

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:31:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013160.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_SRR6013160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:31:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,847,387
Mapped reads	2,956,524 / 76.84%
Unmapped reads	890,863 / 23.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,360 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	485,866 / 12.63%
Duplication rate	11.53%
Clipped reads	1,546,582 / 40.2%

2.2. ACGT Content

Number/percentage of A's	51,476,439 / 26.91%
Number/percentage of C's	35,249,578 / 18.43%
Number/percentage of T's	60,476,793 / 31.62%
Number/percentage of G's	43,769,329 / 22.88%
Number/percentage of N's	294,918 / 0.15%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0618

Standard Deviation	0.6201
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2.4. Mapping Quality

Mean Mapping Quality	45.61
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2.5. Mismatches and indels

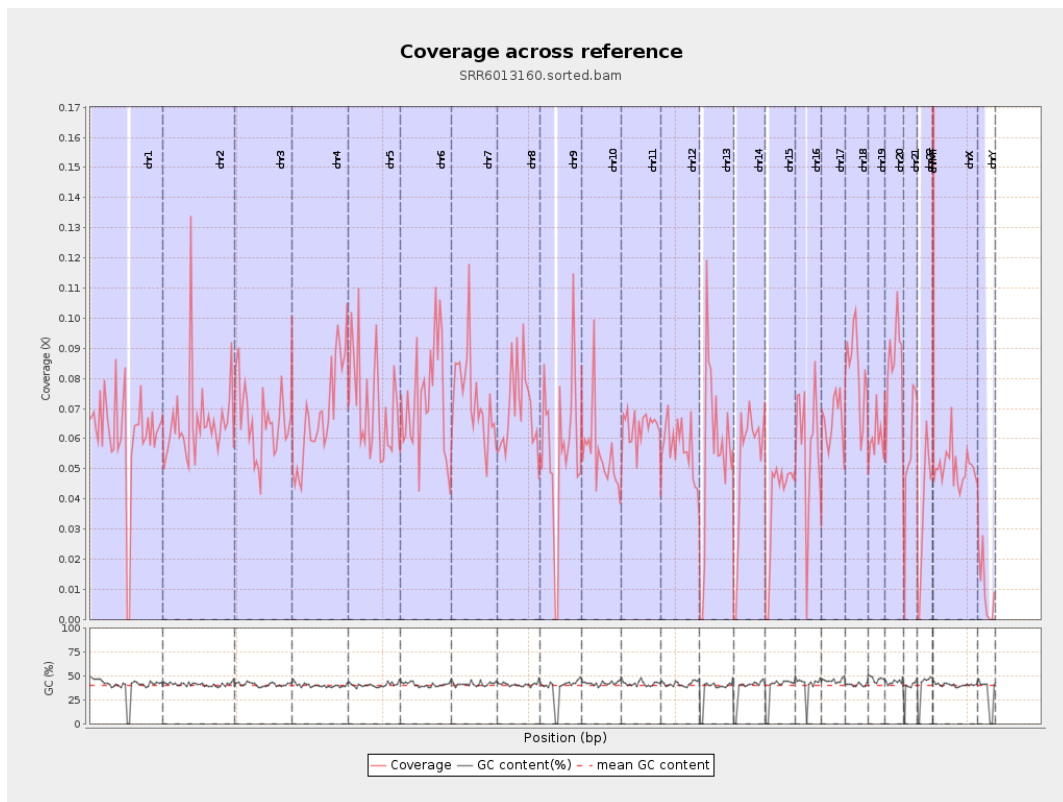
General error rate	0.93%
Mismatches	1,755,942
Insertions	13,018
Mapped reads with at least one insertion	0.44%
Deletions	64,246
Mapped reads with at least one deletion	2.14%
Homopolymer indels	44.43%

2.6. Chromosome stats

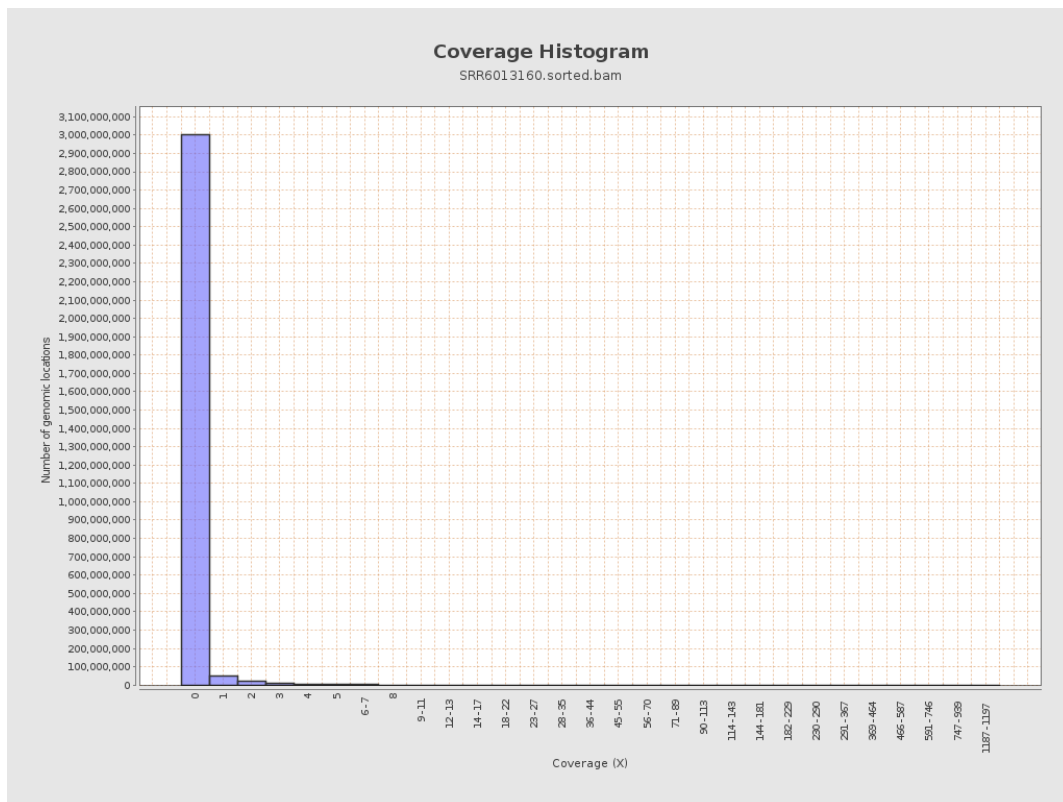
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15241325	0.0611	0.9227
chr2	243199373	15912863	0.0654	0.9007
chr3	198022430	13030607	0.0658	0.4666
chr4	191154276	13035654	0.0682	0.4845
chr5	180915260	12807866	0.0708	0.4846
chr6	171115067	12436504	0.0727	0.5614
chr7	159138663	11628845	0.0731	0.8414

chr8	146364022	10115403	0.0691	0.6791
chr9	141213431	8110625	0.0574	0.596
chr10	135534747	7379845	0.0544	0.5636
chr11	135006516	8610887	0.0638	0.5261
chr12	133851895	7640592	0.0571	0.4386
chr13	115169878	6505916	0.0565	0.4362
chr14	107349540	5643718	0.0526	0.4354
chr15	102531392	3954055	0.0386	0.355
chr16	90354753	5077248	0.0562	0.4565
chr17	81195210	5402281	0.0665	0.4972
chr18	78077248	6453322	0.0827	0.8583
chr19	59128983	3570943	0.0604	0.7246
chr20	63025520	5389424	0.0855	0.5532
chr21	48129895	2730660	0.0567	0.4481
chr22	51304566	1908741	0.0372	0.3462
chrMT	16571	368322	22.2269	13.6607
chrX	155270560	7838193	0.0505	0.4264
chrY	59373566	583909	0.0098	0.1993

