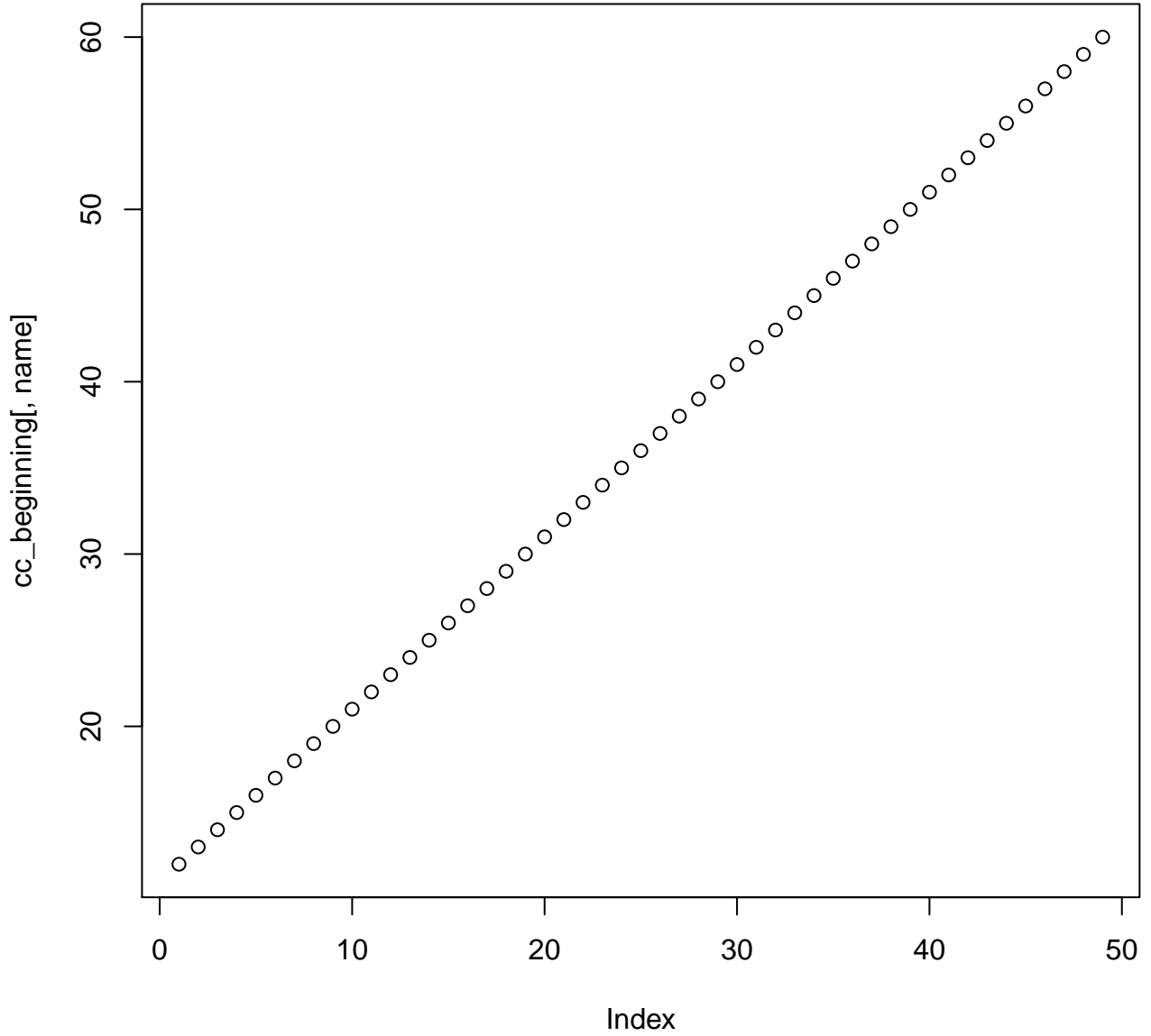
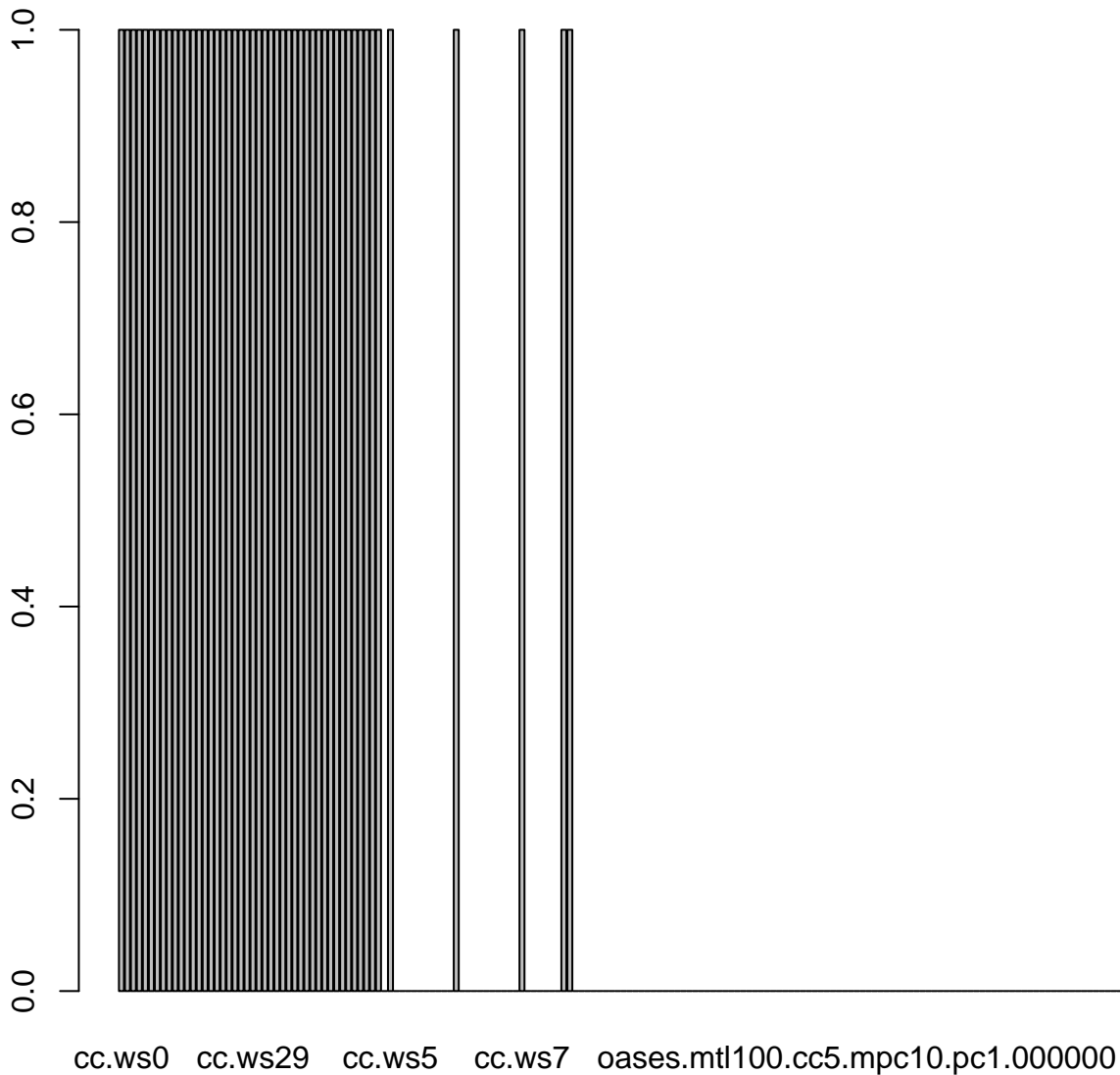


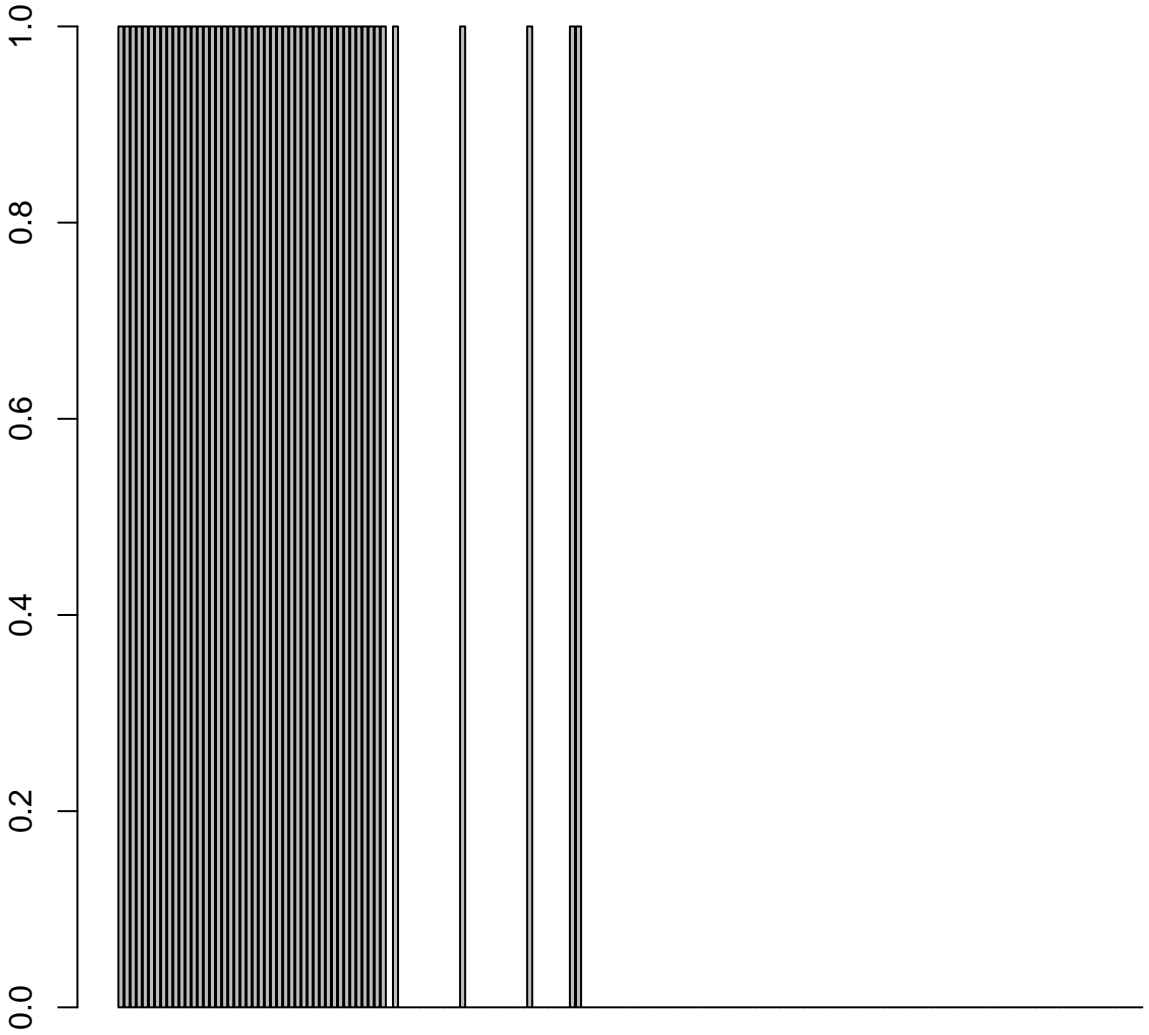
**X**



**name**

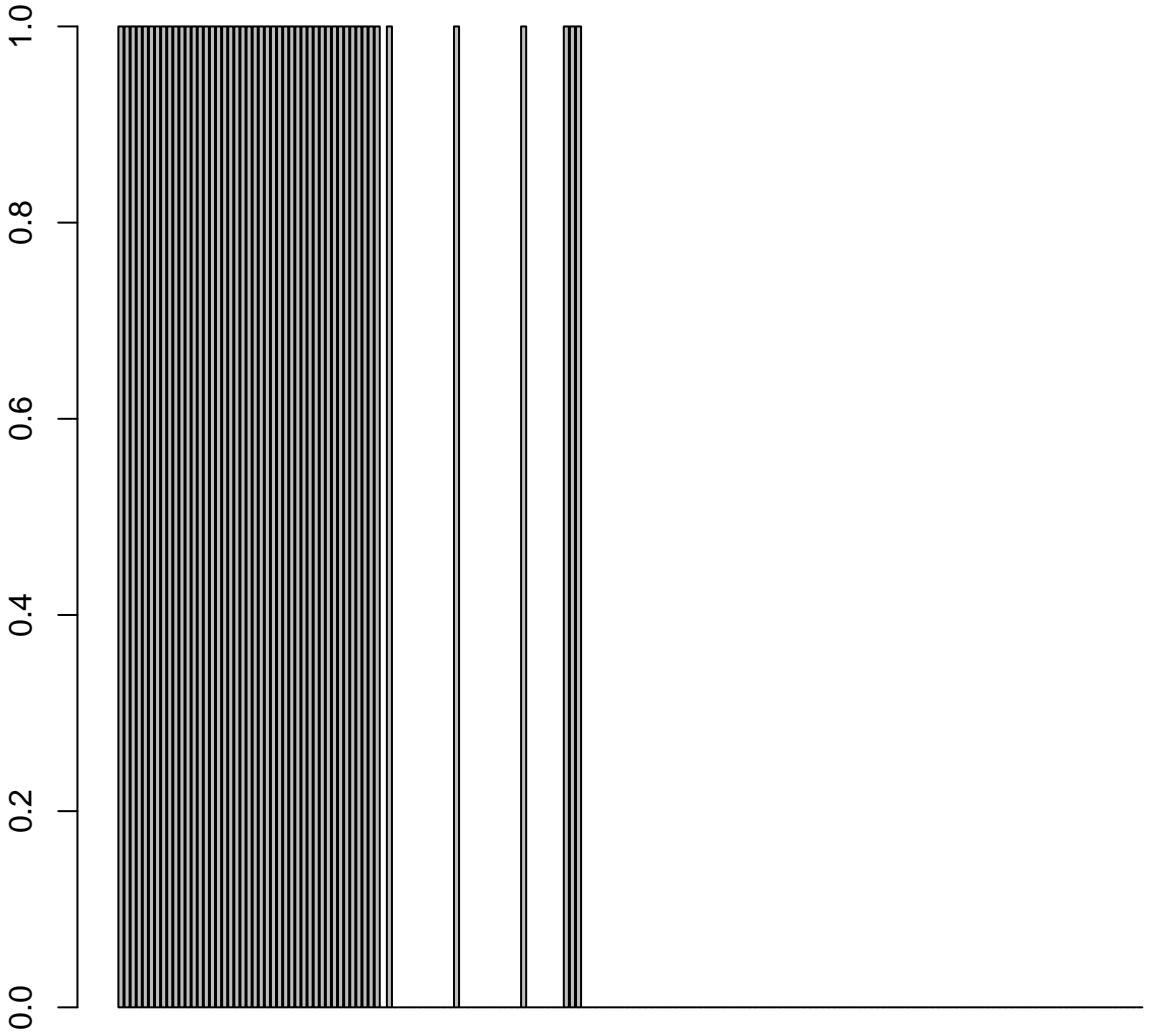


# assembly



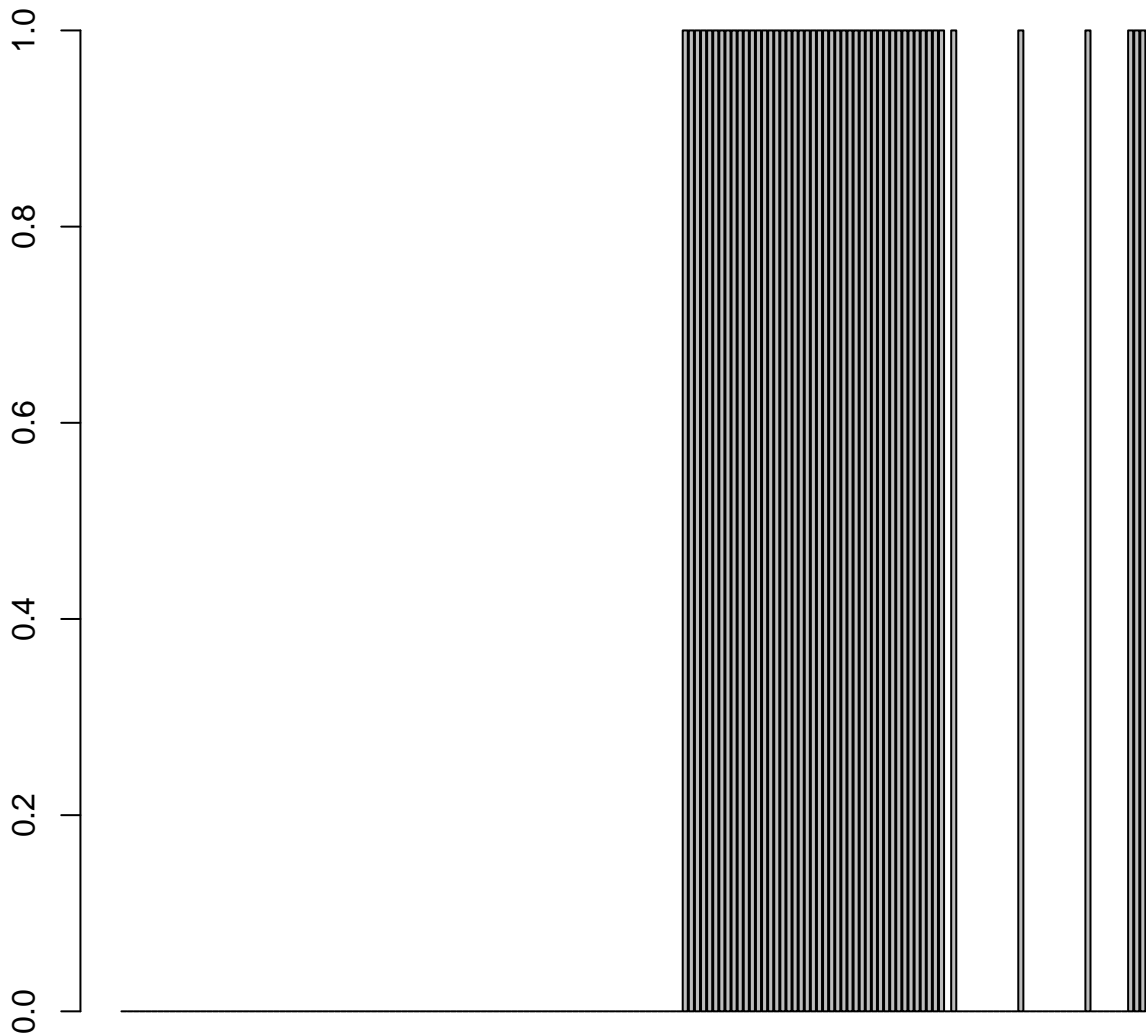
single-full//gridsearch-collectContigs/rsem\_oracleSet.ws0

# summary



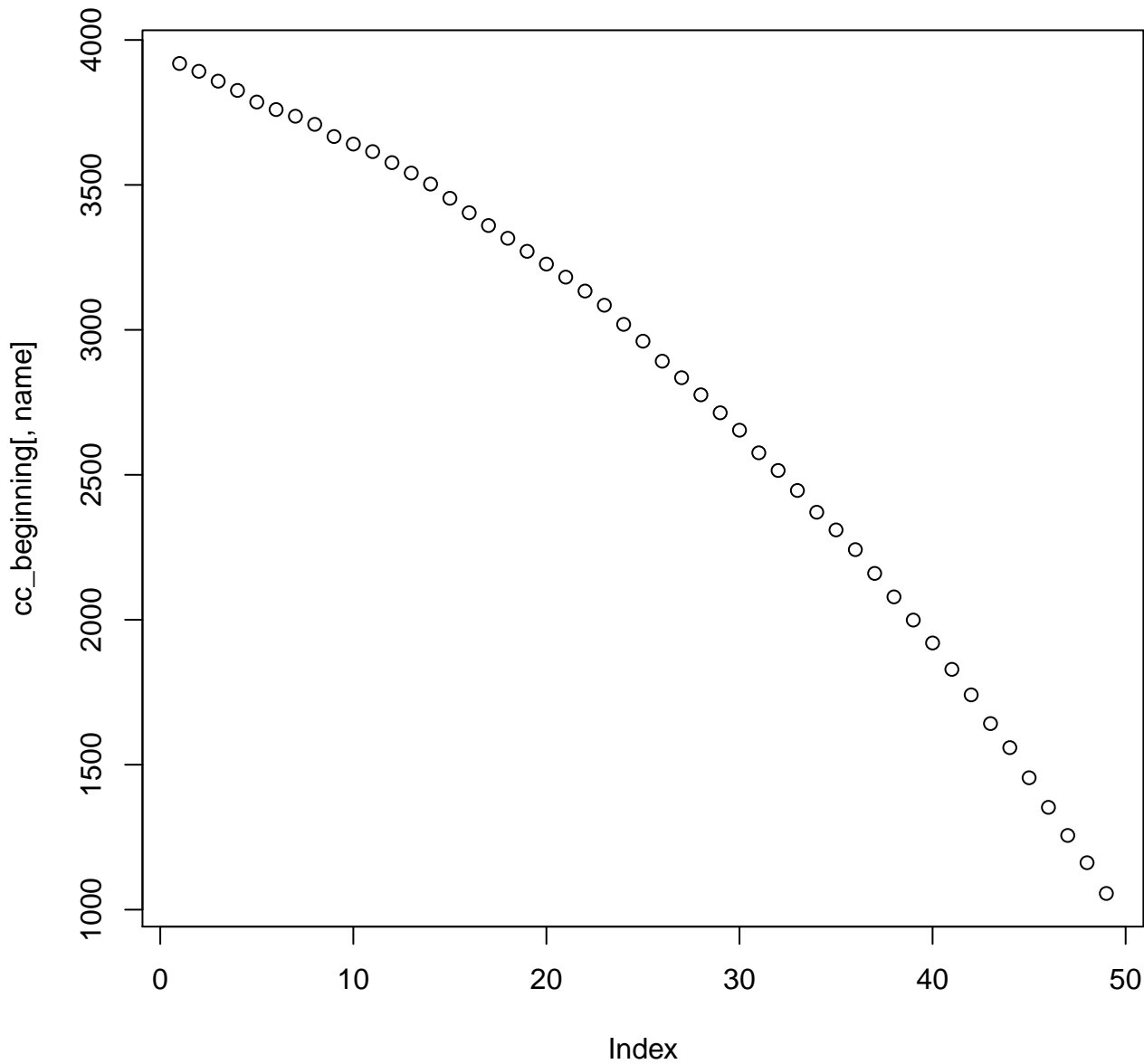
//gridsearch-collectContigs/rsem\_oracleset-summary.ws0/summary

# ssembly\_cmd

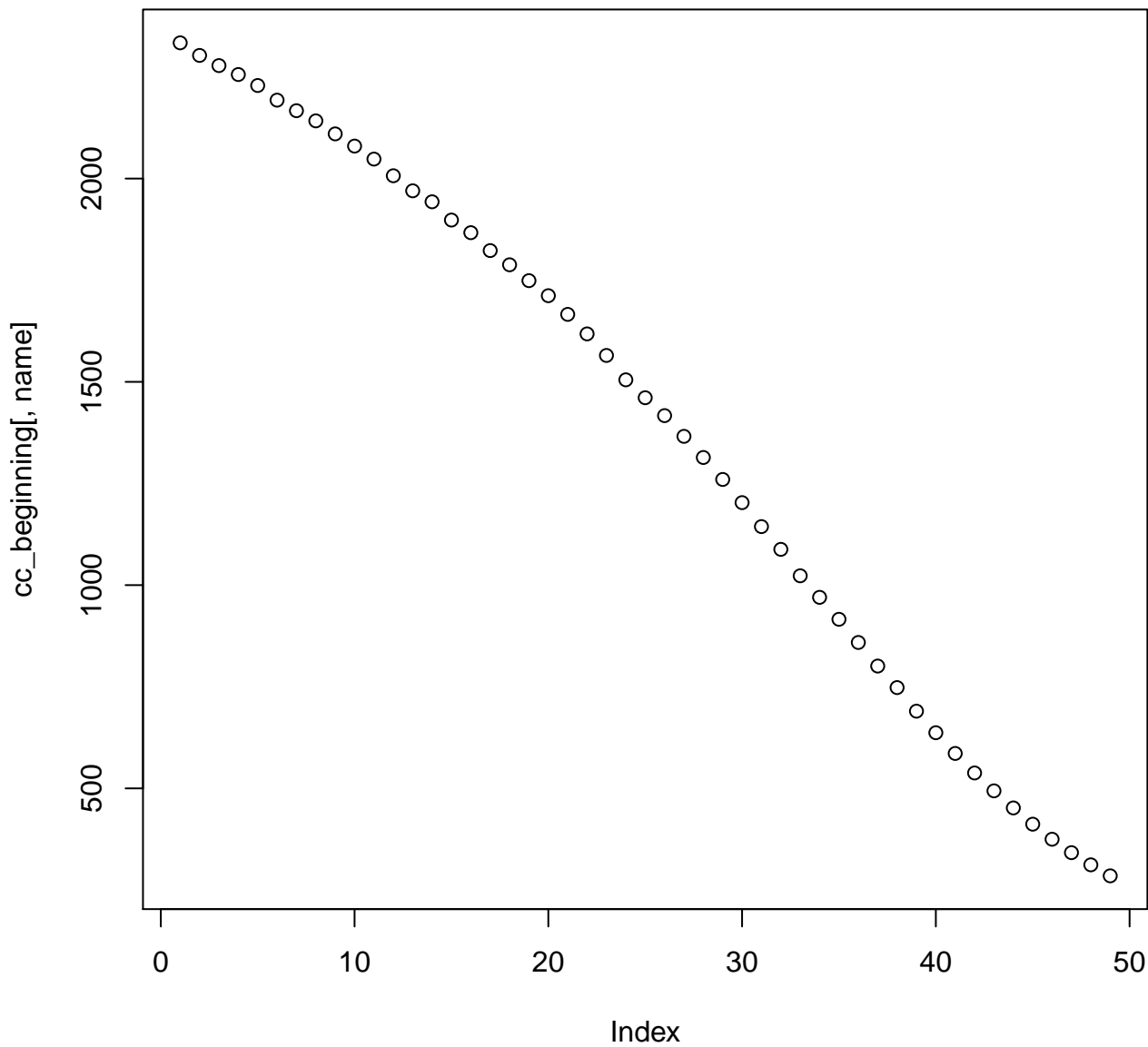


gle-full/SRR203276\_1.fastq --paired-fragment-length=1000 --min-contig-length=0 --output

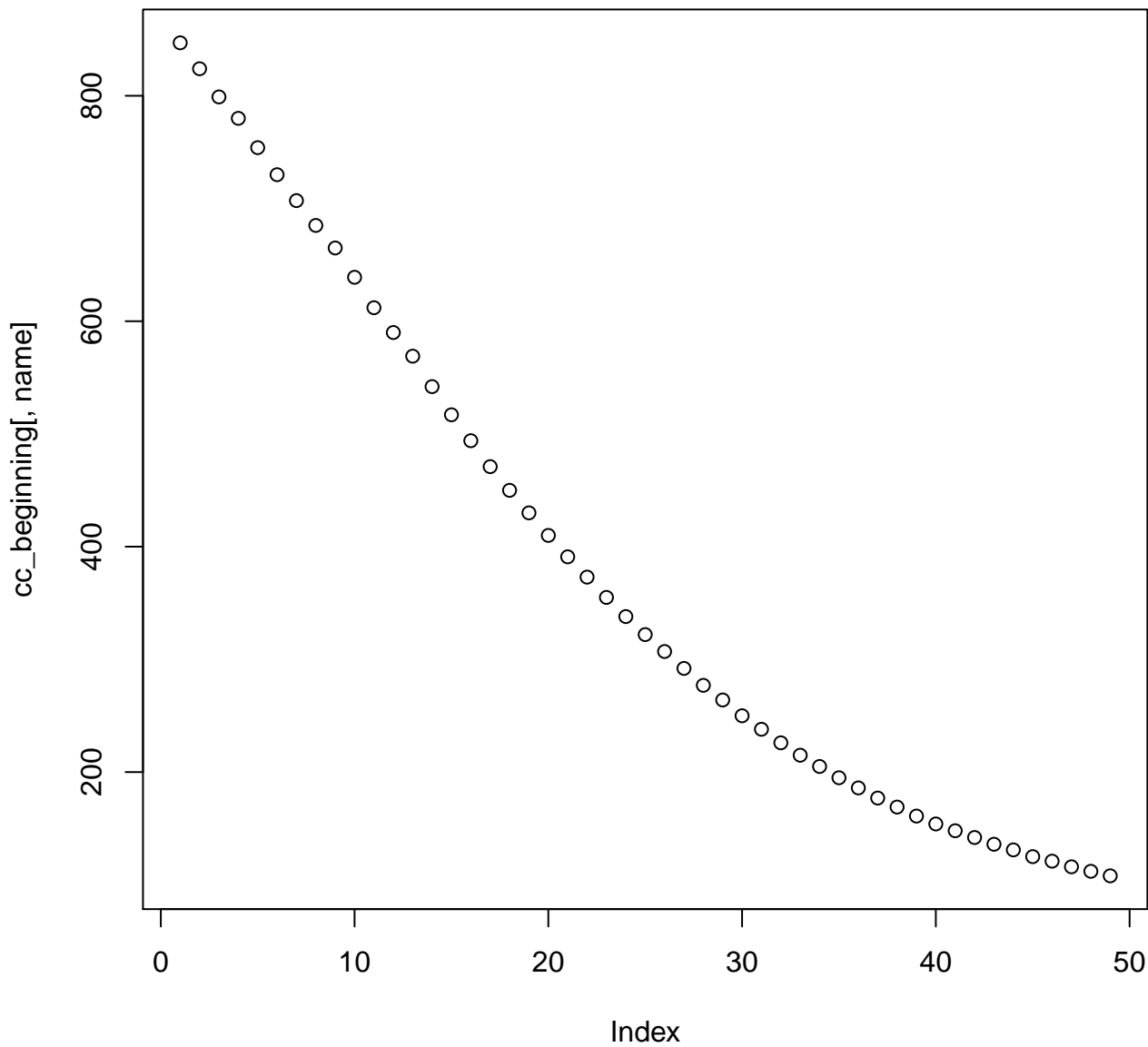
# assembly.N25



# assembly.N50

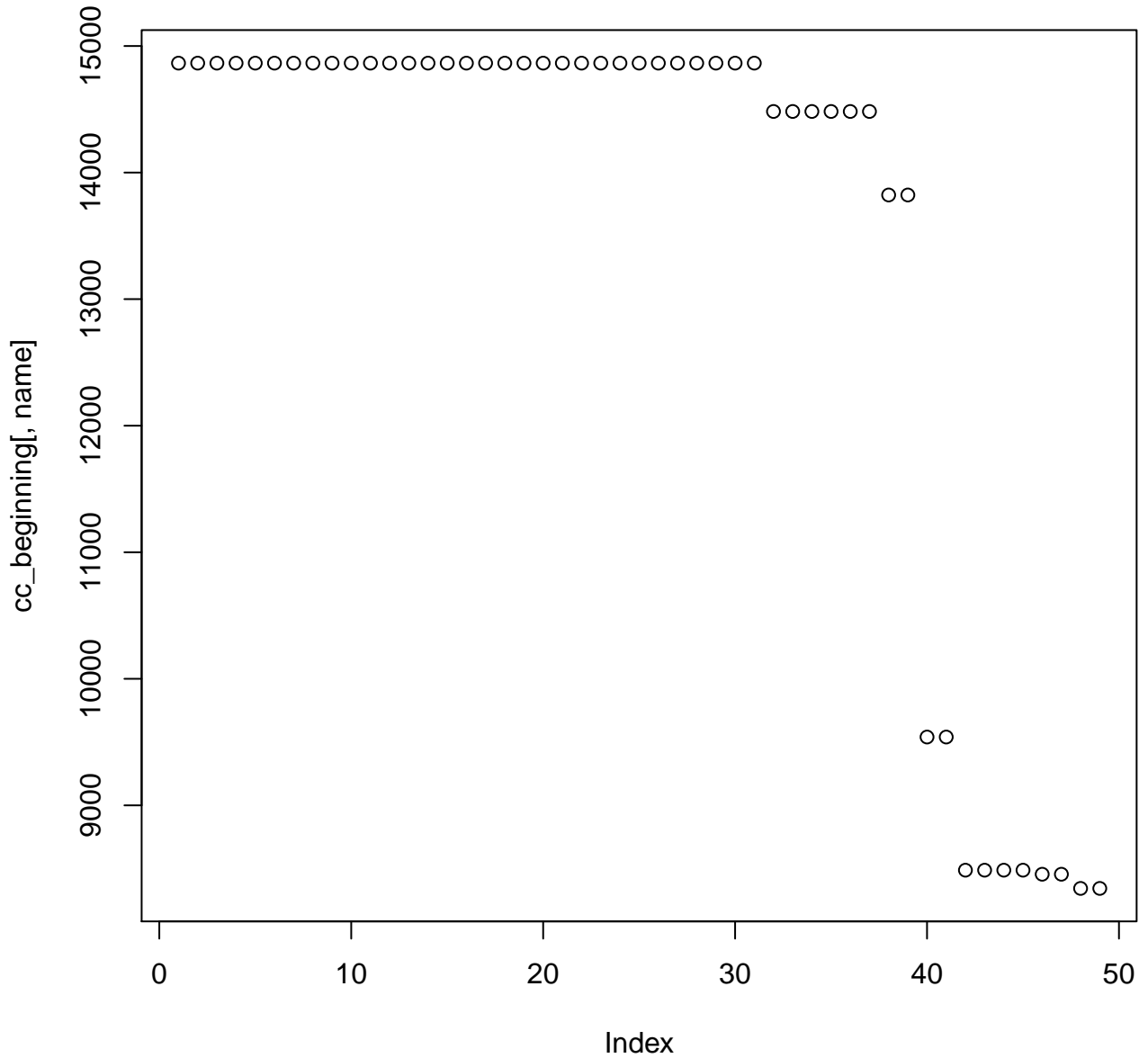


# assembly.N75

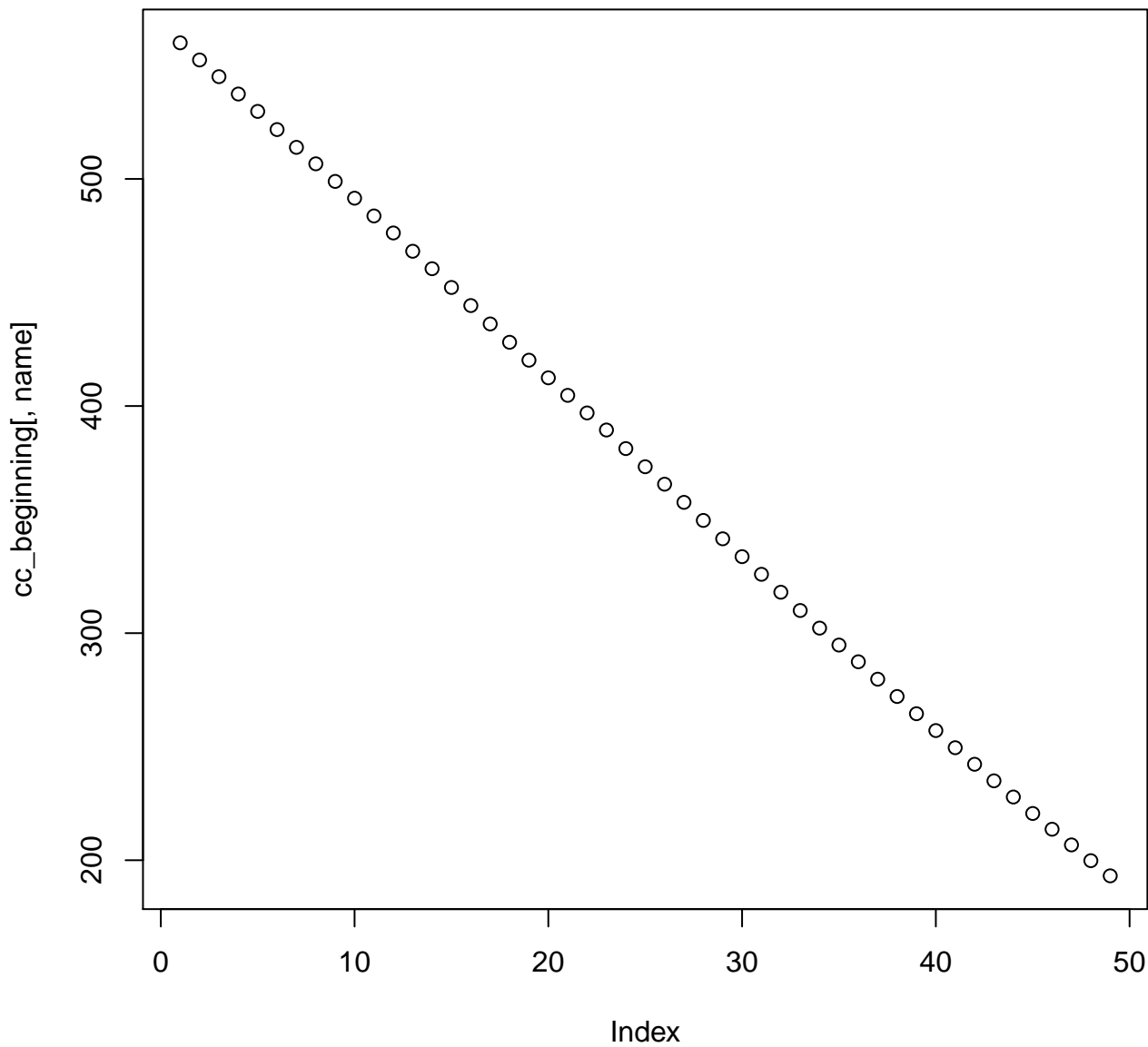




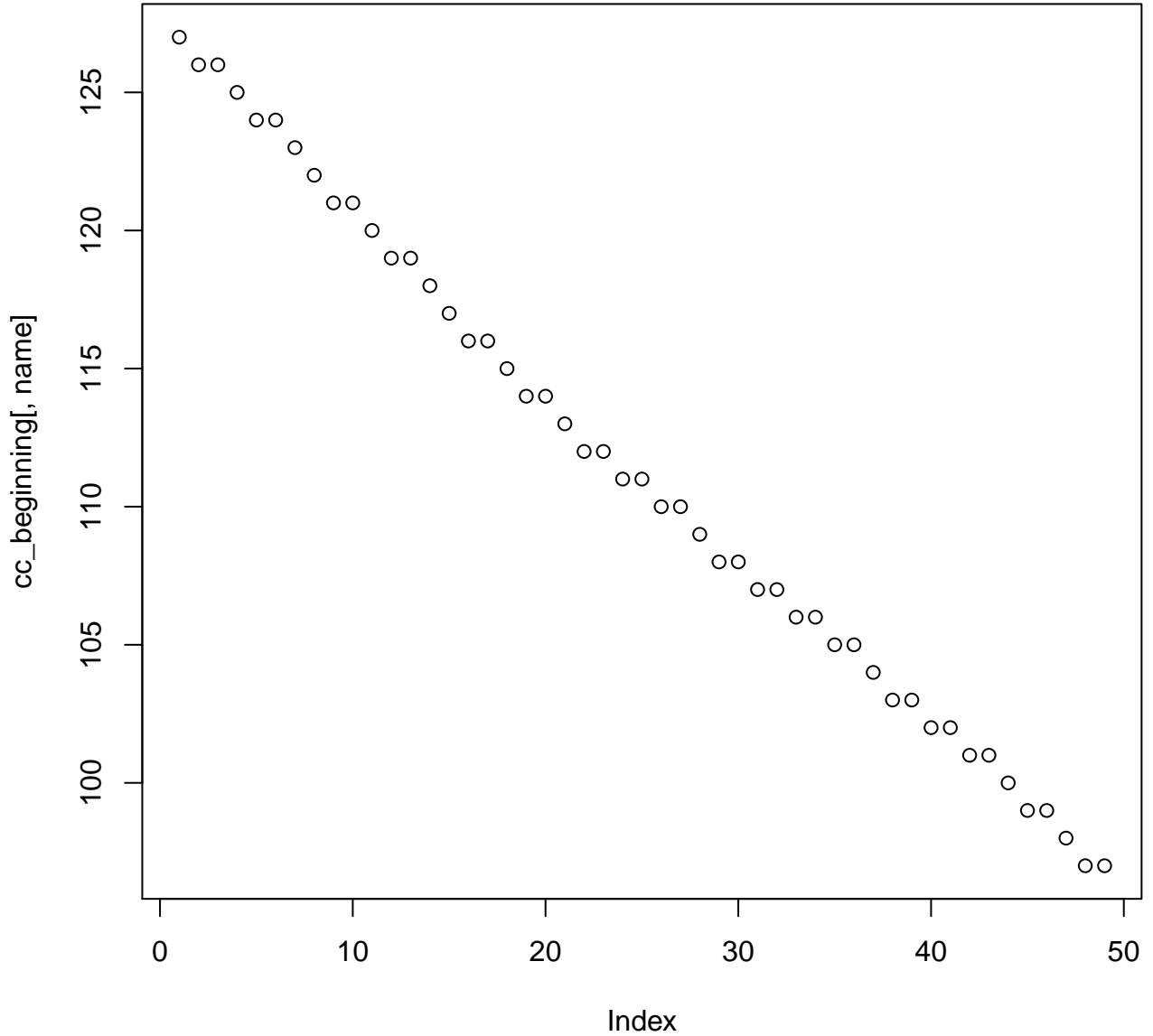
# assembly.longest



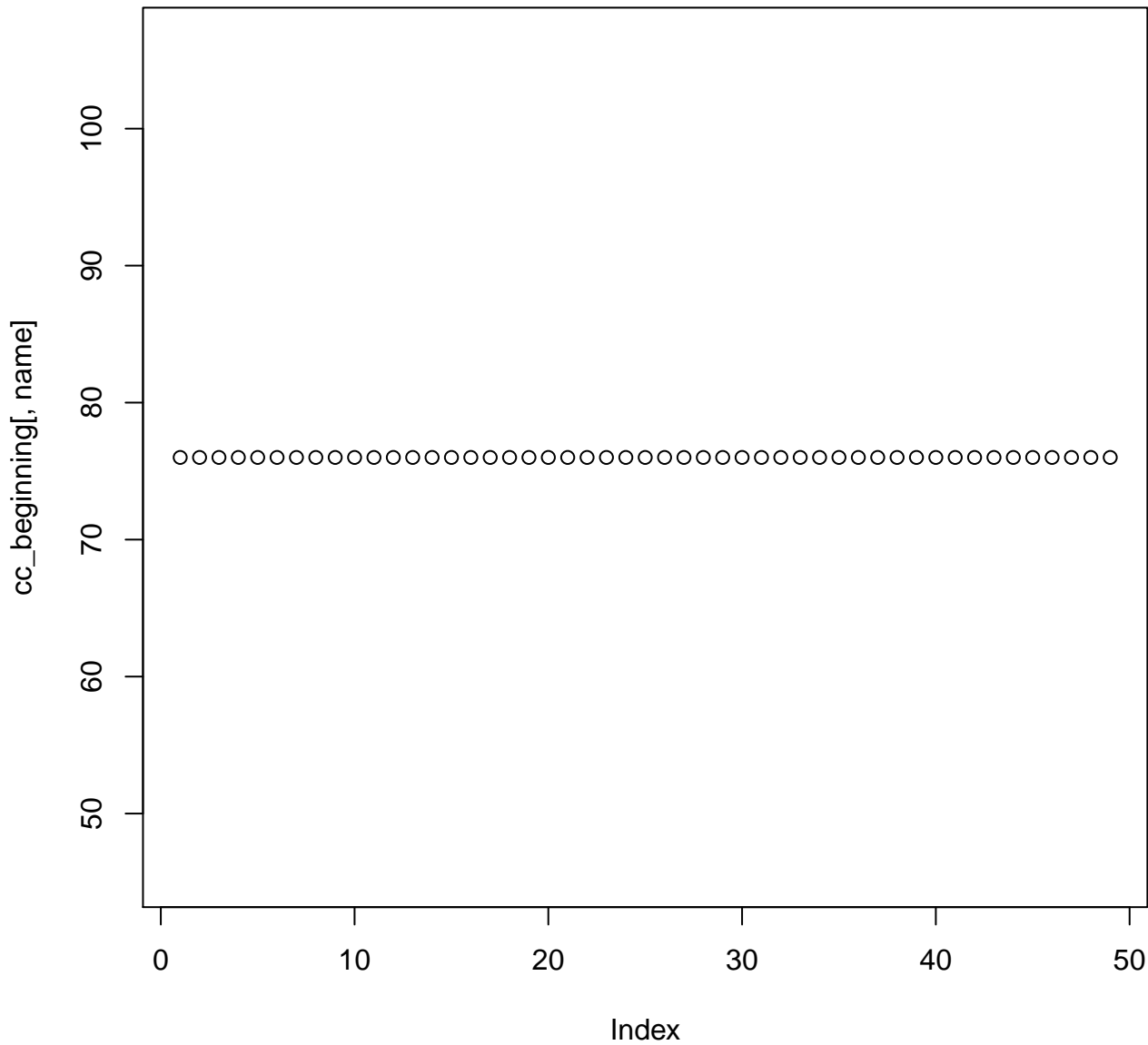
# assembly.mean



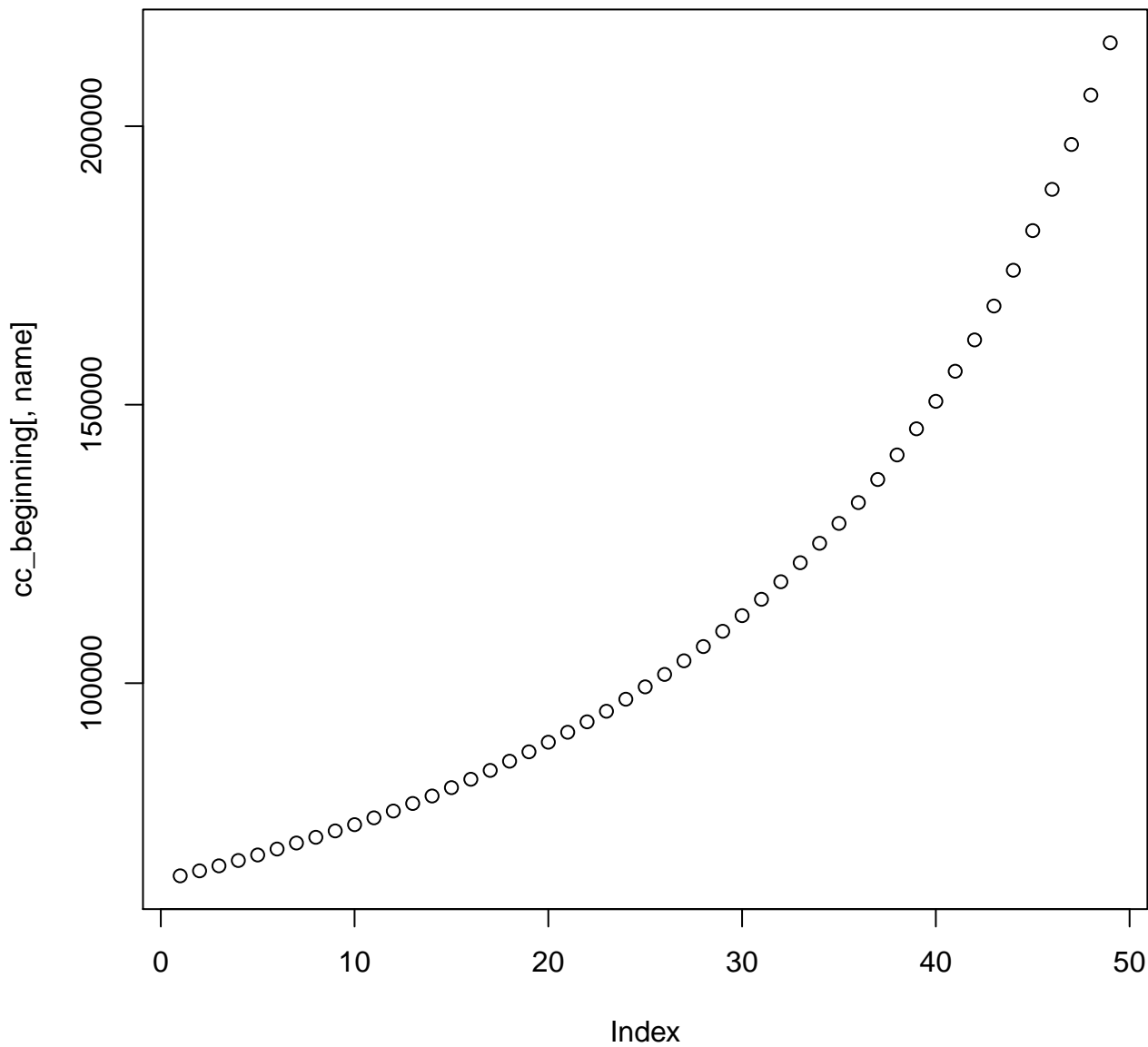
# assembly.median



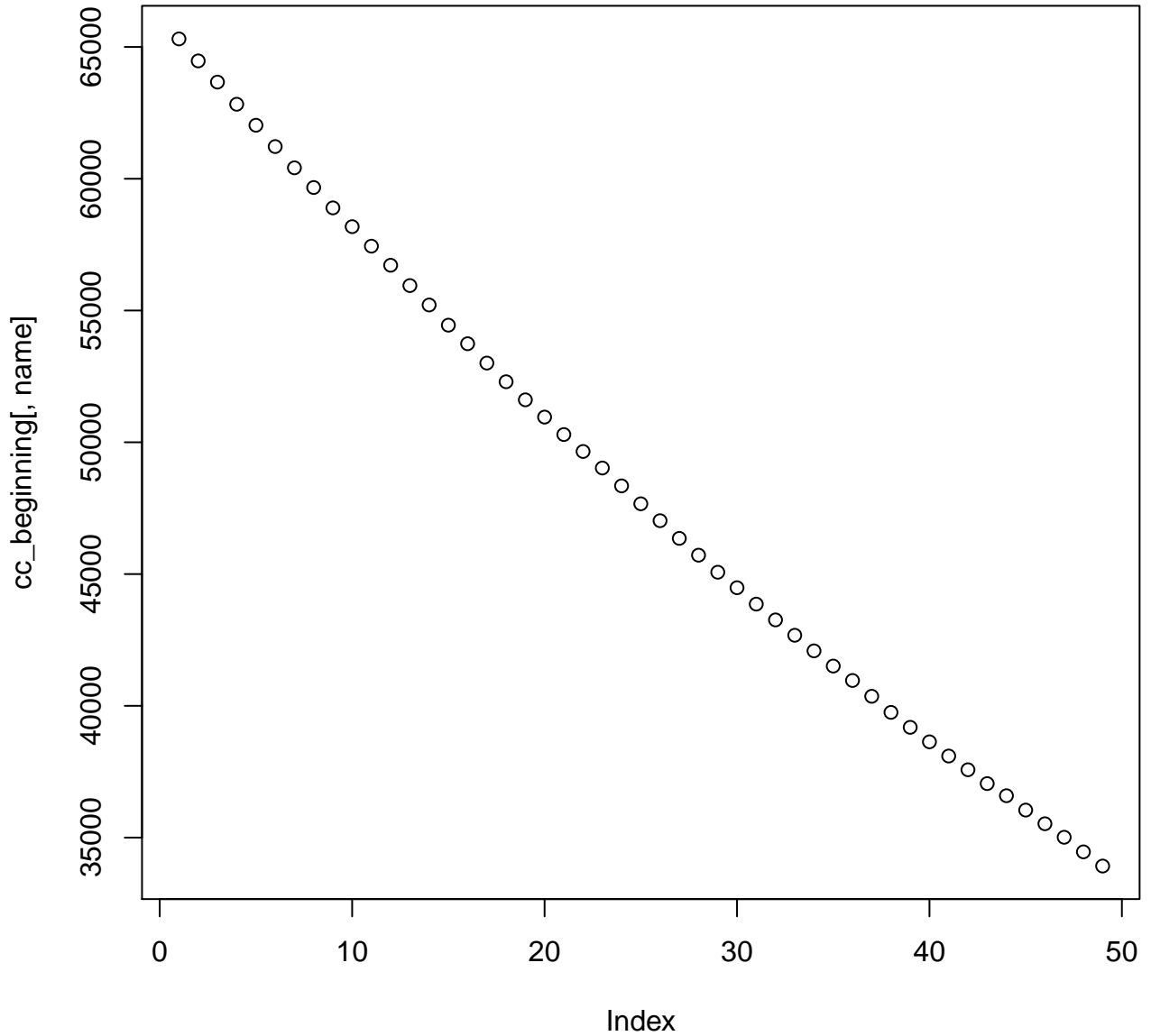
# assembly.shortest



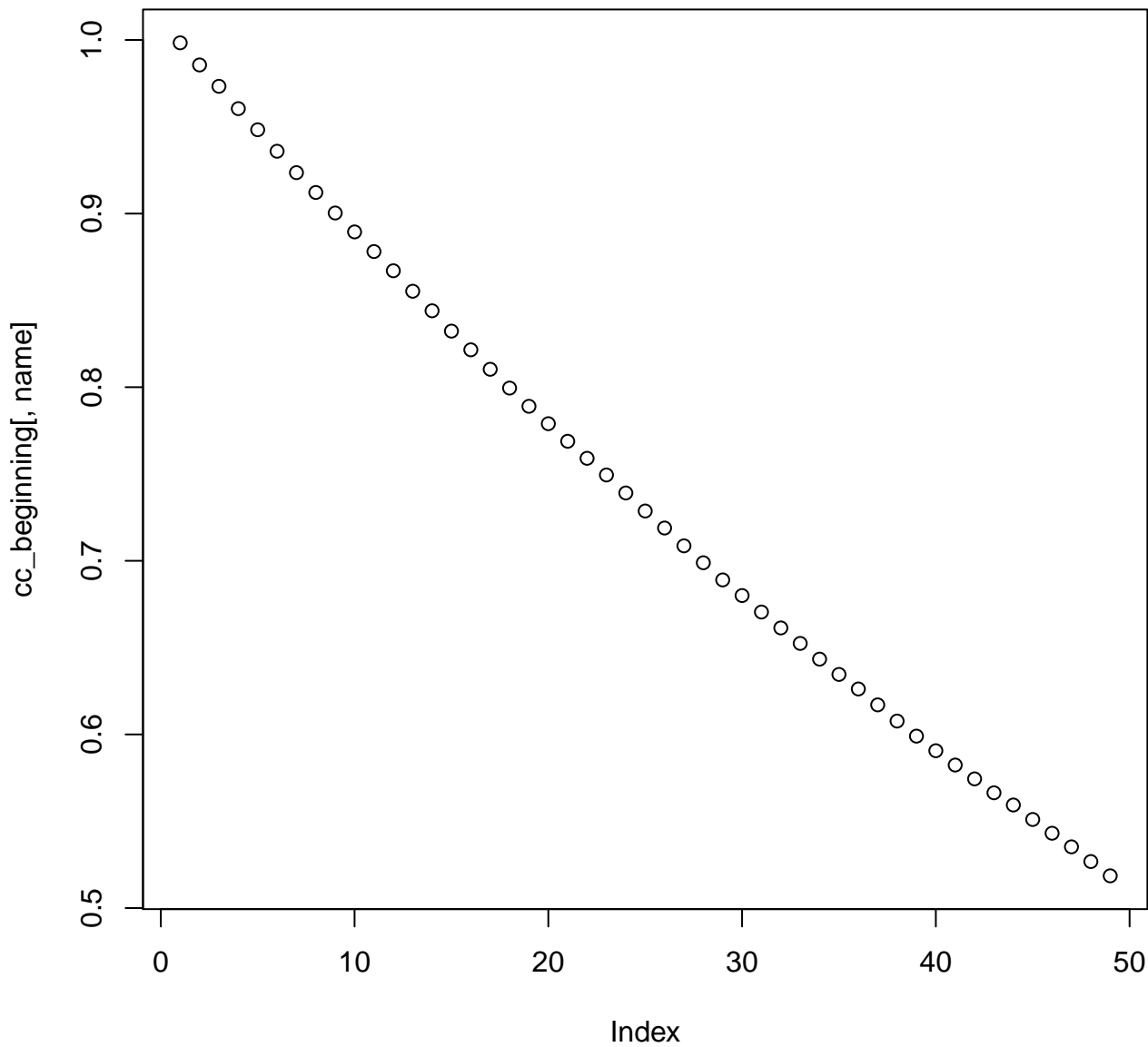
# assembly.num.contigs



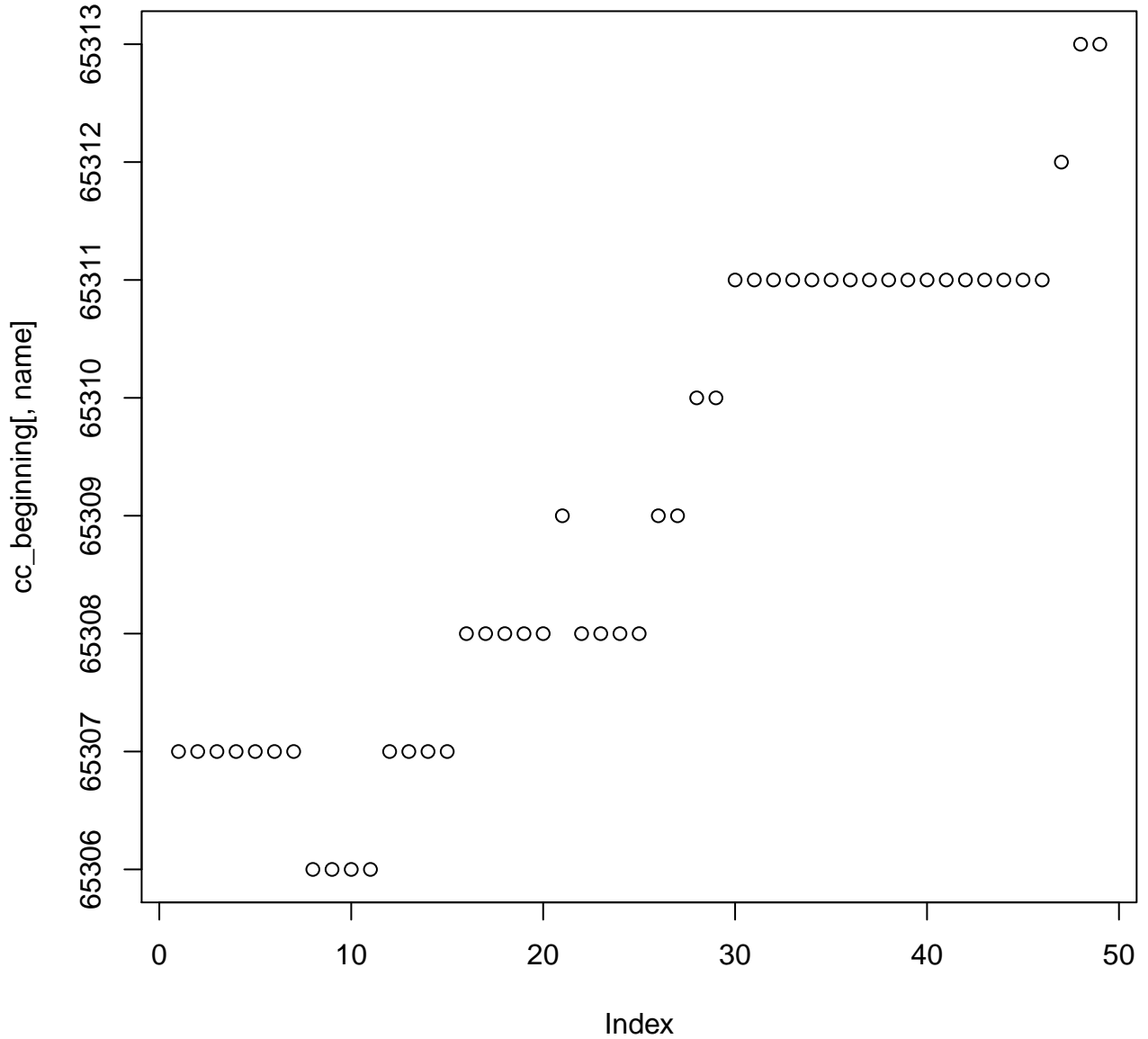
# num.oracleset.in.assembly



# frac.oracle.set.in.assembly

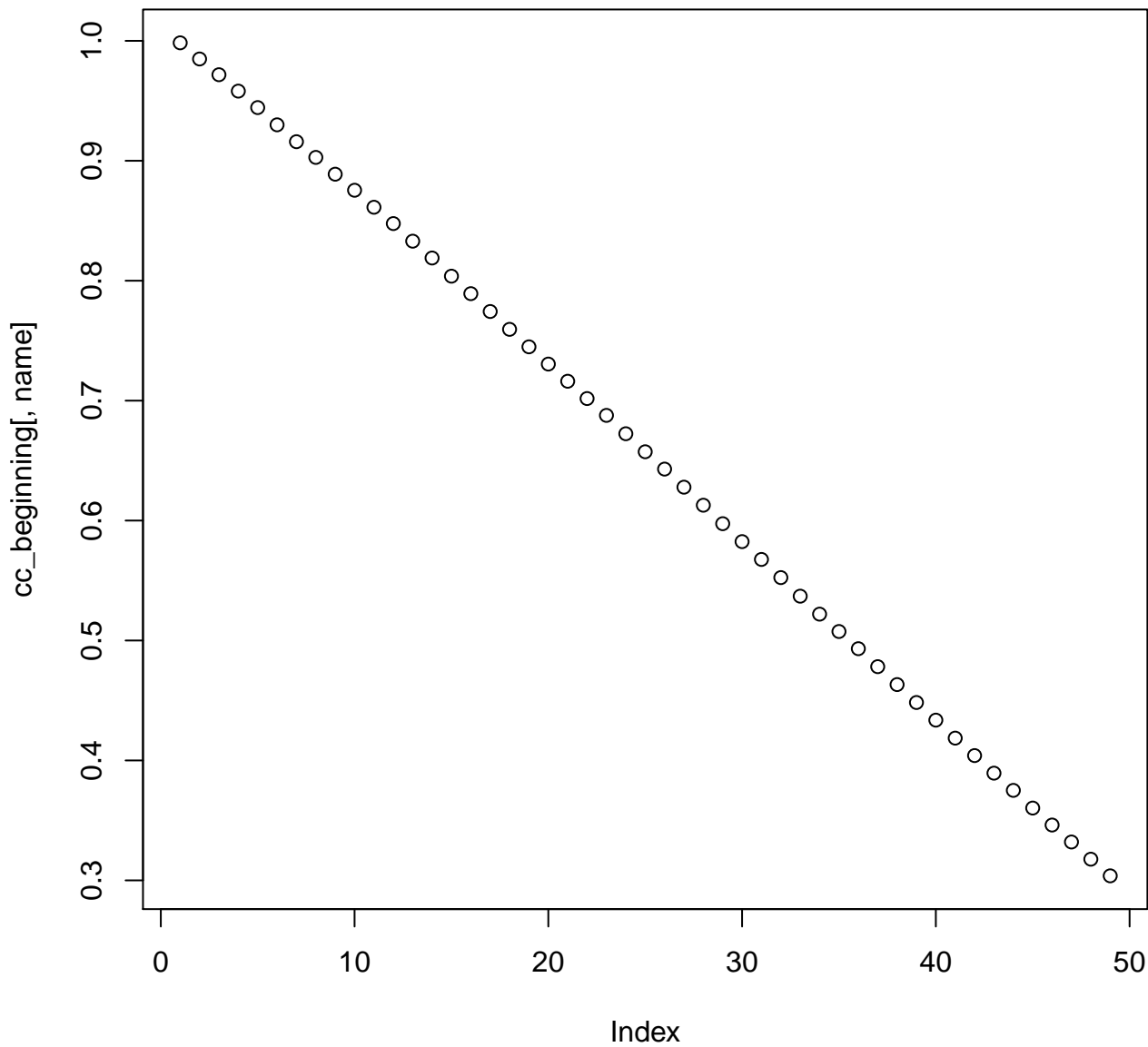


# num.assembly.in.oracleset

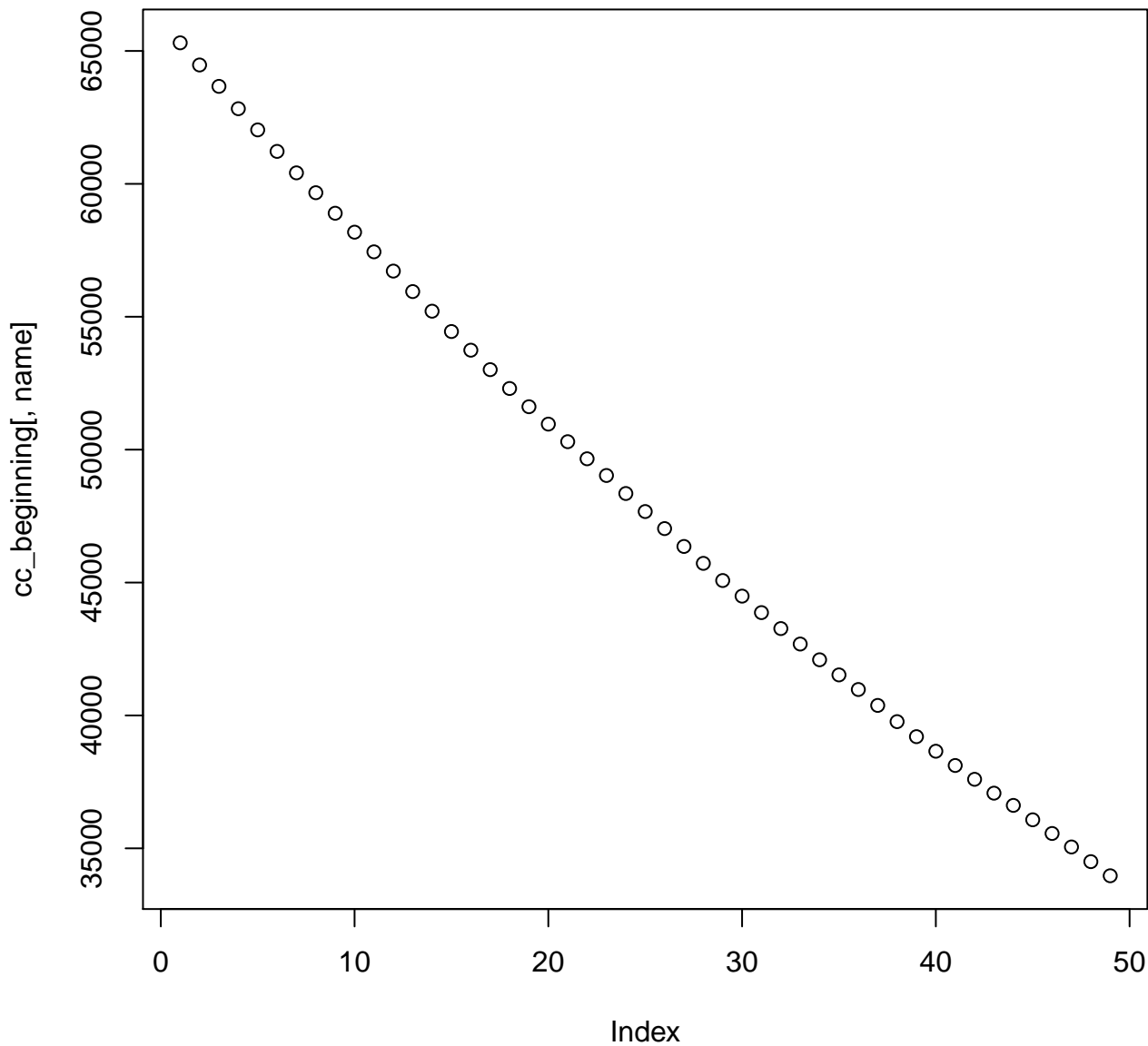




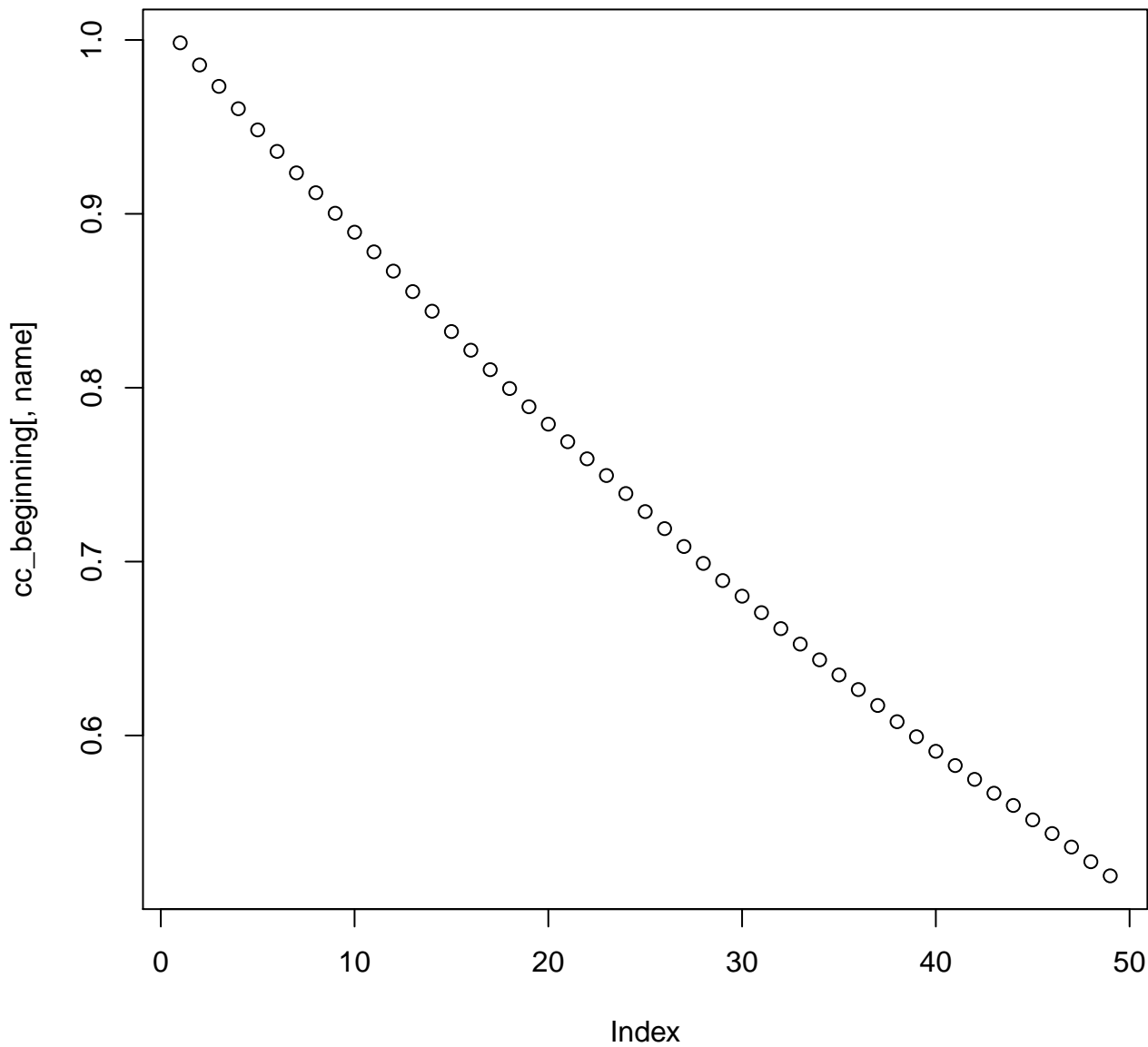
# frac.assembly.in.oracleset



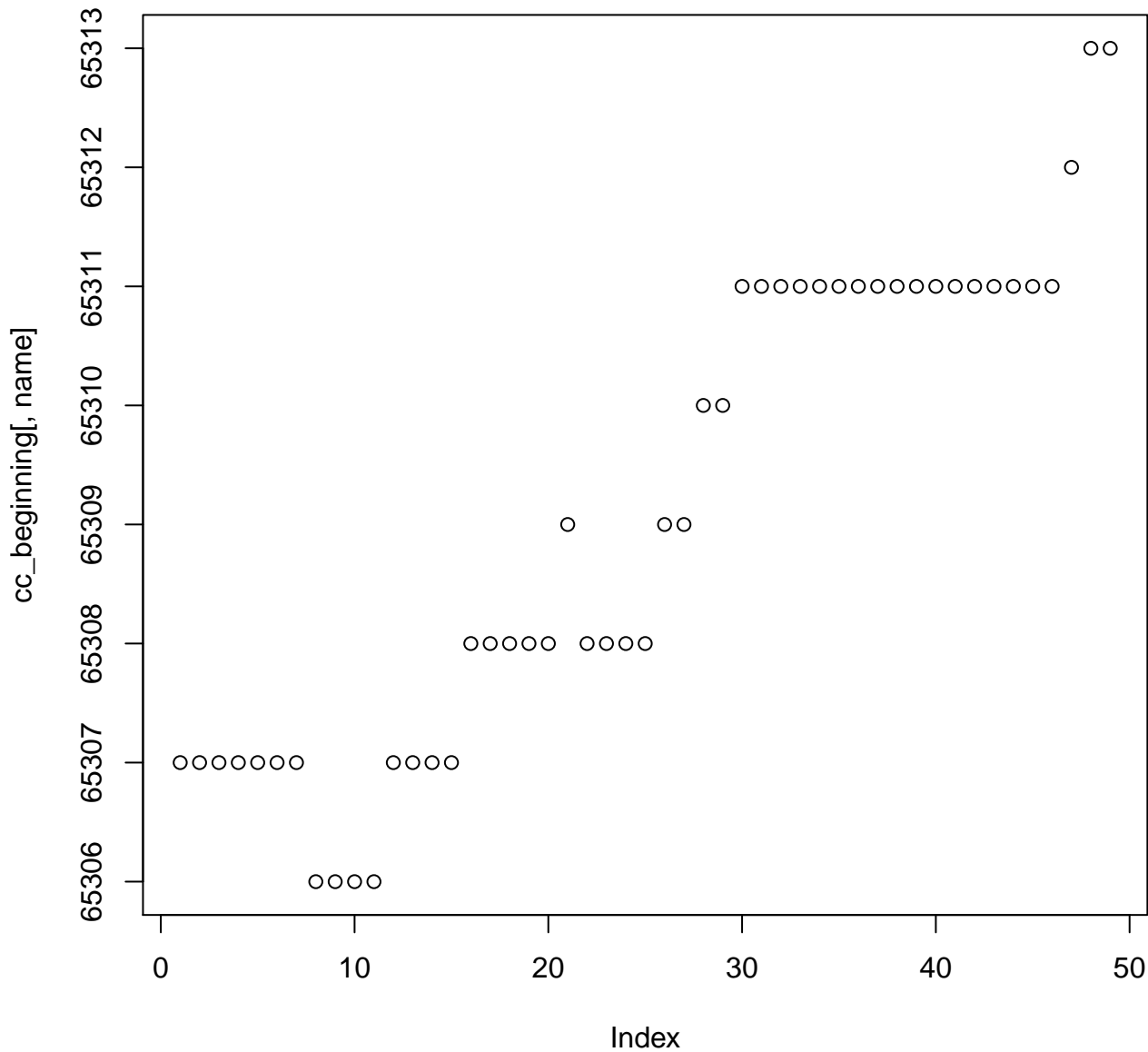
# num.oracleset.in.assembly.without.check.insdel



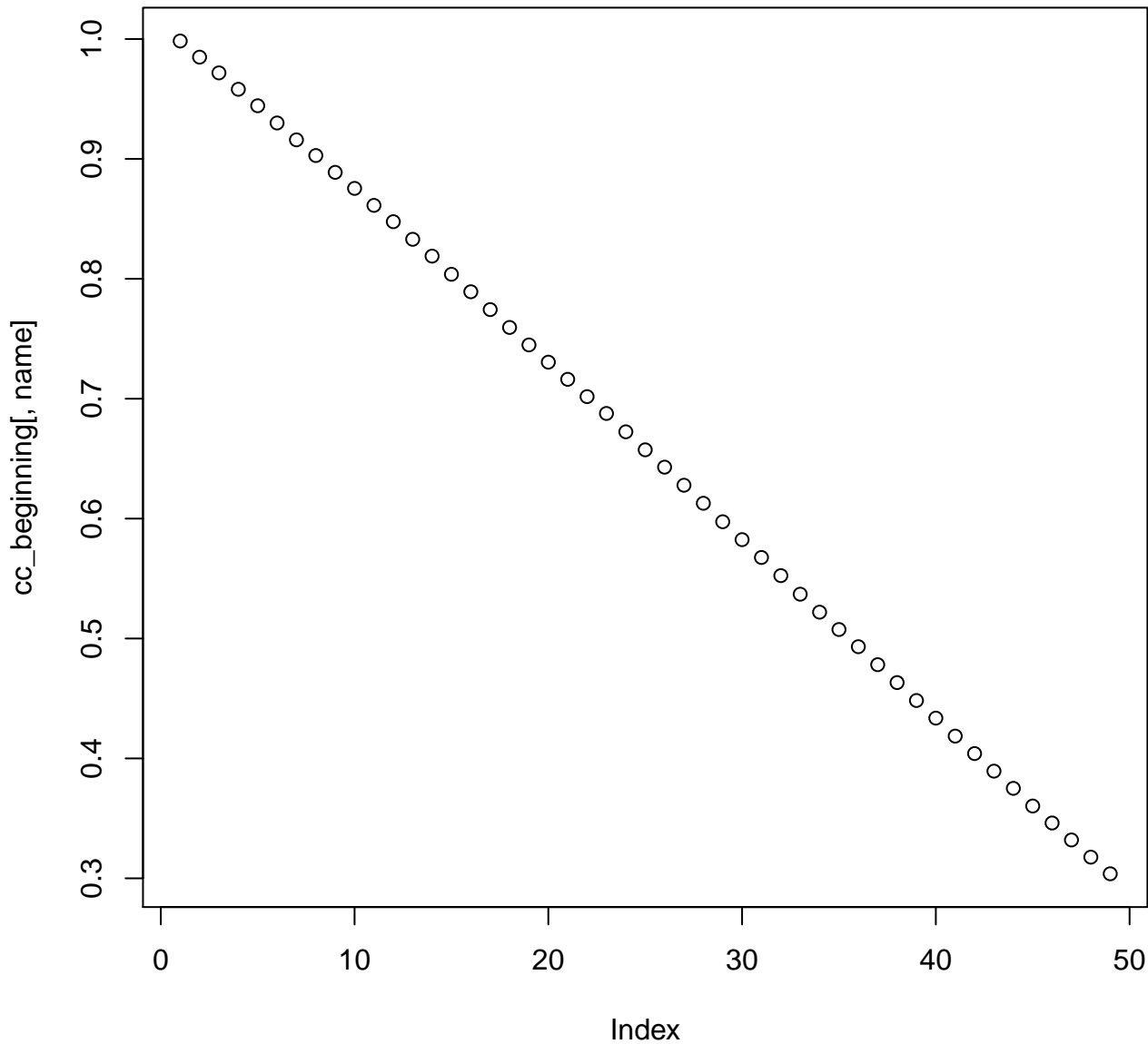
# frac.oracleset.in.assembly.without.check.insdel



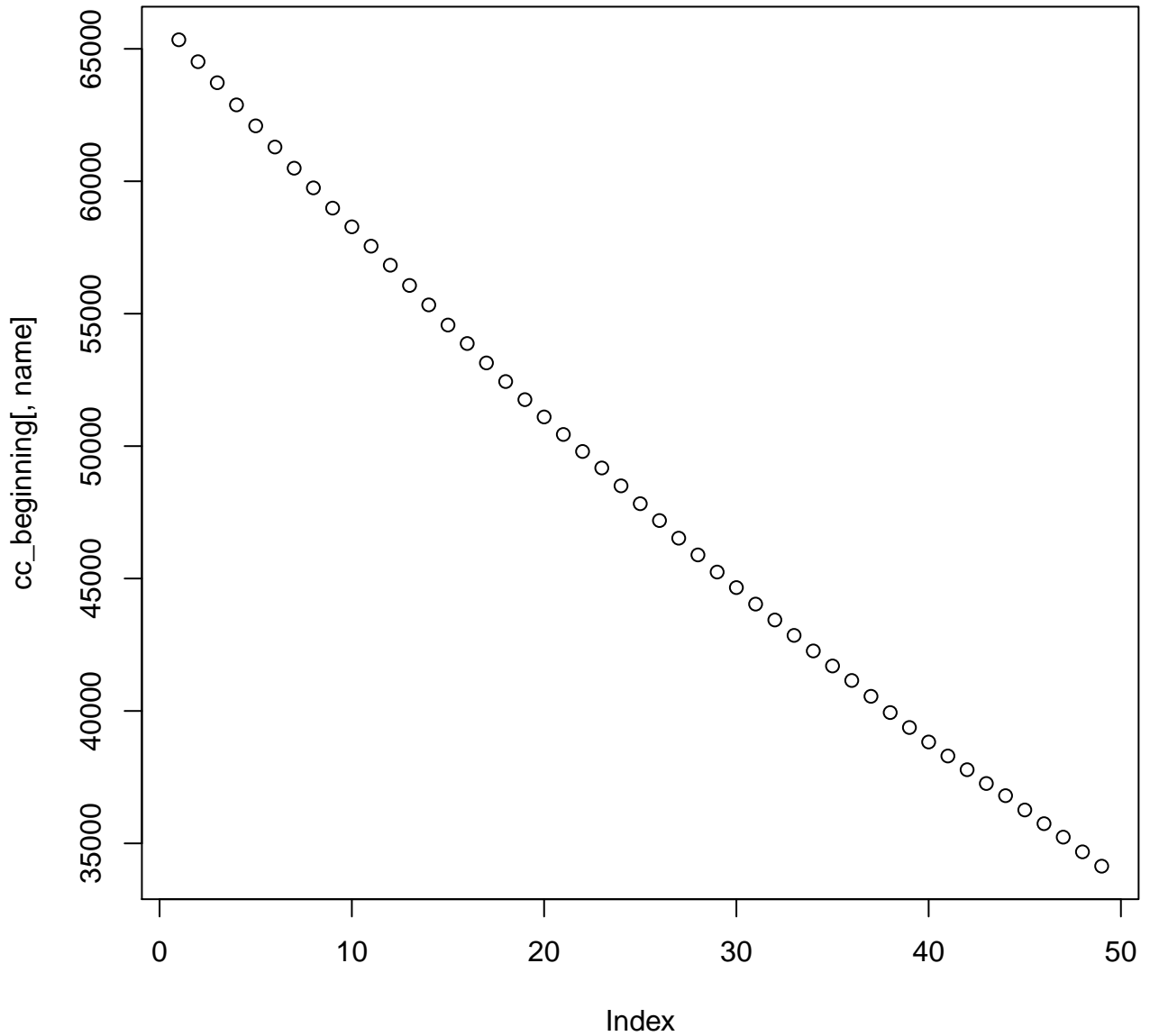
# num.assembly.in.oracle.set.without.check.insdel



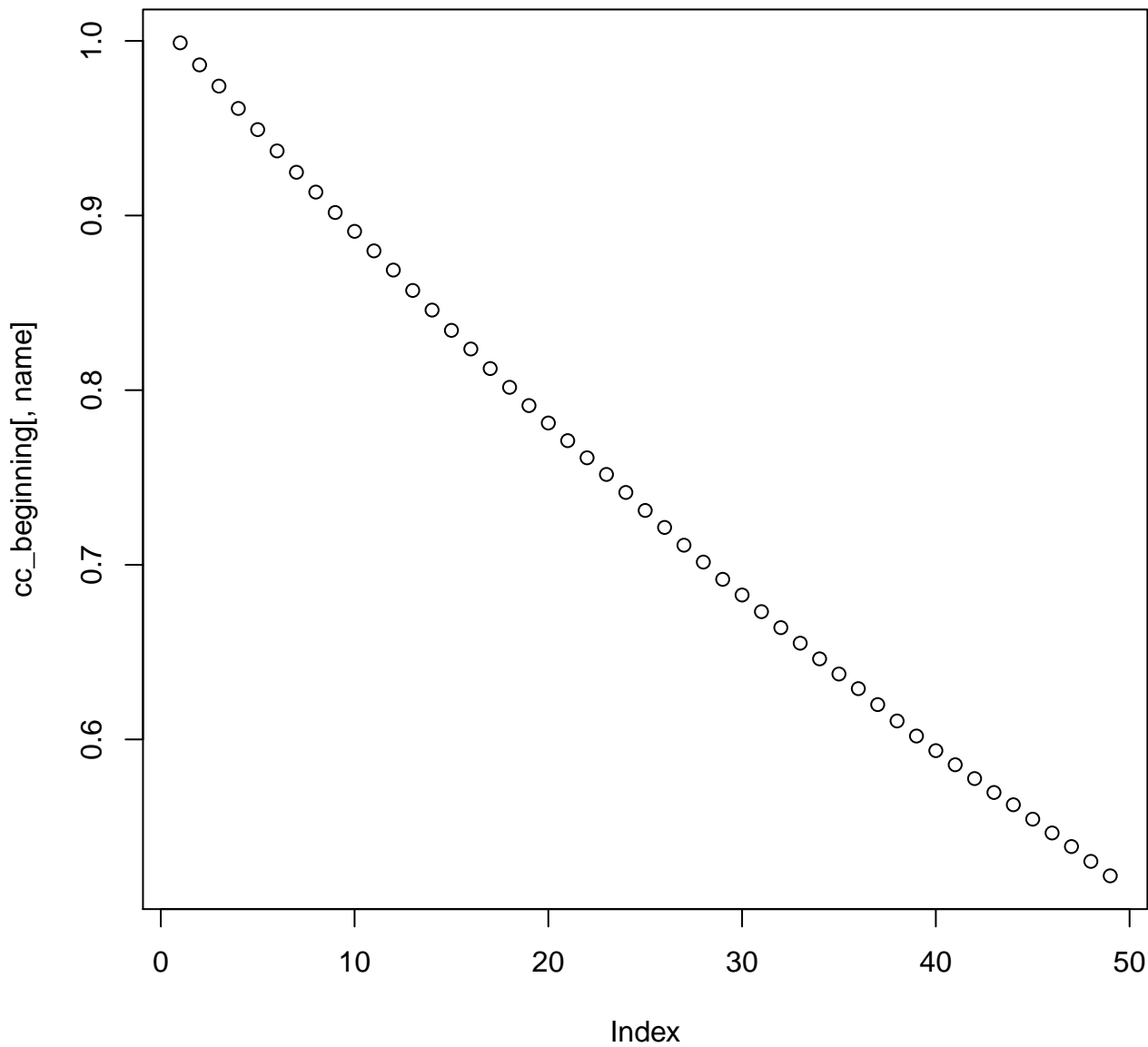
# frac.assembly.in.oracleset.without.check.insdel



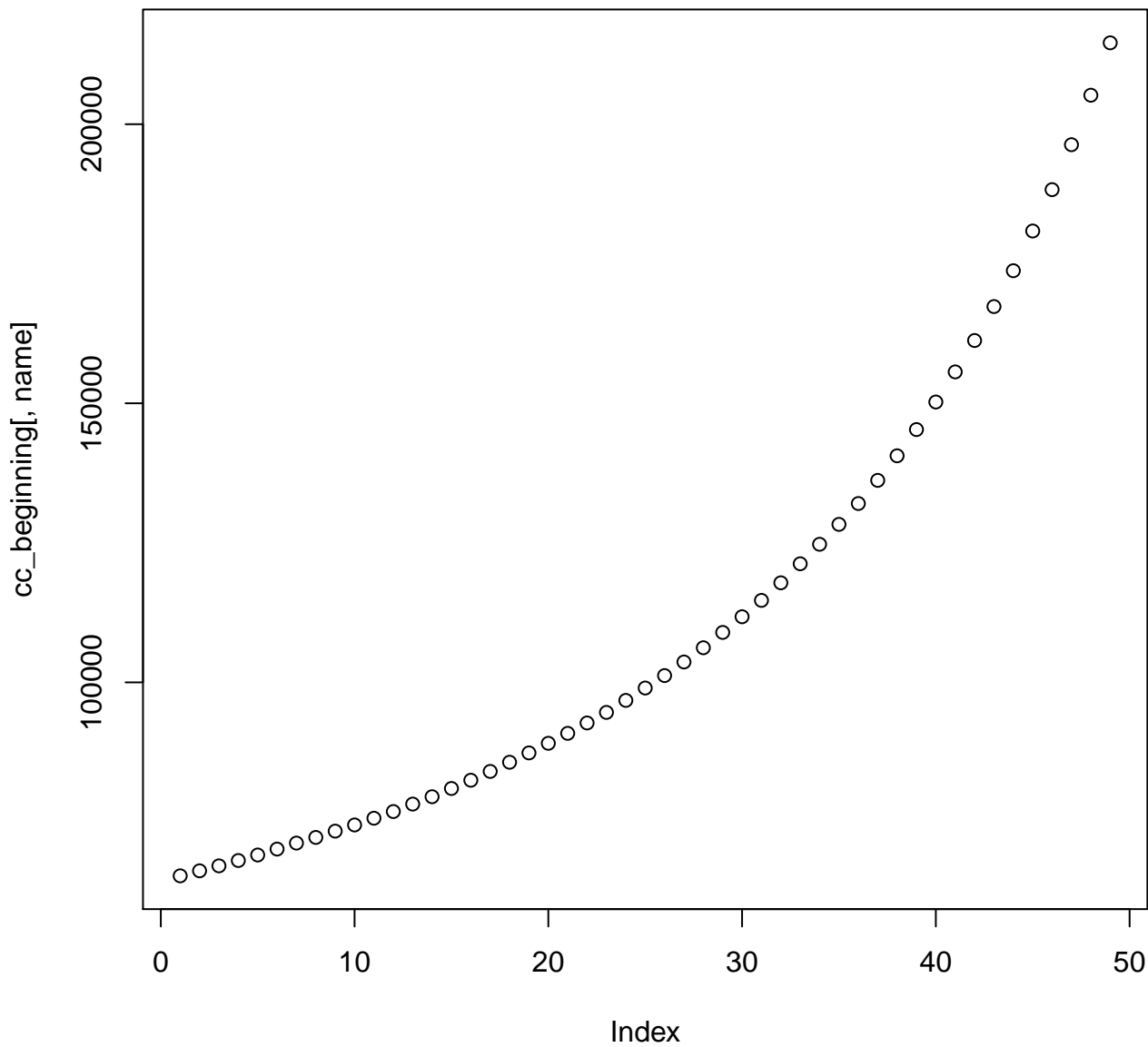
# allmatches.num.oracleset.in.assembly



# allmatches.frac.oracle.set.in.assembly

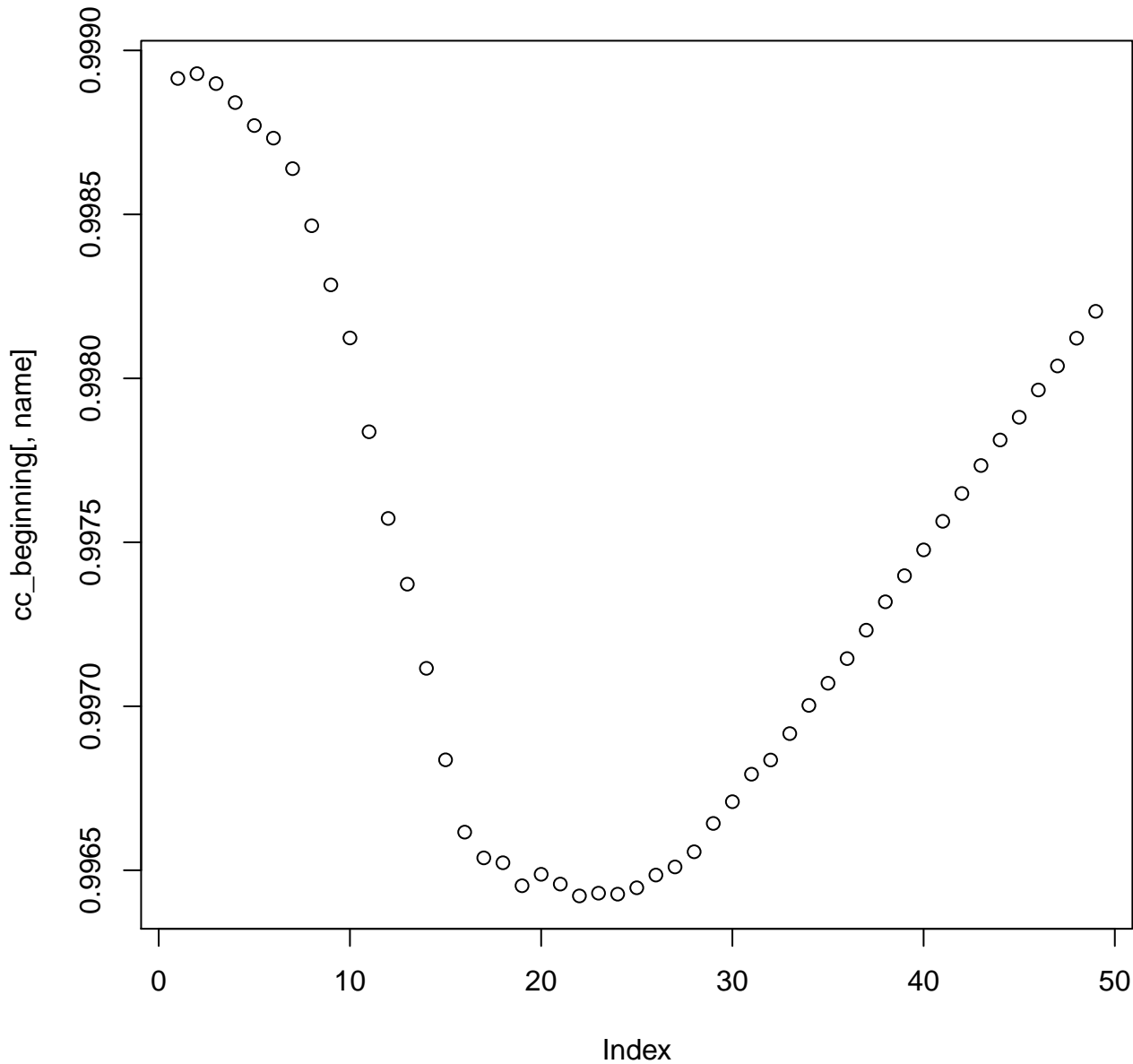


# allmatches.num.assembly.in.oracleset

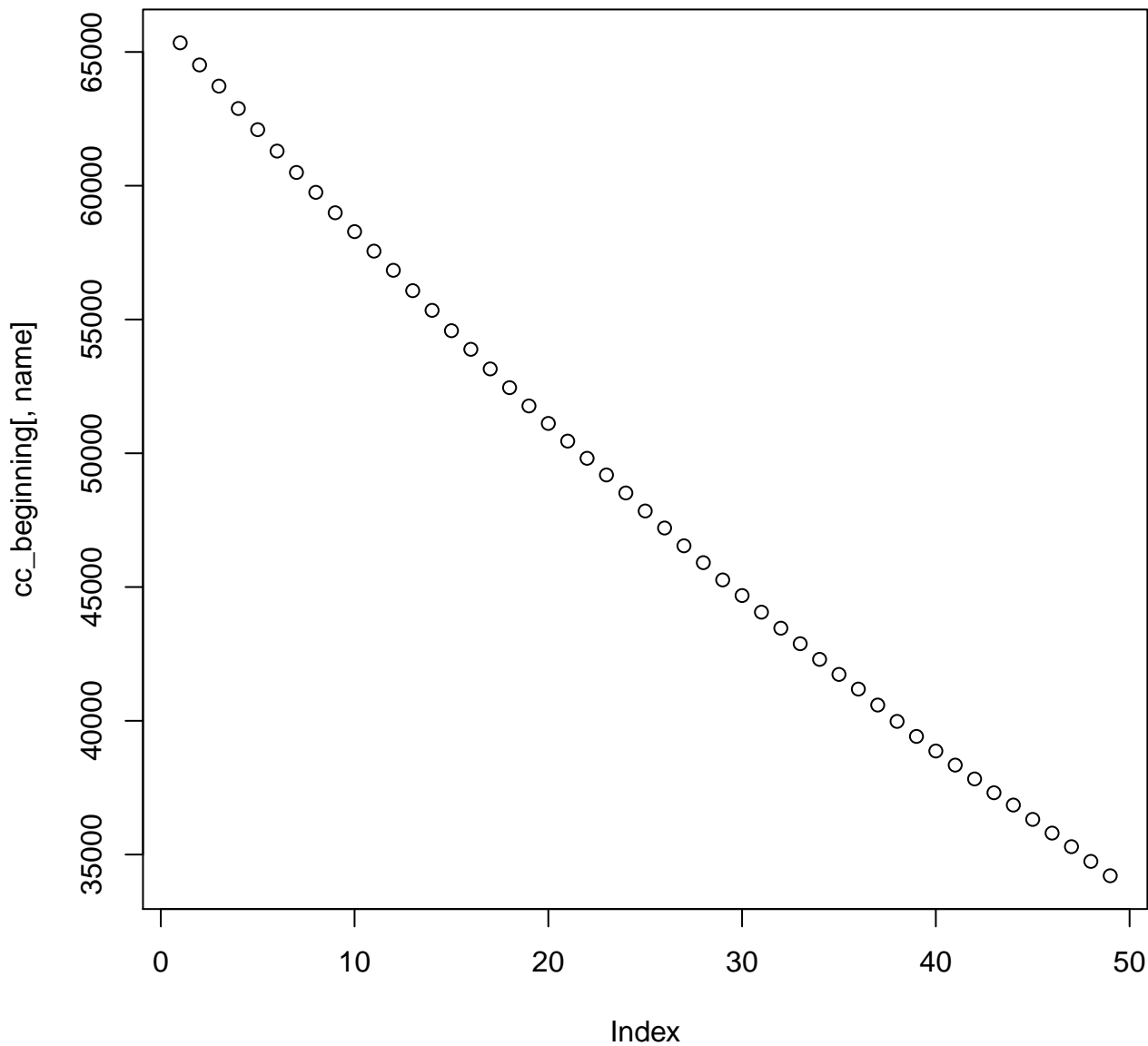




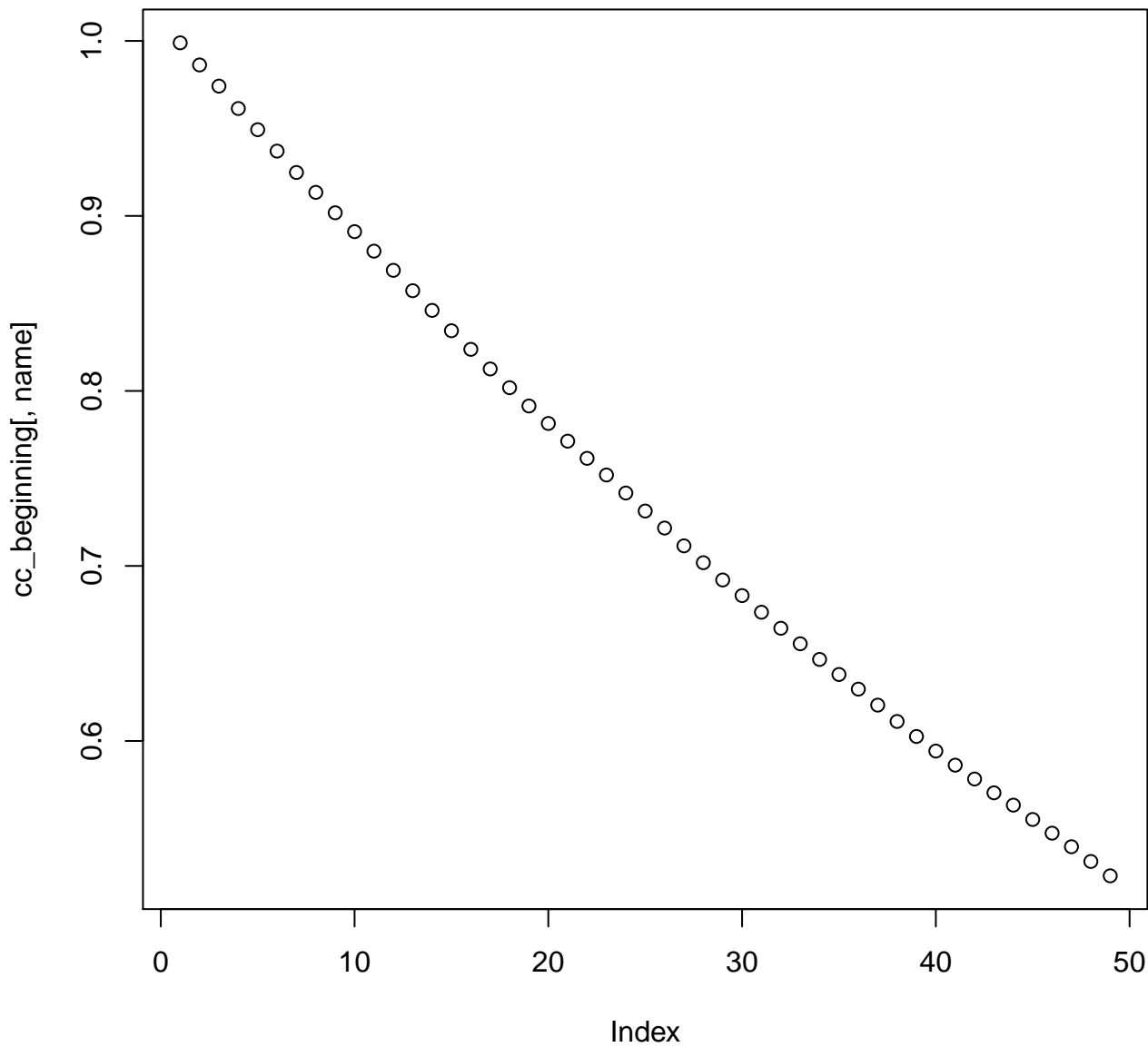
# allmatches.frac.assembly.in.oracleset



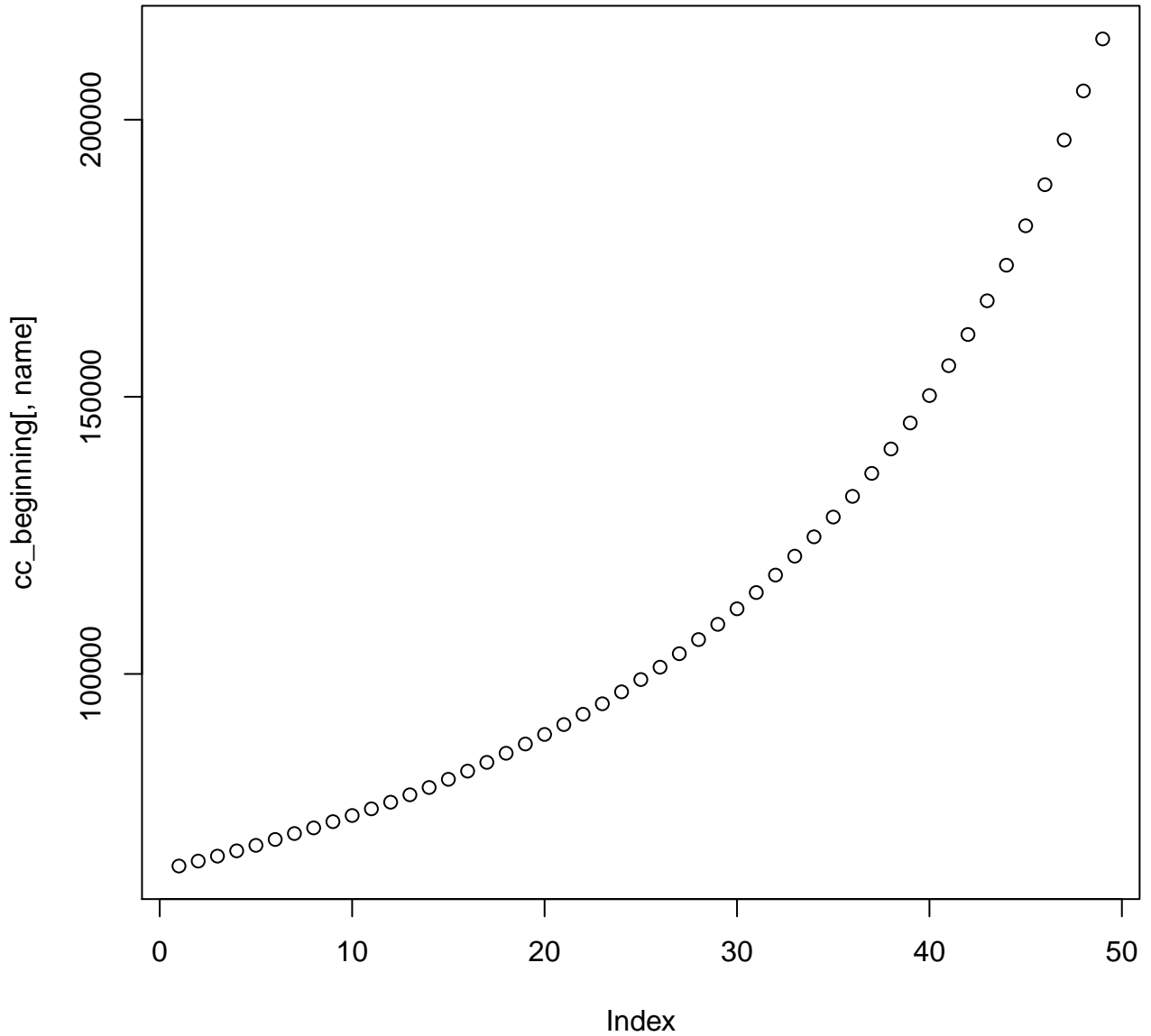
# allmatches.num.oracleset.in.assembly.without.check.insdel



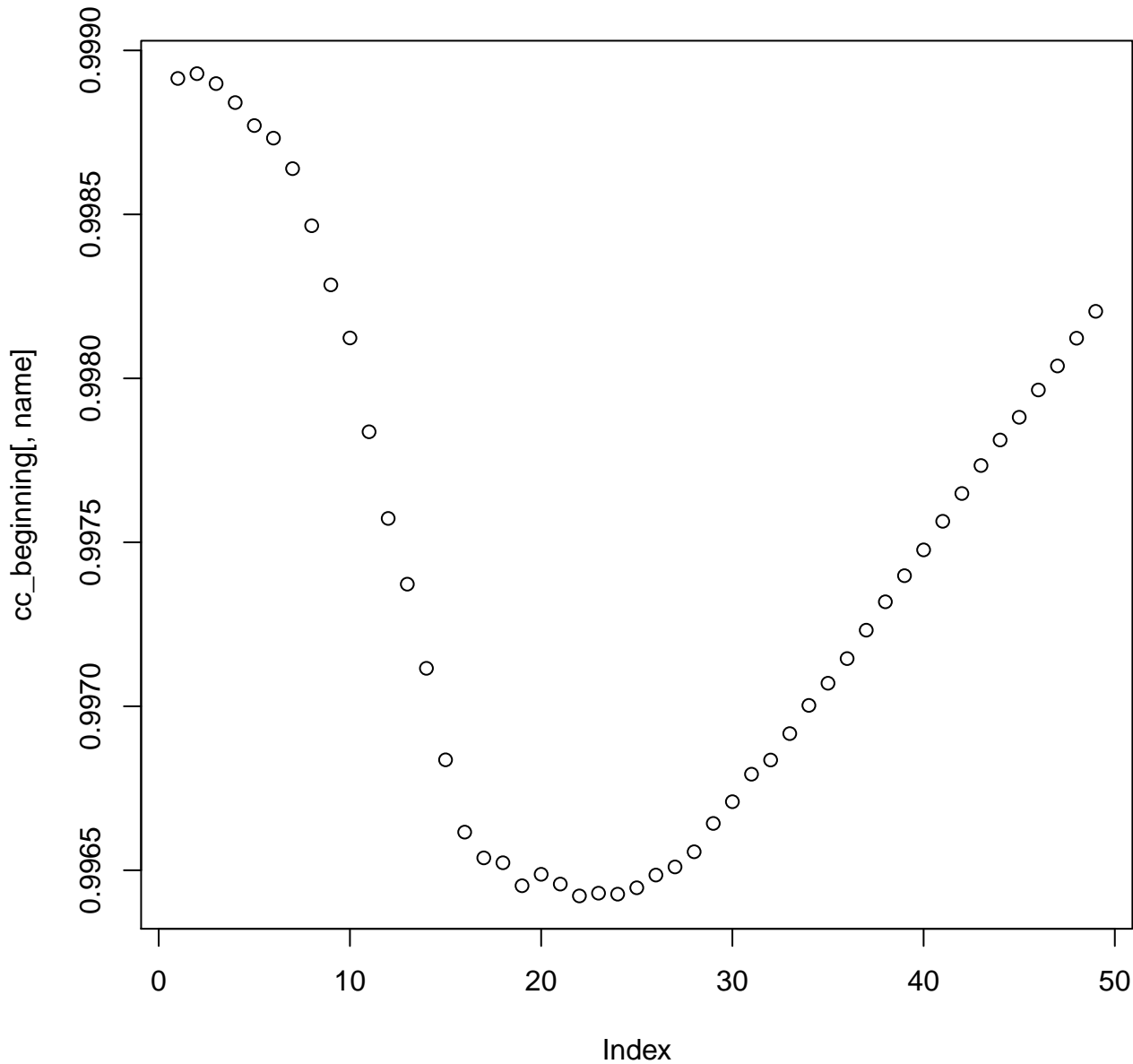
# allmatches.frac.oracleset.in.assembly.without.check.insdel



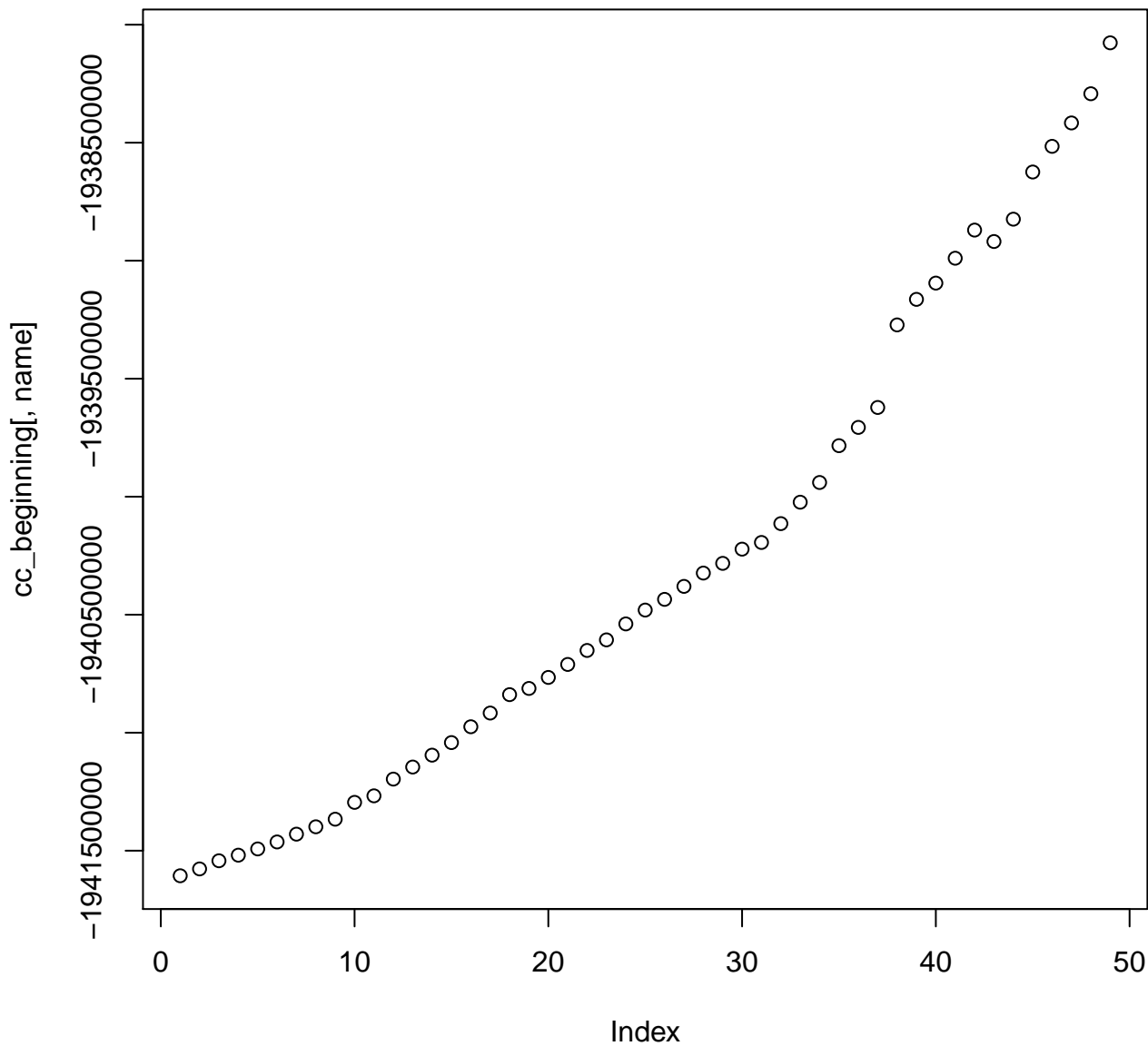
# allmatches.num.assembly.in.oracle.set.without.check.insdel



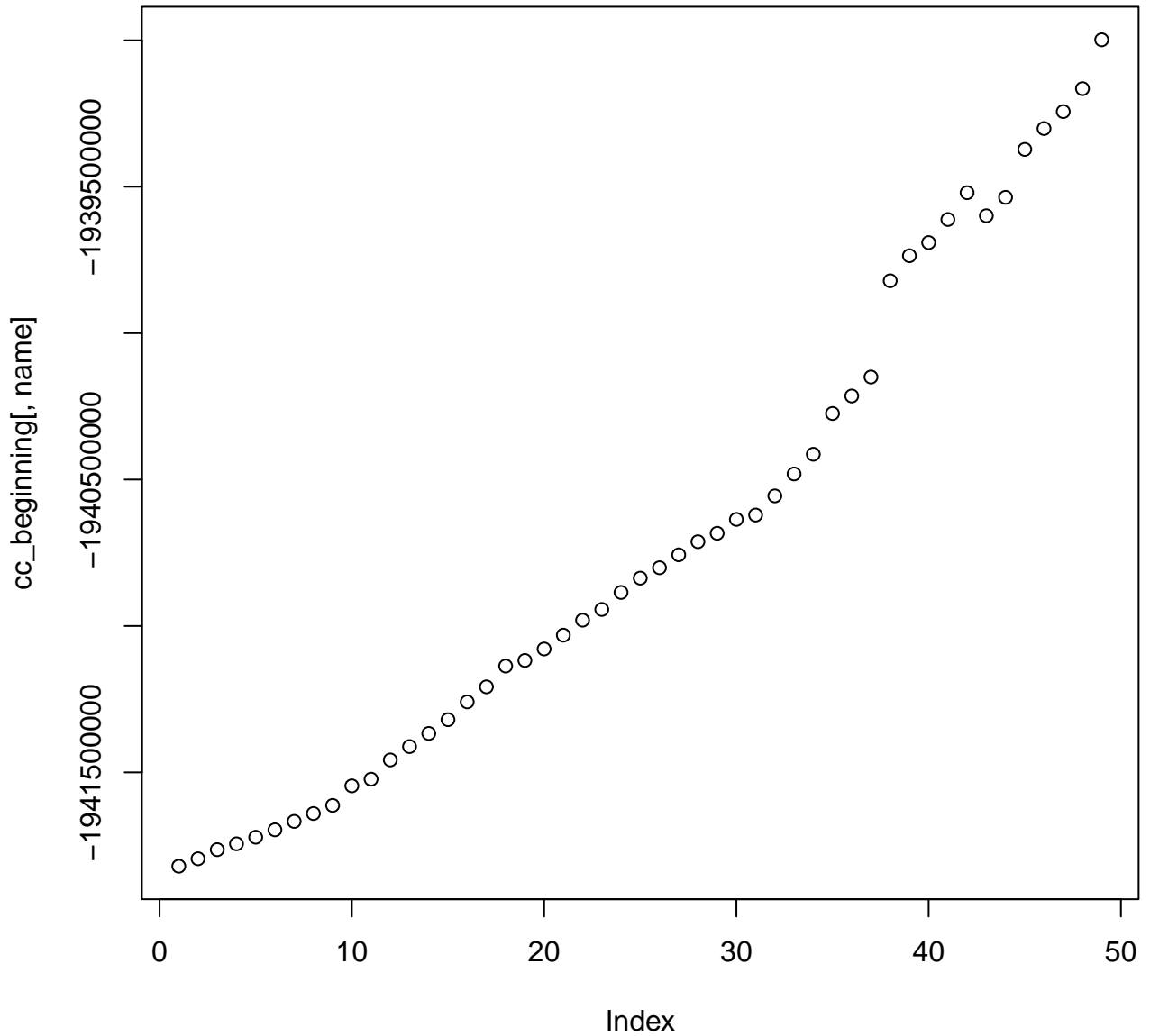
# allmatches.frac.assembly.in.oracle.set.without.check.insdel



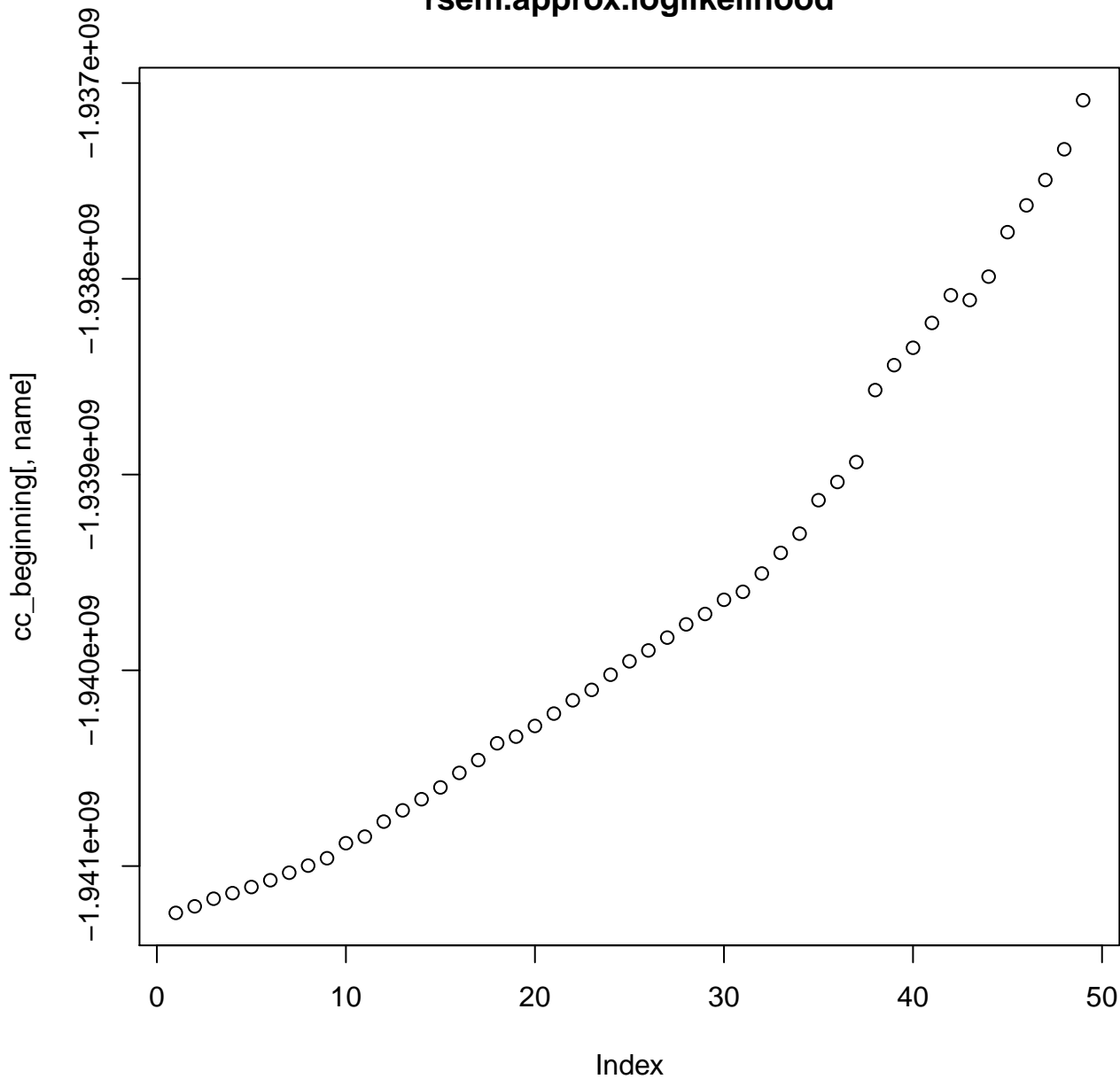
# rsem.approx.approx



# rsem.approx.bic

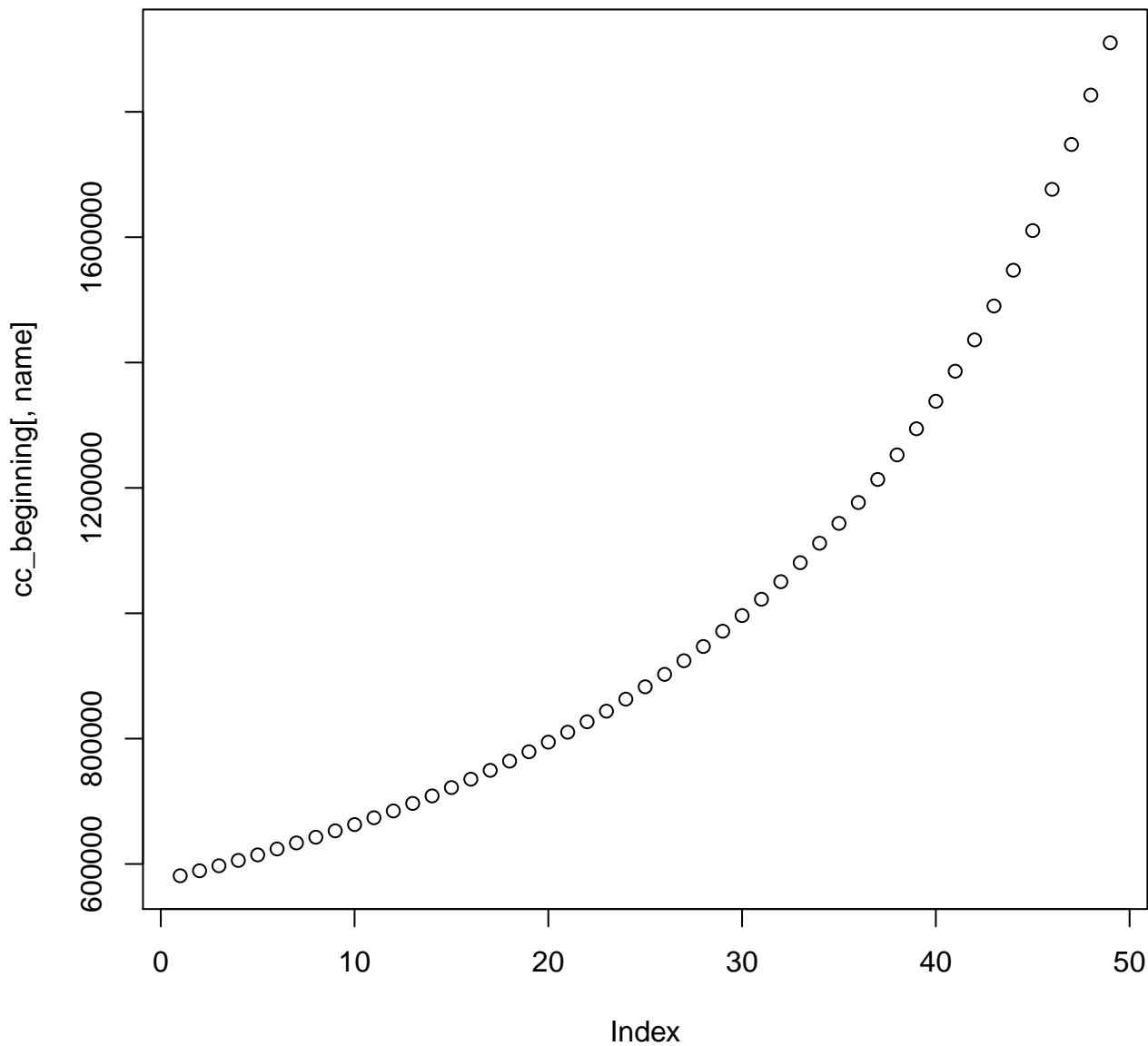


# rsem.approx.loglikelihood

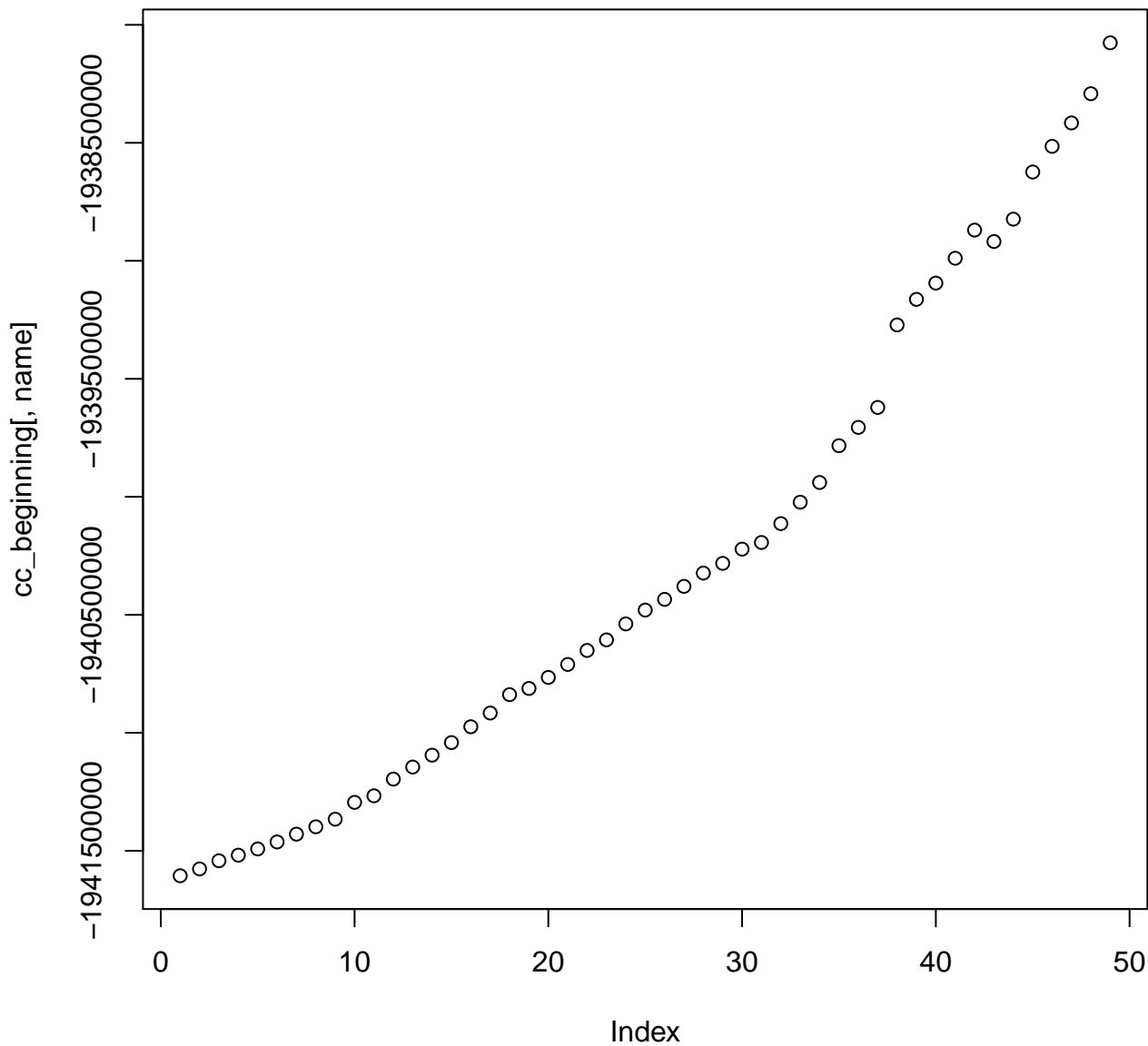




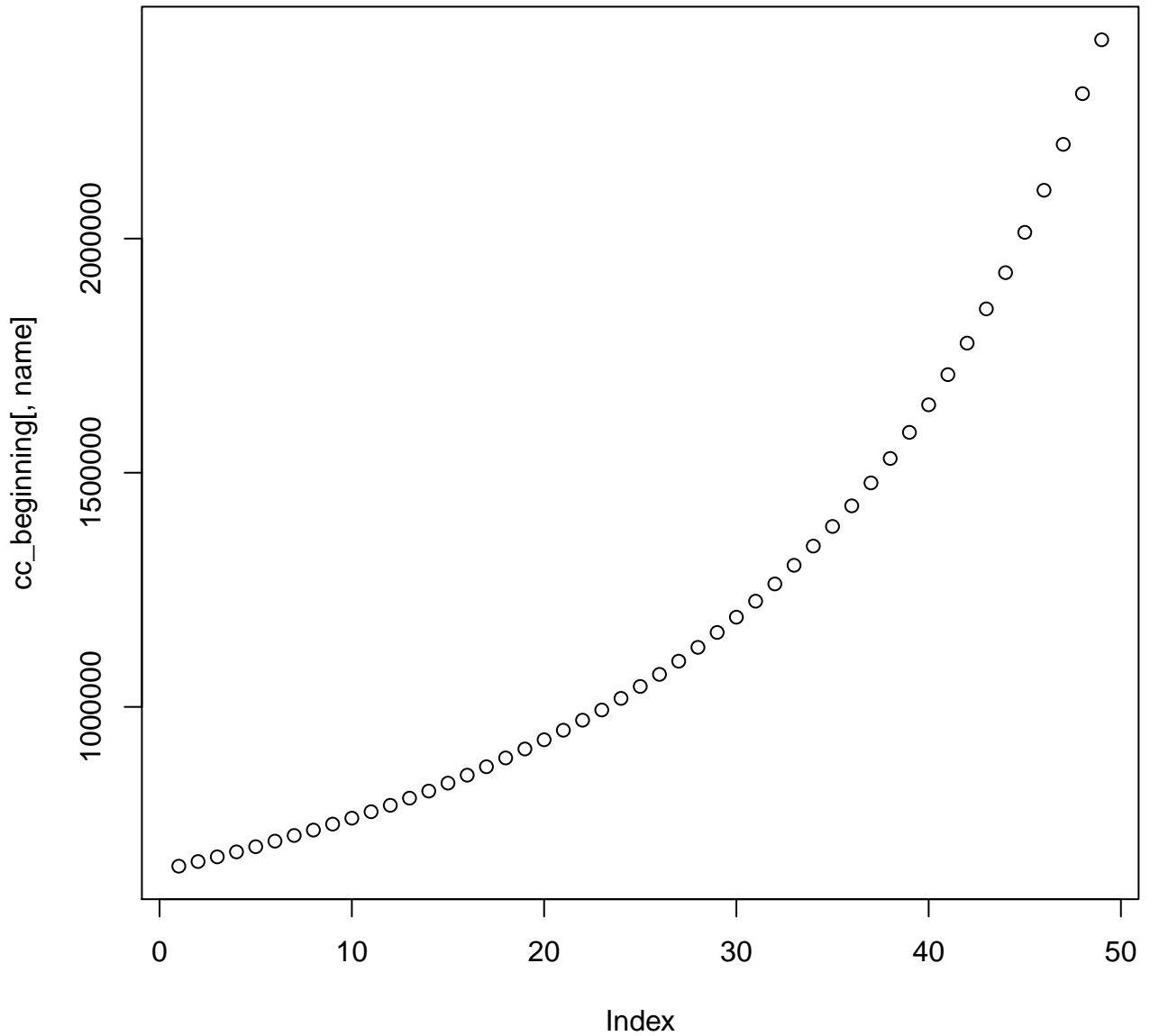
# rsem.approx.loglikelihood.penalty



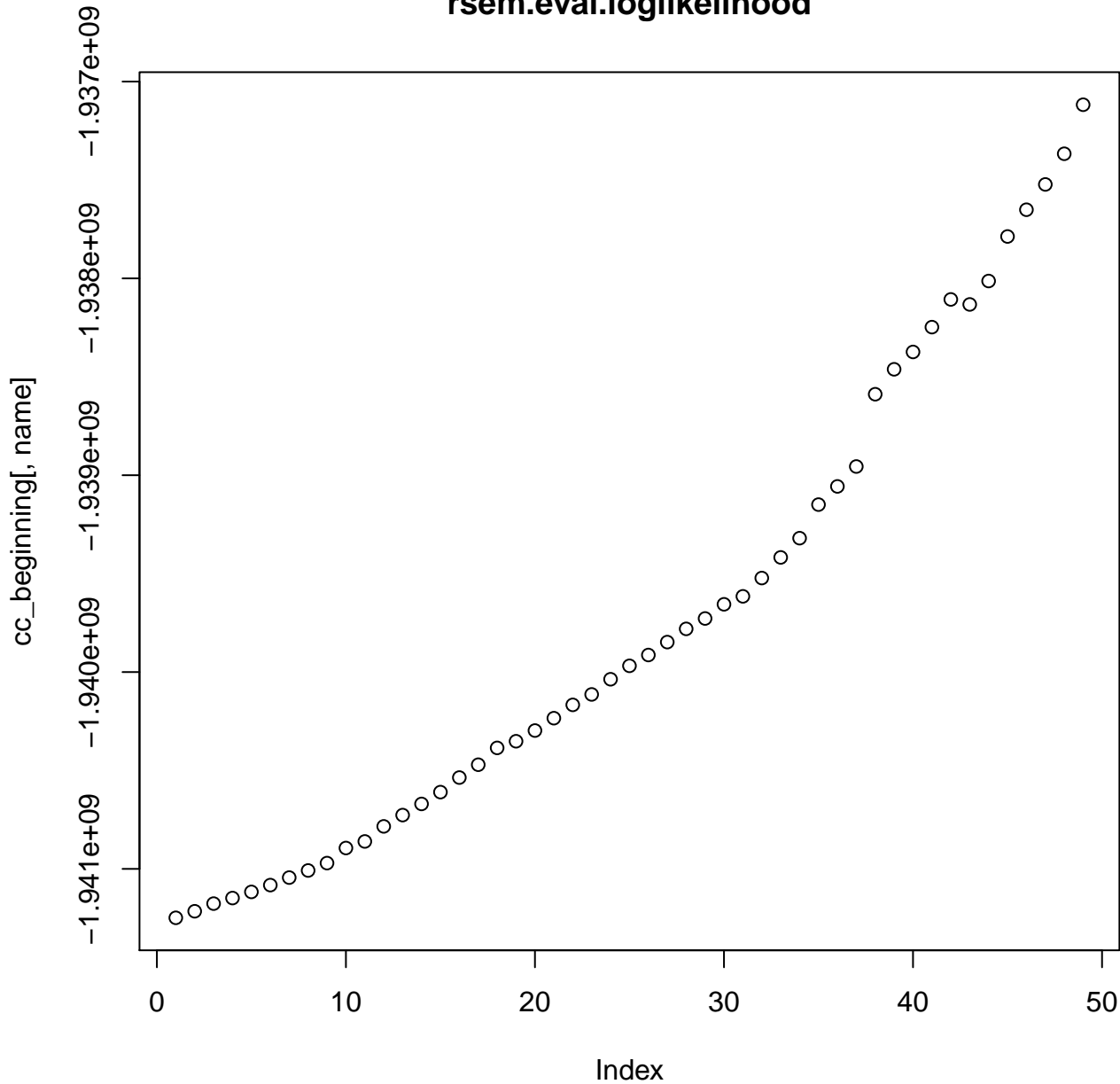
# rsem.eval.lognumer.minus.logdenom



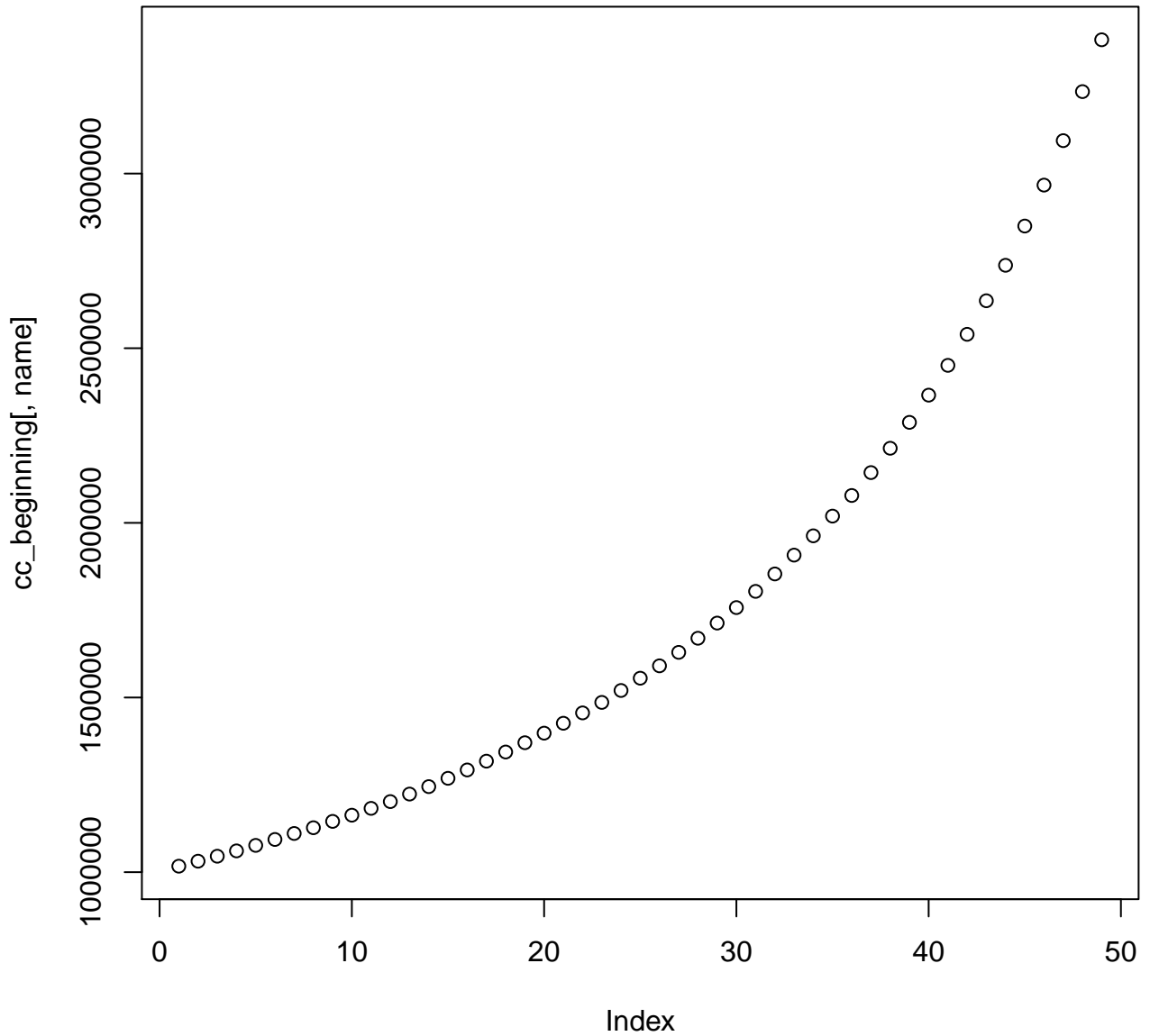
# rsem.eval.logprior



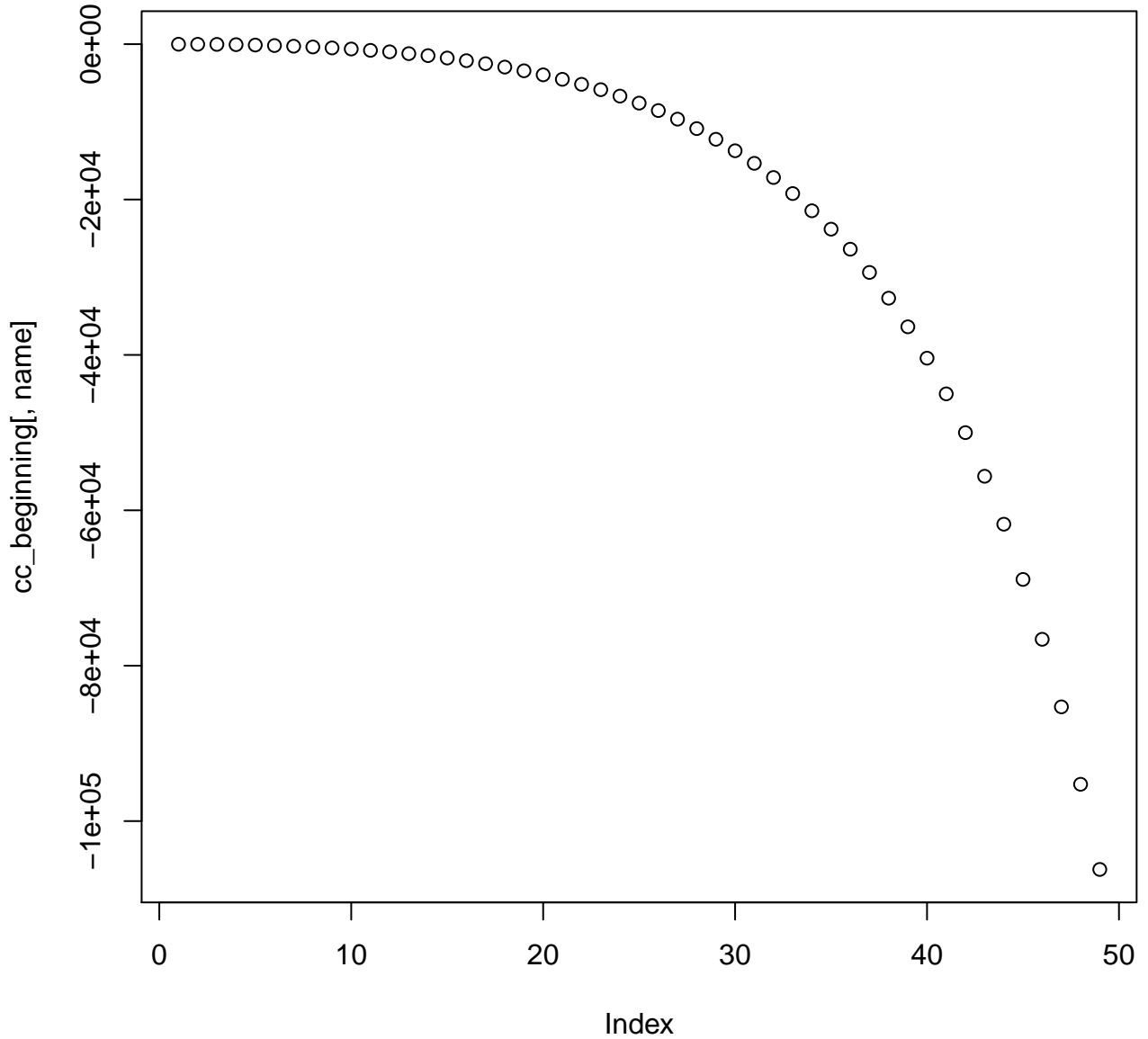
# rsem.eval.loglikelihood



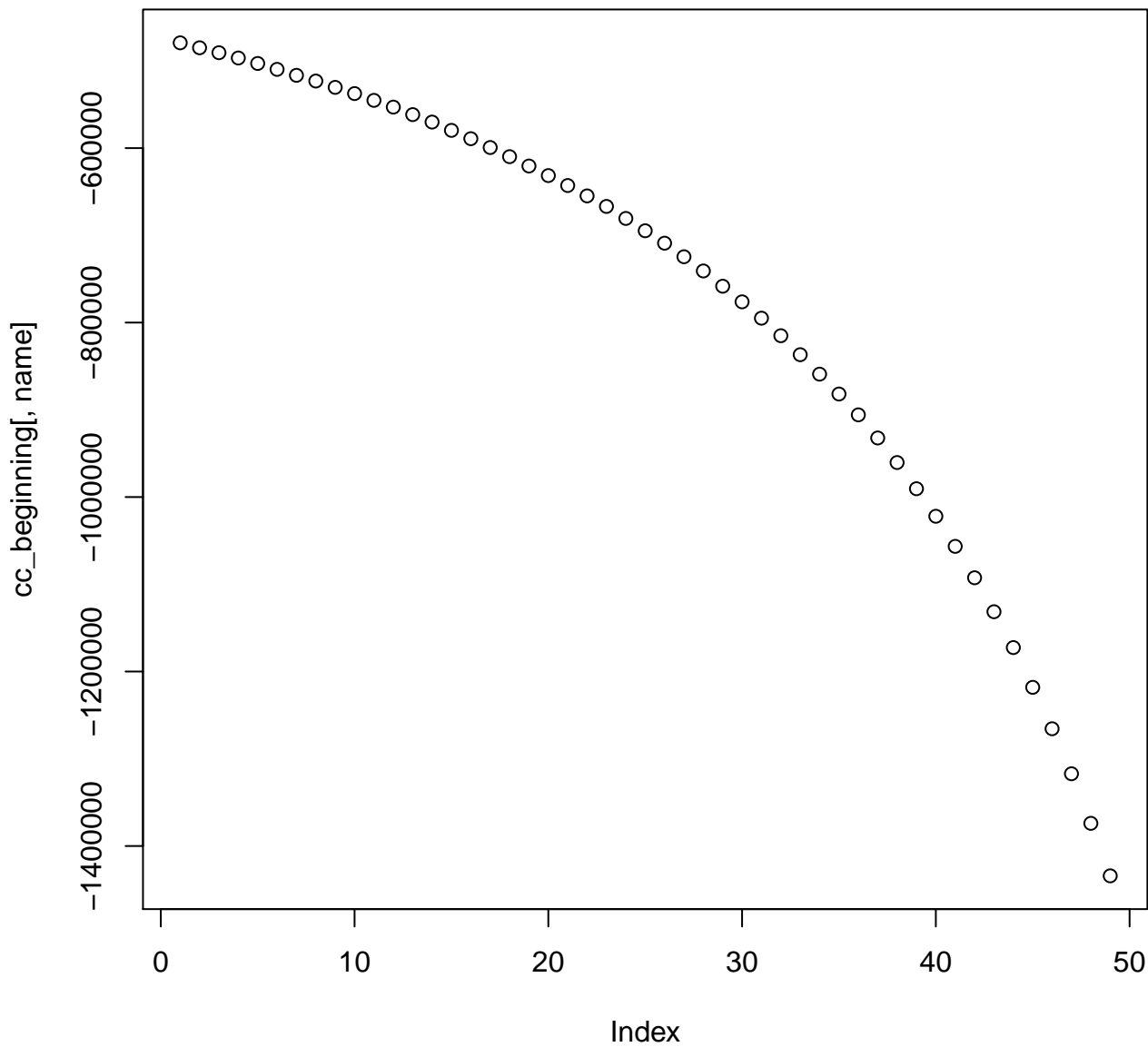
# rsem.eval.logdenom



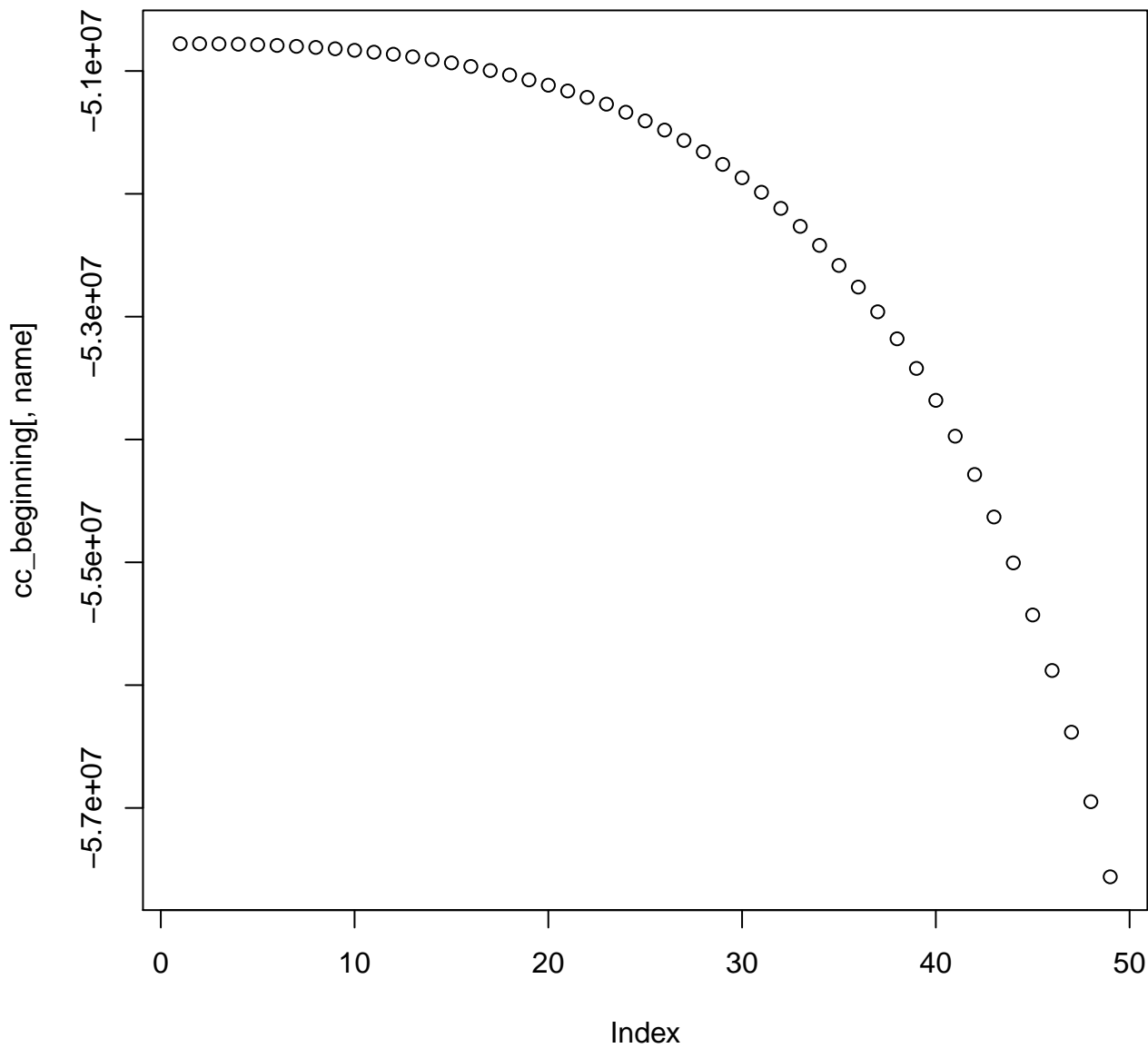
# rsem.prior.log.prob.M



# rsem.prior.log.prob.L.given.M

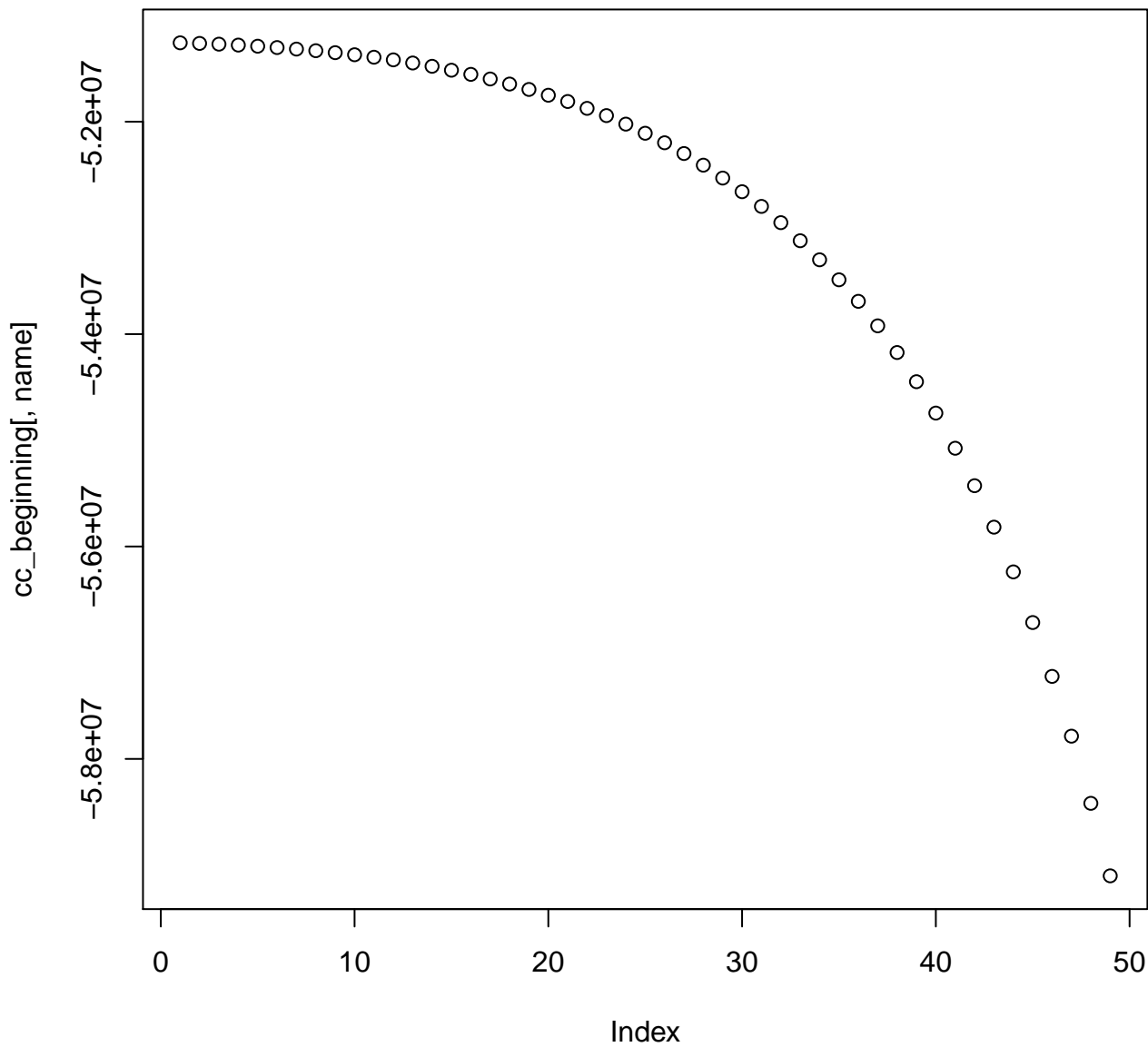


# rsem.prior.log.prob.Sequences.given.L.and.M

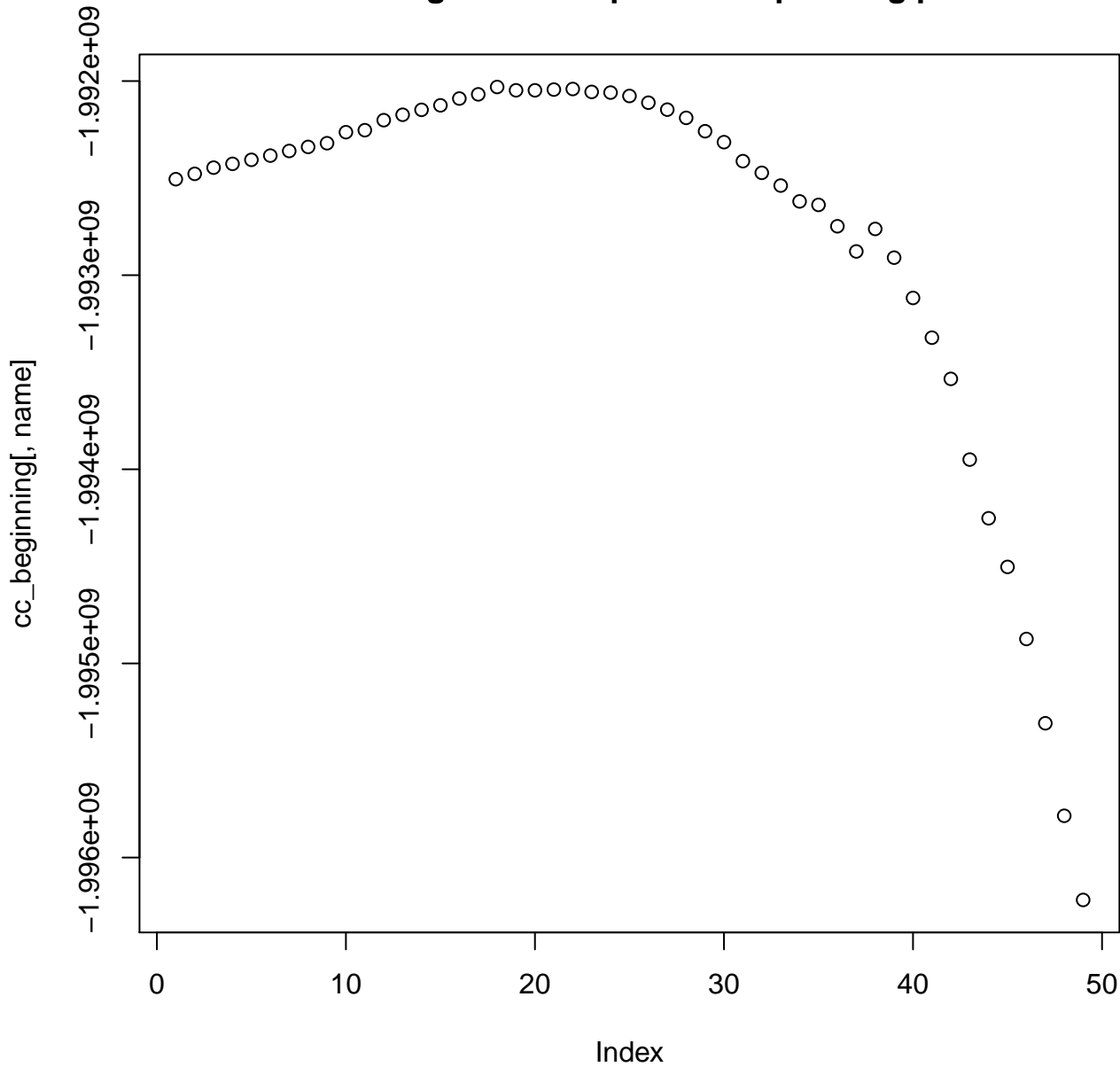




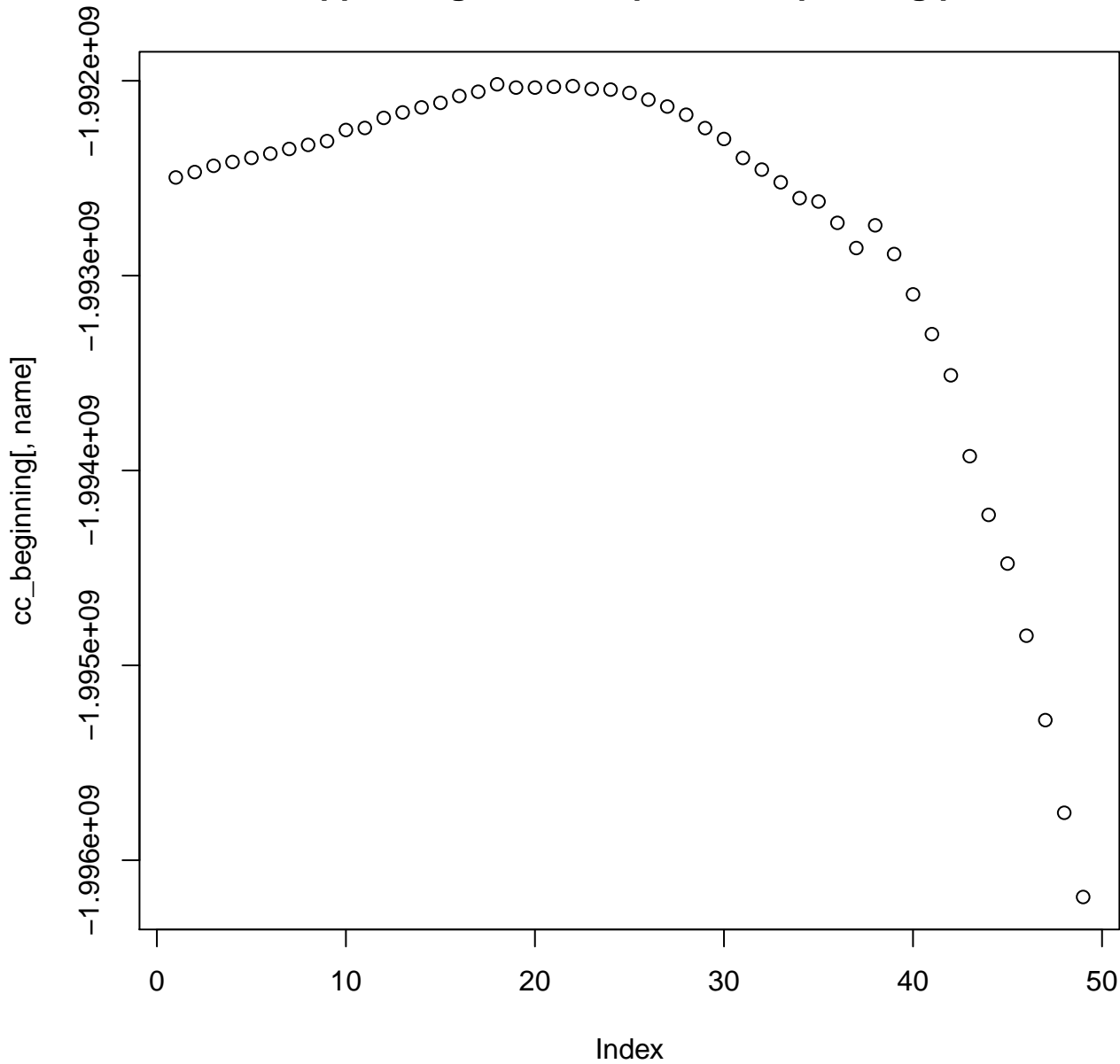
# rsem.prior.log.prob.A



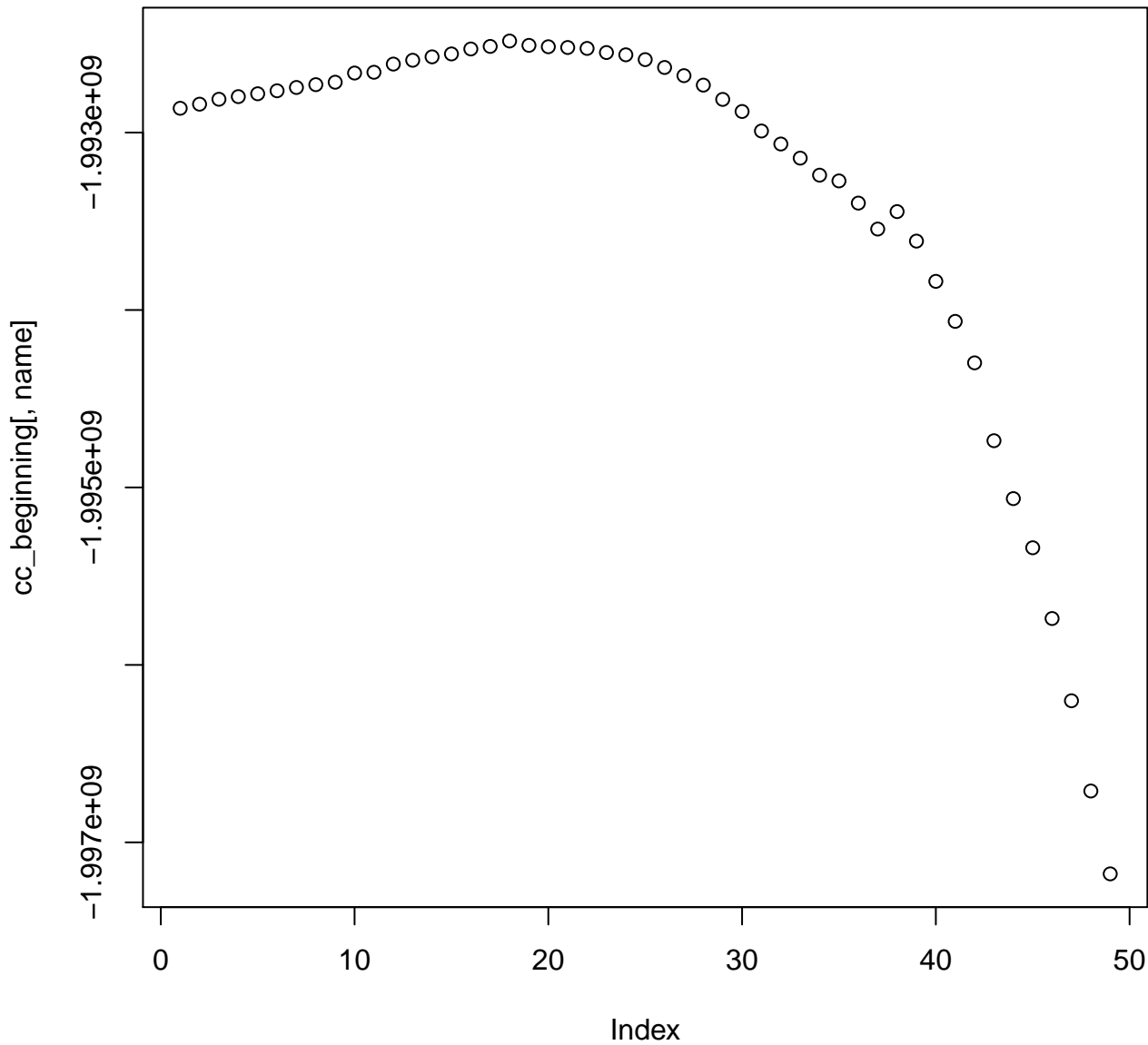
# rsem.eval.loglikelihood.plus.rsem.prior.log.prob.A



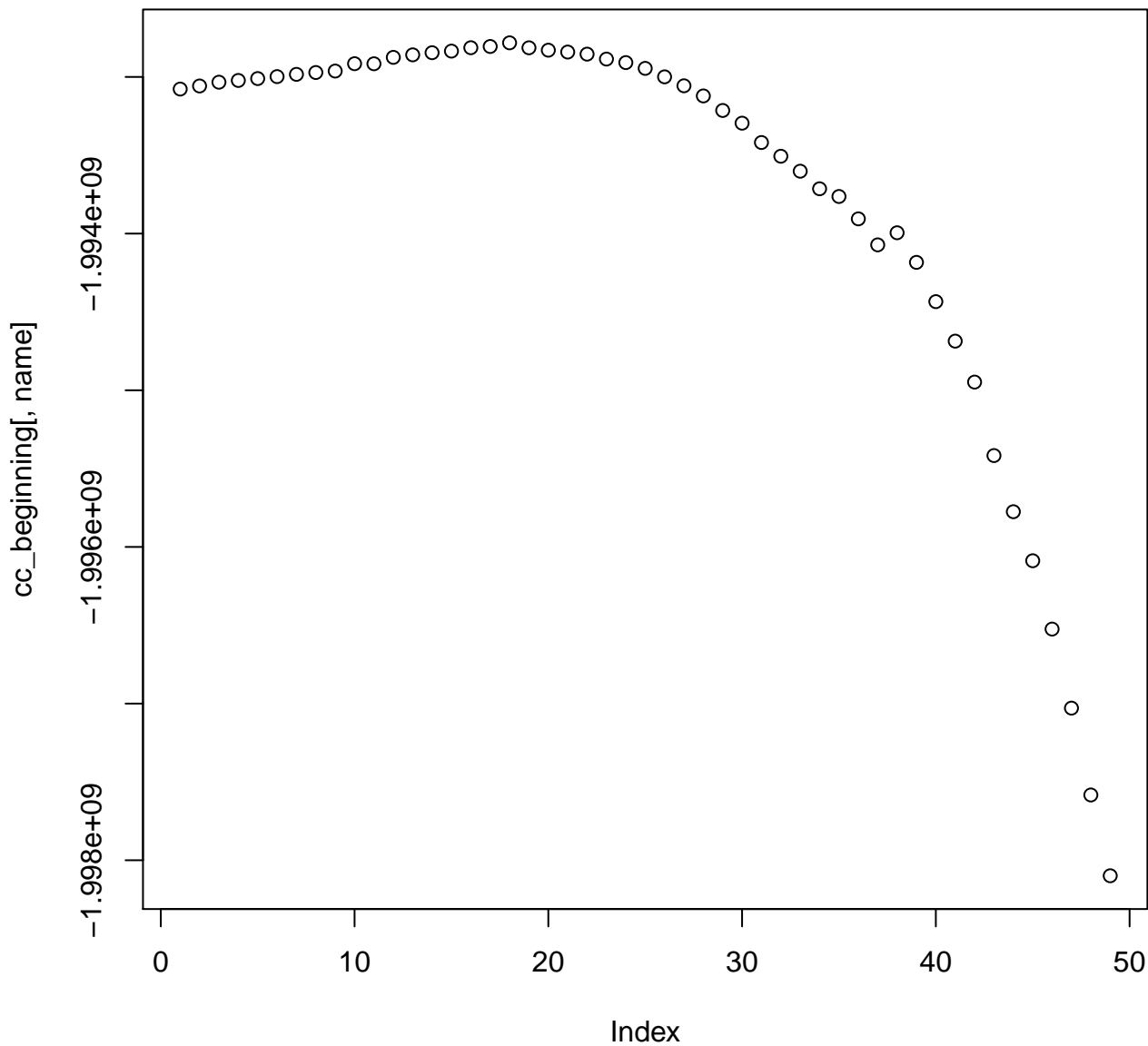
# rsem.approx.loglikelihood.plus.rsem.prior.log.prob.A



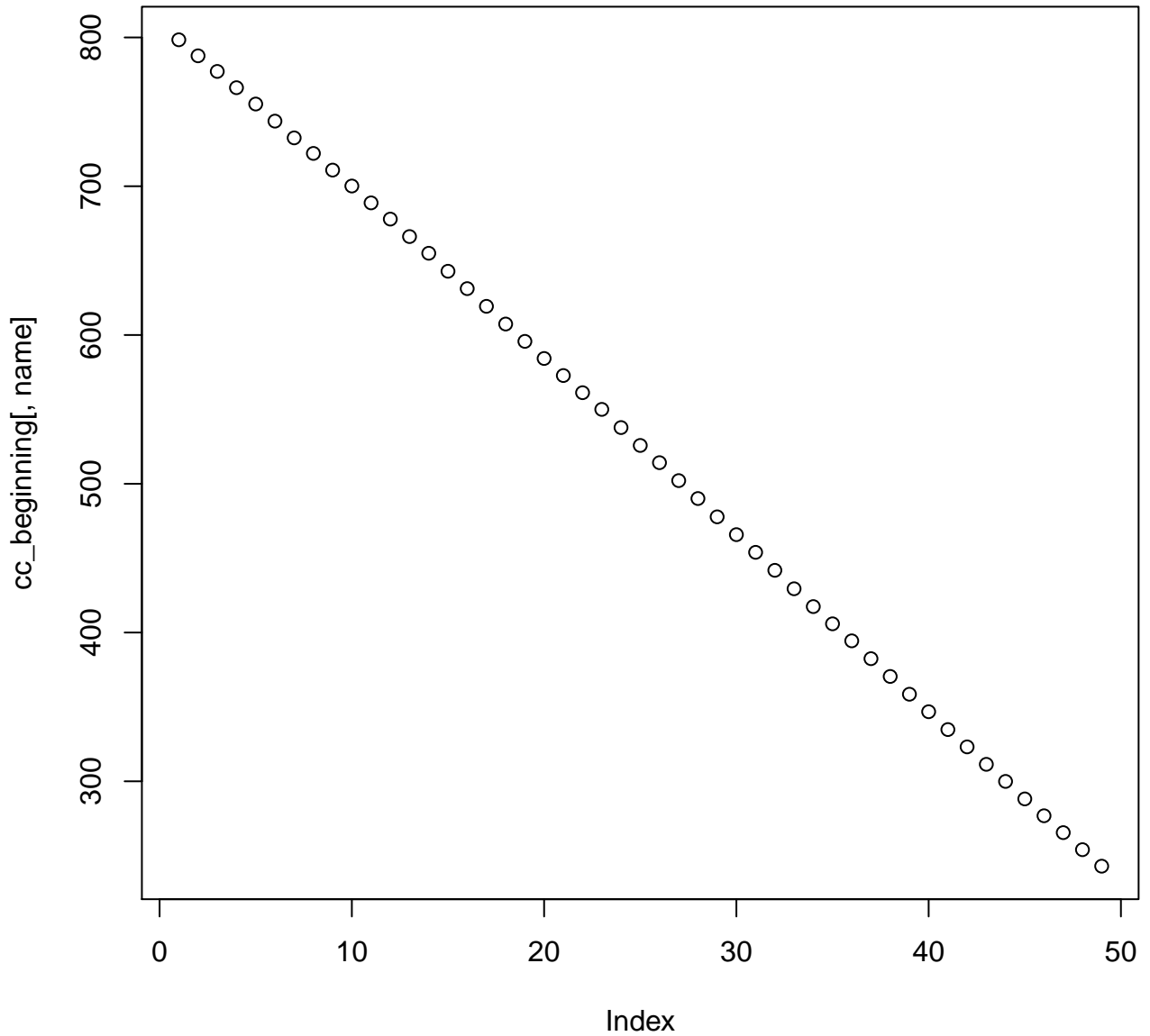
# rsem.approx.approx.plus.rsem.prior.log.prob.A



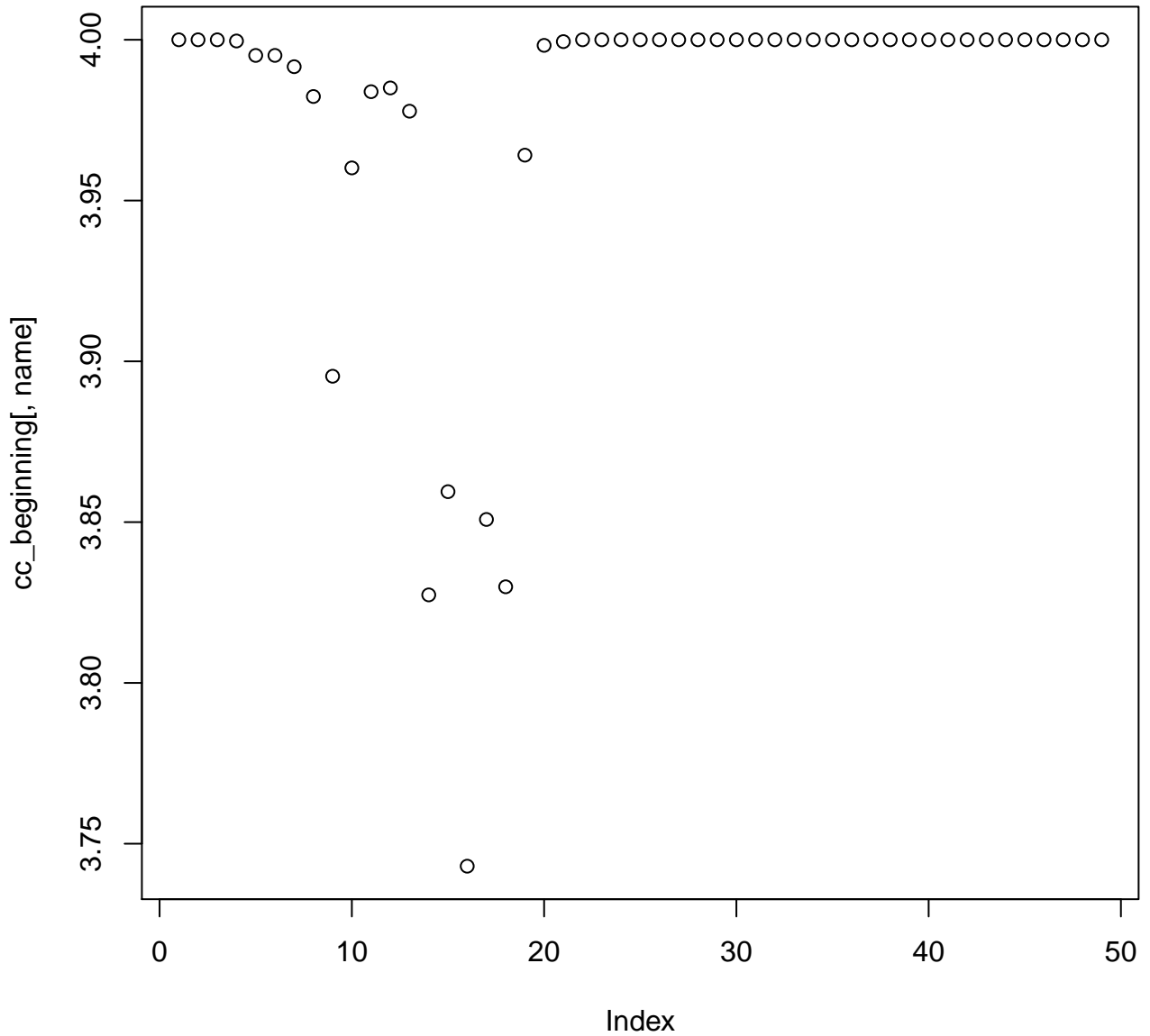
# rsem.approx.bic.plus.rsem.prior.log.prob.A



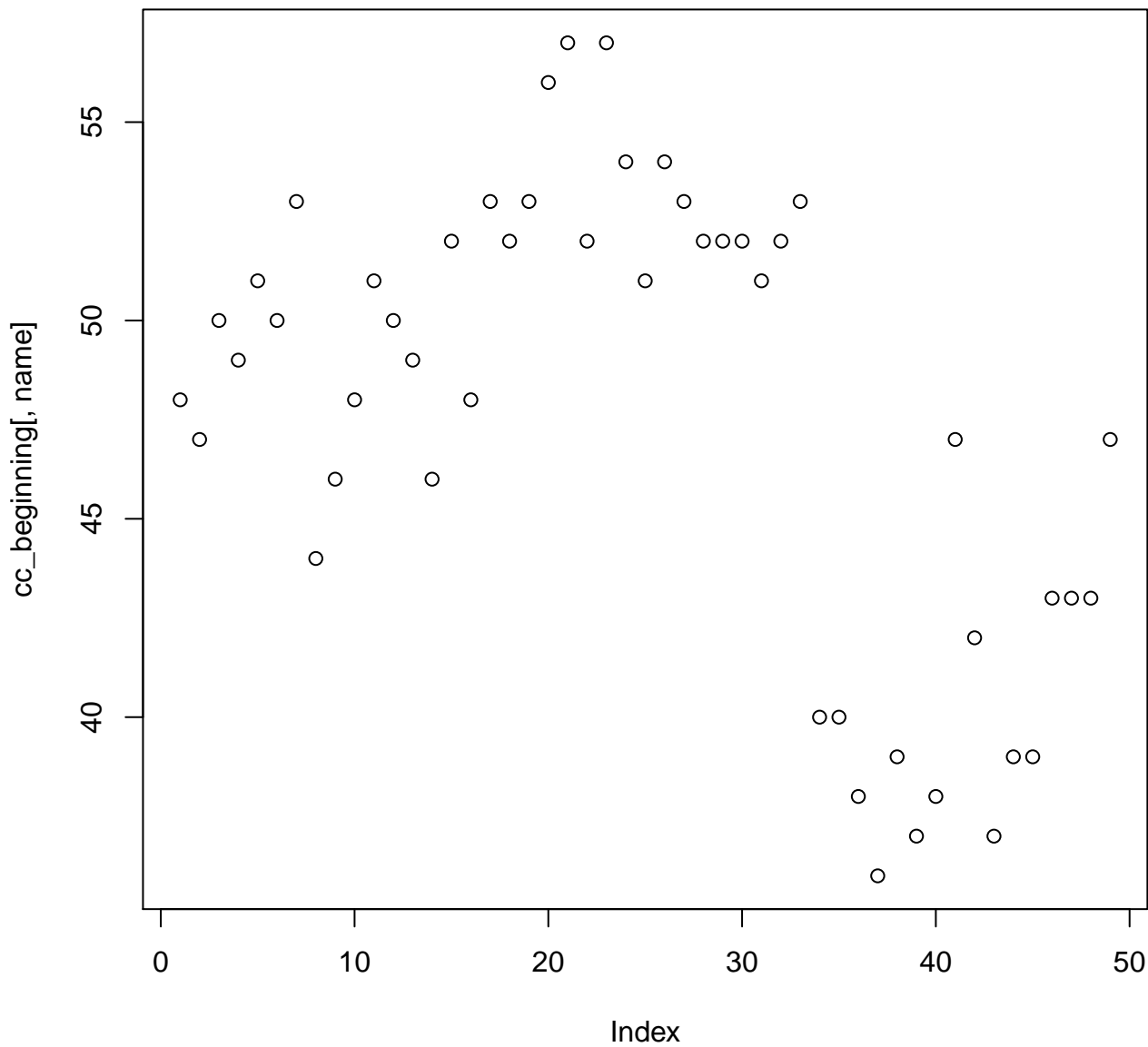
# rsem.ss.mean.num.reads.per.transcript



# rsem.ss.median.num.reads.per.transcript

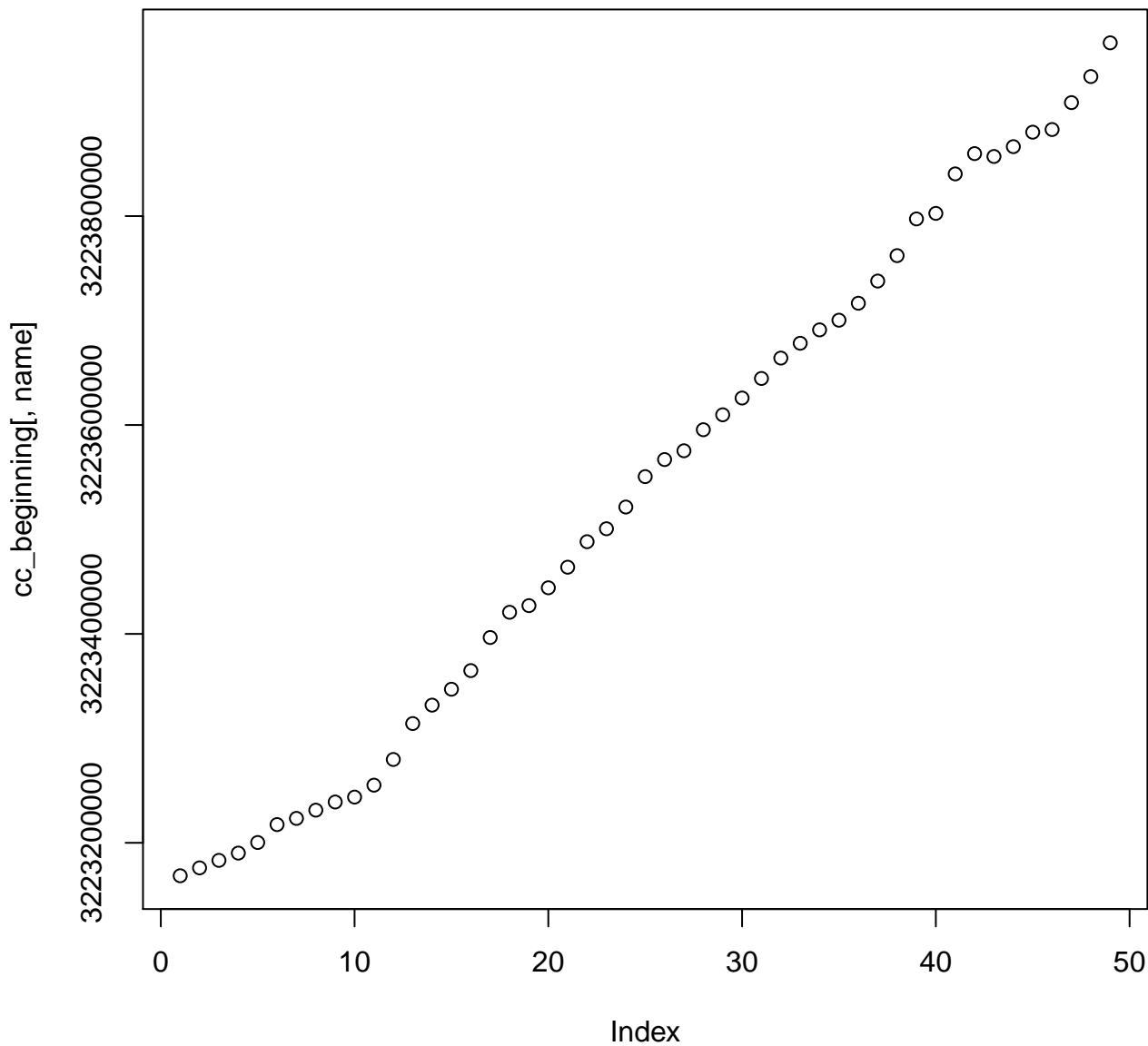


# rsem.ss.num.transcripts.with.zero.reads





# rsem.ss.num.matching.bases



# rsem.ss.num.mismatching.bases

