Direct detection and drug-resistance profiling of bacteremias using inertial microfluidics

Han Wei Hou, Roby P. Bhattacharyya, Deborah T. Hung, Jongyoon Han

Supplementary information

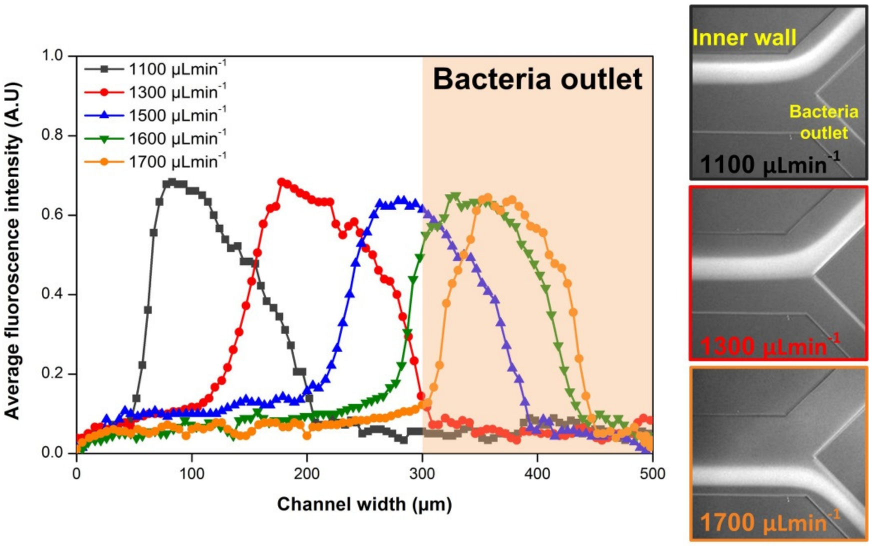

Figure S1 Average fluorescence intensity linescans indicating normalized distribution of FITC-conjugated *E. coli* bioparticles across the channel width (x-axis origin represents inner wall) prior the outlet bifurcation at different flow rates. Approximate position of the bacteria outlet (outer wall region) is shown on the plot. Corresponding average composite images illustrate efficient collection of bacteria into bottom (bacteria) outlet at a flow rate of 1700 μLmin^{-1}.

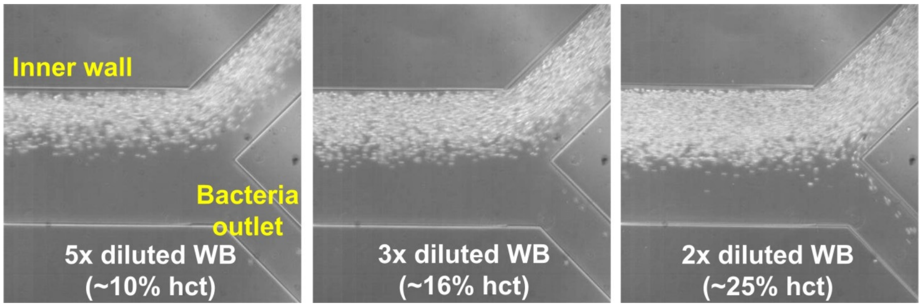

Figure S2 High speed images indicate broadening of RBCs occupied regions at the channel inner wall for increasing hematocrit (hct) prior outlet bifurcation at a sample flow rate of 150 μLmin^{-1} (1500 μLmin^{-1} for sheath flow (1:10)). 3x diluted whole blood (WB) was chosen for subsequent experiments which resulted in minimal RBCs entering the bacteria outlet (bottom).

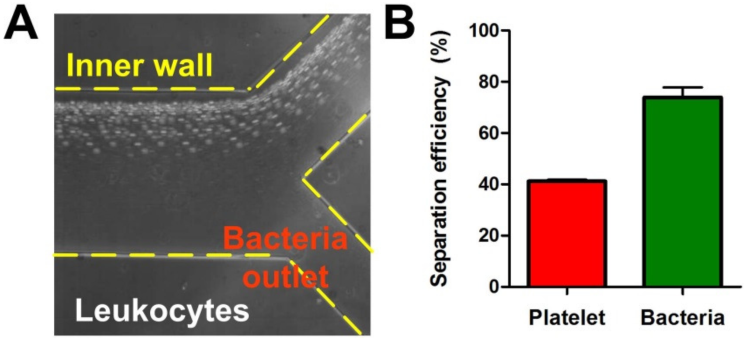

Figure S3 (**A**) Averaged composite high speed image represents the tight focusing of larger leukocytes at the inner wall which resulted in complete removal at the bacteria outlet. Yellow dashed lines indicate position of channel walls. (**B**) Histogram plot showing efficient bacteria recovery (>70%) with lower platelet recovery (~40%) in the sorted samples collected from the bacteria outlet.

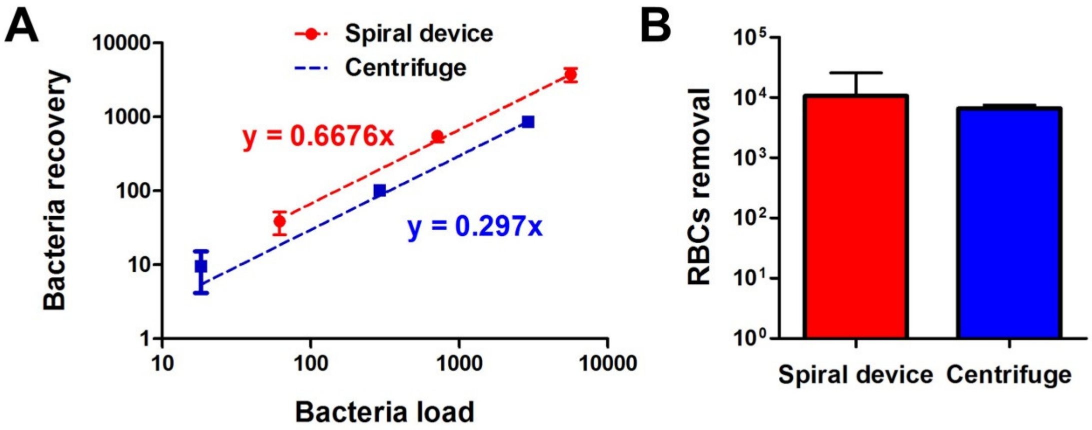

Figure S4 Separation performance comparison between spiral device and centrifuge. (**A**) Higher bacteria recovery was achieved with the spiral device over a range of bacterial loads (*E. coli*) spiked in 1 mL of whole blood. (**B**) Histogram plot indicating similar RBCs removal efficiency (~10^4-fold) for both spiral device and centrifuge.

Figure S5. rRNA probes for specific detection of *P. aeruginosa* (PsA), *E. coli* (Ec), and *K. pneumoniae* (Kp). Probe targets are highlighted in multiple sequence alignments of (A) 16S and (B) 23S rRNA subunits from these three species. Green = PsA-specific probe; Blue = Ec-specific probe; Red = Kp-specific probe; Purple = dual-specificity probe for either Ec or Kp but not PsA. Mismatches in other species corresponding to the region recognized by each probe are shown in lowercase letters; asterisks below the alignment correspond to regions of conservation across the three species. Specific probe sequences designed to target these regions are shown in supplementary Table S1.

A.

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PsA_16S      -----------------------------AACGAGAGGTTGCTGTAGAATGCGCGGCCTC
Ec_16S       AGAAAAATCCTGAAATTCAGGGTTGACTCTGAAAGAGGAAAGCGTAATATACGCCACCTC
Kp_16S       -AGAAAAATCCTGAAAAACGGGTTGACTCTGAAAGAGGATAGCGTAATATACGCCACCTC
                                              *****     ***  ** ***  ****

PsA_16S      GGTT---GAGACGAAAGCCTTGACCAACTGCTCTTTAACAAGTCGAATCAAGCAATTCGT
Ec_16S       GCGACAGTGCGCTAAAGCGCGTCGCAACTGCTCTTTAACAATTTATCA--GACAATCTGT
Kp_16S       GCGACAGAGCGCTAAAGCGCGTCGCAACTGCTCTTTAACAATTTATCA--GACAATCTGT
             *          * *****      ***************** *         ****  **

PsA_16S      GTGGGTGCTTGTGATGTAAGACTGGTGATCGCAAGATTATCAGCAACGCAAGTAACACTC
Ec_16S       GTGGGCACTCGAAG----ATAC-----------GGATTCTTAACG-------------T-
Kp_16S       GTGGGCACTCAAAGTG--ACAT-----------GGATTCTTAACG-------------T-
             *****  **         * *             **** * * *              *

PsA_16S      GTGAATTCGAGAGTTTTATCTCTTTTTAAGAGAATGCGATTGCTGAGCCAAGTTTAGGGT
Ec_16S       CGCAAGACGAAAAATGAATACCAAGTCTCAAGAGTGAACACGTAATTCATTACGAAGCTT
Kp_16S       CCTCGGACGAAAAATGAATACCAAGTCTCAAGAGTGAACACGTAATTCATTACGAAGTTT
                    *** *  *  **  *   *    *** **     *     *       **  *

PsA_16S      TTTCTCAAAACCCAAGCAGTATTGAACTGAAGAGTTTGATCATGGCTCAGATTGAACGCT
Ec_16S       AATTCTTTGAGCATCAAACTTTTAAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCT
Kp_16S       AATTCTTTGAGCATCAAACT--TAAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCT
               *      * *     * *  * ** *********************************

PsA_16S      GGCGGCAGGCCTAACACATGCAAGTCGAgCGGatgaAGGgAGCtt------GCTcCtgga
Ec_16S       GGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACAGGAAGCAGCTTGCTGCTTCGCTG
Kp_16S       GGCGGCAGGCCTAACACATGCAAGTCGAgCGGTAgCAcagAGagc--TtgctCTcgGgTG
             **************************** ***    *   **          **

PsA_16S      accAGcGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGATAACGTCC
Ec_16S       ACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACT
Kp_16S       ACGAGcGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACT
                ** ******************* ** **** ******* * * **********  *

PsA_16S      GGAAACGGGCGCTAATACCGCATACGTCCTGAGGGAGAAAGTGGGGGATCTTCGGACCTC
Ec_16S       GGAAACGGTAGCTAATACCGCATAacgTCgcAAGaccAAAGaGGGGGAcCTTCGGgCCTC
Kp_16S       GGAAACGGTAGCTAATACCGCATAatgTCgcAAGaccAAAGTGGGGGAcCTTCGGgCCTC
             ********  **************    *  * *   **** ****** ****** ****

PsA_16S      ACGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGC
Ec_16S       ttGCcATCGGATGtGCCcAGaTgGGATTAGCTtGTTGGTGGGGTAAcGGCtcACCAAGGC
Kp_16S       AtGCcATCAGATGtGCCcAGaTgGGATTAGCTAGTaGGTGGGGTAAcGGCtcACCtAGGC
               ** *** **** *** ** * ********* ** ********** ***  *** ****

PsA_16S      GACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAG
Ec_16S       GACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAG
Kp_16S       GACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAG
             ******** ** ***************** *** **************************
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PsA_16S      ACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCA
Ec_16S       ACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCA
Kp_16S       ACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCA
             ******************************** ********** ********* ******

PsA_16S      TGCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCA
Ec_16S       TGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAG
Kp_16S       TGCCGCGTGTGTGAAGAAGGCCTTCGGGTTGTAAAGCACTTTCAGCGGGGAGGAAGGCGT
             ********** ********* ****** ******** ***** **  **********

PsA_16S      GTAAGTTAATACCTTGCTGTTTTGACGTTACCAACAGAATAAGCACCGGCTAACTTCGTG
Ec_16S       TAAAGTTAATACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTG
Kp_16S       TAAGGTTAATAACCTTGGCGATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTG
               * ******* * *      ***********  ***** *************** ****

PsA_16S      CCAGCAGCCGCGGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCG
Ec_16S       CCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCG
Kp_16S       CCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCG
             ******************** ***************************************

PsA_16S      CGCGTAGGTGGTTCAGCAAGTTGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATC
Ec_16S       CACGCAGGCGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATC
Kp_16S       CACGCAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATT
             * ** *** ***     ****  ************************************

PsA_16S      CAAAACTACTGAGCTAGAGTACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAAT
Ec_16S       TGATACTGGCAAGCTTGAGTCTCGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAAT
Kp_16S       CGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAAT
               * ***     *** ****   ******** *** ***** *  ***************

PsA_16S      GCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACT
Ec_16S       GCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCT
Kp_16S       GCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCT
             ******* **  * ***** *** ************ ** *******  * ****** **

PsA_16S      GAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
Ec_16S       CAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
Kp_16S       CAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
              ***********************************************************

PsA_16S      GATGTCGACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCGCAGCTAACGCGATAAGTCG
Ec_16S       GATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCG
Kp_16S       GATGTCGATTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAATCG
             ******** * *  * * *   *******   *   *  ** ********** *** ***

PsA_16S      ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
Ec_16S       ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
Kp_16S       ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA
             ************************************************************

PsA_16S      AGCGGTGGAGCATGTGGTTTAATTCGAaGCAACGCGAAGAACCTTACCTGGcCTTGACAT
Ec_16S       AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT
Kp_16S       AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT
             *************************** *********************** ********

PsA_16S      gCtgaGAACTTTcCAGAGATGgattgGTGCCTTCGGGAACTCAGACACAGGTGCTGCATG
Ec_16S       CCACGGAAGTTTTCAGAGATGAGAATGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATG
Kp_16S       CCACaGAACTTagCAGAGATGctttgGTGCCTTCGGGAACTGTGAGACAGGTGCTGCATG
              *   *** **  ********     **************   ** **************

PsA_16S      GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTG
Ec_16S       GCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTA
Kp_16S       GCTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTA
             ****************** **** ****************** ****************
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PsA_16S      TCCTTAGTTACCAGCACCTCGGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG
Ec_16S       TCCTTTGTTGCCAGCGGTCCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAG
Kp_16S       TCCTTTGTTGCCAGCGGTTCGGCCGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAG
             ***** *** *****    ***  *** **** ************ **** **** ****

PsA_16S      GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCAGGGCTACACACGTGCTAC
Ec_16S       GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGaCCAGGGCTACACACGTGCTAC
Kp_16S       GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGaCCAGGGCTACACACGTGCTAC
             ************************************** *********************

PsA_16S      AATGGTCGGTACAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAACCGATCG
Ec_16S       AATGGcgcaTACAAAGaGaaGCgAcctCGCGAGagcaAGCggAcCtCATAAAgtgcgTCG
Kp_16S       AATGGcataTACAAAGaGaaGCgAcctCGCGAGagcaAGCggAcCtCATAAAgtatgTCG
             *****    ******* *  ** *   ******    ***  * * ******     ***

PsA_16S      TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAA
Ec_16S       TAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGA
Kp_16S       TAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTAGA
             ********** * **************** * *************************  *

PsA_16S      TCAGAATGTCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG
Ec_16S       TCAGAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG
Kp_16S       TCAGAATGCTACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG
             ********  **************************************************

PsA_16S      AGTGGGTTGCtccAGAAGTAGcTAGtcTAACCgcaaGGgGGaCGgTTACCACgGAGTGAT
Ec_16S       AGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGAT
Kp_16S       AGTGGGTTGCAAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACTTTGTGAT
             **********   ******** ***  *****    ** ** ** *******   *****

PsA_16S      TCATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCT
Ec_16S       TCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCGGTTGGATCACCT
Kp_16S       TCATGACTGGGGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCGGTTGGATCACCT
             ****************************** ****************** **********

PsA_16S      CCTTAATCGAAGATCTCAGCTTCTTCATAAGCTCCCACACGAA-----TTGCTTGATTCA
Ec_16S       CCTTACCTTAAAGAAGCGTTCTTTGAAGTGCTCACACAGATTGTCTGATGAAAATGAGAA
Kp_16S       CCTTACCTTAAAGAATCTGCCTTTGCAGTGCTCACACAGATTGTCTGATGAAAAACAGCA
             *****    **     *    * *  *       *             *          *

PsA_16S      CTGGTTAGACGATTGGGTCTGTAGCTCAGTTGGTTAGAGCGCACCCCTGATAAGGGTGAG
Ec_16S       GT-AAAACCTCTACAGGCTTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAG
Kp_16S       GTAAAAACCTCTACAGGCTTGTAGCTCAGGTGGTTAGAGCGCACCCCTGATAAGGGTGAG
              *    *        **  ********** ******************************

PsA_16S      GTCGGCAGTTCGAATCTGCCCAGACCCACCAATTGTTGGTGTGCTG--------------
Ec_16S       GTCGGTGGTTCAAGTCCACTCAGGCCTACCAAATTTGCACGGCAAATTTGAAGAGGTTTT
Kp_16S       GTCGGTGGTTCAAGTCCACTCAGGCCTACCAAATTTGCGAAGCAAATTTGAAGAGGTTGC
             *****  **** * **  * *** ** ***** * *

PsA_16S      CGTGATCCGATACGGGGCCATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGT
Ec_16S       AACTACATGTTATGGGGCTATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGG----
Kp_16S       AAA------CGATGGGGCTATAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGT
                        * ***** *************************************

PsA_16S      CAGGAGTTCGATC
Ec_16S       -------------
Kp_16S       CTGCGG-------
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B.

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PsA_23S      GGTCAAGtGAaGAAGCGcAtACGGTGGATGCCtTGGCAGTCAGAGGCGATGAAaGACGTG
Ec_23S       GGTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCAGTCAGAGGCGATGAAGGACGTG
Kp_23S       GGTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCAGTCAGAGGCGATGAAGGACGTG
             *** *** **  ***** * ************ ******************** ******

PsA_23S      gTAgcCTGCGAAAAGCtTCGGggAGtcGgcAaacAgacTTtgAtCCGGAGATCTCTGAAT
Ec_23S       CTAATCTGCGAtAAGCGTCGGTAAGGTGATATGAACCGTTATAACCGGCGATTTCCGAAT
Kp_23S       CTAATCTGCGAAAAGCGTCGGTAAGGTGATATGAACCGTTATAACCGGCGATGTCCGAAT
              **  ****** **** ****  **  *  *   *   **  * **** *** ** ****

PsA_23S      GGGGGAACCCACCTAGGATAACCTAGGTATCTTGTACTGAATCCATAGGTGCAAGAGGCG
Ec_23S       GGGGAAACCCAGTGTGATTCGTCACACTATCATTAACTGAATCCATAGGTTAATGAGGCG
Kp_23S       GGGGAAACCCAGTGCAATTCGTTGCACTATCGTTAACTGAATACATAGGTTAACGAGGCG
             **** ******       *        **** *  ******* *******  * ******

PsA_23S      AACCAGGGGAACTGAAACATCTAAGTACCCTGAGGAAAAGAAATCAACCGAGATTCCCTT
Ec_23S       AACCGGGGGAACTGAAACATCTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCC
Kp_23S       AACCGGGGGAACTGAAACATCTAAGTACCCCGAGGAAAAGAAATCAACCGAGATTCCCCC
             **** ************************* ***************************

PsA_23S      AGTAGTGGCGAGCGAACGGGGAttAGCCCttAagCTtcATt------gaTtTTAGcGGAA
Ec_23S       AGTAGCGGCGAGCGAACGGGGAGCAGCCCAGAGCCTGAATCAGtgTGTGTGTTAGTGGAA
Kp_23S       AGTAGCGGCGAGCGAACGGGGAGCAGCCCAGAGtCTGAATCAGctTGTGTGTTAGTGGAA
             ***** ****************  *****  *  **  **         * **** ****

PsA_23S      CGcTCTGGAAAGtgcgGCcATAgtGGGTGAtAGCCCCGTACgCgAAAggatctttGaaGT
Ec_23S       GCGTCTGGAAAGgCgcgCGaTACAGGGTGAcAGcCCCGTACACaAAAATGCACAtGcTGT
Kp_23S       CGGTCTGGAAAGtCcgaCGgTACAGGGTGAtAGtCCCGTACACcAAAATGCACAGGTTGT
                *********     *  **  ****** ** ******* * ***        *  **

PsA_23S      GAAAT---CGAGTAGGACGGAGCACGAGAAACTTTGTCTGAACATGGGGGGACCATCCTC
Ec_23S       GAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCTGAATATGGGGGGACCATCCTC
Kp_23S       GAACTCGAAGAGTAGGGCGGGACACGTGGTATCCTGTCTGAATATGGGGGGACCATCCTC
             **  *    ******* ***  **** *  *   ******** *****************

PsA_23S      CAAGGCTAAATACTACTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAA
Ec_23S       CAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAA
Kp_23S       CAAGGCTAAATACTCCTGACTGACCGATAGTGAACCAGTACCGTGAGGGAAAGGCGAAAA
             ************** *********************************************

PsA_23S      GAACCCCGGAGAGGGGAGTGAAATAGAACCTGAAACCGTATGCGTACAAGCAGTGGGAGC
Ec_23S       GAACCCCGGCGAGGGGAGTGAAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGC
Kp_23S       GAACCCCGGCGAGGGGAGTGAAAAAGAACCTGAAACCGTGTACGTACAAGCAGTGGGAGC
             ********* ************* *************** * ******************

PsA_23S      CTACT-TGTTAGGTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCAGTGG
Ec_23S       ACGCTtaGgcgtGTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCtGTaG
Kp_23S       ACCT--TCgggtGTGACTGCGTACCTTTTGTATAATGGGTCAGCGACTTATATTCtGTaG
                         ******************************************* ** *

PsA_23S      CAAGCTTAACCGTATAGGGTAGGCGTAGCGAAAGCGAGTCTTAATAGGGCGTTTAGTCGC
Ec_23S       CAAGgTTAACCGaATAGGGgAGCCGaAGgGAAAcCGAGTCTTAACTGGGCGTTAAGTTGC
Kp_23S       CAAGgTTAACCGTATAGGGgAGCCGcAGgGAAAcCGAGTCTTAACTGGGCGTTAAGTTGC
             **** ******* ****** ** ** ** **** **********  ******* *** **

PsA_23S      TGGGTATAGACCCGAAACCGGGCGATCTATCCATGAGCAGGTTGAAGGTTAGGTAACACT
Ec_23S       AGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTGAAGGTTGGGTAACACT
Kp_23S       AGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTGAAGGTTGGGTAACACT
              ****************** ** ****** ***** ************** *********
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PsA_23S      GACTGGAGGACCGAACCCACTCCCGTTGAAAAGGTAGGGGATGACTTGTGGATCGGAGTG
Ec_23S       AACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGATGACTTGTGGCTGGGGGTG
Kp_23S       AACTGGAGGACCGAACCGACTAATGTTGAAAAATTAGCGGATGACTTGTGGCTGGGGGTG
              **************** ***   ********  *** ************* * ** ***

PsA_23S      AAAGGCTAATCAAGCTCGGAGATAGCTGGTTCTCCTCGAAAGCTATTTAGGTAGCGCCTC
Ec_23S       AAAGGCCAATCAAACCGGGAGATAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTC
Kp_23S       AAAGGCCAATCAAACCGGGAGATAGCTGGTTCTCCCCGAAAGCTATTTAGGTAGCGCCTC
             ****** ****** *  ****************** ************************

PsA_23S      ATGTATCACTCT-GGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAA
Ec_23S       GTGAATTCATCTCCGGGGGTAGAGCACTGTTTCGGCAAGGGGGTCATCCCGACTTACCAA
Kp_23S       GTGAATTCATCTTCGGGGGTAGAGCACTGTTTCGGCTAGGGGGTCATCCCGACTTACCAA
              ** **   ***  ********************** ***********************

PsA_23S      ACCGATGCAAACTCCGAATACCCAGAAGTGCCGAGCATGGGAGACACACGGCGGGTGCTA
Ec_23S       CCCGATGCAAACTGCGAATACCGGAGAATG-TTATCACGGGAGACACACGGCGGGTGCTA
Kp_23S       CCCGATGCAAACTACGAATACCGAAGAATG-TTATCACGGGAGACACACGGCGGGTGCTA
              ************ ********    * **   * ** **********************

PsA_23S      ACGTCCGTCGTGAAAAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGTTGTGGTT
Ec_23S       ACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGTCATGGTT
Kp_23S       ACGTCCGTCGTGAAGAGGGAAACAACCCAGACCGCCAGCTAAGGTCCCAAAGTCATGGTT
             ************** **************************************  *****

PsA_23S      AAGTGGTAAACGATGTGGGAAGGCTTAGACAGCTAGGAGGTTGGCTTAGAAGCAGCCACC
Ec_23S       AAGTGGGAAACGATGTGGGAAGGCCCAGACAGCCAGGATGTTGGCTTAGAAGCAGCCATC
Kp_23S       AAGTGGGAAACGATGTGGGAAGGCACAGACAGCCAGGATGTTGGCTTAGAAGCAGCCATC
             ****** *****************  ******* **** ******************* *

PsA_23S      CTTTAAAGAAAGCGTAATAGCTCACTAGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGG
Ec_23S       ATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGG
Kp_23S       ATTTAAAGAAAGCGTAATAGCTCACTGGTCGAGTCGGCCTGCGCGGAAGATGTAACGGGG
              ************************* *********************************

PsA_23S      CTCAAACCACACACCGAAGC--TGCGGGTGTCACGTAAGTGACGCGGTAGAGGAGCGTTC
Ec_23S       CTAAACCATGCACCGAAGCTGCGGCAGCGACACTGTGTGTTGTTGGGTAGGGGAGCGTTC
Kp_23S       CTAAACCATGCACCGAAGCTGCGGCAGCGACACTATGTGTTGTTGGGTAGGGGAGCGTTC
             ** ** *      *  *      ** *        *  **     ***** *********

PsA_23S      TGTAAGCCTGTGAAGGTGaGtTGaGAaGCtTGCTGGAGGTATCAGAAGTGCGAATGCTGA
Ec_23S       TGTAAGCCTGCGAAGGTGTGCTGTGAGGCATGCTGGAGGTATCAGAAGTGCGAATGCTGA
Kp_23S       TGTAAGCCTGCGAAGGTGTGCTGTGAGGCATGCTGGAGGTATCAGAAGTGCGAATGCTGA
             ********** ******* * ** ** ** ******************************

PsA_23S      CATgAGTAACGAcAAtGgGtGTGAAAAaCaCcCaCGCCGaAAGACCAAGGGTTCCTGCGC
Ec_23S       CATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAGACCAAGGGTTCCTGTCC
Kp_23S       CATAAGTAACGATAAAGCGGGTGAAAAGCCCGCTCGCCGGAAGACCAAGGGTTCCTGTCC
             *** ******** ** * * ******* * * * ***** *****************  *

PsA_23S      AACGTTAATCGACGCAGGGTTAGTCGGTTCCTAAGGCGAGGCTGAAAAGCGTAGTCGATG
Ec_23S       AACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCCGAAAGGCGTAGTCGATG
Kp_23S       AACGTTAATCGGGGCAGGGTGAGTCGACCCCTAAGGCGAGGCCGAAAGGCGTAGTCGATG
             ***********  ******* *****   ************* **** ************

PsA_23S      GGAAACAGGTTAATATTCCTGTACTTCTGGTTACTGCGATGGAGGGACGGAGAAGGCTAG
Ec_23S       GGAAACAGGTTAATATTCCTGTACTTggtGTTACTGCGAaGGgGGACGGAGAAGGCTAt
Kp_23S       GGAAACAGGTTAATATTCCTGTACTTggtGTTACTGCGAaGGgGGACGGAGAAGGCTAt
             **************************   ********** ** ****************

PsA_23S      GCCAGCTTGGCGTTGGTTGTCCAAGTTTAAGGTGGTAGGCTGAAATCTTAGGTAAATCCG
Ec_23S       GttGGCcgGGCGacGGTTGTCCcgGTTTAAGcgtGTAGGCTGgttTtcTAGGCAAATCCG
Kp_23S       GttAGCcgGGCGacGGTTGTCCcgGTTTAAGcatGTAGGCTGattGtCCAGGCAAATCCG
             *   **  ****  ********  *******   ********       *** *******
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PsA_23S      GGGTTTCAAGGCCGAGAGCTGATGACGAGTCGTCTTTTAGATGACGAAGTGGTTGATGCC
Ec_23S       GAAAATCAAGGCTGAGGCGTGATGACGAGGCA---CTACGGTGCTGAAGCAACAAATGCC
Kp_23S       GATAATCAAGGCTGAGGTGTGATGACGAGGCA---CTACGGTGCTGAAGTAACAAATGCC
             *    ******* ***   ********** *     *  * **  ****      *****

PsA_23S      ATGCTTCCAAGAAAAGCTTCTAAGCTTCAGGTAACCAGGAACCGTACCCCAAACCGACAC
Ec_23S       CTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTACCCCAAACCGACAC
Kp_23S       CTGCTTCCAGGAAAAGCCTCTAAGCATCAGGTAACATCAAATCGTACCCCAAACCGACAC
              ******** ******* ******* *********    ** ******************

PsA_23S      AGGTGGTCGGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAA
Ec_23S       AGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAA
Kp_23S       AGGTGGTCAGGTAGAGAATACCAAGGCGCTTGAGAGAACTCGGGTGAAGGAACTAGGCAA
             ******** ***************************************************

PsA_23S      AATGGCACCGTAACTTCGGGAGAAGGTGCGCCGGCTAGGGTGAAG---GATTTACTCCGT
Ec_23S       AATGGTGCCGTAACTTCGGGAGAAGGCACGCTGATATGTAGGTGAAGTCCCTCGCGGATG
Kp_23S       AATGGTGCCGTAACTTCGGGAGAAGGCACGCTGGTGTGTAGGTGAAGTCCCT-GCGGATG
             *****  *******************  *** *    *   *         *  *

PsA_23S      AAGCTCTGGCTGGTCGAAGATACCAGGCCGCTGCGACTGTTTATTAAAAACACAGCACTC
Ec_23S       GAGCTGAAATCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTG
Kp_23S       GAGCTGAGACCAGTCGAAGATACCAGCTGGCTGCAACTGTTTATTAAAAACACAGCACTG
              ****       **************   ***** ************************

PsA_23S      TGCAAACACGAAAGTGGACGTATAGGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTG
Ec_23S       TGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTG
Kp_23S       TGCAAACACGAAAGTGGACGTATACGGTGTGACGCCTGCCCGGTGCCGGAAGGTTAATTG
             ************************ ***********************************

PsA_23S      ATGGGGTTAGCGC--AAGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACT
Ec_23S       ATGGGGTCAGCGC--AAGCGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACT
Kp_23S       ATGGGGTTATCCGTAAGGAGAAGCTCTTGATCGAAGCCCCGGTAAACGGCGGCCGTAACT
             ******* * *    * * *****************************************

PsA_23S      ATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCG
Ec_23S       ATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCG
Kp_23S       ATAACGGTCCTAAGGTAGCGAAATTCCTTGTCGGGTAAGTTCCGACCTGCACGAATGGCG
             ************************************************************

PsA_23S      TAACGATGGCGGCGCTGTCTCCACCCGAGACTCAGTGAAATTGAAATCGCTGTGAAGATG
Ec_23S       TAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATG
Kp_23S       TAATGATGGCCAGGCTGTCTCCACCCGAGACTCAGTGAAATTGAACTCGCTGTGAAGATG
             *** ******   ******************************** **************

PsA_23S      CAGTGTATCCGCGGCTAGACGGAAAGACCCCGTGAACCTTTACTGTAGCTTTGCACTGGA
Ec_23S       CAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAA
Kp_23S       CAGTGTACCCGCGGCAAGACGGAAAGACCCCGTGAACCTTTACTATAGCTTGACACTGAA
             ******* ******* **************************** ******  ***** *

PsA_23S      CTTTGAGCCTGCTTGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTTCGCGT
Ec_23S       CATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGTGTGGACGCCAGTCTGCAT
Kp_23S       CATTGAGCCTTGATGTGTAGGATAGGTGGGAGGCTTTGAAGCGTGGACGCCAGTCTGCGT
             * ********   **************************** ************  ** *

PsA_23S      GGAGCCATCCTTGAAATACCACCCTGGCATGCTTGAGGTTCTAACTCTGGTCCGTAATCC
Ec_23S       GGAGCCGACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGTTGACCCGTGATCC
Kp_23S       GGAGCCAACCTTGAAATACCACCCTTTAATGTTTGATGTTCTAACGTTGGCCCCTGACCG
             ******  *****************   *** **** ********  **  ** * * *

PsA_23S      GGATCGAGGACAGTGTATGGTGGGCAGTTTGACTGGGGCGGTCTCCTCCTAAAGAGTAAC
Ec_23S       GGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCTCCTCCTAAAGAGTAAC
Kp_23S       GGGTTGCGGACAGTGTCTGGTGGGTAGTTTGACTGGGGCGGTCTCCTCCCAAAGCGTAAC
             ** * * ********* ******* ************************ **** *****
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PsA_23S      GGAGGAGTACGAAGGTGCGCTCAGACCGGTCGGAAATCGGTCGCAGAGTATAAAGGCAAA
Ec_23S       GGAGGAGCACGAAGGTTGGCTAATCCTGGTCGGACATCAGGAGGTTAGTGCAATGGCATA
Kp_23S       GGAGGAGCACGAAGGTTAGCTAATCCTGGTCGGACATCAGGAGGTTAGTGCAATGGCATA
             ******* ********  *** *  * ******* *** *  *    ***  ** **** *

PsA_23S      AGCGCGCTTGACTGCGAGACAGACACGTCGAGCAGGTACGAAAGTAGGTCTTAGTGATCC
Ec_23S       AGCCAGCTTGACTGCGAGCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCC
Kp_23S       AGCTAGCTTGACTGCGAGCGTGACGGCGCGAGCAGGTGCGAAAGCAGGTCATAGTGATCC
             ***  *************   ***    ********* ****** ***** *********

PsA_23S      GGTGGTTCTGTATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGG
Ec_23S       GGTGGTTCTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGG
Kp_23S       GGTGGTTCTGAATGGAAGGGCCATCGCTCAACGGATAAAAGGTACTCCGGGGATAACAGG
             ********** *************************************************

PsA_23S      CTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGGCTCATC
Ec_23S       CTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGGCTCATC
Kp_23S       CTGATACCGCCCAAGAGTTCATATCGACGGCGGTGTTTGGCACCTCGATGTCGGCTCATC
             ************************************************************

PsA_23S      ACATCCTGGGGCTGAAGCCGGTCCCAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGC
Ec_23S       ACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGC
Kp_23S       ACATCCTGGGGCTGAAGTAGGTCCCAAGGGTATGGCTGTTCGCCATTTAAAGTGGTACGC
             *****************  *****************************************

PsA_23S      GAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGACGTTTGAGAT
Ec_23S       GAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGgCGcTgGAGAa
Kp_23S       GAGCTGGGTTTAGAACGTCGTGAGACAGTTCGGTCCCTATCTGCCGTGGgCGcTgGAGAa
             ************************************************* ** * ****

PsA_23S      TTGAGAGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGAACCTCTGGTGTTCCGGT
Ec_23S       cTGAGgGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGcAtCaCTGGTGTTCgGGT
Kp_23S       TTGAGgGGGGCTGCTCCTAGTACGAGAGGACCGGAGTGGACGcAtCaCTGGTGTTCgGGT
              **** ************************************ * * ********* ***

PsA_23S      TGTCACGCCAGTGGCATTGCCGGGTAGCTATGTTCGGAAAAGATAACCGCTGAAAGCATC
Ec_23S       TGTCAtGCCAaTGGCAcTGCCcGGTAGCTAAATGCGGAAGAGATAAGTGCTGAAAGCATC
Kp_23S       TGTCAtGCCAaTGGCAcTGCCcGGTAGCTAAATGCGGAAGAGATAAGTGCTGAAAGCATC
             ***** **** ***** **** ********  * ***** ******  ************

PsA_23S      TAAGCGGGAAACTTGCCTCAAGATGAGATCTCACTGGGAacTTgAtTCcCCTGAAGGgcC
Ec_23S       TAAGCACGAAACTTGCCCCGAGATGAGTTCTCCCTGActCcTTgAGagTCCTGAAGGAAC
Kp_23S       TAAGCACGAAACTTGCCCCGAGATGAGTTCTCCCTGAGACTTTAAGTCTCCTGAAGGAAC
             *****  ********** * ******* **** ***     ** *    ********  *

PsA_23S      GTcgAAGACtAcGACGTTGATAGGCtGGGTGTGTAAGCGttGTGAgGCGTTGAGCTAACC
Ec_23S       GTTgAAGACGAcGACGTTGATAGGCCGGGTGTGTAAGCGCAGCGATGCGTTGAGCTAACC
Kp_23S       GTTAAAGACGATGACGTTGATAGGCCGGGTGTGTAAGCGCAGCGATGCGTTGAGCTAACC
             **  ***** * ************* *************  * ** **************

PsA_23S      aGTACTAATtgcCCGTGAGGCTTGACCAT--
Ec_23S       GGTACTAATGAACCGTGAGGCTTAACCTT--
Kp_23S       GGTACTAATGAACCGTGAGGCTTAACCTTAC
              ********   *********** *** *
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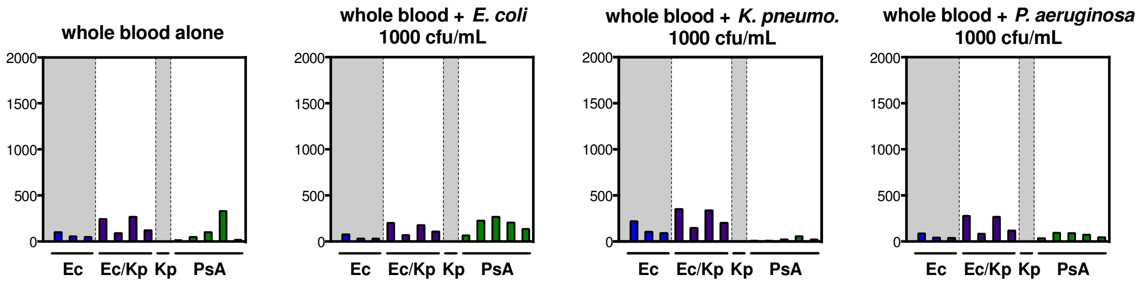
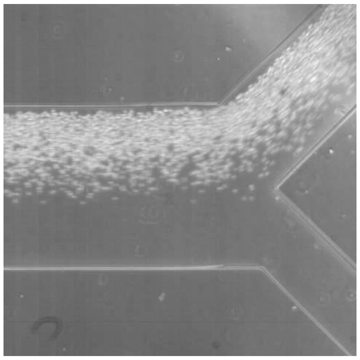


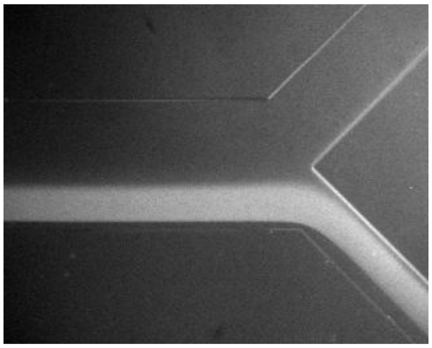
Figure S6 Similar background transcriptional signals from nCounter probes between whole blood and whole blood spiked with 1000 cfu/mL for different bacteria strains.

SI Movie Legends



Movie S1

High speed video (6400 fps) illustrating inertial focusing of RBCs (3x diluted whole blood, ~15% hct) at the inner channel wall at DC 1 and continuous collection into the waste outlet (upper).



Movie S2

Fluoroscent video illustrating focusing of Alexa Fluor® 488 *E. coli* (K-12 strain) BioParticles® conjugates spiked in PBS at the outer wall at DC 1 and collection into the bacterial outlet (bottom).

Table S1. Sequences for rRNA probes targeting the 16S or 23S rRNA subunits from *E. coli* , *K. pneumoniae* , or *P. aeruginosa* . Nucleotide positions are relative to the annotated reference genome sequences of *E. coli* strain EcHS, *K. pneumoniae* strain MGH78578, and *P. aeruginosa* strain PAO1, respectively, from the NCBI database.

	PROBE	SPECIES RECOGNIZED	GENE	NUCLEOTIDES	PROBE 1 SEQUENCE	PROBE 2 SEQUENCE
E. coli	Ec_1	***E. coli***	16S rRNA	5-105	TGTGTTAGGCCTGCCGCCAGCGTTCAATCTGAGCCATGATCAAACTCTT	CCACTCGTCAGCGAAACAGCAAGCTGCTTCCTGTTACCGTTCGACTTGCA
	Ec_2	***E. coli***	16S rRNA	935-1035	GGTAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTT	TCCCGAAGGCACATTCTCATCTCTGAAAACTTCCGTGGATGTCAAGACCA
	Ec_3	***E. coli***	23S rRNA	254-354	ACGCTTCCACTAACACACACACTGATTCAGGCTCTGGGCTGCTCCCCGT	TGTGCATTTTTGTGTACGGGGCTGTCACCCTGTATCGCACGCCTTTCCAG
	Ec/Kp_1	***E. coli, Klebs. pneumo.***	16S rRNA	1370-1470	ACTCCCATGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCA	AGTGGTAAGCGCCCTCCCGAAGGTTAAGCTACCTACTTCTTTTGCAACCC
Klebs. pneumo.	Ec/Kp_2	***E. coli, Klebs. pneumo.***	23S rRNA	5-105	CCTTCATCGCCTCTGACTGCCAGGGCATCCACCGTGTACGCTTAGTCGC	GCTGTAACGGTTCATATCACCTTACCGACGCTTTTCGCAGATTAGCACGT
	Ec/Kp_3	***E. coli, Klebs. pneumo.***	23S rRNA	1210-1310	ATGTCAGCATTCGCACTTCTGATACCTCCAGCATGCCTCACAGCACACC	AACCCTTGGTCTTCCGGCGAGCGGGCTTTTCACCCGCTTTATCGTTACTT
	Ec/Kp_4	***E. coli, Klebs. pneumo.***	23S rRNA	2790-2890	CGGCCTATCAACGTCGTCGTCTTCAACGTTCCTTCAGGAGACTTAAAGT	CACGGTTCATTAGTACCGGTTAGCTCAACGCATCGCTGCGCTTACACACC
	Kp_1	***Klebs. pneumo.***	23S rRNA	260-360	TTCCAGACCGTTCCACTAACACACAAGCTGATTCAGACTCTGGGCTGCT	ACAGCCTGTGCATTTTGGTGTACGGGACTATCACCCTGTACCGTCGGACT
P. aeruginosa	PsA_1	***P. aeruginosa***	16S rRNA	165-265	CATCTGATAGCGTGAGGTCCGAAGATCCCCCACTTTCTCCCTCAGGACC	GTCGCCTTGGTAGGCCTTTACCCCACCAACTAGCTAATCCGACCTAGGCT
	PsA_2	***P. aeruginosa***	16S rRNA	1190-1290	ACCGACCATTGTAGCACGTGTGTAGCCCTGGCCGTAAGGGCCATGATGA	CGATCGGTTTTATGGGATTAGCTCCACCTCGCGGCTTGGCAACCCTTTGT
	PsA_3	***P. aeruginosa***	23S rRNA	525-625	CGCTGACCCATTATACAAAAGGTACGCAGTCACCTAACAAGTAGGCTCC	GCTTTCGCTACGCCTACCCTATACGGTTAAGCTTGCCACTGAATATAAGT
	PsA_4	***P. aeruginosa***	23S rRNA	1375-1475	AGCCTTCTCCGTCCCTCCATCGCAGTAACCAGAAGTACAGGAATATTAA	AGATTTCAGCCTACCACCTTAAACTTGGACAACCAACGCCAAGCTGGCCT
	PsA_5	***P. aeruginosa***	23S rRNA	2605-2705	CGGTCCTCTCGTACTAGGAGCAGCCCCTCTCAAATCTCAAACGTCCACC	CCGGCAATGCCACTGGCGTGACAACCGGAACACCAGAGGTTCGTCCACTC

Table S2. Sequences for mRNA probes targeting ciprofloxacin-responsive ("R_") and control ("C_") transcripts from *E. coli* . Nucleotide position is relative to the annotated reference genome sequence of *E. coli* strain EcHS from the NCBI database.

	PROBE	GENE	NUCLEOTIDES	PROBE 1 SEQUENCE	PROBE 2 SEQUENCE
RESPONSIVE	R_1	*phoB*	50-150	CTTCCGCTTCGACCGGCTGAAAGCCATTTTGTTCGAGCACGAAGCAGAC	AATTAAATCCGGCCAGGGTTCATTCAGTTGATTCACAGCACTGTCATAAT
	R_2	*phoR*	1114-1214	TCCGCTACCGCCGGTTTGCCGGGAACGCGCTTTATCAACGCGATAAAAA	AGGCGACTTTCGTGATGATTCACCGCATGTTTCACGATCGCTAACCCTAA
	R_3	*sulA*	63-163	TAGACAACTTCACTGATAAGCCCGGCTGTAGTGTTTTCCGTAGAGACAC	GTAACAATGGCAACAGTAGAAGTTGCGTCATCATGGGCTGATCTTCGCGA
	R_4	*yebG*	3-103	GACATTTTCTCTTCGCCCTCACGAATGACTACGTATTTAACTTCAACCC	CCGTATCAAGCATTTTGTCATAAGCATCGGCTTCCTTTTTGCTGGTAAAC
	R_5	*recA*	57-157	ATGGAACGGTCTTCACCCAGGCGCATGATGGAGCCTTTACCAAATTGTT	CAAGCGCGATATCCAGTGAAAGCGAACCGGTAGAGATGGTTTCCACATCC
	R_6	*EcHS_A3544*	34-134	GTTCAGTTCTTCAATGGTGATTTCCTGAAAAGCCAGTCGGCTCTCCAGC	AGATGATCGCGCAGTTTCGCCATCTCCATTTCATGAGCGGTCACCGTGAC
CONTROL	C_1	*rcsB*	220-320	GAAATGGCGCTTGATGTACTTGATTAAGGTAATGCCATCGCCGTACTTA	AGAATCGCCGGGTTGTTGTTCATGGTCAGAACAATAATCGACAGGCTTGG
	C_2	*secB*	31-131	GTTCGGCGCTTCGAAAGAGATATCCTTGGTATAAATACGTTGGATCTGC	AGATCAAGTTTAACTTCTGGTTGCCAATCTTTCTGGAAAACGTGCGGCGC
	C_3	*hflC*	361-461	TTTCACGTCCAGGCGACCAATTTCAGAACGCAGACGGTCAGAGAACTTA	GCGTCACGTACTTCGAGGGTCAGACGACCACGGGAATCGGTGACGATGTC