

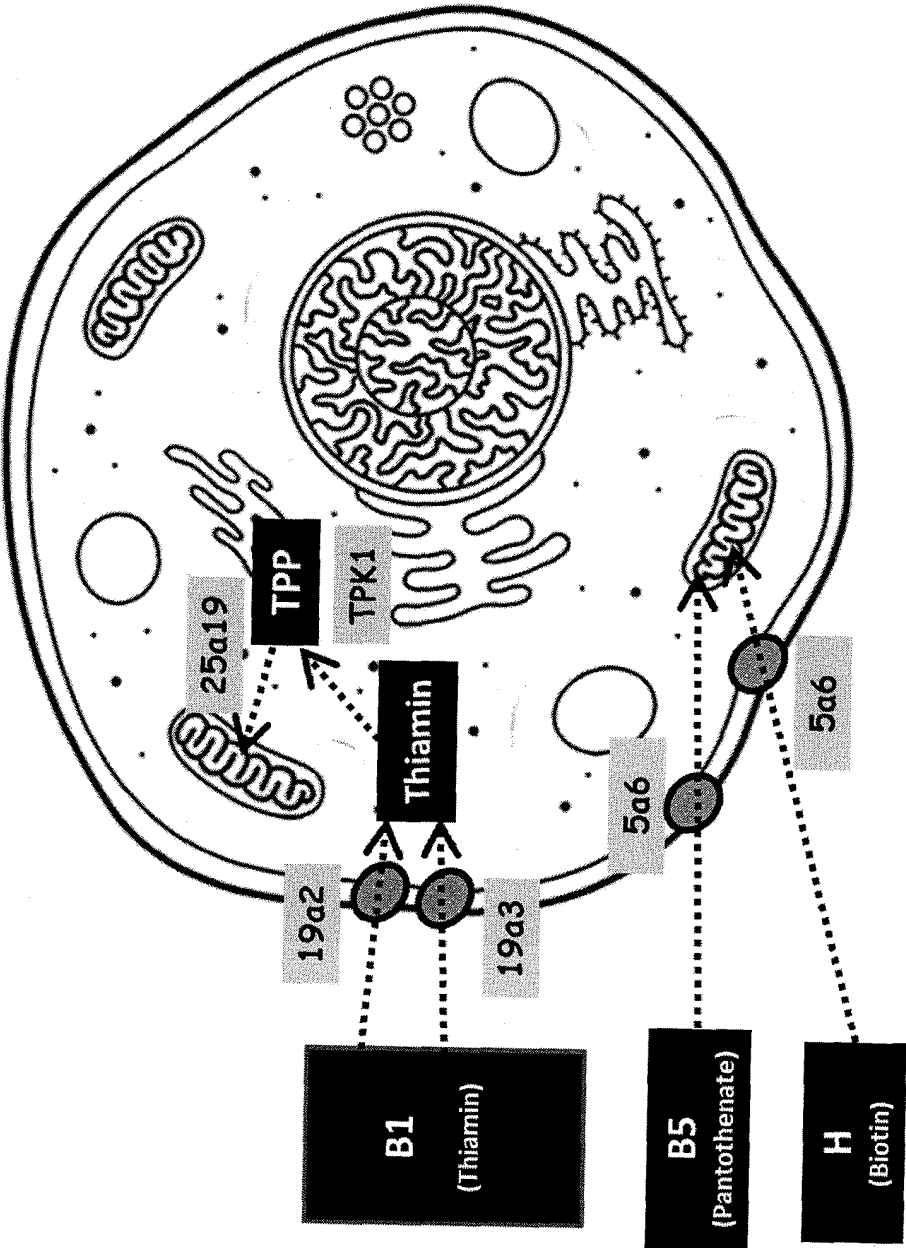


FIG. 1

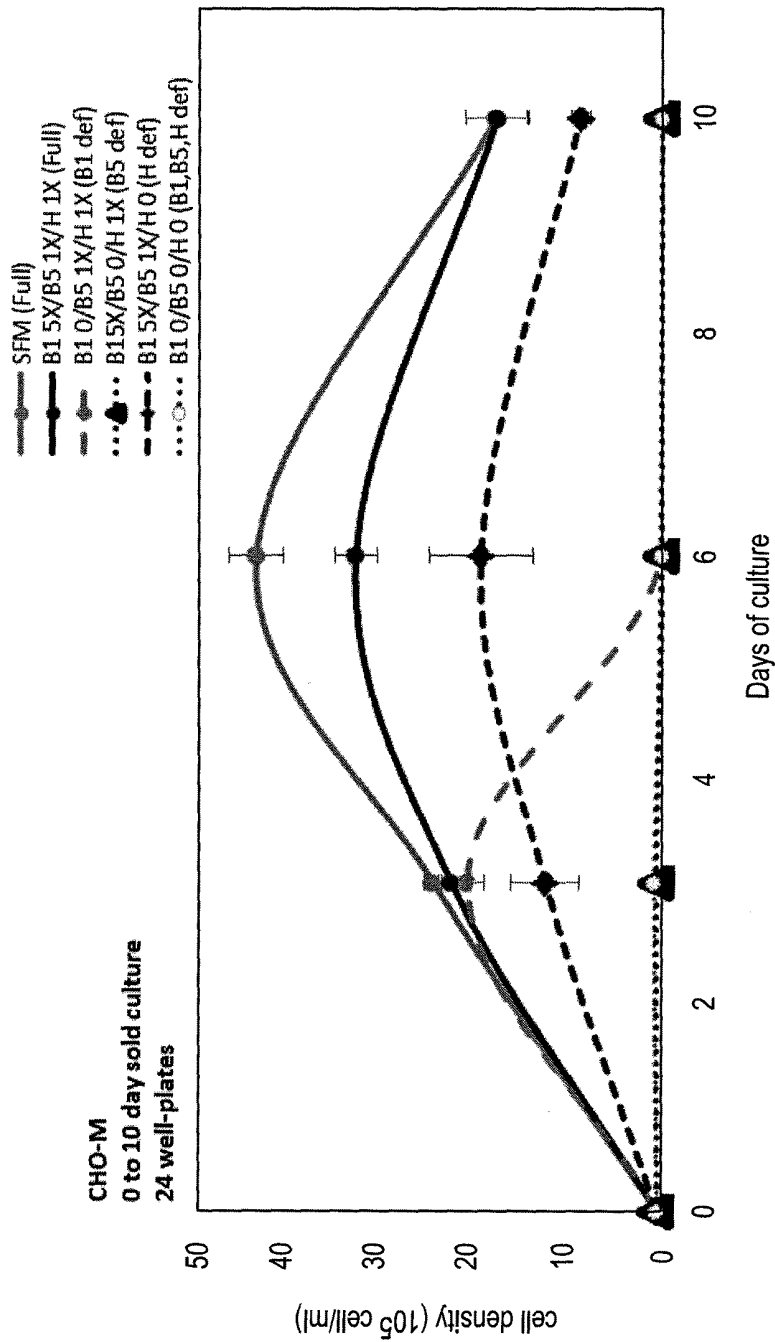


