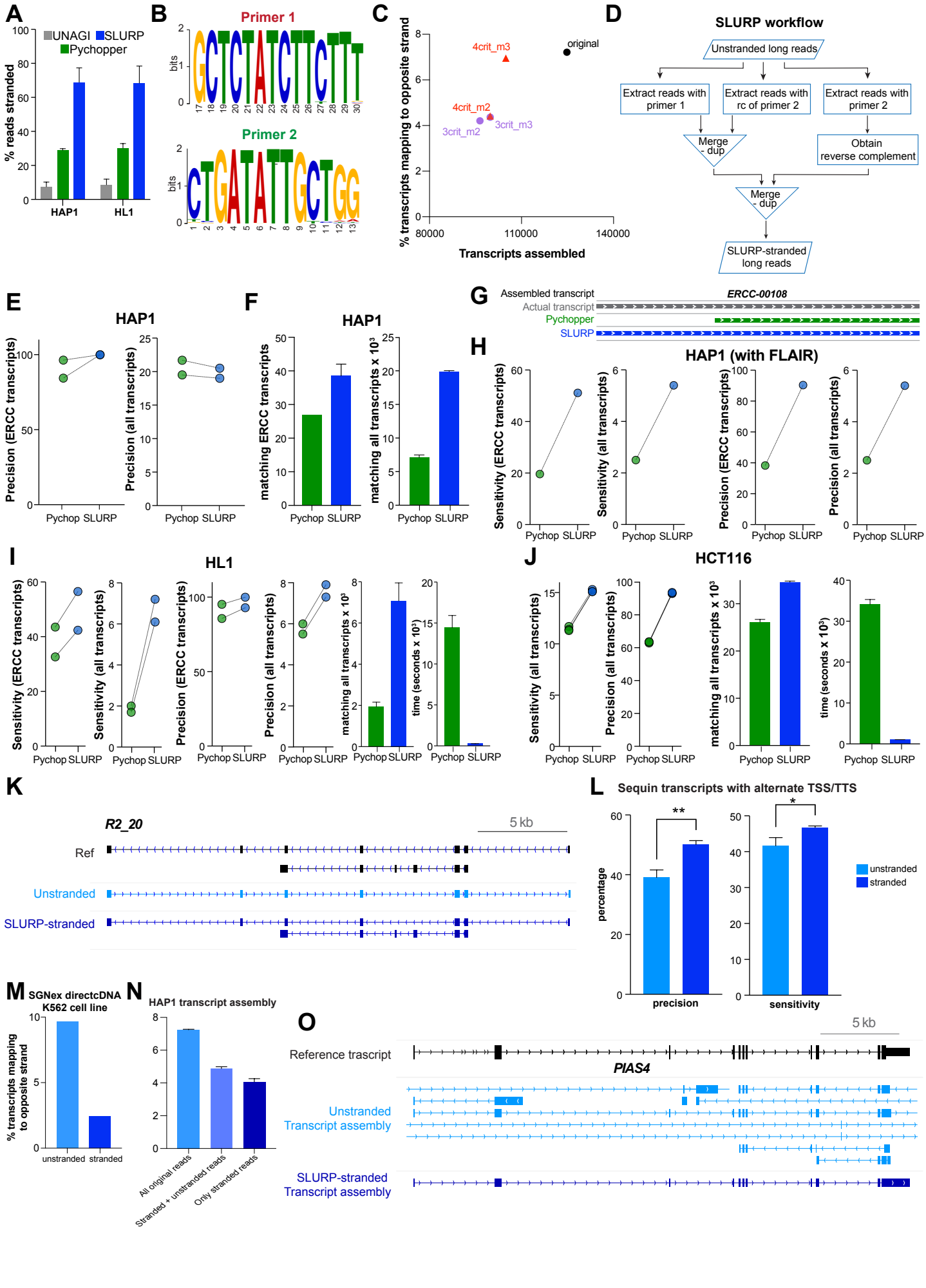
Figure S3


A
UNAGI
SLURP
Pychopper
% reads stranded
HAP1
HL1
B
Primer 1
Primer 2
bits
C
4crit_m3
original
4crit_m2
3crit_m2
3crit_m3
% transcripts mapping to opposite strand
Transcripts assembled
D
SLURP workflow
Unstranded long reads
Extract reads with primer 1
Extract reads with rc of primer 2
Extract reads with primer 2
Merge - dup
Obtain reverse complement
Merge - dup
SLURP-stranded long reads
E
HAP1
Precision (ERCC transcripts)
Precision (all transcripts)
Pychop SLURP
F
HAP1
matching ERCC transcripts
matching all transcripts x 10³
G
Assembled transcript
ERCC-00108
Actual transcript
Pychopper
SLURP
H
HAP1 (with FLAIR)
Sensitivity (ERCC transcripts)
Sensitivity (all transcripts)
Precision (ERCC transcripts)
Precision (all transcripts)
I
HL1
Sensitivity (ERCC transcripts)
Sensitivity (all transcripts)
Precision (ERCC transcripts)
Precision (all transcripts)
matching all transcripts x 10³
time (seconds x 10³)
J
HCT116
Sensitivity (all transcripts)
Precision (all transcripts)
matching all transcripts x 10³
time (seconds x 10³)
K
R2_20
5 kb
Ref
Unstranded
SLURP-stranded
L
Sequin transcripts with alternate TSS/TTS
**
*
percentage
unstranded
stranded
precision
sensitivity
M
SGNex directcDNA K562 cell line
% transcripts mapping to opposite strand
unstranded
stranded
N
HAP1 transcript assembly
All original reads
Stranded + unstranded reads
Only stranded reads
O
5 kb
Reference trascript
PIAS4
Unstranded Transcript assembly
SLURP-stranded Transcript assembly