Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:01:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054600.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_SRR054600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:01:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,294,024
Mapped reads	6,069,883 / 73.18%
Unmapped reads	2,224,141 / 26.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	178 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,256,559 / 15.15%
Duplication rate	15.17%
Clipped reads	629,429 / 7.59%

2.2. ACGT Content

Number/percentage of A's	87,366,201 / 30.58%
Number/percentage of C's	53,840,713 / 18.84%
Number/percentage of T's	87,062,088 / 30.47%
Number/percentage of G's	57,179,546 / 20.01%
Number/percentage of N's	274,378 / 0.1%
GC Percentage	38.86%

2.3. Coverage

Mean	0.0923

Standard Deviation	0.7138

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

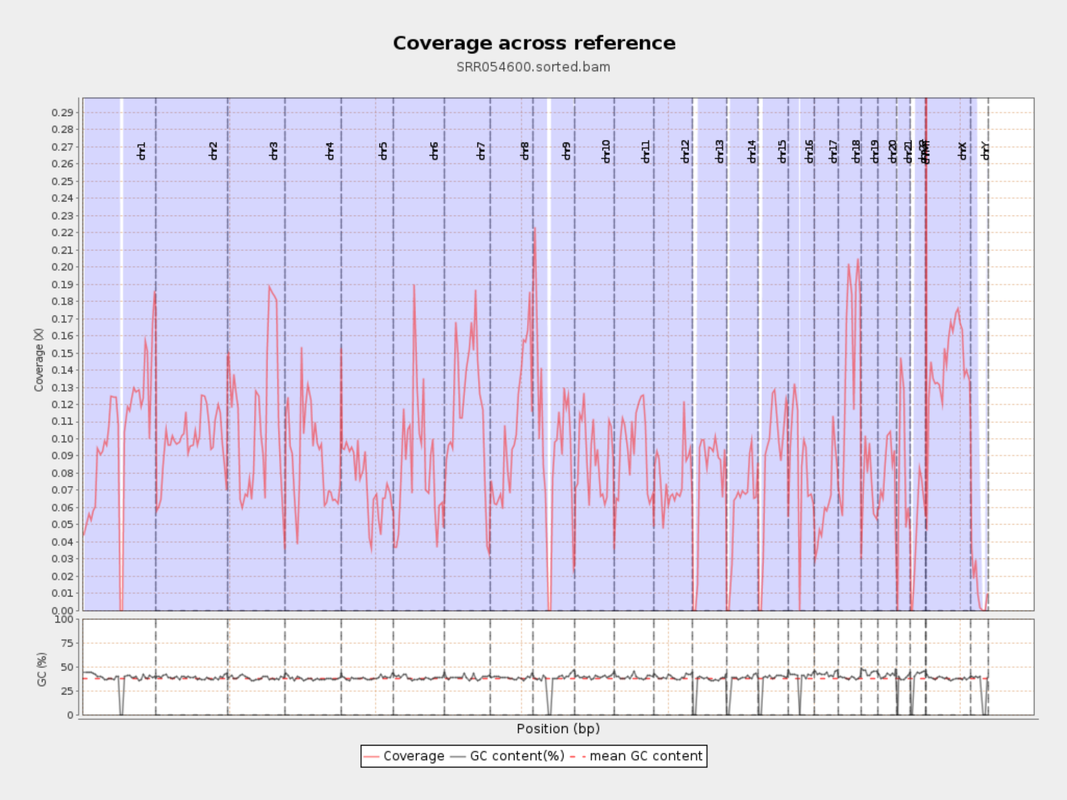
General error rate	0.68%
Mismatches	1,920,893
Insertions	12,670
Mapped reads with at least one insertion	0.21%
Deletions	40,012
Mapped reads with at least one deletion	0.66%
Homopolymer indels	47.01%

2.6. Chromosome stats

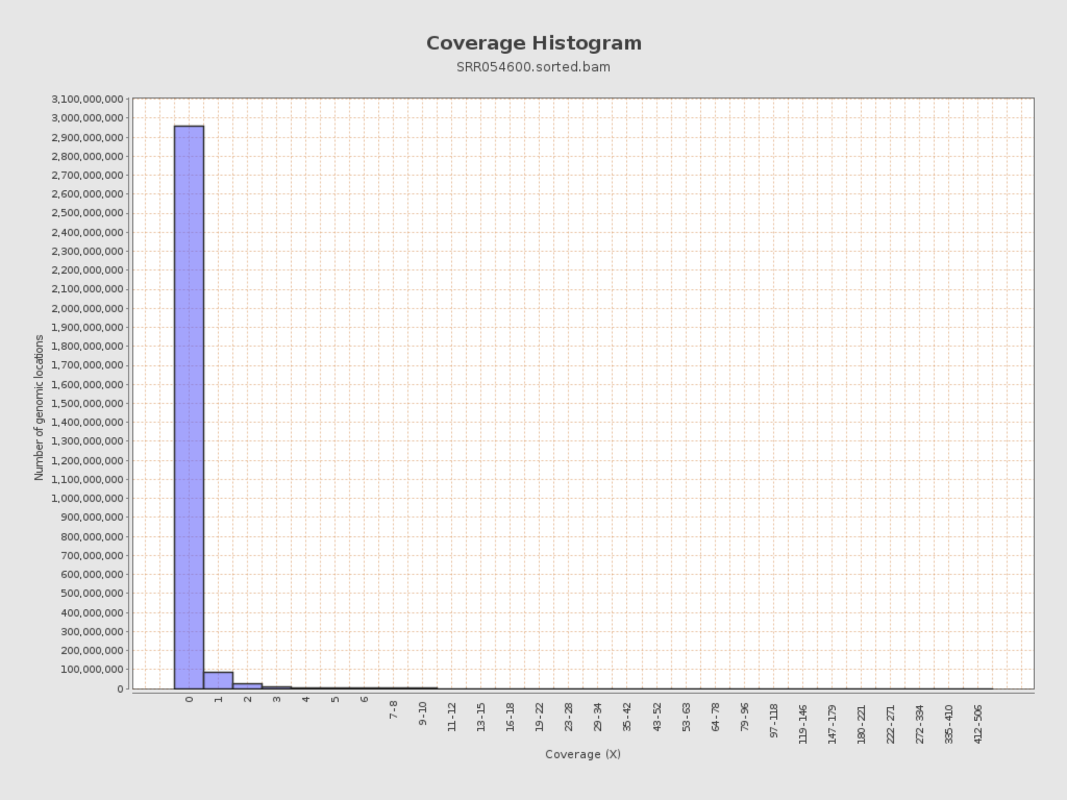
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25347344	0.1017	0.7833
chr2	243199373	23974689	0.0986	0.7802
chr3	198022430	21919075	0.1107	0.7531
chr4	191154276	17251255	0.0902	0.6789
chr5	180915260	13405913	0.0741	0.563
chr6	171115067	14609804	0.0854	0.6962
chr7	159138663	18672773	0.1173	0.8836

chr8	146364022	15282746	0.1044	0.778
chr9	141213431	13826135	0.0979	0.7357
chr10	135534747	12046201	0.0889	0.6808
chr11	135006516	12643442	0.0937	0.6896
chr12	133851895	10324247	0.0771	0.5819
chr13	115169878	8770942	0.0762	0.6067
chr14	107349540	6427521	0.0599	0.5552
chr15	102531392	8866603	0.0865	0.6268
chr16	90354753	7532927	0.0834	0.7195
chr17	81195210	5095487	0.0628	0.5096
chr18	78077248	11176918	0.1432	0.9515
chr19	59128983	4355674	0.0737	0.6311
chr20	63025520	5156017	0.0818	0.6113
chr21	48129895	3699184	0.0769	0.681
chr22	51304566	2456127	0.0479	0.431
chrMT	16571	22600	1.3638	3.638
chrX	155270560	22189936	0.1429	0.9326
chrY	59373566	727799	0.0123	0.2488

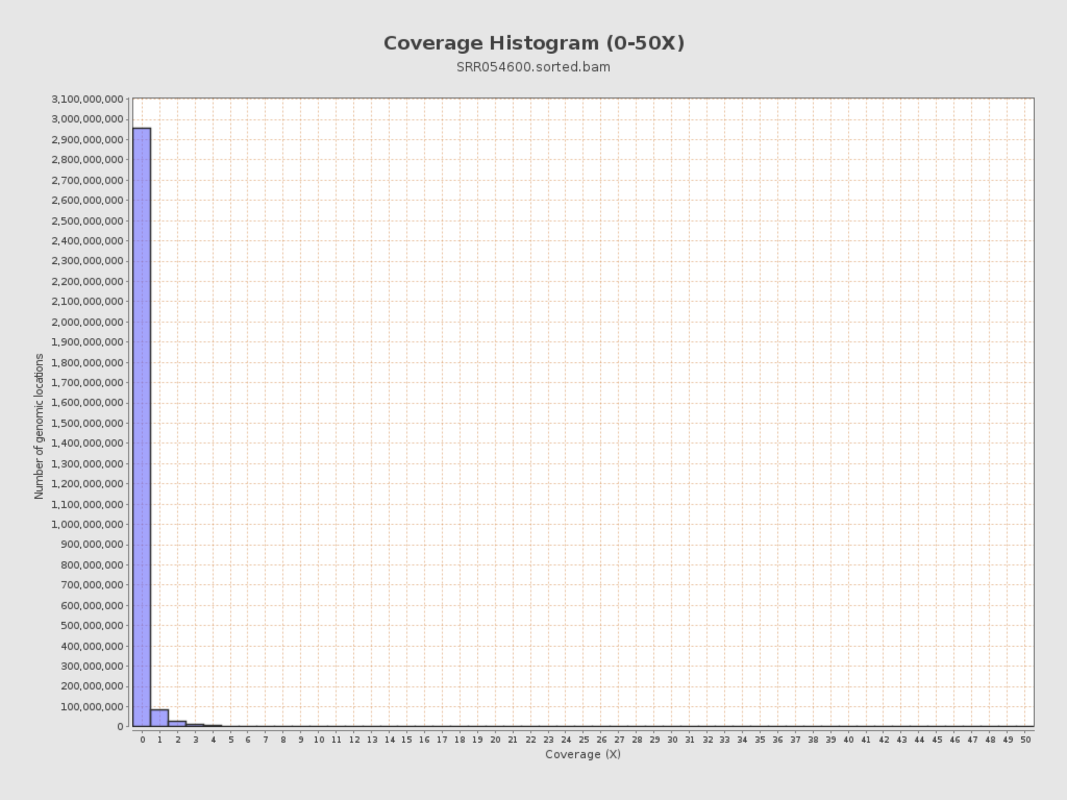
3. Results : Coverage across reference



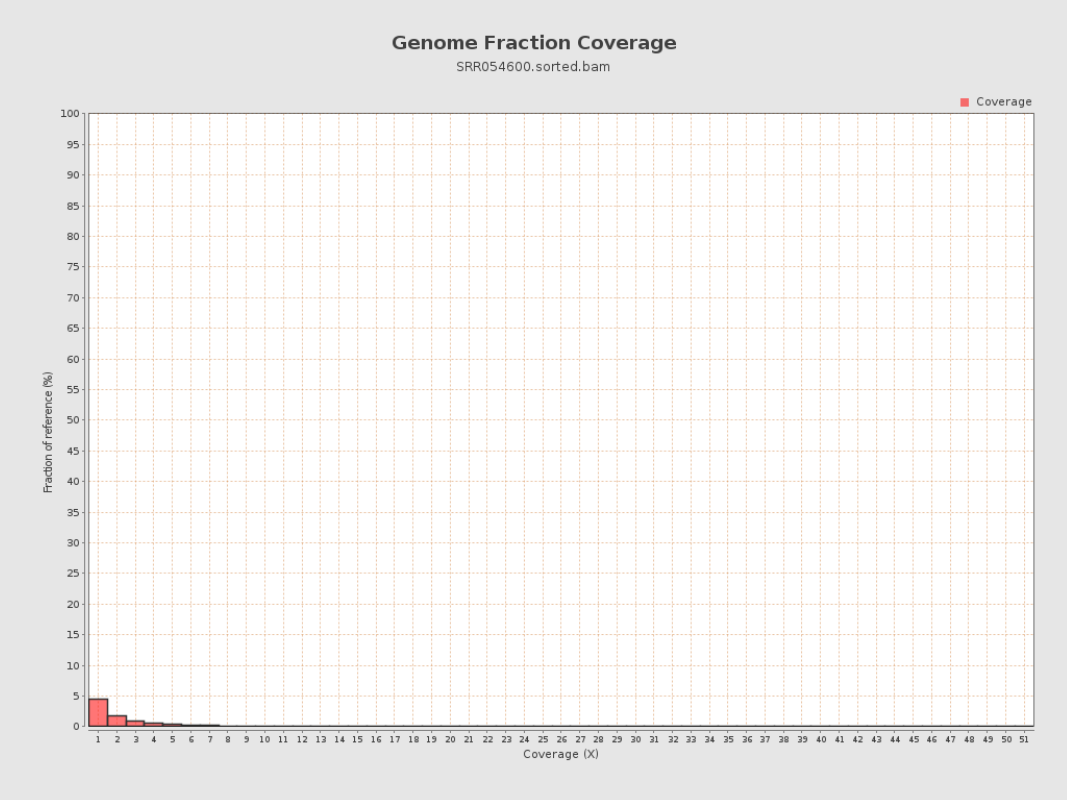
4. Results : Coverage Histogram



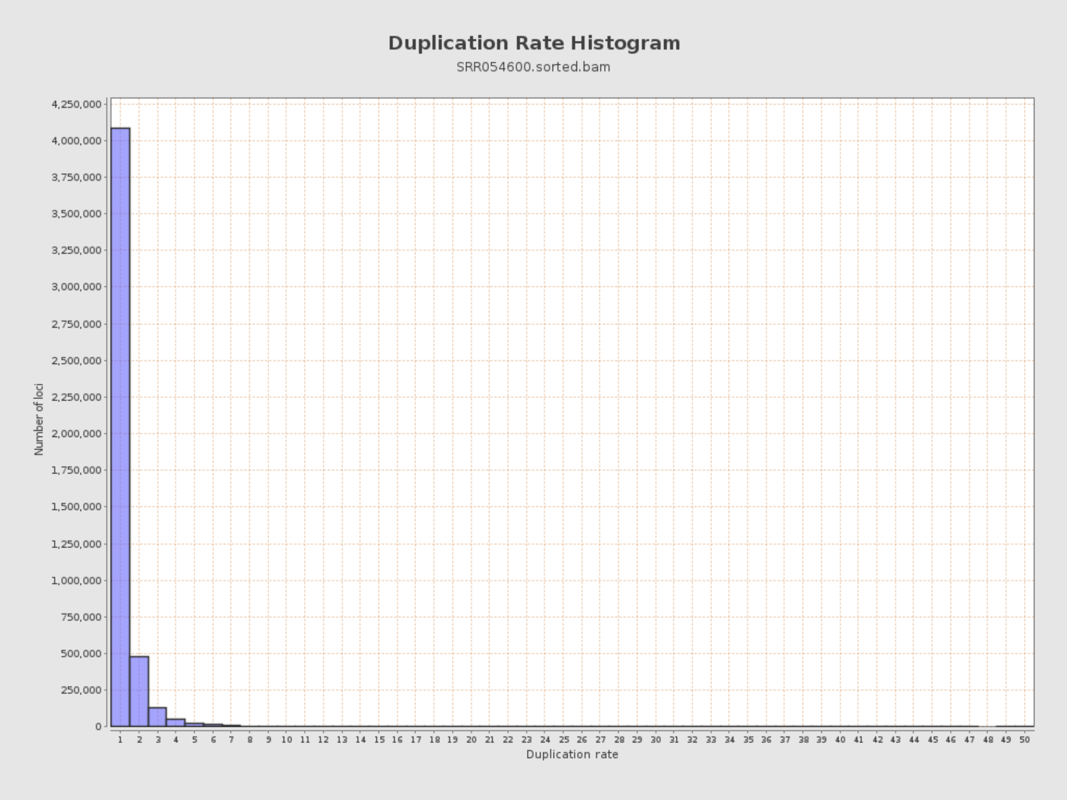
5. Results : Coverage Histogram (0-50X)



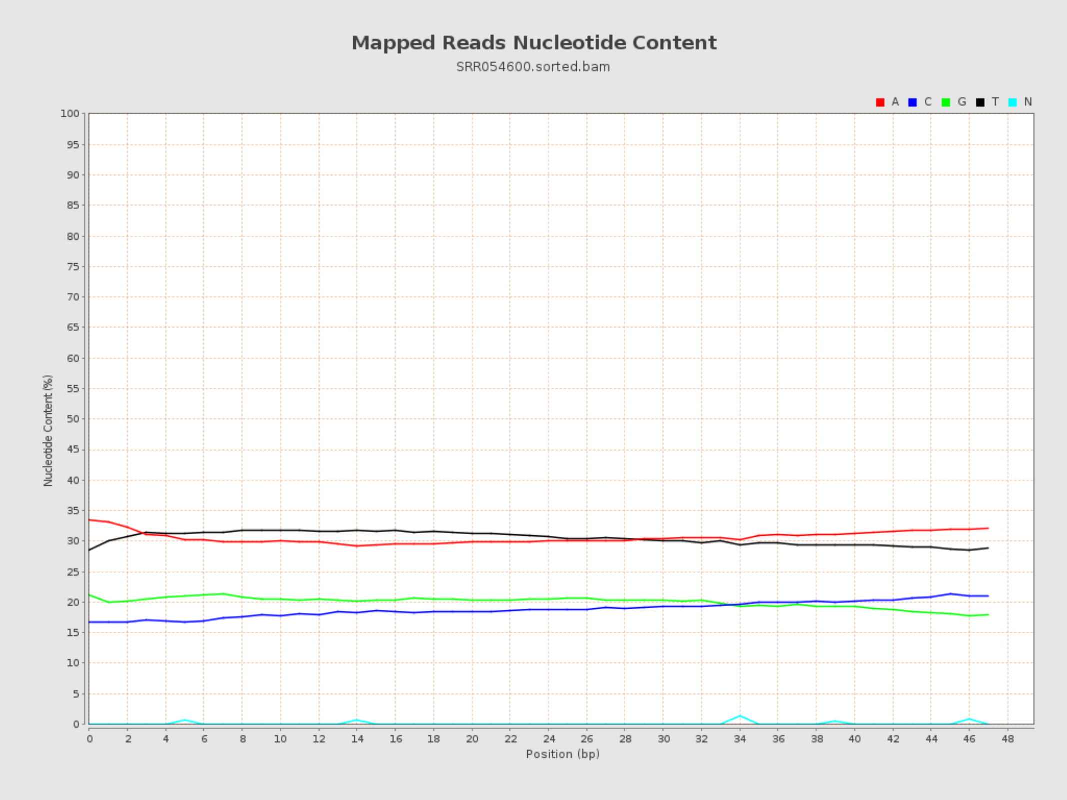
6. Results : Genome Fraction Coverage



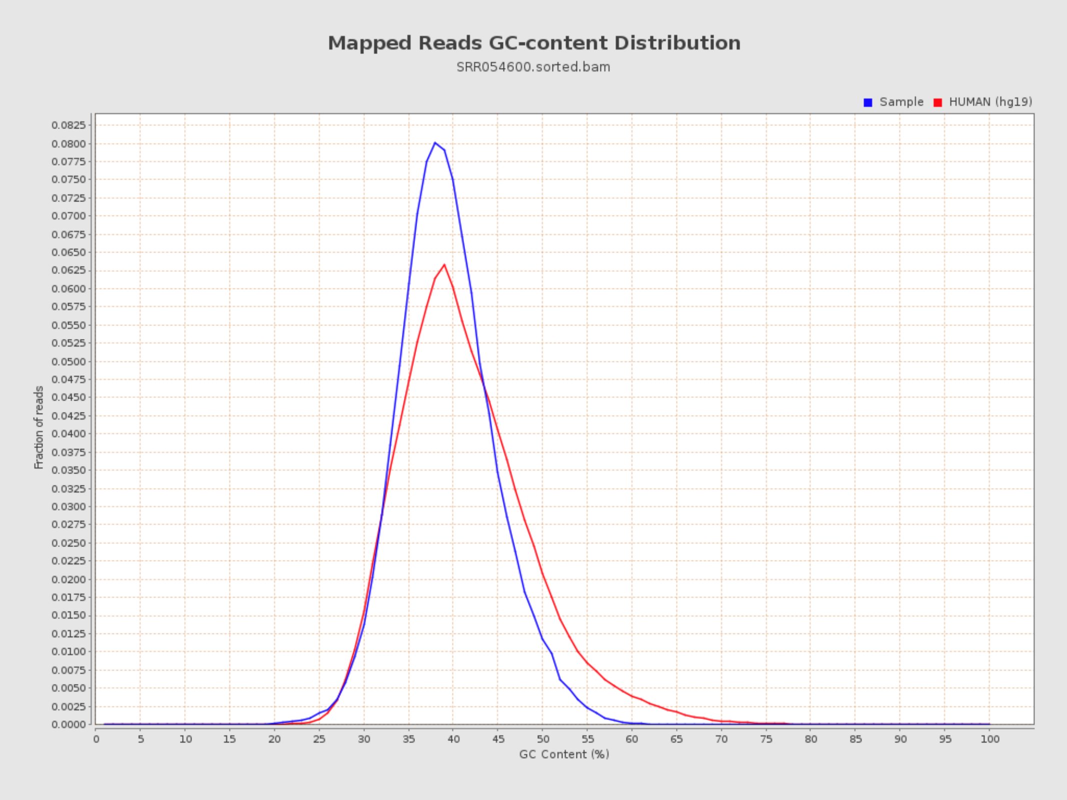
7. Results : Duplication Rate Histogram



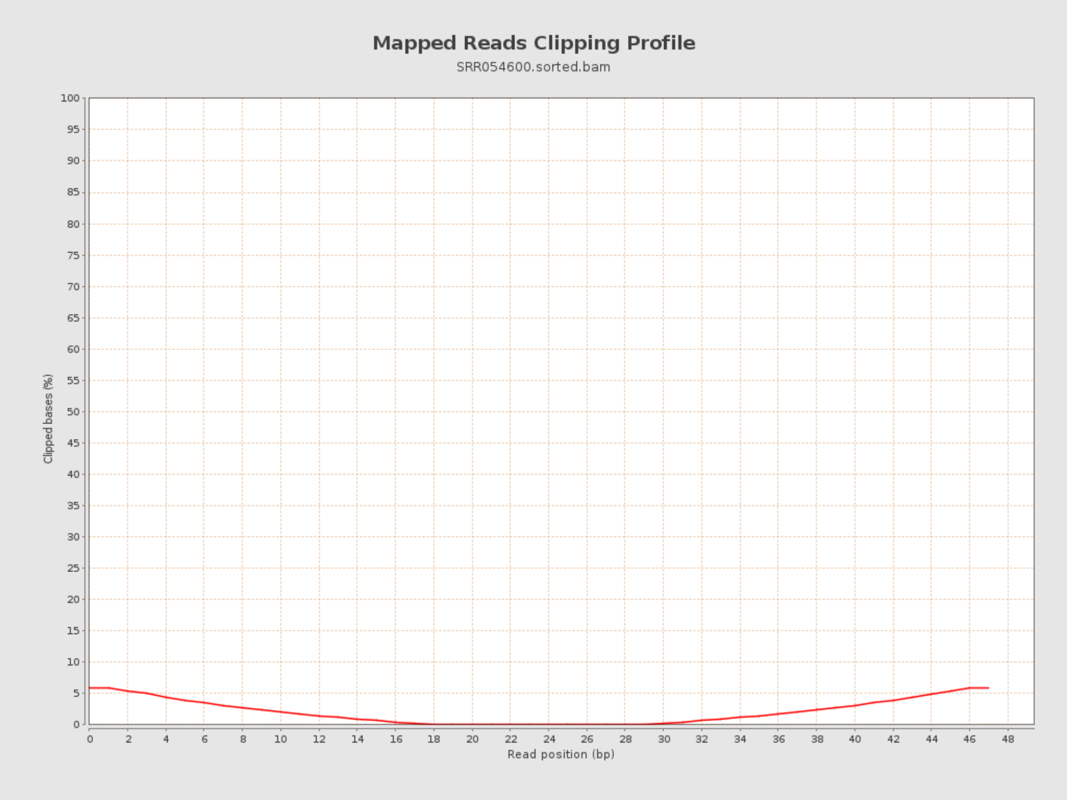
8. Results : Mapped Reads Nucleotide Content



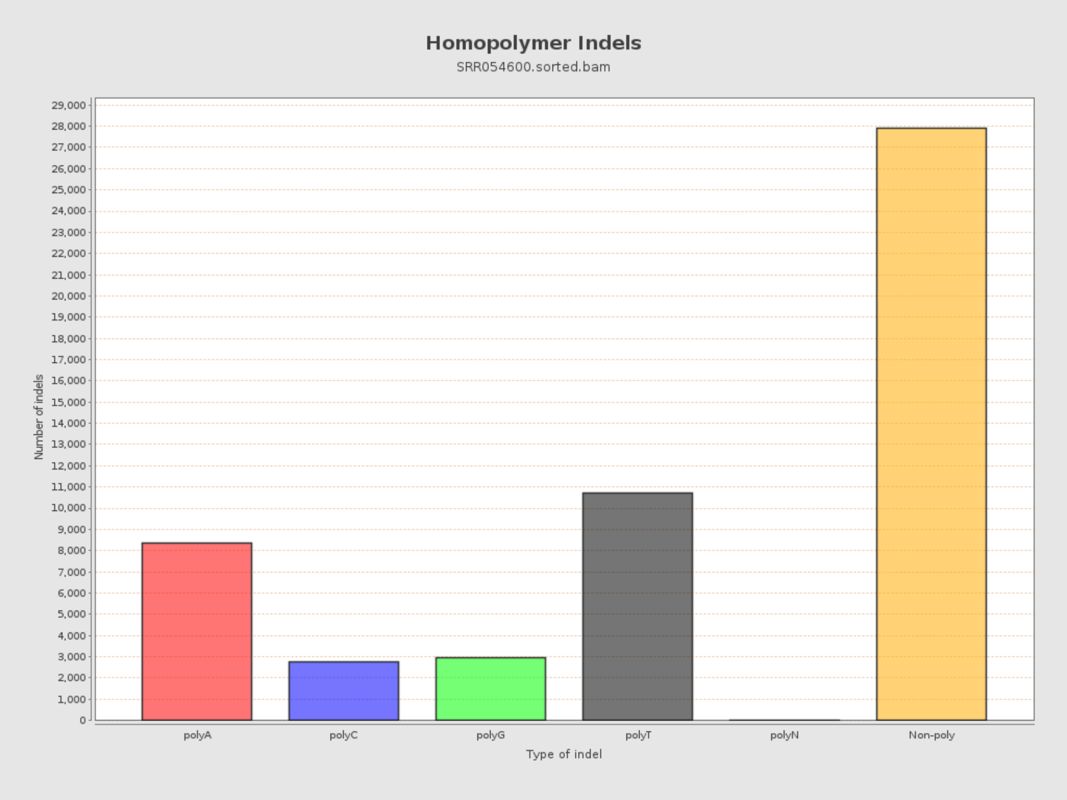
9. Results : Mapped Reads GC-content Distribution



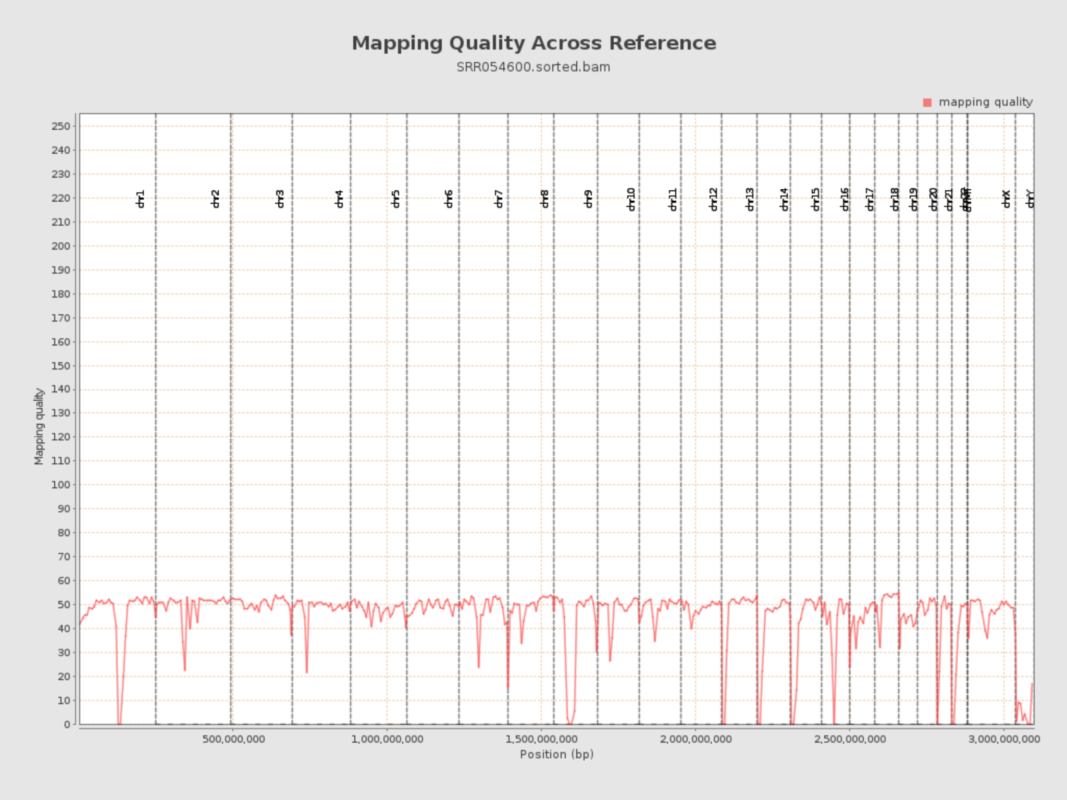
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram