Characterization of an EPS-enriched emulsifying extracellular fraction produced by a Brazilian strain of *Vreelandella zhao-dongensis*

Henrique Alves de Brito[1], Amanda Pasinato Napp[1], Lovaine Silva Duarte[1], Daniel Ubiratan Haas de Brito[1], Eduarda Vargas Abati[1], Francine Melise dos Santos[1], Clarissa Lovato Melo[1], Richard Steiner Salvato[1,2], João Pedro Tauscheck Zielinski[1,*] and Charley Christian Staats[3,*]

[1] Institute of Petroleum and Natural Resources (IPR), Pontifical Catholic University of Rio Grande do Sul (PUCRS), Porto Alegre, Rio Grande do Sul, Brazil; henrique.brito@pucrs.br; amanda.napp@edu.pucrs.br; lovaduarte@gmail.com; daniel.ubiratan@pucrs.br; eduarda.abati@pucrs.br; francinemelise@gmail.com; clamelo30@hotmail.com; joao.zielinski@pucrs.br

[2] Department of Clinical, Toxicological and Bromatological Analyses, School of Pharmaceutical Sciences of Ribeirão Preto (FCFRP), University of São Paulo (USP), Ribeirão Preto, São Paulo, Brazil; salvato@usp.br

[3] Graduate Program in Cellular and Molecular Biology, Center of Biotechnology, Federal University of Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil; staats@ufrgs.br

*Correspondence: joao.zielinski@pucrs.br (J.P.T.Z.); staats@ufrgs.br (C.C.S.).

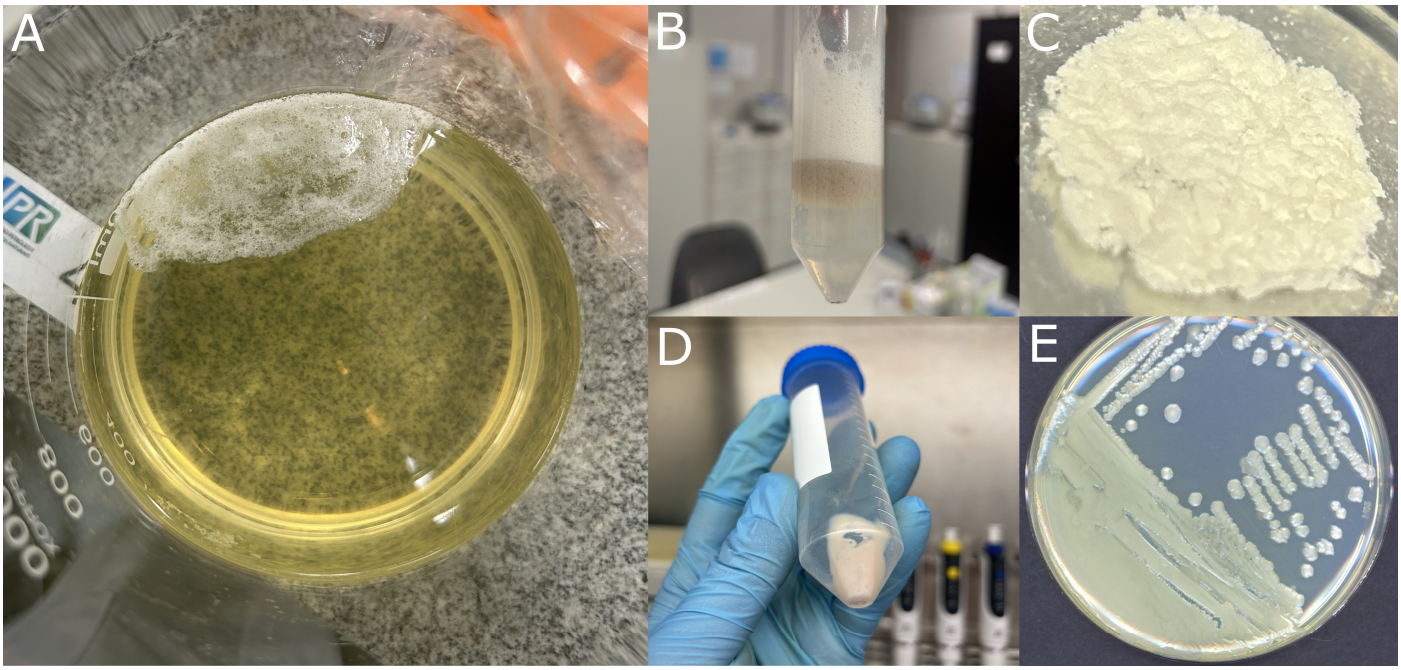


Figure S1. Extraction and enrichment of EPS-EF. (A) Ethanol extraction. The foam-like part is the EPS-EF aggregation. (B) Enrichment of EPS-EF by serial wash after 3 washes with NaOH pH 9, filtration in 0.22 μm, ethanol extraction and centrifugation. (C) EPS-EF lyophilized. (D) Cells from the same culture where EPS-EF was obtained, after 3 washes with NaOH pH 9. (E) Colonies from bacterial growth after serial washes in pH 9. The cell growth after 3 serial washes in pH 9 indicates survivor.

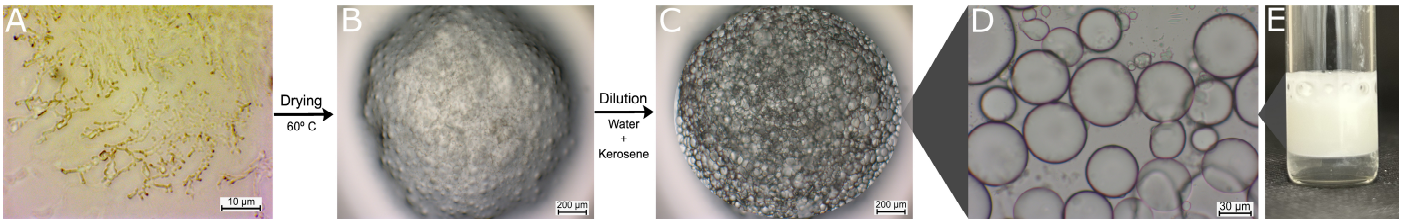


Figure S2. Microscopic observation of emulsification. After enrichment, **(**A) 1mg/mL mg of EPS-EF diluted in water was placed on slide and observed under a microscope at 50x magnification. (B) Dried on the same slide and observed at 10x magnification. (C) Diluted 1:1 in water and kerosene and observed at the same magnification (D) Same condition before at 40x magnification. (E) Emulsification of EPS-EF.

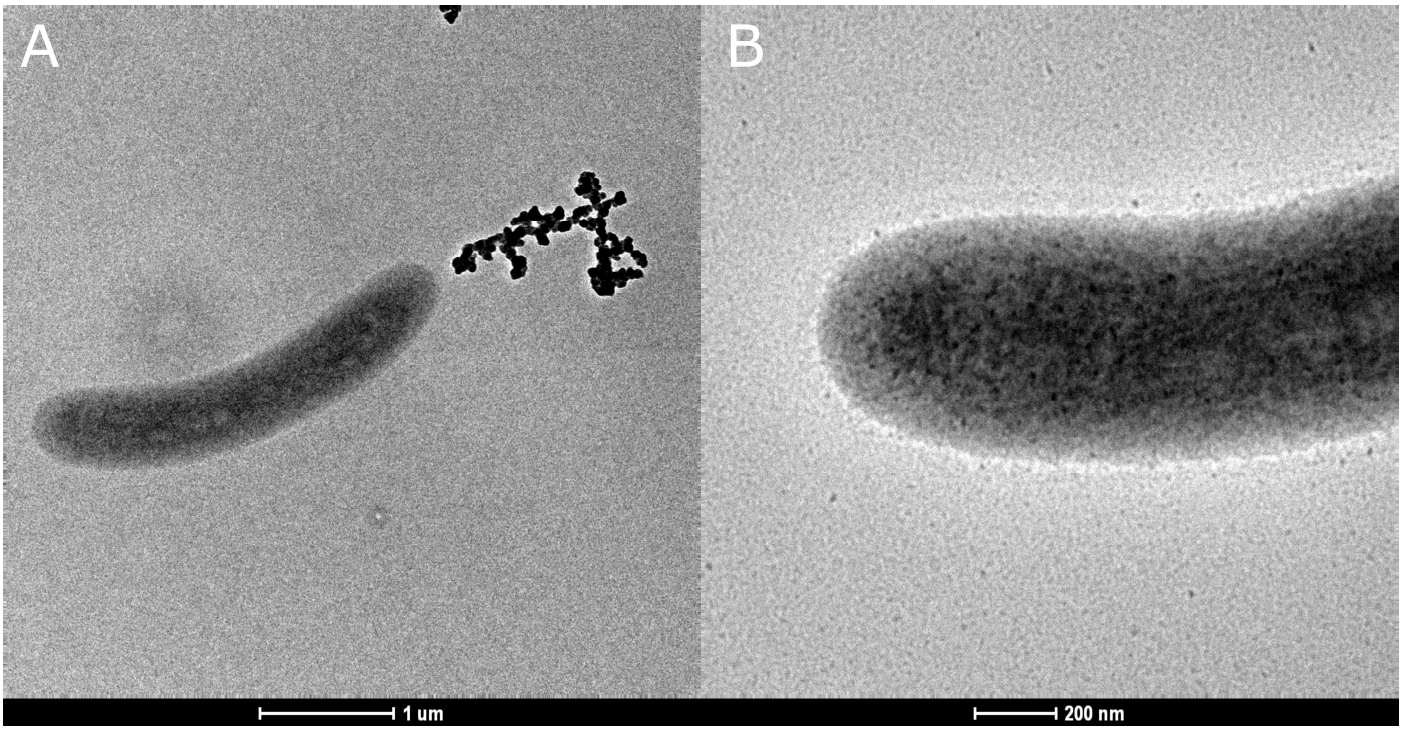


Figure S3. Transmission electron microscopy (TEM) images after culture were treated with pH 9. (A) Extracellular aggregates and fibrillar, hair-like structures were detached from the bacterial surface. (B) Cell membrane structure remains whole with no signs of damage.

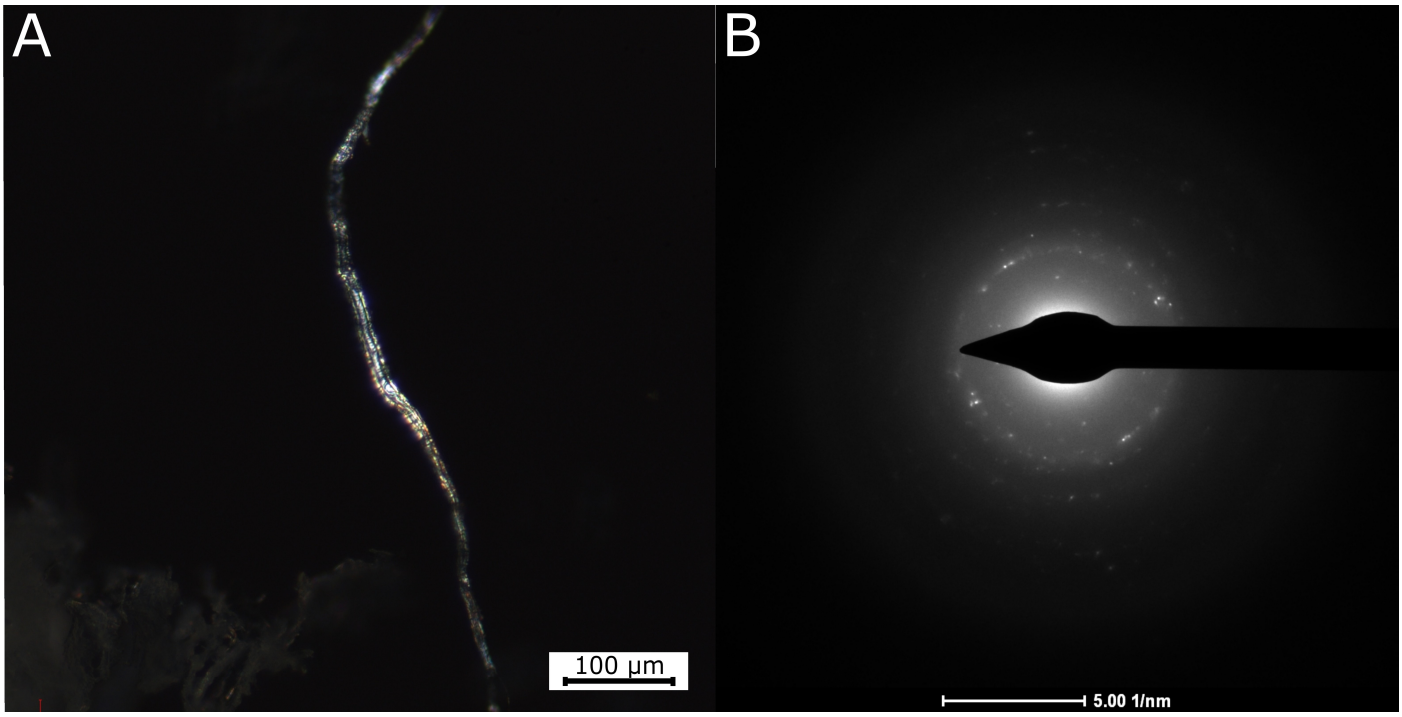


Figure S4. Polarized microscopy of EPS-EF. (A) Polarized Optical Microscopy of EPS-EF 20x. (B) Polarized Transmission Electronic Microscopy of EPS-EF. Both microscopes indicate birefringence.

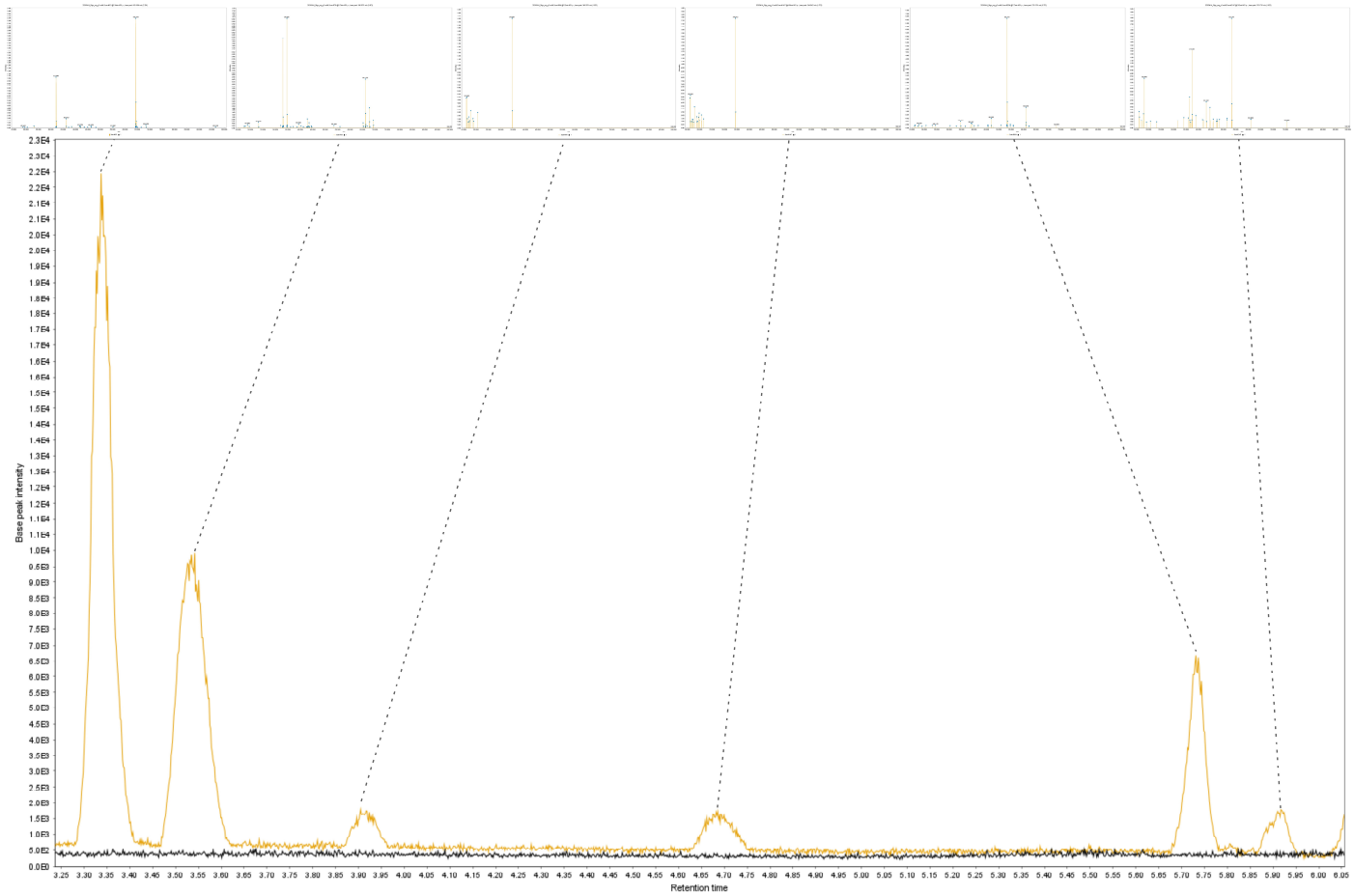


Figure S5. ***V. zhaodongensis*** **BS253 EPS-EF fragments between 3.3-6 min in negative mode [M-H]-.** Chromatogram is on the bottom, and the spectra is on the top of the figure. Black line is control and the brownish line is the EPS-EF sample.

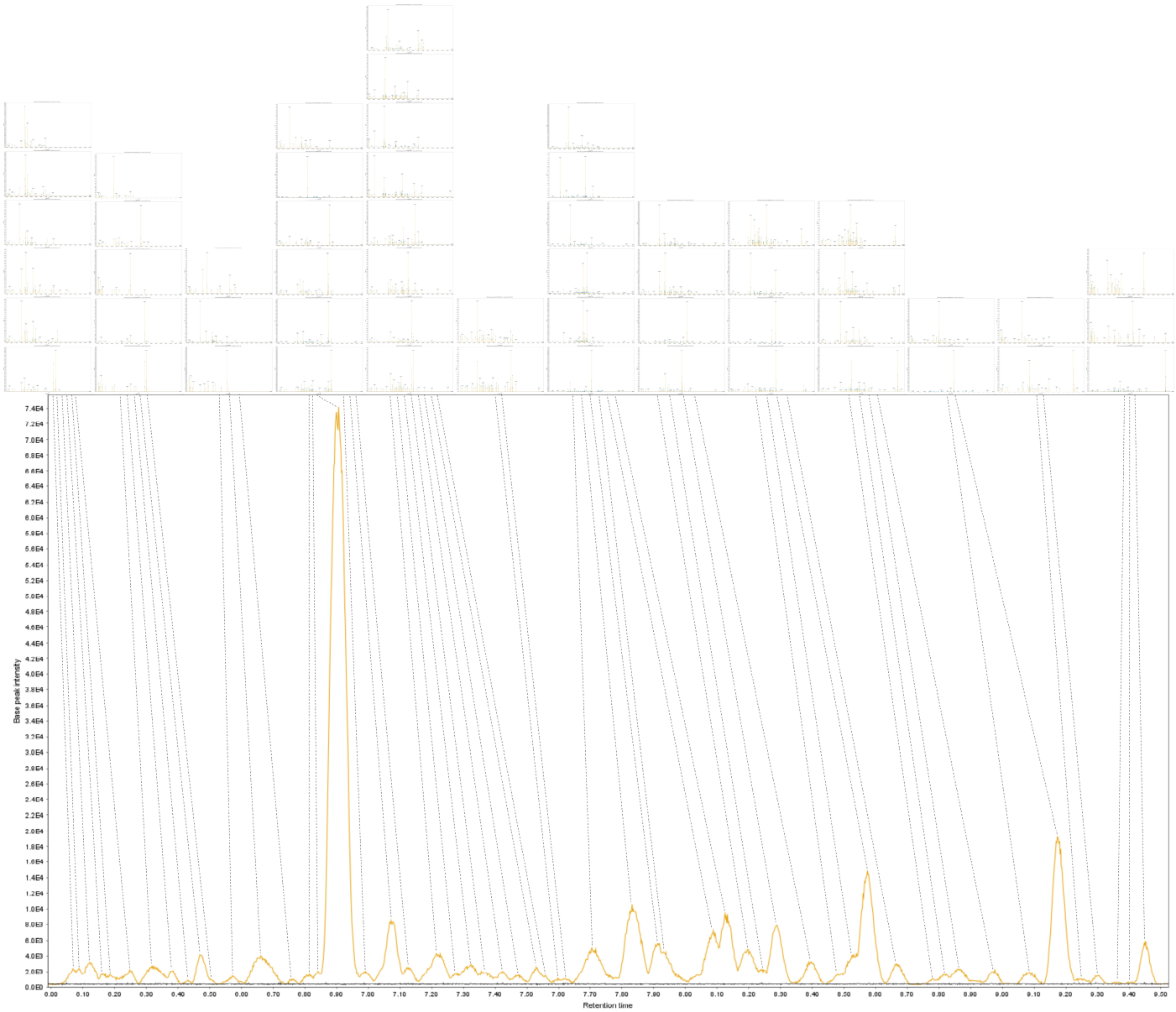


Figure S6. ***V. zhaodongensis*** **BS253 EPS-EF fragments between 6-9.5 min in negative mode [M-H]-.** Chromatogram is on the bottom and the spectra is on the top of the figure. Black line is control and the brownish line is the EPS-EF sample.

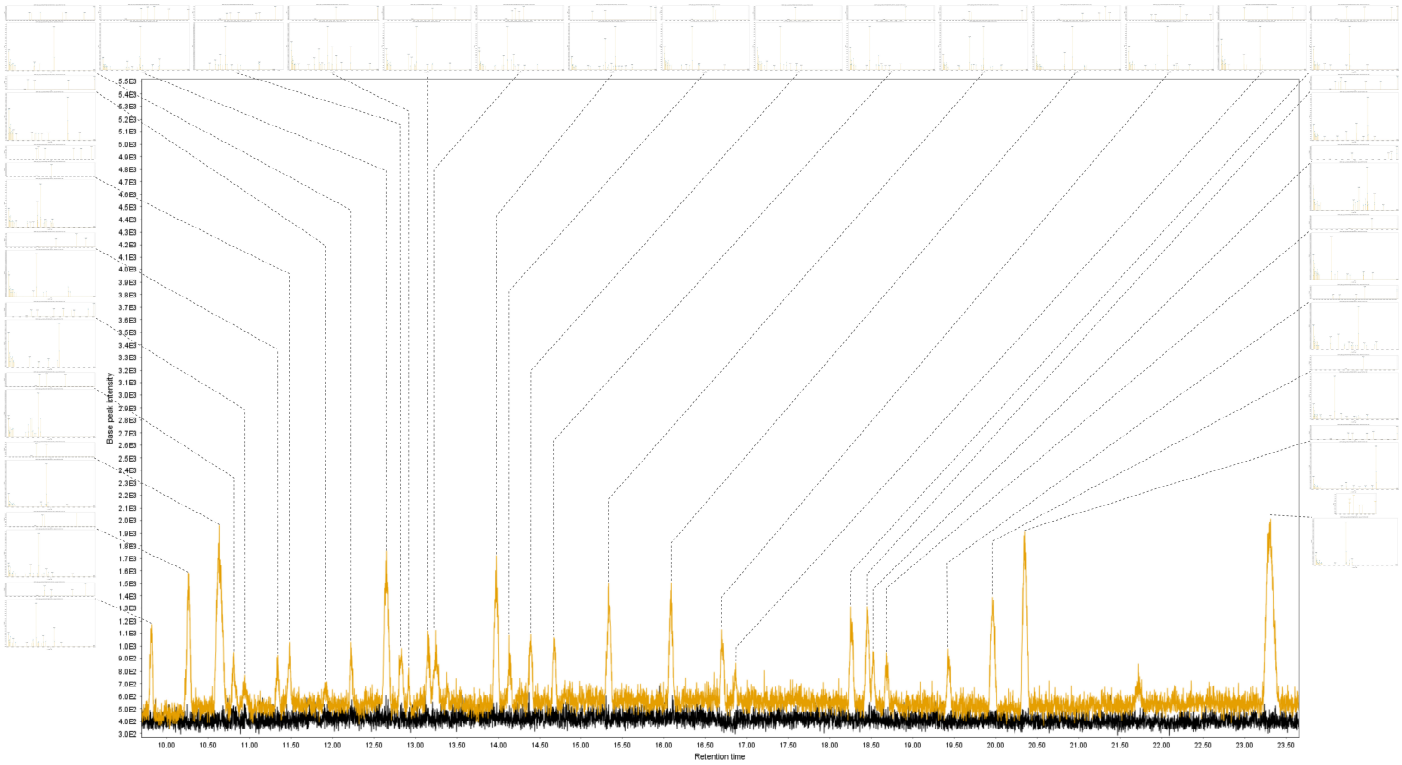


Figure S7. *V. zhaodongensis* BS253 EPS-EF fragments between 9.8-24 min in negative mode [M-H]$^-$. Chromatogram is in the center, and the spectra is around the chromatogram. Each MS/MS is above its respectively MS. Black line is control, and the brownish line is the EPS-EF sample.

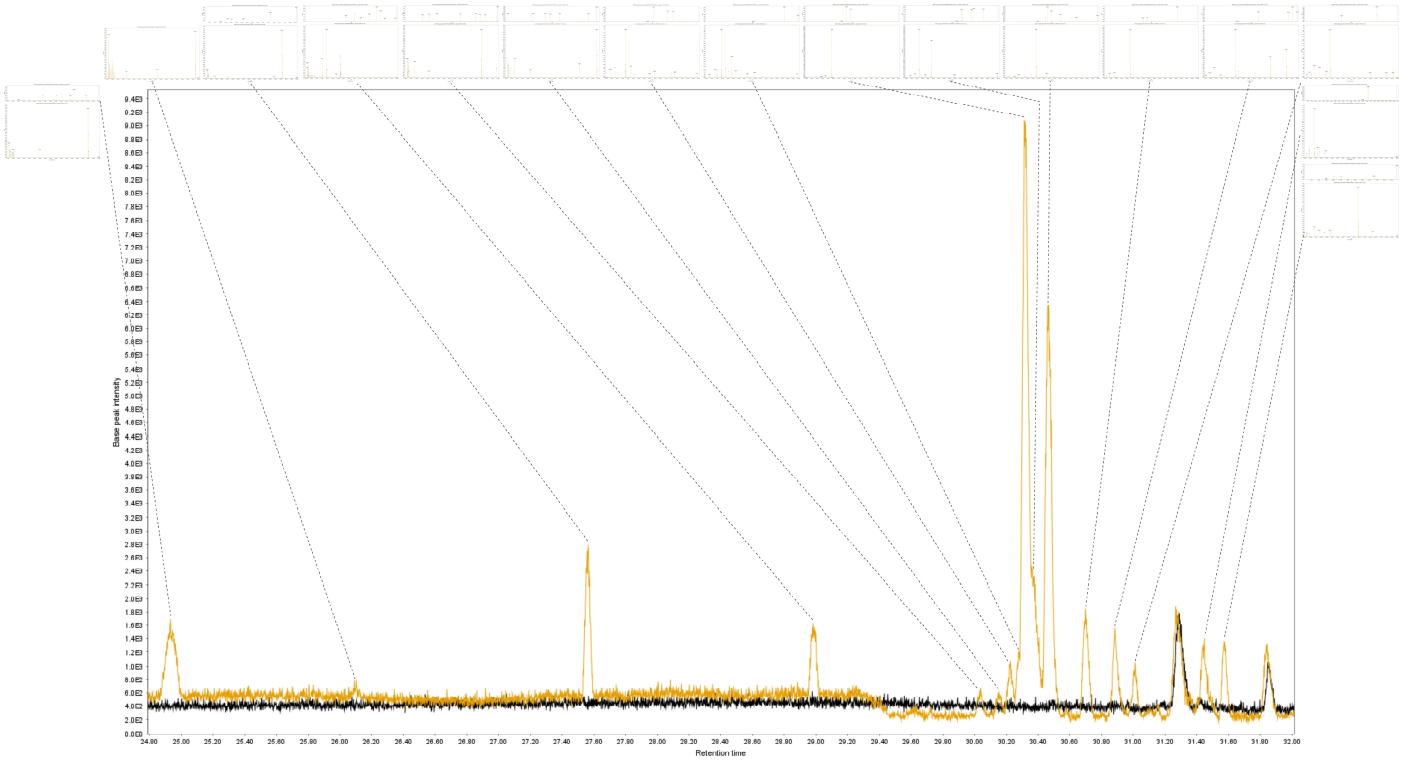


Figure S8. *V. zhaodongensis* BS253 EPS-EF fragments between 24.5-31.2 min in negative mode [M-H]$^-$. Chromatogram is on the bottom, and the spectra is on the top of the figure. Each MS/MS is above its respectively MS. Black line is control, and the brownish line is the EPS-EF sample.

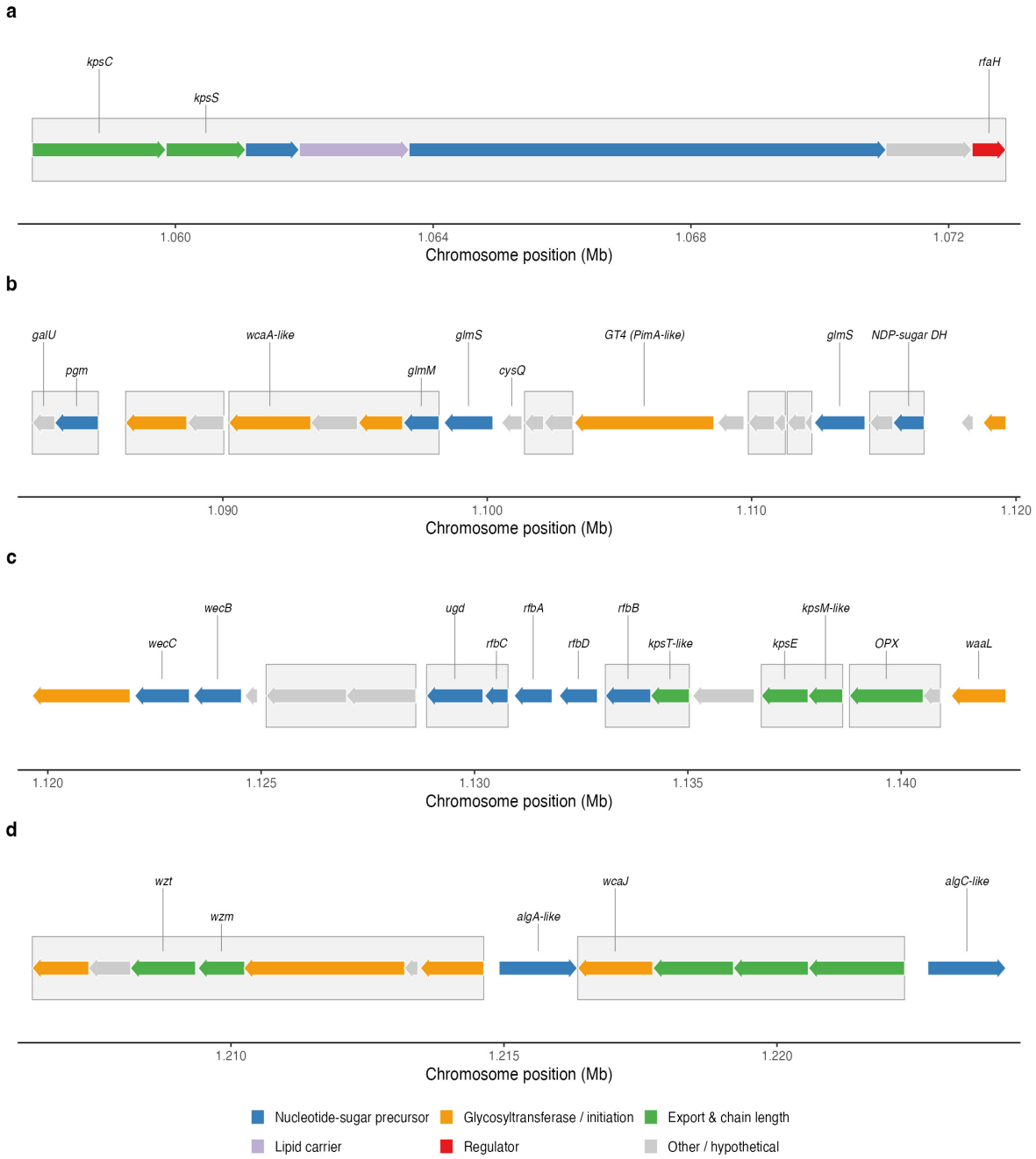


Figure S9. Genomic context of the EPS-related candidate loci in *V. zhaodongensis* BS253. Arrows represent coding sequences drawn to scale on the chromosome (RefSeq NZ_CP195113.1) and point in the direction of transcription; colours denote functional class, as indicated in the key. Grey boxes delimit predicted transcription units, defined as runs of consecutive co-directional coding sequences separated by no more than 50 bp. (a) Group 2 capsule (*kps*) assembly module, positions 1,057,779-1,072,888; all seven coding sequences form a single predicted transcription unit. (b,c) Proximal and distal halves of the 59.7-kb nucleotide-sugar, glycosyltransferase and export island, positions 1,082,793-1,142,454; all 41 coding sequences are transcribed from the same strand. (d) Second glycosyltransferase and ABC-exporter module containing *wcaJ*, positions 1,206,361-1,224,193. Gene symbols in italics are those of the RefSeq annotation; symbols followed by "-like", and the label OPX, denote family-level assignments obtained by NCBI CD-Search. Transcription units shown are computational predictions and were not mapped experimentally.

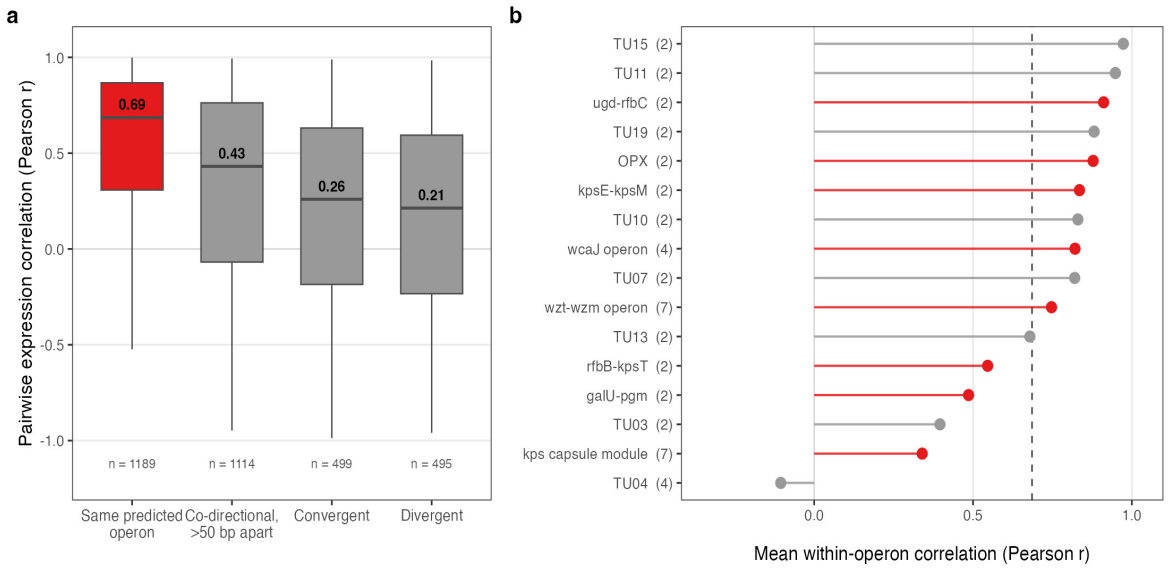


Figure S10. Predicted transcription units of *V. zhaodongensis* BS253 are co-expressed. Adjacent genes sharing a predicted operon are co-expressed, and the export and initiation operons are among the most internally coherent units in the genome, whereas the capsule module is not. (a) Distribution of pairwise Pearson correlations between the variance-stabilised expression profiles of adjacent chromosomal genes across the twelve RNA-Seq samples, grouped by the relative orientation and spacing of each pair. Boxes show the median and interquartile range; whiskers extend to 1.5 times the interquartile range and outliers are omitted. Medians are printed above each box and the number of gene pairs below; the corresponding test statistics are given in the Results. (b) Mean within-unit correlation for each multi-gene predicted transcription unit of the three EPS-related chromosomal modules, showing which operons are co-expressed; the number of coding sequences per unit is given in parentheses and the units discussed in the text are highlighted. The dashed line marks the genome-wide median correlation for pairs sharing a predicted transcription unit. Genes with a mean normalised count below 10 were excluded.

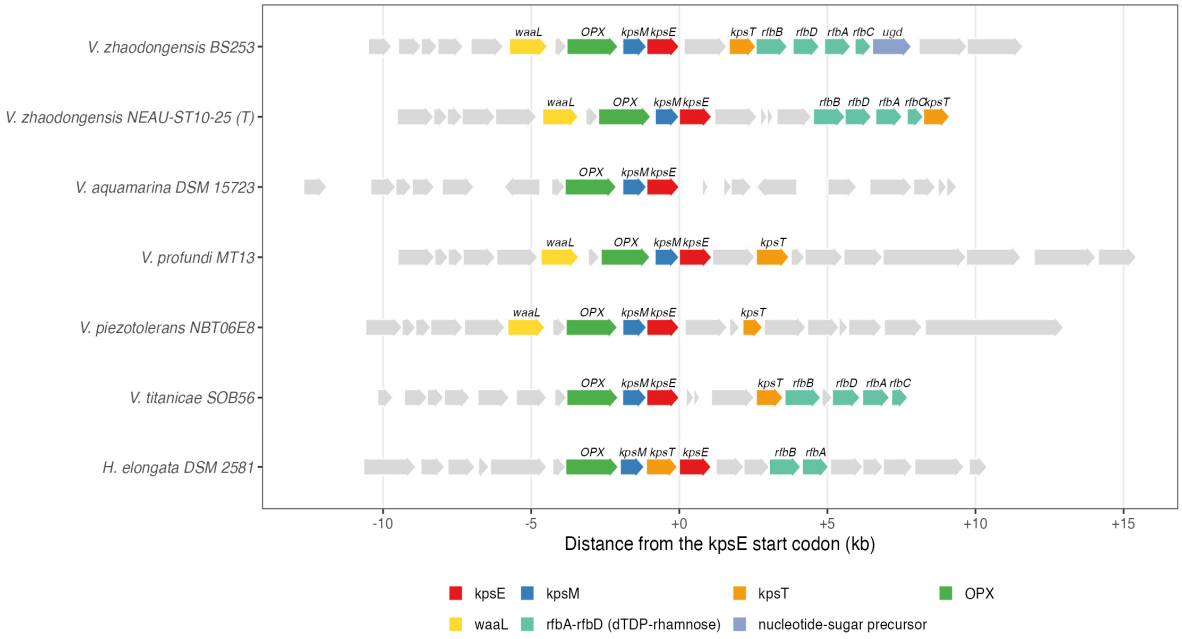


Figure S11. Conservation of the polysaccharide-export locus across related Halomonadaceae. Each row shows the genomic neighbourhood of the kpsE orthologue in one genome, centred on the kpsE start codon and oriented so that kpsE is transcribed left to right; nine coding sequences are shown on either side. Arrows are drawn to scale and point in the direction of transcription. Coloured arrows are orthologues of the V. zhaodongensis BS253 candidate loci,

assigned by reciprocal best DIAMOND hits; grey arrows are coding sequences without an orthologue among the candidate set. Genomes are ordered from BS253 (top) to Halomonas elongata (bottom). Amino-acid identities for every orthologue are given in Table S5.

Table S1. Chromatography gradient used for UHPLC analysis.

Time (minutes)	Flow (mL/min)	Concentration A (%)	Concentration B (%)
0.00	1.0	100.0	0.0
2.00	1.0	100.0	0.0
25.00	1.0	75.0	25.0
40.00	1.0	20.00	80.00
42.00	1.0	0.0	100.0
50.00	1.0	0.0	100.0
50.10	1.0	100.0	0.0
57.00	1.0	100.0	0.0

Table S2. Ions detected at each retention time (RT) after blank subtraction.

RT (min)	Fragments (m/z)
3.34	643.1064, 362.0523, 321.0495,
3.54	693.1225, 677.1261, 661.1325, 428.0292, 346.0551, 330.0611
3.92	346.0551
4.69	344.0421
5.73	609.0760, 533.1761, 469.2099, 346.1590
5.92	755.0893, 610.0626, 533.1761, 446.1908, 431.1797, 374.1557, 364.2006
6.07	544.1889, 418.1936, 362.0523, 342.1672, 332.1474
6.09	522.2320, 418.1936, 362.0523, 342.1672, 332.1474, 280.0720, 271.0598
6.12	628.0731, 561.1445, 404.9389, 360.1256, 343.0652, 280.0690
6.17	629.0576, 490.2158, 443.2283, 418.1936, 346.0551, 302.1343, 280.0690
6.19	667.0959, 443.2283, 418.1936, 359.1592, 346.0584, 330.1689, 302,1343
6.25	649.0815, 627.0895, 465.2077, 374.1253, 330.1689, 302.1373
6.32	489.2310, 316.1497
6.38	595.0994, 373.1740, 346.1655, 332.1474, 316.1528
6.43	487.2644, 346.1655
6.47	633.0864, 490.2197
6.50	650.0689, 633.0908, 490.2158, 324.5297
6.57	634.0704, 628.0731, 577.0851, 476.5569, 346.1623, 302.1343
6.66	549.1956, 436.9351, 434.9348, 398.9595, 337.0922, 274.0937
6.76	547.1240, 430.2416, 405.2023, 355.1949, 316.1559, 274.0937
6.81	673.0951, 476.5607, 430.2416, 426.9142, 388.9390, 327.0686, 274.0937
6.84	673.0951, 446.1429, 387.1892, 264.0748
6.91	893.2921, 668.0788, 544.1075, 446.1429, 374.0882
6.99	707.0997, 588.2311, 566.2242, 472.2048, 446.1429, 402.1973, 344.1845
7.08	662.2188, 652.0861, 587.1270, 468.5600, 401.0240, 346.1623
7.13	691.1070, 662.2188, 619.1133, 502.2161, 485.5670, 416.1797, 389.1697, 331.1590, 280.0690, 274.0937, 271.0598, 264.0748
7.22	707.1043, 691.1070, 668.0788, 651.0971, 486.0632, 460.2038, 435.1277, 342.1672, 330.1689
7.28	652.0816, 544.2337, 517.2231, 505.5733, 486.0555, 415.1834, 316.1528, 307.0500
7.32	652.0816, 619.2740, 610.0971, 426.9467, 417.1503, 316.1528, 307.0500, 299.0632
7.37	978.1381, 691.1070, 675.2565, 643.1330, 630.2749, 610.0971, 585.2932, 560.2231, 488.5634, 476.1989, 430.1982, 392.1464, 316.1869, 307.0500
7.42	651.1016, 617.0915, 585.3059, 501.2311, 392.1464, 375.1894, 371.1944, 359.1592, 346.1655, 316.1900
7.47	852.1595, 621.0819, 558.2092, 548.2226, 499.2560, 489.0612, 485.5670, 446.2314, 425.5775, 416.1761, 389.1697, 371.1944, 360.1786, 346.1623, 274.1428, 259.1296
7.53	884.1462, 791.2643, 716.3272, 638.5782, 601.0957, 588.1084, 548.1001, 503.2491, 461.5750, 446.1945, 403.1843, 371.1944, 274.1457
7.56	956.1368, 791.2545, 716.3272, 601.0957, 588.1126, 517.5724, 503.2569, 477.5670, 460.2076, 446.1908, 430.1982, 403.1849, 389.1697, 371.1944, 330.1689, 274.1400

7.60	726.2586, 691.1070, 675.1114, 638.0844, 610.2523, 567.2088, 492.1845, 477.5708, 446.1871, 430.1982, 403.1884, 387.1892, 371.1944, 359.1592, 330.1689, 274.1400
7.62	963.1214, 726.2680, 691.1024, 675.1068, 661.0966, 638.0888, 619.0785, 610.2523, 546.2549, 525.5713, 517.2310, 492.1845, 481.0629, 477.5746, 474.2244, 457.1988, 446.1945, 430.1982, 417.1700, 403.1849, 387.1926, 371.1911, 359.1559, 330.1689, 296.1280, 284.1609, 274.1400
7.71	962.1468, 892.1658, 853.1583, 729.3282, 641.0855, 592.0891, 570.2136, 540.1701, 534.2445, 513.2342, 480.5731, 477.1743, 460.2076, 446.1908, 429.2034, 417.2021, 403.1884, 399.1966, 388.1754, 359.1923, 342.1672, 316.1528
7.83	661.0921, 650.5852, 601.0273, 587.1270, 525.5713, 519.2452, 511.1330, 506.0639, 497.5730, 489.2387, 478.0629, 461.5713, 433.1968, 399.1896, 379.9265, 373.1740, 345.1792, 341.1801, 334.9872, 318.0578, 291.0417, 255.0611
7.92	996.1496, 853.1481, 791.2594, 670.5891, 650.5807, 630.0866, 589.2135, 545.2561, 529.2264, 519.2413, 504.2322, 497.5730, 488.2009, 453.1628, 447.2125, 433.1932, 414.1990, 403.1814, 399.1896, 359.1559, 292.0489, 255.0611
7.93	996.1496, 908.1665, 685.2335, 670.5891, 650.5807, 630.0866, 603.3055, 589.2135, 564.2161, 545.2561, 529.2264, 519.2413, 504.2322, 497.5730, 488.2009, 453.1628, 447.2125, 433.1932, 414.1990, 403.1814, 399.1896, 359.1559, 292.0489, 255.0611
8.09	932.1838, 687.3090, 575.1876, 518.2516, 509.5797, 502.2161, 489.2310, 473.5786, 465.5842, 463.1887, 403.1849, 399.1896, 356.1823
8.13	854.1373, 645.0951, 634.2769, 575.1834, 544.2419, 518.2516, 506.0600, 486.2248, 403.1884, 375.1894, 356.1823, 345.1792, 328.1900
8.20	997.1358, 917.1607, 791.2692, 703.3320, 670.0921, 646.2657, 580.2378, 531.2437, 509.5758, 501.2311, 498.0636, 472.5727, 460.2076, 431.1797, 403.1849, 399.1896, 394.1637, 344.1845
8.24	980.1586, 930.1549, 682.1032, 646.2702, 627.1375, 588.1126, 570.2094, 561.2520, 543.2429, 531.2437, 518.2158, 503.2491, 489.5785, 464.5794, 447.2088, 431.1833, 403.1814, 394.1637, 360.1786, 344.1845, 288.1610
8.29	920.3133, 876.1782, 682.1078, 646.2702, 627.1332, 619.2609, 588.1084, 558.2463, 518.2118, 502.220, 490.2158, 479.1777, 460.2038, 447.2088, 430.1946, 403.1814, 394.1325, 373.1740, 302.1373
8.40	916.1885, 794.6256, 662.6006, 603.2712, 571.1308, 531.2437, 501.5788, 490.2158, 461.1890, 442.1965, 430.1982, 402.2008, 385.2104, 375.1894, 351.0367, 342.1317
8.49	933.1751, 876.1730, 715.3000, 642.0890, 605.2403, 589.2177, 573.2514, 565.2322, 530.2627, 518.2118, 510.1866, 466.0776, 446.2240, 437.5847, 431.1797, 403.1879, 395.1587, 373.1740, 356.1823, 345.1759, 330.1689
8.54	932.1625, 877.1548, 730.3277, 670.5982, 642.0934, 611.1407, 575.1876, 561.2479, 518.2118, 504.2322, 460.0728, 442.2332, 416.2153, 403.1849, 395.1587, 356.1823, 345.1759
8.58	956.1907, 878.1474, 670.5891, 611.1407, 604.2961, 572.1154, 504.2362, 477.5899, 469.0739, 461.1927, 403.1849, 389.2110, 356.1823, 345.1759, 316.1559
8.67	920.3028, 914.1718, 900.1851, 673.1630, 615.2764, 591.2613, 561.2479, 500.2353, 473.2407, 459.6462, 445.1961, 403.1849, 373.1740, 328.1868, 302.1373
8.79	916.1780, 559.2734, 531.2437, 523.1656, 517.2628, 510.1905, 488.2048, 457.5869, 444.2135, 431.2123, 403.1849, 373.1740, 344.1813, 328.7656
8.82	956.1907, 916.1727, 900.1903, 627.3124, 510.1866, 486.2248, 477.5899, 457.5832, 444.2135, 433.1968, 417.2021, 403.1849, 358.2008, 345.1792, 328.1520
8.87	956.1853, 877.1651, 627.367, 604.2618, 556.2771, 545.2561, 486.2210, 470.2274, 438.0777, 417.1985, 403.1884, 358.2008, 336.1221, 298.1766
8.97	978.1545, 962.1847, 940.1932, 917.1607, 901.1749, 807.3584, 674.3000, 615.2764, 599.3172, 556.2771, 546.2100, 469.5918, 460.2413, 449.1706, 359.1956, 298.1796

9.09	733.3397, 640.2639, 599.3214, 556.2771, 503.2413, 480.1791, 460.2488, 445.1961, 433.2331, 416.2188, 387.1892, 329.1866, 316.1528, 298.1766
9.17	940.1879, 789.3706, 722.0087, 684.0325, 640.2639, 595.1419, 565.2322, 532.1491, 486.2248, 473.2407, 469.5956, 444.2172, 417.1985, 393.1423, 375.1894, 359.1956, 350.1381, 342.1672, 300.1960
9.30	938.1396, 922.1831, 900.1851, 761.3381, 728.3059, 652.2153, 577.2318, 548.2594, 532.1491, 484.2873, 474.2282, 449.5923, 432.2094, 387.1926, 373.1740, 342.1640
9.45	962.1576, 946.1852, 924.2110, 727.2937, 627.3552, 599.3086, 587.2834, 561.2520, 541.2618, 531.2437, 515.2525, 494.1881, 461.5938, 444.2098, 417.2056, 403.1849, 392.1498, 342.1672, 300.1960
9.82	677.3169, 607.2813, 526.2197, 500.2353, 456.2478, 430.2344, 401.2040, 350.1348, 341.1866, 328.7624
10.27	554.1429, 531.2799, 508.2097, 457.2436, 442.2332, 432.2130, 408.1832, 389.2041, 376.1500, 369.2167, 328.7688
10.64	547.2710, 530.2466, 529.2665, 484.2835, 479.1854
10.81	474.2331, 451.2331, 429.2431, 418.1900, 400.2224, 390.1687, 376.1568, 355.2014, 330.7685
10.94	655.3478, 640.2595, 458.2293, 369.2133
11.34	761.4440, 742.3796, 528.2793, 502.2513, 431.2521, 401.2075
11.48	589.2855, 476.2217, 470.2084, 445.2292, 440.2500, 401.2075, 373.2145, 342.1704
11.92	856.4135, 738.3814, 548.2472, 484.2412, 454.2705, 426.2402, 413.2442, 387.1892
12.23	604.3218, 465.1701, 454.2705, 413.2442, 401.2075
12.65	714.3342, 703.3736, 649.2949, 552.2876, 528.2312, 517.2668, 498.2622, 399.1757
12.83	860.3658, 850.3723, 674.2275, 649.2860, 527.2851, 476.2179, 463.1887, 426.2366, 373.2078
12.92	924.4050, 850.3571, 738.2628, 649.2949, 597.2427, 557.2242, 515.2841, 430.2344, 383.2263
13.16	796.3040, 621.2820, 575.3090, 484.2796, 463.1849, 443.2136, 413.2442, 401.1865, 383.2298
13.25	743.3925, 615.2937, 520.2439, 508.2412, 484.2796, 443.2136, 408.1796, 324.1903
13.98	763.3377, 702.3003, 665.3256, 632.3314, 595.3208, 575.2838, 557.3024, 528.3034, 494.2269, 476.2217, 454.2668, 437.2051, 344.1813
14.14	763.3281, 562.0751, 500.2001, 437.2051, 421.1716, 380.1817
14.39	600.3002, 553.0384, 490.2428, 453.2037, 426.1790, 390.2032, 330.7621, 257.1501
14.68	664.3042, 565.2654, 555.3185, 516.2671, 486.2018, 476.2255, 447.1904, 431.2521, 421.1788, 358.1975, 328.7624, 315.1204
15.34	735.2975, 658.3444, 593.2659, 565.2654, 544.2704, 491.1977, 445.2219, 428.1953, 315.1204, 257.8222
16.09	660.3609, 643.2746, 522.2599, 447.2273
16.71	767.3642, 656.3623, 641.3109, 613.3645, 579.2461, 550.2185, 529.2545, 519.2492, 501.2271, 459.2459, 427.2533, 327.0907
16.86	573.3266, 548.2390, 415.2617, 387.2270
18.26	699.3020, 521.2275, 489.2310, 2717.1633
18.45	814.4000, 702.3326, 627.3124, 587.3426, 485.2056, 461.2452, 398.2000, 392.1637, 271.1662
18.52	858.46.26, 772.3127, 697.3927, 680.2950, 657.3015, 615.2980, 600.2788, 577.2696, 563.2797
18.69	754.3672, 663.3420, 657.3060, 503.0651, 403.2199, 376.2041, 340.2266, 330.7653
19.43	789.3166, 771.3819, 740.3412, 692.3279, 669.3515, 611.3435, 548.2758, 516.3067, 474.2586, 447.2383, 411.2599, 333.1340
19.96	698.3793, 626.2550, 612.2759, 592.2589, 569.2930, 535.0556, 437.2088, 410.1847, 374.2097, 328.7688
20.35	785.3503, 747.3759, 682.3767, 621.2646, 564.2327, 486.2941, 445.2476

