Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 22:49:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053600.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_SRR053600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 22:49:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,957,655
Mapped reads	4,987,559 / 62.68%
Unmapped reads	2,970,096 / 37.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	197 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,338,948 / 16.83%
Duplication rate	19.9%
Clipped reads	768,041 / 9.65%

2.2. ACGT Content

Number/percentage of A's	70,744,661 / 30.46%
Number/percentage of C's	44,912,596 / 19.34%
Number/percentage of T's	68,738,173 / 29.59%
Number/percentage of G's	47,769,040 / 20.57%
Number/percentage of N's	100,821 / 0.04%
GC Percentage	39.9%

2.3. Coverage

Mean	0.075

Standard Deviation	0.92

2.4. Mapping Quality

Mean Mapping Quality	44.36

2.5. Mismatches and indels

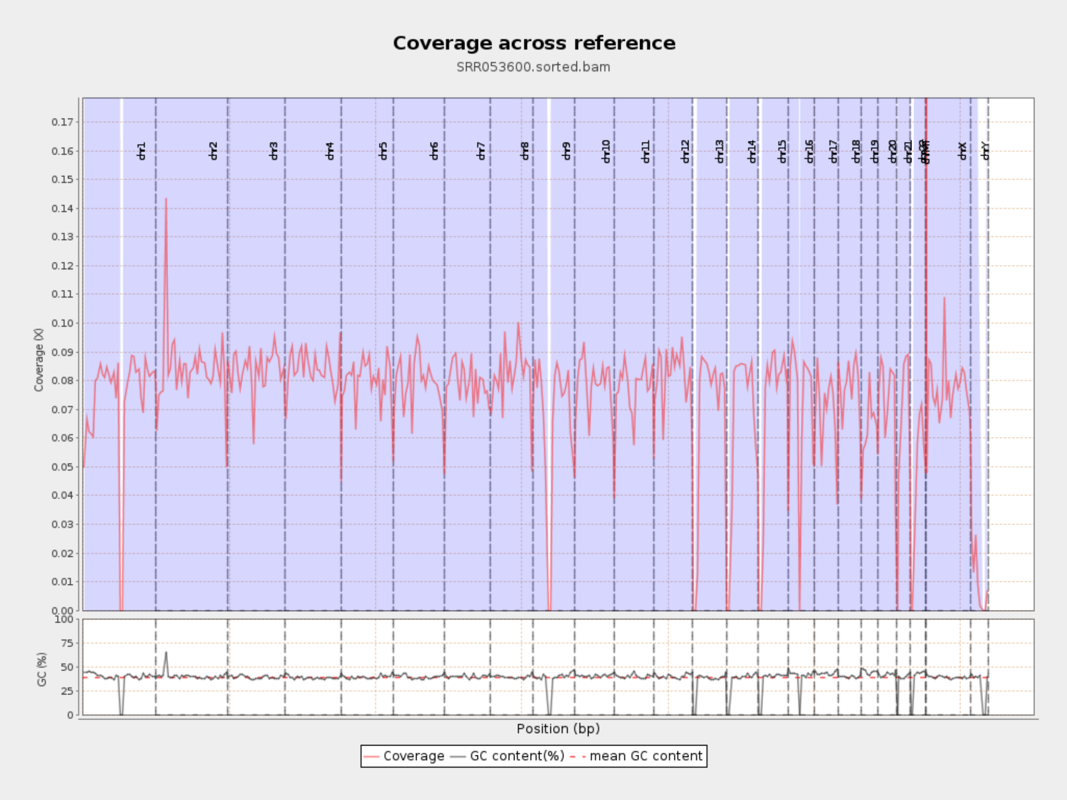
General error rate	0.99%
Mismatches	2,271,613
Insertions	13,218
Mapped reads with at least one insertion	0.26%
Deletions	33,413
Mapped reads with at least one deletion	0.67%
Homopolymer indels	45.52%

2.6. Chromosome stats

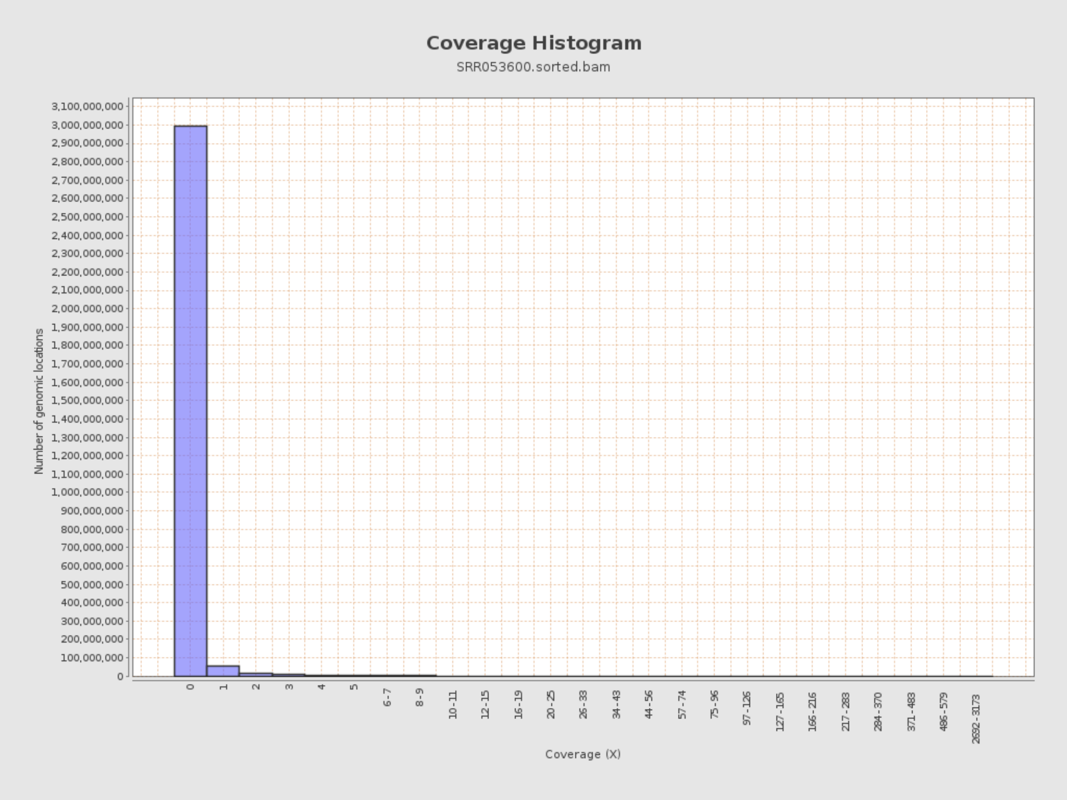
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18258763	0.0733	0.7346
chr2	243199373	20525098	0.0844	2.4036
chr3	198022430	16624122	0.084	0.6504
chr4	191154276	16149269	0.0845	0.6671
chr5	180915260	14411186	0.0797	0.6366
chr6	171115067	13670890	0.0799	0.7182
chr7	159138663	12534158	0.0788	0.7189

chr8	146364022	11955241	0.0817	0.6765
chr9	141213431	9350640	0.0662	0.6054
chr10	135534747	10720024	0.0791	0.6801
chr11	135006516	10476991	0.0776	0.6976
chr12	133851895	11033831	0.0824	0.6401
chr13	115169878	7778659	0.0675	0.5885
chr14	107349540	7150758	0.0666	0.6273
chr15	102531392	6893018	0.0672	0.5698
chr16	90354753	6360149	0.0704	0.6078
chr17	81195210	5731890	0.0706	0.5861
chr18	78077248	6149443	0.0788	0.7434
chr19	59128983	3773689	0.0638	0.6661
chr20	63025520	4801965	0.0762	0.6221
chr21	48129895	3115569	0.0647	0.5896
chr22	51304566	2256987	0.044	0.4286
chrMT	16571	52531	3.1701	5.6259
chrX	155270560	11962814	0.077	0.6505
chrY	59373566	574659	0.0097	0.2015

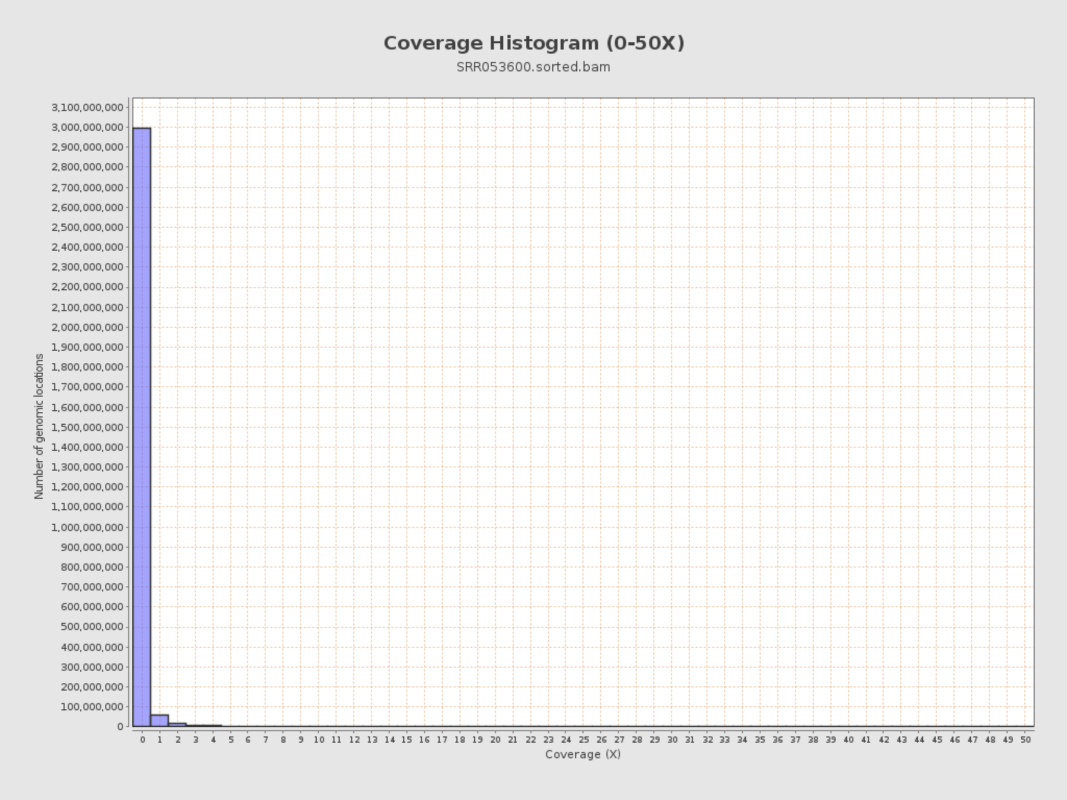
3. Results : Coverage across reference



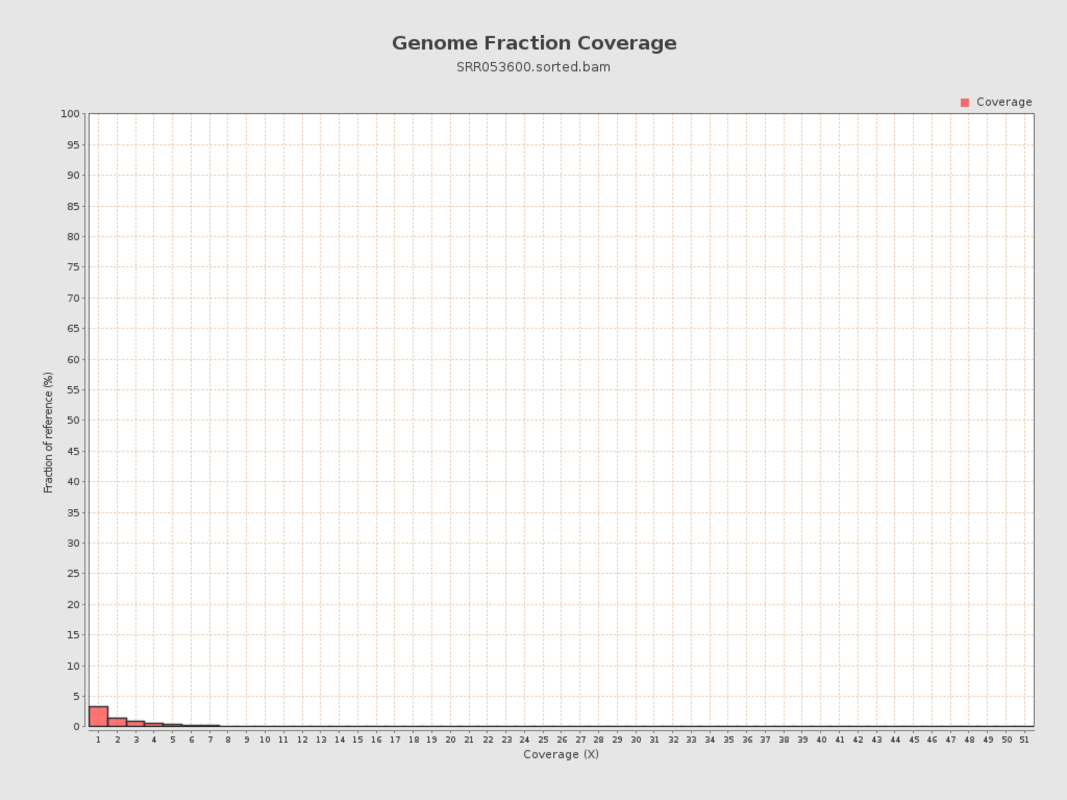
4. Results : Coverage Histogram



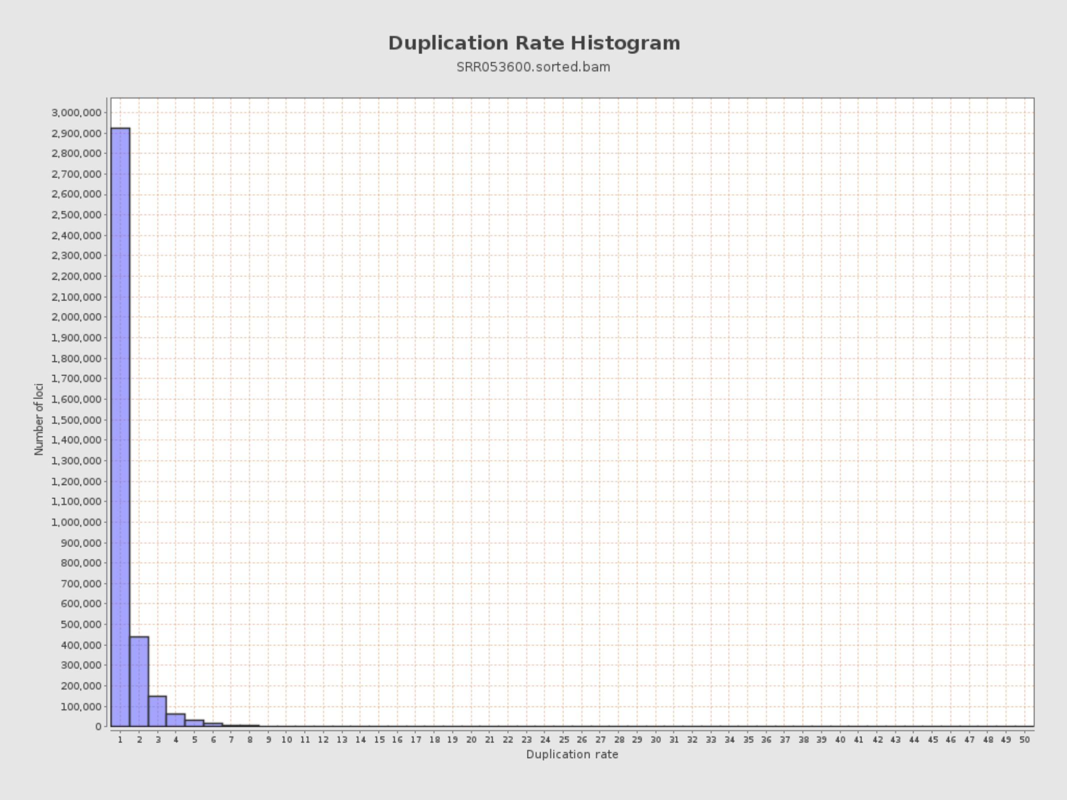
5. Results : Coverage Histogram (0-50X)



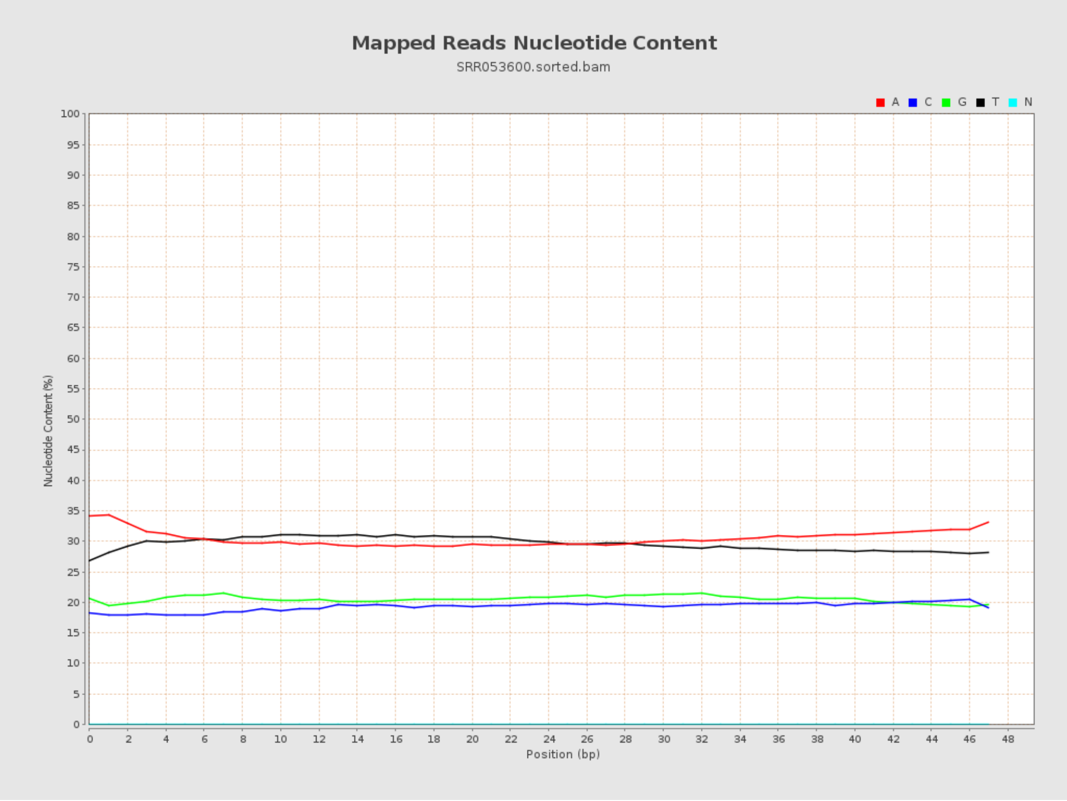
6. Results : Genome Fraction Coverage



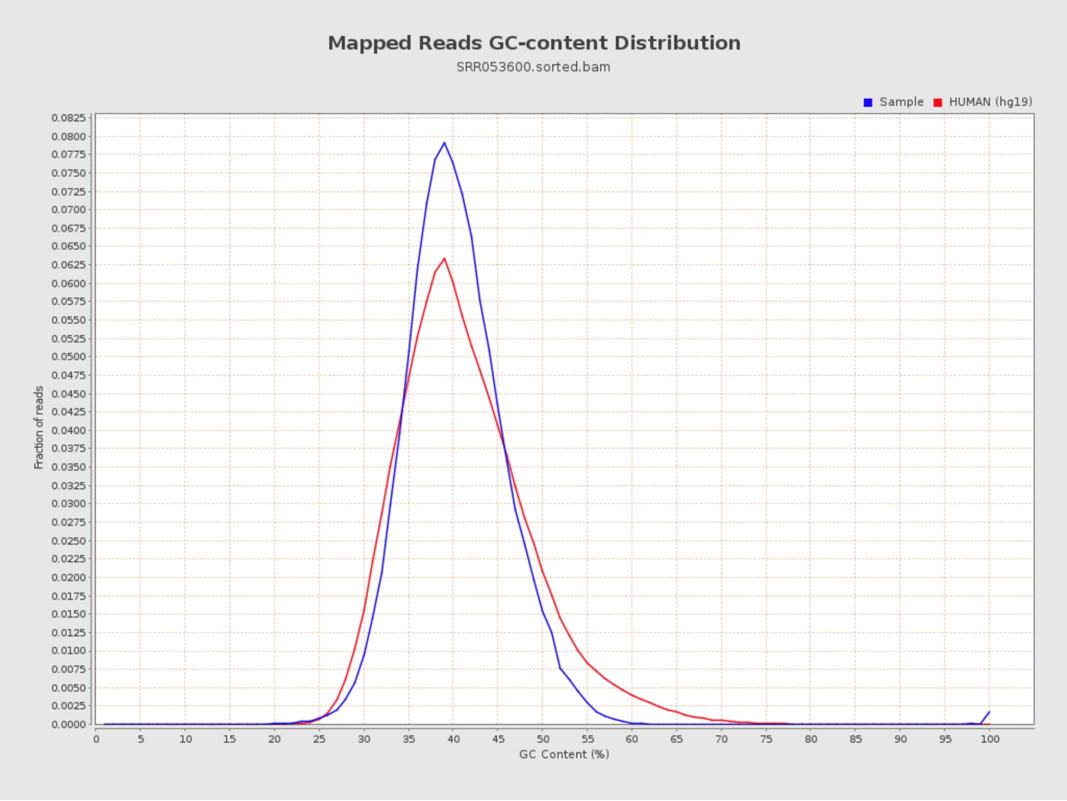
7. Results : Duplication Rate Histogram



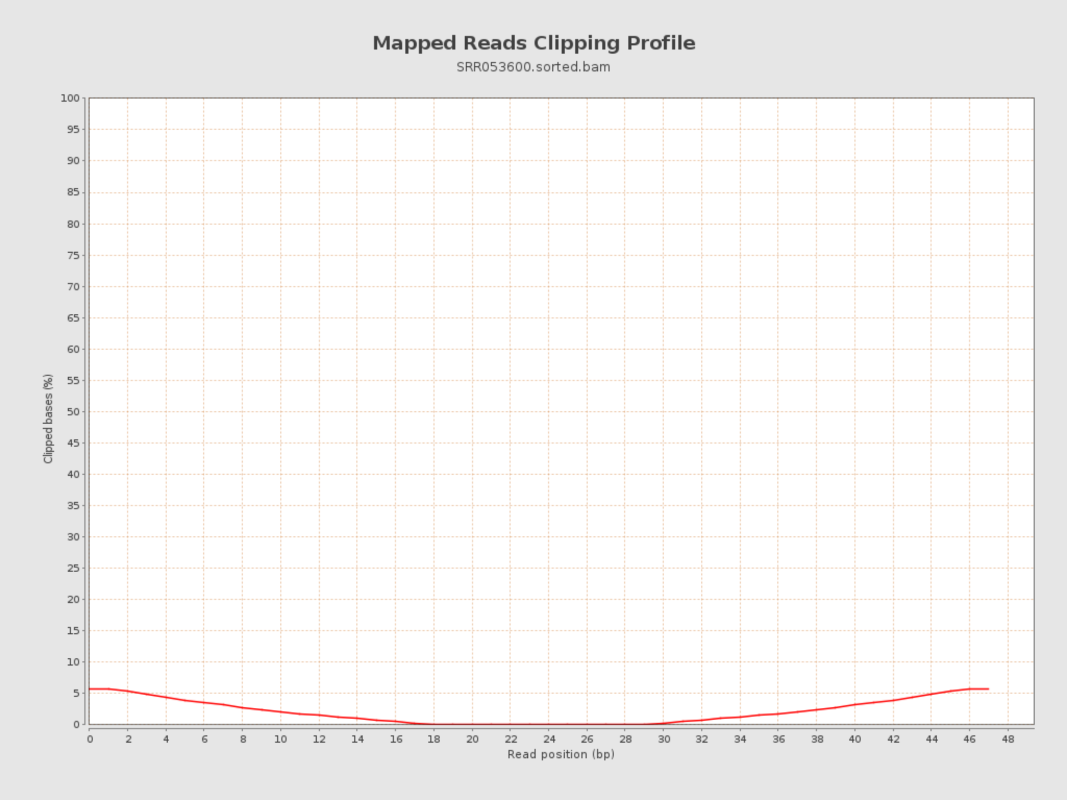
8. Results : Mapped Reads Nucleotide Content



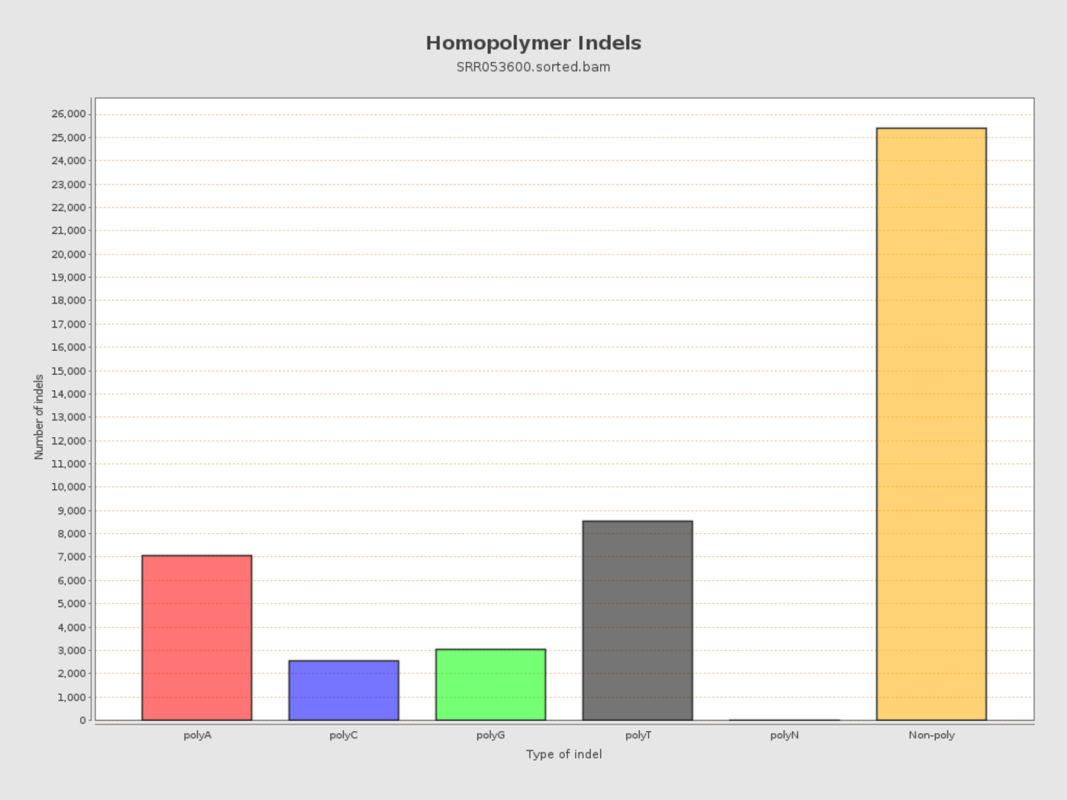
9. Results : Mapped Reads GC-content Distribution



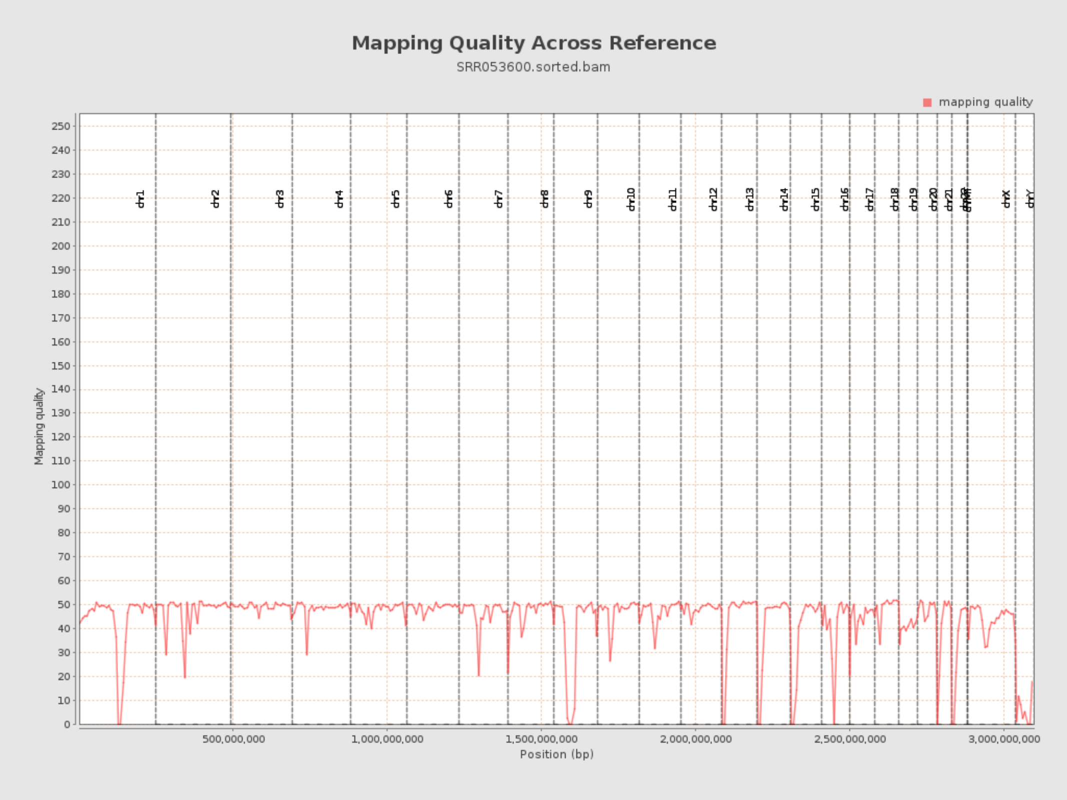
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram