

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:38:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525178.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_SRR10525178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:38:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,396,722
Mapped reads	4,064,878 / 92.45%
Unmapped reads	331,844 / 7.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,145 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	285,224 / 6.49%
Duplication rate	5.13%
Clipped reads	4,075,112 / 92.69%

2.2. ACGT Content

Number/percentage of A's	59,705,708 / 25.35%
Number/percentage of C's	47,101,404 / 20%
Number/percentage of T's	72,673,453 / 30.86%
Number/percentage of G's	56,024,097 / 23.79%
Number/percentage of N's	5,477 / 0%
GC Percentage	43.79%

2.3. Coverage

Mean	0.0761

Standard Deviation	0.661
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	44.67
----------------------	-------

2.5. Mismatches and indels

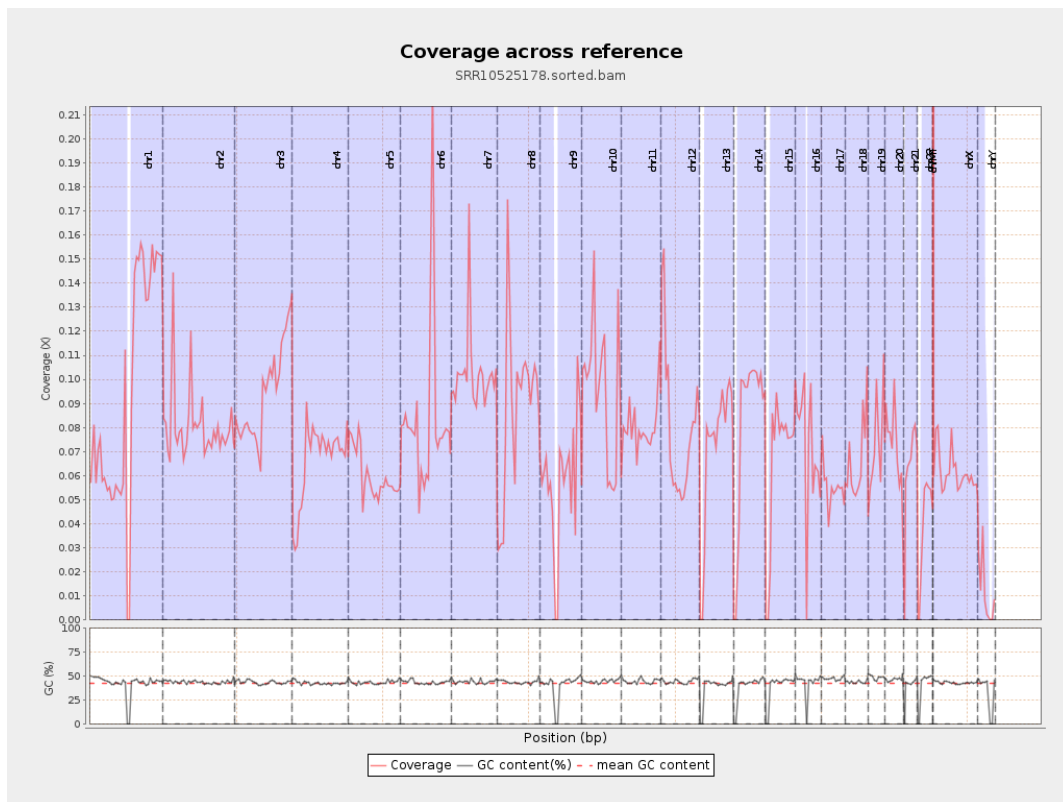
General error rate	0.51%
Mismatches	1,186,586
Insertions	13,887
Mapped reads with at least one insertion	0.34%
Deletions	47,110
Mapped reads with at least one deletion	1.15%
Homopolymer indels	45.11%

2.6. Chromosome stats

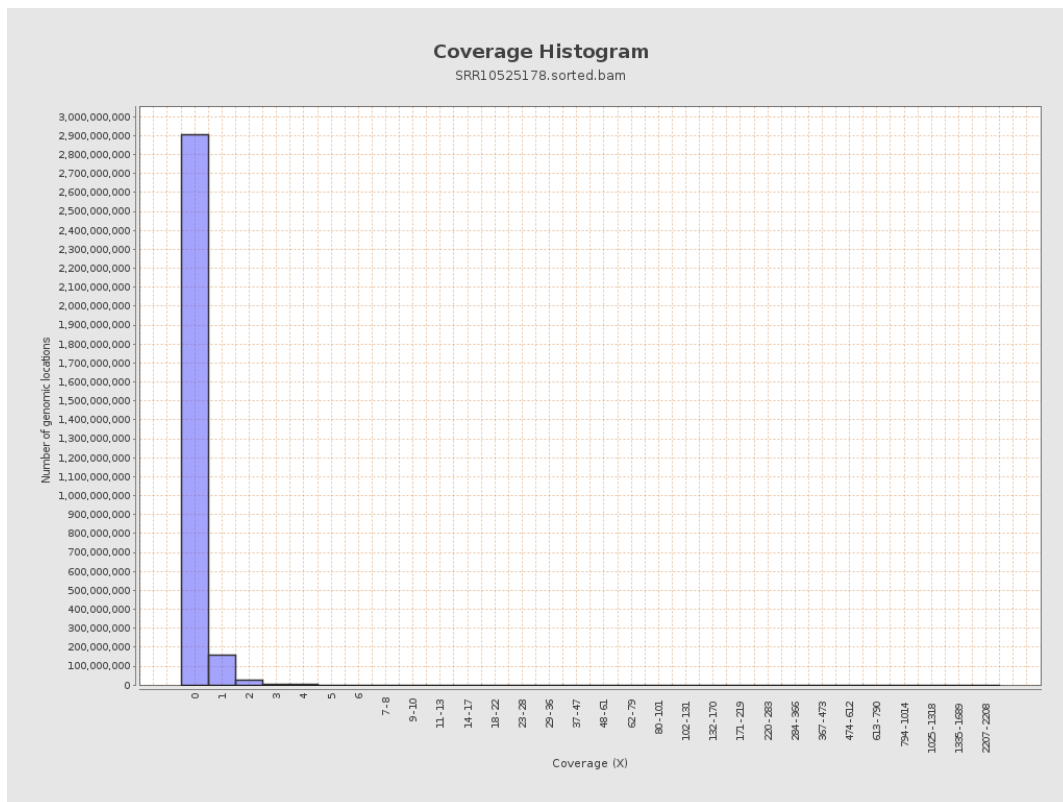
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23470694	0.0942	1.2217
chr2	243199373	19575323	0.0805	0.9837
chr3	198022430	18534477	0.0936	0.3785
chr4	191154276	12764182	0.0668	0.3558
chr5	180915260	10838078	0.0599	0.3006
chr6	171115067	14226735	0.0831	0.4378
chr7	159138663	16336770	0.1027	1.2383

chr8	146364022	13231843	0.0904	0.6128
chr9	141213431	8018856	0.0568	0.458
chr10	135534747	12816970	0.0946	0.6301
chr11	135006516	10812299	0.0801	0.5046
chr12	133851895	10688693	0.0799	0.3497
chr13	115169878	8271375	0.0718	0.3277
chr14	107349540	8875850	0.0827	0.3686
chr15	102531392	6594576	0.0643	0.3191
chr16	90354753	6442329	0.0713	0.3861
chr17	81195210	4501759	0.0554	0.3083
chr18	78077248	5145376	0.0659	0.8994
chr19	59128983	4365911	0.0738	0.8419
chr20	63025520	4579600	0.0727	0.3388
chr21	48129895	3042981	0.0632	0.3528
chr22	51304566	1972940	0.0385	0.2358
chrMT	16571	208582	12.5872	7.1593
chrX	155270560	9589681	0.0618	0.3637
chrY	59373566	679148	0.0114	0.3091

