

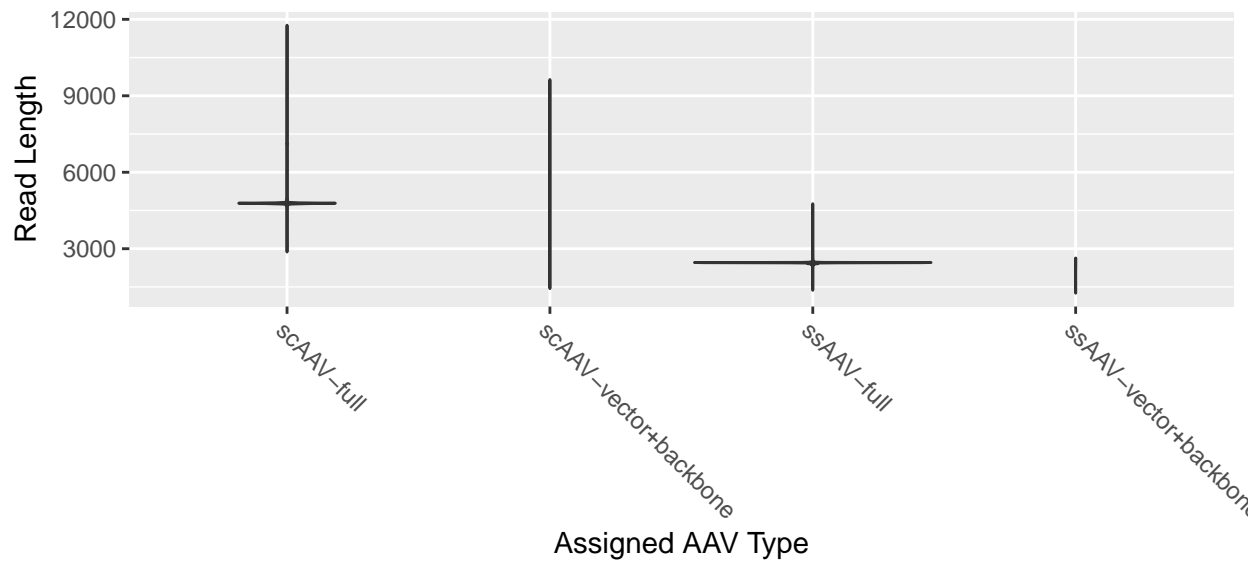
AAV Report

Assigned Types By Read Alignment Characteristics, overview

Assigned Type	Count	Frequency (%)
ssAAV	28262	68.66
scAAV	11291	27.43
other	1535	3.73
unmapped	73	0.18

Assigned Type	Count	Frequency (%)
ssAAV	28262	71.45
scAAV	11291	28.55

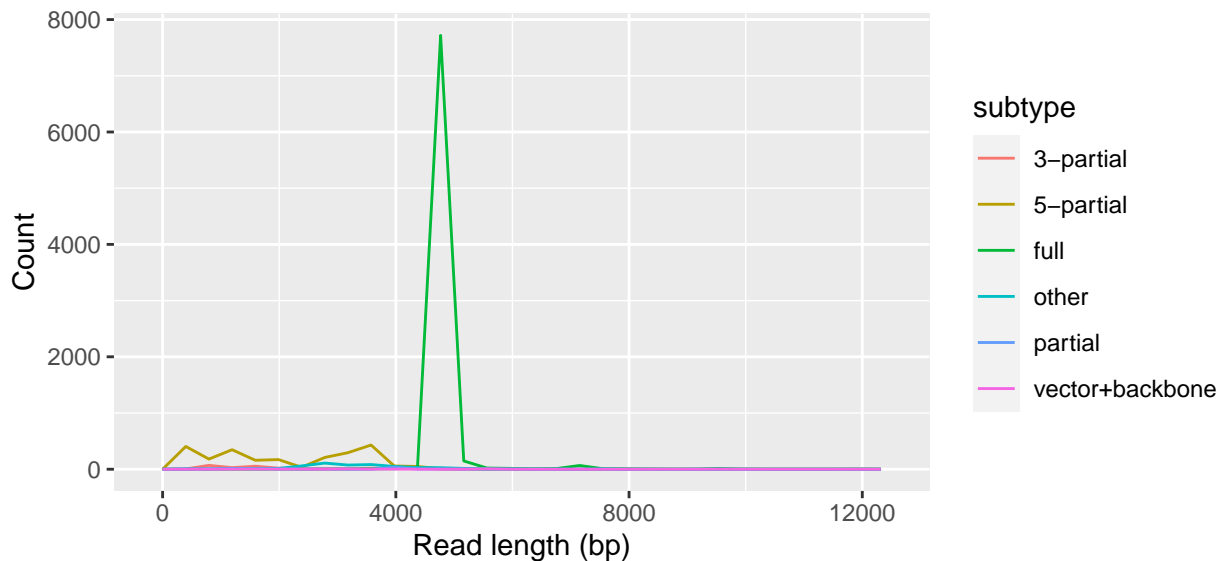
Distribution of Read Lengths by Assigned AAV Type