23.31	536.2754, 509.2528, 473.2786, 360.2415
24.94	898.4371, 447.2051
26.10	969.4738, 616.3374, 330.7589, 328.7688
27.56	914.3565, 898.4005, 882.4242, 860.4426, 784.8271, 361.2160, 343.2656
28.99	478.9065, 468.8736, 433.9090, 344.0097, 330.7653, 300.0207
30.05	987.4715, 846.4380
30.15	987.4770, 828.4144, 375.1927, 329.2372
30.23	987.4770, 782.36.50, 753.3566, 594.4482, 549.2283, 412.2373, 386.1700, 375.1894, 329.2309, 249.1536
30.28	987.4715, 594.4439, 529.387, 417.2128, 385.0494, 357.0589, 329.2341, 289.0890, 255.1057
30.32	987.4770, 594.4482, 529.3308, 417.2092, 385.0494, 375.1860, 357.0622, 329.2341, 289.0890, 269.1325
30.37	987.4770, 594.4524, 385.0528, 269.1225
30.47	594.4567, 526.2437, 491.2751, 464.2559, 428.2783, 385.0494, 377.1999, 327.1633, 283.0999, 269.1325
30.70	385.0494, 377.1999, 265.1535
30.88	895.4005, 746.9132, 456.2030, 426.9683, 321.1026, 291.1072
31.01	958.80.97, 895.3953, 746.9180, 386.2009, 377.1999, 344.2428, 330.7621, 281.1214
31.44	341.1769, 329.2309, 281.1214, 266.9896, 237.1162
31.57	877.3822, 740.5786, 637.0312, 444.9715, 379.2159, 339.1620, 329.2372, 281.1243

Table S3. Coordinates, strand, intergenic distances, predicted transcription units, conserved-domain assignments and within-unit expression correlations for the coding sequences of the three EPS-related chromosomal modules of *V. zhaodongensis* BS253 (RefSeq GCF_051175405.1). Intergenic distance is measured to the immediate upstream coding sequence; negative values indicate overlapping coding sequences. The final column indicates whether each coding sequence was included in the targeted gene set used for the differential-expression and co-expression analyses.

Region	Predicted_TU	Locus_tag	Protein_ID	Assigned_name	RefSeq_gene_symbol	RefSeq_product	Replicon	Start	End	Strand	Intergenic_gap_to_upstream_CDS_bp	CD_Search_top_hits	In_author_gene_set	Mean_within_TU_correlation
A	TU01	ACR0PX_RS04745	WP_434986121.1	kpsC		capsular polysaccharide biosynthesis protein	NZ_CP195113.1	1057779	1059854	+	305.0	KpsC (E=0e+00)	no	0.34
A	TU01	ACR0PX_RS04750	WP_434986122.1	kpsS		capsule biosynthesis protein	NZ_CP195113.1	1059856	1061091	+	2.0	KpsS (E=0e+00)	no	0.34
A	TU01	ACR0PX_RS04755	WP_434986124.1			SDR family NAD(P)-dependent oxidoreductase	NZ_CP195113.1	1061088	1061921	+	-3.0		no	0.34
A	TU01	ACR0PX_RS04760	WP_434986126.1			LTA synthase family protein	NZ_CP195113.1	1061923	1063629	+	2.0		no	0.34
A	TU01	ACR0PX_RS04765	WP_434986127.1			SDR family NAD(P)-dependent oxidoreductase	NZ_CP195113.1	1063626	1071029	+	-3.0		no	0.34
A	TU01	ACR0PX_RS04770	WP_179926796.1			aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	NZ_CP195113.1	1071026	1072360	+	-3.0		no	0.34
A	TU01	ACR0PX_RS04775	WP_162218250.1	rfaH	rfaH	transcription/translation regulatory transformer protein RfaH	NZ_CP195113.1	1072364	1072888	+	4.0		no	0.34
B	TU02	ACR0PX_RS04815	WP_434986136.1	galU		UTP--glucose-1-phosphate uridylyltransferase	NZ_CP195113.1	1082793	1083647	-	124.0	GalU (E=3e-148)	yes	0.486
B	TU02	ACR0PX_RS04820	WP_434987019.1	pgm	pgm	phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	NZ_CP195113.1	1083644	1085290	-	-3.0	PGM_like3 (E=0e+00)	yes	0.486
B	TU03	ACR0PX_RS04825	WP_434986138.1			glycosyltransferase family 2 protein	NZ_CP195113.1	1086323	1088635	-	1033.0		yes	0.396
B	TU03	ACR0PX_RS04830	WP_434986139.1			hypothetical protein	NZ_CP195113.1	1088672	1090039	-	37.0		no	0.396
B	TU04	ACR0PX_RS04835	WP_434986141.1	wcaA-like		glycosyltransferase	NZ_CP195113.1	1090230	1093325	-	191.0	WcaA (E=2e-46)		
B	TU04	ACR0PX_RS04840	WP_434986142.1			hypothetical protein	NZ_CP195113.1	1093328	1095088	-	3.0		no	-0.105
B	TU04	ACR0PX_RS04845	WP_434986143.1			glycosyltransferase family 2 protein	NZ_CP195113.1	1095133	1096797	-	45.0		yes	-0.105
B	TU04	ACR0PX_RS04850	WP_434986144.1	glmM	glmM	phosphoglucosamine mutase	NZ_CP195113.1	1096838	1098175	-	41.0		yes	-0.105

B	TU05	ACR0PX_RS04855	WP_434986146.1	glmS	glmS	glutamine--fructose-6-phosphate transaminase (isomerizing)	NZ_CP195113.1	1098368	1100215	-	193.0		yes	
B	TU06	ACR0PX_RS04860	WP_434986148.1	cysQ	cysQ	3'(2'),5'-bisphosphate nucleotidase CysQ	NZ_CP195113.1	1100544	1101314	-	329.0		no	
B	TU07	ACR0PX_RS04865	WP_434986149.1			DUF6270 domain-containing protein	NZ_CP195113.1	1101410	1102129	-	96.0		no	0.82
B	TU07	ACR0PX_RS04870	WP_434986150.1			hypothetical protein	NZ_CP195113.1	1102155	1103237	-	26.0		no	0.82
B	TU08	ACR0PX_RS04875	WP_434986151.1	GT4 (PimA-like)		glycosyltransferase	NZ_CP195113.1	1103301	1108571	-	64.0	COG4641 (E=2e-50)		
B	TU09	ACR0PX_RS04880	WP_434986152.1			hypothetical protein	NZ_CP195113.1	1108722	1109708	-	151.0		no	
B	TU10	ACR0PX_RS04885				nucleotidyl transferase AbiEii/AbiGii toxin family protein	NZ_CP195113.1	1109874	1110863	-	166.0		no	0.83
B	TU10	ACR0PX_RS04890	WP_434986153.1			DUF6088 family protein	NZ_CP195113.1	1110860	1111276	-	-3.0		no	0.83
B	TU11	ACR0PX_RS04895	WP_434986154.1			zeta toxin family protein	NZ_CP195113.1	1111345	1112037	-	69.0		no	0.948
B	TU11	ACR0PX_RS04900	WP_434986155.1			hypothetical protein	NZ_CP195113.1	1112019	1112282	-	-18.0		no	0.948
B	TU12	ACR0PX_RS04905	WP_434986156.1	glmS	glmS	glutamine--fructose-6-phosphate transaminase (isomerizing)	NZ_CP195113.1	1112373	1114286	-	91.0		yes	
B	TU13	ACR0PX_RS04910	WP_434986157.1			class I SAM-dependent methyltransferase	NZ_CP195113.1	1114465	1115337	-	179.0		no	0.679
B	TU13	ACR0PX_RS04915	WP_434986159.1	NDP-sugar DH		nucleotide sugar dehydrogenase	NZ_CP195113.1	1115355	1116521	-	18.0	PRK15057 superfamily (E=0e+00)	yes	0.679
B	TU14	ACR0PX_RS04920	WP_434986160.1			IS3 family transposase	NZ_CP195113.1	1117925	1118378	-	1404.0		no	
B	TU15	ACR0PX_RS04925	WP_434986161.1			ATP-grasp fold amidoligase family protein	NZ_CP195113.1	1118761	1119618	-	383.0		no	0.973
B	TU15	ACR0PX_RS04930	WP_434986162.1			glycosyltransferase family protein	NZ_CP195113.1	1119636	1121927	-	18.0		yes	0.973
B	TU16	ACR0PX_RS04935	WP_434986163.1	wecC	wecC	UDP-N-acetyl-D-mannosamine dehydrogenase	NZ_CP195113.1	1122038	1123318	-	111.0		yes	
B	TU17	ACR0PX_RS04940	WP_434986165.1	wecB	wecB	non-hydrolyzing UDP-N-acetylglucosamine 2-epimerase	NZ_CP195113.1	1123419	1124537	-	101.0		yes	

B	TU18	ACR0PX_RS04945	WP_434986166.1		hypothetical protein	NZ_CP195113.1	1124621	1124911	-	84.0		no	
B	TU19	ACR0PX_RS04950	WP_434986167.1		hypothetical protein	NZ_CP195113.1	1125114	1127000	-	203.0		no	0.881
B	TU19	ACR0PX_RS04955	WP_434986168.1		hypothetical protein	NZ_CP195113.1	1126997	1128625	-	-3.0		no	0.881
B	TU20	ACR0PX_RS04960	WP_434986169.1	ugd	UDP-glucose dehydrogenase family protein	NZ_CP195113.1	1128876	1130198	-	251.0	Ugd (E=0e+00)	yes	0.911
B	TU20	ACR0PX_RS04965	WP_434986170.1	rfbC rfbC	dTDP-4-dehydrorhamnose 3,5-epimerase	NZ_CP195113.1	1130241	1130786	-	43.0		yes	0.911
B	TU21	ACR0PX_RS04970	WP_434986171.1	rfbA rfbA	glucose-1-phosphate thymidylyltransferase RfbA	NZ_CP195113.1	1130929	1131819	-	143.0		yes	
B	TU22	ACR0PX_RS04975	WP_434986172.1	rfbD rfbD	dTDP-4-dehydrorhamnose reductase	NZ_CP195113.1	1131986	1132879	-	167.0		yes	
B	TU23	ACR0PX_RS04980	WP_434986173.1	rfbB rfbB	dTDP-glucose 4,6-dehydratase	NZ_CP195113.1	1133066	1134130	-	187.0		yes	0.546
B	TU23	ACR0PX_RS04985	WP_434986175.1	kpsT-like	ABC transporter ATP-binding protein	NZ_CP195113.1	1134127	1135035	-	-3.0	TagH (E=9e-105)	no	0.546
B	TU24	ACR0PX_RS04990	WP_434986176.1		MBL fold metallo-hydrolase RNA specificity domain-containing protein	NZ_CP195113.1	1135112	1136554	-	77.0		no	
B	TU25	ACR0PX_RS04995	WP_434986177.1	kpsE	chain-length determining protein	NZ_CP195113.1	1136720	1137817	-	166.0	KpsE (E=1e-124)	yes	0.835
B	TU25	ACR0PX_RS05000	WP_434986178.1	kpsM-like	ABC transporter permease	NZ_CP195113.1	1137821	1138630	-	4.0	TagG (E=2e-34)	yes	0.835
B	TU26	ACR0PX_RS05005	WP_434986179.1	OPX	polysaccharide biosynthesis/export family protein	NZ_CP195113.1	1138786	1140513	-	156.0	Wza (E=1e-39)		
B	TU26	ACR0PX_RS05010	WP_434986180.1		DVU3141 family protein	NZ_CP195113.1	1140516	1140920	-	3.0		no	0.878
B	TU27	ACR0PX_RS05015	WP_434986182.1	waaL	O-antigen ligase family protein	NZ_CP195113.1	1141174	1142454	-	254.0	RfaL (E=1e-27)	yes	
C	TU28	ACR0PX_RS05295	WP_434986229.1		glycosyltransferase family 4 protein	NZ_CP195113.1	1206361	1207395	-	606.0		yes	0.747
C	TU28	ACR0PX_RS05300	WP_434986231.1		DUF4214 domain-containing protein	NZ_CP195113.1	1207392	1208162	-	-3.0		no	0.747
C	TU28	ACR0PX_RS05305	WP_434986232.1	wzt	ABC transporter ATP-binding protein	NZ_CP195113.1	1208159	1209352	-	-3.0	TagH (E=9e-132)		
C	TU28	ACR0PX_RS05310	WP_434986233.1	wzm	ABC transporter permease	NZ_CP195113.1	1209400	1210251	-	48.0	TagG (E=2e-54)	no	0.747
C	TU28	ACR0PX_RS05315	WP_434986234.1		glycosyltransferase	NZ_CP195113.1	1210235	1213183	-	-16.0		yes	0.747

C	TU28	ACR0PX_RS05320	WP_434986235.1			hypothetical protein	NZ_CP195113.1	1213173	1213424	-	-10.0		no	0.747
C	TU28	ACR0PX_RS05325	WP_434986237.1			glycosyltransferase	NZ_CP195113.1	1213471	1214628	-	47.0		no	0.747
C	TU29	ACR0PX_RS05330	WP_434986238.1	algA-like		mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	NZ_CP195113.1	1214911	1216344	+	283.0	Glyco_tranf_GTA_type superfamily (E=0e+00)	yes	
C	TU30	ACR0PX_RS05335	WP_434986240.1	wcaJ		undecaprenyl-phosphate glucose phosphotransferase	NZ_CP195113.1	1216350	1217723	-	6.0	PRK10124 superfamily (E=3e-151)	no	0.821
C	TU30	ACR0PX_RS05340	WP_434986242.1			TolC family outer membrane protein	NZ_CP195113.1	1217730	1219202	-	7.0		no	0.821
C	TU30	ACR0PX_RS05345	WP_434986244.1			HlyD family type I secretion periplasmic adaptor subunit	NZ_CP195113.1	1219202	1220575	-	0.0		no	0.821
C	TU30	ACR0PX_RS05350	WP_434986246.1			type I secretion system permease/ATPase	NZ_CP195113.1	1220577	1222337	-	2.0		no	0.821
C	TU31	ACR0PX_RS05355	WP_434986248.1	algC-like		phosphomannomutase	NZ_CP195113.1	1222763	1224193	+	426.0	ManB (E=0e+00)	yes	

Table S4. Correspondence between the gene symbols used in this study and the locus tags, product descriptions and conserved-domain assignments of RefSeq assembly GCF_051175405.1.

Author_label	Author_product	Locus_tag	RefSeq_product	CD_Search_top_hits	Module	Predicted_TU	Start	End	Strand	Action
glcP	MFS transporter	ACR0PX_RS06105	MFS transporter	FucP (E=2e-35)	outside	732	1381756	1382934	+	UNSUPPORTED as glcP â€" CD-Search: FucP. No GlcP-type glucose/galactose porter
glcP	MFS transporter	ACR0PX_RS03095	MFS transporter	MFS_YcxA_like (E=2e-79)	outside	373	702163	703371	+	UNSUPPORTED as glcP â€" CD-Search: MFS_YcxA_like. No GlcP-type glucose/galactose porter
glcP	MFS transporter	ACR0PX_RS05445	MFS transporter	UhpC superfamily (E=3e-03)	outside	648	1255399	1256712	+	UNSUPPORTED as glcP â€" CD-Search: UhpC superfamily. No GlcP-type glucose/galactose porter
glcP	MFS transporter	ACR0PX_RS10815	MFS transporter	UhpC (E=1e-37)	outside	1343	2443329	2444624	-	UNSUPPORTED as glcP â€" CD-Search: UhpC. No GlcP-type glucose/galactose porter
gntP	GntP family permease	ACR0PX_RS03090	GntP family permease	not run	outside	372	700696	702090	+	consistent
glk	glk	ACR0PX_RS00600	glucokinase	not run	outside	80	179980	180945	-	consistent
gntK	gluconokinase	ACR0PX_RS15625	gluconokinase	not run	outside	1935	3453300	3453824	+	consistent

pgm	pgm	ACR0PX_RS04820	phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	PGM_like3 (E=0e+00)	B	573	1083644	1085290	-	consistent
glmS	glmS	ACR0PX_RS04855	glutamine--fructose-6-phosphate transaminase (isomerizing)	not run	B	576	1098368	1100215	-	consistent
glmS	glmS	ACR0PX_RS04905	glutamine--fructose-6-phosphate transaminase (isomerizing)	not run	B	583	1112373	1114286	-	consistent
algC	phosphomannomutase/phosphoglucomutase	ACR0PX_RS13380	phosphomannomutase/phosphoglucomutase	not run	outside	1641	2981374	2982762	-	consistent
algC	phosphomannomutase/phosphoglucomutase	ACR0PX_RS05355	phosphomannomutase	ManB (E=0e+00)	C	638	1222763	1224193	+	consistent
galU	UTP--glucose-1-phosphate uridylyltransferase	ACR0PX_RS04815	UTP--glucose-1-phosphate uridylyltransferase	GalU (E=3e-148)	outside	573	1082793	1083647	-	consistent
glmM	glmM	ACR0PX_RS04850	phosphoglucosamine mutase	not run	B	575	1096838	1098175	-	consistent
glmM	glmM	ACR0PX_RS12555	phosphoglucosamine mutase	not run	outside	1536	2798245	2799594	+	consistent
algA	mannose-1-P guanylyltransferase/mannose-6-P isomerase	ACR0PX_RS05330	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	Glyco_tranf_GTA_type superfamily (E=0e+00)	C	636	1214911	1216344	+	consistent
algA	mannose-1-P guanylyltransferase/mannose-6-P isomerase	ACR0PX_RS15510	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	not run	outside	1917	3430410	3431819	+	consistent
hypothetic dehydrogenase #1	UDP-glucose dehydrogenase family protein	ACR0PX_RS04960	UDP-glucose dehydrogenase family protein	Ugd (E=0e+00)	B	591	1128876	1130198	-	RENAME to ugd â€″ CD-Search: Ugd (E=0). Locus listed 3x in the table

tuaD	UDP-glucose dehydrogenase family protein	ACR0PX_RS04960	UDP-glucose dehydrogenase family protein	Ugd (E=0e+00)	B	591	1128876	1130198	-	RENAME to ugd â€" CD-Search: Ugd (E=0). Locus listed 3x in the table
ugd	nucleotide sugar dehydrogenase	ACR0PX_RS04915	nucleotide sugar dehydrogenase	PRK15057 superfamily (E=0e+00)	B	584	1115355	1116521	-	RENAME â€" CD-Search gives PRK15057, not Ugd
glmU	glmU	ACR0PX_RS10800	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU	not run	outside	1341	2438997	2440364	+	consistent
hypothetic dehydrogenase #2	UDP-glucose dehydrogenase family protein	ACR0PX_RS04960	UDP-glucose dehydrogenase family protein	Ugd (E=0e+00)	B	591	1128876	1130198	-	RENAME to ugd â€" CD-Search: Ugd (E=0). Locus listed 3x in the table
wecB	wecB	ACR0PX_RS04940	non-hydrolyzing UDP-N-acetylglucosamine 2-epimerase	not run	B	588	1123419	1124537	-	consistent
wecC	wecC	ACR0PX_RS04935	UDP-N-acetyl-D-mannosamine dehydrogenase	not run	B	587	1122038	1123318	-	consistent
rffG	rfbA	ACR0PX_RS04970	glucose-1-phosphate thymidylyltransferase RfbA	not run	B	592	1130929	1131819	-	consistent
rfbB	rfbB	ACR0PX_RS04980	dTDP-glucose 4,6-dehydratase	not run	B	594	1133066	1134130	-	consistent
rfbC	rfbC	ACR0PX_RS04965	dTDP-4-dehydrorhamnose 3,5-epimerase	not run	B	591	1130241	1130786	-	consistent
rfbD	rfbD	ACR0PX_RS04975	dTDP-4-dehydrorhamnose reductase	not run	B	593	1131986	1132879	-	consistent
uppS	uppS	ACR0PX_RS13495	polyprenyl diphosphate synthase	not run	outside	1656	3002725	3003510	+	consistent
uppP	undecaprenyl-diphosphate phosphatase	ACR0PX_RS10790	undecaprenyl-diphosphate phosphatase	not run	outside	1341	2437046	2437846	+	consistent
glycosyltransferase	glycosyltransferase	ACR0PX_RS04835	glycosyltransferase	WcaA (E=2e-46)						

glycosyltransferase	glycosyltransferase	ACR0PX_RS04875	glycosyltransferase	COG4641 (E=2e-50)						
glycosyltransferase	glycosyltransferase	ACR0PX_RS04930	glycosyltransferase family protein	not run	B	586	1119636	1121927	-	consistent
glycosyltransferase	glycosyltransferase	ACR0PX_RS05315	glycosyltransferase	not run	C	635	1210235	1213183	-	consistent
glycosyltransferase family 2 protein	GT2	ACR0PX_RS04825	glycosyltransferase family 2 protein	not run	B	574	1086323	1088635	-	consistent
glycosyltransferase family 2 protein	GT2	ACR0PX_RS04845	glycosyltransferase family 2 protein	not run	B	575	1095133	1096797	-	consistent
glycosyltransferase family 2 protein	GT2	ACR0PX_RS08630	glycosyltransferase family 2 protein	not run	outside	1069	1958571	1959995	-	consistent
glycosyltransferase family 2 protein	GT2	ACR0PX_RS11040	glycosyltransferase family 2 protein	not run	outside	1372	2499919	2500749	-	consistent
glycosyltransferase family 4 protein	GT4	ACR0PX_RS05295	glycosyltransferase family 4 protein	not run	C	635	1206361	1207395	-	consistent
glycosyltransferase family 4 protein	GT4	ACR0PX_RS11030	glycosyltransferase family 4 protein	not run	outside	1372	2497948	2498925	-	consistent
glycosyltransferase family 4 protein	GT4	ACR0PX_RS11045	glycosyltransferase family 2 protein	not run	outside	1372	2500746	2501504	-	consistent
glycosyltransferase family 4 protein	GT4	ACR0PX_RS12105	glycosyltransferase family 4 protein	not run	outside	1477	2703327	2704487	-	consistent
glycosyltransferase family 9 protein	GT9	ACR0PX_RS11055	glycosyltransferase family 9 protein	not run	outside	1373	2502251	2503348	+	consistent

msbA	msbA	ACR0PX_RS03900	lipid A export permease/ATP-binding protein MsbA	not run	outside	470	878651	880387	-	consistent
kpsE	chain-length determining protein	ACR0PX_RS04995	chain-length determining protein	KpsE (E=1e-124)	B	596	1136720	1137817	-	consistent
kpsE	chain-length determining protein	ACR0PX_RS05000	ABC transporter permease	TagG (E=2e-34)	B	596	1137821	1138630	-	MISLABELLED â€" this is the ABC permease (KpsM-like, CDD TagG)
kpsD	polysaccharide biosynthesis/export family protein	ACR0PX_RS05005	polysaccharide biosynthesis/export family protein	Wza (E=1e-39)						
waaL	O-antigen ligase family protein	ACR0PX_RS05015	O-antigen ligase family protein	RfaL (E=1e-27)	B	598	1141174	1142454	-	consistent
PEP-CTERM exosortase A EpsH	glycosyltransferase	ACR0PX_RS04875	glycosyltransferase	COG4641 (E=2e-50)						
WaaA	WaaA	ACR0PX_RS11065	lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase	not run	outside	1373	2504768	2506057	+	consistent
WaaF	WaaF	ACR0PX_RS11020	lipopolysaccharide heptosyltransferase II	not run	outside	1370	2495101	2496120	+	consistent
lptF	lptF	ACR0PX_RS13775	LPS export ABC transporter permease LptF	not run	outside	1688	3062509	3063588	+	consistent
lptG	lptG	ACR0PX_RS13780	LPS export ABC transporter permease LptG	not run	outside	1688	3063588	3064664	+	consistent
lptB	lptB	ACR0PX_RS04185	LPS export ABC transporter ATP-binding protein	not run	outside	497	935309	936091	+	consistent
lptA	lptA	ACR0PX_RS04180	lipopolysaccharide transport periplasmic protein LptA	not run	outside	497	934771	935280	+	consistent
lptE	lptE	ACR0PX_RS01275	LPS assembly lipoprotein LptE	not run	outside	157	322275	322787	-	consistent
lptD	lptD	ACR0PX_RS06720	LPS-assembly protein LptD	not run	outside	820	1521480	1523927	-	consistent
(not in table)		ACR0PX_RS05335	undecaprenyl-phosphate glucose phosphotransferase	PRK10124 superfamily (E=3e-151)	C	637	1216350	1217723	-	ADD to the analysed set â€" wcaJ â€" named in Abstract/Results/Fig 11C but ABSENT from the gene set

(not in table)	ACR0PX_RS04985	ABC transporter ATP-binding protein	TagH (E=9e-105)	B	594	1134127	1135035	-	ADD to the analysed set â€″ KpsT-like ABC ATP-binding â€″ completes the kps export system
(not in table)	ACR0PX_RS05305	ABC transporter ATP-binding protein	TagH (E=9e-132)						
(not in table)	ACR0PX_RS05310	ABC transporter permease	TagG (E=2e-54)	C	635	1209400	1210251	-	ADD to the analysed set â€″ Wzm-type ABC permease (2nd exporter)
(not in table)	ACR0PX_RS04745	capsular polysaccharide biosynthesis protein	KpsC (E=0e+00)	A	567	1057779	1059854	+	ADD to the analysed set â€″ KpsC â€″ group 2 capsule assembly
(not in table)	ACR0PX_RS04750	capsule biosynthesis protein	KpsS (E=0e+00)	A	567	1059856	1061091	+	ADD to the analysed set â€″ KpsS â€″ group 2 capsule assembly
(not in table)	ACR0PX_RS04775	transcription/translation regulatory transformer protein RfaH	not run	A	567	1072364	1072888	+	ADD to the analysed set â€″ RfaH â€″ antiterminator of kps/O-antigen operons

Table S5. Orthologues of the EPS-related candidate loci of *V. zhaodongensis* BS253 in six related Halomonadaceae genomes, with amino-acid identities from reciprocal best DIAMOND hits, and the number of intervening coding sequences between orthologues of adjacent BS253 genes.

gene	BS253_locus	*V. zhaodongensis* BS253	*V. zhaodongensis* NEAU-ST10-25 (T)	*V. aquamarina* DSM 15723	*V. profundi* MT13	*V. piezotolerans* NBT06E8	*V. titanicae* SOB56	*H. elongata* DSM 2581
kpsC	ACR0PX_RS04745	â€″	99%	73%	73%	74%	73%	56%
kpsS	ACR0PX_RS04750	â€″	99%	88%	81%	88%	84%	63%
kpsE	ACR0PX_RS04995	â€″	90%	87%	83%	88%	84%	65%
kpsM	ACR0PX_RS05000	â€″	91%	77%	85%	82%	83%	70%
kpsT	ACR0PX_RS04985	â€″	75%	83%	86%	84%	84%	74%
OPX	ACR0PX_RS05005	â€″	90%	80%	85%	80%	79%	66%
waaL	ACR0PX_RS05015	â€″	78%	58%	65%	68%	absent	absent
ugd	ACR0PX_RS04960	â€″	absent	71%	absent	65%	73%	73%

NDP-sugar DH	ACR0PX_RS04915	â€″	78%	absent	81%	absent	81%	absent
wecB	ACR0PX_RS04940	â€″	absent	absent	absent	89%	absent	absent
wecC	ACR0PX_RS04935	â€″	absent	absent	absent	88%	absent	absent
rfbA	ACR0PX_RS04970	â€″	94%	89%	absent	absent	92%	74%
rfbB	ACR0PX_RS04980	â€″	91%	82%	26%	absent	75%	81%
rfbC	ACR0PX_RS04965	â€″	87%	57%	absent	absent	80%	absent
rfbD	ACR0PX_RS04975	â€″	89%	61%	absent	absent	79%	absent
galU	ACR0PX_RS04815	â€″	98%	94%	87%	95%	54%	57%
pgm	ACR0PX_RS04820	â€″	94%	85%	81%	84%	82%	absent
glmM	ACR0PX_RS04850	â€″	absent	85%	absent	84%	82%	absent
wzt	ACR0PX_RS05305	â€″	absent	32%	absent	absent	89%	43%
wzm	ACR0PX_RS05310	â€″	absent	absent	absent	absent	87%	27%
wcaJ	ACR0PX_RS05335	â€″	42%	65%	42%	44%	70%	37%
algA	ACR0PX_RS05330	â€″	absent	absent	absent	absent	72%	absent
algC	ACR0PX_RS05355	â€″	absent	absent	absent	absent	77%	absent
rfaH	ACR0PX_RS04775	â€″	100%	83%	85%	86%	80%	63%
uppS	ACR0PX_RS13495	â€″	100%	91%	84%	93%	85%	69%
uppP	ACR0PX_RS10790	â€″	98%	81%	79%	82%	80%	69%
glmU	ACR0PX_RS10800	â€″	96%	86%	84%	88%	86%	76%