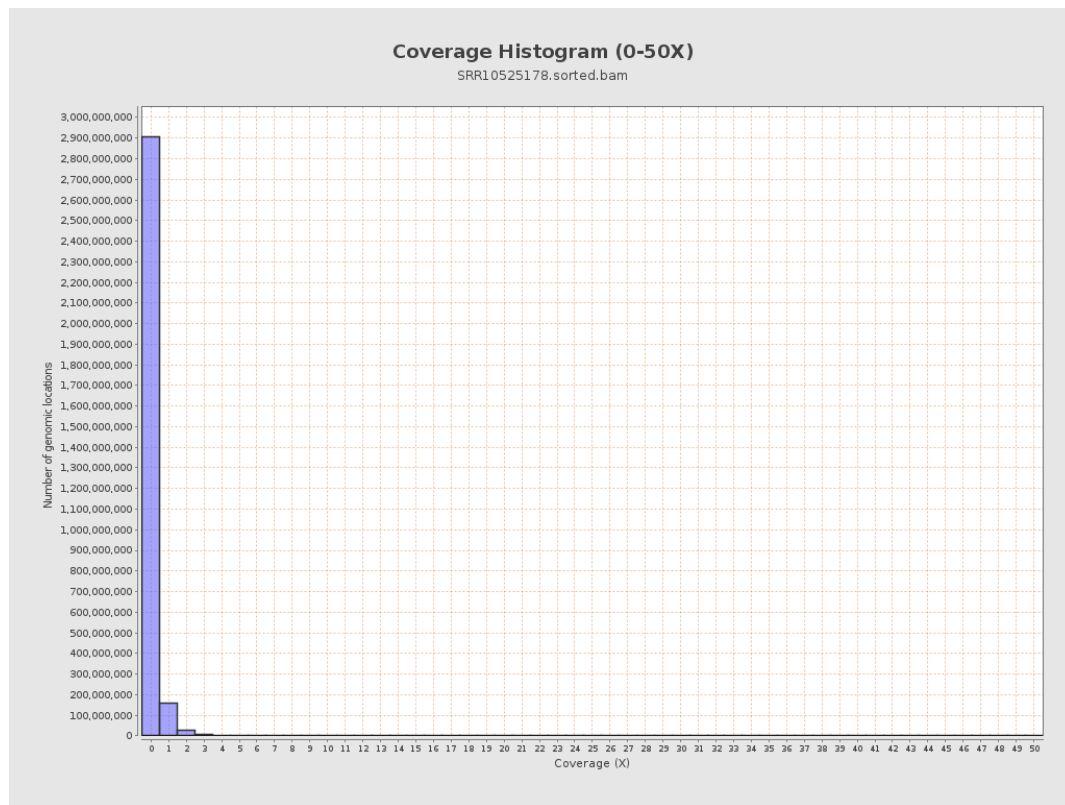
3. Results : Coverage across reference



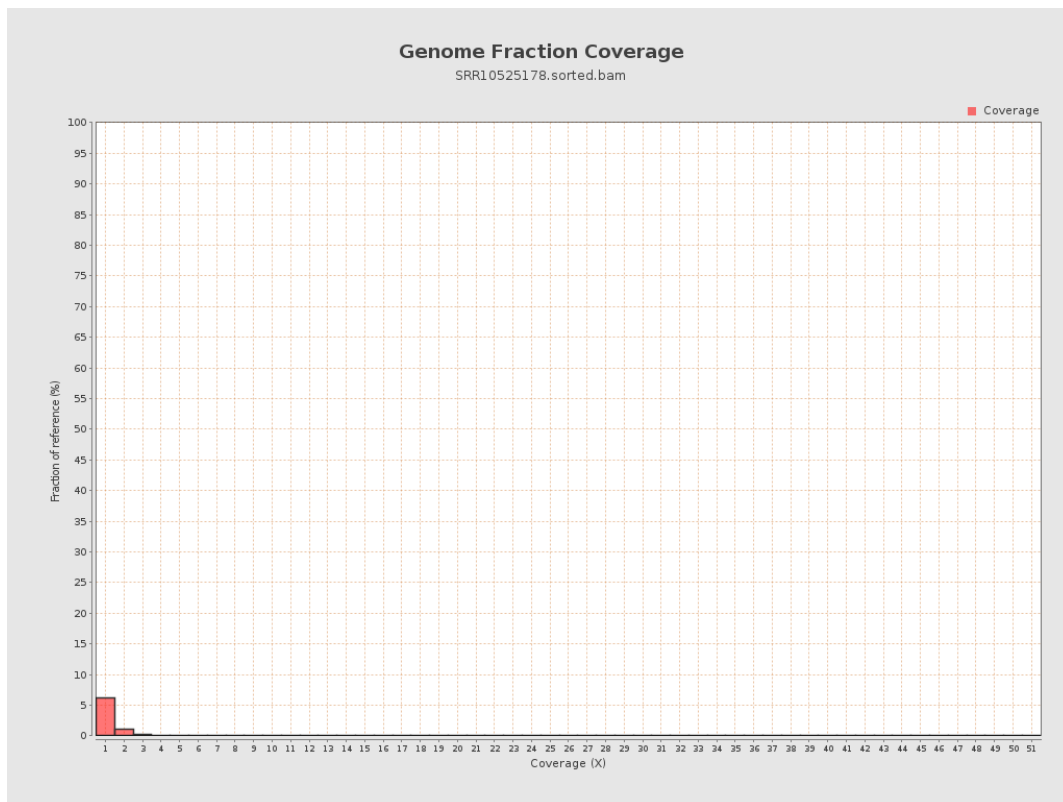
