1- Selection of reference sequences for the Zika analysis

KF383115.1
1
KF268948.1
1
KF268950.1
1
KF268949.1

East Africa

KF383118.1
1
KF383119.1
0,5
LC002520.1

West Africa

1
KF383116.1
1
HQ234501.1
0,744
KF383117.1
1
HQ234500.1

EU545988.1
1
JN860885.1
0,981
KF993678.1
1
KJ776791.2

KY317936.1
0,954
KY317939.1
0,901
KY317938.1
0,642
KY317940.1
1
KY317937.1
0,876
KU501215.1
0,472
KU321639.1
0,516
KU527068.1
0,708
KU853012.1
0,403
KU501216.1
1
KU501217.1

Asia

HQ234499.1

2.0

Phylogenetic tree obtained from the alignment of 27 Zika genomes. The studied genomes appears in a red box and the selected reference genomes in a green box.

Phylogenic tree was built with MEGA (option -a infer_NJ_nucleotide.mao) (Kumar et al., 2016) from the alignment of 27 Zika sequences with MAFFT (Katoh et al., 2002) . The phylogenetic tree picture was generated with figtree (http://tree.bio.ed.ac.uk/). Zika sequences were clustered depending to their location: Asia, east Africa and west africa. We selected 2 Asian sequences, 1 west African sequence and 1 east African sequence for the analysis.

Katoh, K., Misawa, K., Kuma, K., Miyata, T., 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 30, 3059–3066.

Kumar, S., Stecher, G., Tamura, K., 2016. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol. Biol. Evol. 33, 1870–1874. https://doi.org/10.1093/molbev/msw054

2- Primers used for amplification of long viral genome fragments

| RT-PCR number	Forward primer ID	Forward primer sequence	Reverse primer ID	Reverse primer sequence	Expected amplicon length (pb)	PCR extension time
a	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR01_R	CCAAAACTGCTTCACGGGAC	525	1 min
b	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR03_R	GCCATCTGCAAGACTACCAGT	1013	1 min 30
c	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR05_R	TGCTGGACTCCAATACACACA	1637	2 min
d	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR06_R	TGCTTGACCACTTACTGCCA	2012	2 min 30
e	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR08_R	TCACCAGCCTTGGCCATATAA	2695	3 min
f	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR09_R	AGGCACTAACTTTAGCACCTACA	3009	3 min 30
g	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR11_R	TGCAACACACTGCCAATCAC	3653	4 min
h	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR12_R	TGAAAATGACATACCATGCCCAA	3989	4 min 30
i	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR14_R	AAAGACGCGCTGCCAATTTC	4548	5 min
j	PCR01_F	ATTGTGAGCGATTTGCGTGC	PCR16_R	CCAAAACTTTCACCAACAGGCA	4975	5 min 30

Primers used for amplification of long viral genome fragments by testing RT-PCR amplifications of different lengths, from ~500bp to ~5000bp with an increment-step of ~500 bp.

**3- Accession numbers of the 47 HCoV-OC43 genomes aligned to design the primer set**

Accession	Description
KP198610.1	Human coronavirus OC43 strain 2058A/10
AY903460.1	Human coronavirus OC43 strain 19572 Belgium 2004
AY585229.1	Human coronavirus OC43 serotype OC43-Paris
AY903459.1	Human coronavirus OC43 strain 87309 Belgium 2003
KF923904.1	Human coronavirus OC43 isolate 12694/2012
KJ958219.1	Human coronavirus OC43 strain LY342
KF530078.1	Human coronavirus OC43 strain OC43/human/USA/9612-29/1996
KF530068.1	Human coronavirus OC43 strain OC43/human/USA/007-11/2000
KF923897.1	Human coronavirus OC43 isolate 3269A/2012
KF923925.1	Human coronavirus OC43 isolate 10574/2010
JN129834.1	Human coronavirus OC43 strain HK04-01
KF530099.1	Human coronavirus OC43 strain OC43/human/USA/971-5/1997
KF530098.1	Human coronavirus OC43 strain OC43/human/USA/965-6/1996
KF530097.1	Human coronavirus OC43 strain OC43/human/USA/9211-43/1992
KF530096.1	Human coronavirus OC43 strain OC43/human/USA/911-38/1991
KF530095.1	Human coronavirus OC43 strain OC43/human/USA/912-6/1991
KF530094.1	Human coronavirus OC43 strain OC43/human/USA/912-36/1991
KF530092.1	Human coronavirus OC43 strain OC43/human/USA/008-5/2000
KF530091.1	Human coronavirus OC43 strain OC43/human/USA/911-58/1991
KF530090.1	Human coronavirus OC43 strain OC43/human/USA/931-85/1993
KF530089.1	Human coronavirus OC43 strain OC43/human/USA/911-66/1991
KF530088.1	Human coronavirus OC43 strain OC43/human/USA/901-54/1990
KF530087.1	Human coronavirus OC43 strain OC43/human/USA/873-6/1987
KF530086.1	Human coronavirus OC43 strain OC43/human/USA/872-5/1987
KF530085.1	Human coronavirus OC43 strain OC43/human/USA/871-25/1987
KF530084.1	Human coronavirus OC43 strain OC43/human/USA/951-18/1995
KF530083.1	Human coronavirus OC43 strain OC43/human/USA/873-19/1987
KF530082.1	Human coronavirus OC43 strain OC43/human/USA/912-11/1991
KF530081.1	Human coronavirus OC43 strain OC43/human/USA/991-5/1999
KF530080.1	Human coronavirus OC43 strain OC43/human/USA/9712-31/1997
KF530079.1	Human coronavirus OC43 strain OC43/human/USA/913-29/1991
KF530077.1	Human coronavirus OC43 strain OC43/human/USA/873-16/1987
KF530076.1	Human coronavirus OC43 strain OC43/human/USA/911-11/1991
KF530075.1	Human coronavirus OC43 strain OC43/human/USA/953-23/1995
KF530074.1	Human coronavirus OC43 strain OC43/human/USA/9212-33/1992
KF530073.1	Human coronavirus OC43 strain OC43/human/USA/8912-37/1989
KF530072.1	Human coronavirus OC43 strain OC43/human/USA/9712-13/1997
KF530071.1	Human coronavirus OC43 strain OC43/human/USA/925-1/1992
KF530070.1	Human coronavirus OC43 strain OC43/human/USA/991-19/1999
KF530069.1	Human coronavirus OC43 strain OC43/human/USA/982-4/1998
KF530067.1	Human coronavirus OC43 strain OC43/human/USA/912-10/1991
KF530066.1	Human coronavirus OC43 strain OC43/human/USA/901-33/1990
KF530065.1	Human coronavirus OC43 strain OC43/human/USA/901-41/1990
KF530064.1	Human coronavirus OC43 strain OC43/human/USA/9612-9/1996
KF530063.1	Human coronavirus OC43 strain OC43/human/USA/9612-48/1996
KF530061.1	Human coronavirus OC43 strain OC43/human/USA/901-43/1990
KF530060.1	Human coronavirus OC43 strain OC43/human/USA/851-15/1985

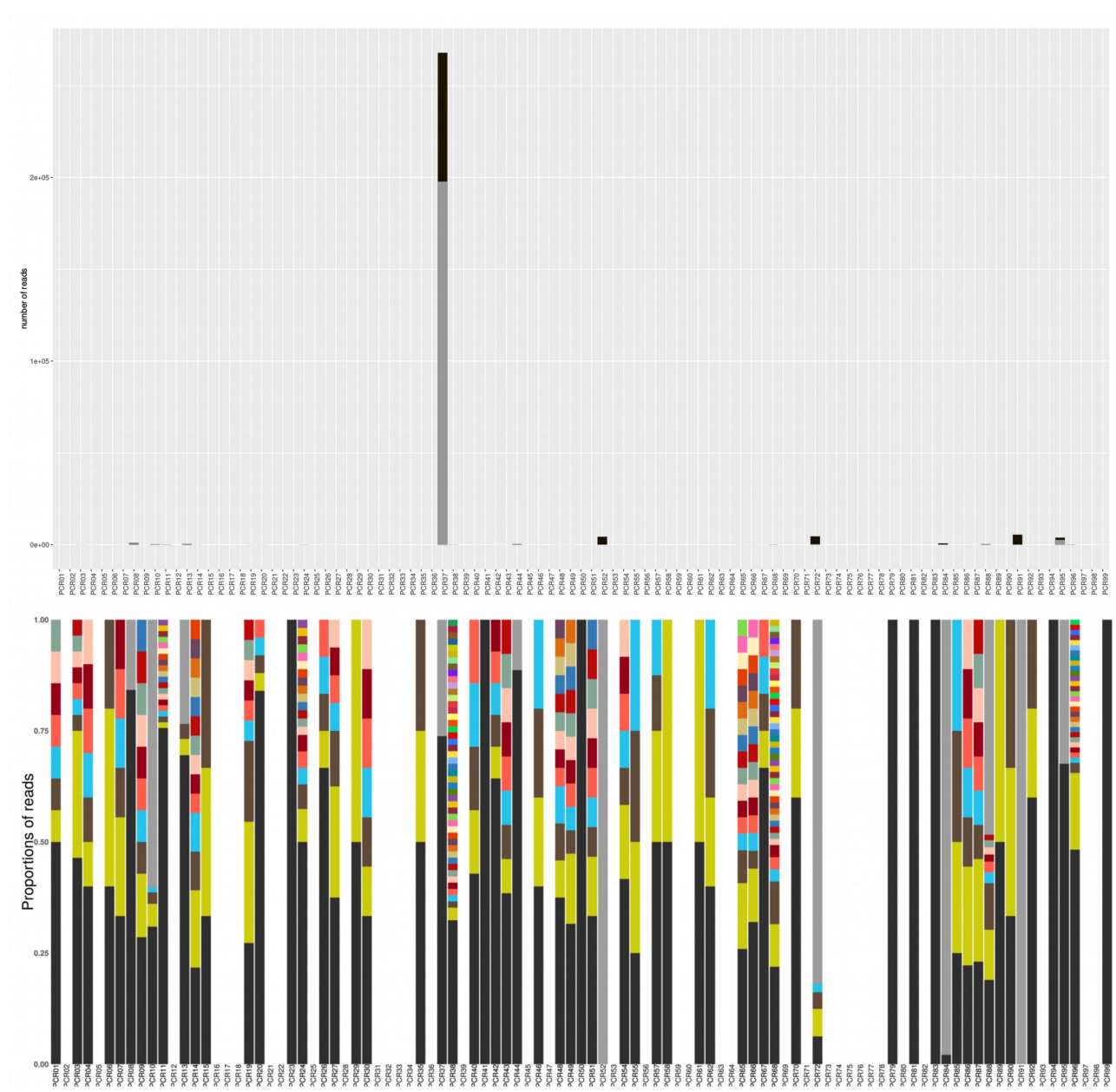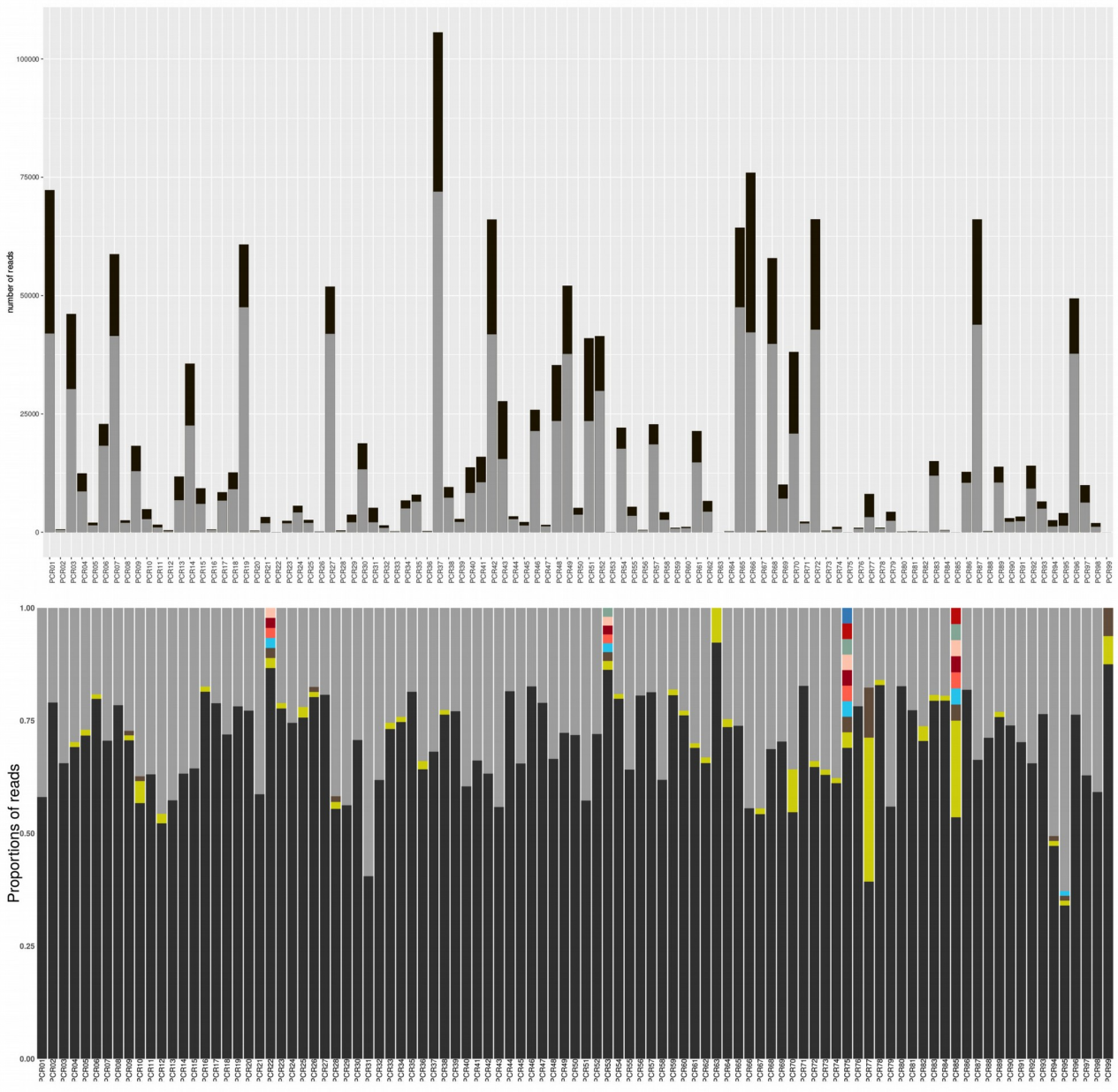# 4- Study of the cluster size distribution for the 99 amplicons
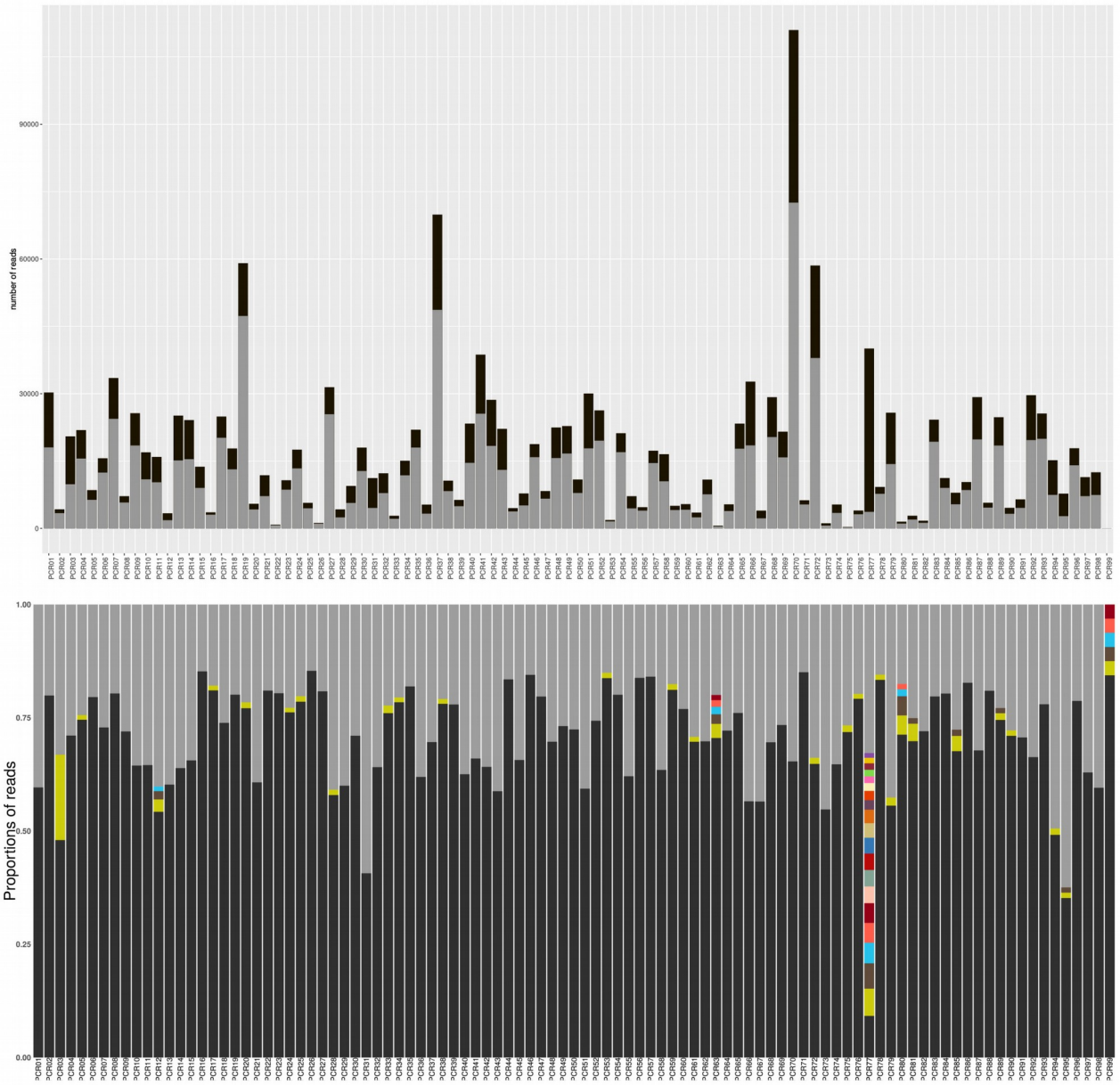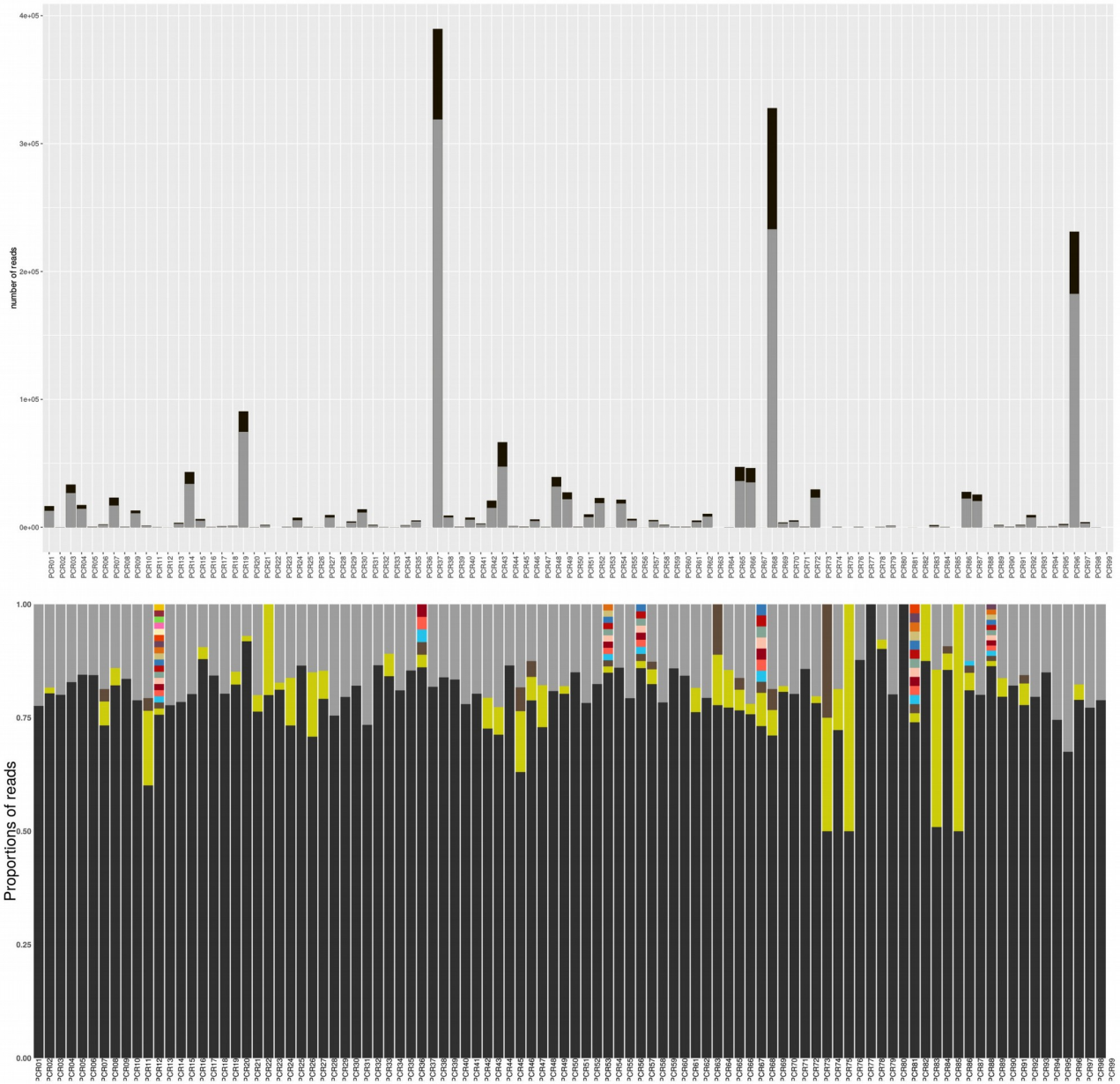