Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:30:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230343.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_SRR6230343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:30:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,040,335
Mapped reads	2,869,753 / 94.39%
Unmapped reads	170,582 / 5.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,082 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	102,797 / 3.38%
Duplication rate	2.23%
Clipped reads	755,560 / 24.85%

2.2. ACGT Content

Number/percentage of A's	62,600,686 / 30.42%
Number/percentage of C's	40,642,839 / 19.75%
Number/percentage of T's	61,095,013 / 29.69%
Number/percentage of G's	41,313,775 / 20.08%
Number/percentage of N's	118,286 / 0.06%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0665

Standard Deviation	0.7078

2.4. Mapping Quality

Mean Mapping Quality	47.42

2.5. Mismatches and indels

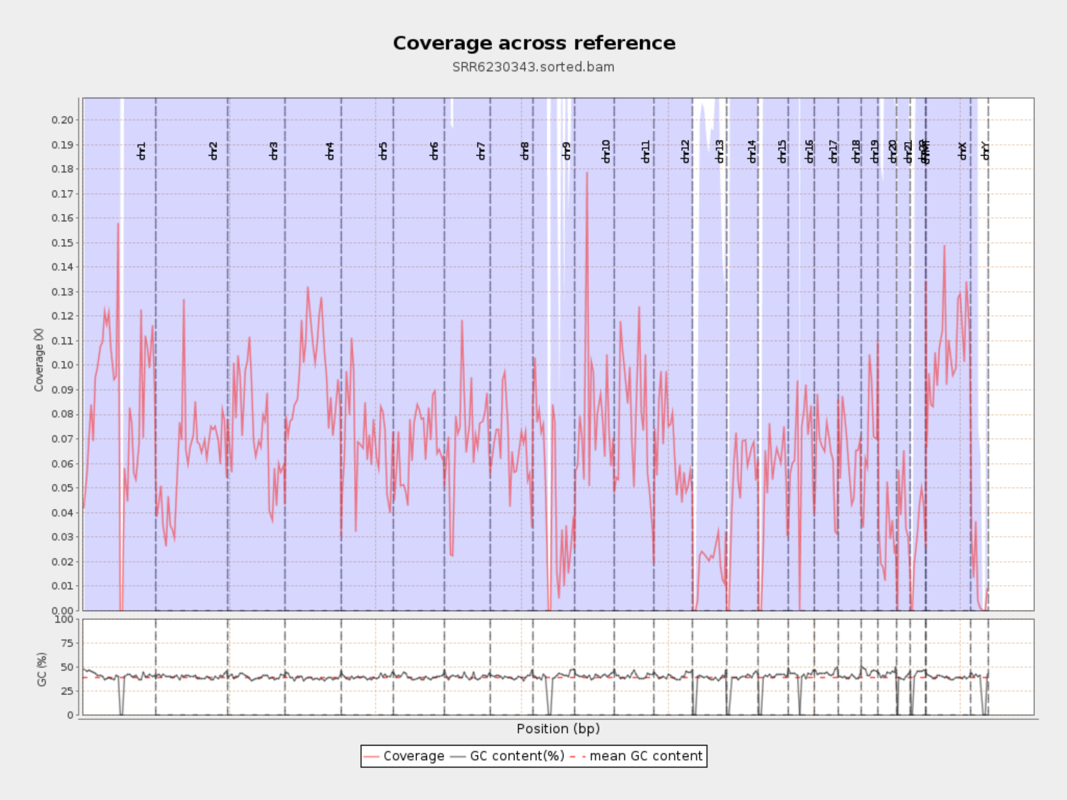
General error rate	0.93%
Mismatches	1,876,916
Insertions	17,949
Mapped reads with at least one insertion	0.62%
Deletions	61,244
Mapped reads with at least one deletion	2.11%
Homopolymer indels	45.71%

2.6. Chromosome stats

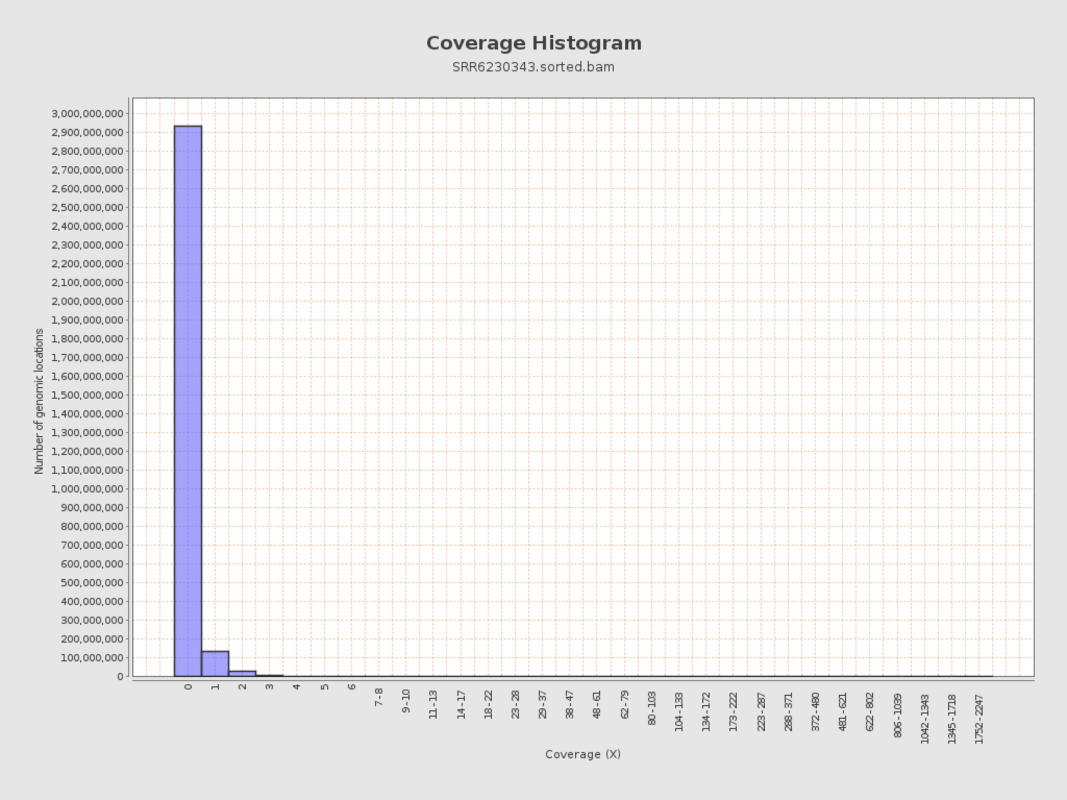
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21011836	0.0843	1.7043
chr2	243199373	15092200	0.0621	0.55
chr3	198022430	14618847	0.0738	0.3507
chr4	191154276	18450921	0.0965	0.41
chr5	180915260	12557592	0.0694	0.3211
chr6	171115067	11633906	0.068	0.4104
chr7	159138663	11296934	0.071	0.751

chr8	146364022	9621184	0.0657	0.6324
chr9	141213431	6295775	0.0446	0.5509
chr10	135534747	10820801	0.0798	0.8555
chr11	135006516	10463841	0.0775	0.7316
chr12	133851895	8890352	0.0664	0.3288
chr13	115169878	2071971	0.018	0.1566
chr14	107349540	5652953	0.0527	0.3231
chr15	102531392	5099489	0.0497	0.2645
chr16	90354753	5752743	0.0637	0.4351
chr17	81195210	5114989	0.063	0.3703
chr18	78077248	5072259	0.065	1.113
chr19	59128983	4165473	0.0704	1.1114
chr20	63025520	1741533	0.0276	0.2183
chr21	48129895	1820452	0.0378	0.328
chr22	51304566	1497602	0.0292	0.2004
chrMT	16571	2230	0.1346	0.3821
chrX	155270560	16480609	0.1061	0.4855
chrY	59373566	648433	0.0109	0.2867

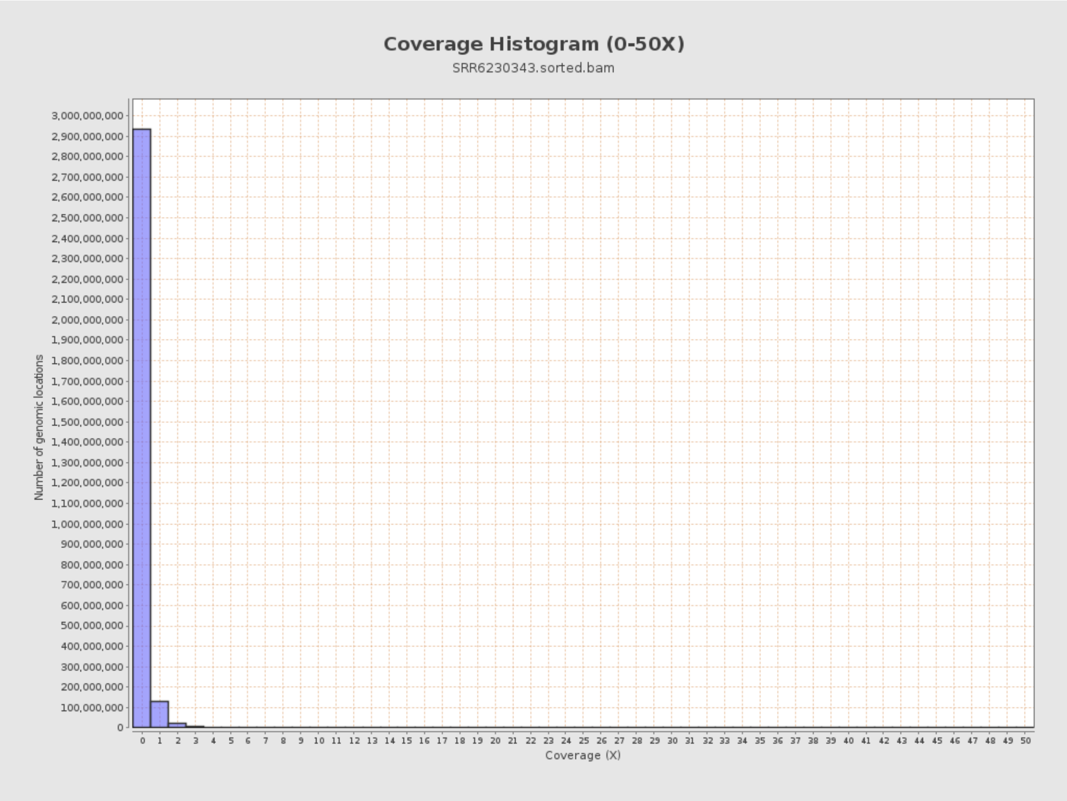
3. Results : Coverage across reference



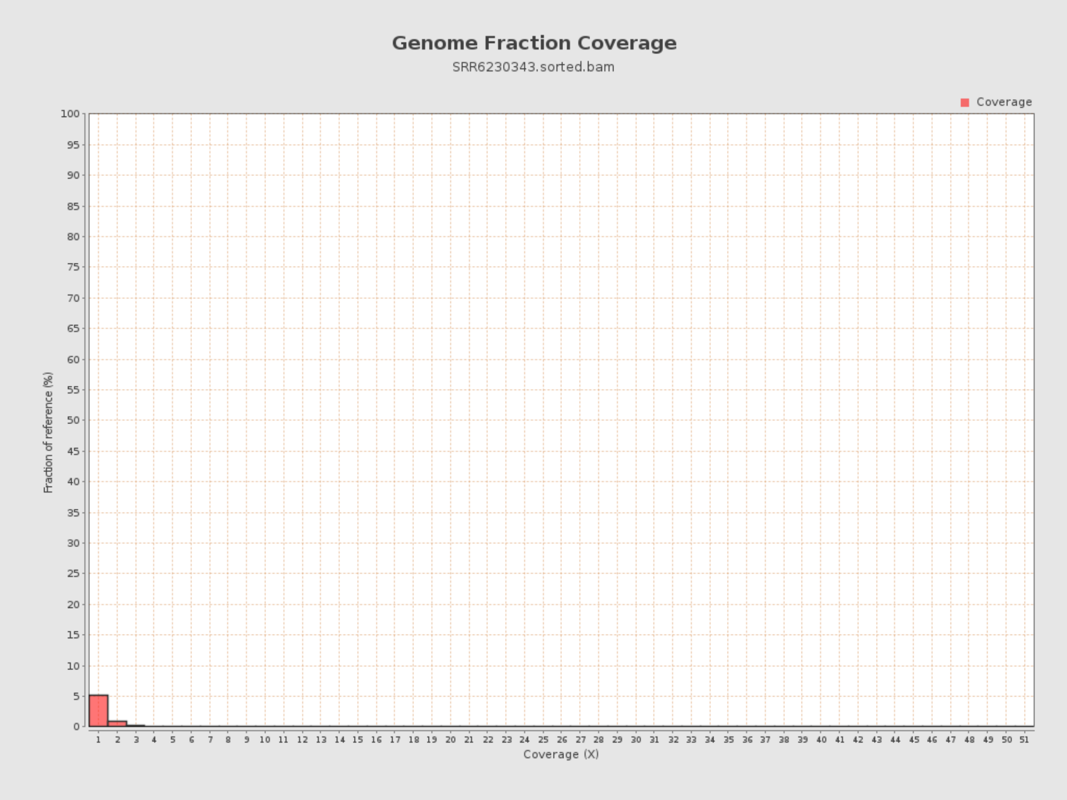
4. Results : Coverage Histogram



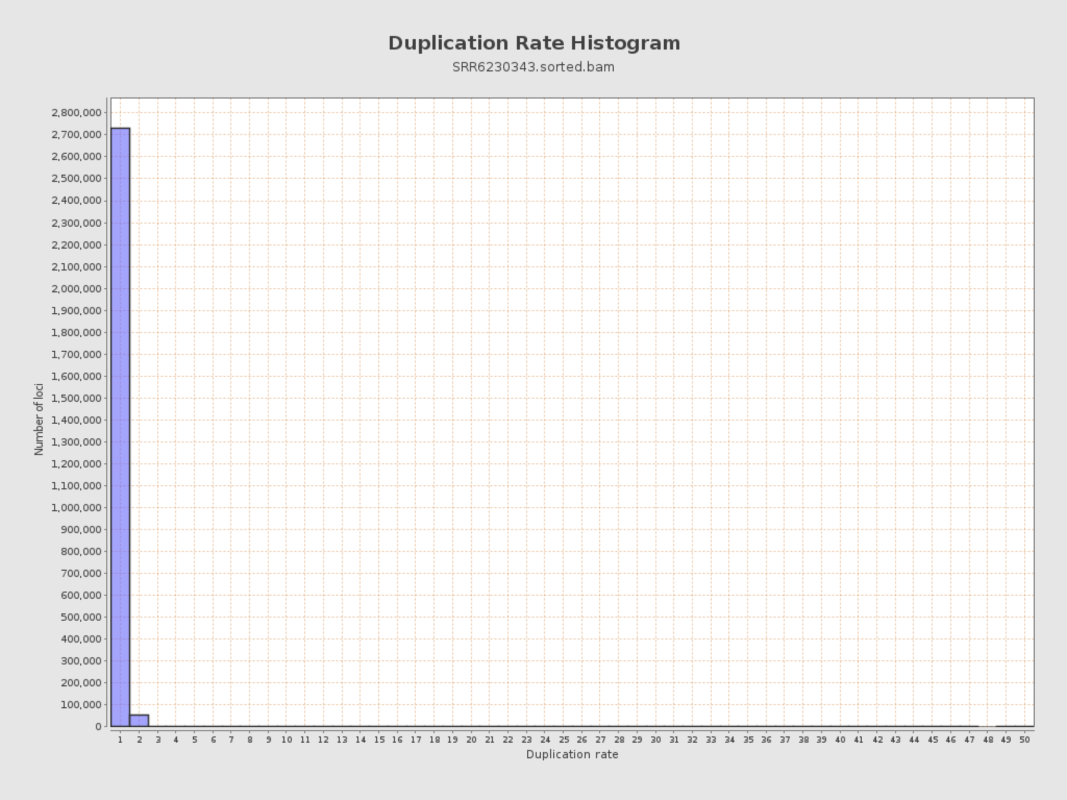
5. Results : Coverage Histogram (0-50X)



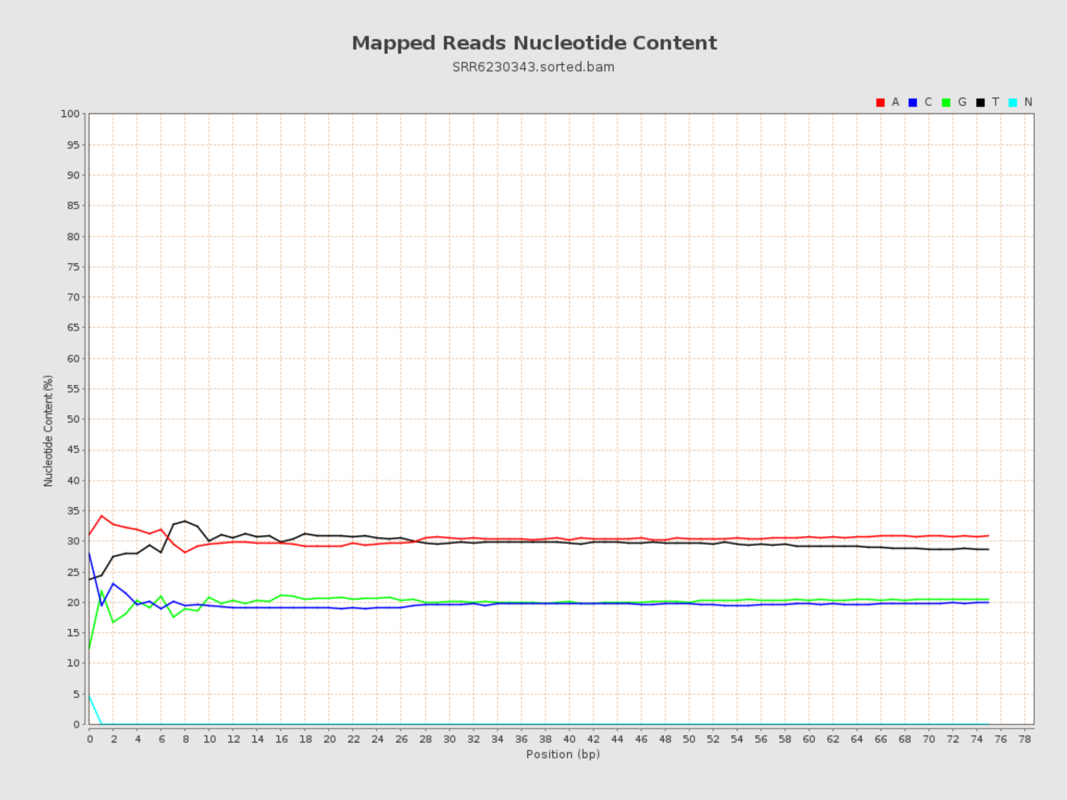
6. Results : Genome Fraction Coverage



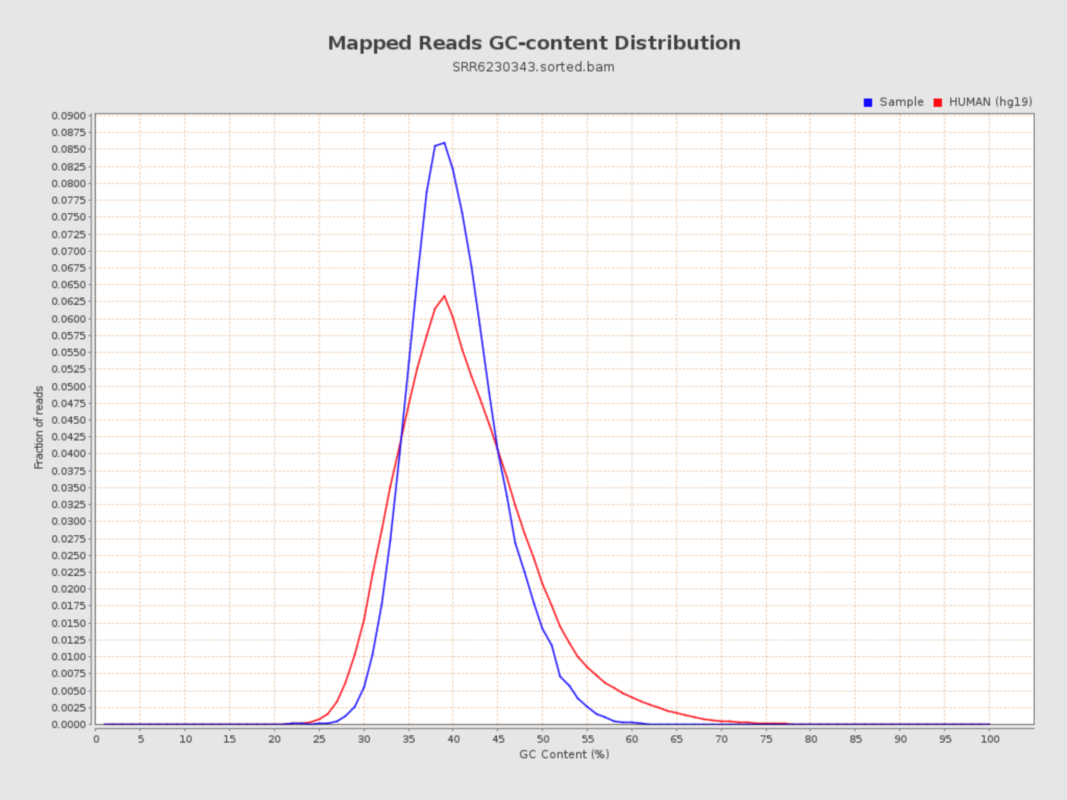
7. Results : Duplication Rate Histogram



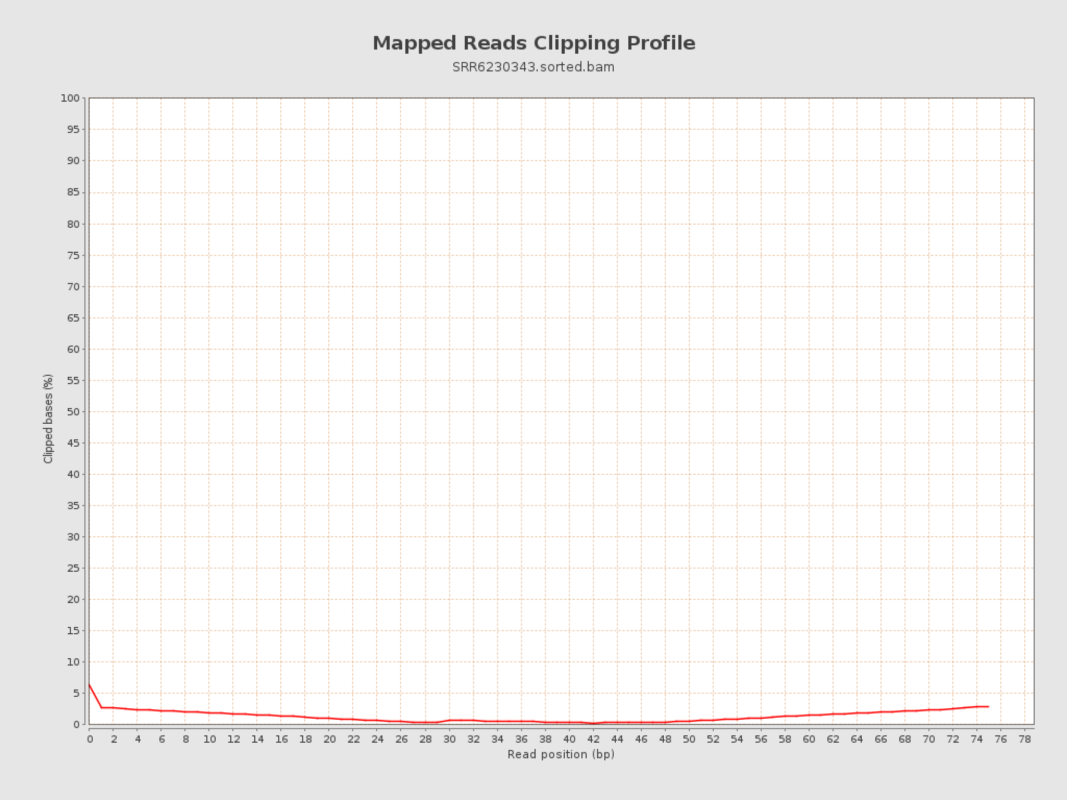
8. Results : Mapped Reads Nucleotide Content



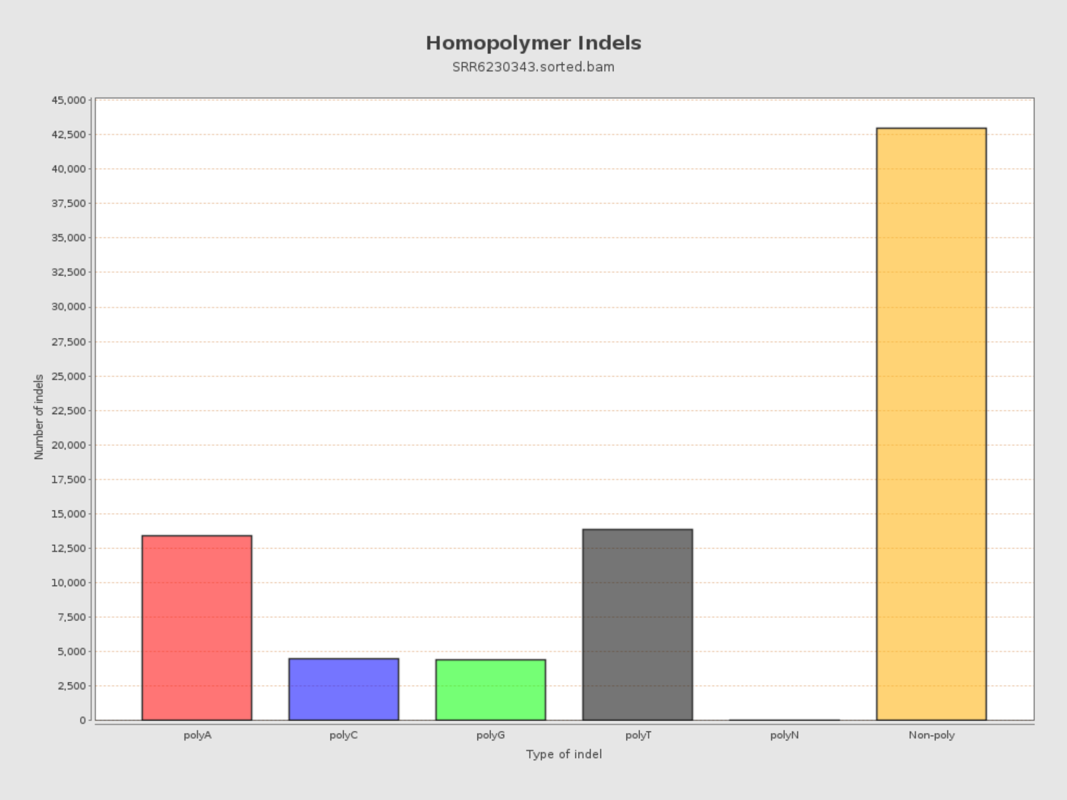
9. Results : Mapped Reads GC-content Distribution



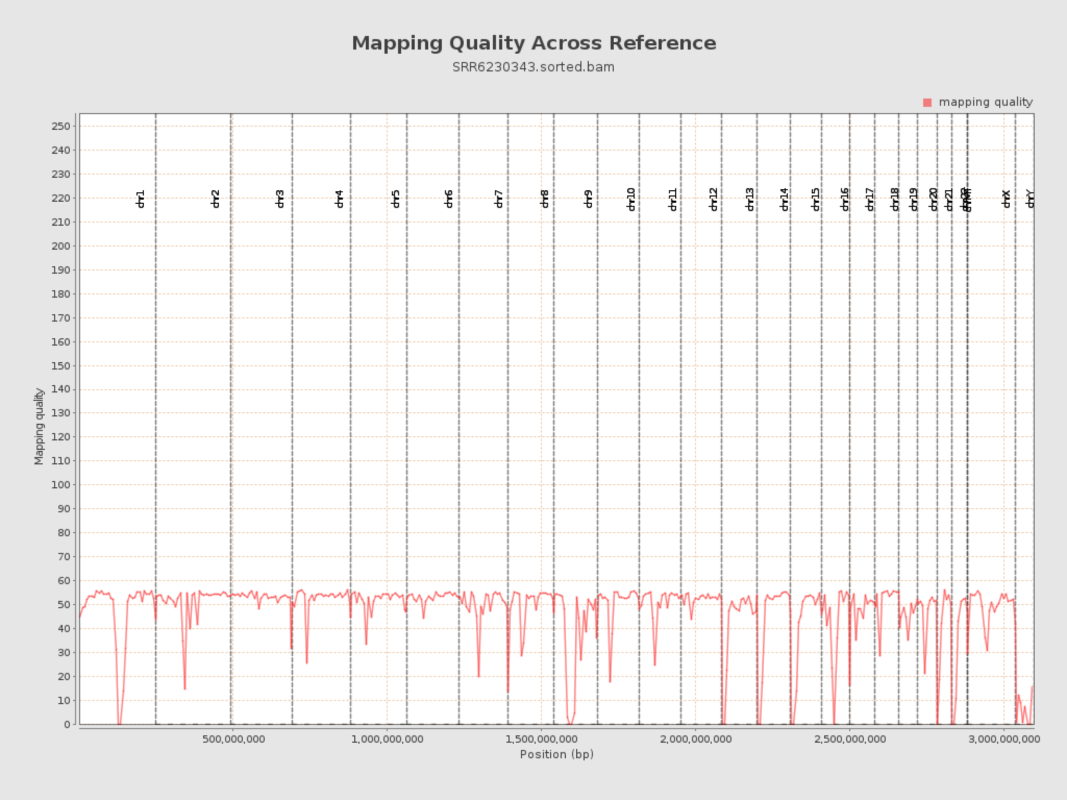
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram