

COVID-19 subject 437

2021-04-30

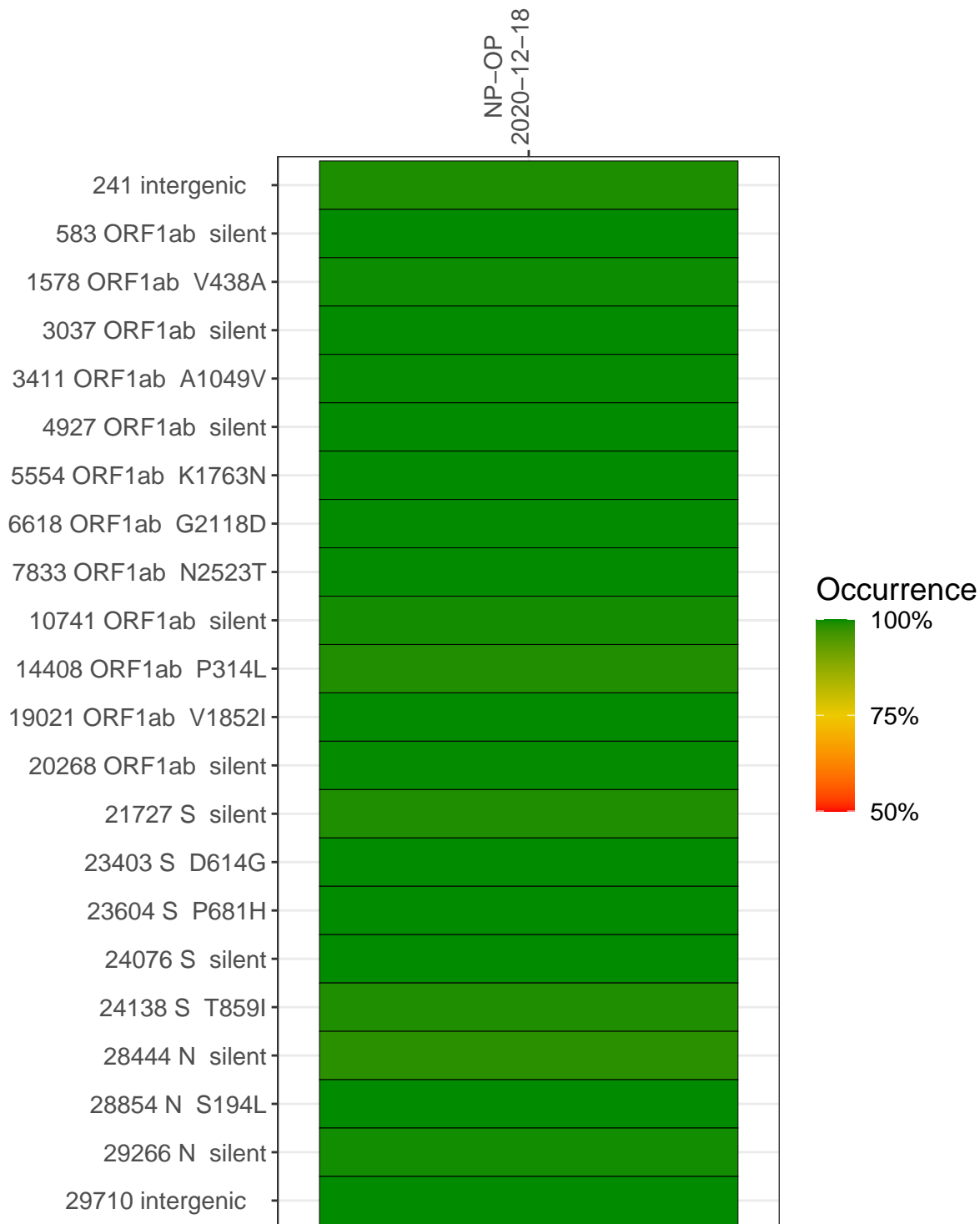
The table below provides a summary of subject samples for which sequencing data is available. The experiments column shows the number of sequencing experiments performed for each specimen. Experiment specific analyses are shown at the end of this report. Lineages are called with the Pangolin software tool (Rambaut et al 2020) for genomes with $> 90\%$ sequence coverage.

Table 1. Sample summary.

Experiment	Type	Genomes	Sample type	Sample date	Largest contig (KD)	Lineage	Reference read coverage	Reference read coverage (≥ 5 reads)
VSP0560	composite	NA	NP-OP	2020-12-18	28.05	B.1.243	99.9%	99.8%
VSP0560-1	single experiment	NA	NP-OP	2020-12-18	29.87	B.1.243	99.9%	99.8%
VSP0560-2	single experiment	NA	NP-OP	2020-12-18	15.09	B.1.243	99.7%	99.7%

Variants shared across samples

The heat map below shows how variants (reference genome /home/everett/projects/SARS-CoV-2-Philadelphia/Wuhan-Hu-1) are shared across subject samples where the percent variance is colored. Variants are called if a variant position is covered by 5 or more reads, the alternative base is found in > 50% of read pairs and the variant yields a PHRED score > 20. Gray tiles denote positions where the variant was not the major variant or no variants were found. The relative base compositions of each experiment used to calculate tiles are shown in the following plot where the total number of position reads are shown atop of each plot.



NP-OP
2020-12-18

interj6N 1 N 4 N 3 S 6 S 7 S 8 S 9 S 10 S 11 S 12 S 13 S 14 S 15 S 16 S 17 S 18 S 19 S 20 S 21 S 22 S 23 S 24 S 25 S 26 S 27 S 28 S 29 S 30 S 31 S 32 S 33 S 34 S 35 S 36 S 37 S 38 S 39 S 40 S 41 S 42 S 43 S 44 S 45 S 46 S 47 S 48 S 49 S 50 S 51 S 52 S 53 S 54 S 55 S 56 S 57 S 58 S 59 S 60 S 61 S 62 S 63 S 64 S 65 S 66 S 67 S 68 S 69 S 70 S 71 S 72 S 73 S 74 S 75 S 76 S 77 S 78 S 79 S 80 S 81 S 82 S 83 S 84 S 85 S 86 S 87 S 88 S 89 S 90 S 91 S 92 S 93 S 94 S 95 S 96 S 97 S 98 S 99 S 100 S 101 S 102 S 103 S 104 S 105 S 106 S 107 S 108 S 109 S 110 S 111 S 112 S 113 S 114 S 115 S 116 S 117 S 118 S 119 S 120 S 121 S 122 S 123 S 124 S 125 S 126 S 127 S 128 S 129 S 130 S 131 S 132 S 133 S 134 S 135 S 136 S 137 S 138 S 139 S 140 S 141 S 142 S 143 S 144 S 145 S 146 S 147 S 148 S 149 S 150 S 151 S 152 S 153 S 154 S 155 S 156 S 157 S 158 S 159 S 160 S 161 S 162 S 163 S 164 S 165 S 166 S 167 S 168 S 169 S 170 S 171 S 172 S 173 S 174 S 175 S 176 S 177 S 178 S 179 S 180 S 181 S 182 S 183 S 184 S 185 S 186 S 187 S 188 S 189 S 190 S 191 S 192 S 193 S 194 S 195 S 196 S 197 S 198 S 199 S 200 S 201 S 202 S 203 S 204 S 205 S 206 S 207 S 208 S 209 S 210 S 211 S 212 S 213 S 214 S 215 S 216 S 217 S 218 S 219 S 220 S 221 S 222 S 223 S 224 S 225 S 226 S 227 S 228 S 229 S 230 S 231 S 232 S 233 S 234 S 235 S 236 S 237 S 238 S 239 S 240 S 241 S 242 S 243 S 244 S 245 S 246 S 247 S 248 S 249 S 250 S 251 S 252 S 253 S 254 S 255 S 256 S 257 S 258 S 259 S 260 S 261 S 262 S 263 S 264 S 265 S 266 S 267 S 268 S 269 S 270 S 271 S 272 S 273 S 274 S 275 S 276 S 277 S 278 S 279 S 280 S 281 S 282 S 283 S 284 S 285 S 286 S 287 S 288 S 289 S 290 S 291 S 292 S 293 S 294 S 295 S 296 S 297 S 298 S 299 S 300 S 301 S 302 S 303 S 304 S 305 S 306 S 307 S 308 S 309 S 310 S 311 S 312 S 313 S 314 S 315 S 316 S 317 S 318 S 319 S 320 S 321 S 322 S 323 S 324 S 325 S 326 S 327 S 328 S 329 S 330 S 331 S 332 S 333 S 334 S 335 S 336 S 337 S 338 S 339 S 340 S 341 S 342 S 343 S 344 S 345 S 346 S 347 S 348 S 349 S 350 S 351 S 352 S 353 S 354 S 355 S 356 S 357 S 358 S 359 S 360 S 361 S 362 S 363 S 364 S 365 S 366 S 367 S 368 S 369 S 370 S 371 S 372 S 373 S 374 S 375 S 376 S 377 S 378 S 379 S 380 S 381 S 382 S 383 S 384 S 385 S 386 S 387 S 388 S 389 S 390 S 391 S 392 S 393 S 394 S 395 S 396 S 397 S 398 S 399 S 400 S 401 S 402 S 403 S 404 S 405 S 406 S 407 S 408 S 409 S 410 S 411 S 412 S 413 S 414 S 415 S 416 S 417 S 418 S 419 S 420 S 421 S 422 S 423 S 424 S 425 S 426 S 427 S 428 S 429 S 430 S 431 S 432 S 433 S 434 S 435 S 436 S 437 S 438 S 439 S 440 S 441 S 442 S 443 S 444 S 445 S 446 S 447 S 448 S 449 S 450 S 451 S 452 S 453 S 454 S 455 S 456 S 457 S 458 S 459 S 460 S 461 S 462 S 463 S 464 S 465 S 466 S 467 S 468 S 469 S 470 S 471 S 472 S 473 S 474 S 475 S 476 S 477 S 478 S 479 S 480 S 481 S 482 S 483 S 484 S 485 S 486 S 487 S 488 S 489 S 490 S 491 S 492 S 493 S 494 S 495 S 496 S 497 S 498 S 499 S 500 S 501 S 502 S 503 S 504 S 505 S 506 S 507 S 508 S 509 S 510 S 511 S 512 S 513 S 514 S 515 S 516 S 517 S 518 S 519 S 520 S 521 S 522 S 523 S 524 S 525 S 526 S 527 S 528 S 529 S 530 S 531 S 532 S 533 S 534 S 535 S 536 S 537 S 538 S 539 S 540 S 541 S 542 S 543 S 544 S 545 S 546 S 547 S 548 S 549 S 550 S 551 S 552 S 553 S 554 S 555 S 556 S 557 S 558 S 559 S 560 S 561 S 562 S 563 S 564 S 565 S 566 S 567 S 568 S 569 S 570 S 571 S 572 S 573 S 574 S 575 S 576 S 577 S 578 S 579 S 580 S 581 S 582 S 583 S 584 S 585 S 586 S 587 S 588 S 589 S 590 S 591 S 592 S 593 S 594 S 595 S 596 S 597 S 598 S 599 S 600 S 601 S 602 S 603 S 604 S 605 S 606 S 607 S 608 S 609 S 610 S 611 S 612 S 613 S 614 S 615 S 616 S 617 S 618 S 619 S 620 S 621 S 622 S 623 S 624 S 625 S 626 S 627 S 628 S 629 S 630 S 631 S 632 S 633 S 634 S 635 S 636 S 637 S 638 S 639 S 640 S 641 S 642 S 643 S 644 S 645 S 646 S 647 S 648 S 649 S 650 S 651 S 652 S 653 S 654 S 655 S 656 S 657 S 658 S 659 S 660 S 661 S 662 S 663 S 664 S 665 S 666 S 667 S 668 S 669 S 670 S 671 S 672 S 673 S 674 S 675 S 676 S 677 S 678 S 679 S 680 S 681 S 682 S 683 S 684 S 685 S 686 S 687 S 688 S 689 S 690 S 691 S 692 S 693 S 694 S 695 S 696 S 697 S 698 S 699 S 700 S 701 S 702 S 703 S 704 S 705 S 706 S 707 S 708 S 709 S 710 S 711 S 712 S 713 S 714 S 715 S 716 S 717 S 718 S 719 S 720 S 721 S 722 S 723 S 724 S 725 S 726 S 727 S 728 S 729 S 730 S 731 S 732 S 733 S 734 S 735 S 736 S 737 S 738 S 739 S 740 S 741 S 742 S 743 S 744 S 745 S 746 S 747 S 748 S 749 S 750 S 751 S 752 S 753 S 754 S 755 S 756 S 757 S 758 S 759 S 760 S 761 S 762 S 763 S 764 S 765 S 766 S 767 S 768 S 769 S 770 S 771 S 772 S 773 S 774 S 775 S 776 S 777 S 778 S 779 S 780 S 781 S 782 S 783 S 784 S 785 S 786 S 787 S 788 S 789 S 790 S 791 S 792 S 793 S 794 S 795 S 796 S 797 S 798 S 799 S 800 S 801 S 802 S 803 S 804 S 805 S 806 S 807 S 808 S 809 S 810 S 811 S 812 S 813 S 814 S 815 S 816 S 817 S 818 S 819 S 820 S 821 S 822 S 823 S 824 S 825 S 826 S 827 S 828 S 829 S 830 S 831 S 832 S 833 S 834 S 835 S 836 S 837 S 838 S 839 S 840 S 841 S 842 S 843 S 844 S 845 S 846 S 847 S 848 S 849 S 850 S 851 S 852 S 853 S 854 S 855 S 856 S 857 S 858 S 859 S 860 S 861 S 862 S 863 S 864 S 865 S 866 S 867 S 868 S 869 S 870 S 871 S 872 S 873 S 874 S 875 S 876 S 877 S 878 S 879 S 880 S 881 S 882 S 883 S 884 S 885 S 886 S 887 S 888 S 889 S 890 S 891 S 892 S 893 S 894 S 895 S 896 S 897 S 898 S 899 S 900 S 901 S 902 S 903 S 904 S 905 S 906 S 907 S 908 S 909 S 910 S 911 S 912 S 913 S 914 S 915 S 916 S 917 S 918 S 919 S 920 S 921 S 922 S 923 S 924 S 925 S 926 S 927 S 928 S 929 S 930 S 931 S 932 S 933 S 934 S 935 S 936 S 937 S 938 S 939 S 940 S 941 S 942 S 943 S 944 S 945 S 946 S 947 S 948 S 949 S 950 S 951 S 952 S 953 S 954 S 955 S 956 S 957 S 958 S 959 S 960 S 961 S 962 S 963 S 964 S 965 S 966 S 967 S 968 S 969 S 970 S 971 S 972 S 973 S 974 S 975 S 976 S 977 S 978 S 979 S 980 S 981 S 982 S 983 S 984 S 985 S 986 S 987 S 988 S 989 S 990 S 991 S 992 S 993 S 994 S 995 S 996 S 997 S 998 S 999 S 1000 S

10010	4023
6449	2322
1523	517
6583	2438
9707	3422
12817	4833
6898	2330
8722	3589
12358	4416
6185	2127
15332	5351
12614	4576
1885	530
4778	1676
18984	6842
15563	5779
3446	1165
4906	1693
23936	7475
2675	931
9815	3305
1010	380

VSP0560-1

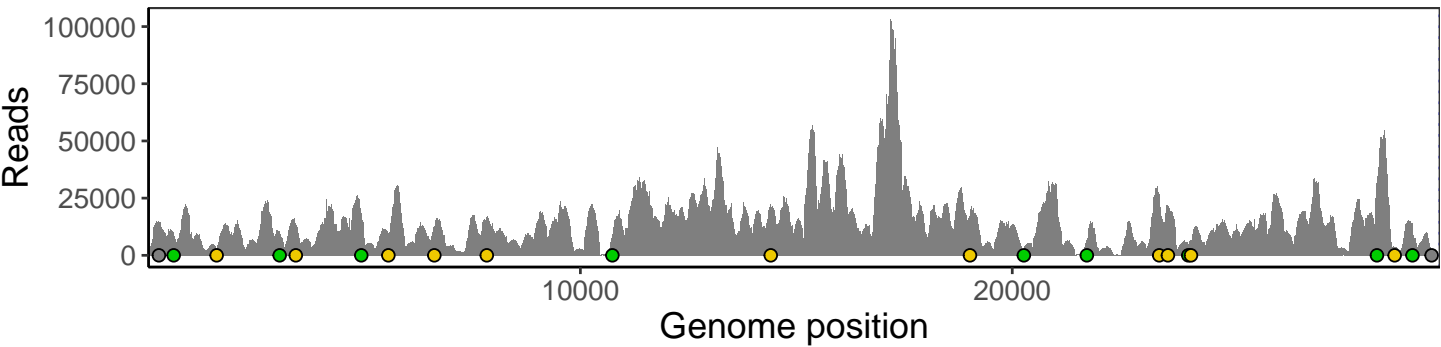
VSP0560-2



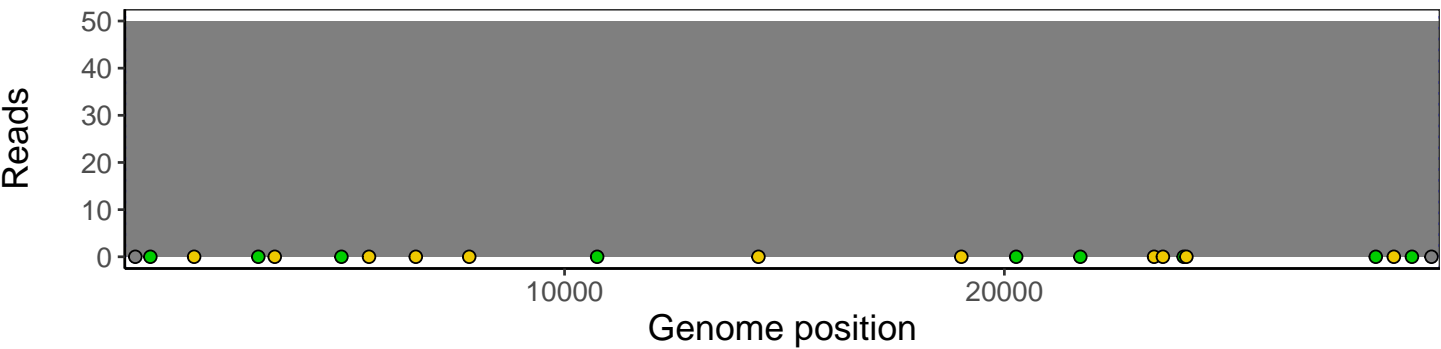
Analyses of individual experiments and composite results

VSP0560 | 2020-12-18 | NP-OP | 437no | composite result

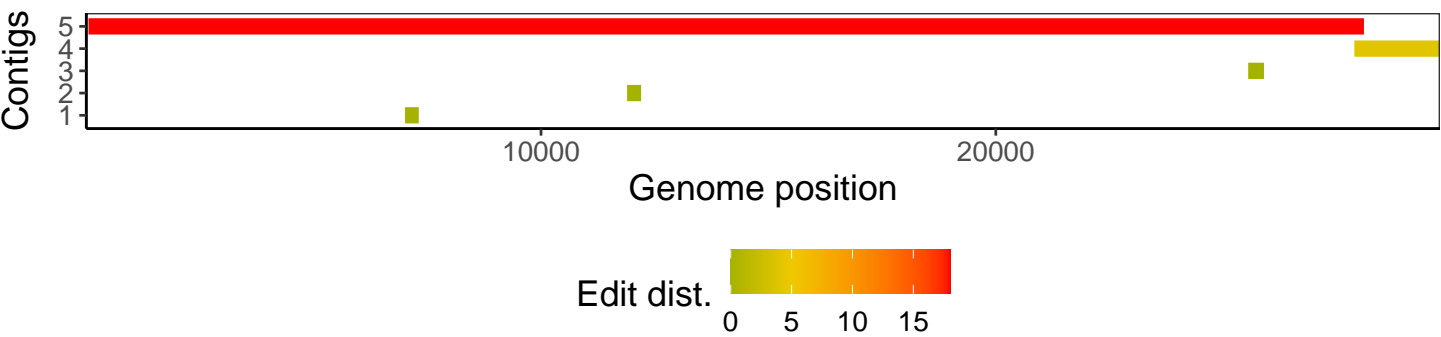
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according to variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



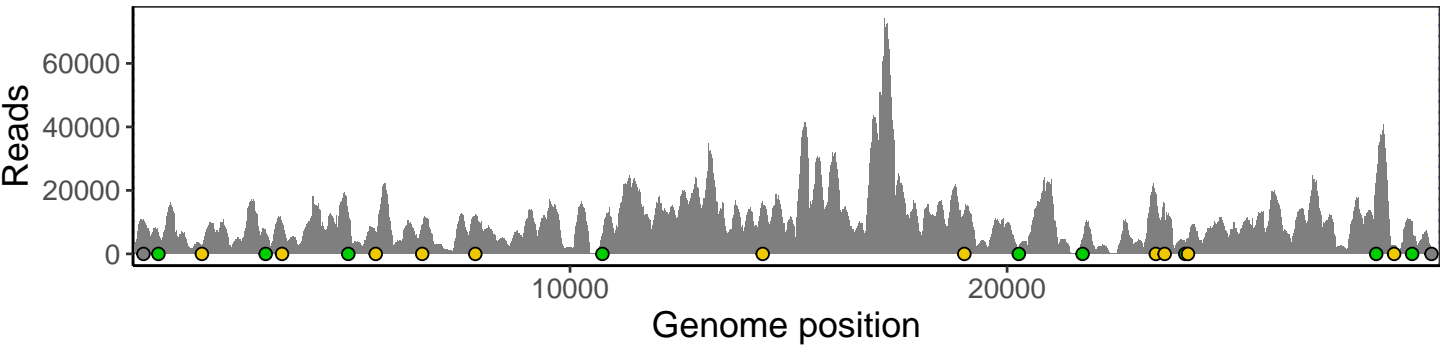
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



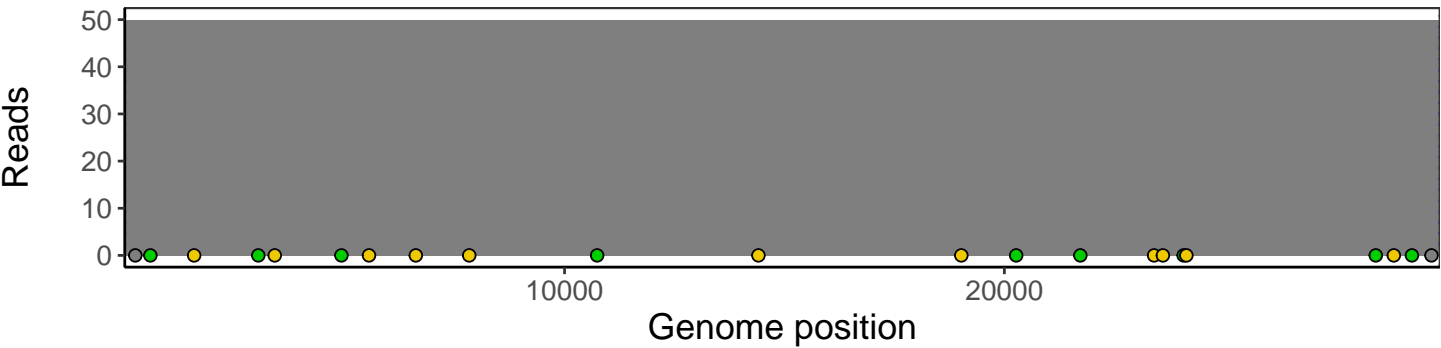
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



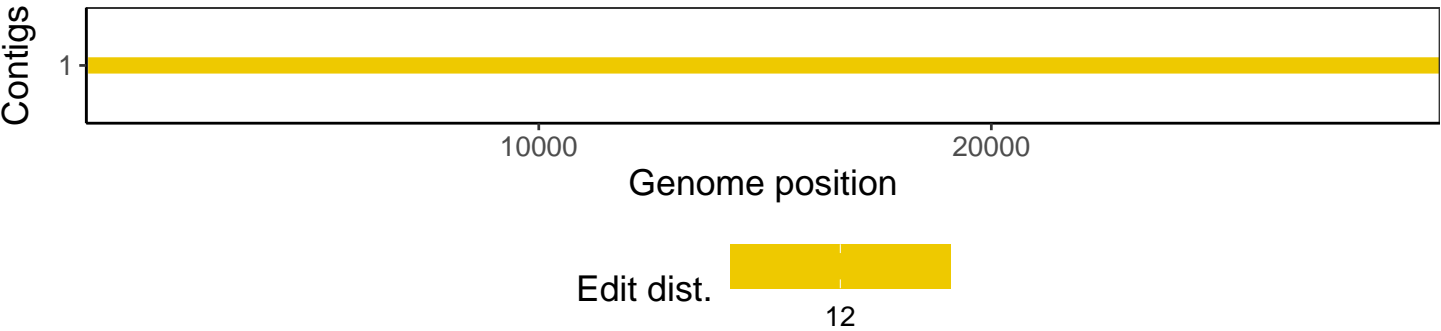
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



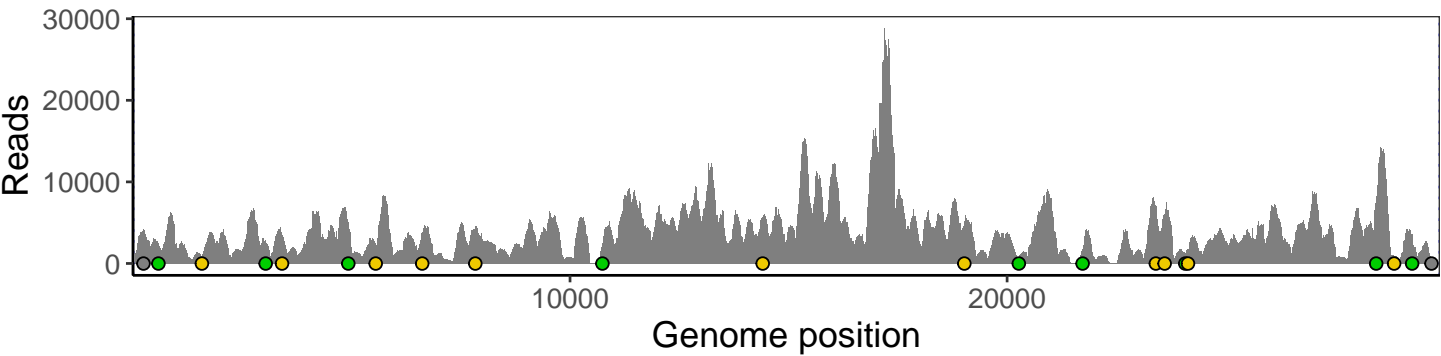
Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



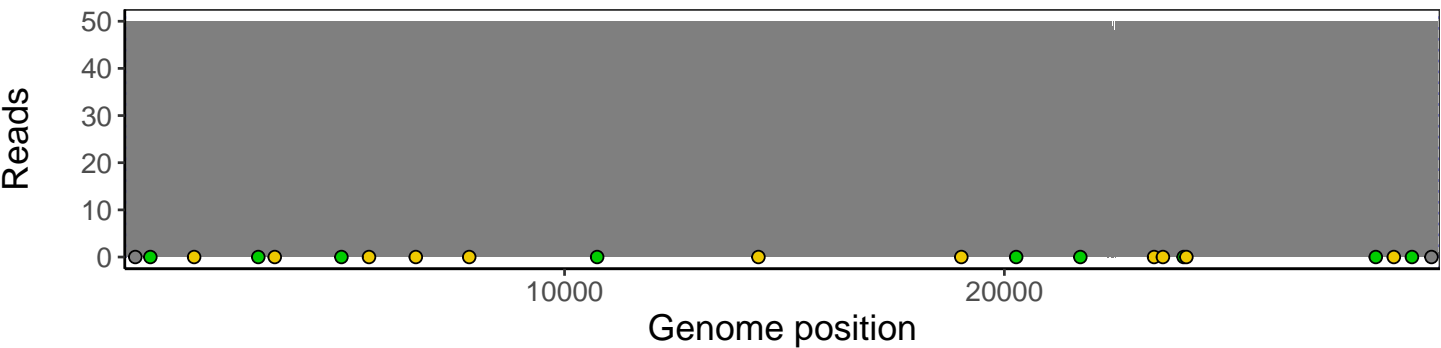
The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



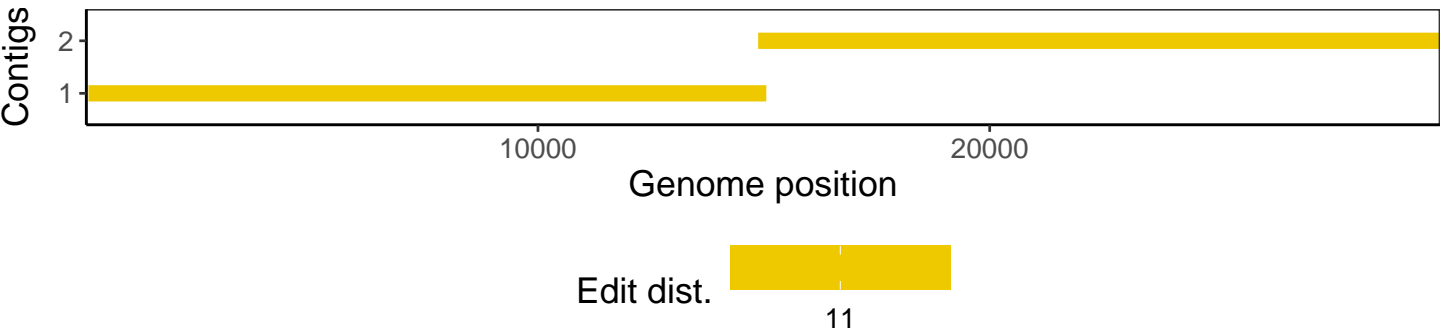
The plot below shows the number of reads covering each nucleotide position in the reference genome. Variants are shown as colored dots along the bottom of the plot and are color coded according by variant types: gray - transgenic, green - silent, gold - missense, red - nonsense, black - indel.



Excerpt from plot above focusing on reads coverage from 0 to 50 NT.



The longest five assembled contigs are shown below colored by their edit distance to the reference genome.



Software environment

Software/R package	Version
R	3.4.0
bwa	0.7.17-r1198-dirty
samtools	1.10 Using htlib 1.10
bcftools	1.10.2-34-g1a12af0-dirty Using htlib 1.10.2-57-gf58a6f3
pangolin	2.3.8
genbankr	1.4.0
optparse	1.6.0
forcats	0.3.0
stringr	1.4.0
dplyr	0.8.1
purrr	0.2.5
readr	1.1.1
tidyr	0.8.1
tibble	2.1.2
ggplot2	3.0.0
tidyverse	1.2.1
ShortRead	1.34.2
GenomicAlignments	1.12.2
SummarizedExperiment	1.6.5
DelayedArray	0.2.7
matrixStats	0.54.0
Biobase	2.36.2
Rsamtools	1.28.0
GenomicRanges	1.28.6
GenomeInfoDb	1.12.3
Biostrings	2.44.2
XVector	0.16.0
IRanges	2.10.5
S4Vectors	0.14.7
BiocParallel	1.10.1
BiocGenerics	0.22.1