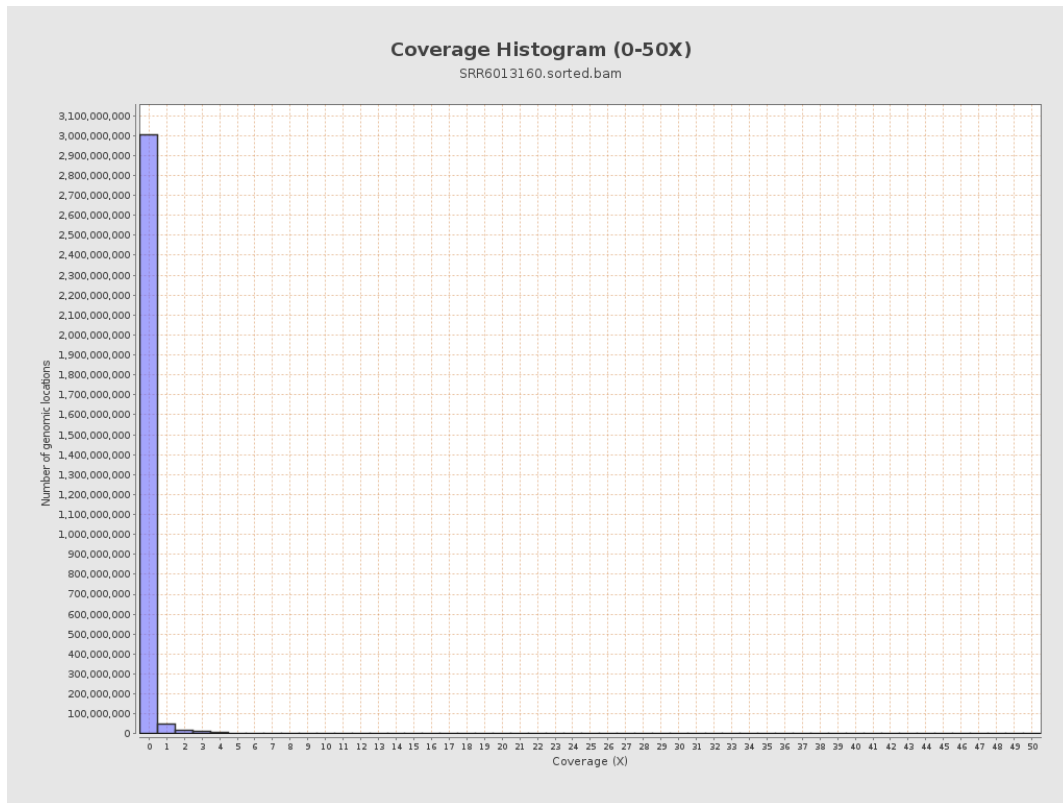
3. Results : Coverage across reference



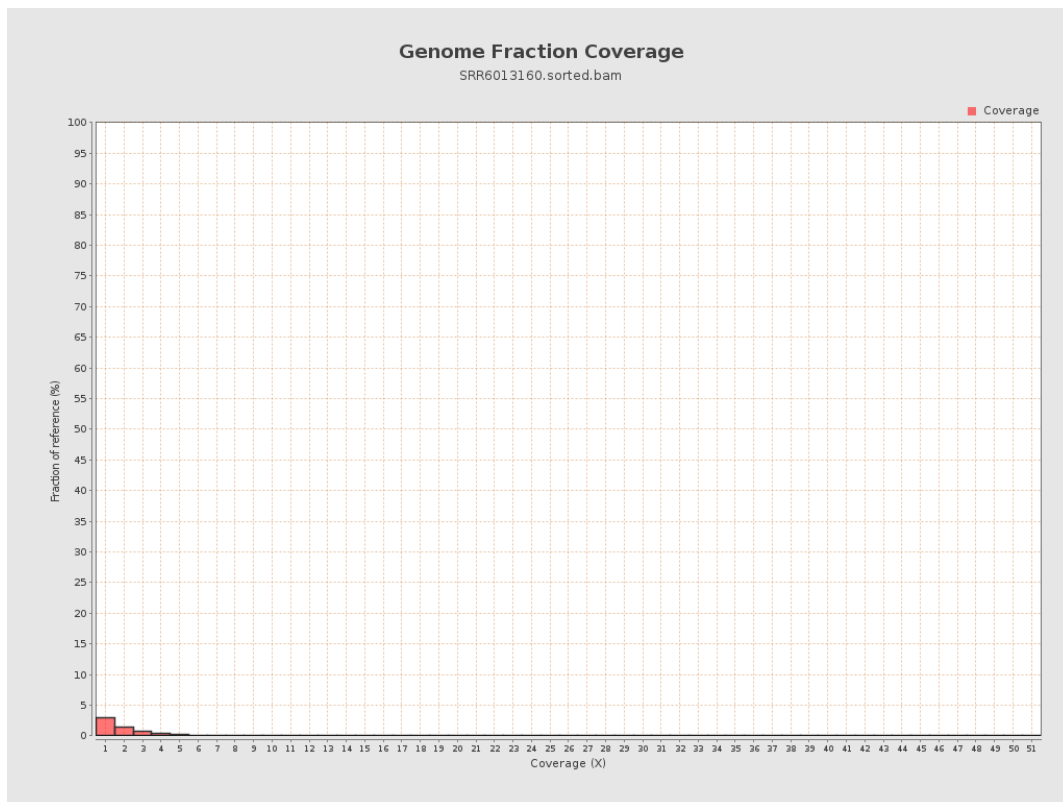
