**Supporting information**

**Table S1.** Characteristics of the pig manure and digestate samples

| Parameters | Site 1<br>Pig manure | Site 2<br>Pig manure | Site 3<br>Digestate |
|---|---|---|---|
| TSS [$gL^{-1}$] | 3 | 4.9 | 1.8 |
| VSS [% of TSS] | 83.3 | 78 | 67.8 |
| COD [$gL^{-1}$] | 11.3 | 11.8 | 19.5 |
| $NH_4^+$ - N [$gL^{-1}$] | 4.4 | 2.9 | 1.8 |
| $PO_4^{-3}$ [$mgL^{-1}$] | 394 | 323 | 245 |
| pH | 7.8 | 7.8 | 7.8 |
| TOC [$gL^{-1}$] | 4.9 | 4.3 | 3.9 |
| DOC [$gL^{-1}$] | 3.3 | 3 | 1.8 |
| DTN [$gL^{-1}$] | 3 | 2 | 1.5 |
| Acetic acid [$mgL^{-1}$] | 3637 | 2211 | <100 |
| $K^+$ [$mgL^{-1}$] | 1794 | 1698 | 2663 |

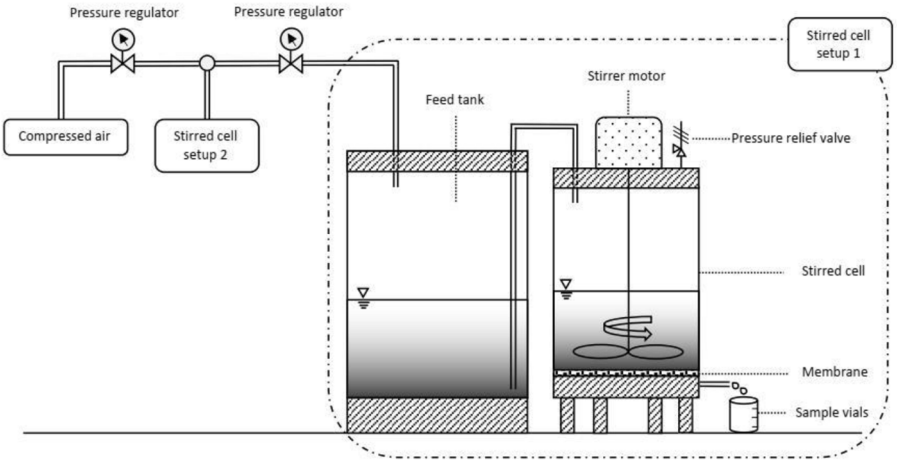
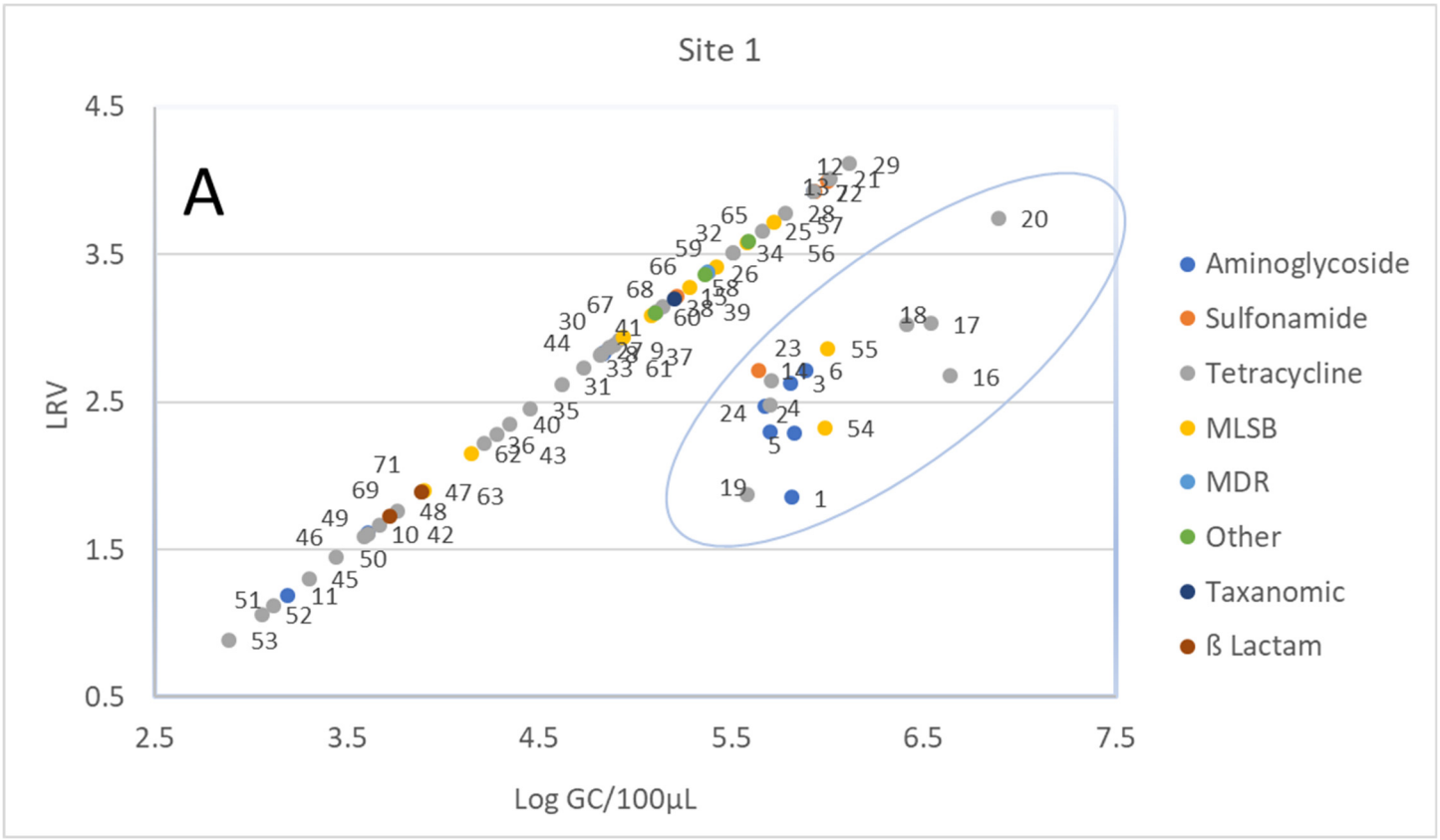
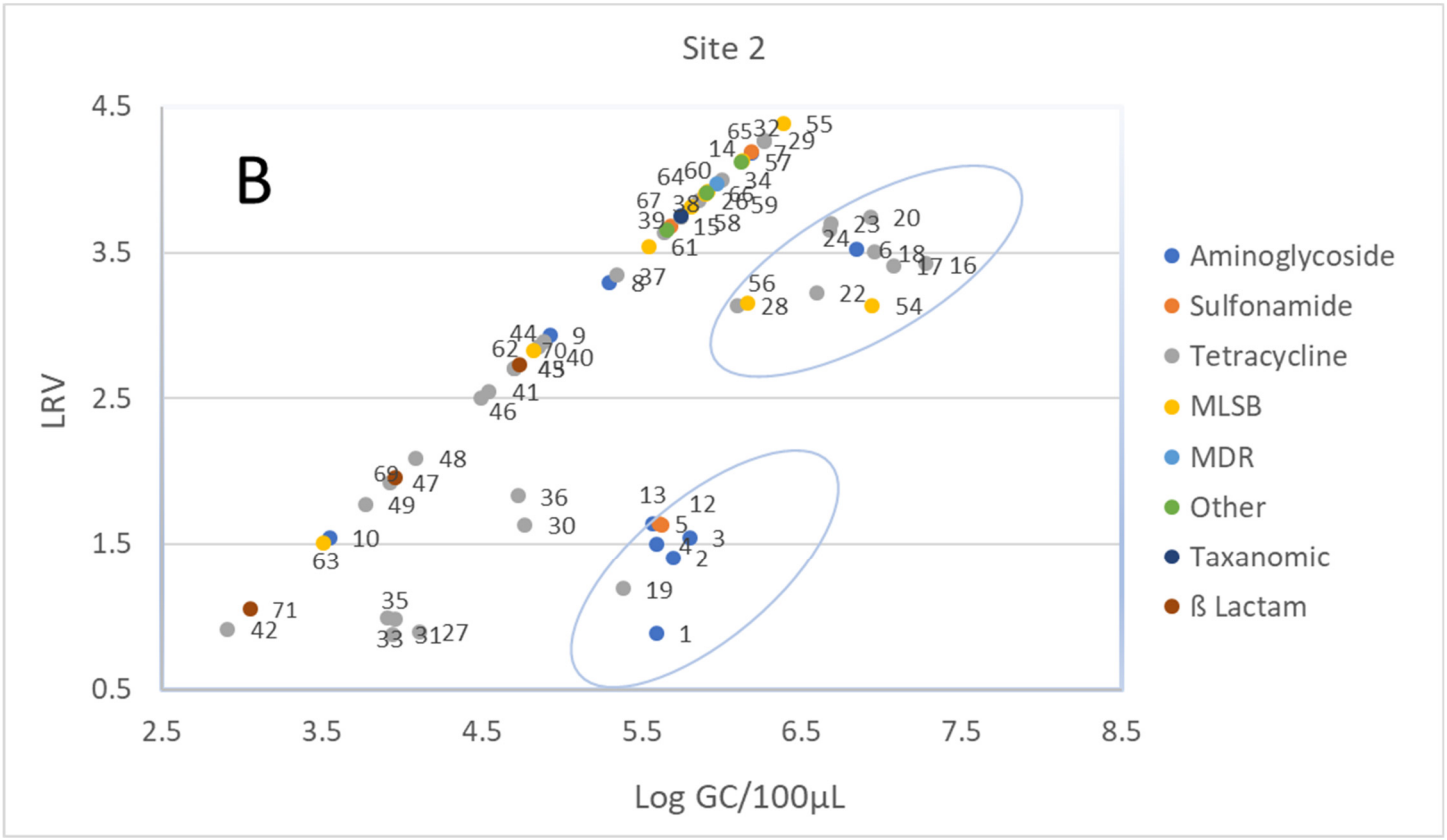



**Figure S1.** Stirred cell dead end membrane filtration system

| Description | Total genes No. | Tetracycline | Aminoglycoside | MLSB | Sulfonamide | Other | Beta Lactam | Taxanomic | MDR |
|---|---|---|---|---|---|---|---|---|---|
| Site 1 manure | 70 | 38 | 11 | 10 | 4 | 3 | 2 | 1 | 1 |
| Site 2 manure | 66 | 34 | 10 | 10 | 4 | 3 | 3 | 1 | 1 |
| Site 3 digestate | 53 | 26 | 8 | 8 | 4 | 3 | 2 | 1 | 1 |
| Site 1 N270 perm | 16 | 7 | 6 | 2 | 1 | 0 | 0 | 0 | 0 |
| Site 2 NF270 perm | 25 | 15 | 6 | 2 | 2 | 0 | 0 | 0 | 0 |
| Site 3 NF270 perm | 13 | 4 | 6 | 1 | 2 | 0 | 0 | 0 | 0 |

**Figure S2**. Number of detected ARGs.





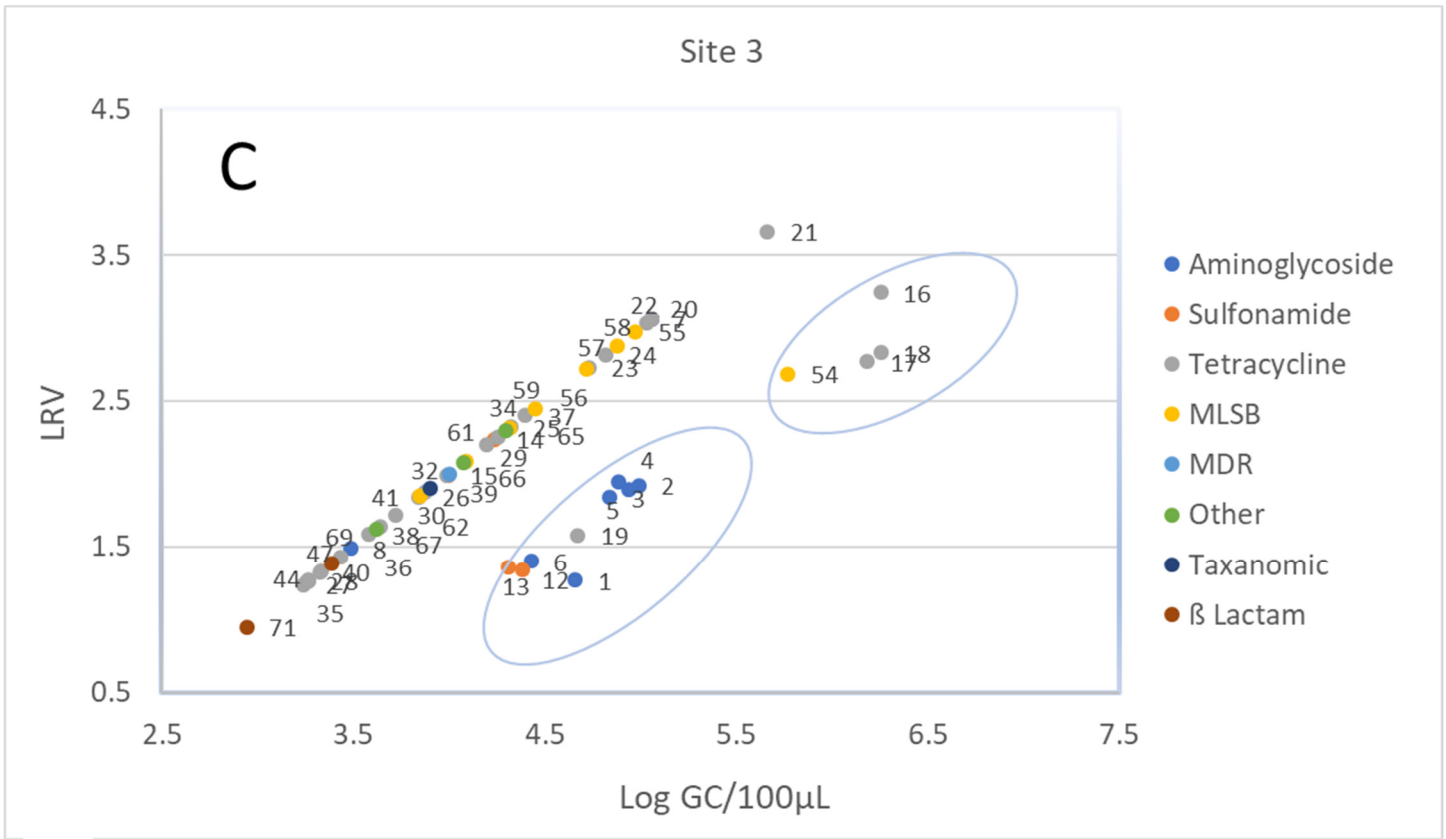




**Figure S3.** Relation between ARG concentration in the feed and their consequent removal by MF-NF process. Every ARG is represented with a unique serial number which is mentioned in Table SD2.

**Table S2.** ARG charcteristics

| AB groups | SL No. | ARGs | Forward Primer | Reverse Primer |
|---|---|---|---|---|
| | | | | |
| Aminoglycoside | 1 | strB | GCTCGGTCGTGAGAACAATCT | CAATTTCGGTCGCCTGGTAGT |
| | 2 | aadA_1 | GTTGTGCACGACGACATCATT | GGCTCGAAGATACCTGCAAGAA |
| | 3 | aadA2_3 | CAATGACATTCTTGCGGGTATC | GACCTACCAAGGCAACGCTATG |
| | 4 | aadA1 | TGTACGGCTCCGCAGTG | CACGGAATGATGTCGTCGTG |
| | 5 | aadA_2 | CGAGATTCTCCGCGCTGTA | GCTGCCATTCTCCAAATTGC |
| | 6 | str | AATGAGTTTTGGAGTGTCTCAACGTA | AATCAAAACCCCTATTAAAGCCAAT |
| | 7 | aadE | TACCTTATTGCCCTTGGAAGAGTTA | GGAACTATGTCCCTTTTAATTCTACAATCT |
| | 8 | aadA2_1 | ACGGCTCCGCAGTGGAT | GGCCACAGTAACCAACAAATCA |
| | 9 | aadD | CCGACAACATTTCTACCATCCTT | ACCGAAGCGCTCGTCGTATA |
| | 10 | strA | CCGGTGGCATTTGAGAAAAA | GTGGCTCAACCTGCGAAAAG |
| | 11 | aacC2 | ACGGCATTCTCGATTGCTTT | CCGAGCTTCACGTAAGCATTT |
| Sulfonamide | 12 | sul2_2 | TCATCTGCCAAACTCGTCGTTA | GTCAAAGAACGCCGCAATGT |
| | 13 | sul2_1 | TCCGGTGGAGGCCGGTATCTGG | CGGGAATGCCATCTGCCTTGAG |
| | 14 | sul1_1 | CGCACCGGAAACATCGCTGCAC | TGAAGTTCCGCCGCAAGGCTCG |
| | 15 | sul1_2 | GCCGATGAGATCAGACGTATTG | CGCATAGCGCTGGGTTTC |
| Tetracycline | 16 | tetM | GGAGCGATTACAGAATTAGGAAGC | TCCATATGTCCTGGCGTGTC |
| | 17 | tetM_3 | CATCATAGACACGCCAGGACATAT | CGCCATCTTTTGCAGAAATCA |
| | 18 | tetM_2 | GCAATTCTACTGATTTCTGC | CTGTTTGATTACAATTTCCGC |
| | 19 | tetH | TTTGGGTCATCTTACCAGCATTAA | TTGCGCATTATCATCGACAGA |
| | 20 | tetPA | GGAAACCTTAGTTCAGTGACTTGG | CCCATTTAACCACGCACTGAA |
| | 21 | tetM_1 | TAATATTGGAGTTTTAGCTCATGTTGATG | CCTCTCTGACGTTCTAAAAGCGTATTAT |
| | 22 | tetW | ATGAACATTCCCACCGTTATCTTT | ATATCGGCGGAGAGCTTATCC |
| | 23 | tet36_1 | AGAATACTCAGCAGAGGTCAGTTCCT | TGGTAGGTCGATAACCCGAAAAT |
| | 24 | tetT | CCATATAGAGGTTCCACCAAATCC | TGACCCTATTGGTAGTGGTTCTATTG |
| | 25 | tet36_2 | TGCAGGAAAGACCTCCATTACAG | CTTTGTCCACACTTCCACGTACTATG |
| | 26 | tetPB_1 | TGGGCGACAGTAGGCTTAGAA | TGACCCTACTGAAACATTAGAAATATACCT |
| | 27 | tetA/B_2 | GCCCAGTGCTGTTGTTGTCAT | TGAAAGCAAACGGCCTAAATACA |
| | 28 | tetQ | CGCCTCAGAAGTAAGTTCATACACTAAG | TCGTTCATGCGGATATTATCAGAAT |
| | 29 | tetA(P) | AGTTGCAGATGTGTATAGTCGTAAACTATCTATT | TGCTACAAGTACGAAAACAAAACTAGAA |
| | 30 | tetX | AAATTTGTTACCGACACGGAAGTT | CATAGCTGAAAAAATCCAGGACAGTT |
| | 31 | tetR_4 | CGCGATGGAGCAAAAGTACAT | AGTGAAAAACCTTGTTGGCATAAAA |
| | 32 | tet44 | CTCATGTAGATGCAGGAAAGACG | GTAACTGCTGCCTGAATTGTGA |
| | 33 | tetA/B_1 | AGTGCGCTTTGGATGCTGTA | AGCCCCAGTAGCTCCTGTGA |
| | 34 | tetO_2 | CAACATTAACGGAAAGTTTATTGTATACCA | TTGACGCTCCAAATTCATTGTATC |
| | 35 | tetD | AATTGCACTGCCTGCATTGC | GACAGATTGCCAGCAGCAGA |
| | 36 | tetR_3 | CGCGATAGACGCCTTCGA | TCCTGACAACGAGCCTCCTT |
| | 37 | tetL_2 | ATGGTTGTAGTTGCGCGCTATAT | ATCGCTGGACCGACTCCTT |
| | 38 | tetO_1 | ATGTGGATACTACAACGCATGAGATT | TGCCTCCACATGATATTTTTCCT |
| | 39 | tet32 | CCATTACTTCGGACAACGGTAGA | CAATCTCTGTGAGGGCATTTAACA |
| | 40 | tetA_2 | CTCACCAGCCTGACCTCGAT | CACGTTGTTATAGAAGCCGCATAG |
| | 41 | tetG_2 | CATCAGCGCCGGTCTTATG | CCCCATGTAGCCGAACCA |
| | 42 | tetC_1 | CATATCGCAATACATGCGAAAAA | AAAGCCGCGGTAAATAGCAA |
| | 43 | tetR | CCGTCAATGCGCTGATGAC | GCCAATCCATCGACAATCACC |
| | 44 | tetG | TCGCGTTCCTGCTTGCC | CCGCGAGCGACAAACCA |
| | 45 | tetC_3 | TGCGTTGATGCAATTTCTATGC | GGAATGGTGCATGCAAGGAG |
| | 46 | tetS | TTAAGGACAAACTTTCTGACGACATC | TGTCTCCCATTGTTCTGGTTCA |
| | 47 | tetG_1 | TCAACCATTGCCGATTCGA | TGGCCCGGCAATCATG |
| | 48 | tetR_1 | CAATCCATCGACAATCAC | GACAATCAGCTACTTCAC |
| | 49 | tet39 | TATAGCGGGTCCGGTAATAGGTG | CCATAACGATCCTGCCCATAGATAAC |
| | 50 | tetM_4 | TGGCAAGACGAGTTTGACTGA | GATCGCTCCACTTCAGCGATAA |
| | 51 | tetPB_3 | ACACCTGGACACGCTGATTTT | ACCGTCTAGAACGCGGAATG |
| | 52 | tetK | CAGCAGTCATTGGAAAATTATCTGATTATA | CCTTGTACTAACCTACCAAAAATCAAAATA |
| | 53 | tetR_2 | ATGAGTTCGGCCAGAATTTCC | GGTTGTGCGCGAAATGATT |
| MLSB | 54 | ermB_2 | GAACACTAGGGTTGTTCTTGCA | CTGGAACATCTGTGGTATGGC |
| | 55 | lnuB | GGATCGTTTACCAAAGGAGAAGG | AGCATAGCCTTCGTATCAGGAA |
| | 56 | mefA_1 | CCGTAGCATTGGAACAGCTTTT | AAACGGAGTATAAGAGTGCTGCAA |
| | 57 | lnuB_2 | AAAGGAGAAGGTGACCAATACTCTGA | GGAGCTACGTCAAACAACCAGTT |
| | 58 | ermF | TCTGATGCCCGAAATGTTCAAG | TGAAGGACAATTGAACCTCCCA |
| | 59 | lnuB_1 | TGAACATAATCCCCTCGTTTAAAGAT | TAATTGCCCTGTTTCATCGTAAATAA |
| | 60 | erm35 | TTGAAAACGATGTTGCATTAAGTCA | TCTATAATCACAACTAACCACTTGAACGT |
| | 61 | mefA | CCGTAGCATTGGAACAGCTTTT | AAACGGAGTATAAGAGTGCTGCAA |
| | 62 | mphA | TCAGCGGGATGATCGACTG | GAGGGCGTAGAGGGCGTA |
| | 63 | mphA_1 | CTGACGCGCTCCGTGTT | GGTGGTGCATGGCGATCT |
| MDR | 64 | cefa_qacelta | TAGTTGGCGAAGTAATCGCAAC | TGCGATGCCATAACCGATTATG |
| Other | 65 | qacEΔ1_2 | CCCCTTCCGCCGTTGT | CGACCAGACTGCATAAGCAACA |
| | 66 | qacEΔ1_3 | GTCGGTGTTGCTTATGCAGTCT | CAACCAGGCAATGGCTGTAA |
| | 67 | qacEΔ1_1 | TCGCAACATCCGCATTAAAA | ATGGATTTCAGAACCAGAGAAAGAAA |
| Taxanomic | 68 | Enterococci | AGAAATTCCAAACGAACTTG | CAGTGCTCTACCTCCATCATT |
| Beta Lactam | 69 | blaSFO | CCGCCGCCATCCAGTA | GGGCCGCCAAGATGCT |
| | 70 | cfxA | TCATTCCTCGTTCAAGTTTTCAGA | TGCAGCACCAAGAGGAGATGT |
| | 71 | blaOXY | CGTTCAGGCGGCAGGTT | GCCGCGATATAAGATTTGAGAATT |