

Supporting materials

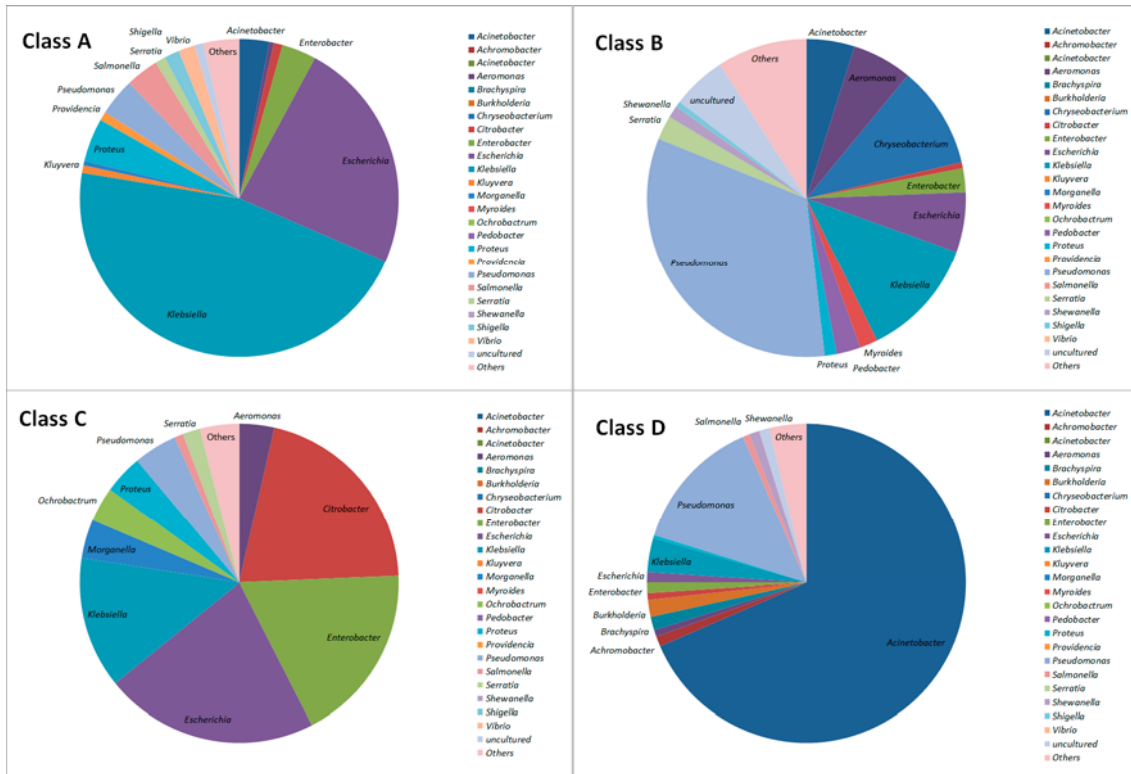


Fig. S1 Relative contribution of different bacterial genera to the description of new beta-lactamases sequences of each class of beta-lactamase genes

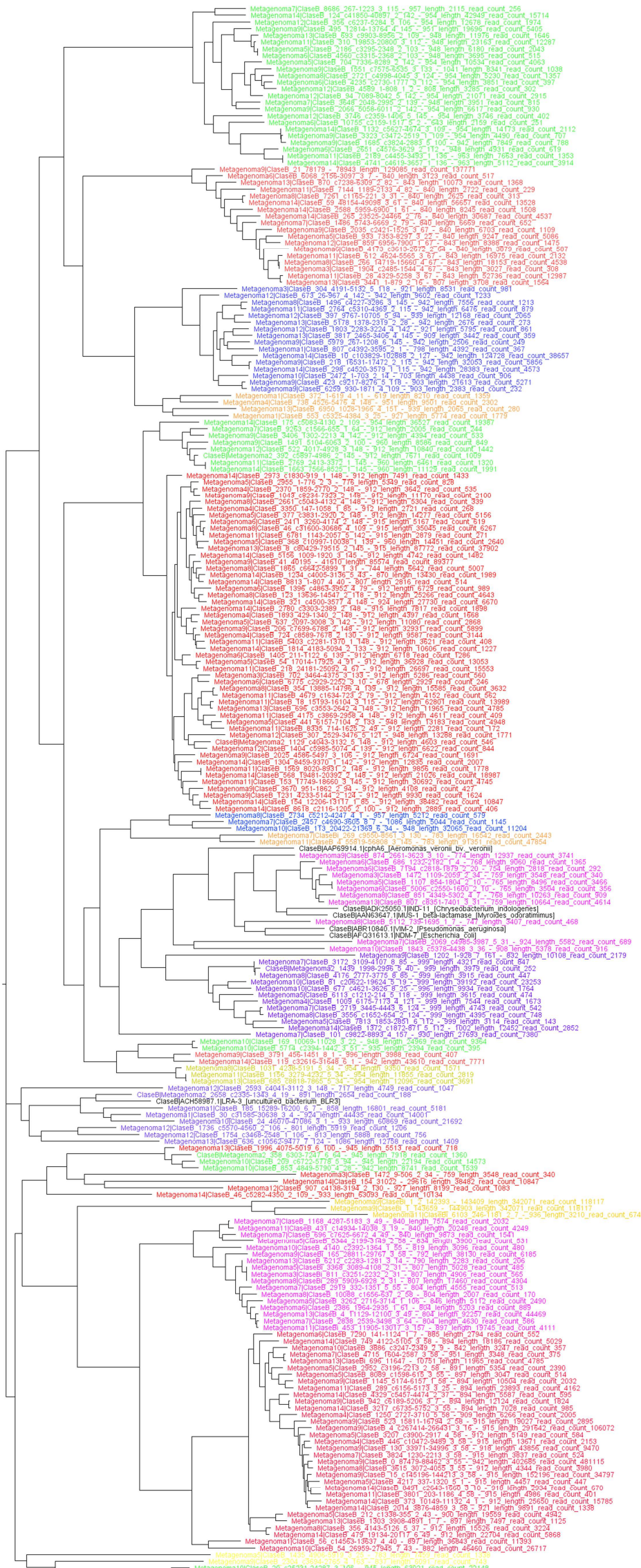


Fig. S2 Phylogenetic tree constructed with deduced amino acid sequences of class B beta-lactamases identified in Antarctic microbial mat metagenomes. Representative reference sequences were also included in the tree. The tree was constructed using Neighbor Joining algorithm. All sequences are shown and clusters are represented in different colors

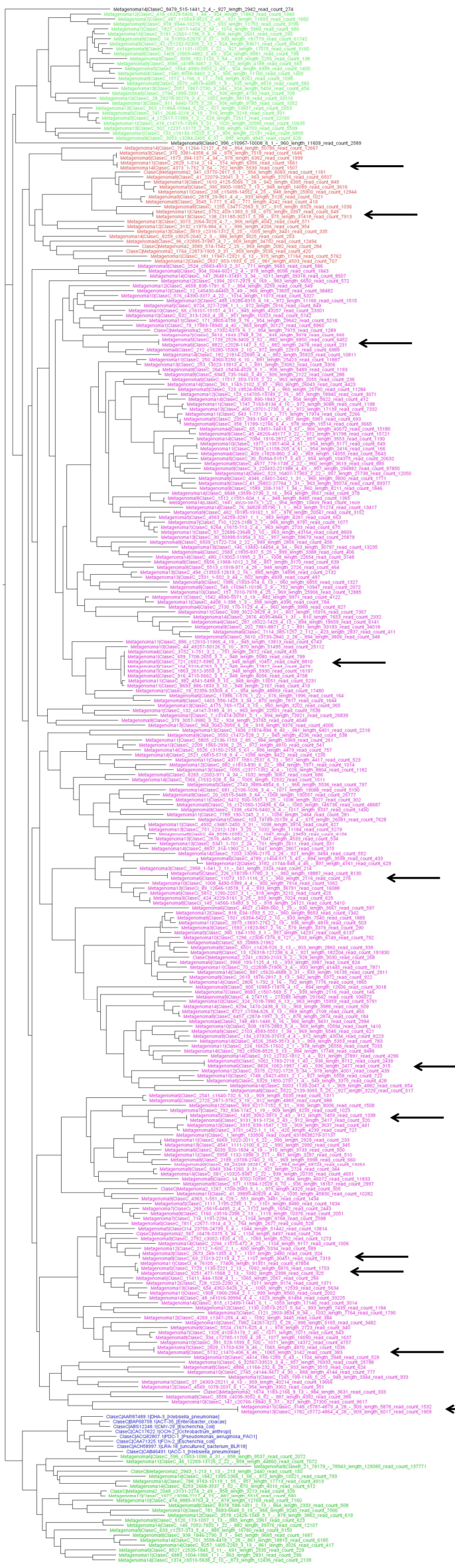


Fig. S3 Phylogenetic tree constructed with deduced amino acid sequences of class C beta-lactamases identified in Antarctic microbial metagenomes. Representative reference sequences were also included in the tree. The tree was constructed using Neighbor Joining algorithm. All sequences are shown and clusters are represented in different colors

Table S1 Data about metagenomics

Sample	Read length	Reads	bases	Filtered Reads	Concentration (ng/ μ L)	insert size	#contigs	total contig length	max contig length	N50 contig	N90 contig	assembly_idba_ud_scaffolds_statistics	aligned reads	expected_coverage-full metagenome-
Met_1	151	48720224	7356753824	48382778	0.924792	400	14345	26277856	139542	3021	696	scaffolds: 14312 n50: 3136 max: 139542 mean: 1835 total length: 26272956 n80: 1121	3725361 aligned reads	expected coverage 0.154412
Met_2	151	49571536	7485301936	49228170	0.40213536	400	11311	24258161	115178	3513	928	scaffolds: 10847 n50: 3719 max: 115178 mean: 2228 total length: 24176850 n80: 1599	3156151 aligned reads	expected coverage 0.139887
Met_3	151	51486780	7774503780	51138354	2.22367728	451	17047	28679046	76805	2622	669	scaffolds: 16970 n50: 2714 max: 76805 mean: 1688 total length: 28646295 n80: 1113	4014577 aligned reads	expected coverage 0.153685
Met_4	151	44170014	6669672114	43864896	5.5129536	428	19554	43565110	176118	4952	793	scaffolds: 19524 n50: 5209 max: 178674 mean: 2229 total length: 43521507 n80: 1390	7685093 aligned reads	expected coverage 0.189139
Met_5	151	80342346	12131694246	79787584	2.6968128	426	62551	109465657	102763	2702	736	scaffolds: 62425 n50: 2831 max: 139332 mean: 1751 total length: 109314890 n80: 1157	18189783 aligned reads	expected coverage 0.181746
Met_6	151	76432590	11541321090	75905826	2.19981168	405	47446	83192253	67877	2581	769	scaffolds: 47386 n50: 2658 max: 67877 mean: 1753 total length: 83098484 n80: 1166	12678391 aligned reads	expected coverage 0.166652
Met_7	151	59174324	8935322924	58762486	0.82157328	414	35849	69755911	358740	3420	753	scaffolds: 35906 n50: 3597 max: 359076 mean: 1941 total length: 69712750 n80: 1311	13362777 aligned reads	expected coverage 0.207558
Met_8	151	48383076	7305844476	48051082	1.52978496	505	53174	83777672	72718	2953	568	scaffolds: 54302 n50: 3212 max: 74621 mean: 1544 total length: 83856067 n80: 971	14504583 aligned reads	expected coverage 0.191331
Met_9	151	33405258	5044193958	33174278	4.16812704	431	17447	67226753	402685	9113	1539	scaffolds: 16969 n50: 9902 max: 453598 mean: 3956 total length: 67145737 n80: 2810	10255142 aligned reads	expected coverage 0.158725
Met_10	151	45302832	6840727632	44989458	0.51490032	415	18089	51076287	124478	4658	1198	scaffolds: 17786 n50: 4863 max: 128267 mean: 2868 total length: 51013721 n80: 1854	8084374 aligned reads	expected coverage 0.16716
Met_11	151	43073298	6504067998	42775934	4.32683328	429	24919	75528956	107363	6668	1215	scaffolds: 23654 n50: 7503 max: 132871 mean: 3184 total length: 75321931 n80: 2363	9488840 aligned reads	expected coverage 0.132172
Met_12	151	60291510	9104018010	59869488	2.05482816	380	23874	56525696	57945	3613	1085	scaffolds: 35906 n50: 3597 max: 359076 mean: 1941 total length: 69712750 n80: 1311	6562607 aligned reads	expected coverage 0.123952
Met_13	151	49993630	7549038130	49645462	2.26186224	422	23997	58290664	142874	4826	936	scaffolds: 23288 n50: 5265 max: 185499 mean: 2497 total length: 58172782 n80: 1730	8004955 aligned reads	expected coverage 0.146363
Met_14	151	36888162	5570112462	36629882	0.52921968	415	34862	101298892	296354	7146	1089	scaffolds: 32911 n50: 8228 max: 371234 mean: 3069 total length: 101034532 n80: 2427	14930069 aligned reads	expected coverage 0.155409

Notes: The average reads is 51945399; the average bases is 7843755184; the average filtered_reads is 51586120. The s.d. of reads is 13342882; the s.d. of bases is 2014775227; the s.d. of filtered_reads is 13250855. The total bases is 109812572580.