

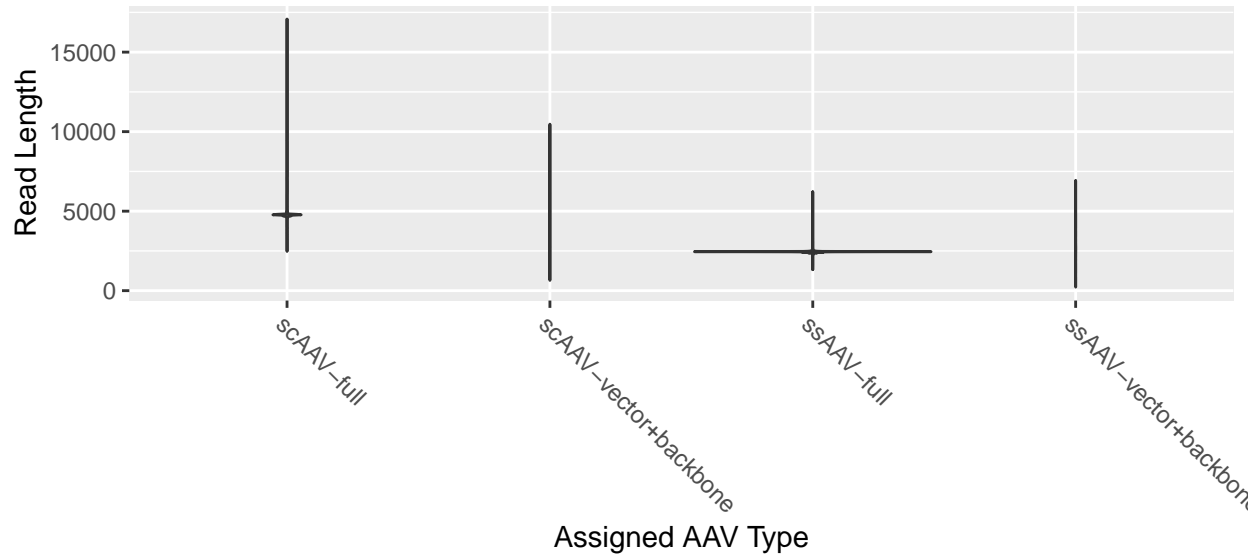
# *AAV Report*

## *Assigned Types By Read Alignment Characteristics, overview*

<b>Assigned Type</b>	<b>Count</b>	<b>Frequency (%)</b>
scAAV	346577	49.75
ssAAV	298385	42.83
other	39430	5.66
unmapped	12304	1.77

Assigned Type	Count	Frequency (%)
scAAV	346577	53.74
ssAAV	298385	46.26

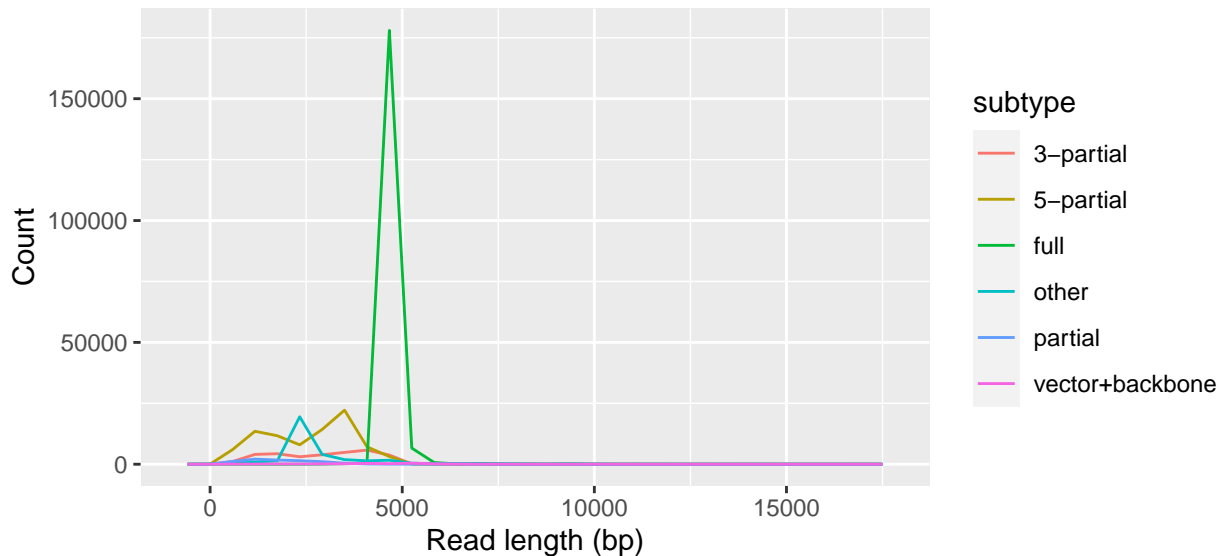
Distribution of Read Lengths by Assigned AAV Type



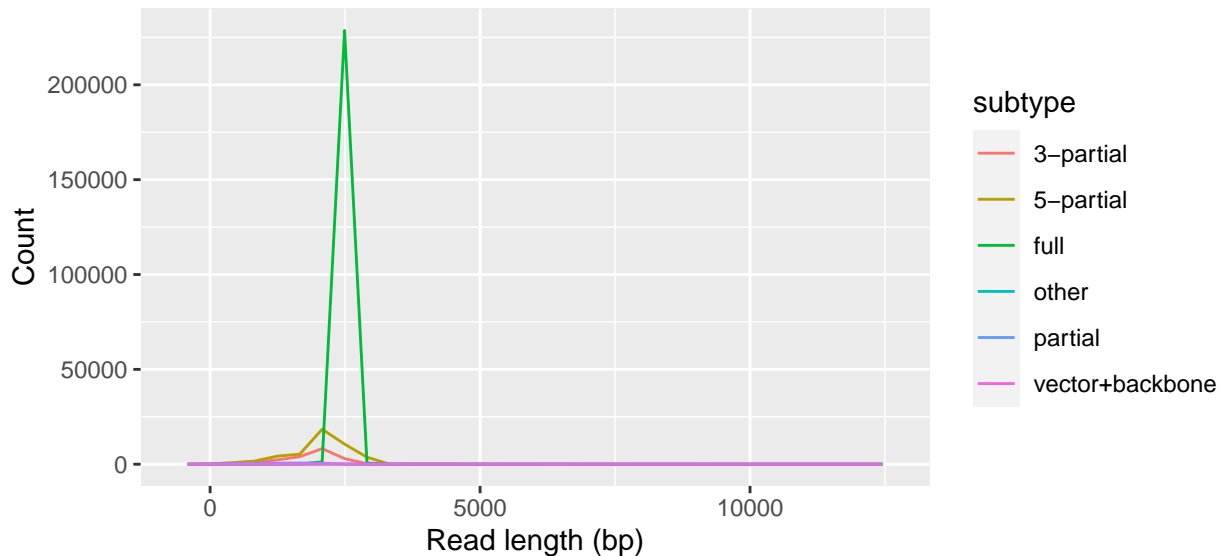
## *Assigned AAV Types, detailed (top 20 only)*

<b>Assigned Type, detailed</b>	<b>Assigned Subtype</b>	<b>Count</b>	<b>Frequency (%)</b>
ssAAV	full	230733	35.77
scAAV	full	186735	28.95
scAAV	5-partial	86131	13.35
ssAAV	5-partial	45067	6.99
scAAV	3-partial	30882	4.79
scAAV	full 5-partial	21180	3.28
ssAAV	3-partial	19270	2.99
scAAV	partial	8077	1.25
scAAV	backbone	3307	0.51
scAAV	full 3-partial	3079	0.48
ssAAV	partial	2646	0.41
scAAV	vector+backbone	1921	0.30
scAAV	5-partial partial	1448	0.22
scAAV	3-partial partial	647	0.10
scAAV	backbone 5-partial	568	0.09
scAAV	3-partial 5-partial	548	0.08
scAAV	5-partial 3-partial	466	0.07
scAAV	full backbone	399	0.06
ssAAV	vector+backbone	397	0.06
scAAV	vector+backbone 5-partial	271	0.04

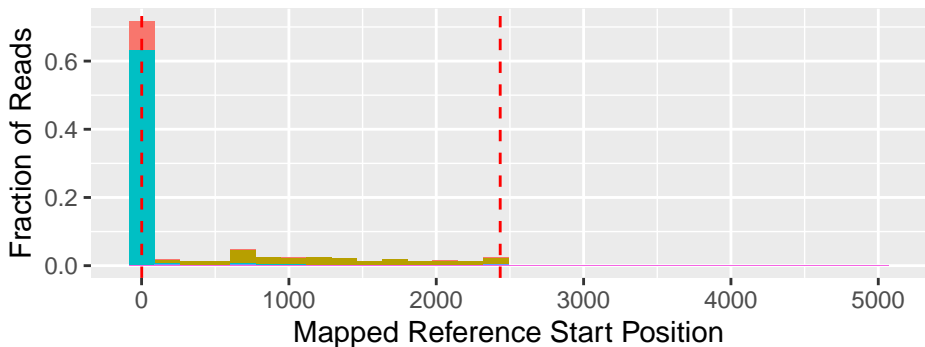
### Distribution of read length, scAAV, by subtype



### Distribution of read length, ssAAV, by subtype



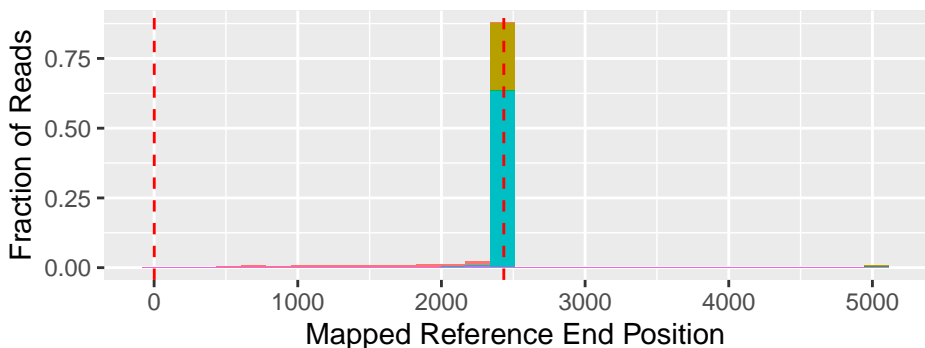
### Distribution of Mapped Reference Start Position



map\_subtype



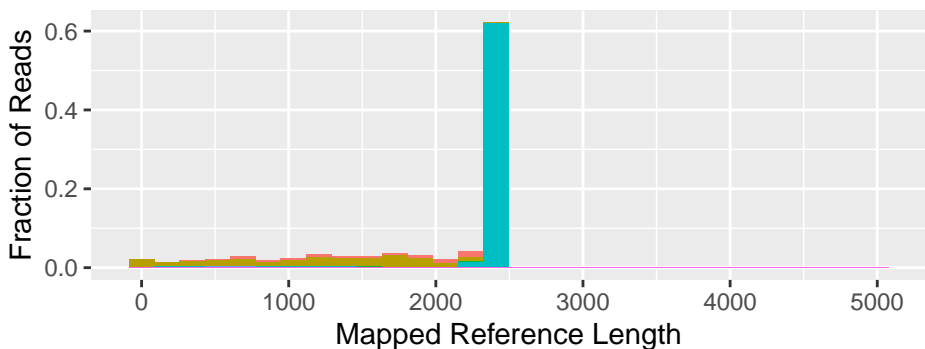
### Distribution of Mapped Reference End Position



map\_subtype



### Distribution of Mapped Reference Spanning Region Size

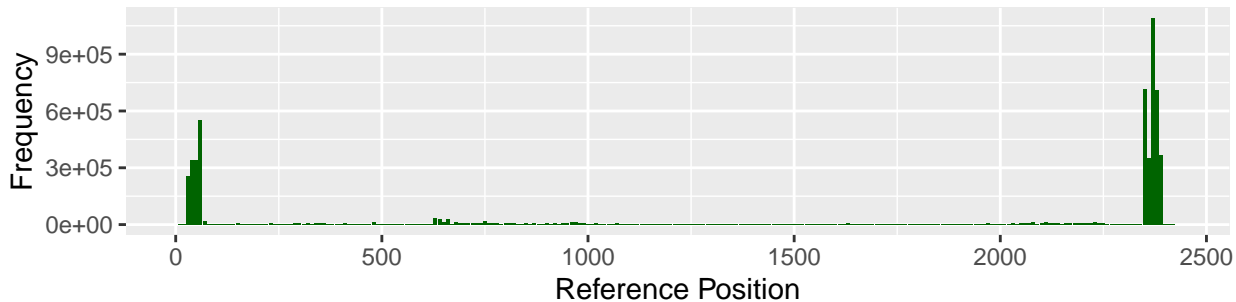


map\_subtype



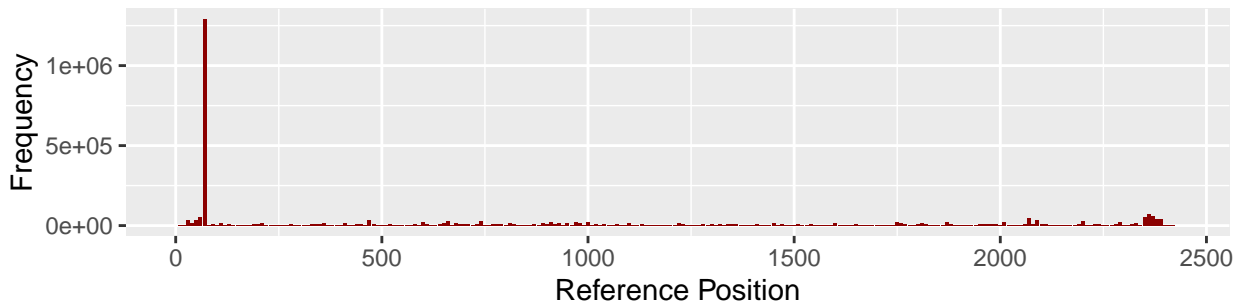
## Distribution of Non-matches by Reference Position, Substitutions

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



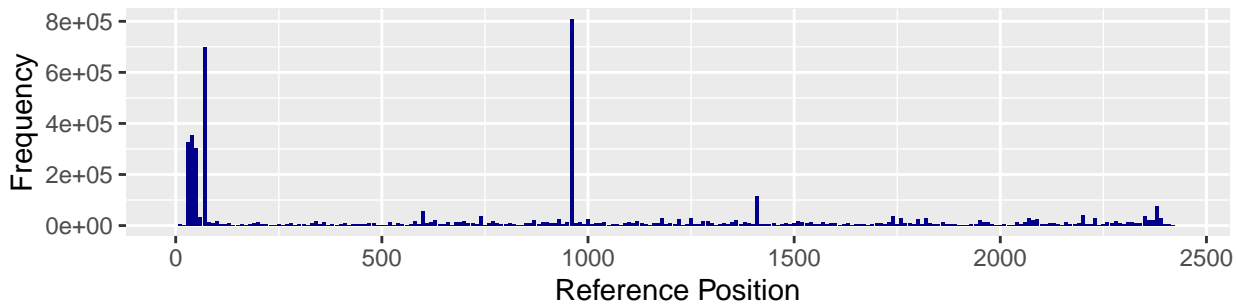
## Distribution of Non-matches by Reference Position, Deletions

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

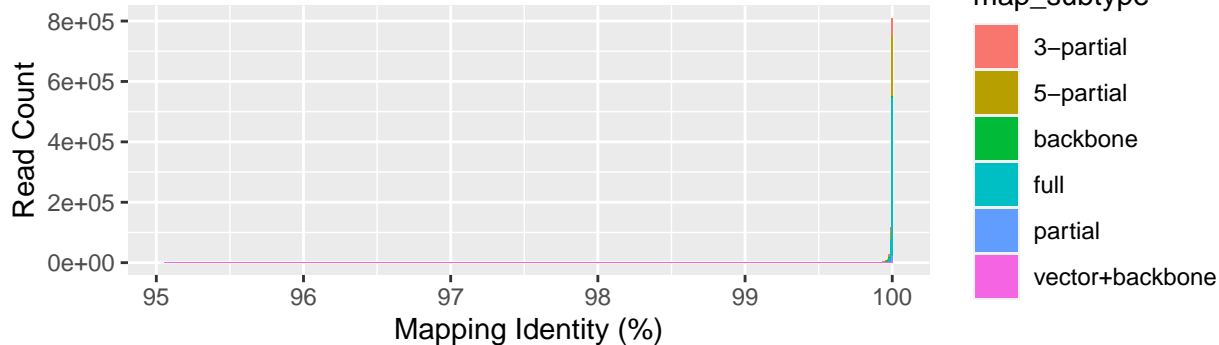


## Distribution of Non-matches by Reference Position, Insertions

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

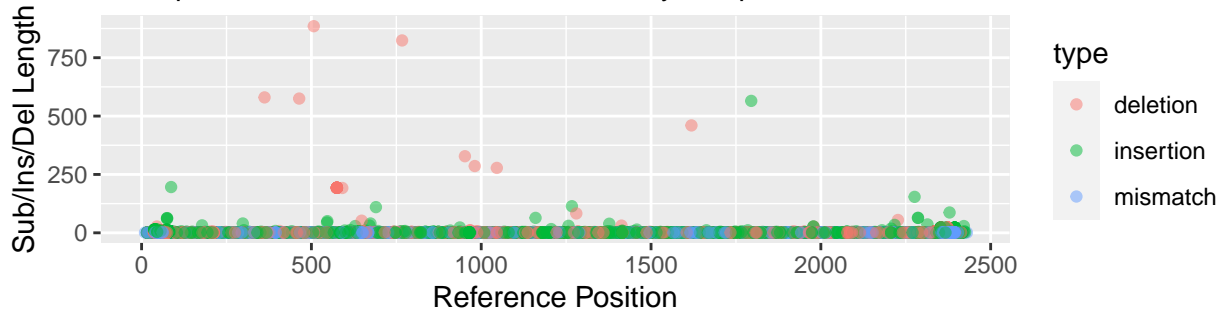


## Distribution of Mapped Identity to Reference



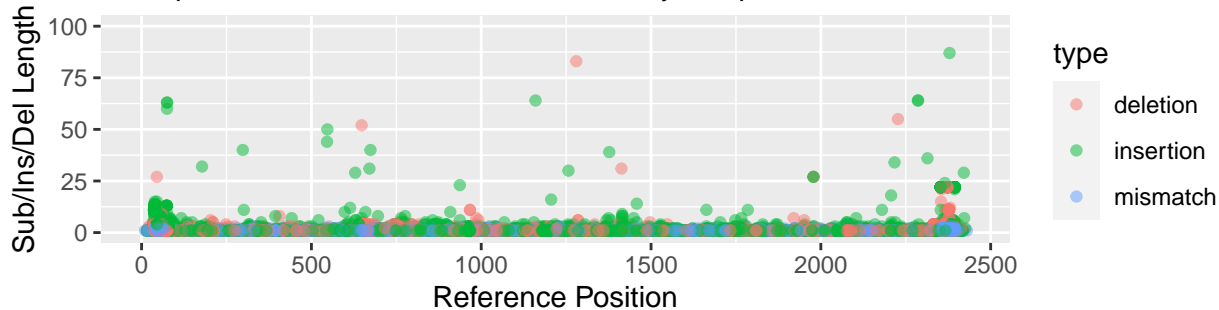
## Distribution of Non-Matches

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*

<b>Err Type</b>	<b>Err Length</b>	<b>Count</b>	<b>Frequency (%)</b>
deletion	1-10	3321751	23.23
deletion	11-100	35725	0.25
deletion	100-500	3635	0.03
deletion	>500	890	0.01
insertion	1-10	4801393	33.57
insertion	11-100	284907	1.99
insertion	100-500	1540	0.01
insertion	>500	233	0.00
mismatch	1-10	5850966	40.91
mismatch	11-100	1	0.00