Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/01/21 18:25:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR620536.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR620536.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 21 18:25:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR620536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,692,981
Mapped reads	5,106,494 / 58.74%
Unmapped reads	3,586,487 / 41.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	504 / 0.01%
Read min/max/mean length	30 / 49 / 49
Duplicated reads (estimated)	310,997 / 3.58%
Duplication rate	3.4%
Clipped reads	1,262,817 / 14.53%

2.2. ACGT Content

Number/percentage of A's	63,422,425 / 27.21%
Number/percentage of C's	44,829,156 / 19.23%
Number/percentage of T's	71,366,083 / 30.62%
Number/percentage of G's	53,432,014 / 22.93%
Number/percentage of N's	14,562 / 0.01%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0753

Standard Deviation	0.8429

2.4. Mapping Quality

Mean Mapping Quality	42.29

2.5. Mismatches and indels

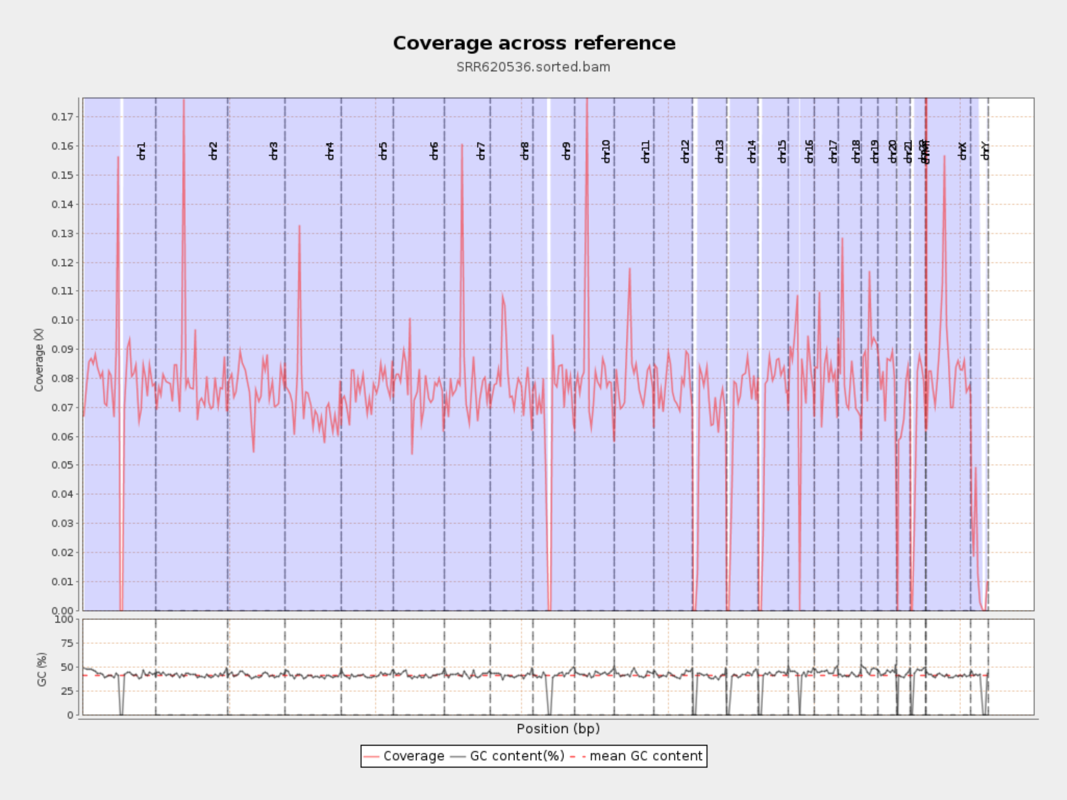
General error rate	0.74%
Mismatches	1,706,098
Insertions	15,441
Mapped reads with at least one insertion	0.3%
Deletions	37,713
Mapped reads with at least one deletion	0.73%
Homopolymer indels	45.22%

2.6. Chromosome stats

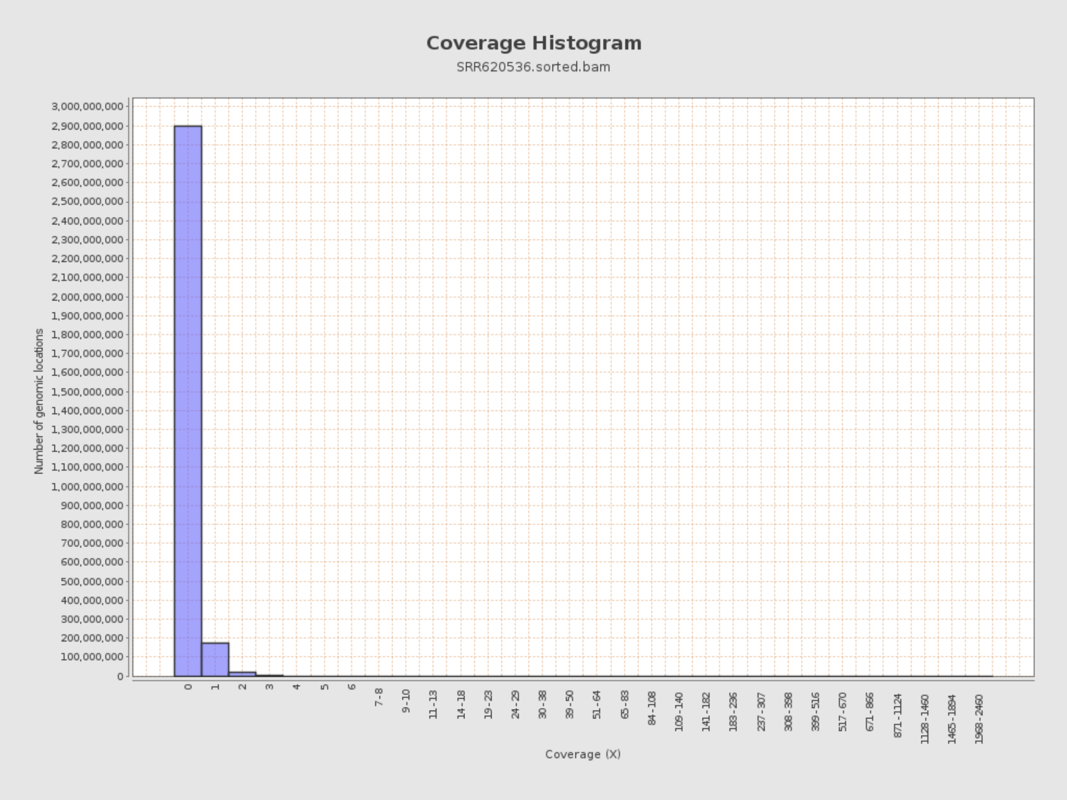
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19245725	0.0772	1.5035
chr2	243199373	19461371	0.08	0.8291
chr3	198022430	15251436	0.077	0.4122
chr4	191154276	13793869	0.0722	0.4655
chr5	180915260	13793371	0.0762	0.3591
chr6	171115067	13165170	0.0769	0.5127
chr7	159138663	12654626	0.0795	1.067

chr8	146364022	11549617	0.0789	0.9216
chr9	141213431	9519459	0.0674	0.621
chr10	135534747	11226313	0.0828	0.8137
chr11	135006516	10883831	0.0806	1.1826
chr12	133851895	10501380	0.0785	0.4204
chr13	115169878	7042776	0.0612	0.3185
chr14	107349540	7061113	0.0658	0.3537
chr15	102531392	6767886	0.066	0.3374
chr16	90354753	7102004	0.0786	0.471
chr17	81195210	6747314	0.0831	0.5408
chr18	78077248	6311941	0.0808	2.2588
chr19	59128983	5335450	0.0902	0.9968
chr20	63025520	5048352	0.0801	0.4451
chr21	48129895	3037094	0.0631	0.4211
chr22	51304566	2921179	0.0569	0.2839
chrMT	16571	498564	30.0865	23.5578
chrX	155270560	13303914	0.0857	0.6747
chrY	59373566	898094	0.0151	0.3003

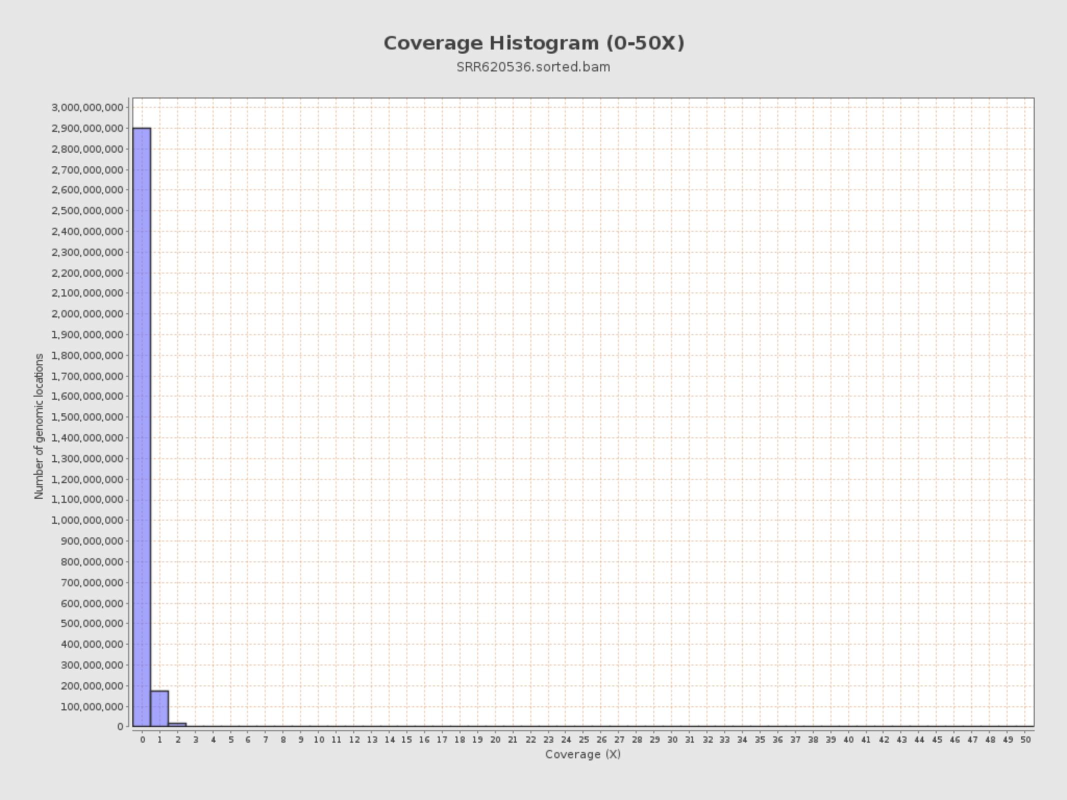
3. Results : Coverage across reference



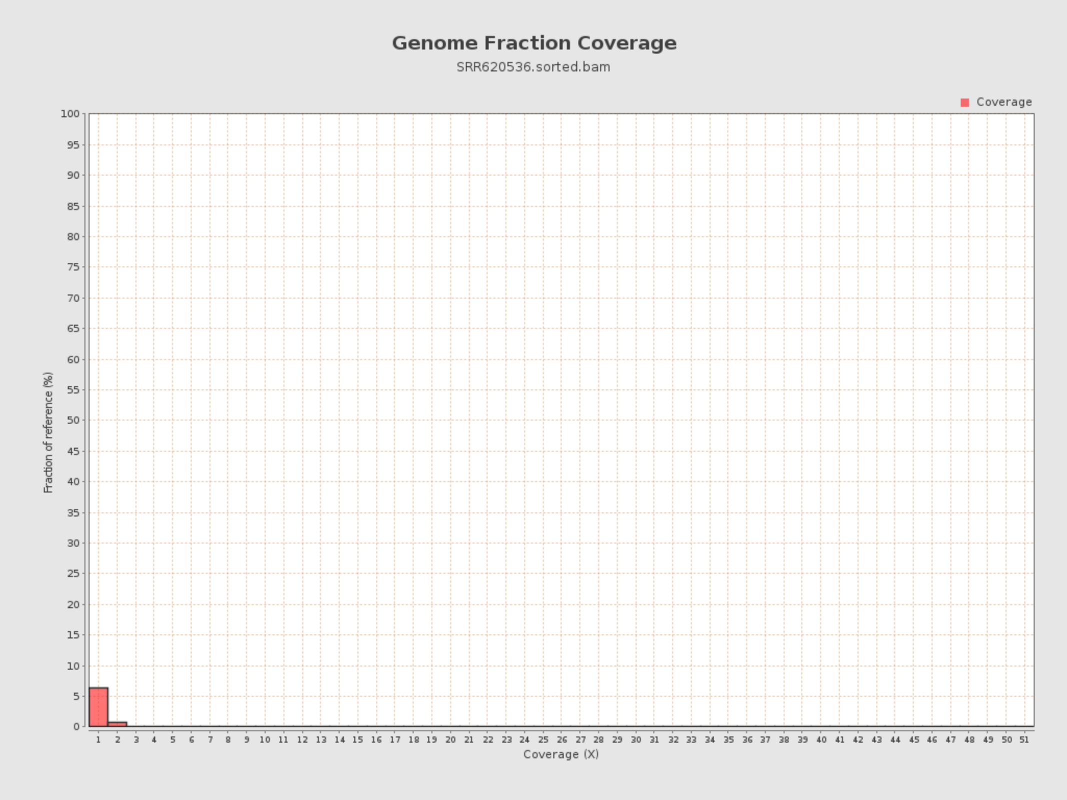
4. Results : Coverage Histogram



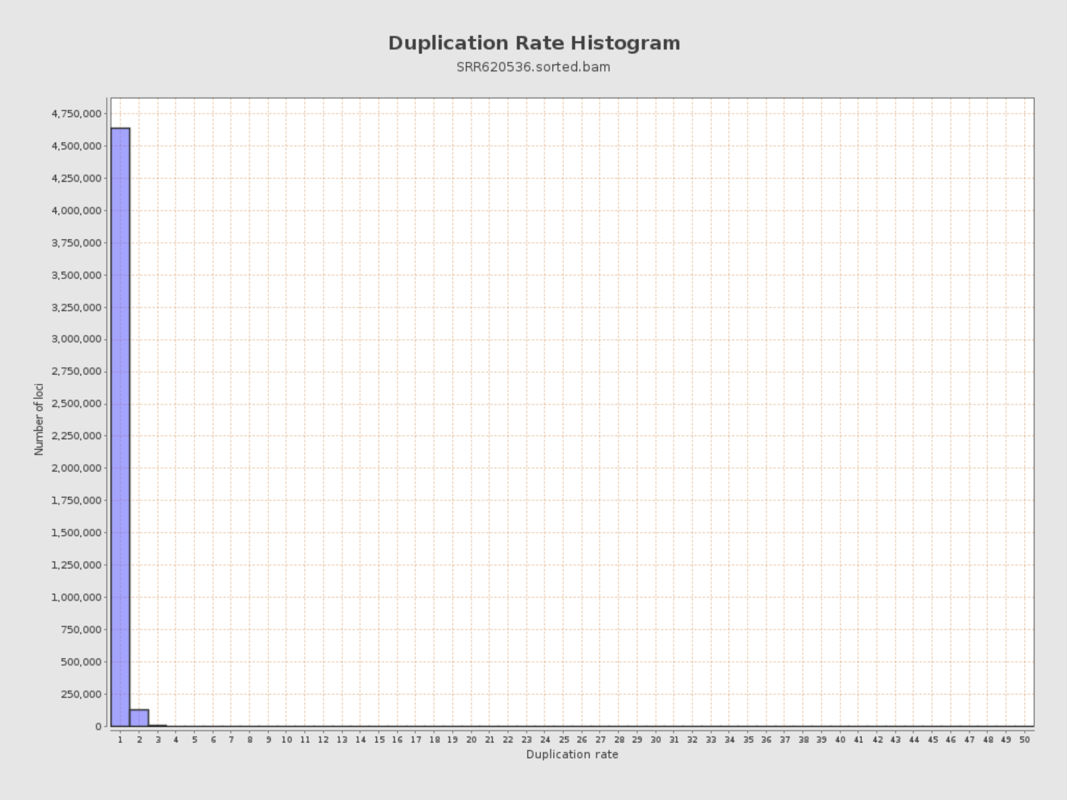
5. Results : Coverage Histogram (0-50X)



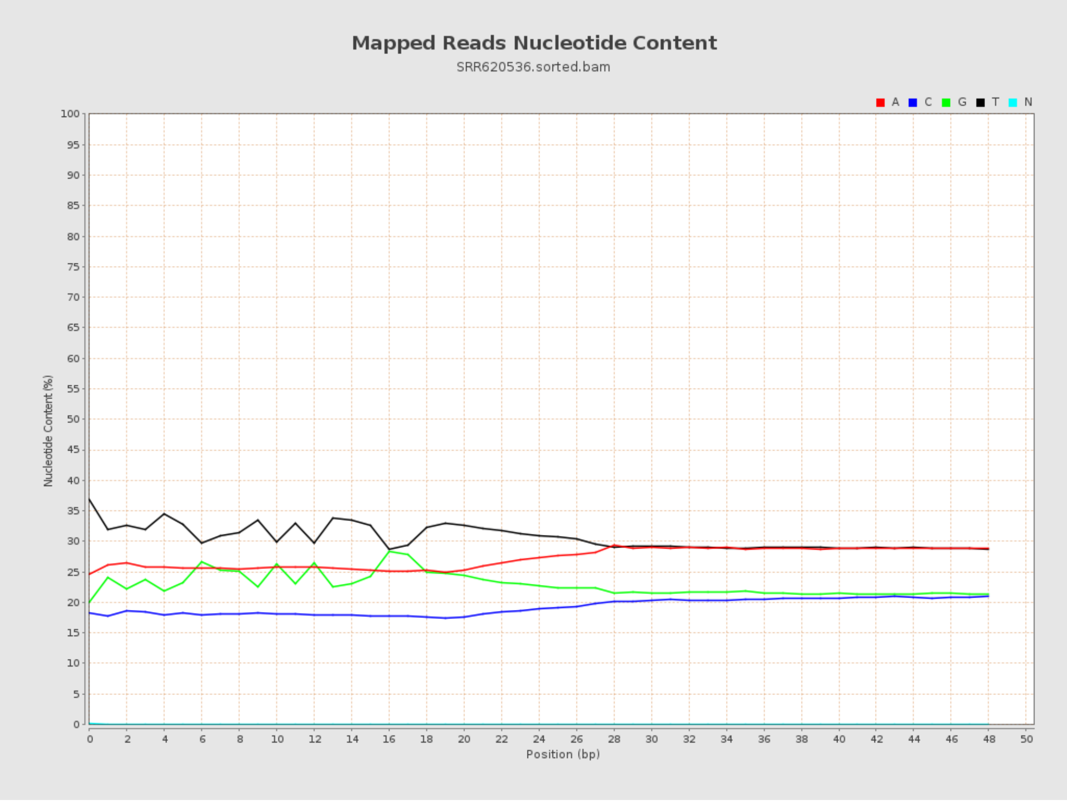
6. Results : Genome Fraction Coverage



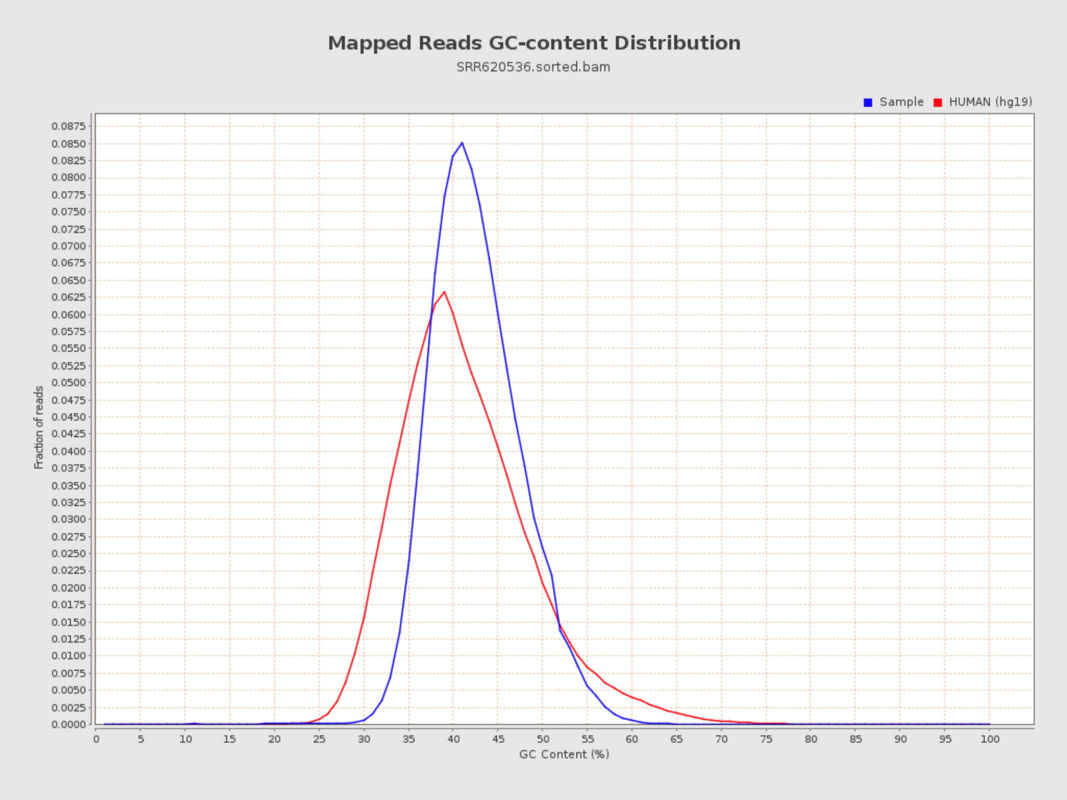
7. Results : Duplication Rate Histogram



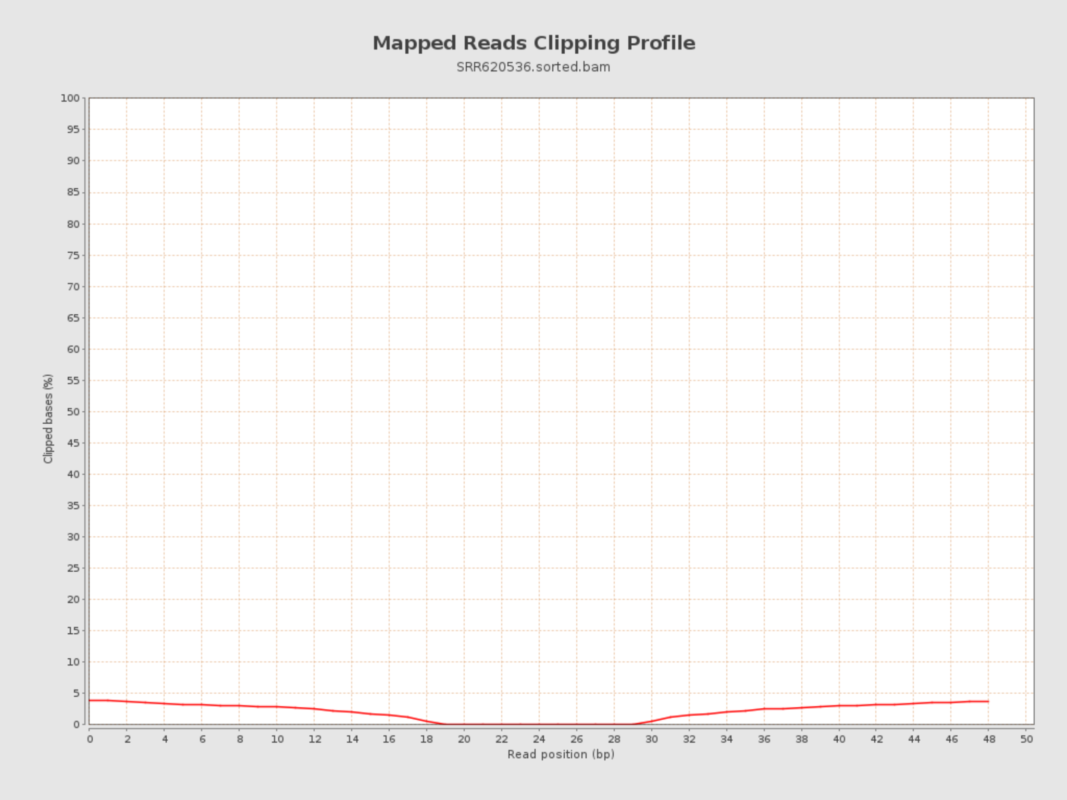
8. Results : Mapped Reads Nucleotide Content



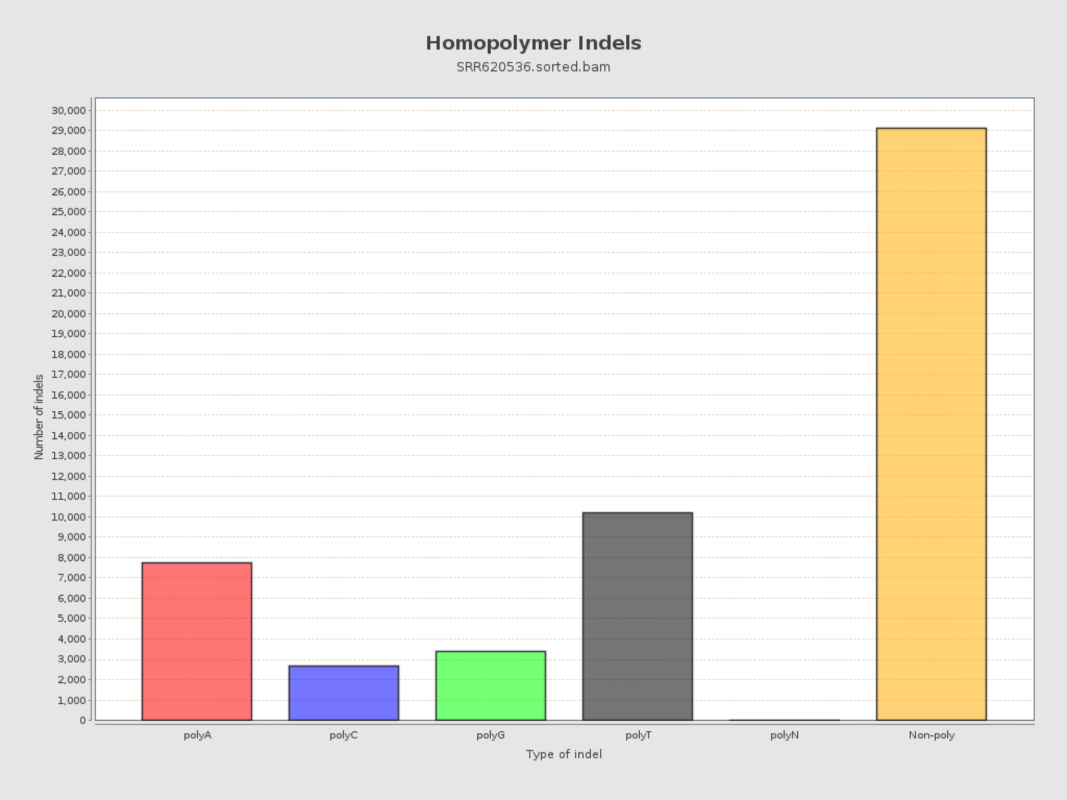
9. Results : Mapped Reads GC-content Distribution



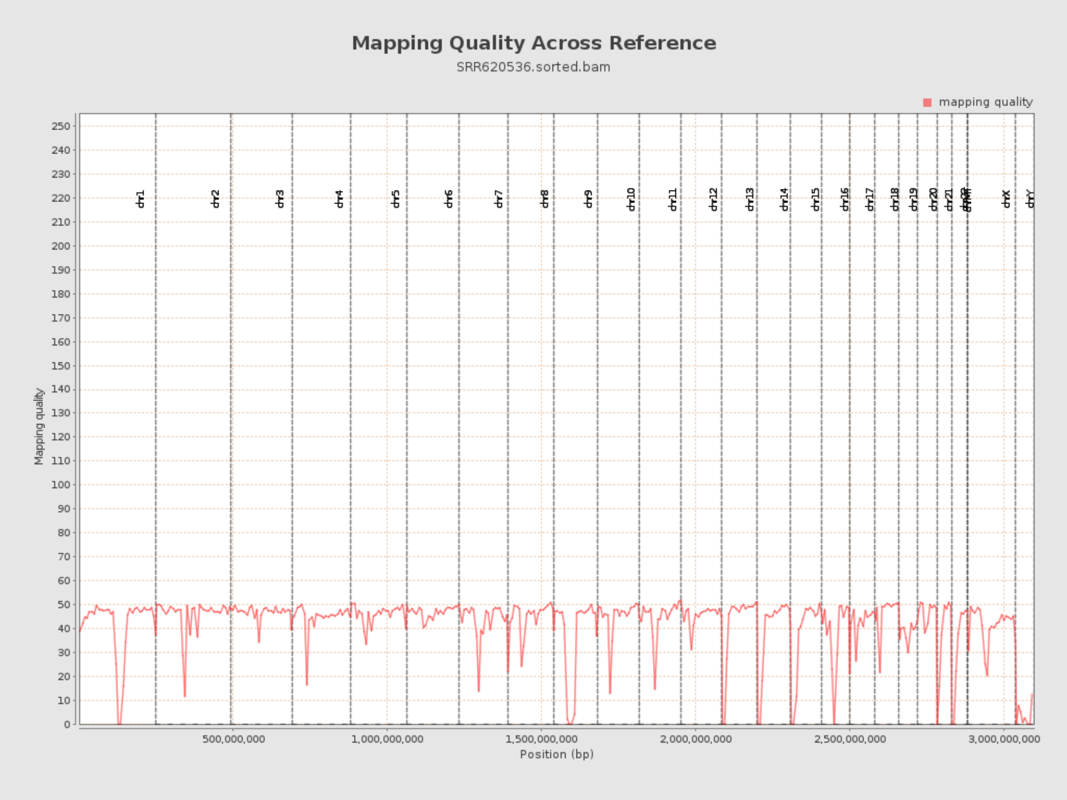
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram