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1. Summary mapping report

1.1 Summary statistics

	Count	Average length	Total bases
Reads	164,864,080	97.67	16,101,974,443
Matched	141,788,128	97.95	13,888,621,494
Not matched	23,075,952	95.92	2,213,352,949
Contigs	175,162	1,634	286,273,807
Reads in pairs	65,532,548	226.66	
Broken paired reads	76,255,580	97.88	

1.2 General algorithm parameters

Parameter	Value
Conflict resolution	Unknown nucleotide (N)
Non specific matches	ignore

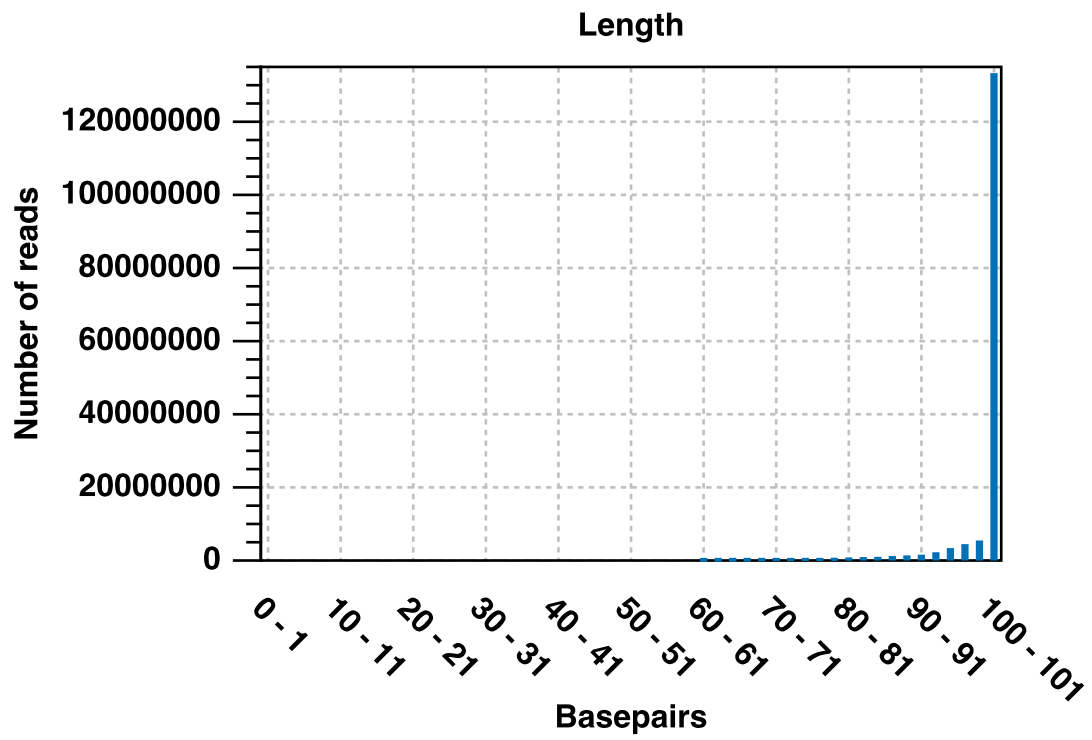
1.3 Reads parameters

Reads	Length	Type	Parameters
Prep7_1-1_1_sequence (paired)	Long	Paired	Default

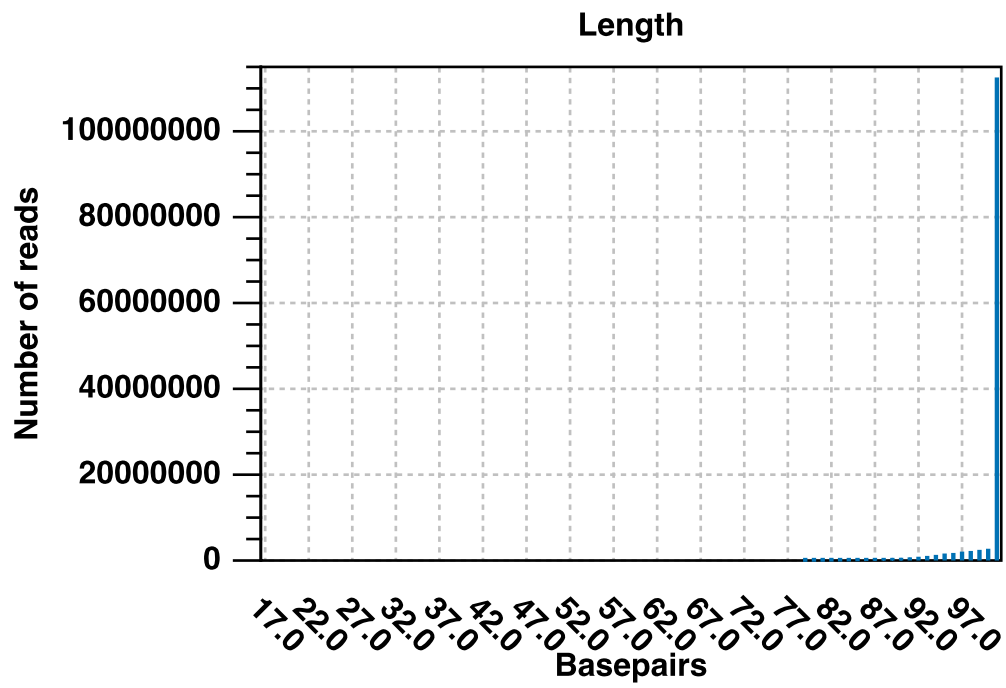
1.4 Quality measurement

N75	1,136
N50	2,250
N25	4,439

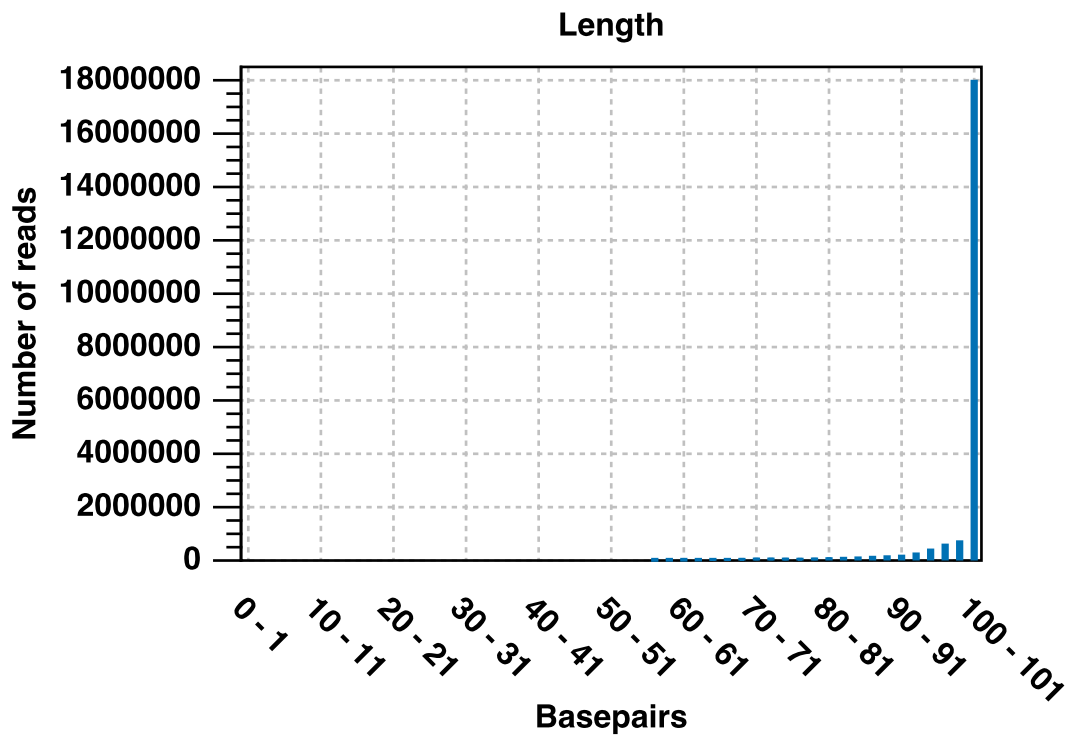
1.5 Distribution of read length



1.6 Distribution of matched read length



1.7 Distribution of non-matched read length



1.8 Paired reads distance distribution

