

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:13:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237582.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_SRR6237582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237582.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:13:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,370,995
Mapped reads	1,915,945 / 80.81%
Unmapped reads	455,050 / 19.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,718 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	128,482 / 5.42%
Duplication rate	4.44%
Clipped reads	1,175,733 / 49.59%

2.2. ACGT Content

Number/percentage of A's	30,712,132 / 25.43%
Number/percentage of C's	23,123,372 / 19.15%
Number/percentage of T's	36,323,825 / 30.08%
Number/percentage of G's	30,563,869 / 25.31%
Number/percentage of N's	28,200 / 0.02%
GC Percentage	44.46%

2.3. Coverage

Mean	0.039

Standard Deviation	0.3743
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2.4. Mapping Quality

Mean Mapping Quality	39.19
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2.5. Mismatches and indels

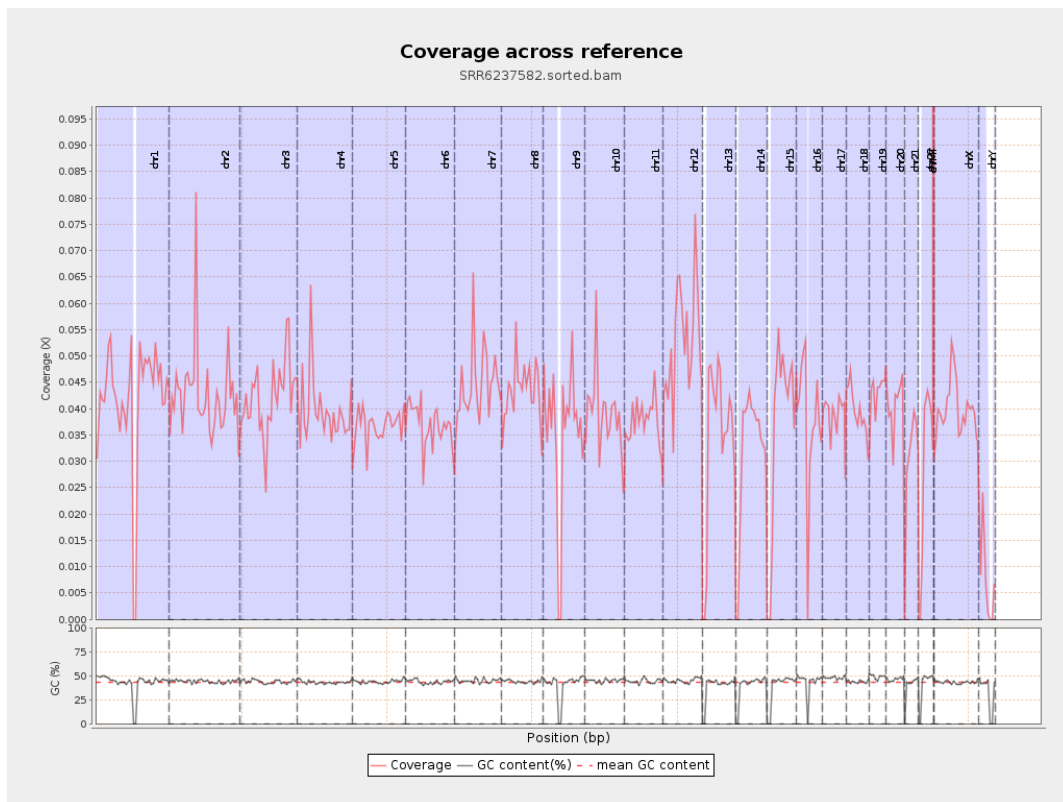
General error rate	0.97%
Mismatches	1,150,278
Insertions	11,510
Mapped reads with at least one insertion	0.59%
Deletions	43,614
Mapped reads with at least one deletion	2.24%
Homopolymer indels	45.91%

2.6. Chromosome stats

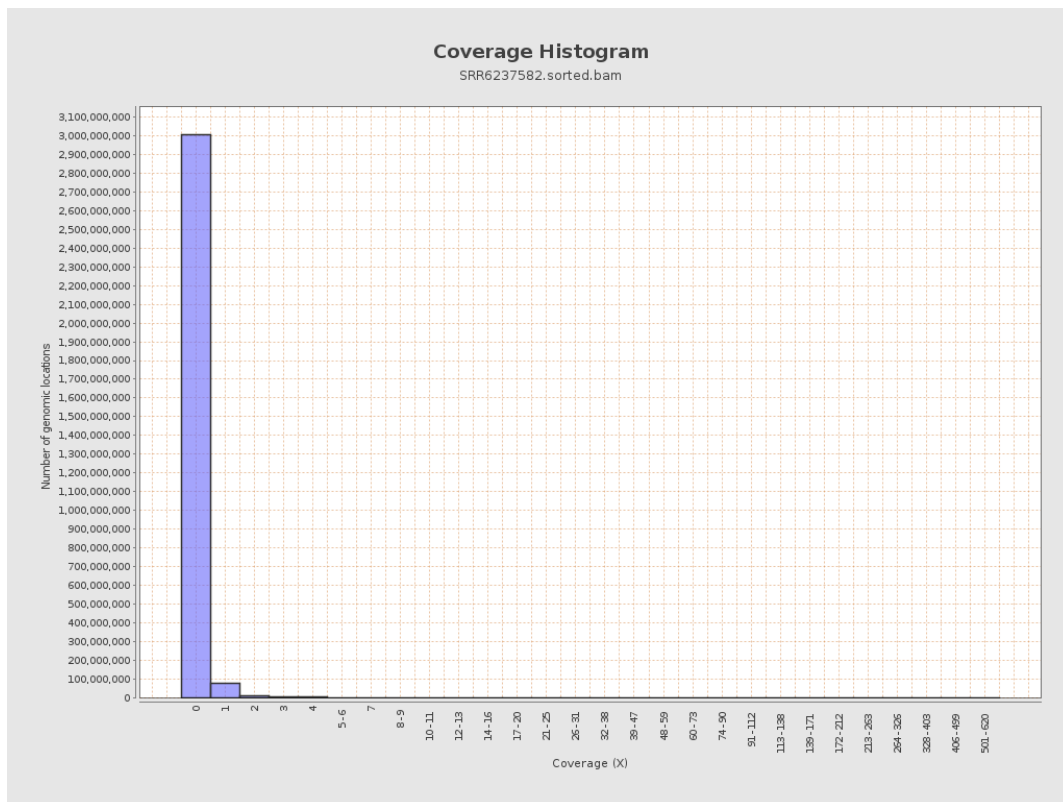
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10403883	0.0417	0.456
chr2	243199373	10381630	0.0427	0.5367
chr3	198022430	8317514	0.042	0.2939
chr4	191154276	7539186	0.0394	0.3034
chr5	180915260	6653770	0.0368	0.2617
chr6	171115067	6310266	0.0369	0.2908
chr7	159138663	7110928	0.0447	0.5475

chr8	146364022	6318067	0.0432	0.3536
chr9	141213431	4914409	0.0348	0.4041
chr10	135534747	5274506	0.0389	0.3728
chr11	135006516	5038252	0.0373	0.4104
chr12	133851895	7115735	0.0532	0.3471
chr13	115169878	3913533	0.034	0.2624
chr14	107349540	3398716	0.0317	0.2871
chr15	102531392	3791004	0.037	0.2842
chr16	90354753	3409169	0.0377	0.3204
chr17	81195210	3130691	0.0386	0.2987
chr18	78077248	3100161	0.0397	0.536
chr19	59128983	2553515	0.0432	0.388
chr20	63025520	2520971	0.04	0.2905
chr21	48129895	1471603	0.0306	0.2766
chr22	51304566	1431990	0.0279	0.2411
chrMT	16571	110247	6.653	5.6812
chrX	155270560	6162808	0.0397	0.3127
chrY	59373566	451281	0.0076	0.1824

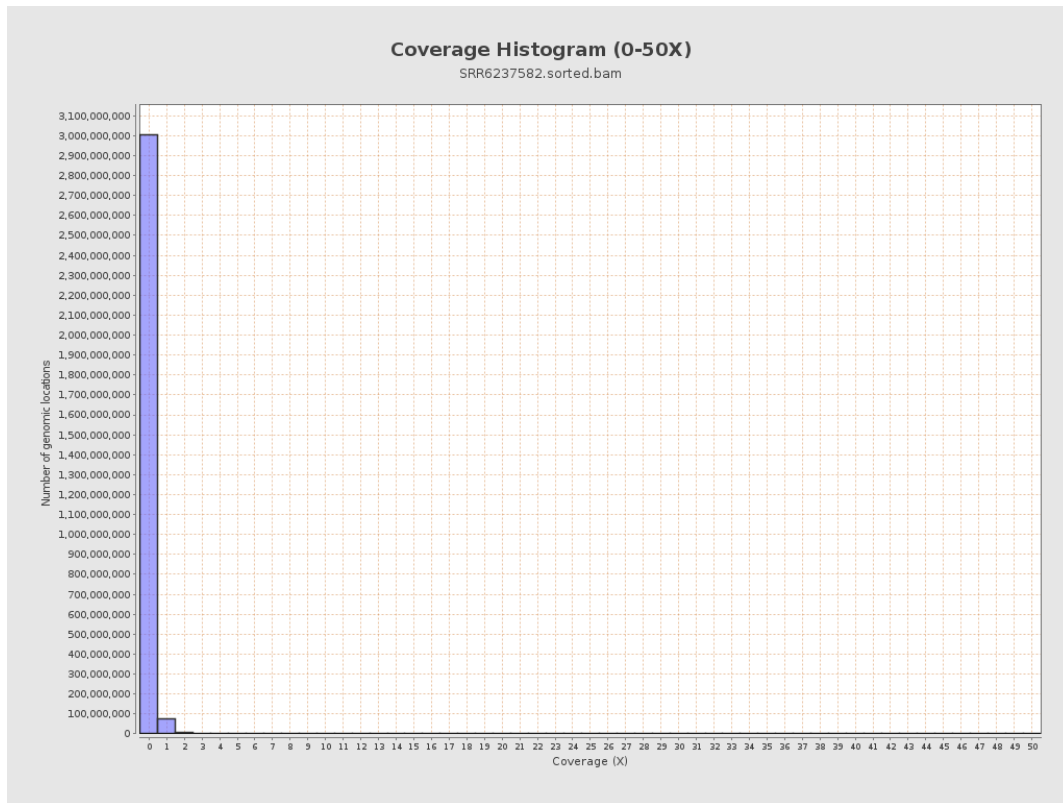
3. Results : Coverage across reference



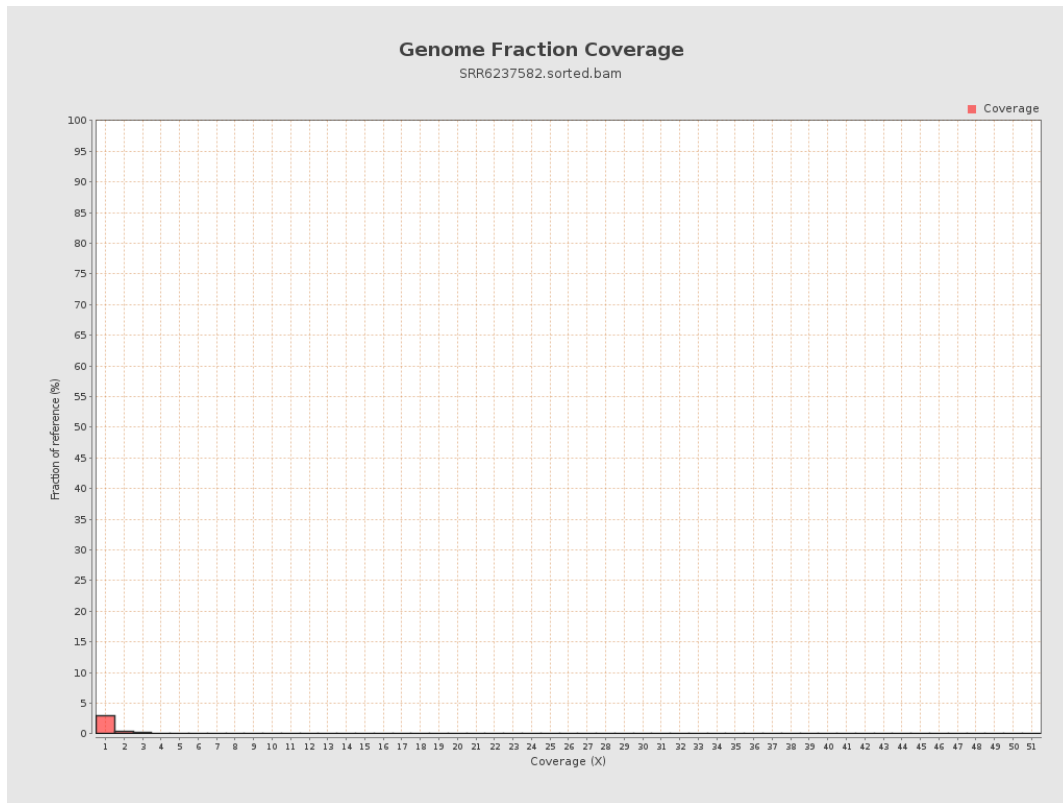
4. Results : Coverage Histogram



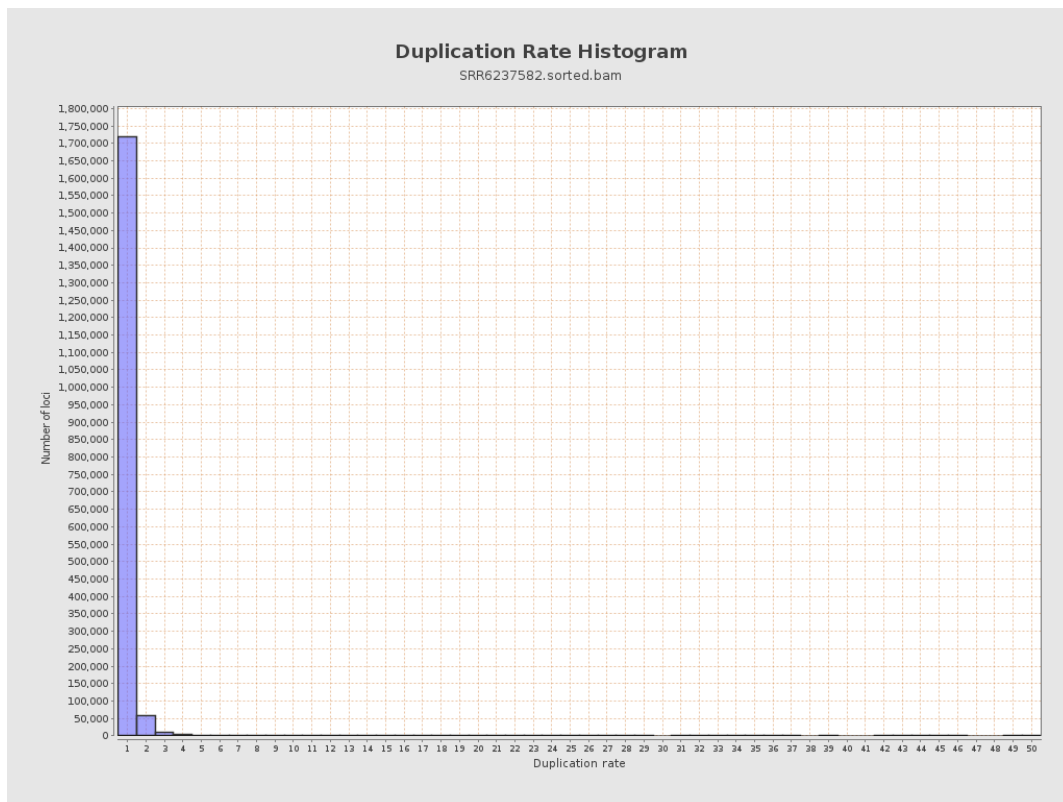
5. Results : Coverage Histogram (0-50X)



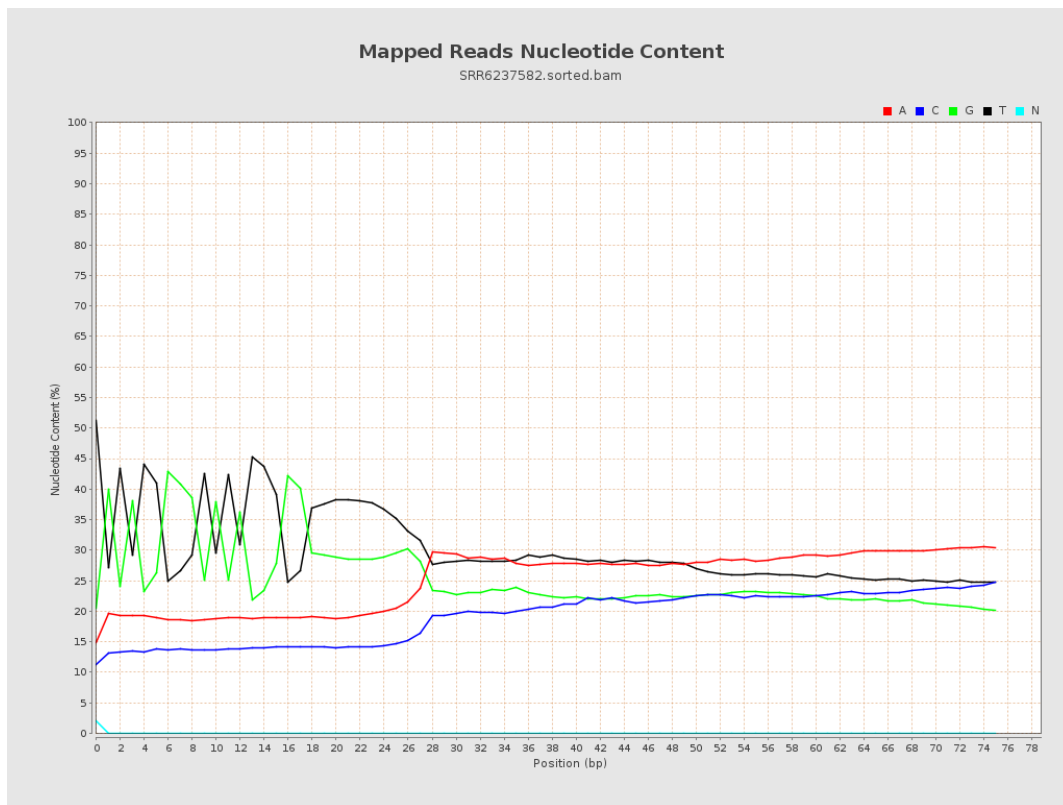
6. Results : Genome Fraction Coverage



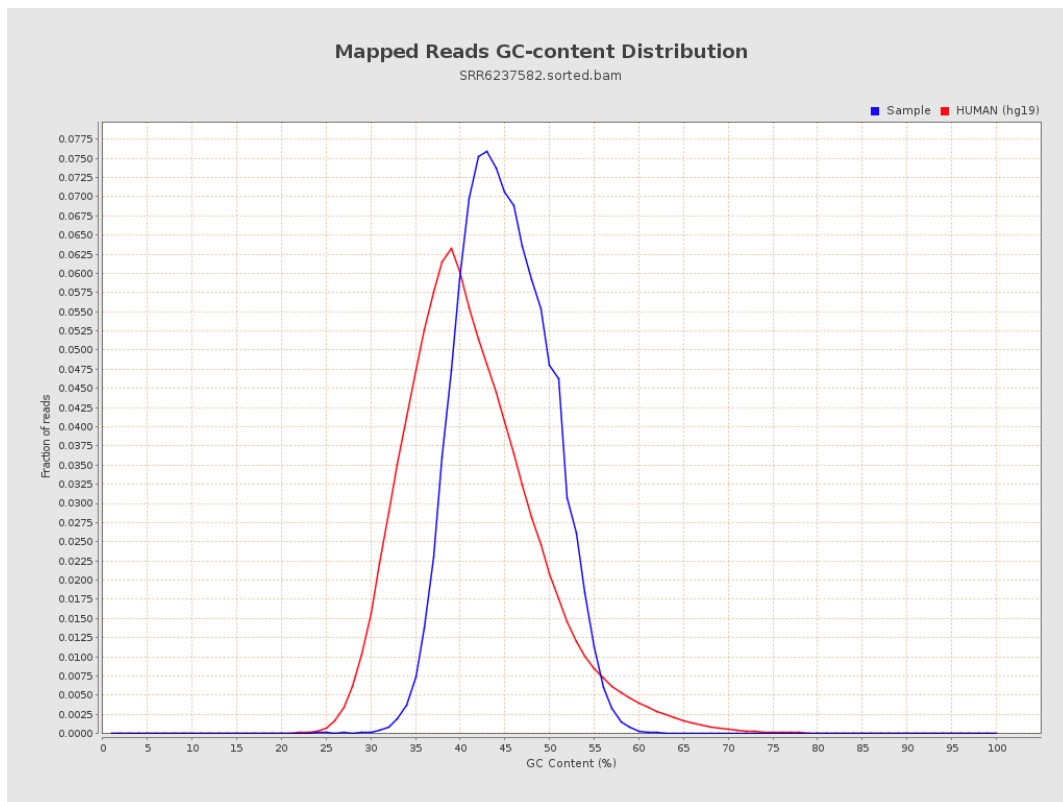
7. Results : Duplication Rate Histogram



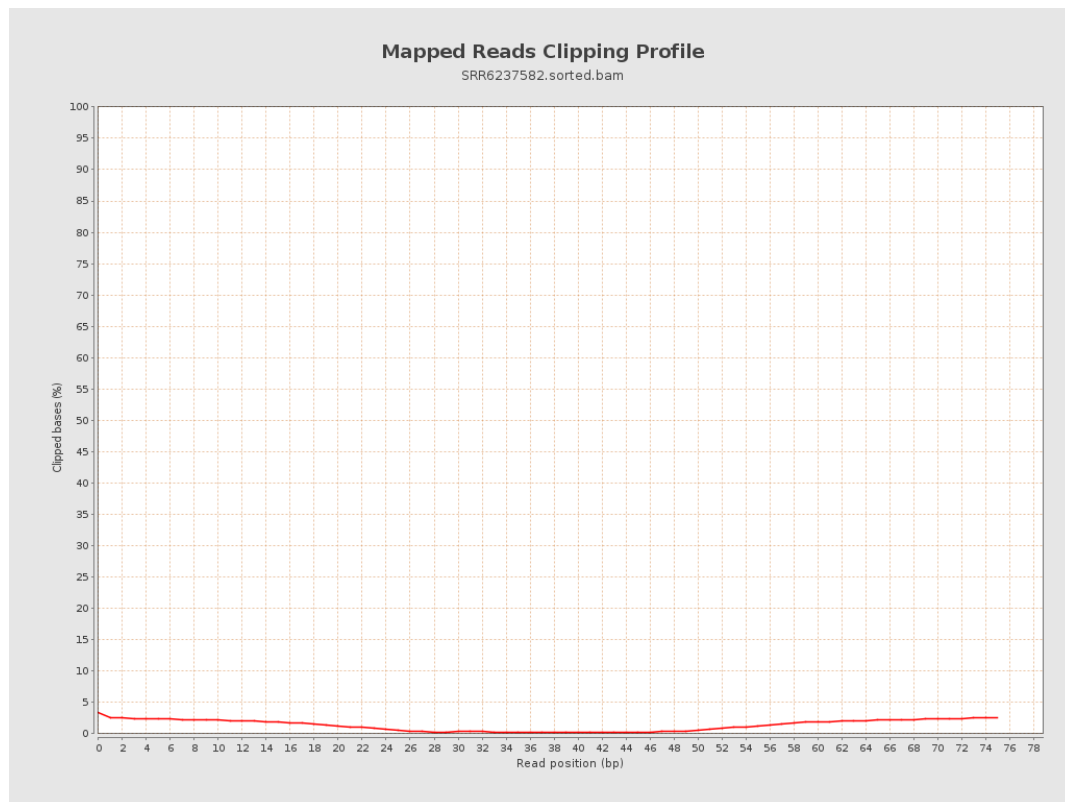
8. Results : Mapped Reads Nucleotide Content



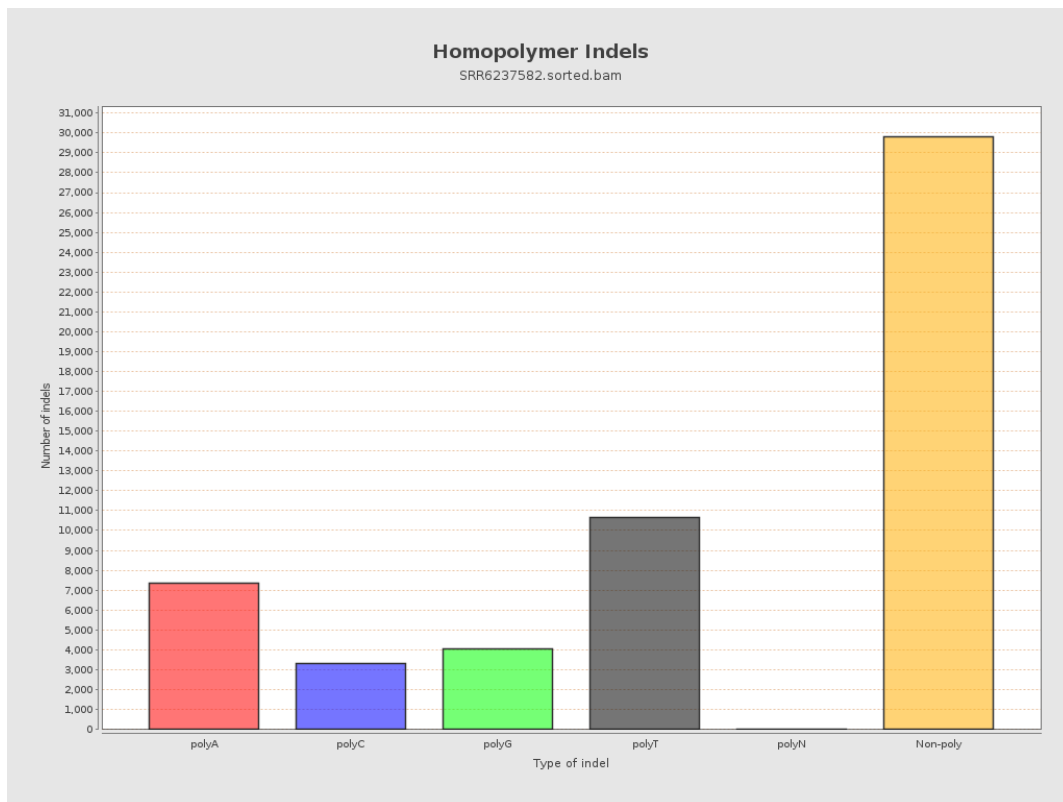
9. Results : Mapped Reads GC-content Distribution



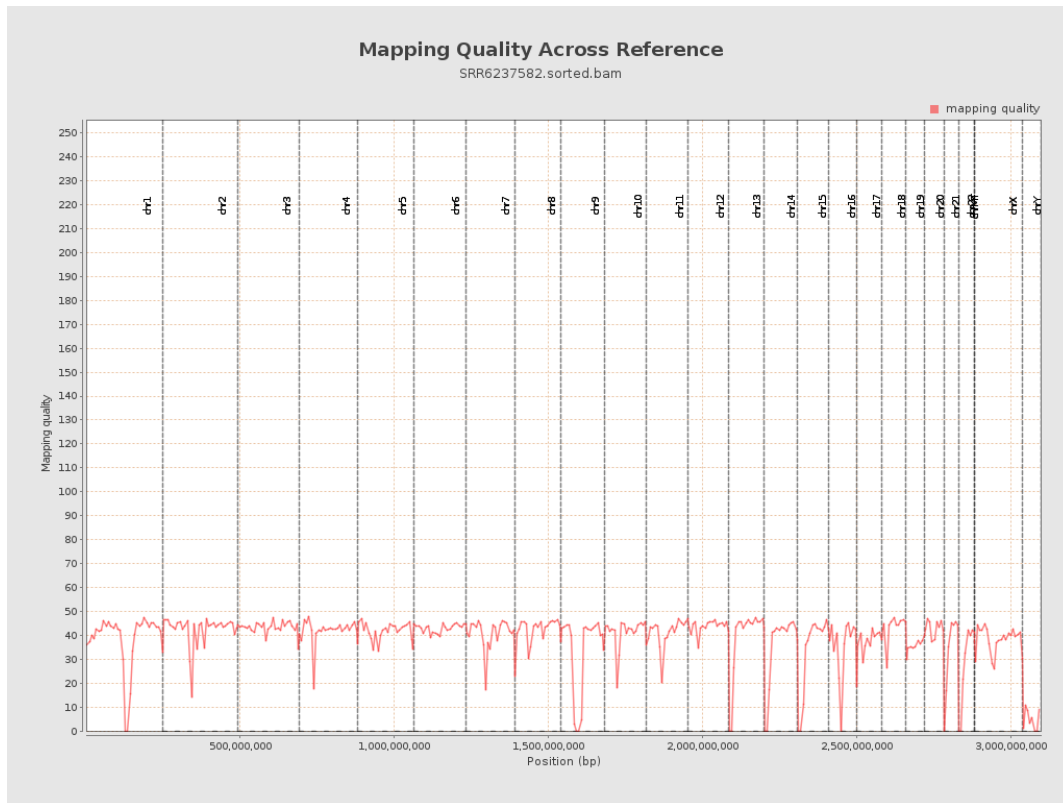
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