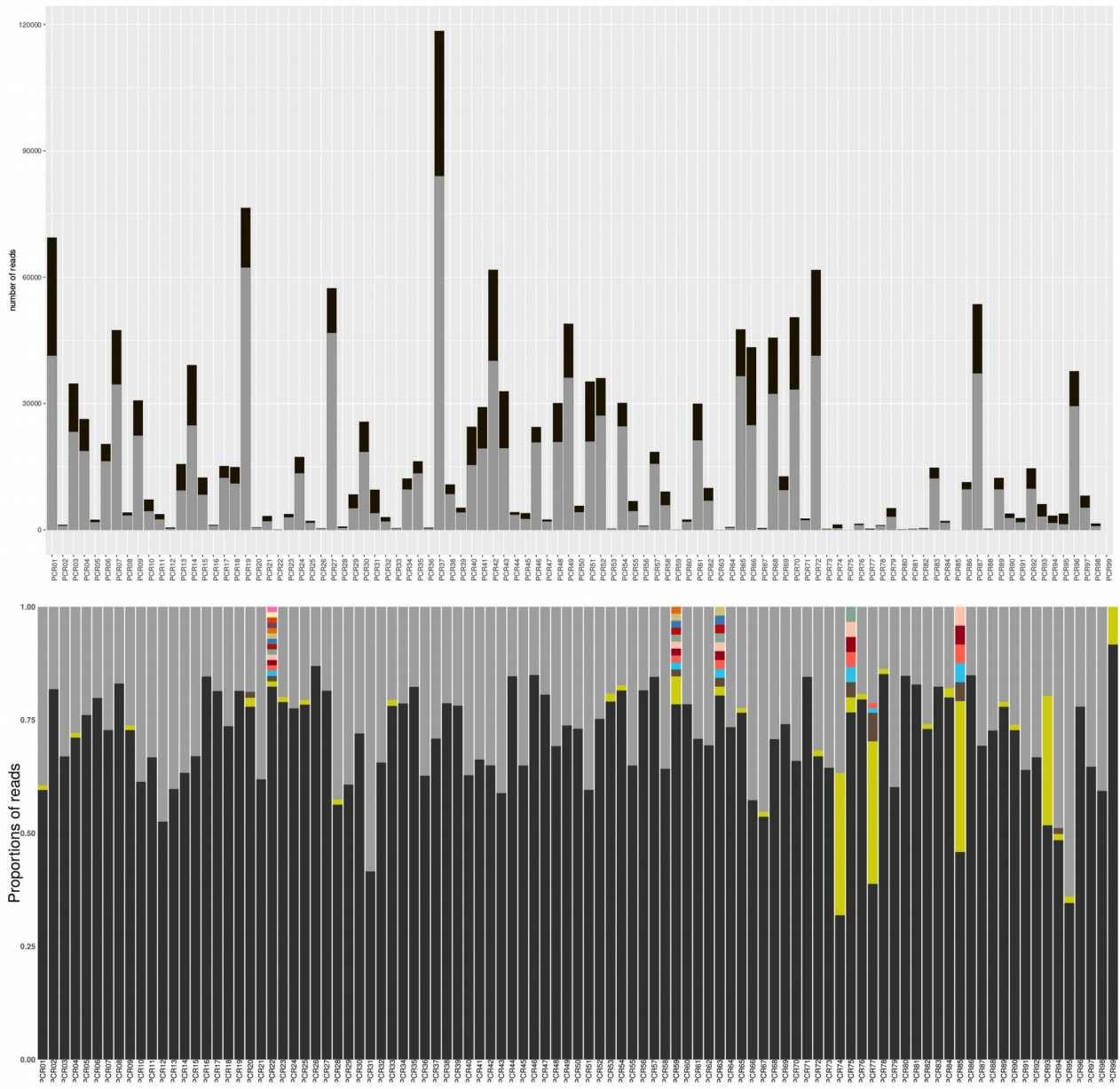
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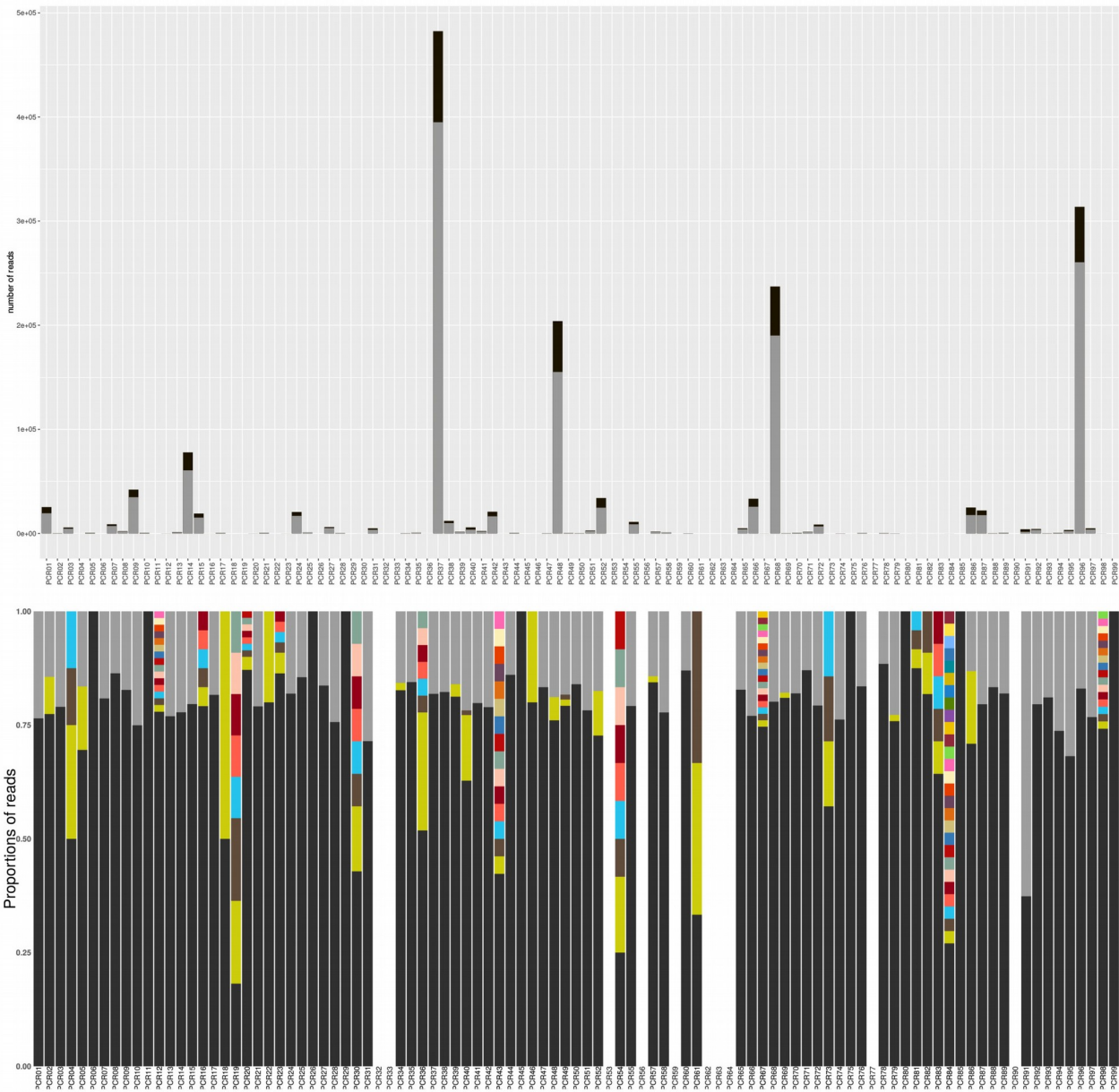
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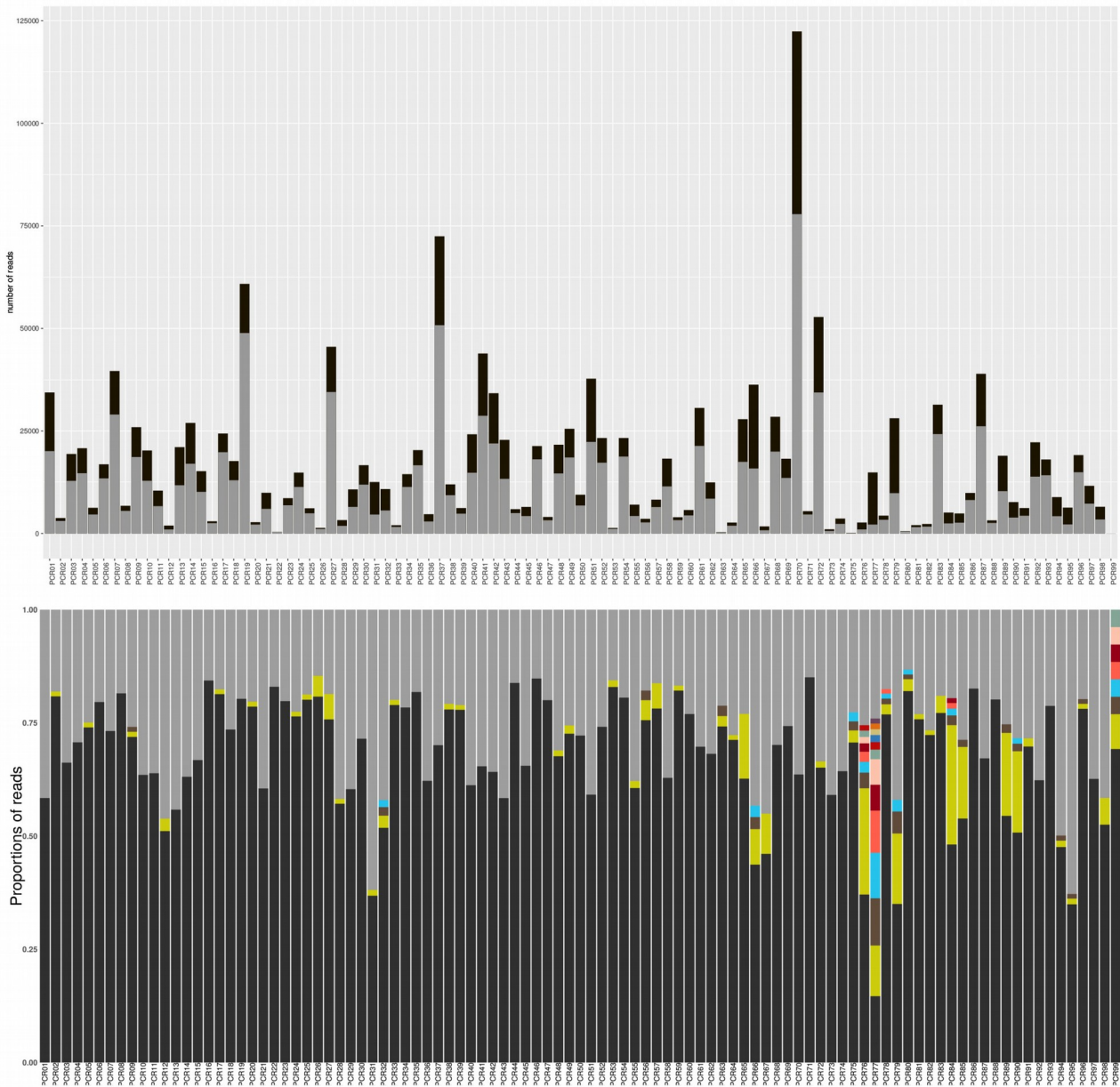
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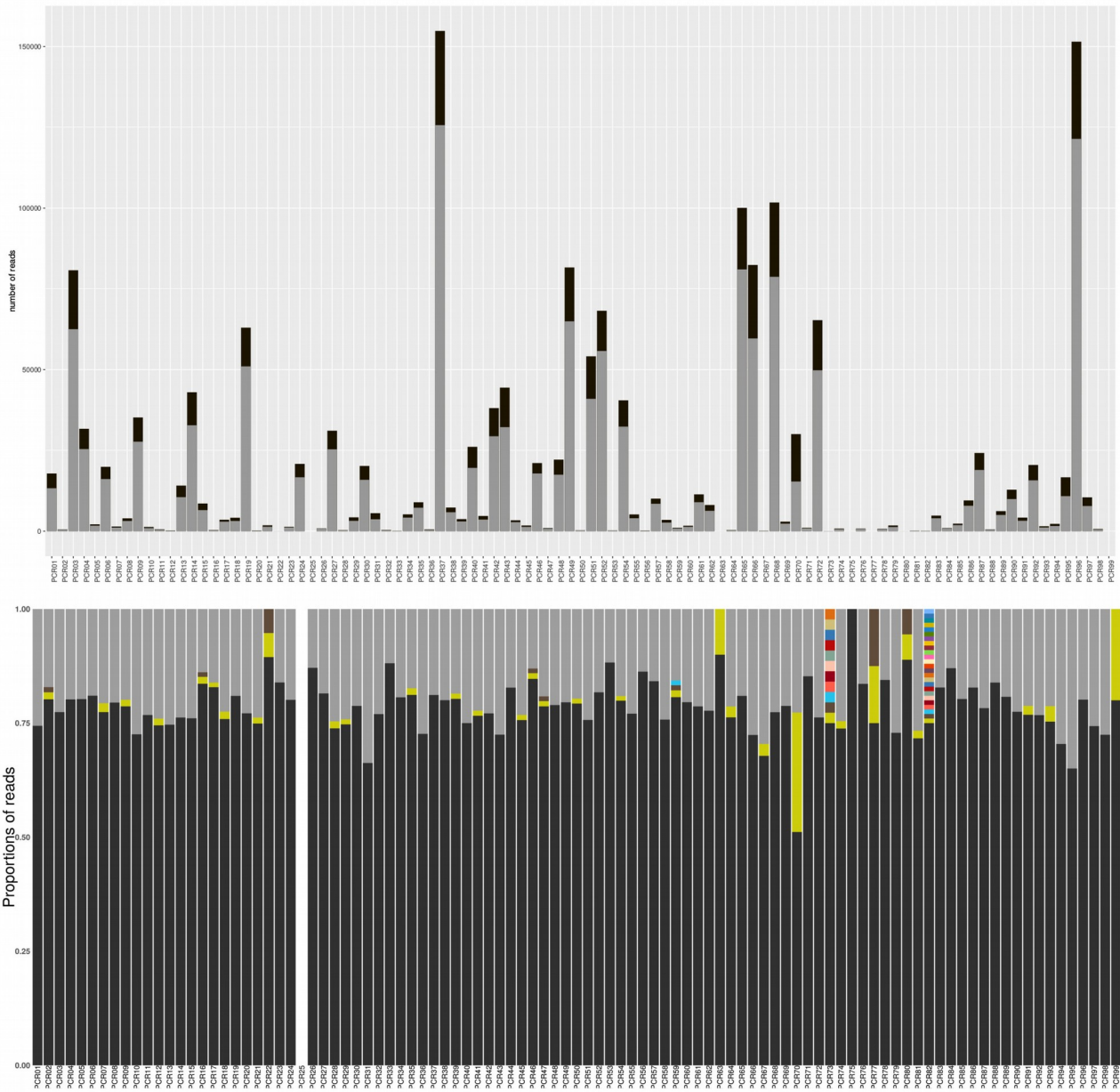
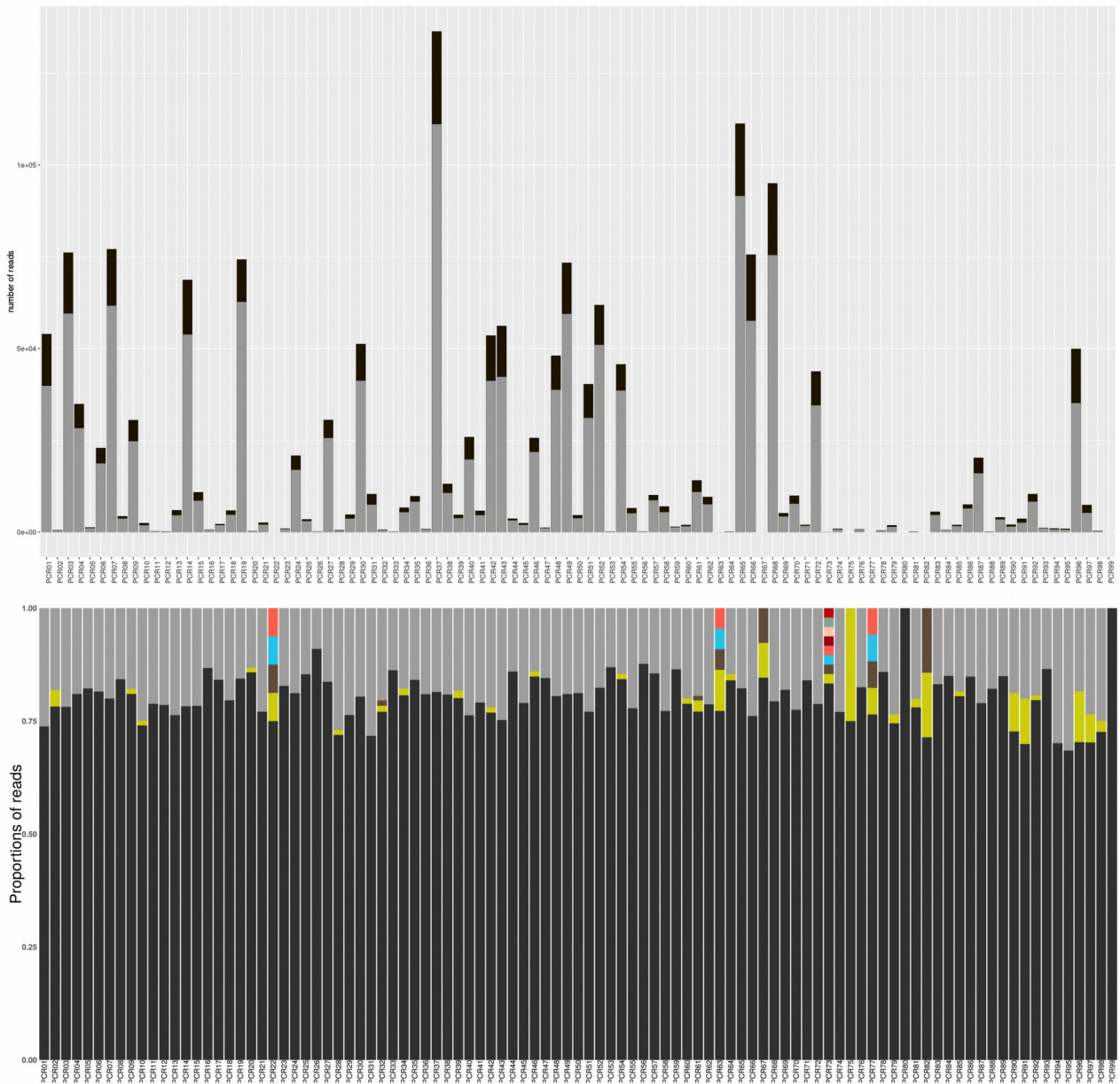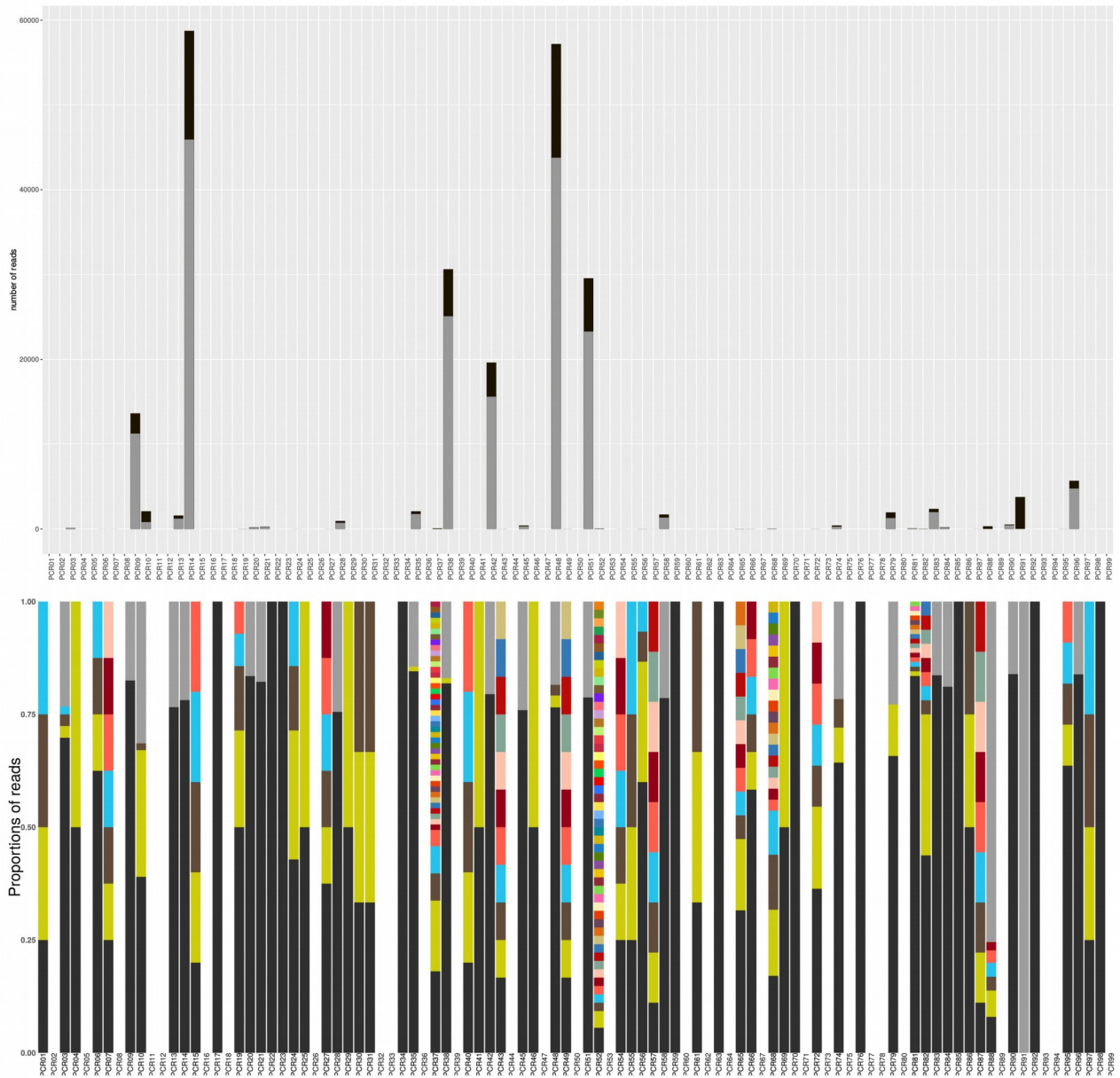# MDS-6

MDS-11

MDS-12

MDS-14

MDS-15

MDS-16

PR2

5- Primers used as input of V-ASAP for Zika data

List of the primers used as input of V-ASAP in the Zika study. These primers correspond to the 22 nucleotides following the forward primers designed in the original study.

ID	Forward primers
1	CTAGCAACAGTATCAACAGGTT
2	TGAGAATAATCAATGCTAGGAA
3	AACACGACGTCAACTTGGGTTG
4	TAGGGACTTTGTGGAAGGTATG
5	GGGGAAATGGATGTGGACTTTT
6	CCTTGACTTTTCAGATTTGTAT
7	GTGTACCGCAGCGTTCACATTC
8	CTGGCACAGGAGTGGCAGCACC
9	TCTTATCCACAGCCGTCTCTGC
10	AAAACCCCATGTGGAGAGGTCC
11	TAAGGGAAAGGAGGCTGTACAC
12	ACATGTGGAACAAGAGGACCAT
13	CCTGGGAGGATTTTCAATGAGT
14	TTGGCAATACGAGCGATGGTTG
15	GTTGGCCTGATATGCGCATTGG
16	ACCCTTTGCAGCTGGAGCGTGG
17	CGCCTGGGACGGGCACAGCGAG
18	GATGCTGAAGAAGAAGCAGCTA
19	GATCCCTCAAGTATAGCAGCAA
20	CTCAGCAGAAAGACTTTTGAGA
21	CACTGGCTTGAAGCAAGAATGC
22	GAGTGCTCAAACCGAGGTGGAT
23	ATAGGGAAGATGGGCTTTGGAA
24	AGCAACCATAGGATTCTCAATG
25	CATTTTGCTCGTGGCGCACTAC
26	TTCACTGTGTAACATTTTTAGG
27	TGGAGCGGGGATACCTGCAGCC
28	AGACCAGGAGCCTTTTGTATAA
29	CACGCGGGCTGTGGTAAGCTGC
30	GACCCCCAAGAAGGCACTCGTC
31	AAGGGCAGCCGCGCCATCTGGT
32	CTTGGCATTGGCCATAATCAAG
33	GATGATTGCGTTGTGAAGCCAA
34	ACTGATGGCCAATGCCATTTGT
35	AAAACACAGTCAACATGGTGCG