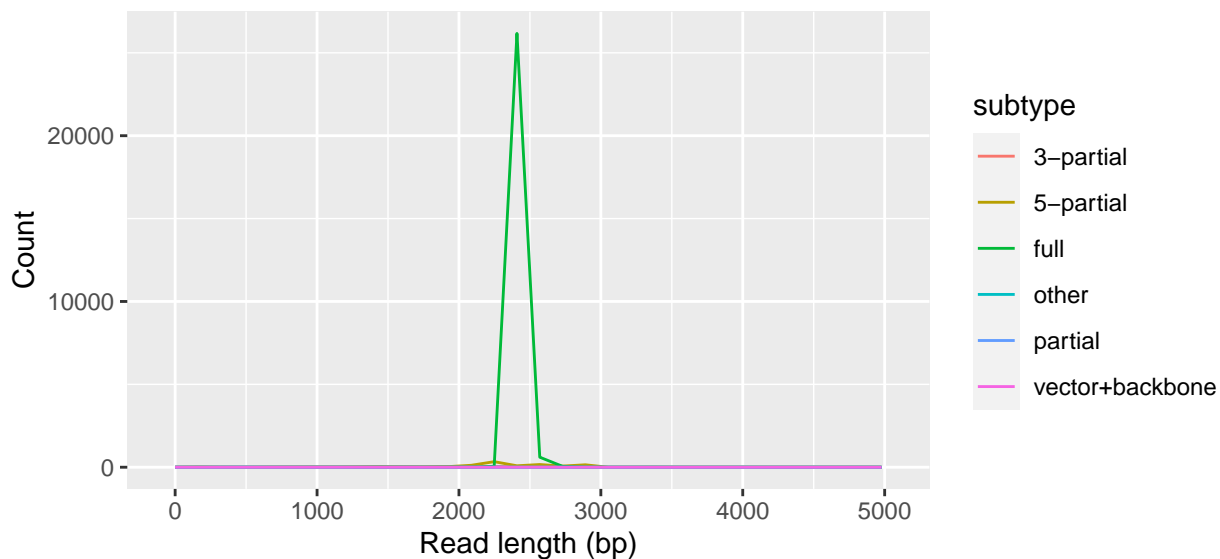
Assigned AAV Types, detailed (top 20 only)

Assigned Type, detailed	Assigned Subtype	Count	Frequency (%)
ssAAV	full	26911	68.04
scAAV	full	8054	20.36
scAAV	5-partial	2347	5.93
ssAAV	5-partial	1102	2.79
scAAV	3-partial	262	0.66
scAAV	full 5-partial	237	0.60
ssAAV	3-partial	216	0.55
scAAV	full 3-partial	100	0.25
scAAV	backbone	82	0.21
scAAV	partial	83	0.21
ssAAV	partial	29	0.07
scAAV	vector+backbone	22	0.06
scAAV	vector+backbone 5-partial	24	0.06
scAAV	backbone 5-partial	17	0.04
scAAV	partial 5-partial	14	0.04
scAAV	5-partial partial	10	0.03
scAAV	3-partial 5-partial	6	0.02
scAAV	5-partial 3-partial	7	0.02
scAAV	3-partial partial	5	0.01
scAAV	full backbone	5	0.01

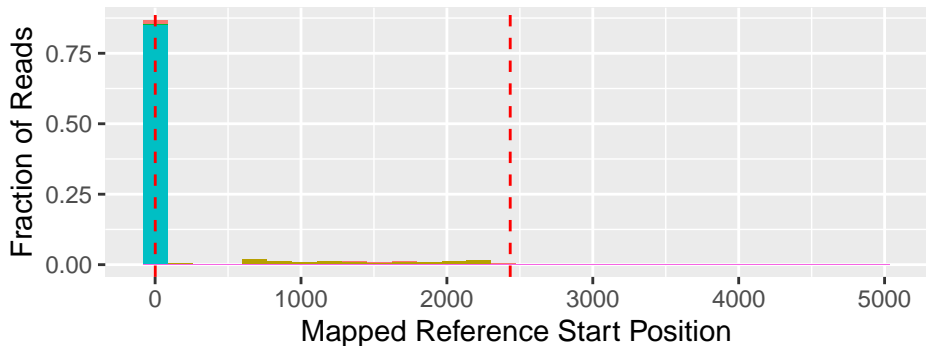
Distribution of read length, scAAV, by subtype



Distribution of read length, ssAAV, by subtype



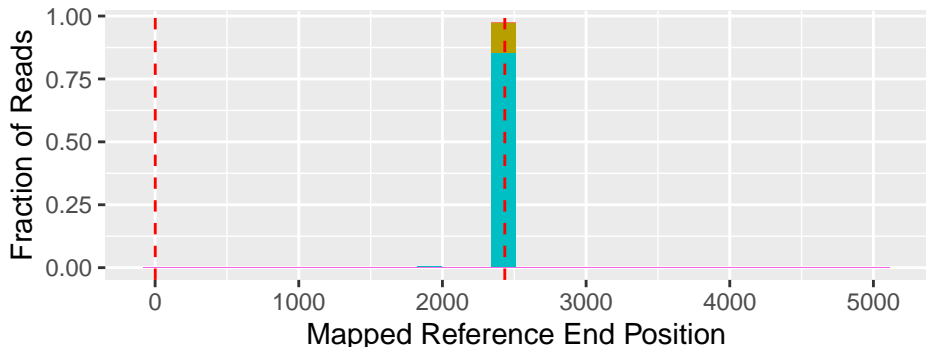
Distribution of Mapped Reference Start Position



map_subtype



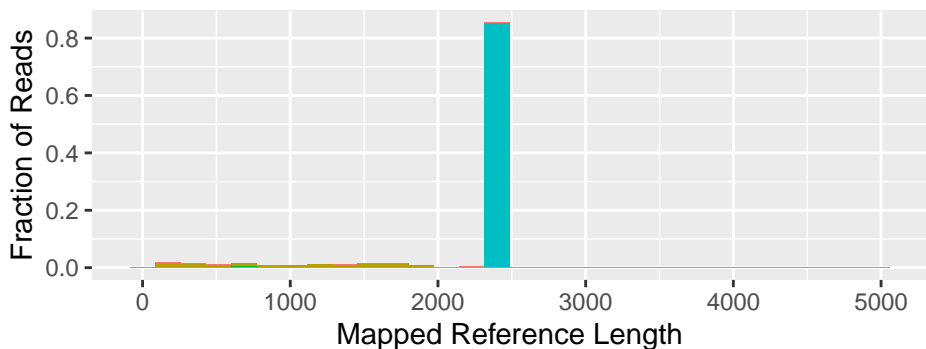
Distribution of Mapped Reference End Position



map_subtype



Distribution of Mapped Reference Spanning Region Size

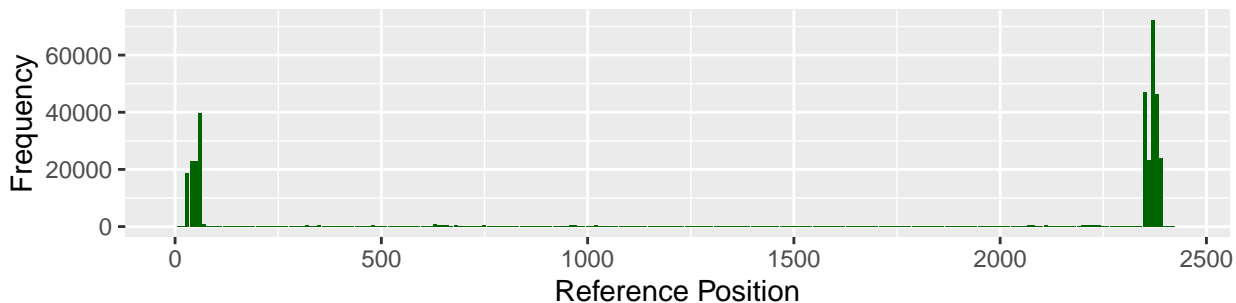


map_subtype



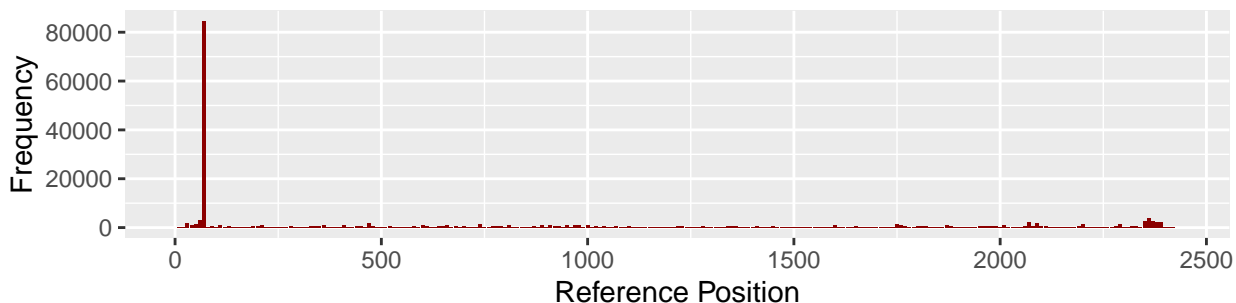
Distribution of Non-matches by Reference Position, Substitutions

Higher bars indicate hot spots for substitutions w.r.t reference



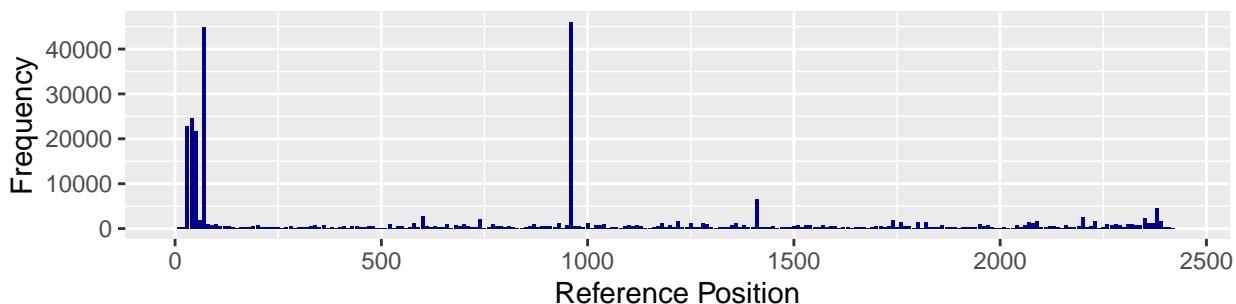
Distribution of Non-matches by Reference Position, Deletions

Higher bars indicate hot spots for deletion w.r.t reference

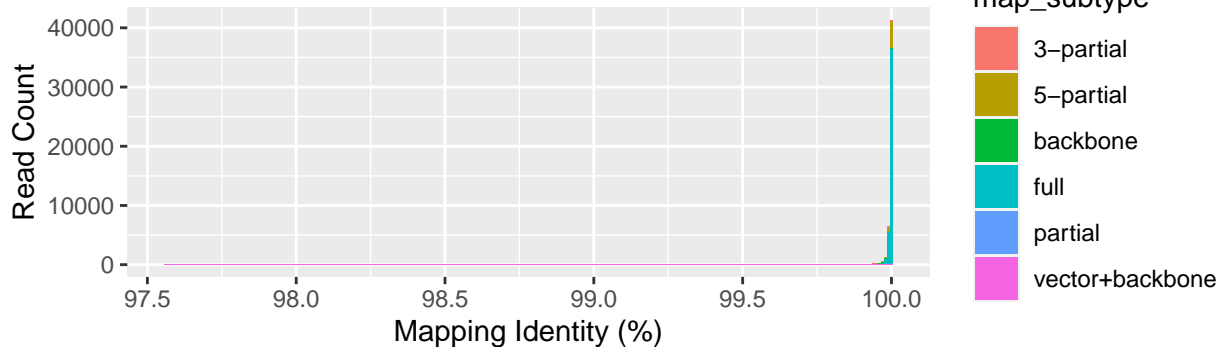


Distribution of Non-matches by Reference Position, Insertions

Higher bars indicate hot spots for insertion w.r.t reference

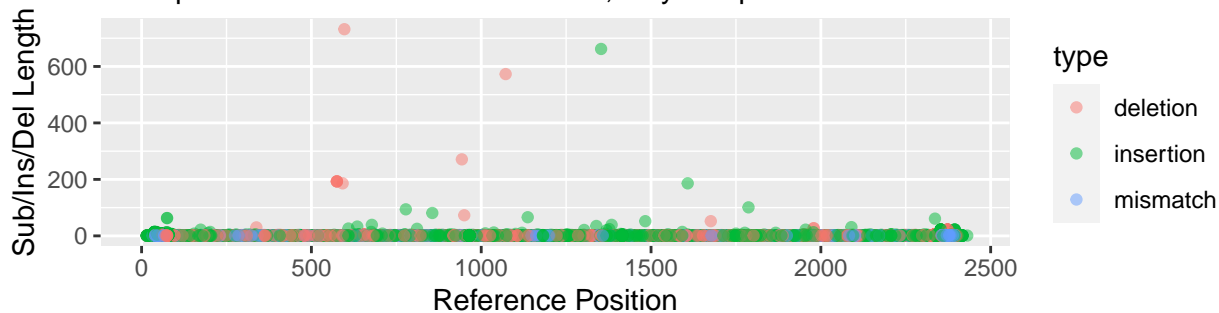


Distribution of Mapped Identity to Reference



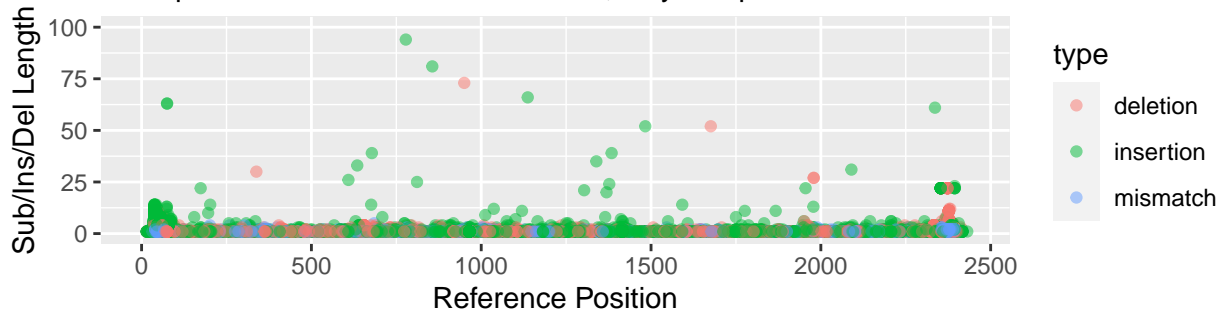
Distribution of Non-Matches

Each point is a non-match from a read, only 50k points at most



Distribution of Non-Matches (of sizes <100 only)

Each point is a non-match from a read, only 50k points at most



Length Distribution of Different Non-matches

Err Type	Err Length	Count	Frequency (%)
deletion	1-10	193841	22.57
deletion	11-100	992	0.12
deletion	100-500	105	0.01
deletion	>500	31	0.00
insertion	1-10	286130	33.32
insertion	11-100	19312	2.25
insertion	100-500	53	0.01
insertion	>500	19	0.00
mismatch	1-10	358179	41.71