4. Results : Coverage Histogram



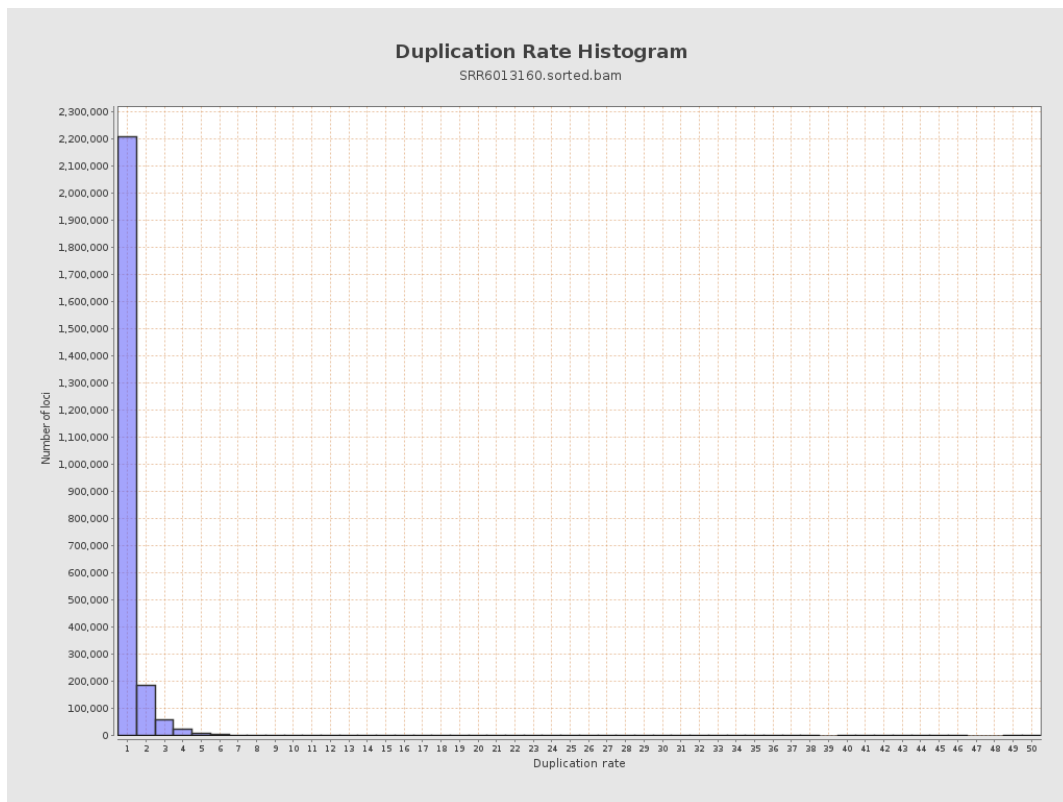
5. Results : Coverage Histogram (0-50X)



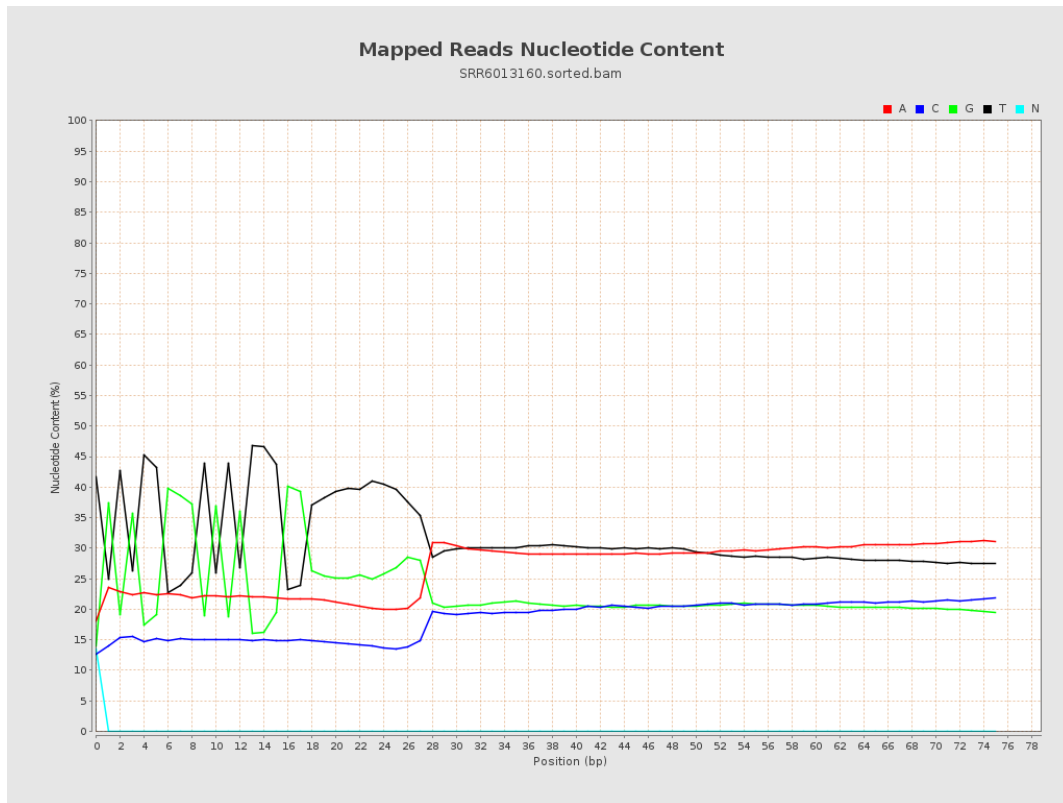
6. Results : Genome Fraction Coverage



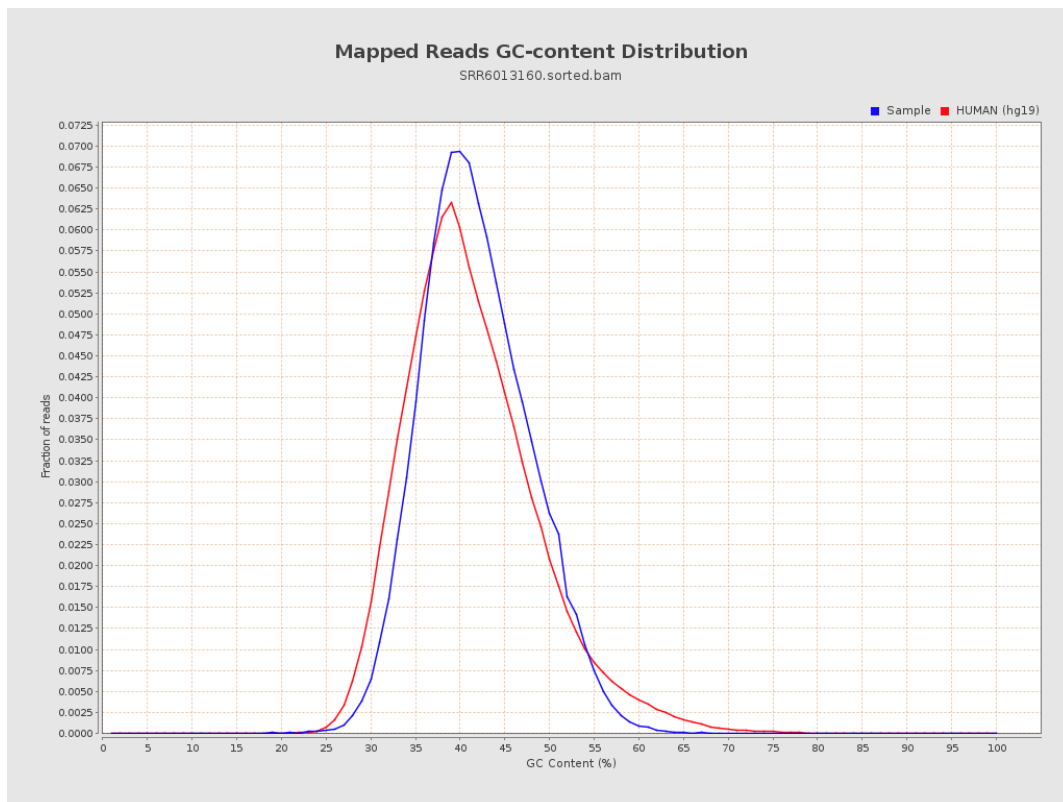
