

Supplementary Information

Interspecies chemical signaling in a methane-oxidizing bacterial community

Aaron W. Puri^{1*#}, Darren Liu¹, Amy L. Schaefer², Zheng Yu¹, Mitchell W. Pesesky¹,
E. Peter Greenberg², and Mary E. Lidstrom^{1,2}

Departments of ¹Chemical Engineering and ²Microbiology,
University of Washington, Seattle, WA 98105

*Present affiliation:

Department of Chemistry and the Henry Eyring Center for Cell and Genome Science,
University of Utah, Salt Lake City, UT 84112

#Corresponding author: a.puri@utah.edu

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Supplementary Figures

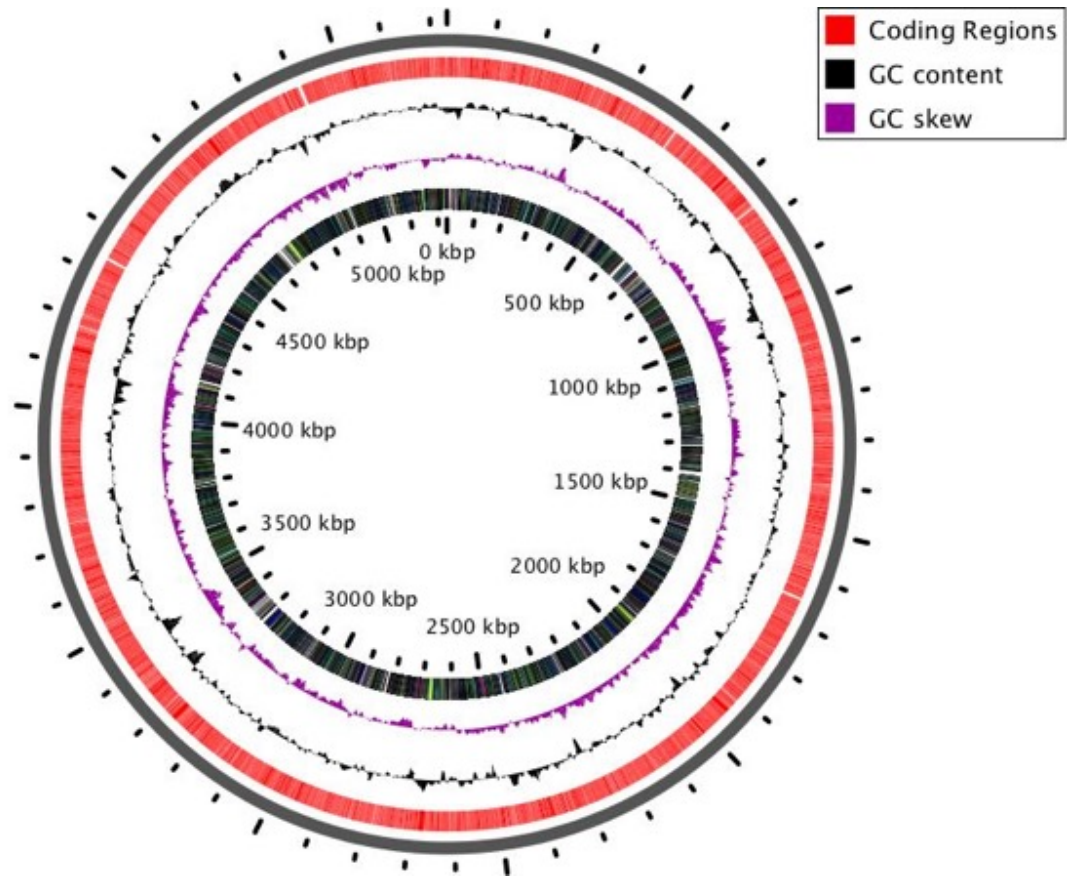


Figure S1. Overview of finished LW13 genome. Visualization using GView (1).

