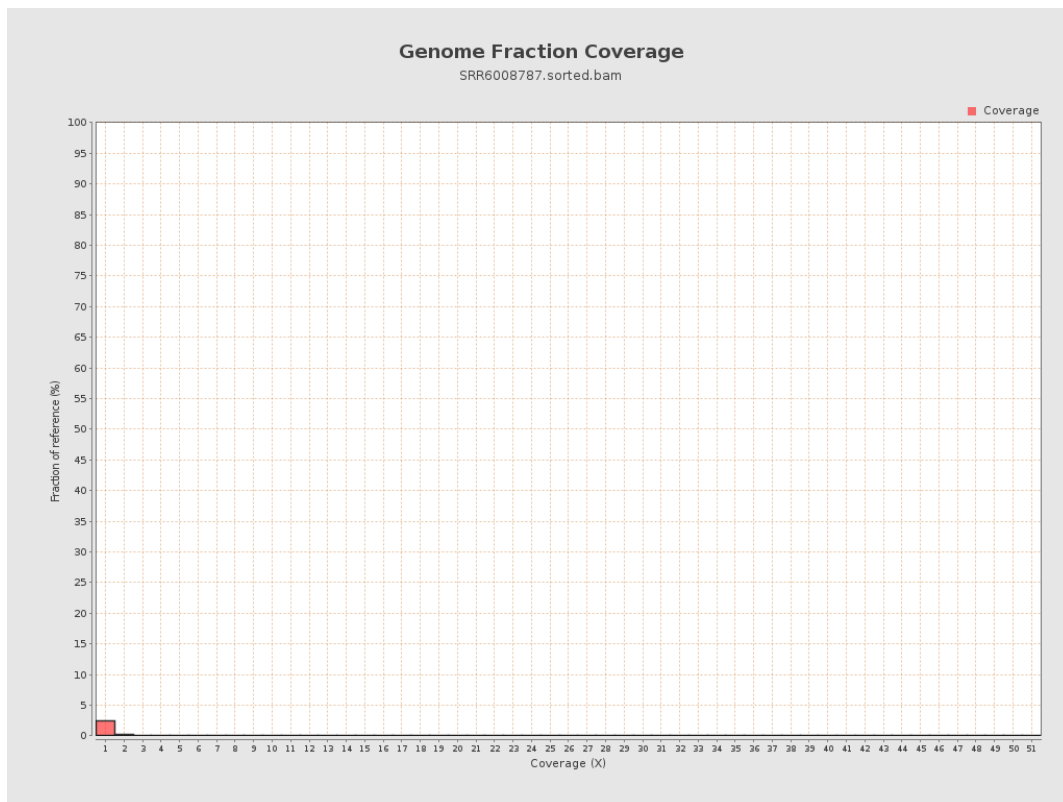
4. Results : Coverage Histogram



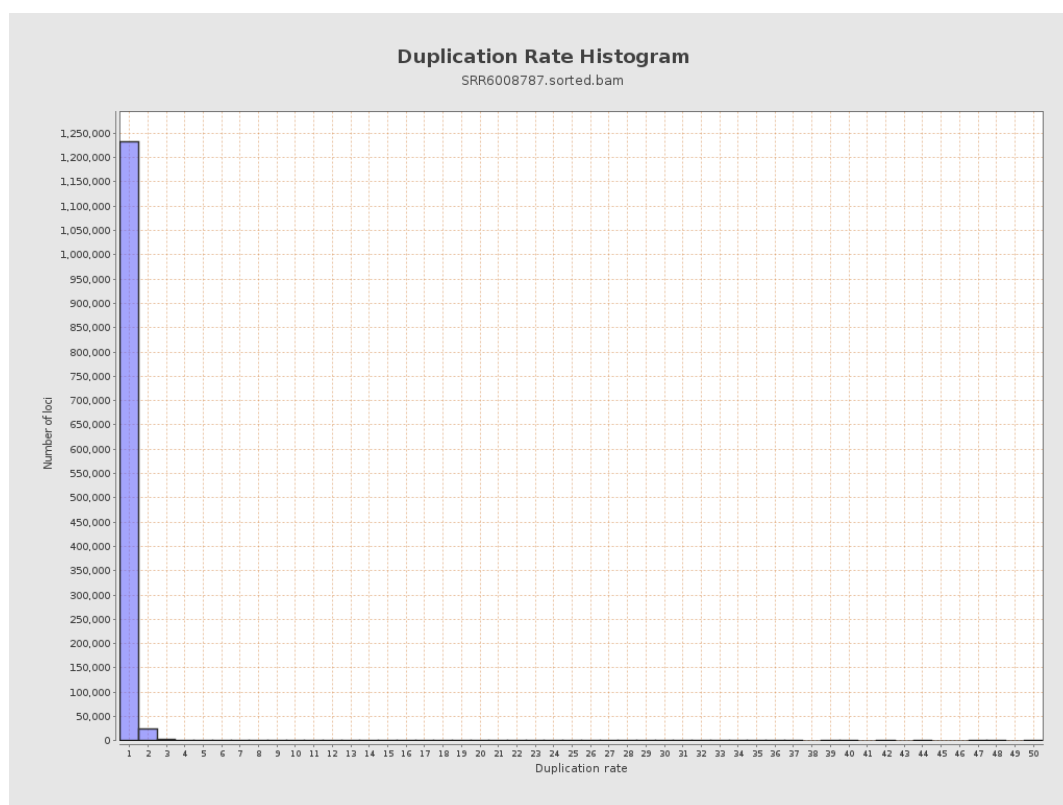
5. Results : Coverage Histogram (0-50X)



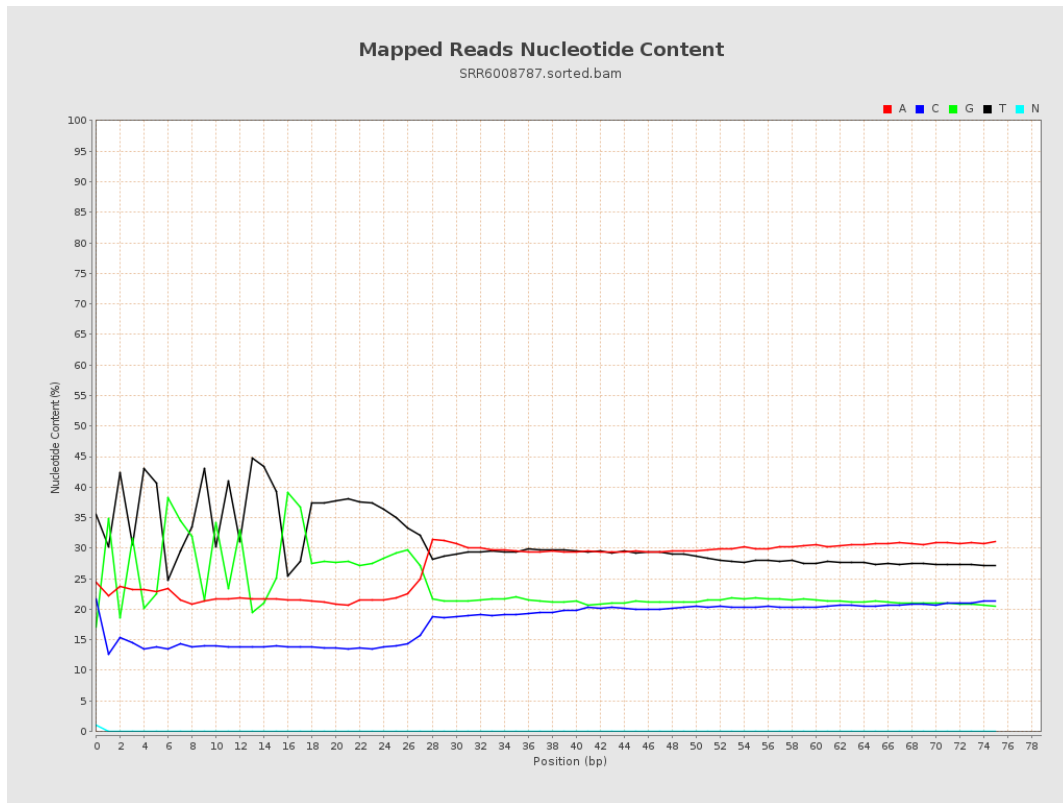
6. Results : Genome Fraction Coverage



