

Sample	number of trimmed reads*	unique sequences within sample**	unique sequences among duplicates***
RH89-a	6280	2371	
RH89-b	3804	1620	572
sh83-a	3330	1443	
sh83-b	5147	2035	511
average	4640	1867	

* UID and NBS are trimmed at 5' side, successive 100nt are retained, 3' remaining sequence is discarded

** Sequences occurring at least once among trimmed reads

*** Sequences occurring at least once in both samples