

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:54:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004136.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_SRR6004136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:54:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,712,821
Mapped reads	1,410,996 / 82.38%
Unmapped reads	301,825 / 17.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,102 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	66,444 / 3.88%
Duplication rate	3.68%
Clipped reads	783,951 / 45.77%

2.2. ACGT Content

Number/percentage of A's	24,634,786 / 27.14%
Number/percentage of C's	16,341,683 / 18%
Number/percentage of T's	29,036,188 / 31.99%
Number/percentage of G's	20,743,599 / 22.85%
Number/percentage of N's	15,253 / 0.02%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.2948
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2.4. Mapping Quality

Mean Mapping Quality	45.51
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2.5. Mismatches and indels

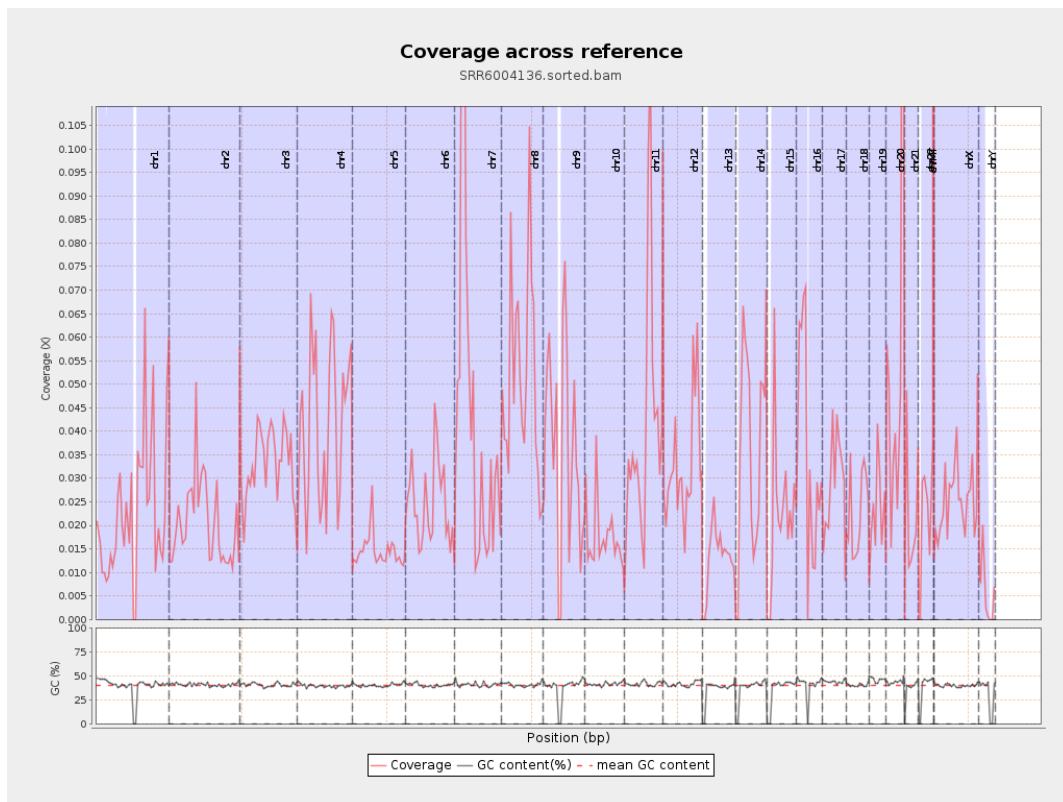
General error rate	0.98%
Mismatches	876,719
Insertions	7,589
Mapped reads with at least one insertion	0.53%
Deletions	25,457
Mapped reads with at least one deletion	1.78%
Homopolymer indels	44.93%

2.6. Chromosome stats

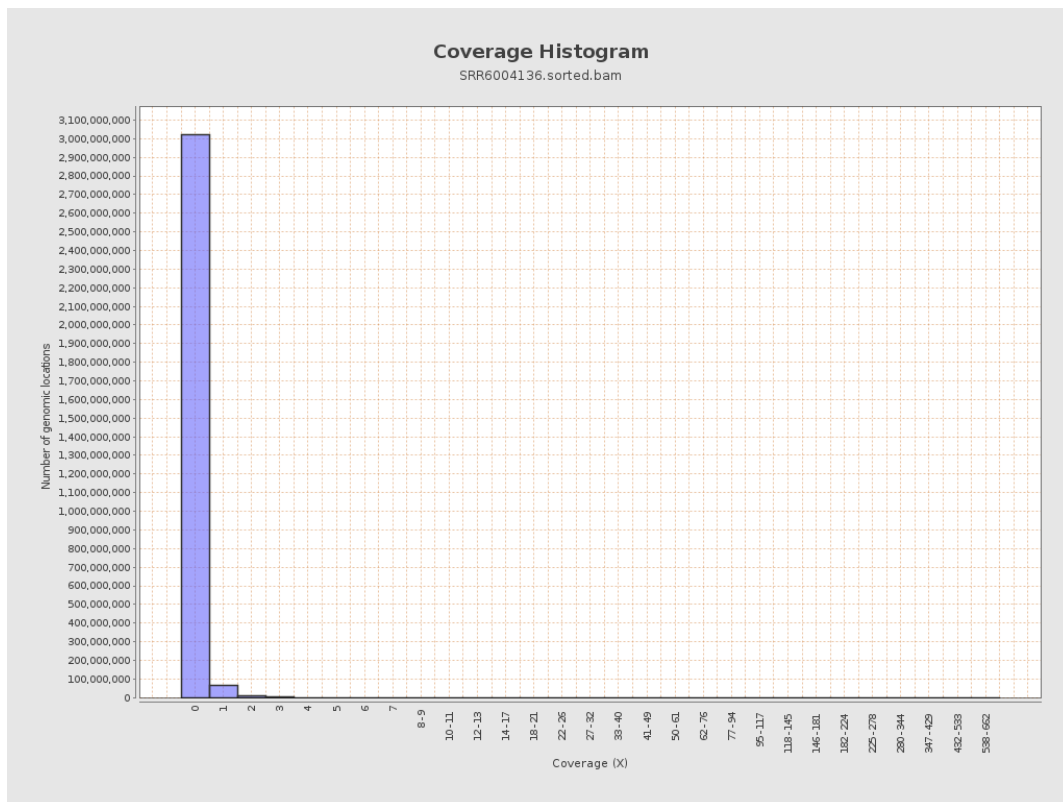
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5647450	0.0227	0.353
chr2	243199373	5017910	0.0206	0.331
chr3	198022430	6658650	0.0336	0.2086
chr4	191154276	7962557	0.0417	0.2544
chr5	180915260	2629098	0.0145	0.1418
chr6	171115067	4191279	0.0245	0.1864
chr7	159138663	7110870	0.0447	0.4116

chr8	146364022	7421887	0.0507	0.4232
chr9	141213431	5237376	0.0371	0.3726
chr10	135534747	2361400	0.0174	0.2235
chr11	135006516	5579476	0.0413	0.3071
chr12	133851895	4389929	0.0328	0.2136
chr13	115169878	1492135	0.013	0.132
chr14	107349540	3855335	0.0359	0.2468
chr15	102531392	2284891	0.0223	0.1731
chr16	90354753	3269745	0.0362	0.2634
chr17	81195210	2360448	0.0291	0.2124
chr18	78077248	1805688	0.0231	0.6995
chr19	59128983	1407574	0.0238	0.2942
chr20	63025520	3820098	0.0606	0.2987
chr21	48129895	1002627	0.0208	0.2076
chr22	51304566	1068457	0.0208	0.1652
chrMT	16571	38826	2.343	2.1476
chrX	155270560	3861951	0.0249	0.205
chrY	59373566	338014	0.0057	0.1477

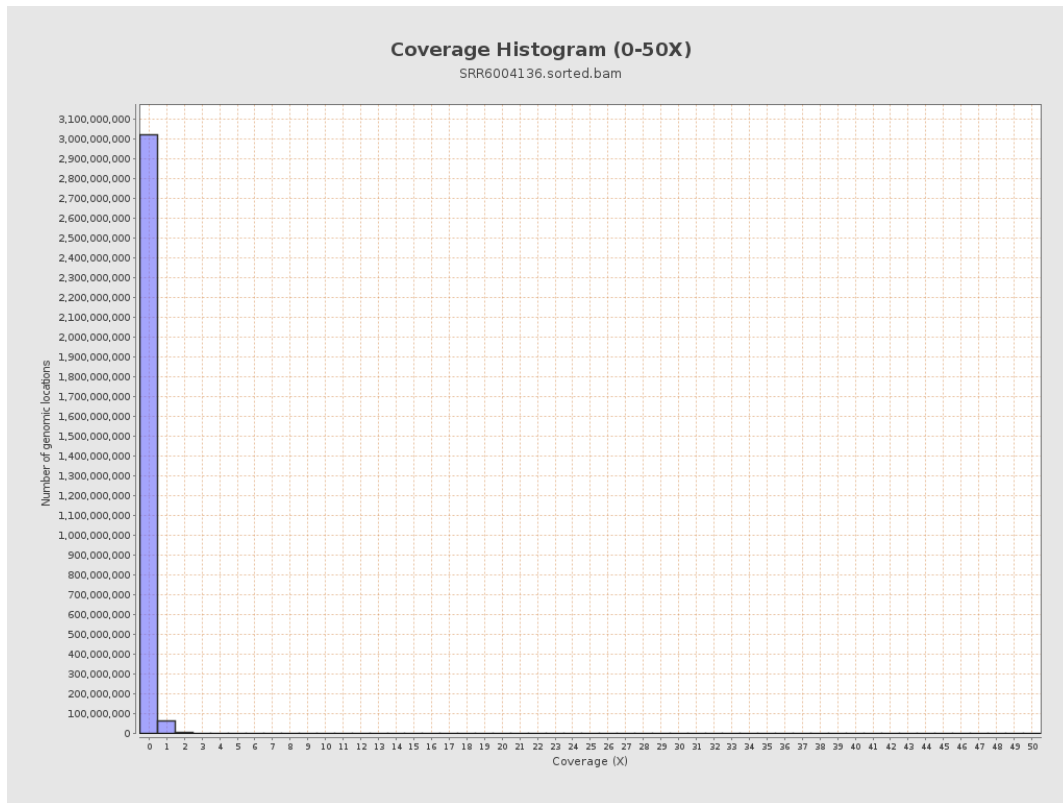
3. Results : Coverage across reference



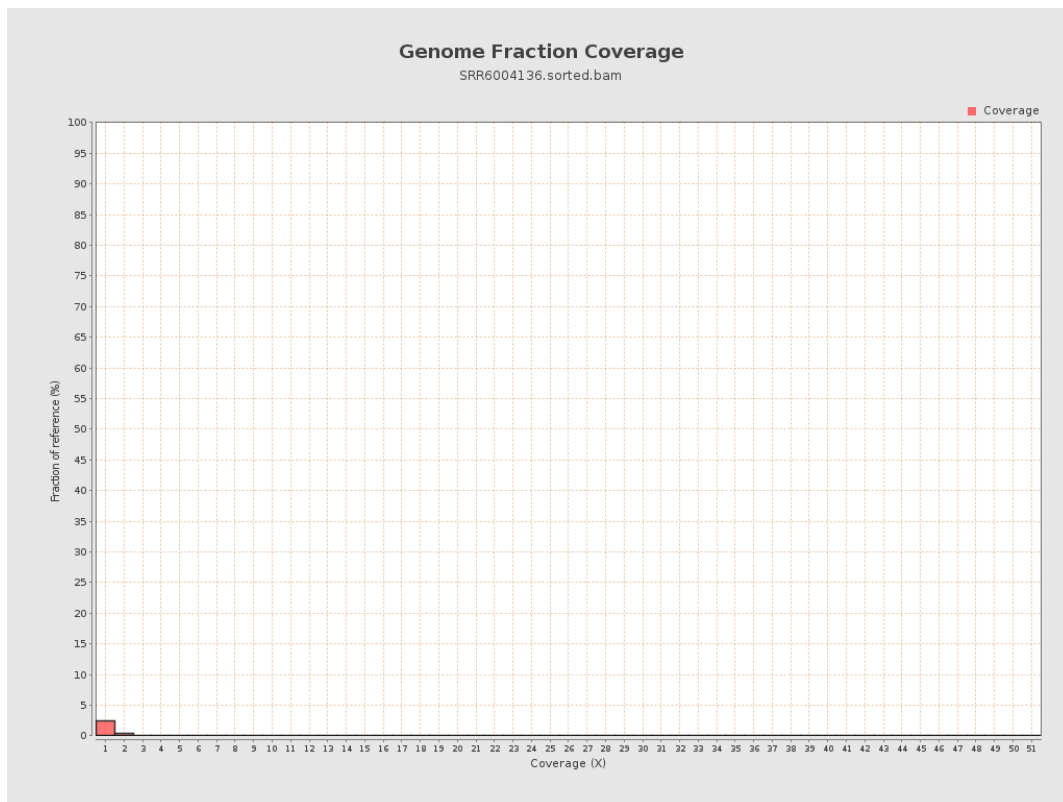
