

DNA160609__spike__only__contamination

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Overview

In the control batch DNA160609LC, samples 1-20 contain only spike-ins and primers (no DNA). During our pipeline, we run a spike removal tool that searches for a 9-bp barcode within fastq reads and removes those reads. After running this program on the spike-only samples, we still have reads in these samples.

We need to find out what proportion of total reads are not spikes, as well as what the source of these reads are. One likely cause is from the p14 DNA that contaminated the batch. They could also be spikes that were not removed in the spike removal step.

Set up

We need the PEAR'ed fastq files for samples 1-20. These will act as the baseline counts for each sample. The despiked fastq files produced by the spike removal tool will be our comparison counts. Lastly, we'll need the exported alignment files in order to determine p14 contamination.

Analysis

Using these files, we'll determine

1. The proportion of reads that aren't spikes
2. The proportion of non-spiked reads that are from p14
3. The proportion of reads that aren't spikes, but also are not p14 (unaccounted reads)

```
## [1] 0.8684770 0.7461521 0.6332091 0.5951745 0.5924477 0.6092125 0.5999344
## [8] 0.4702209 0.5948057 0.5691646 0.5466388 0.5635463 0.6388492 0.7837993
## [15] 0.6802170 0.7016472 0.7637548 0.6541527 0.6115455 0.5104863
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.4702  0.5866  0.6104  0.6367  0.6856  0.8685
```

```
## [1] 0.016775709 0.011079105 0.018254838 0.015337423 0.011680878
## [6] 0.014916468 0.011623852 0.011407712 0.012655024 0.016294606
## [11] 0.009543806 0.017550018 0.020370748 0.025094103 0.015885624
## [16] 0.019884669 0.016708438 0.022603978 0.016747613
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.009544 0.012170 0.016290 0.016020 0.017900 0.025090
```

Only a small percentage of the total reads are not the spike-ins (less than 1%). Of these non-spike reads, a small amount are accounted for by the p14 contamination, with the rest of unknown origin.

```
## [1] 0.8683313 0.7460694 0.6330936 0.5950832 0.5923785 0.6091216 0.5998647
## [8] 0.4701673 0.5947305 0.5690718 0.5465866 0.5634474 0.6387190 0.7836026
## [15] 0.6801089 0.7015077 0.6540434 0.6114073 0.5104008
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	0.4702	0.5807	0.6091	0.6299	0.6671	0.8683

Removing p14 contamination doesn't significantly change the proportion of contaminated reads. Are there any primer combinations that stand out as being overrepresented?

##	sample	total.count	Best V hit	Best J hit	N	proportion
## 1:	1	5531	V13-3	J2-4	246	4.447659
## 2:	1	5531	V20	J2-1	231	4.176460
## 3:	1	5531	V13-1	J1-6	93	1.681432
## 4:	1	5531	V24	J1-6	84	1.518713
## 5:	1	5531	V13-2	J2-1	83	1.500633
## 6:	2	8311	V13-3	J2-4	321	3.862351
## 7:	2	8311	V20	J2-1	256	3.080255
## 8:	2	8311	V12-1	J1-2	136	1.636386
## 9:	2	8311	V13-1	J2-4	122	1.467934
## 10:	2	8311	V13-3	J2-5	121	1.455902
## 11:	3	4968	V13-1	J2-1	76	1.529791
## 12:	3	4968	V13-1	J2-5	75	1.509662
## 13:	3	4968	V20	J2-1	75	1.509662
## 14:	3	4968	V13-1	J2-4	75	1.509662
## 15:	3	4968	V1	J1-2	68	1.368760
## 16:	4	5702	V1	J1-2	110	1.929148
## 17:	4	5702	V13-3	J2-4	106	1.858997
## 18:	4	5702	V12-1	J1-2	98	1.718695
## 19:	4	5702	V13-1	J2-1	91	1.595931
## 20:	4	5702	V13-1	J2-5	85	1.490705
## 21:	5	7844	V20	J2-1	127	1.619072
## 22:	5	7844	V12-1	J1-2	120	1.529832
## 23:	5	7844	V1	J1-2	111	1.415094
## 24:	5	7844	V13-1	J2-1	103	1.313106
## 25:	5	7844	V13-2	J2-2	99	1.262111
## 26:	6	6250	V12-1	J1-2	101	1.616000
## 27:	6	6250	V20	J2-1	94	1.504000
## 28:	6	6250	V13-1	J2-3	92	1.472000
## 29:	6	6250	V13-1	J1-6	92	1.472000
## 30:	6	6250	V13-3	J2-4	89	1.424000
## 31:	7	7837	V13-3	J2-4	170	2.169197
## 32:	7	7837	V12-1	J1-2	129	1.646038
## 33:	7	7837	V13-1	J2-4	120	1.531198
## 34:	7	7837	V1	J1-2	116	1.480158
## 35:	7	7837	V20	J2-1	114	1.454638
## 36:	8	7887	V12-1	J1-2	134	1.698998
## 37:	8	7887	V1	J1-2	123	1.559528
## 38:	8	7887	V13-3	J2-4	122	1.546849
## 39:	8	7887	V13-1	J2-3	115	1.458096
## 40:	8	7887	V13-1	J2-4	113	1.432737
## 41:	9	6939	V13-3	J2-4	216	3.112840
## 42:	9	6939	V1	J1-2	137	1.974348
## 43:	9	6939	V13-1	J2-4	127	1.830235
## 44:	9	6939	V13-1	J2-3	114	1.642888
## 45:	9	6939	V13-1	J2-1	114	1.642888
## 46:	10	5617	V13-3	J2-4	183	3.257967
## 47:	10	5617	V13-1	J2-1	84	1.495460

## 48:	10	5617	V13-1	J2-4	82	1.459854
## 49:	10	5617	V13-1	J1-6	80	1.424248
## 50:	10	5617	V24	J1-6	77	1.370839
## 51:	11	9475	V13-3	J2-4	248	2.617414
## 52:	11	9475	V12-1	J1-2	163	1.720317
## 53:	11	9475	V13-1	J2-5	150	1.583113
## 54:	11	9475	V1	J1-2	139	1.467018
## 55:	11	9475	V13-1	J2-1	134	1.414248
## 56:	12	5095	V13-3	J2-4	144	2.826300
## 57:	12	5095	V12-1	J1-2	88	1.727184
## 58:	12	5095	V13-1	J2-4	80	1.570167
## 59:	12	5095	V13-1	J2-1	76	1.491658
## 60:	12	5095	V13-2	J1-6	74	1.452404
## 61:	13	4434	V20	J2-1	169	3.811457
## 62:	13	4434	V13-3	J2-4	82	1.849346
## 63:	13	4434	V13-1	J2-5	74	1.668922
## 64:	13	4434	V1	J1-2	72	1.623816
## 65:	13	4434	V13-1	J2-4	69	1.556157
## 66:	14	3520	V13-3	J2-4	93	2.642045
## 67:	14	3520	V20	J2-1	77	2.187500
## 68:	14	3520	V12-1	J1-2	67	1.903409
## 69:	14	3520	V13-1	J2-1	58	1.647727
## 70:	14	3520	V13-1	J2-5	49	1.392045
## 71:	15	5723	V13-3	J2-4	123	2.149222
## 72:	15	5723	V12-1	J1-2	97	1.694915
## 73:	15	5723	V20	J2-1	96	1.677442
## 74:	15	5723	V13-1	J2-1	82	1.432815
## 75:	15	5723	V13-1	J2-3	81	1.415342
## 76:	16	4628	V1	J1-2	82	1.771824
## 77:	16	4628	V20	J2-1	79	1.707001
## 78:	16	4628	V13-1	J2-4	77	1.663786
## 79:	16	4628	V12-1	J1-2	63	1.361279
## 80:	16	4628	V13-3	J2-4	63	1.361279
## 81:	18	5479	V13-3	J2-4	84	1.533126
## 82:	18	5479	V12-1	J1-2	84	1.533126
## 83:	18	5479	V20	J2-1	80	1.460120
## 84:	18	5479	V13-1	J2-4	79	1.441869
## 85:	18	5479	V1	J1-2	77	1.405366
## 86:	19	3968	V13-3	J2-4	73	1.839718
## 87:	19	3968	V13-1	J2-1	69	1.738911
## 88:	19	3968	V1	J1-2	69	1.738911
## 89:	19	3968	V20	J2-1	54	1.360887
## 90:	19	3968	V13-1	J1-6	53	1.335685
## 91:	20	5307	V13-3	J2-4	129	2.430752
## 92:	20	5307	V13-1	J2-4	96	1.808932
## 93:	20	5307	V1	J1-2	87	1.639344
## 94:	20	5307	V13-1	J2-1	85	1.601658
## 95:	20	5307	V12-1	J1-2	79	1.488600
##	sample total.count	Best V hit	Best J hit	N	proportion	

None of the primer combinations have particularly high proportions. One thing of note, however, is that V13-1, V13-2, and V13-3 seem to appear often. We can group by V's instead of V/J and see if any particular V's are messing things up.

##	sample	total.count	Best V hit	N	proportion
## 1:	1	5531	V13-3	591	10.685229
## 2:	1	5531	V13-1	533	9.636594
## 3:	1	5531	V24	482	8.714518
## 4:	1	5531	V13-2	438	7.919002
## 5:	1	5531	V1	375	6.779967
## 6:	2	8311	V13-1	871	10.480087
## 7:	2	8311	V13-3	831	9.998797
## 8:	2	8311	V24	725	8.723379
## 9:	2	8311	V13-2	652	7.845025
## 10:	2	8311	V1	610	7.339670
## 11:	3	4968	V13-1	543	10.929952
## 12:	3	4968	V24	443	8.917069
## 13:	3	4968	V13-2	432	8.695652
## 14:	3	4968	V1	408	8.212560
## 15:	3	4968	V13-3	351	7.065217
## 16:	4	5702	V13-1	640	11.224132
## 17:	4	5702	V24	508	8.909155
## 18:	4	5702	V1	499	8.751315
## 19:	4	5702	V13-2	470	8.242722
## 20:	4	5702	V13-3	427	7.488600
## 21:	5	7844	V13-1	788	10.045895
## 22:	5	7844	V24	673	8.579806
## 23:	5	7844	V13-2	641	8.171851
## 24:	5	7844	V1	635	8.095360
## 25:	5	7844	V12-1	534	6.807751
## 26:	6	6250	V13-1	672	10.752000
## 27:	6	6250	V24	590	9.440000
## 28:	6	6250	V1	516	8.256000
## 29:	6	6250	V13-2	497	7.952000
## 30:	6	6250	V13-3	409	6.544000
## 31:	7	7837	V13-1	836	10.667347
## 32:	7	7837	V1	664	8.472630
## 33:	7	7837	V24	638	8.140870
## 34:	7	7837	V13-3	621	7.923950
## 35:	7	7837	V13-2	608	7.758071
## 36:	8	7887	V13-1	877	11.119564
## 37:	8	7887	V13-2	661	8.380880
## 38:	8	7887	V24	659	8.355522
## 39:	8	7887	V1	643	8.152656
## 40:	8	7887	V13-3	537	6.808672
## 41:	9	6939	V13-1	887	12.782822
## 42:	9	6939	V1	682	9.828506
## 43:	9	6939	V13-3	674	9.713215
## 44:	9	6939	V13-2	595	8.574723
## 45:	9	6939	V24	557	8.027093
## 46:	10	5617	V13-1	629	11.198148
## 47:	10	5617	V13-3	529	9.417839
## 48:	10	5617	V24	496	8.830336
## 49:	10	5617	V13-2	479	8.527684
## 50:	10	5617	V1	458	8.153819
## 51:	11	9475	V13-1	1061	11.197889
## 52:	11	9475	V13-3	823	8.686016
## 53:	11	9475	V13-2	812	8.569921

## 54:	11	9475	V1	785	8.284960
## 55:	11	9475	V24	773	8.158311
## 56:	12	5095	V13-1	597	11.717370
## 57:	12	5095	V13-3	477	9.362120
## 58:	12	5095	V24	439	8.616290
## 59:	12	5095	V13-2	424	8.321884
## 60:	12	5095	V1	415	8.145240
## 61:	13	4434	V13-1	511	11.524583
## 62:	13	4434	V1	412	9.291836
## 63:	13	4434	V13-2	361	8.141633
## 64:	13	4434	V13-3	354	7.983762
## 65:	13	4434	V24	345	7.780785
## 66:	14	3520	V13-1	403	11.448864
## 67:	14	3520	V24	308	8.750000
## 68:	14	3520	V13-2	307	8.721591
## 69:	14	3520	V13-3	305	8.664773
## 70:	14	3520	V1	287	8.153409
## 71:	15	5723	V13-1	636	11.113053
## 72:	15	5723	V13-2	493	8.614363
## 73:	15	5723	V24	443	7.740695
## 74:	15	5723	V13-3	441	7.705749
## 75:	15	5723	V1	412	7.199021
## 76:	16	4628	V13-1	483	10.436474
## 77:	16	4628	V24	403	8.707865
## 78:	16	4628	V1	377	8.146067
## 79:	16	4628	V13-2	369	7.973207
## 80:	16	4628	V12-1	311	6.719965
## 81:	18	5479	V13-1	596	10.877897
## 82:	18	5479	V1	474	8.651214
## 83:	18	5479	V24	469	8.559956
## 84:	18	5479	V13-2	451	8.231429
## 85:	18	5479	V13-3	368	6.716554
## 86:	19	3968	V13-1	428	10.786290
## 87:	19	3968	V1	363	9.148185
## 88:	19	3968	V13-2	337	8.492944
## 89:	19	3968	V24	313	7.888105
## 90:	19	3968	V13-3	293	7.384073
## 91:	20	5307	V13-1	627	11.814585
## 92:	20	5307	V13-3	450	8.479367
## 93:	20	5307	V1	447	8.422838
## 94:	20	5307	V24	435	8.196721
## 95:	20	5307	V13-2	432	8.140192
##	sample total.count Best V hit N proportion				

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	41.70	42.95	43.82	44.20	44.98	48.93

##	Best V hit N	
## 1:	V13-3	17
## 2:	V13-1	19
## 3:	V24	19
## 4:	V13-2	19
## 5:	V1	19
## 6:	V12-1	2

The same 5 V's are almost always the top 5, and they generally make up about 43.8204509 percent of all of the reads. Is this the same in the spike count files?

```
##      V4  N
## 1: V13-1 19
## 2:   V1 19
## 3:  V29 19
## 4:  V24 19
## 5:  V23 16
## 6: V13-2  3
```

The unique V's that are in the top 5 in at least one sample are not the same between the left-over reads and the spiked reads, although 3 of them are the same. In fact, V13-1, V1, and V24 are in the top 5 in all samples. Let's try and see if they're primer-dimers or some chimeric read caused by mis-amplification. Process:

1. For each entry in an alignment file, extract the V and J hits
2. Use V and J to extract appropriate 34-bp synthetic template from spike file
3. Divide synthetic template into 6 9-bp strings ([1:9], [5:14], [10:19], [15:24], [20:29], [25:34])
4. Search the fastq read of the alignment entry for these strings
5. Observe distribution of hits

```
# Each entry in the align file has a V and J as well as a sequence.
# Can take the V and J identities and search for them in the spike file.
# Then take the spike sequence from the spike file.
# Split into a few substrings (first try strings of length 9, every 5)
# Use vcountPattern to check if they're there.
spikes <- read.table("~/Desktop/OHSU/tcr_spike/text_barcode.vj.txt", header = T, sep = ' ',
                    stringsAsFactors = F)
spikes.v122 <- spikes[spikes$V == "V12-1-2-",]
spikes.v122$V <- gsub("V12-1-2-", "V12-2", spikes.v122$V)
spikes$V <- gsub("V12-1-2-", "V12-1", spikes$V)
spikes$V <- gsub("-$", "", spikes$V)

test <- list()
for (i in 1:length(align.files)){
  curr.align <- suppressWarnings(fread(paste(align.dir, align.files[i], sep = ''), na.strings = c('', ' ',
                                                showProgress = F))
  curr.align$`Best V hit` <- gsub("TRB|\\*00", '', curr.align$`Best V hit`)
  curr.align$`Best J hit` <- gsub("TRB|\\*00", '', curr.align$`Best J hit`)
  index <- gsub(".*_S|_align.*", '', align.files[i])
  align.query.results <- NULL
  for (j in 1:length(curr.align$`Read(s) sequence`)){
    V <- curr.align$`Best V hit`[j]
    J <- curr.align$`Best J hit`[j]
    if (V %in% spikes$V && J %in% spikes$J){
      fastq.read <- curr.align$`Read(s) sequence`[j]
      query <- spikes[spikes$V == V & spikes$J == J, "SPIKE"]
      query <- unlist(strsplit(query, split = ''))
      sub.query <- c(paste(query[1:9], collapse = ''), paste(query[5:14], collapse = ''),
                    paste(query[10:19], collapse = ''), paste(query[15:24], collapse = ''),
                    paste(query[20:29], collapse = ''), paste(query[25:34], collapse = ''))
      query.results <- vector(mode = "numeric", length = 6)
      for (k in 1:length(sub.query)){
```

```

    query.results[k] <- vcountPattern(sub.query[k], fastq.read)
  } # for k
  align.query.results <- rbind(align.query.results, query.results)
} # if
} # for j
test[[i]] <- align.query.results
} # for i

# Now we have a list containing 19 data frames with nrow = number of alignments and ncol = 6 (one for e
# For each list, take the row sum and add it as a column
for (i in 1:length(test)){
  test[[i]] <- data.table(test[[i]])
  test[[i]]$sum <- apply(test[[i]], 1, sum)
}

results <- matrix(nrow = length(test), ncol = 9)
for (i in 1:length(test)){
  pass.4 <- length(test[[i]][test[[i]]$sum >= 4, `sum`])
  pass.3 <- length(test[[i]][test[[i]]$sum >= 3, `sum`])
  pass.2 <- length(test[[i]][test[[i]]$sum >= 2, `sum`])
  pass.1 <- length(test[[i]][test[[i]]$sum >= 1, `sum`])
  total <- length(test[[i]][, `sum`])
  proportion.4 <- round(pass.4 / total * 100, digits = 2)
  proportion.3 <- round(pass.3 / total * 100, digits = 2)
  proportion.2 <- round(pass.2 / total * 100, digits = 2)
  proportion.1 <- round(pass.1 / total * 100, digits = 2)
  new.row <- c(total, pass.4, proportion.4, pass.3, proportion.3, pass.2, proportion.2, pass.1, proportion.1)
  results[i,] <- new.row
}
colnames(results) <- c("total.reads", "Reads.4.hits", "Proportion.4", "Reads.3.hits",
                      "Proportion.3", "Reads.2.hits", "Proportion.2", "Reads.1.hit", "Proportion.1")
rownames(results) <- c(1:16, 18:20)
results

```

##	total.reads	Reads.4.hits	Proportion.4	Reads.3.hits	Proportion.3
## 1	5507	1154	20.96	1668	30.29
## 2	8278	1974	23.85	2782	33.61
## 3	4955	1452	29.30	2033	41.03
## 4	5680	1622	28.56	2333	41.07
## 5	7831	2227	28.44	3222	41.14
## 6	6235	1674	26.85	2441	39.15
## 7	7809	2189	28.03	3064	39.24
## 8	7867	2509	31.89	3494	44.41
## 9	6908	1880	27.21	2634	38.13
## 10	5604	1606	28.66	2254	40.22
## 11	9451	2838	30.03	3949	41.78
## 12	5080	1505	29.63	2101	41.36
## 13	4412	1131	25.63	1618	36.67
## 14	3503	870	24.84	1227	35.03
## 15	5715	1609	28.15	2261	39.56
## 16	4623	1278	27.64	1818	39.33
## 18	5465	1540	28.18	2237	40.93
## 19	3956	1212	30.64	1673	42.29

## 20	5296	1607	30.34	2254	42.56
##	Reads.2.hits	Proportion.2	Reads.1.hit	Proportion.1	
## 1	2239	40.66	2688	48.81	
## 2	3700	44.70	4442	53.66	
## 3	2644	53.36	3108	62.72	
## 4	3100	54.58	3707	65.26	
## 5	4201	53.65	4968	63.44	
## 6	3188	51.13	3779	60.61	
## 7	3999	51.21	4753	60.87	
## 8	4516	57.40	5307	67.46	
## 9	3466	50.17	4129	59.77	
## 10	2929	52.27	3445	61.47	
## 11	5075	53.70	6010	63.59	
## 12	2671	52.58	3109	61.20	
## 13	2113	47.89	2549	57.77	
## 14	1569	44.79	1885	53.81	
## 15	2967	51.92	3507	61.36	
## 16	2417	52.28	2892	62.56	
## 18	2860	52.33	3439	62.93	
## 19	2176	55.01	2554	64.56	
## 20	2959	55.87	3488	65.86	

Using this method, it looks like 50-60 percent of the reads are some version of spikes. One suggestion from this is to incorporate the secondary barcode from the spike file during our spike removal step. A spike sequence is 34-bp long, the first 9 are a universal spike barcode, the last 9 are a different universal barcode, and the remaining 16 are unique identifiers for each individual spike.

Currently, we identify spikes for removal using the first 9-bp sequence only. We could potentially use both the first and the second 9-bp sequences to remove spikes.