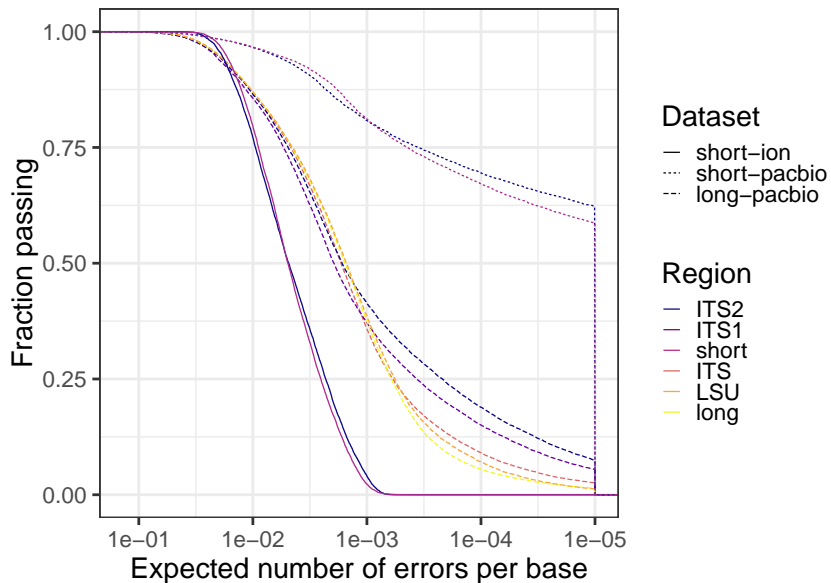
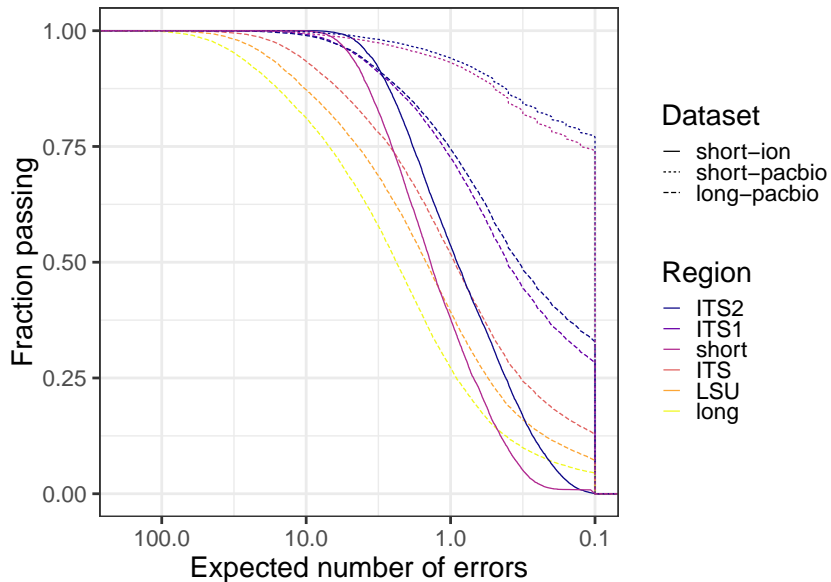


Read quality check

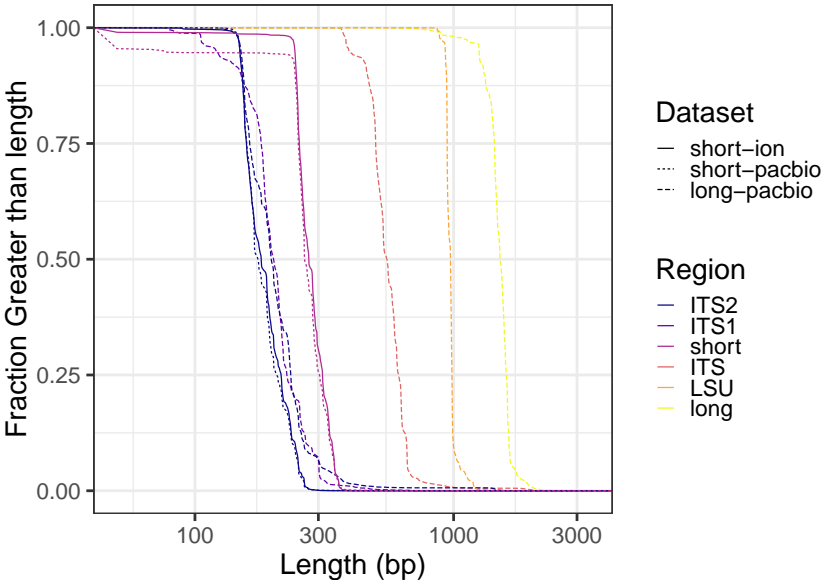
Expected error rate



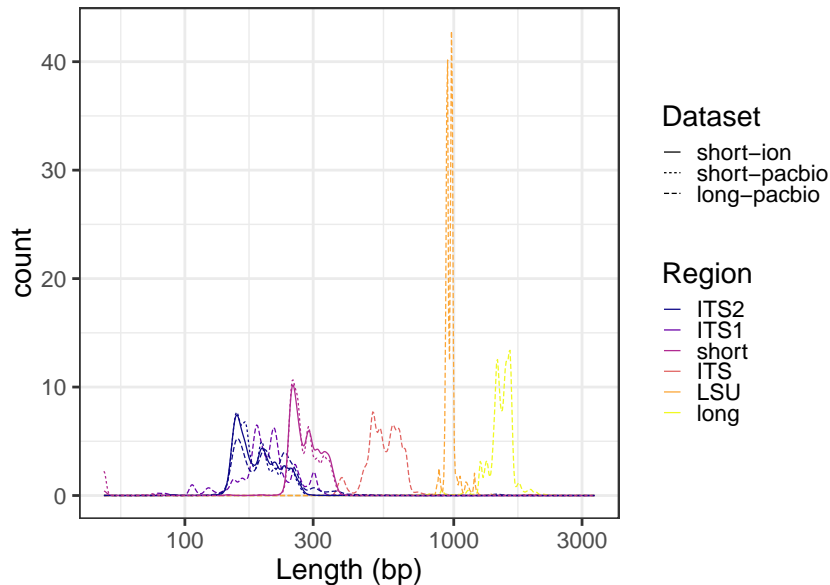
Expected number of errors



Read length



Read length density



Expected error-free reads

Dataset	Plate	Region	Expected Error-Free	Total
short-ion	001	ITS2	5818508.232	14931799
short-ion	001	short	4474677.801	15447116
short-pacbio	001	ITS2	20261.470	22956
short-pacbio	001	short	20996.139	24356
short-pacbio	002	ITS2	6930.194	7813
short-pacbio	002	short	7485.751	8607
long-pacbio	001	ITS2	16495.323	26923
long-pacbio	001	ITS1	15568.549	26806
long-pacbio	001	ITS	10831.268	26750
long-pacbio	001	LSU	8506.286	26658
long-pacbio	001	long	7674.849	31683
long-pacbio	002	ITS2	15349.279	25542
long-pacbio	002	ITS1	14767.305	25393
long-pacbio	002	ITS	9893.460	25372
long-pacbio	002	LSU	7128.997	25508
long-pacbio	002	long	5298.393	27650

ASV correspondences

- ▶ IonTorrent reads which match a PacBio ASV:
`filter(crosstab, pb.reads > 0) %$$ sum(ion.reads)`
- ▶ IonTorrent reads which do NOT match PacBio:
`filter(crosstab, pb.reads == 0) %$$
sum(ion.reads)`
- ▶ PacBio reads which match an IonTorrent ASV:
`filter(crosstab, ion.reads > 0) %$$ sum(pb.reads)`
- ▶ PacBio reads which do NOT match IonTorrent:
`filter(crosstab, ion.reads == 0) %$$
sum(pb.reads)`