Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 14:20:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089583.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_SRR089583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 14:20:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,017,685
Mapped reads	7,013,618 / 77.78%
Unmapped reads	2,004,067 / 22.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	262 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,382,564 / 26.42%
Duplication rate	26.36%
Clipped reads	829,337 / 9.2%

2.2. ACGT Content

Number/percentage of A's	105,054,616 / 31.92%
Number/percentage of C's	63,462,245 / 19.28%
Number/percentage of T's	88,080,989 / 26.76%
Number/percentage of G's	72,419,212 / 22%
Number/percentage of N's	123,791 / 0.04%
GC Percentage	41.28%

2.3. Coverage

Mean	0.1063

Standard Deviation	0.9403

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

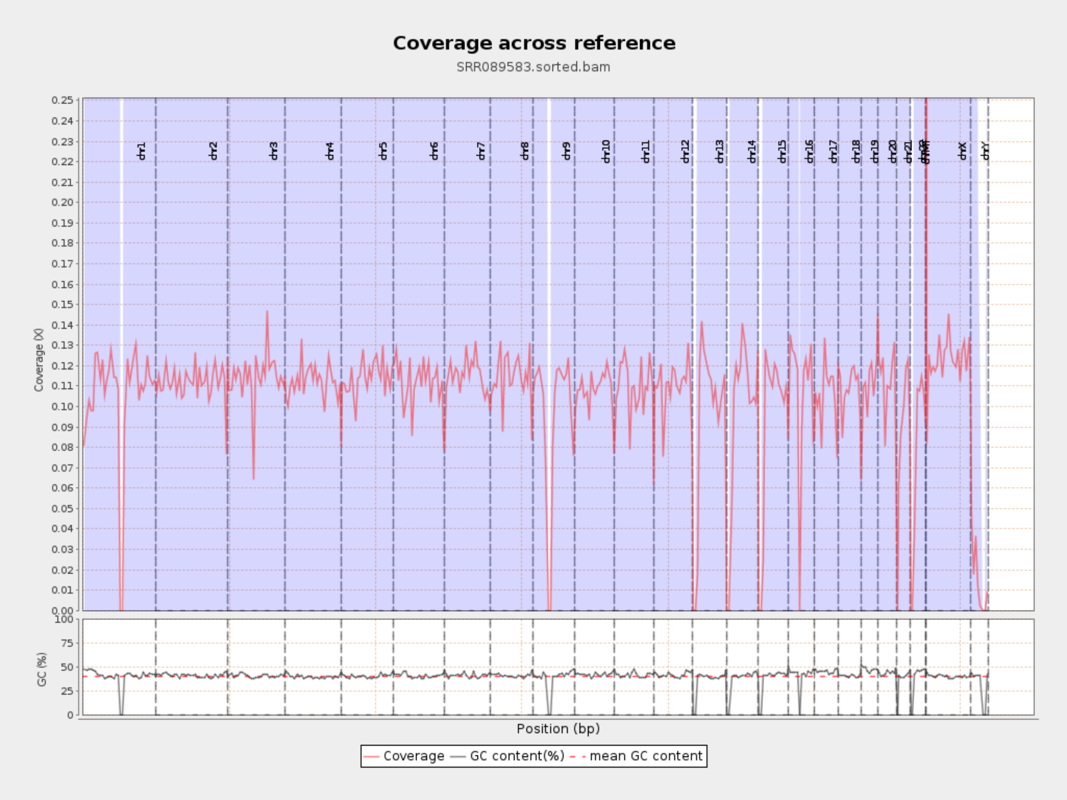
General error rate	0.59%
Mismatches	1,914,701
Insertions	14,819
Mapped reads with at least one insertion	0.21%
Deletions	42,765
Mapped reads with at least one deletion	0.61%
Homopolymer indels	44.18%

2.6. Chromosome stats

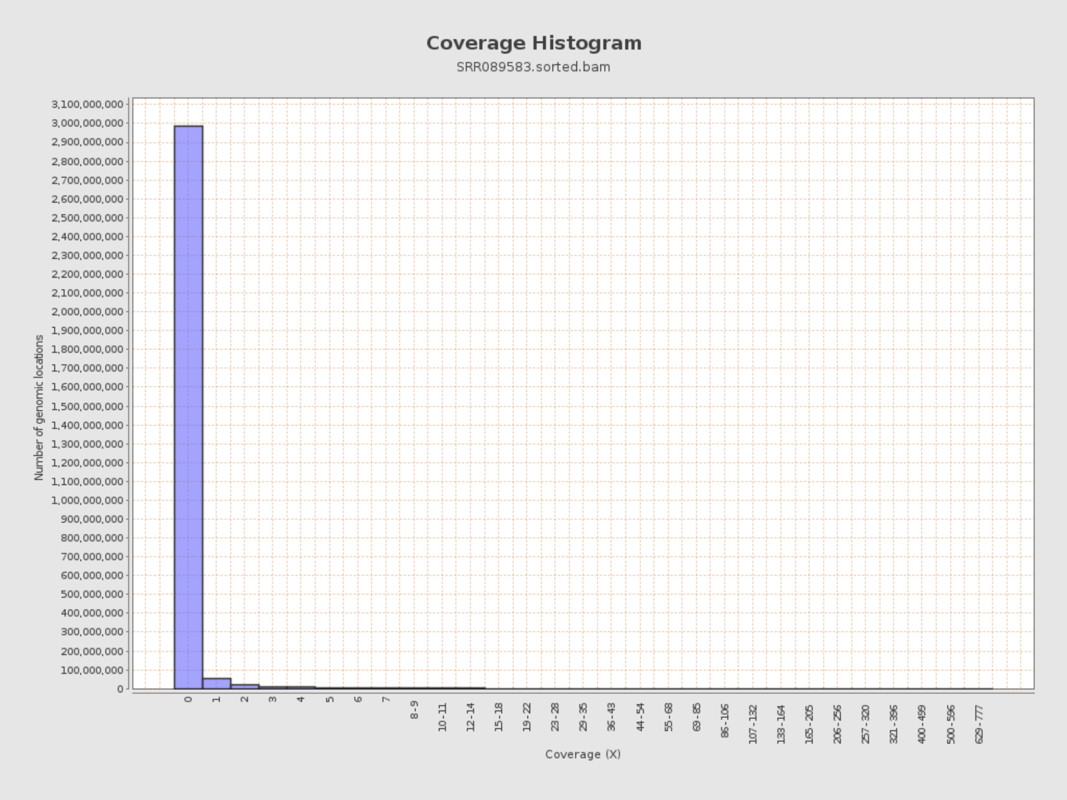
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26190773	0.1051	0.9976
chr2	243199373	27261811	0.1121	1.0104
chr3	198022430	22670753	0.1145	0.9452
chr4	191154276	21522184	0.1126	0.9456
chr5	180915260	20652371	0.1142	0.9319
chr6	171115067	19158729	0.112	0.9844
chr7	159138663	18243175	0.1146	1.038

chr8	146364022	16723621	0.1143	1.0456
chr9	141213431	13461818	0.0953	0.8402
chr10	135534747	14826395	0.1094	0.9412
chr11	135006516	14786293	0.1095	0.9907
chr12	133851895	14835959	0.1108	0.9139
chr13	115169878	10858077	0.0943	0.8599
chr14	107349540	10275198	0.0957	0.9151
chr15	102531392	9337958	0.0911	0.8183
chr16	90354753	9455760	0.1047	0.9052
chr17	81195210	8659376	0.1066	0.8724
chr18	78077248	8516894	0.1091	0.9375
chr19	59128983	6558304	0.1109	0.9371
chr20	63025520	7136150	0.1132	0.9131
chr21	48129895	4206396	0.0874	0.8378
chr22	51304566	3851369	0.0751	0.7163
chrMT	16571	83657	5.0484	8.9083
chrX	155270560	19094262	0.123	0.9969
chrY	59373566	837570	0.0141	0.2916

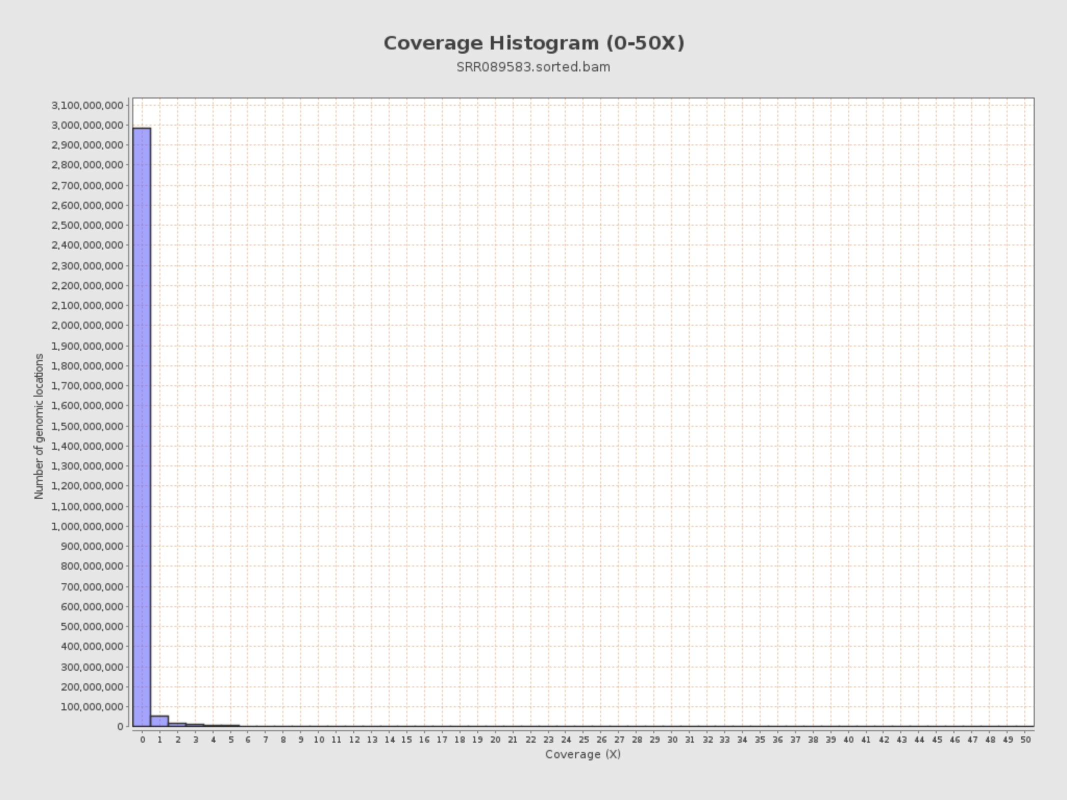
3. Results : Coverage across reference



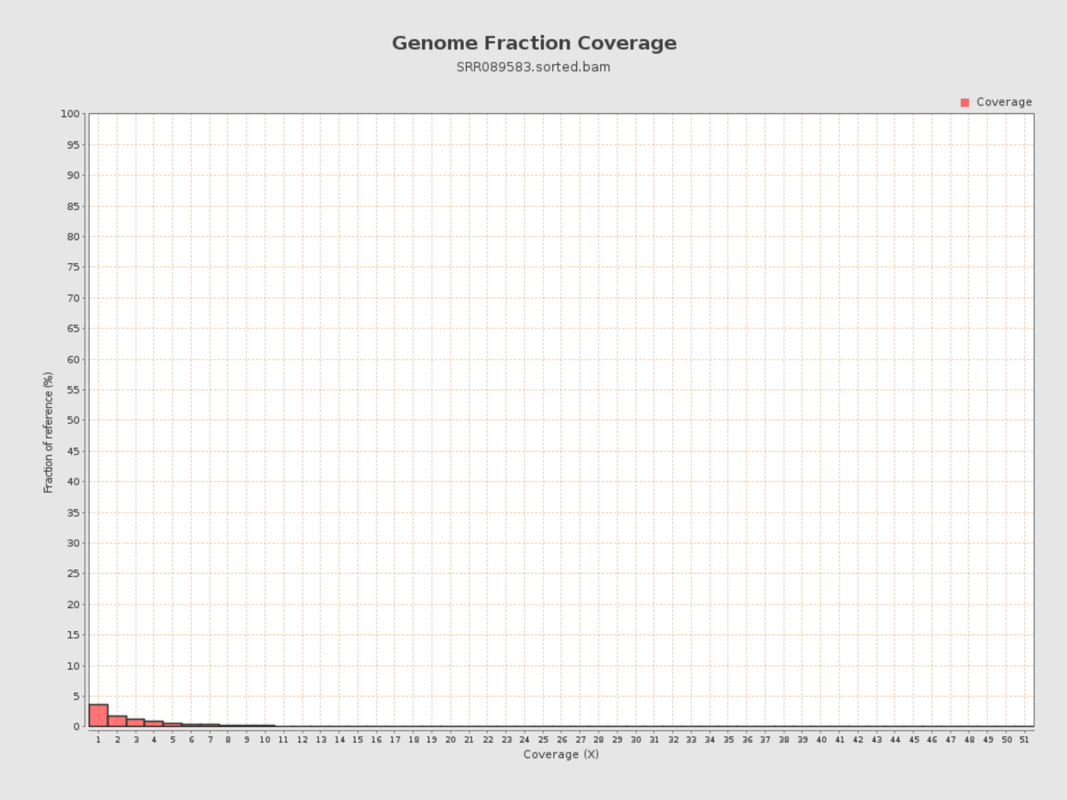
4. Results : Coverage Histogram



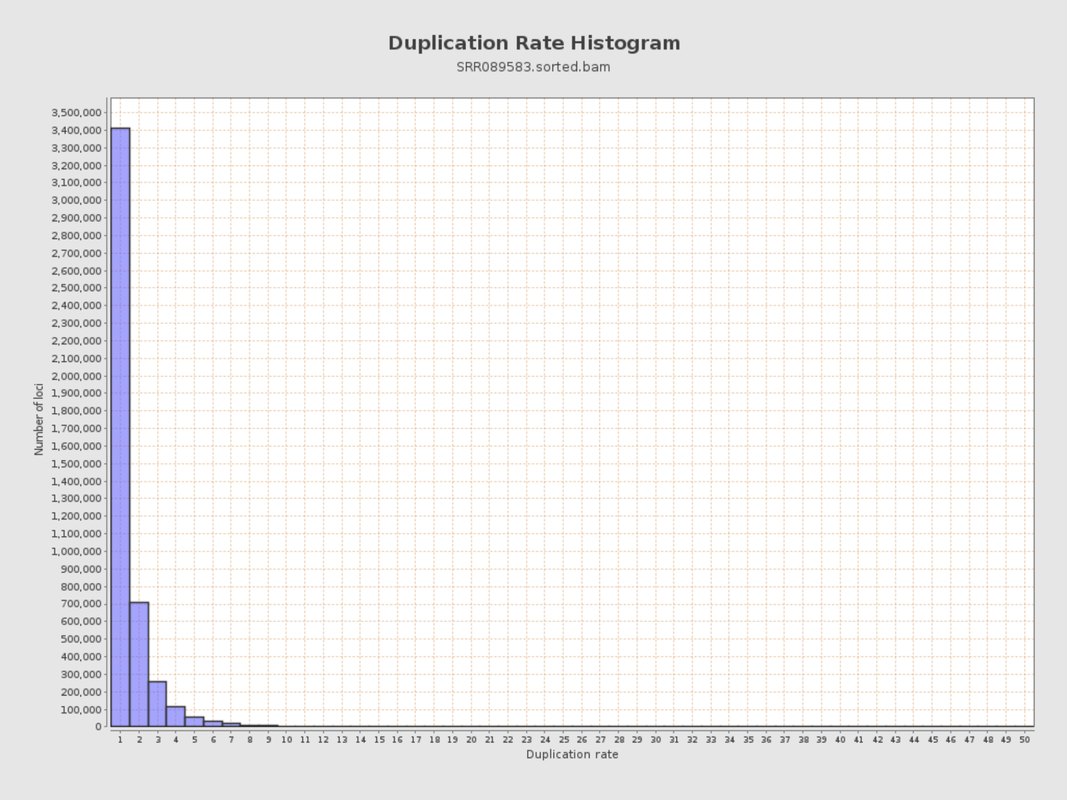
5. Results : Coverage Histogram (0-50X)



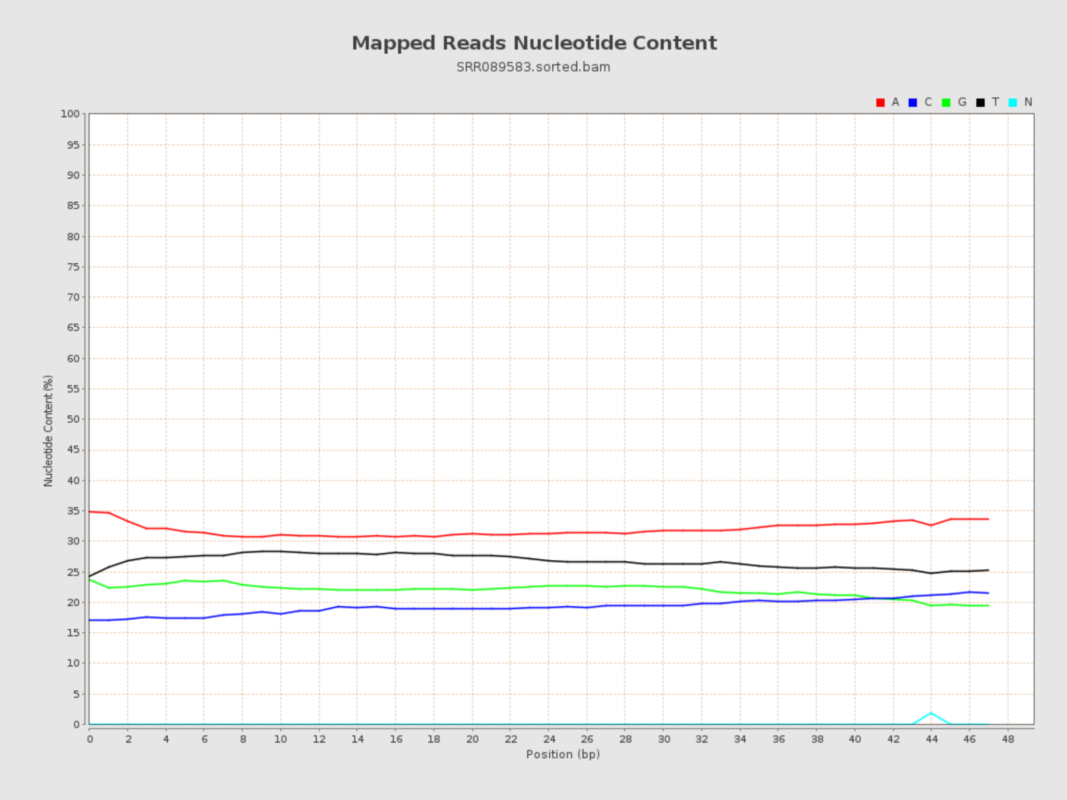
6. Results : Genome Fraction Coverage



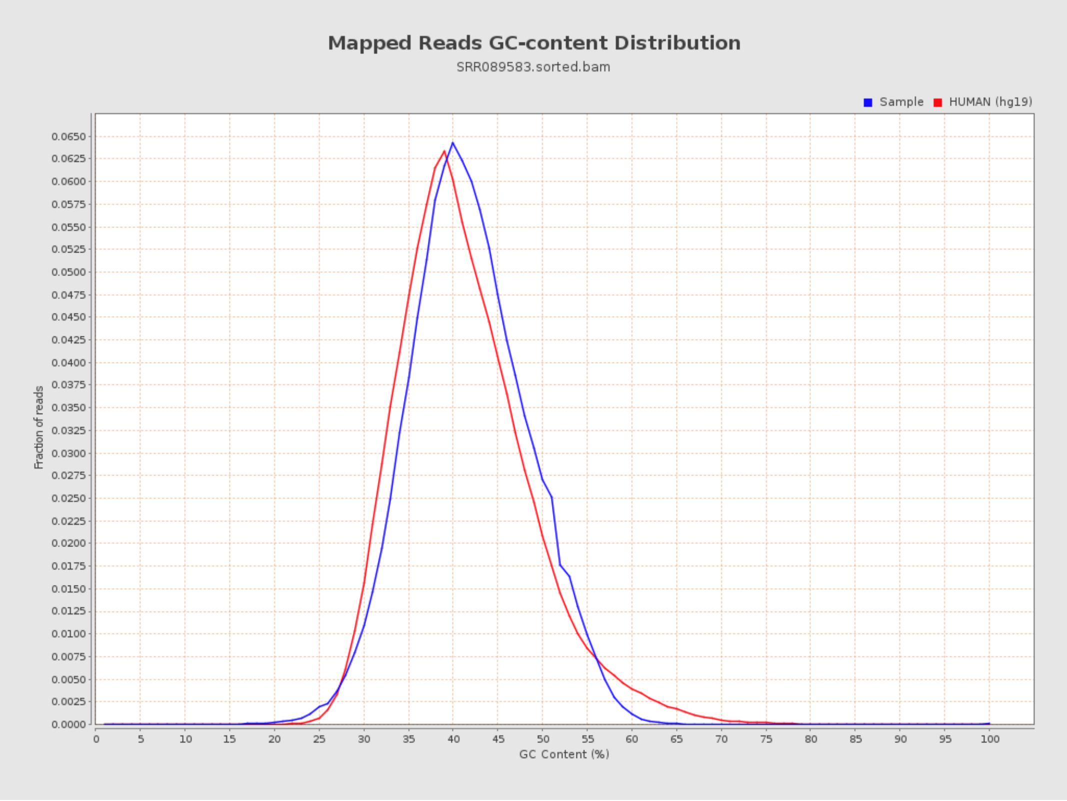
7. Results : Duplication Rate Histogram



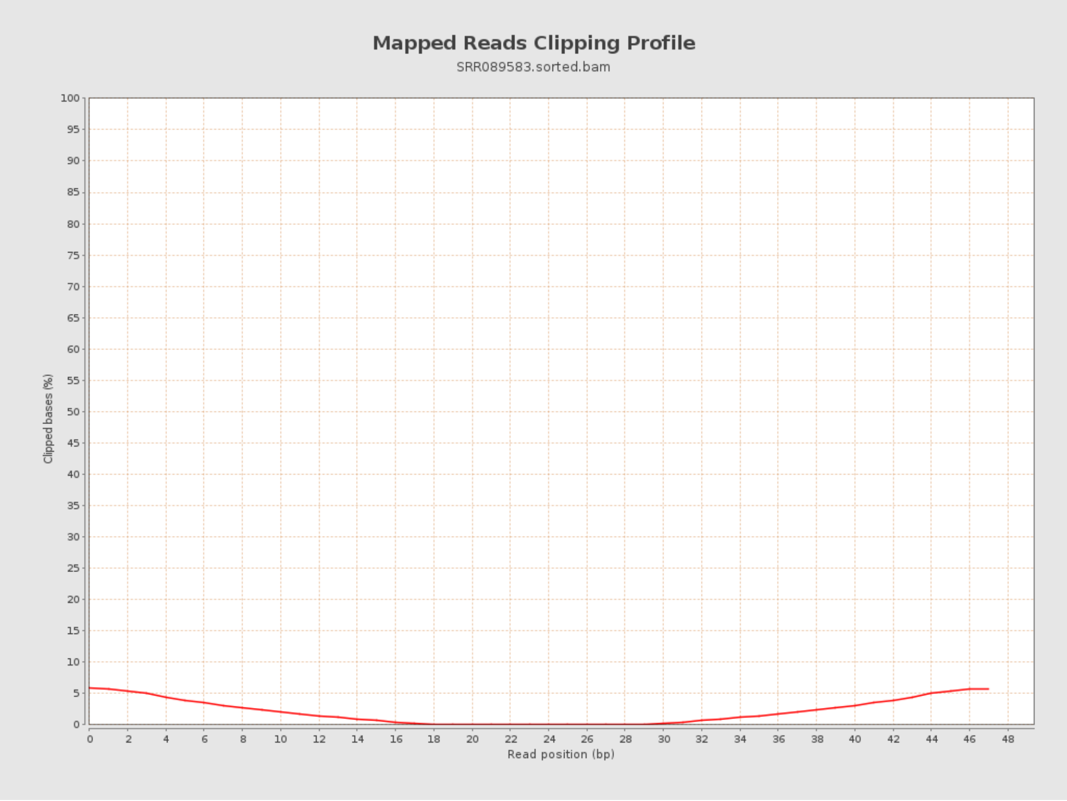
8. Results : Mapped Reads Nucleotide Content



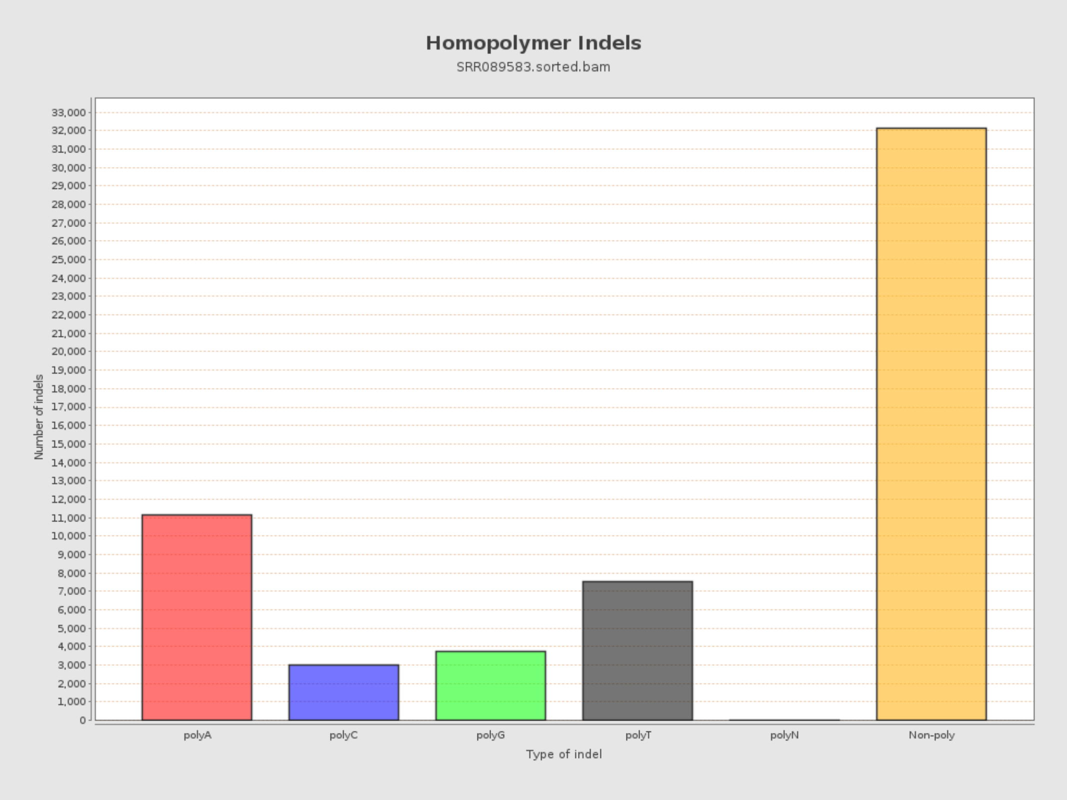
9. Results : Mapped Reads GC-content Distribution



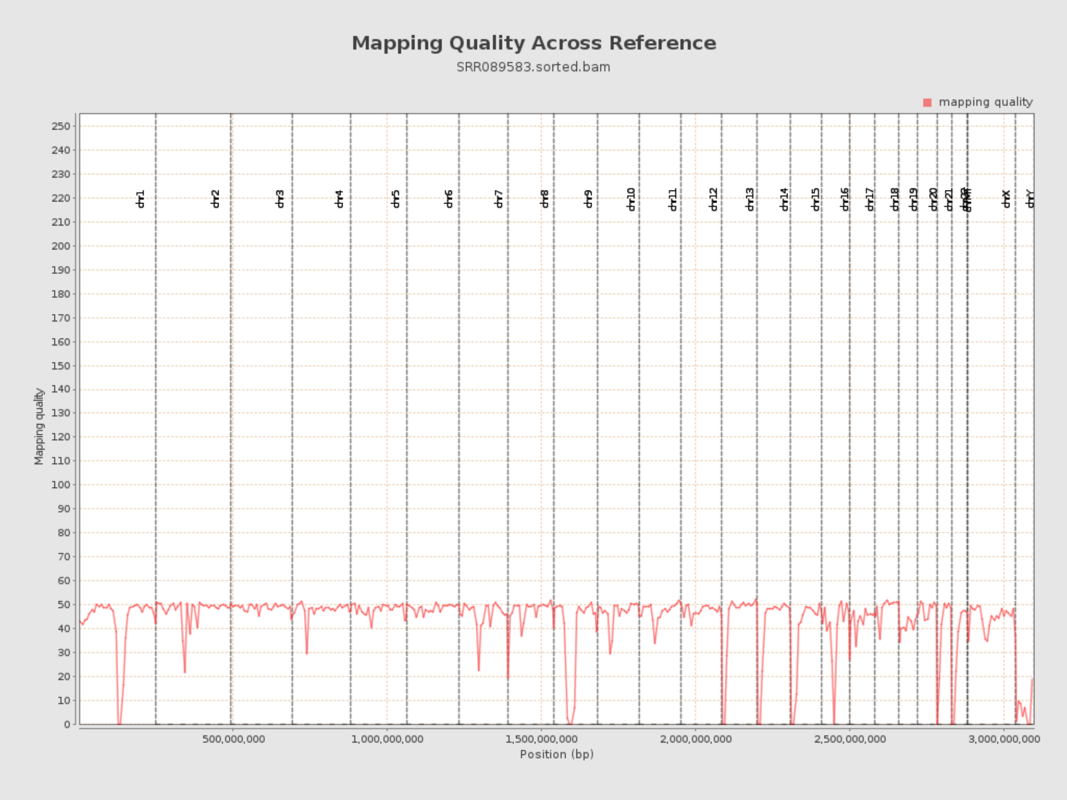
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram