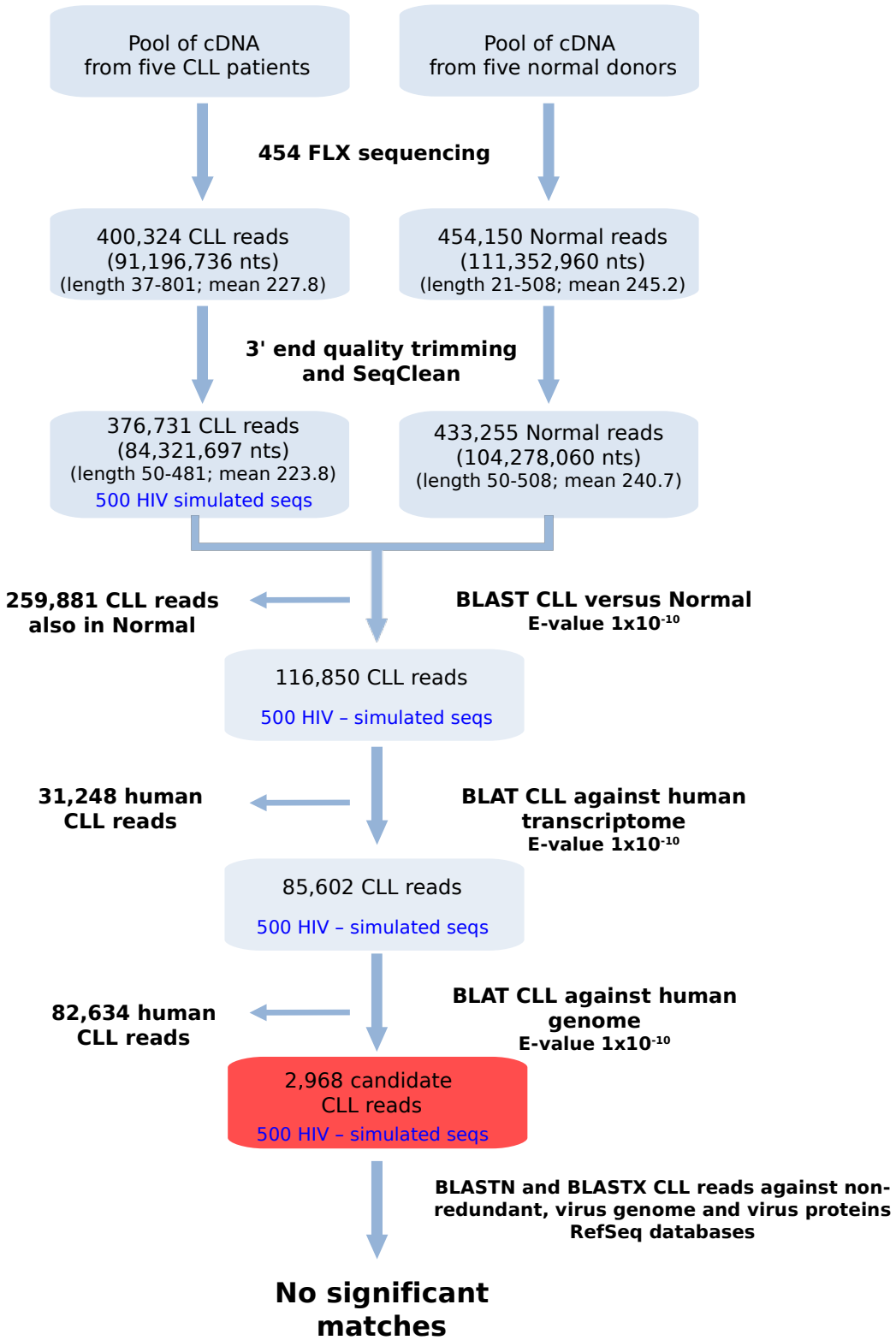
Pool of cDNA
from five CLL patients
Pool of cDNA
from five normal donors
454 FLX sequencing
400,324 CLL reads
(91,196,736 nts)
(length 37-801; mean 227.8)
454,150 Normal reads
(111,352,960 nts)
(length 21-508; mean 245.2)
3' end quality trimming
and SeqClean
376,731 CLL reads
(84,321,697 nts)
(length 50-481; mean 223.8)
500 HIV simulated seqs
433,255 Normal reads
(104,278,060 nts)
(length 50-508; mean 240.7)
259,881 CLL reads
also in Normal
BLAST CLL versus Normal
E-value 1x10-10
116,850 CLL reads
500 HIV – simulated seqs
31,248 human
CLL reads
BLAT CLL against human
transcriptome
E-value 1x10-10
85,602 CLL reads
500 HIV – simulated seqs
82,634 human
CLL reads
BLAT CLL against human
genome
E-value 1x10-10
2,968 candidate
CLL reads
500 HIV – simulated seqs
BLASTN and BLASTX CLL reads against non-
redundant, virus genome and virus proteins
RefSeq databases
No significant
matches