

Supplementary Material

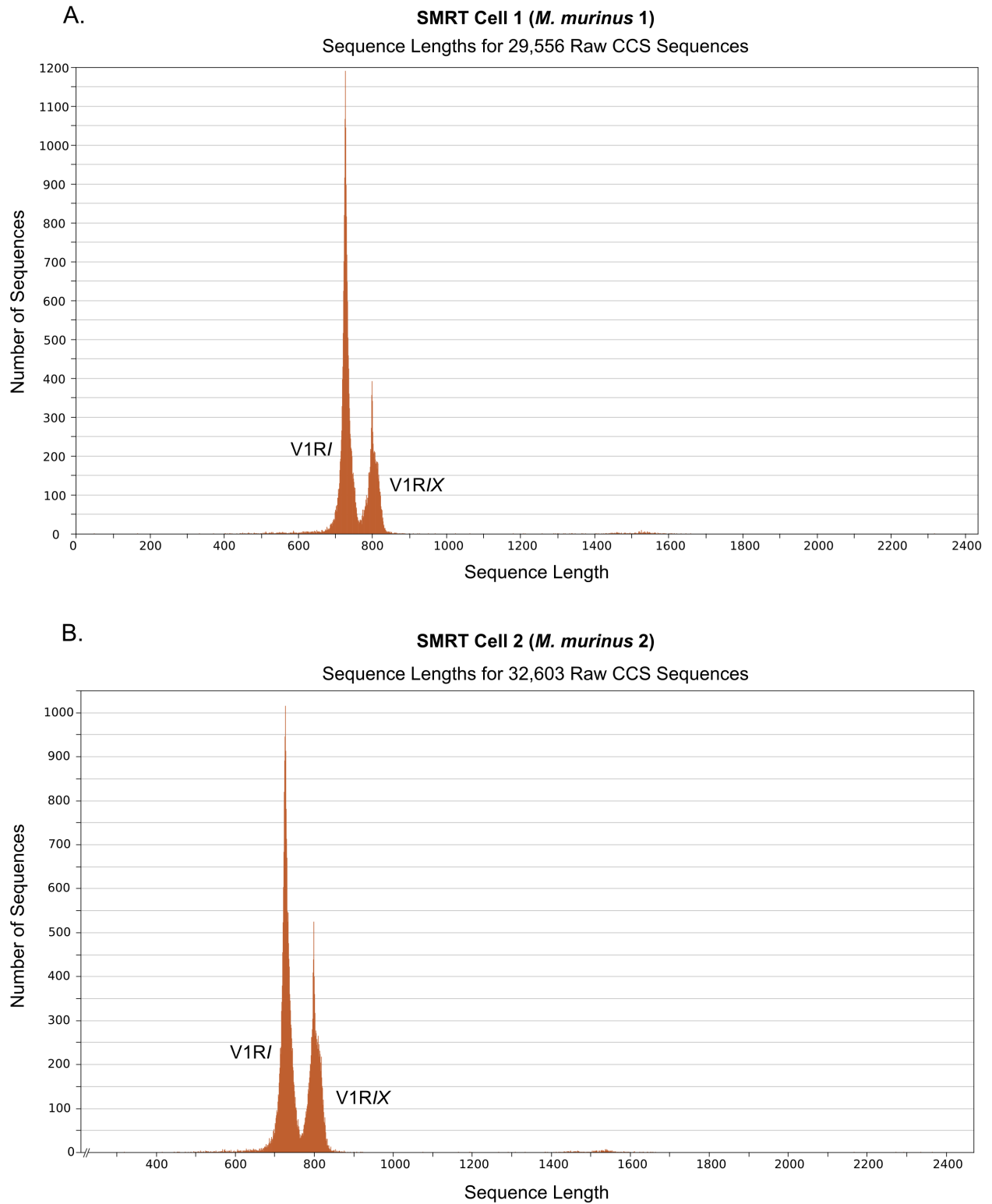
Larsen et al.

Utility of PacBio CCS for characterizing multigene family diversity

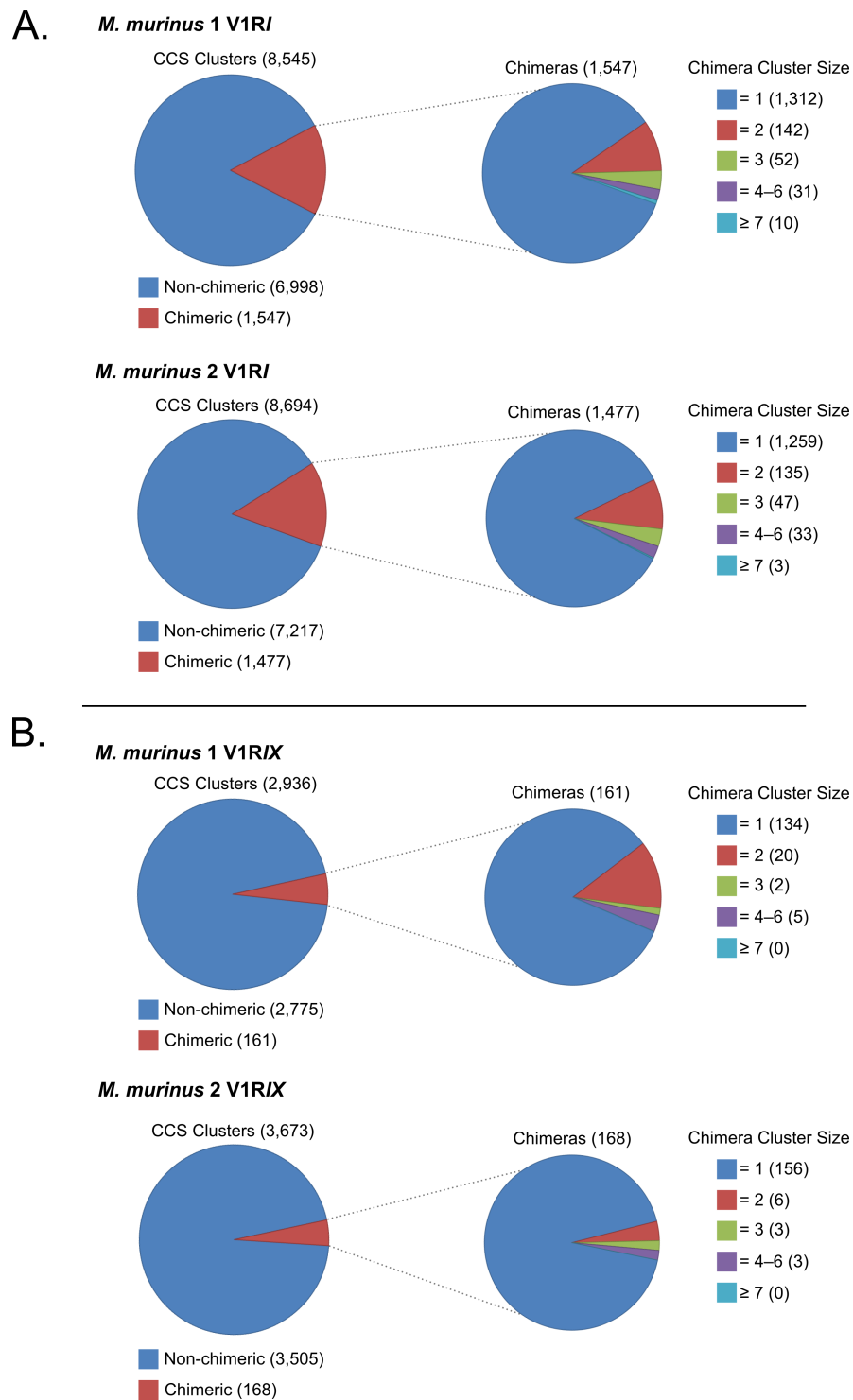
Supplementary Data

Supplementary Datasets are located at www.labarchives.com with the following DOI:
10.6070/H4G73BN0

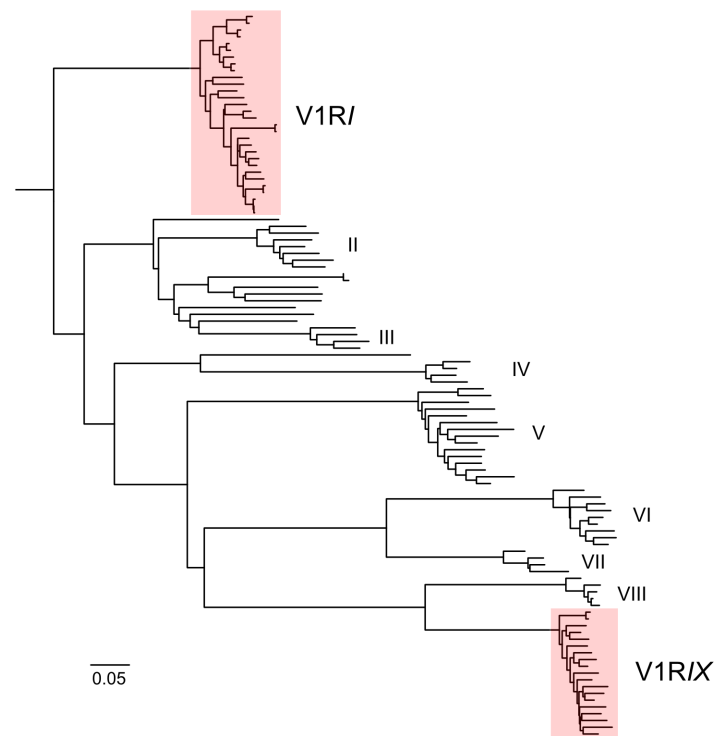
Supplementary Figures



Supplementary Figure 1. Read lengths of raw PacBio CCS sequences for two SMRT cells. Pooled amplicons for V1R subfamilies *I* and *IX* were sequenced from two individuals of *Microcebus murinus* (SMRT cells 1 [A] and 2 [B]; see Methods and Results).



Supplementary Figure 2. Results of *de novo* chimera detection analysis of CCS sequence data. Number of CCS clusters and putative chimeras for V1RI (A) and V1RIX (B) subfamily sequences from *M. murinus* 1 and 2, respectively.



Supplementary Figure 3. Neighbor-joining phylogeny of functional V1R sequences mined from the draft *M. murinus* genome. Highlighted clades were selected for CCS sequencing. Subfamily nomenclature follows Hohenbrink *et al.* (2012; *I–IX*).

Supplementary Tables

Supplementary Table 1. Primer sequences used to amplify *Microcebus murinus* V1R/ and V1R/X subfamilies.

Primer	V1R Subfamily	Orientation	Primer Sequence	Source
V1RG1F	V1R/	Forward	CTC AAC CAG CTG GTC TTA GCY AAC	Yoder et al. 2014
V1RG1R	V1R/	Reverse	GAC AAT GAA CAC AAA GGG GCT GAA	Yoder et al. 2014
MMV1RIXF	V1R/X	Forward	CAY AGC CAA YAY CTT	This paper
MMV1RIXR	V1R/X	Reverse	ATT ATC ACH AAA GGA CTY A	This paper

Supplementary Table 2. Results of Chi-squared tests of genetic differentiation.

<i>M. murinus 1</i>	χ^2	<i>P</i>	d.f.
V1R/ CCS vs. genome	36	0.879	47
V1R/X CCS vs. genome	32.86	0.663	37
<i>M. murinus 2</i>			
V1R/ CCS vs. Sanger	59.44	0.638	64
Final repertoire comparisons			
V1R/ <i>M. murinus 1</i> vs. <i>M. murinus 2</i>	88	0.450	87
V1R/X <i>M. murinus 1</i> vs. <i>M. murinus 2</i>	58.99	0.470	59

Supplementary Table 3. Intra- and inter- V1R subfamily genetic distances (percentages) for *M. murinus*.

<i>Intra-individual</i>	Nucleotide	Amino Acid
<i>M. murinus 1</i> (V1R/)	9.6	14.4
<i>M. murinus 2</i> (V1R/)	9.8	14.8
<i>M. murinus 1</i> (V1R/X)	6.3	11.2
<i>M. murinus 2</i> (V1R/X)	6.4	10.8
<i>Inter-individual</i>		
<i>M. murinus 1</i> vs. 2 (V1R/)	9.6	14.4
<i>M. murinus 1</i> vs. 2 (V1R/X)	6.4	10.8

Hohenbrink P, Radespiel U, Mundy NI: **Pervasive and ongoing positive selection in the vomeronasal-1 receptor (V1R) repertoire of mouse lemurs.** *Molecular biology and evolution* 2012, **29**:3807-3816.

Yoder A, Chan L, dos Reis M, Larsen P, Campbell C, Rasolarison R, Barrett M, Roos C, Kappeler P, Bielawski J, Yang Z: **Molecular evolutionary characterization of a novel V1R subfamily in strepsirrhine primates.** *Genome biology and evolution* 2014, **6**:213-227.

Young JM, Massa HF, Hsu L, Trask BJ: **Extreme variability among mammalian V1R gene families.** *Genome research* 2010, **20**:10-18.