4. Results : Coverage Histogram



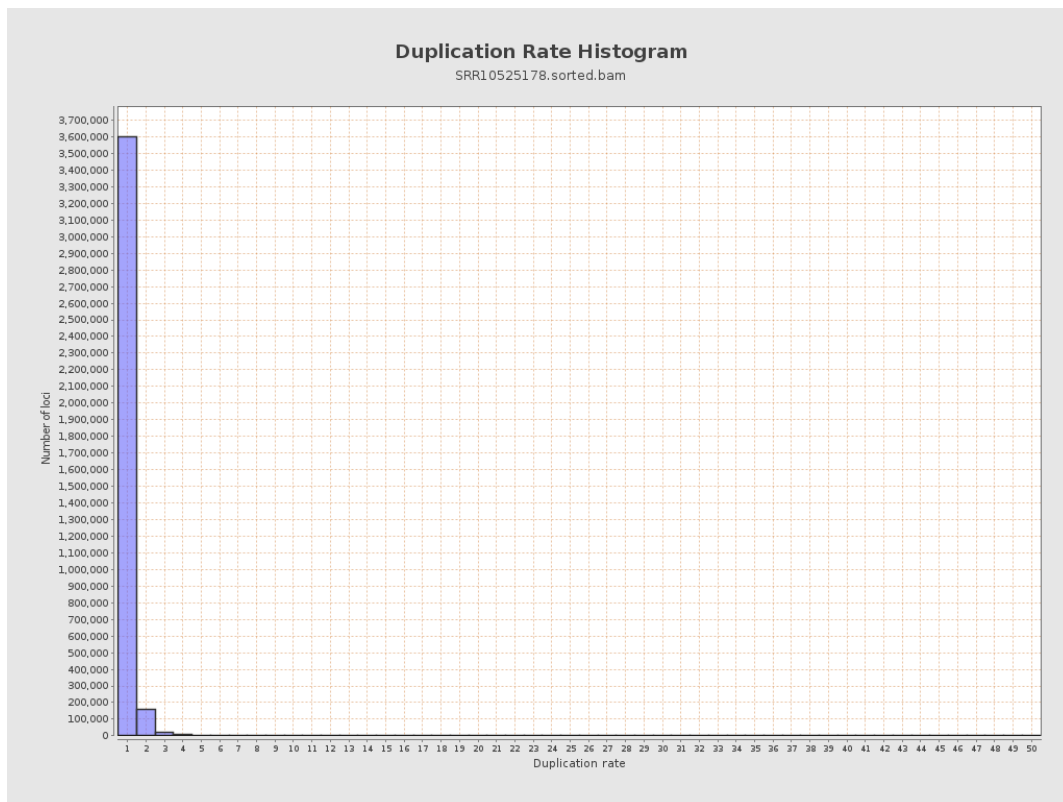
5. Results : Coverage Histogram (0-50X)



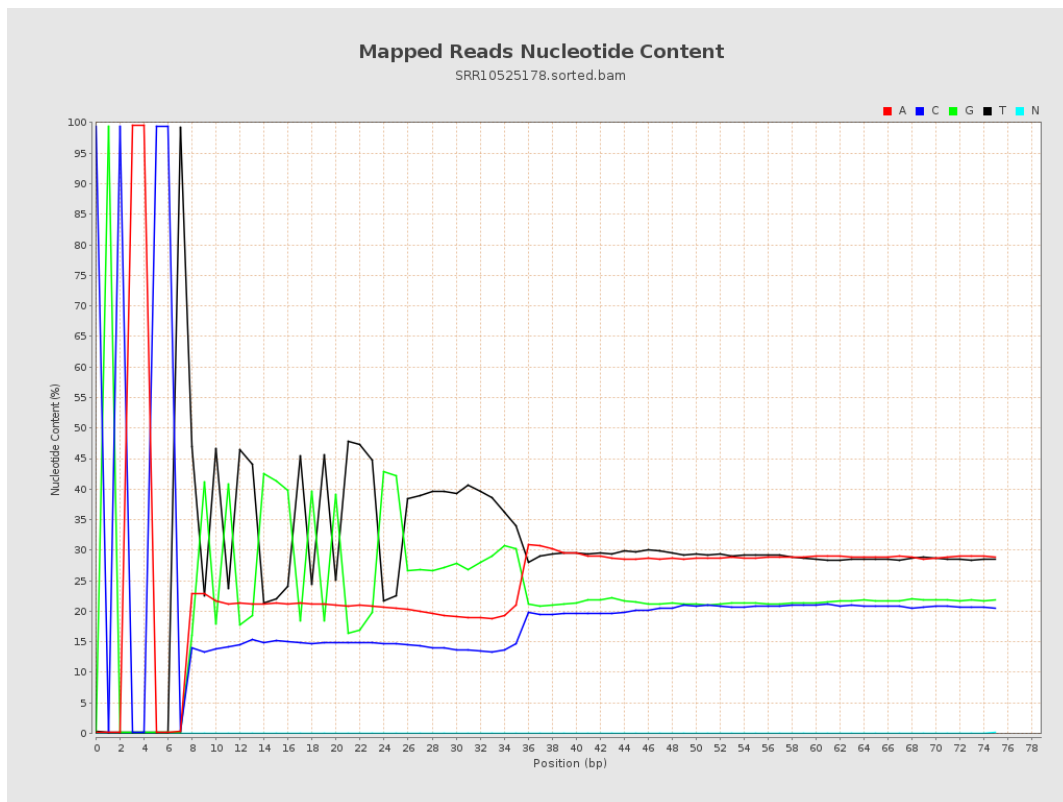
6. Results : Genome Fraction Coverage



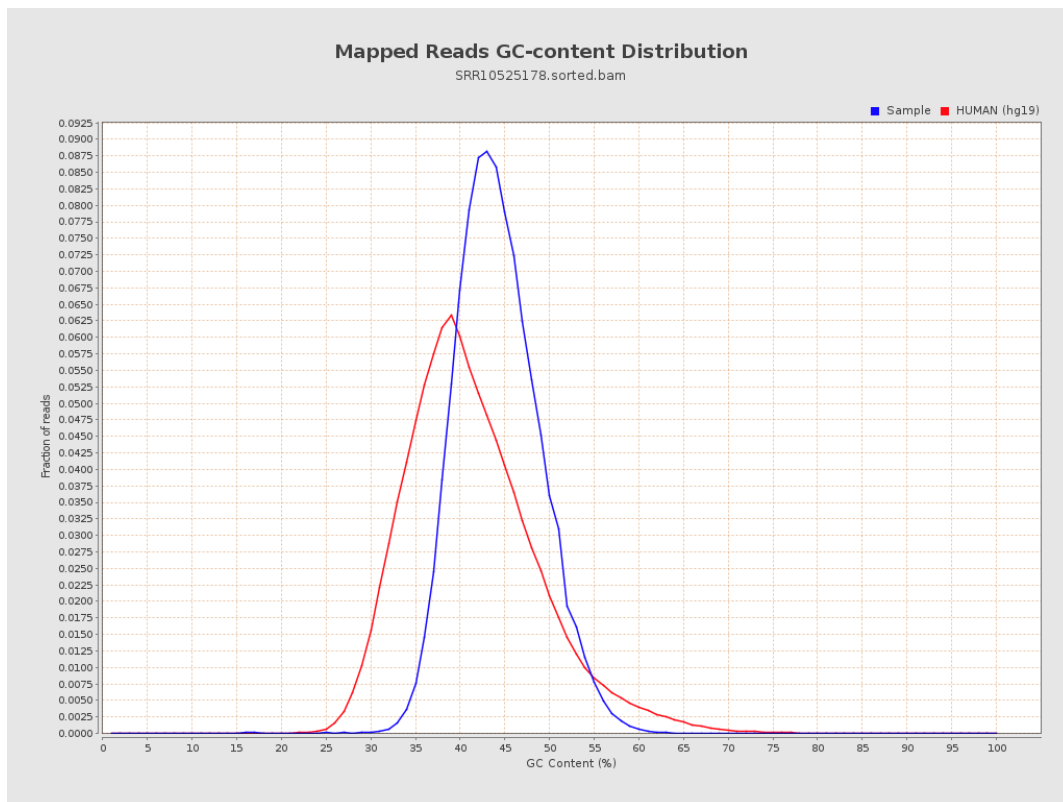
7. Results : Duplication Rate Histogram



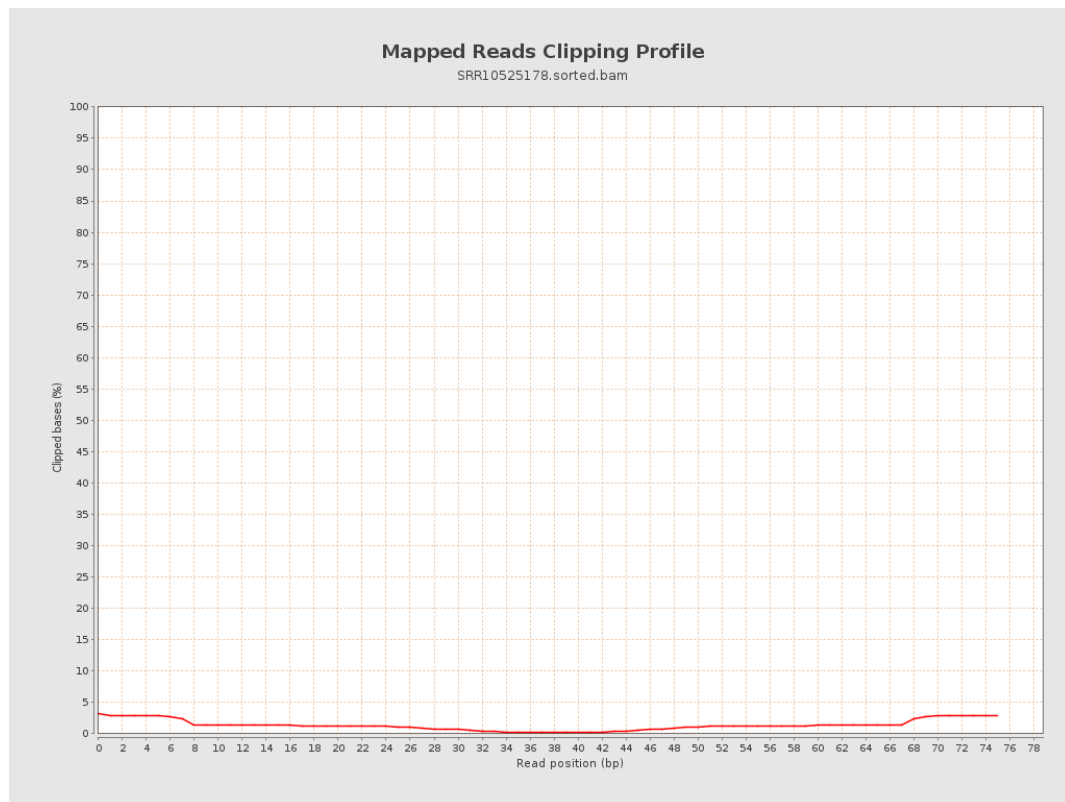
8. Results : Mapped Reads Nucleotide Content



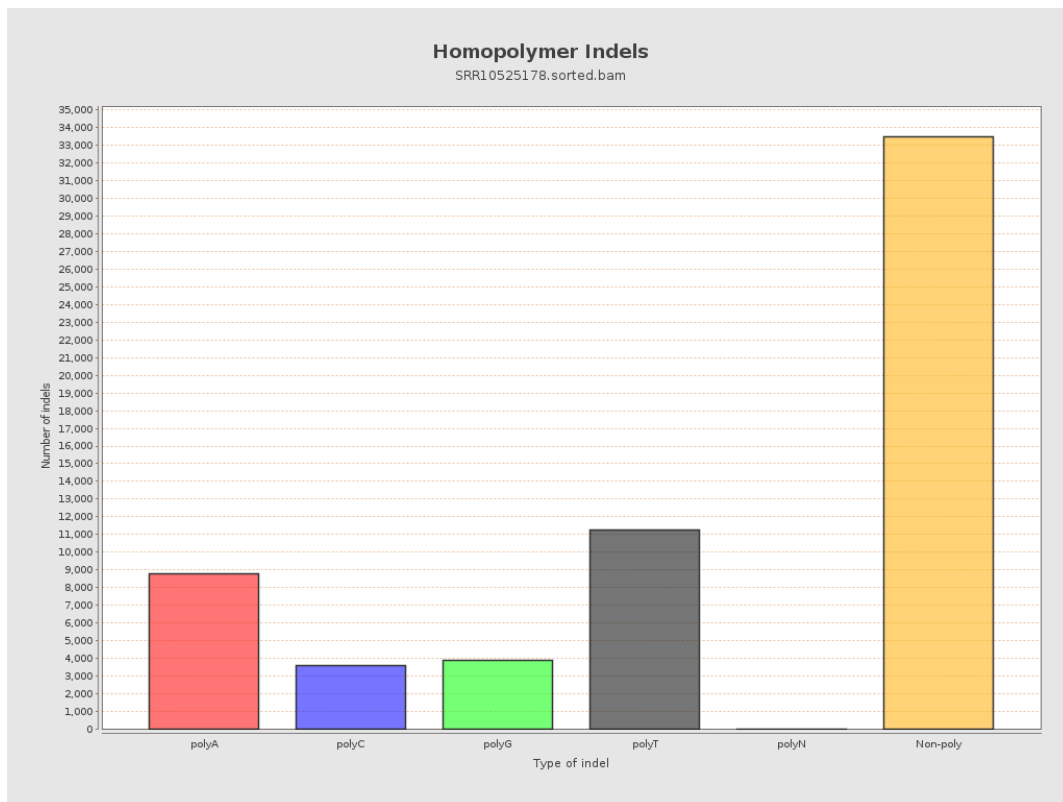
9. Results : Mapped Reads GC-content Distribution



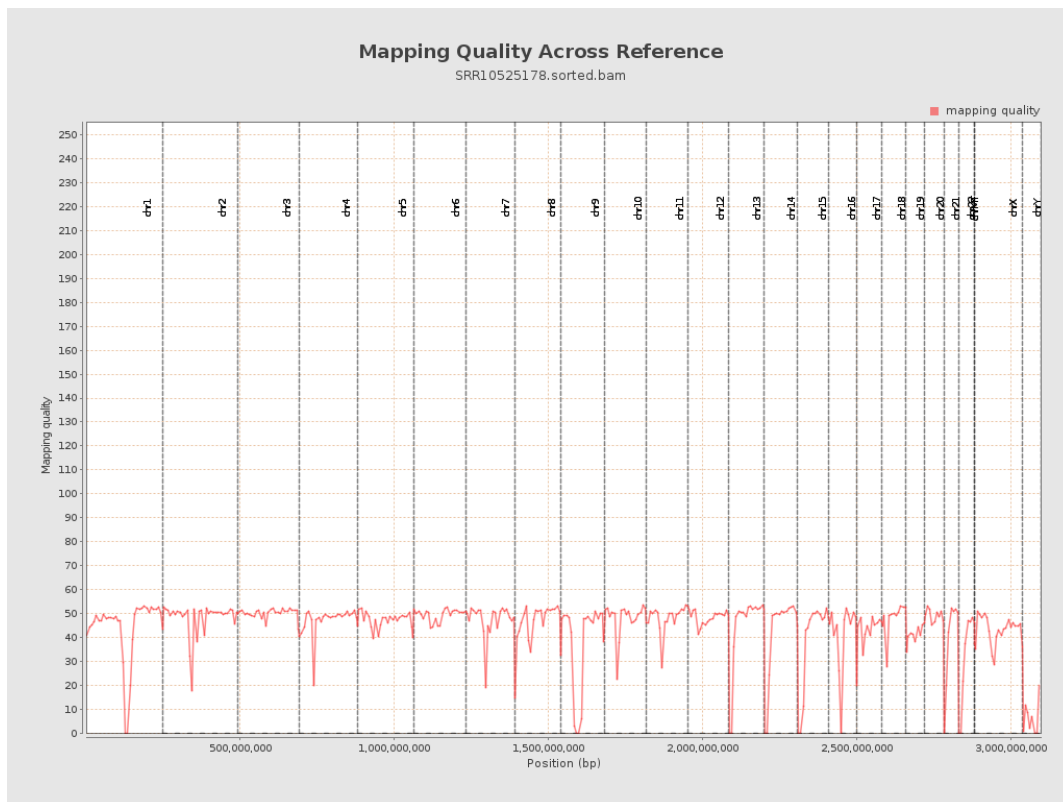
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

