Good paper for references

1. High-salt ponds from around the world, extracted and compared viruses, used individual assembly (*1*)
2. General best practices for metagenomic analysis (*2*)
3. Hypersaline soils from saltmarshes, extracted good MAGs, functional and amino acid analysis, cool taxonomy analysis of MAGs (*3*)
4. Studies a variety of halophile metagenomes, extracted lot of MAGs, and found general functional adaptations that allow *Halobacteria* to be osmo-tolerant (*4*)
5. Review discussing survival of halophiles on other plants (*5*)
6. Review study that compiled the genomes of 1000 known halophiles into a database (*6*)
7. Review about what hypersaline ecosystems have been studied in metagenomics. Discusses the taxonomic diversity of halophiles and the dominance of *Salinibacter*, Nanohaloarchaea, and *Euryarchaeaota* (*7*)
8. Saline lake surface, extracted Nanohaloarchaea for the first time, used co-assembly (*8*)
9. Lake metavirome study, virus dynamics over time (*9*)
10. Antarctica lake metagenome, looked at evolution dynamics of halophiles, co-assembly (*10*)
11. Review proposing the power of SAGs to de-convolute extremophile microbiome. Also mentions the power of metagenomic binning (surface-level, however) (*11*)
12. Comparison of functional potential across a salinity gradient in ponds, produced lots of MAGs, found pathways that correlate with salinity (*12*)
13. Hypersaline soda lakes, many MAGs extracted, pI and functional potential of MAGs analyzed (*13*)
14. Review outlining the difficulties of binning in halophile metagenomes... Halophiles have very low species diversity, but high intraspecific diversity, making assembly and binning difficult. High microdiversity makes abundant halophiles a pain to extract. <https://doi.org/10.1016/j.syapm.2018.11.001> (*14*)
15. Importance of uncultured microbial dark matter (*15*)
16. High GC content makes assembly worse, lowers kmer diversity (*16*)
17. Low kmer diversity reduces kmer-based binning power (*17*)
18. Paper showing the power of using two approaches to extract MAGs (*18*)

1. S. Roux *et al.*, Analysis of metagenomic data reveals common features of halophilic viral communities across continents. *Environ Microbiol* **18**, 889-903 (2016).

2. C. Quince, A. W. Walker, J. T. Simpson, N. J. Loman, N. Segata, Corrigendum: Shotgun metagenomics, from sampling to analysis. *Nat Biotechnol* **35**, 1211 (2017).

3. B. Vera-Gargallo, A. Ventosa, Metagenomic Insights into the Phylogenetic and Metabolic Diversity of the Prokaryotic Community Dwelling in Hypersaline Soils from the Odiel Saltmarshes (SW Spain). *Genes (Basel)* **9**, (2018).

4. E. A. Becker *et al.*, Phylogenetically driven sequencing of extremely halophilic archaea reveals strategies for static and dynamic osmo-response. *PLoS Genet* **10**, e1004784 (2014).

5. A. Oren, Halophilic archaea on Earth and in space: growth and survival under extreme conditions. *Philos Trans A Math Phys Eng Sci* **372**, (2014).

6. A. Loukas, I. Kappas, T. J. Abatzopoulos, HaloDom: a new database of halophiles across all life domains. *J Biol Res (Thessalon)* **25**, 2 (2018).

7. A. Ventosa, R. R. de la Haba, C. Sanchez-Porro, R. T. Papke, Microbial diversity of hypersaline environments: a metagenomic approach. *Curr Opin Microbiol* **25**, 80-87 (2015).

8. P. Narasingarao *et al.*, De novo metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. *ISME J* **6**, 81-93 (2012).

9. J. B. Emerson *et al.*, Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. *Appl Environ Microbiol* **78**, 6309-6320 (2012).

10. M. Z. DeMaere *et al.*, High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. *Proc Natl Acad Sci U S A* **110**, 16939-16944 (2013).

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12. J. A. Kimbrel *et al.*, Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. *Front Microbiol* **9**, 1492 (2018).

13. C. D. Vavourakis *et al.*, Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. *Front Microbiol* **7**, 211 (2016).

14. M. D. Ramos-Barbero *et al.*, Recovering microbial genomes from metagenomes in hypersaline environments: the Good, the Bad and the Ugly. *Systematic and Applied Microbiology*, (2018).

15. C. Rinke *et al.*, Insights into the phylogeny and coding potential of microbial dark matter. *Nature* **499**, 431-437 (2013).

16. Y. C. Chen, T. Liu, C. H. Yu, T. Y. Chiang, C. C. Hwang, Effects of GC bias in next-generation-sequencing data on de novo genome assembly. *PLoS One* **8**, e62856 (2013).

17. K. Sedlar, K. Kupkova, I. Provaznik, Bioinformatics strategies for taxonomy independent binning and visualization of sequences in shotgun metagenomics. *Comput Struct Biotechnol J* **15**, 48-55 (2017).

18. R. D. Stewart *et al.*, Assembly of 913 microbial genomes from metagenomic sequencing of the cow rumen. *Nat Commun* **9**, 870 (2018).