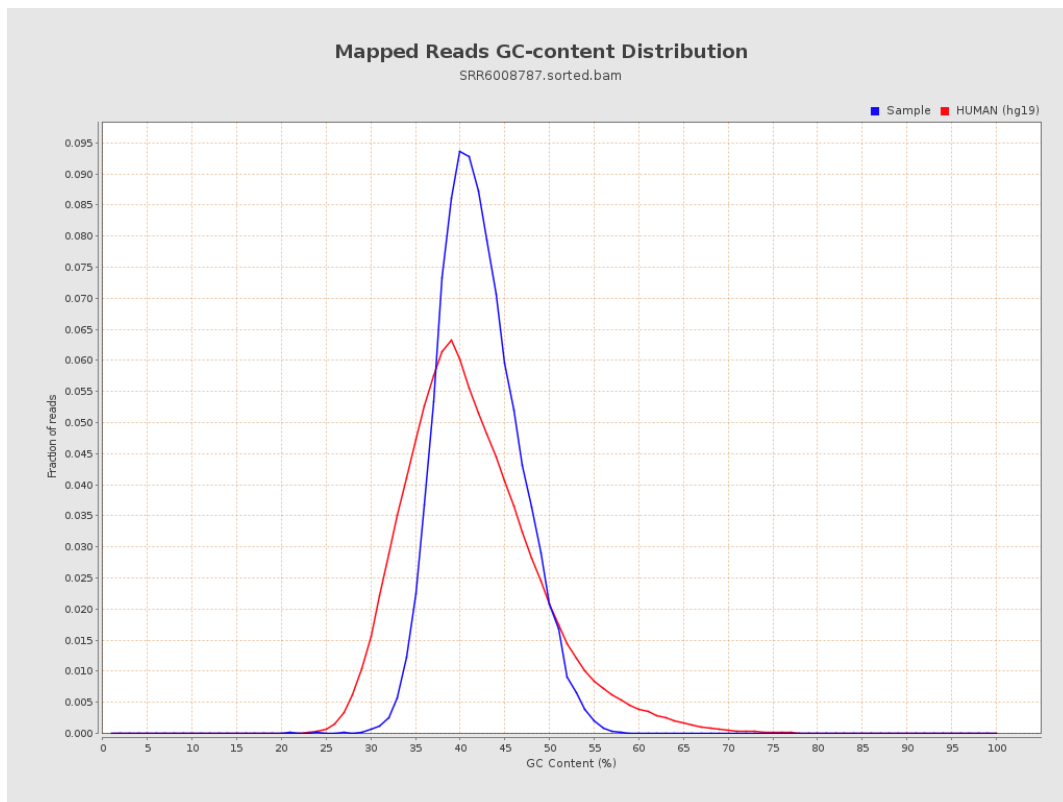
7. Results : Duplication Rate Histogram



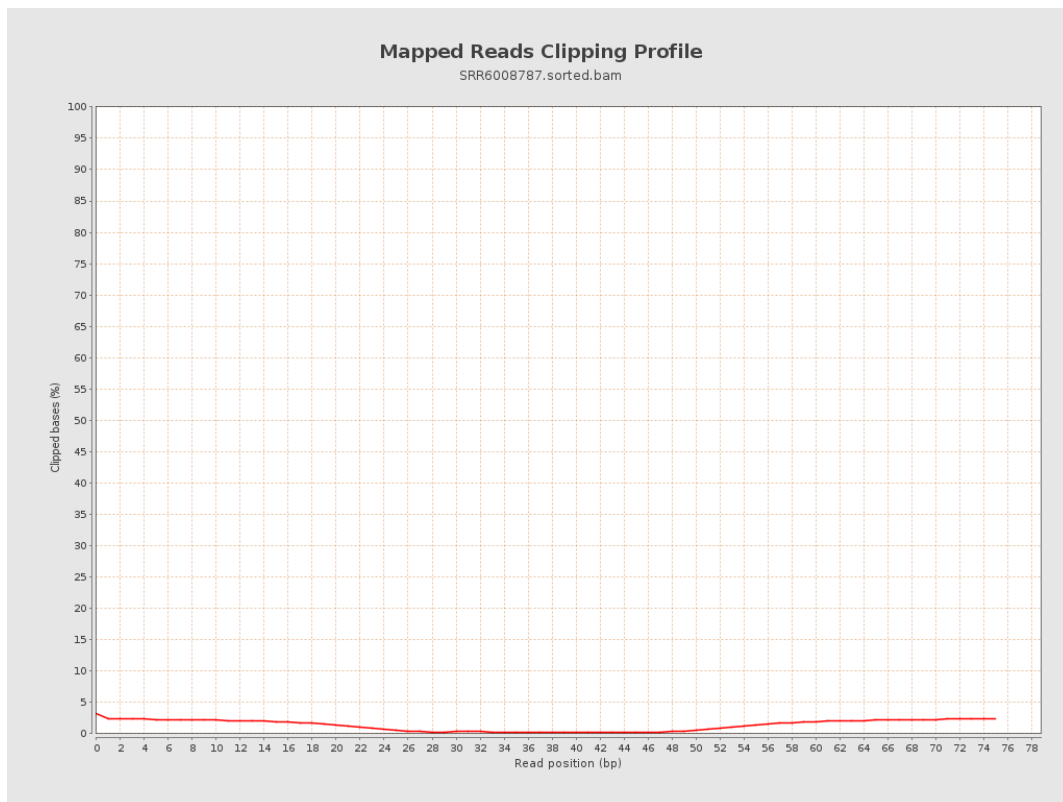
8. Results : Mapped Reads Nucleotide Content



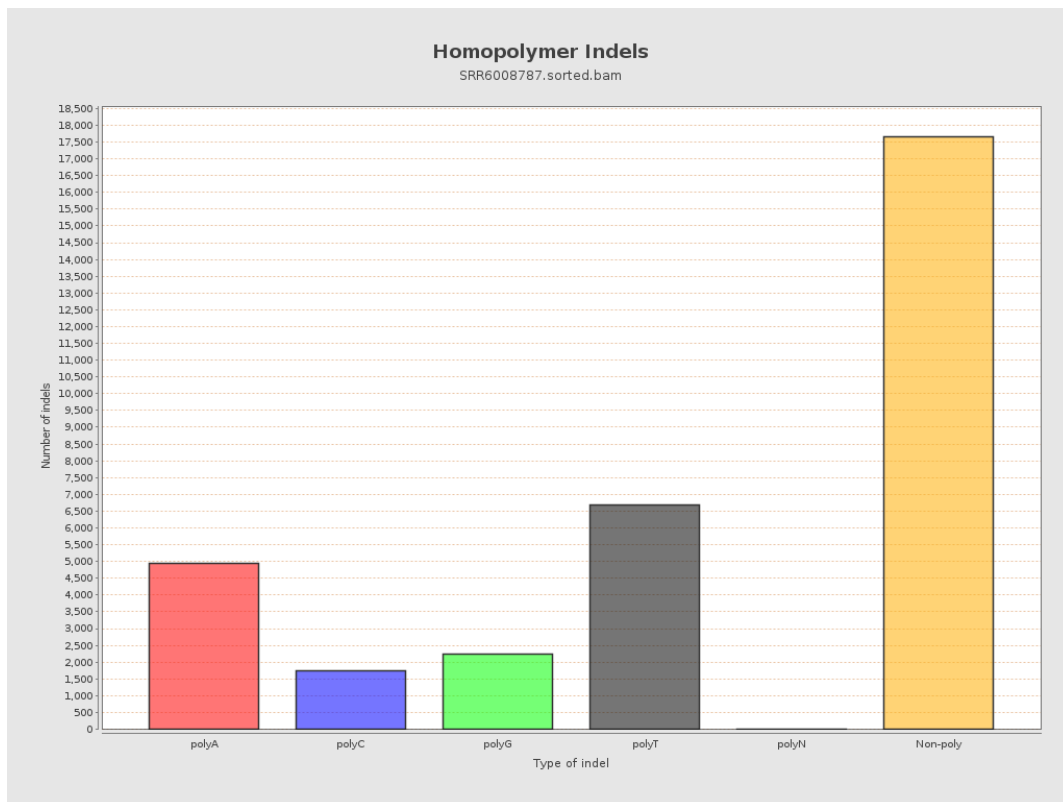
9. Results : Mapped Reads GC-content Distribution



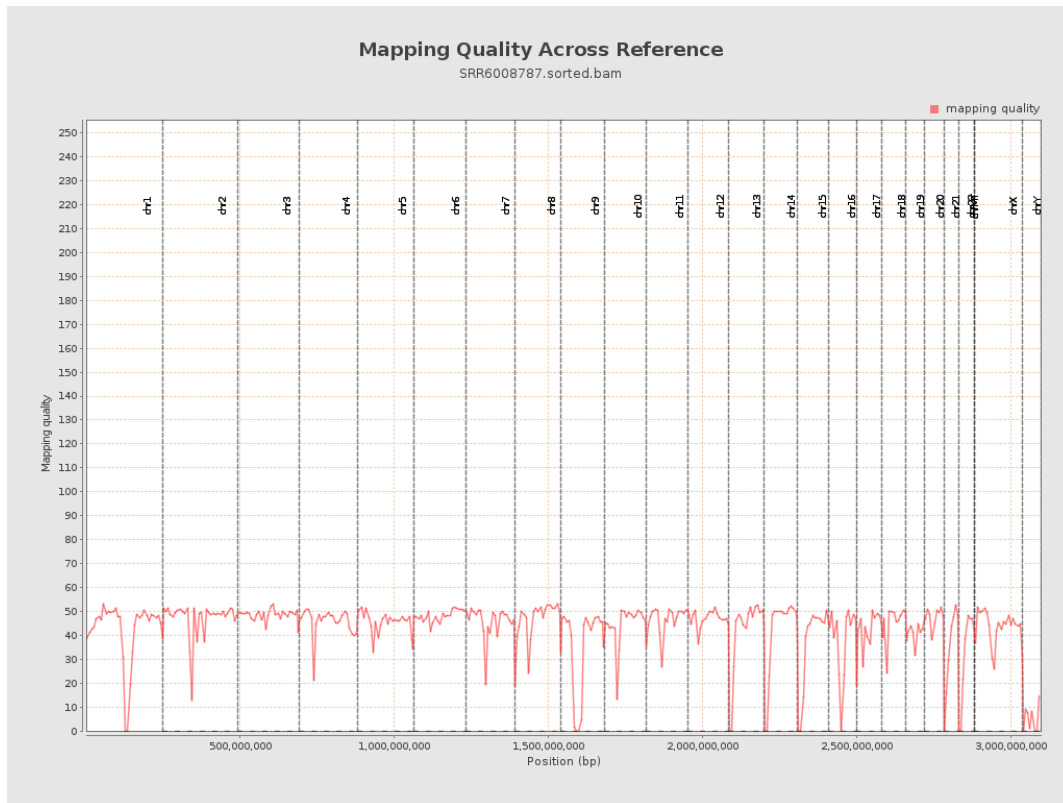
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