4. Results : Coverage Histogram



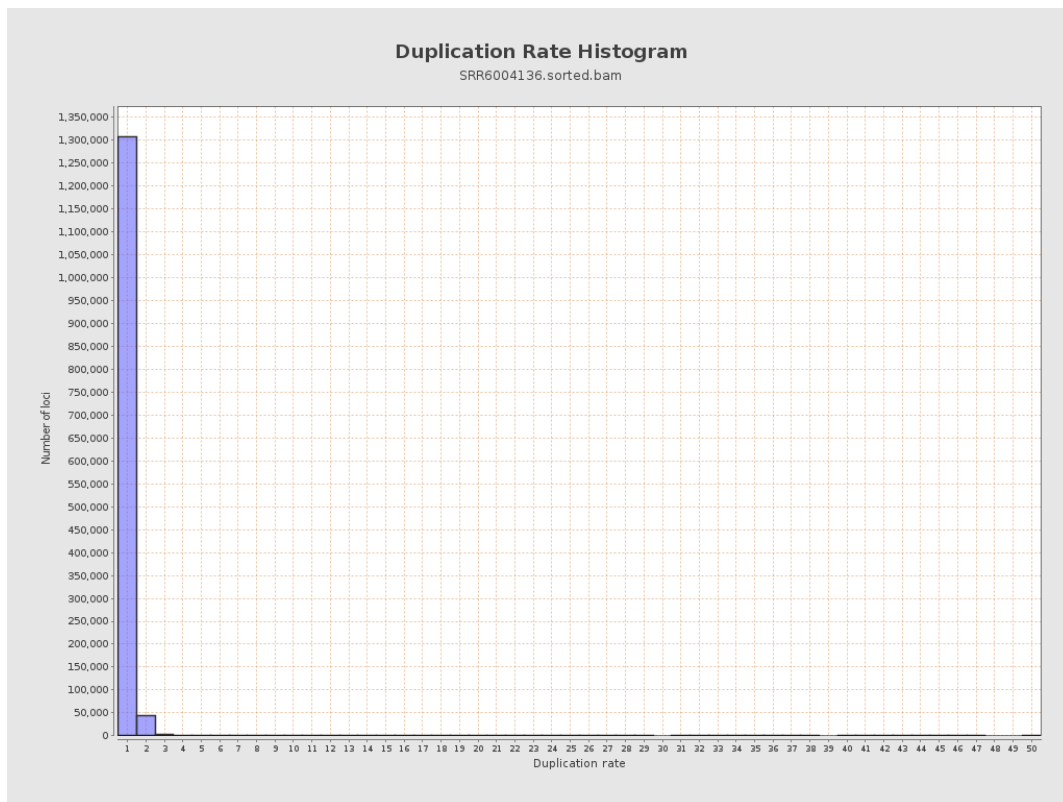
5. Results : Coverage Histogram (0-50X)



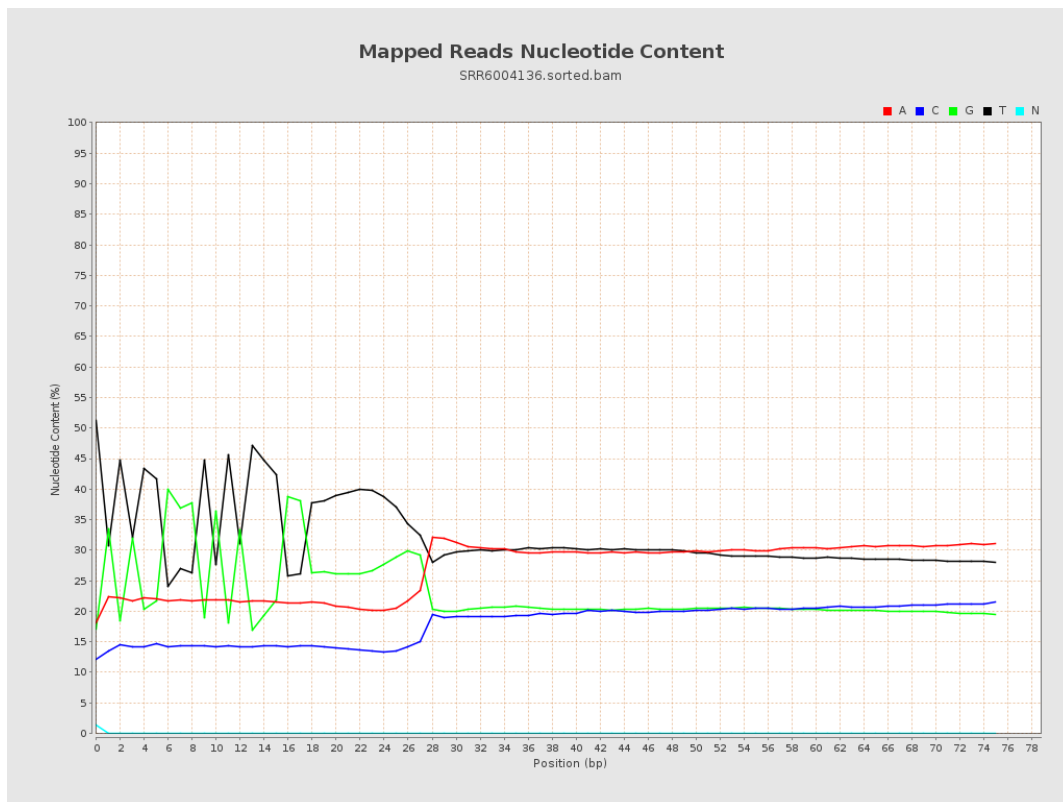
6. Results : Genome Fraction Coverage



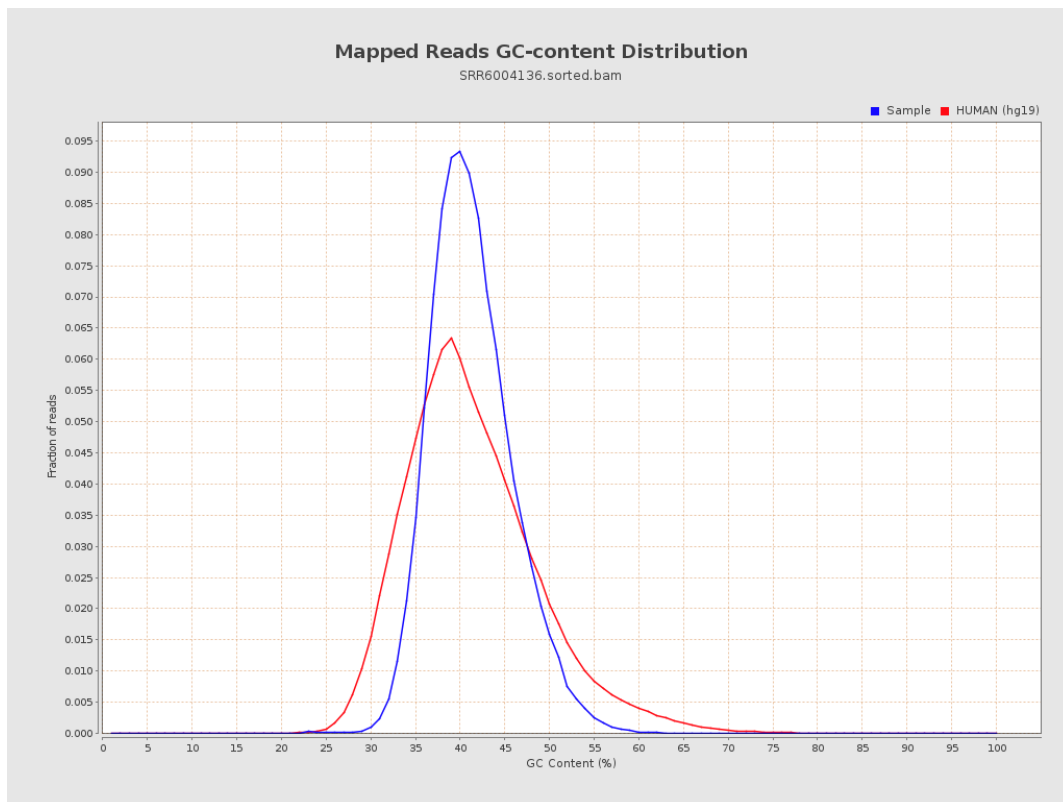
7. Results : Duplication Rate Histogram



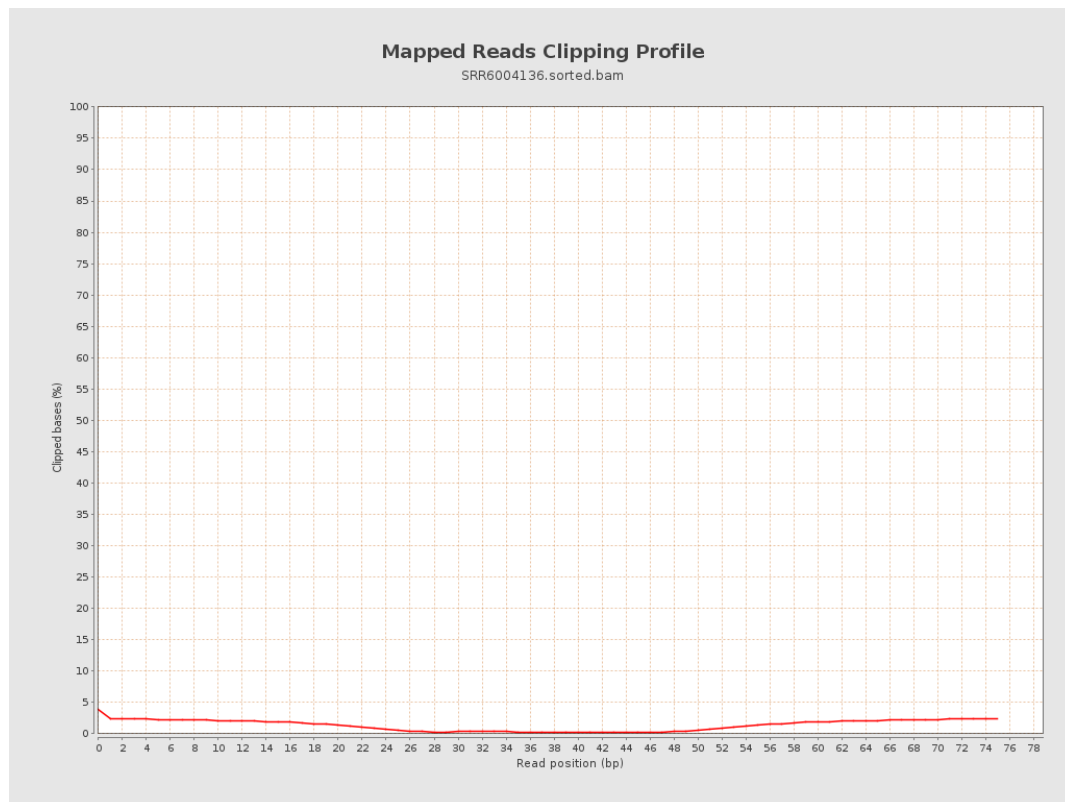
8. Results : Mapped Reads Nucleotide Content



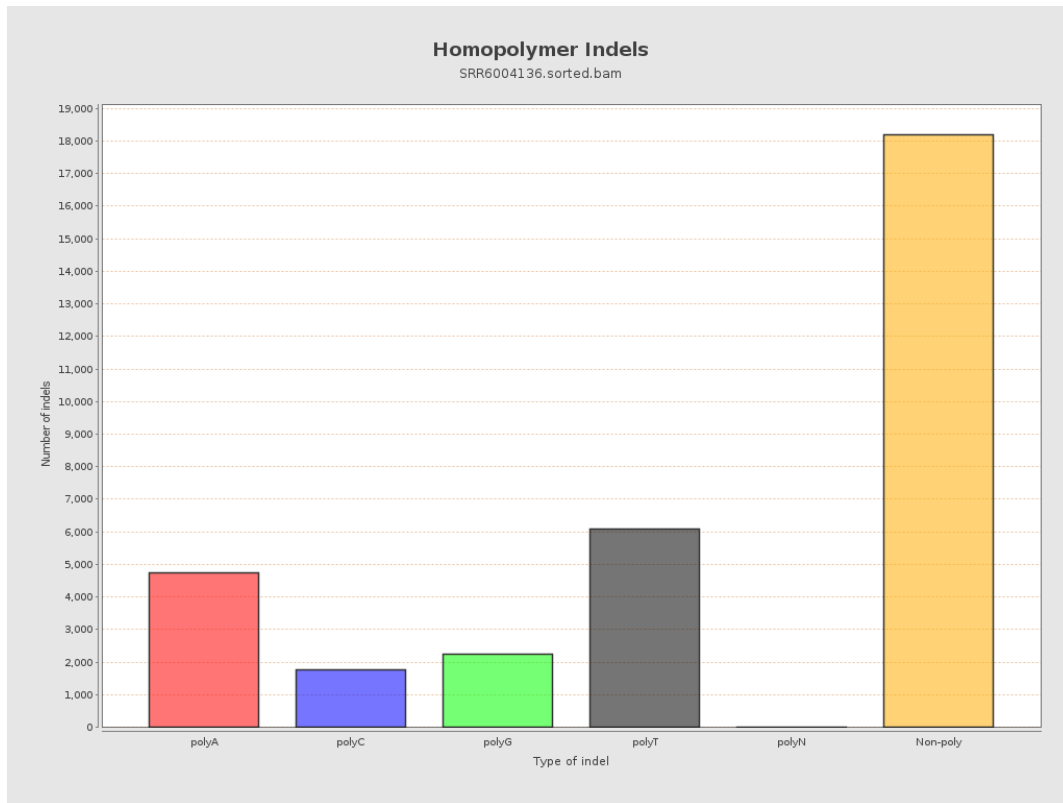
9. Results : Mapped Reads GC-content Distribution



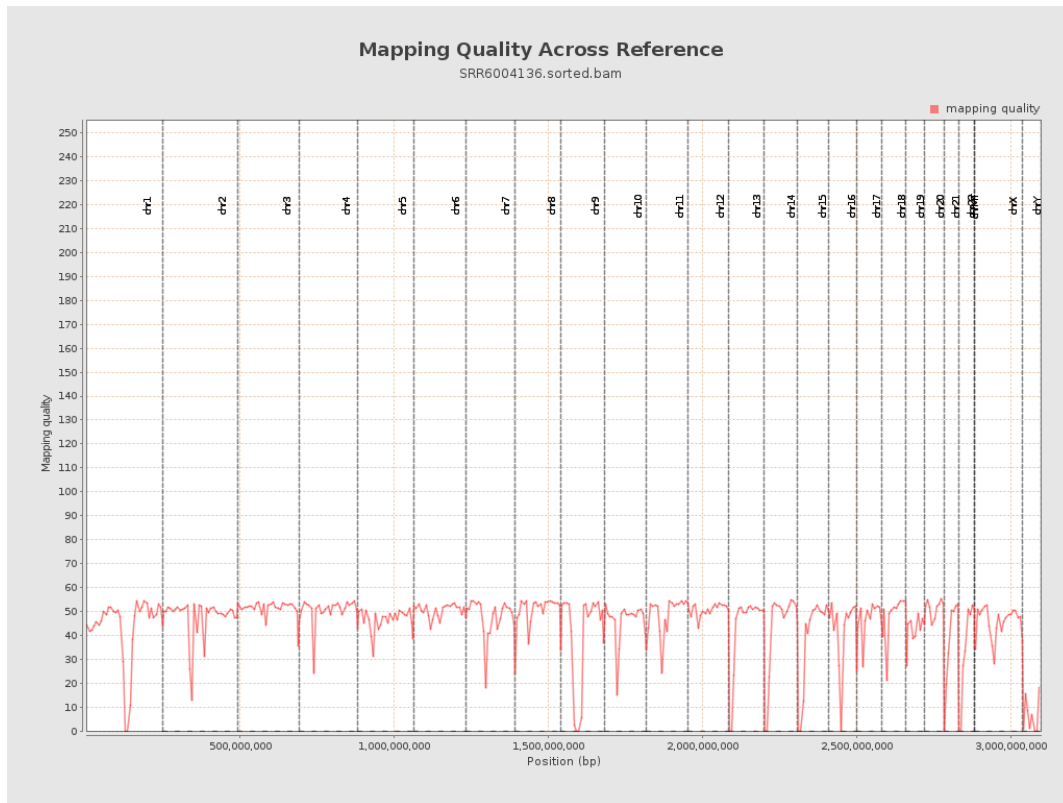
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