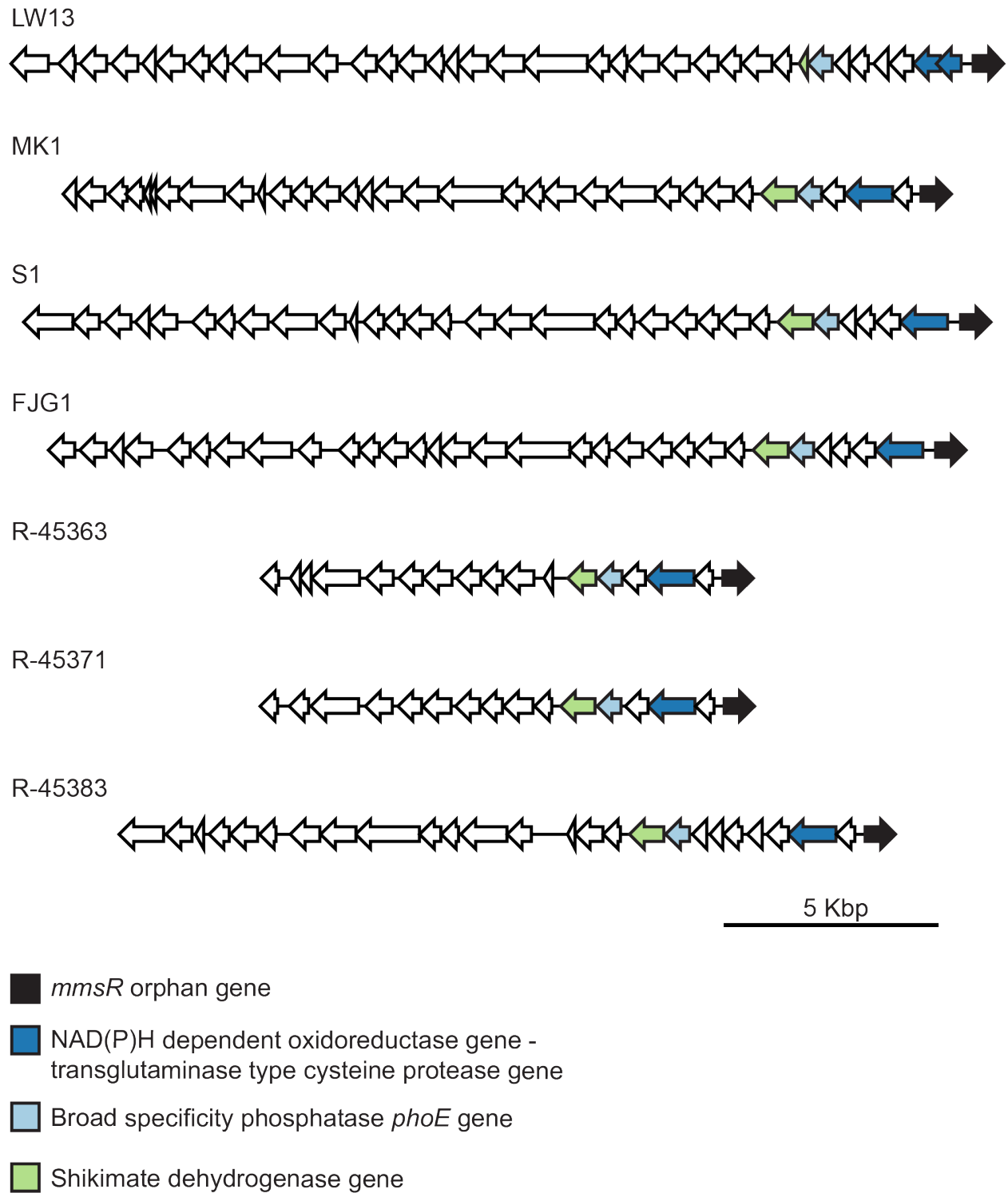


Figure S2. The *mmsR* orphan *luxR*-type receptor/transcription factor gene and neighboring gene cluster is conserved in several *Methylomonas* species. The following genomic regions are shown: *Methylomonas* sp. LW13: U737_12580 - U737_12750; *Methylomonas* sp. MK1: G006DRAFT_0572 - G006DRAFT_0604; *Methylomonas methanica* S1/NCIMB 11130:

Ga0133021_10132 - Ga0133021_101333; *Methylomonas denitrificans* FJG1:
Ga0213656_112900 - Ga0213656_112931; *Methylomonas methanica* R-45363:
Ga0133022_10999 - Ga0133022_109925 (reverse, end of contig); *Methylomonas methanica* R-45371:
Ga0133023_10646 - Ga0133023_106421 (reverse); *Methylomonas koyamae* R-45383:
Ga0133025_11938 - Ga0133025_119320 (reverse). All gene locus tags are from the Integrated Microbial Genomes system (2), except for LW13 genes which refer to the new genome reported in this manuscript. Gene clusters drawn using Easyfig (3).

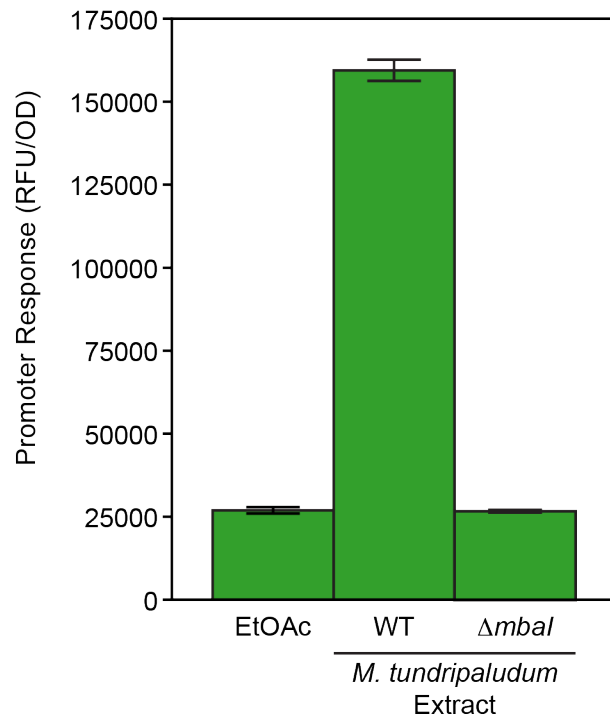


Figure S3. The *E. coli* reporter strain P₁₂₇₄₅-*gfp* responds to an ethyl acetate extract from the supernatant of wild-type *M. tundripaludum*, but not a $\Delta mbal$ mutant strain.

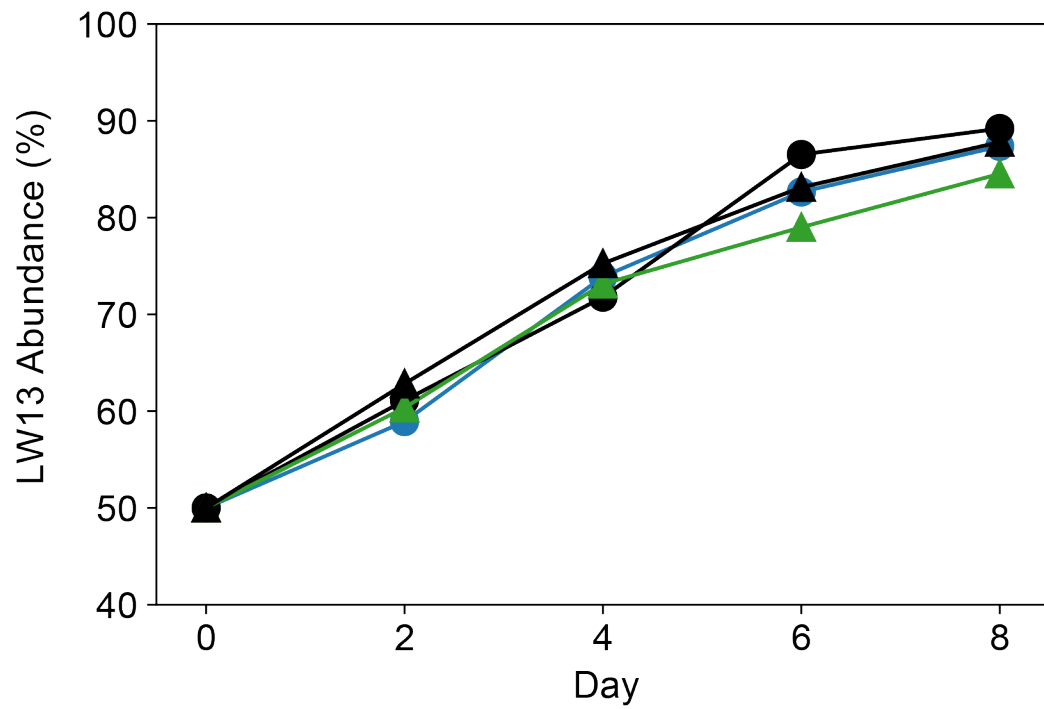


Figure S4. MmsR does not affect the outcome of a co-culture competition between LW13 and *M. tundripaludum* 21/22. Black and blue circles: Abundance of wild-type LW13 in co-culture with *M. tundripaludum*. Black and green triangles: Abundance of LW13 $\Delta mmsR$ in co-culture with *M. tundripaludum*. Two separate co-cultures of each condition are shown and the results are representative of two independent experiments.

WT + EtOAc	WT + 3-OH-C₁₀-HSL	$\Delta mmsR$ + EtOAc	$\Delta mmsR$ + 3-OH-C₁₀-HSL
10.1 (9.9-10.3)	11.3 (10.1-12.6)	10.9 (10.1-11.7)	11.0 (10.4-11.5)

Table S1. Doubling times for LW13 wild-type (WT) and $\Delta mmsR$ mutant strains in the absence or presence of 2 μ M 3-OH-C₁₀-HSL. Data are the mean of two independent experiments, with the range shown in parentheses. There are no significant differences in the doubling times of any pair of strains (two-tailed homoscedastic t-test, p-value < 0.01). EtOAc, ethyl acetate solvent control.

References

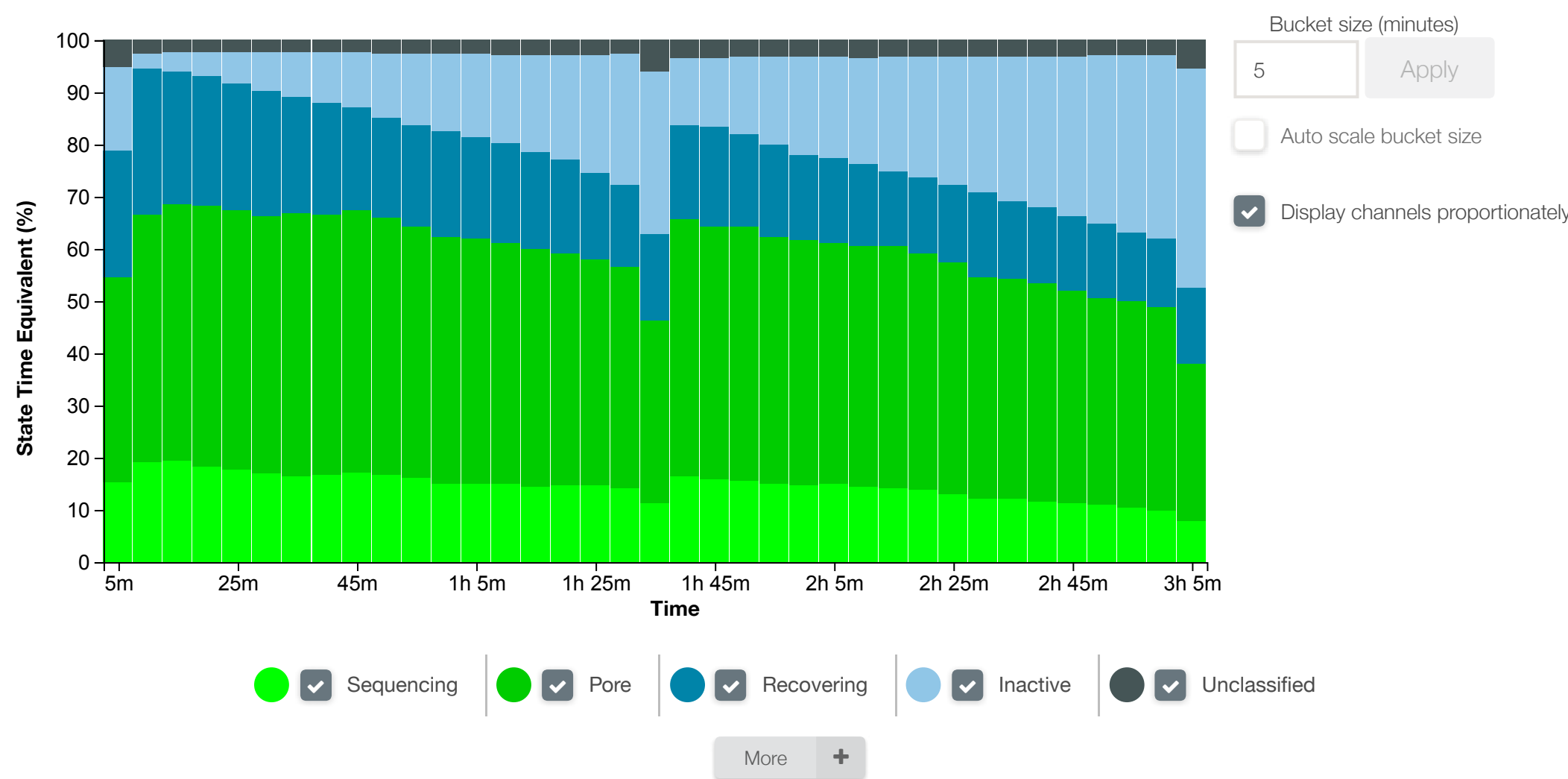
1. Petkau A, Stuart-Edwards M, Stothard P, Van Domselaar G. 2010. Interactive microbial genome visualization with GView. *Bioinformatics* 26:3125–3126.
2. Chen I-MA, Chu K, Palaniappan K, Pillay M, Ratner A, Huang J, Huntemann M, Varghese N, White JR, Seshadri R, Smirnova T, Kirton E, Jungbluth SP, Woyke T, Elie-Fadrosh EA, Ivanova NN, Kyrpides NC. 2018. IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. *Nucleic Acids Res.* [Epub ahead of print]
3. Sullivan MJ, Petty NK, Beatson SA. 2011. Easyfig: a genome comparison visualizer. *Bioinformatics* 27:1009–1010.

Experiment complete

Export PDF Report

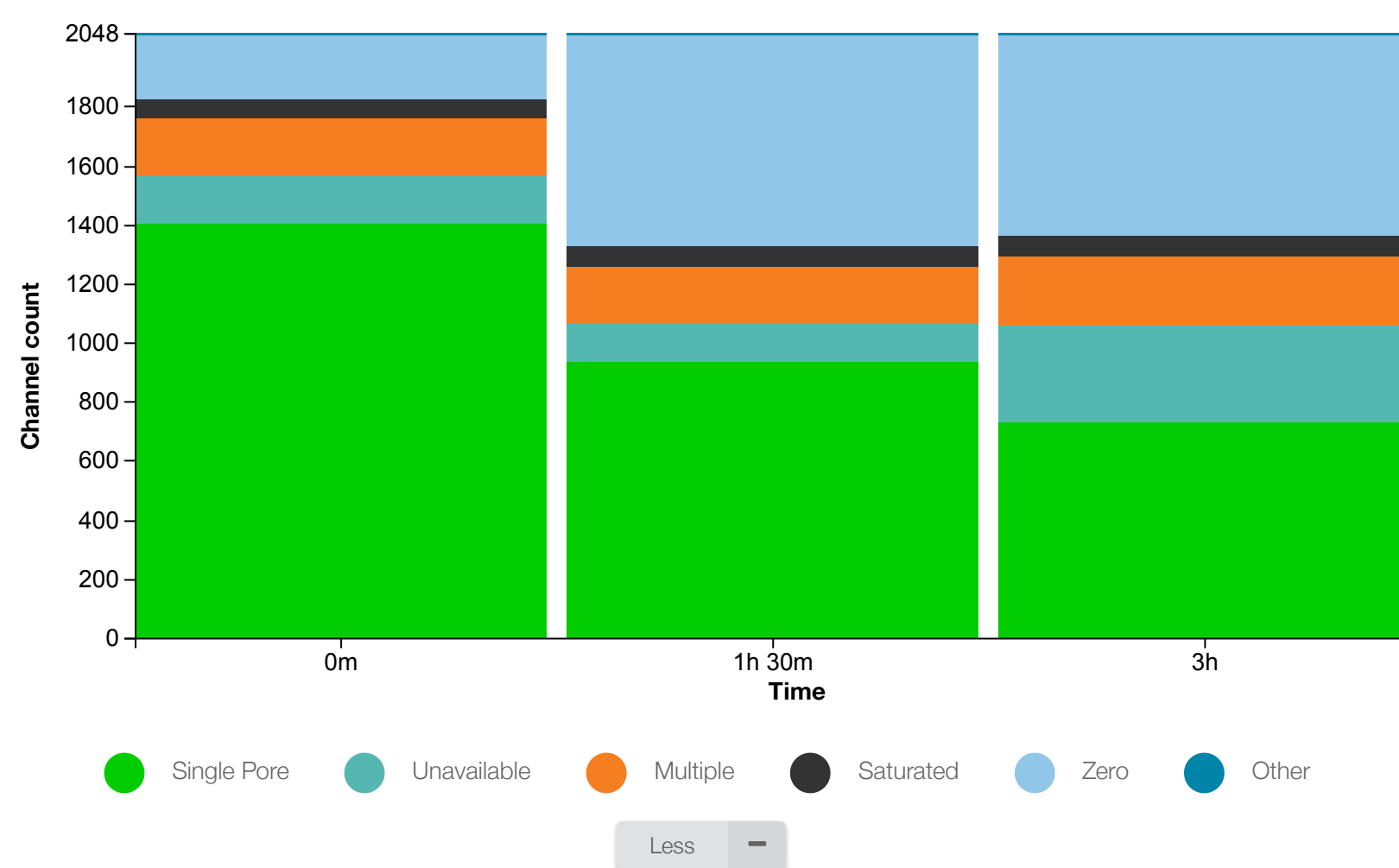
Duty Time

Summary of channel states over time



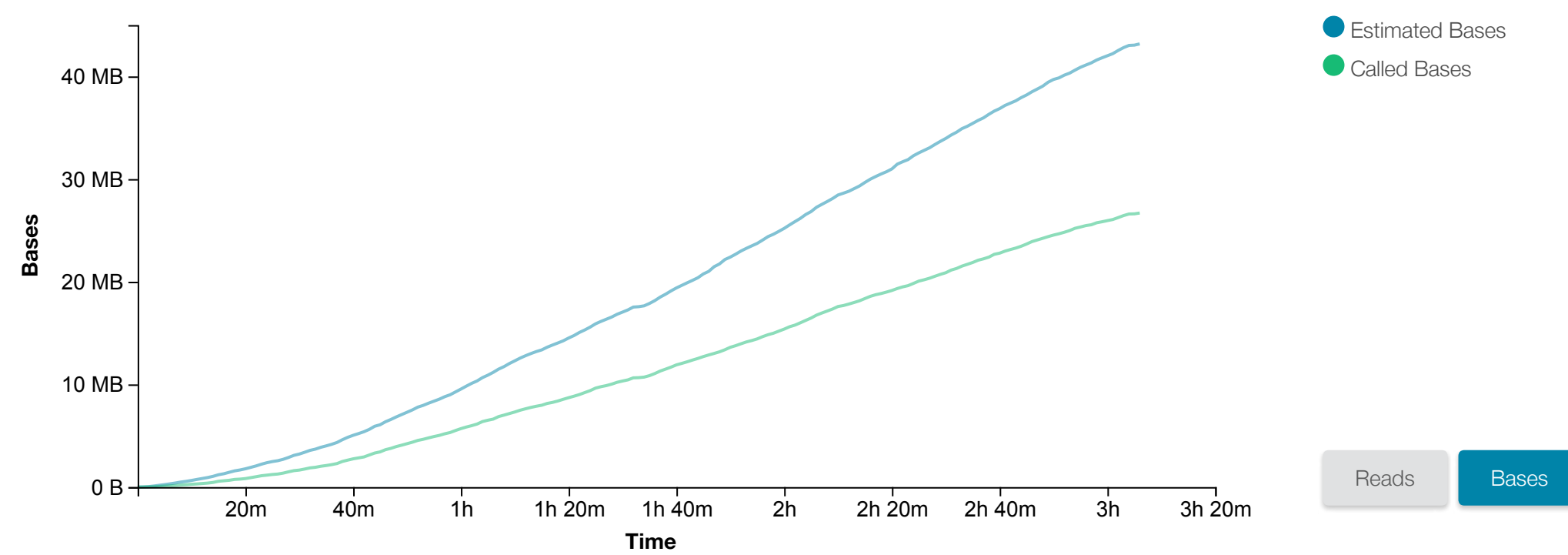
Mux Scan Results

Channel counts per category after each mux scan



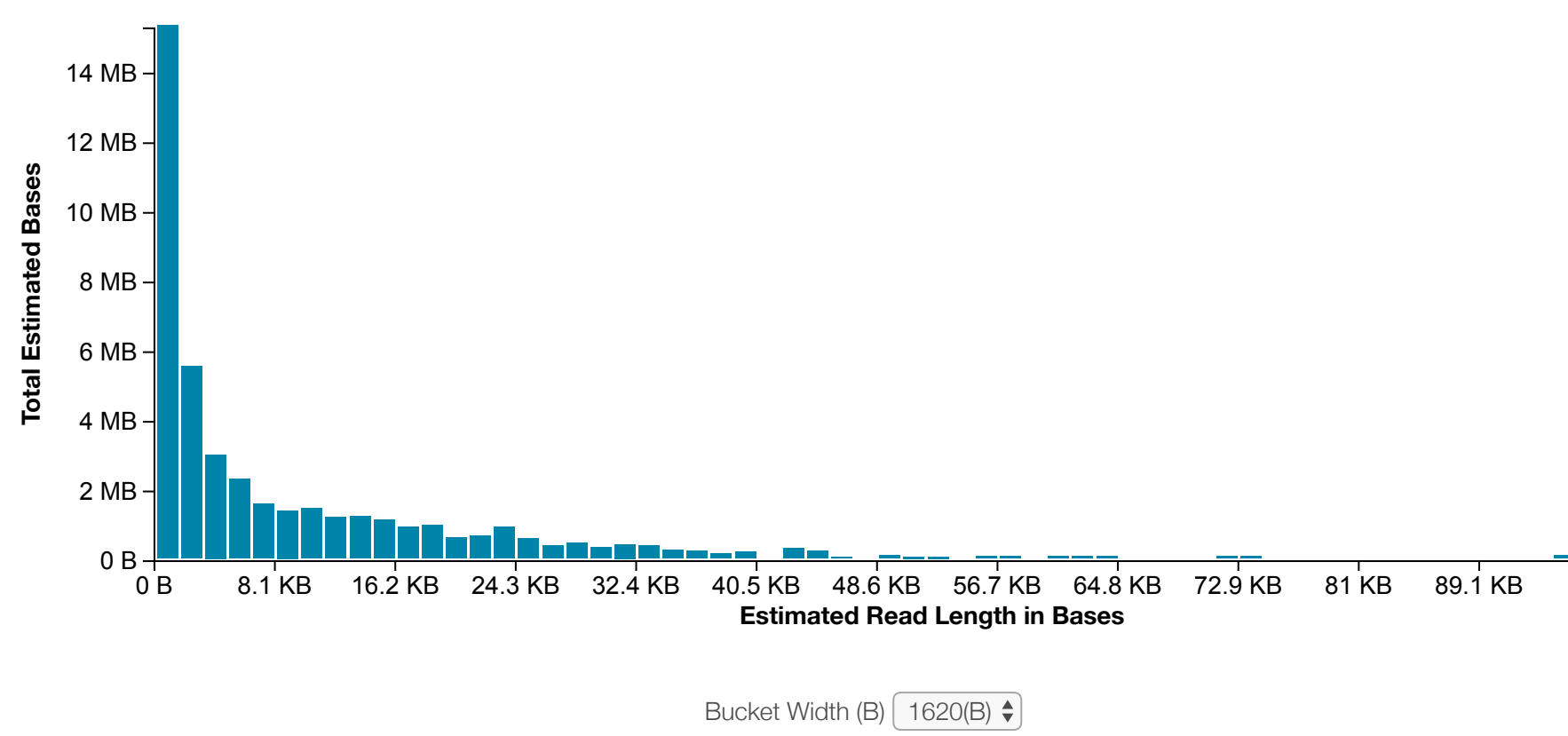
Cumulative Throughput

Throughput of run over time



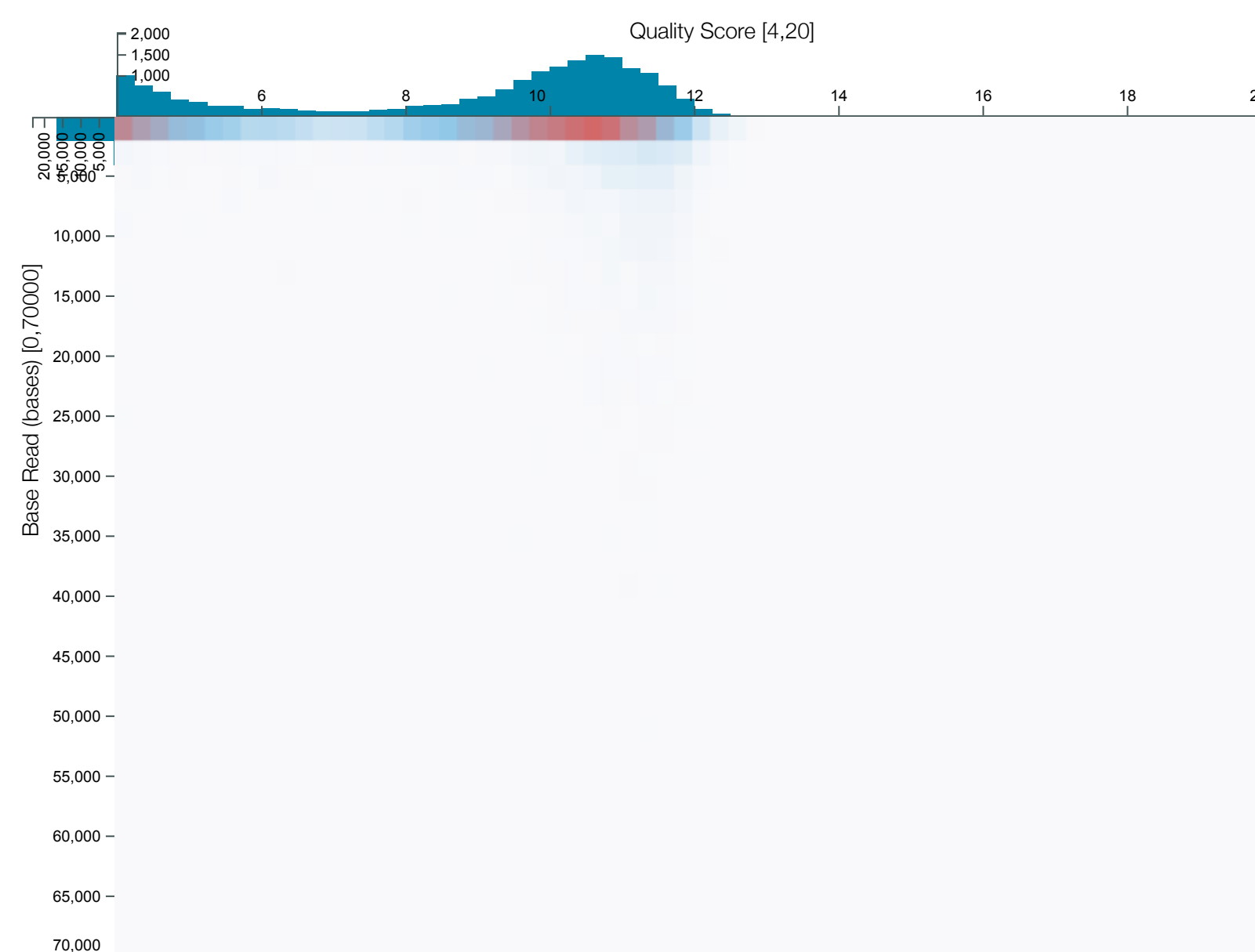
Read Length Histogram

Summary read length distribution



Basecall

Heatmap of read length vs basecall quality score



- Finished Mux Scan**
MN27905 2 minutes ago
- Group 4 has 17 active channels**
MN27905 2 minutes ago
- Group 3 has 88 active channels**
MN27905 2 minutes ago
- Group 2 has 230 active channels**
MN27905 2 minutes ago
- Group 1 has 399 active channels**
MN27905 2 minutes ago
- a total of 734 wells have been selected and split into the following groups**
MN27905 2 minutes ago
- Processing Mux 4**
MN27905 2 minutes ago
- advancing to group 4**
MN27905 2 minutes ago
- Processing Mux 3**
MN27905 3 minutes ago
- advancing to group 3**
MN27905 3 minutes ago
- Processing Mux 2**
MN27905 3 minutes ago
- advancing to group 2**
MN27905 3 minutes ago
- Processing Mux 1**
MN27905 3 minutes ago
- Starting Mux Scan**
MN27905 3 minutes ago
- Finished Mux Scan**
MN27905 1 hour ago
- Group 4 has 32 active channels**
MN27905 1 hour ago
- Group 3 has 145 active channels**
MN27905 1 hour ago
- Group 2 has 307 active channels**
MN27905 1 hour ago
- Group 1 has 453 active channels**
MN27905 1 hour ago
- a total of 937 wells have been selected and split into the following groups**
MN27905 1 hour ago
- Processing Mux 4**
MN27905 1 hour ago
- advancing to group 4**
MN27905 1 hour ago
- Processing Mux 3**
MN27905 1 hour ago
- advancing to group 3**
MN27905 1 hour ago
- Processing Mux 2**
MN27905 1 hour ago
- advancing to group 2**
MN27905 1 hour ago
- Processing Mux 1**
MN27905 1 hour ago
- Starting Mux Scan**
MN27905 1 hour ago
- Starting Sequencing**
MN27905 3 hours ago
- Finished Mux Scan**
MN27905 3 hours ago
- Group 4 has 128 active channels**
MN27905 3 hours ago
- Group 3 has 320 active channels**
MN27905 3 hours ago
- Group 2 has 452 active channels**
MN27905 3 hours ago
- Group 1 has 503 active channels**
MN27905 3 hours ago
- a total of 1403 wells have been selected and split into the following groups**
MN27905 3 hours ago
- Processing Mux 4**
MN27905 3 hours ago
- advancing to group 4**
MN27905 3 hours ago
- Processing Mux 3**
MN27905 3 hours ago
- advancing to group 3**
MN27905 3 hours ago
- Processing Mux 2**
MN27905 3 hours ago
- advancing to group 2**
MN27905 3 hours ago
- Processing Mux 1**
MN27905 3 hours ago
- Starting Mux Scan**
MN27905 3 hours ago
- Experimental Parameters Complete**
MN27905 3 hours ago
- Setting Experimental Parameters**
MN27905 3 hours ago
- calibration finished successfully**
MN27905 3 hours ago