7. Results : Duplication Rate Histogram



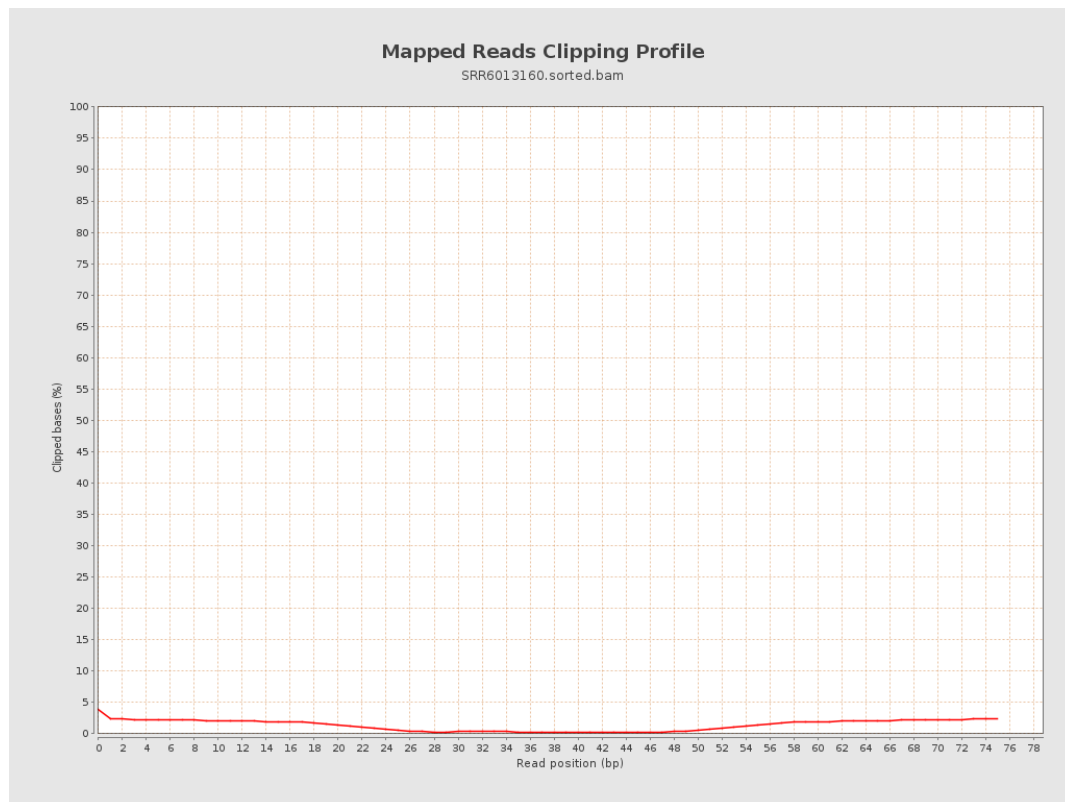
8. Results : Mapped Reads Nucleotide Content



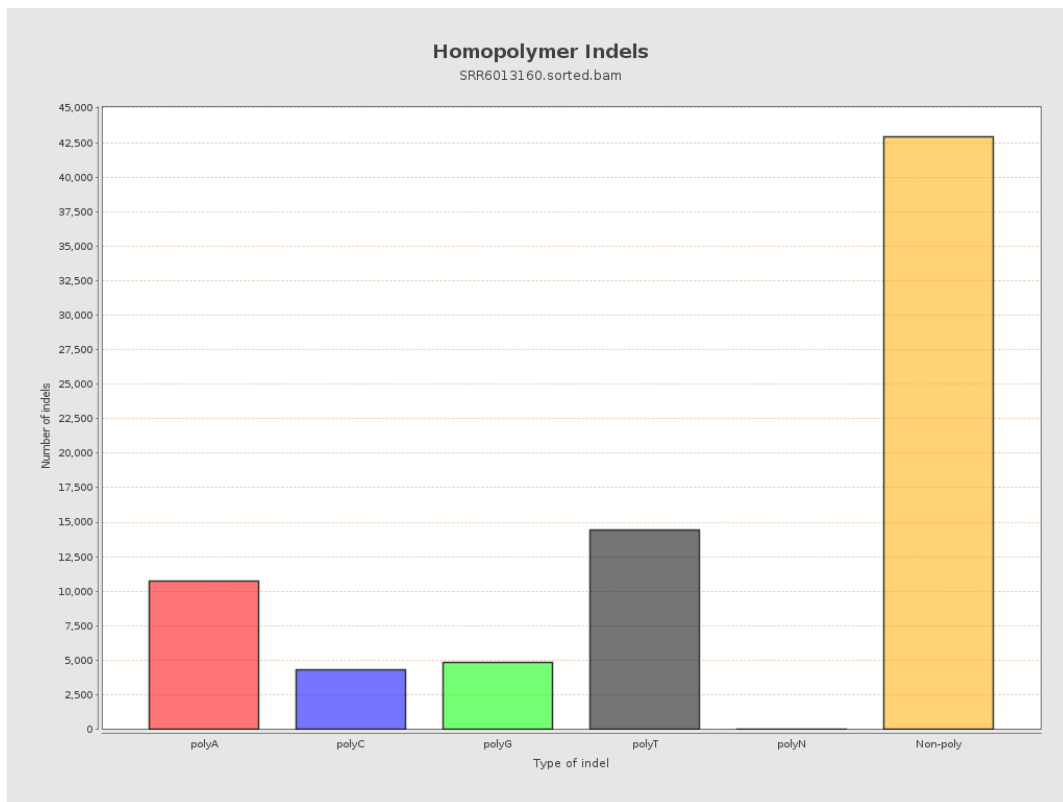
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