FIG. 2A

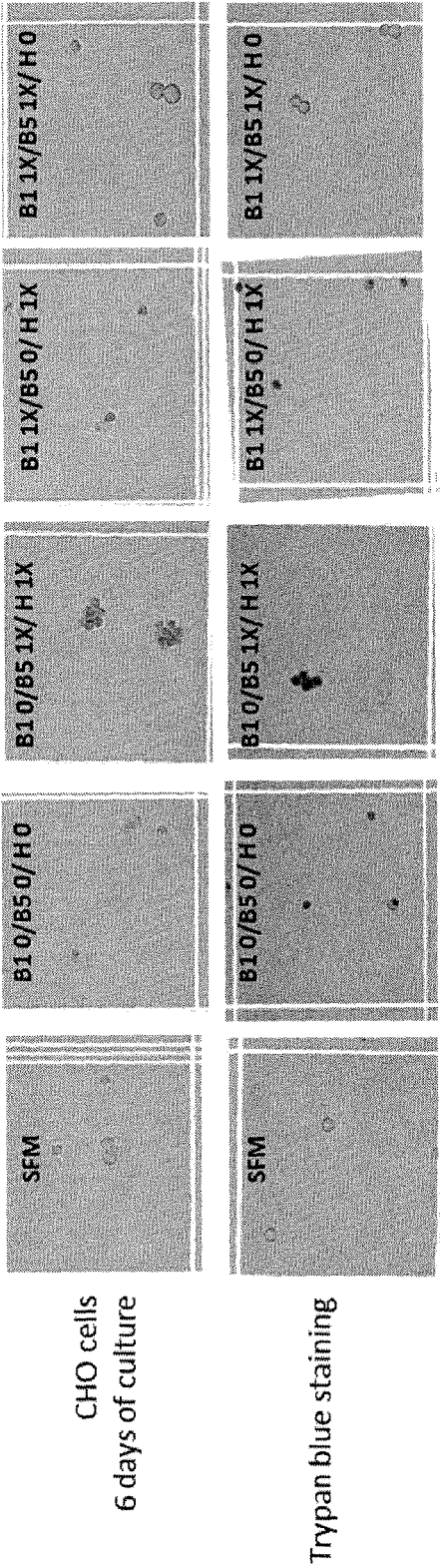


FIG. 2B

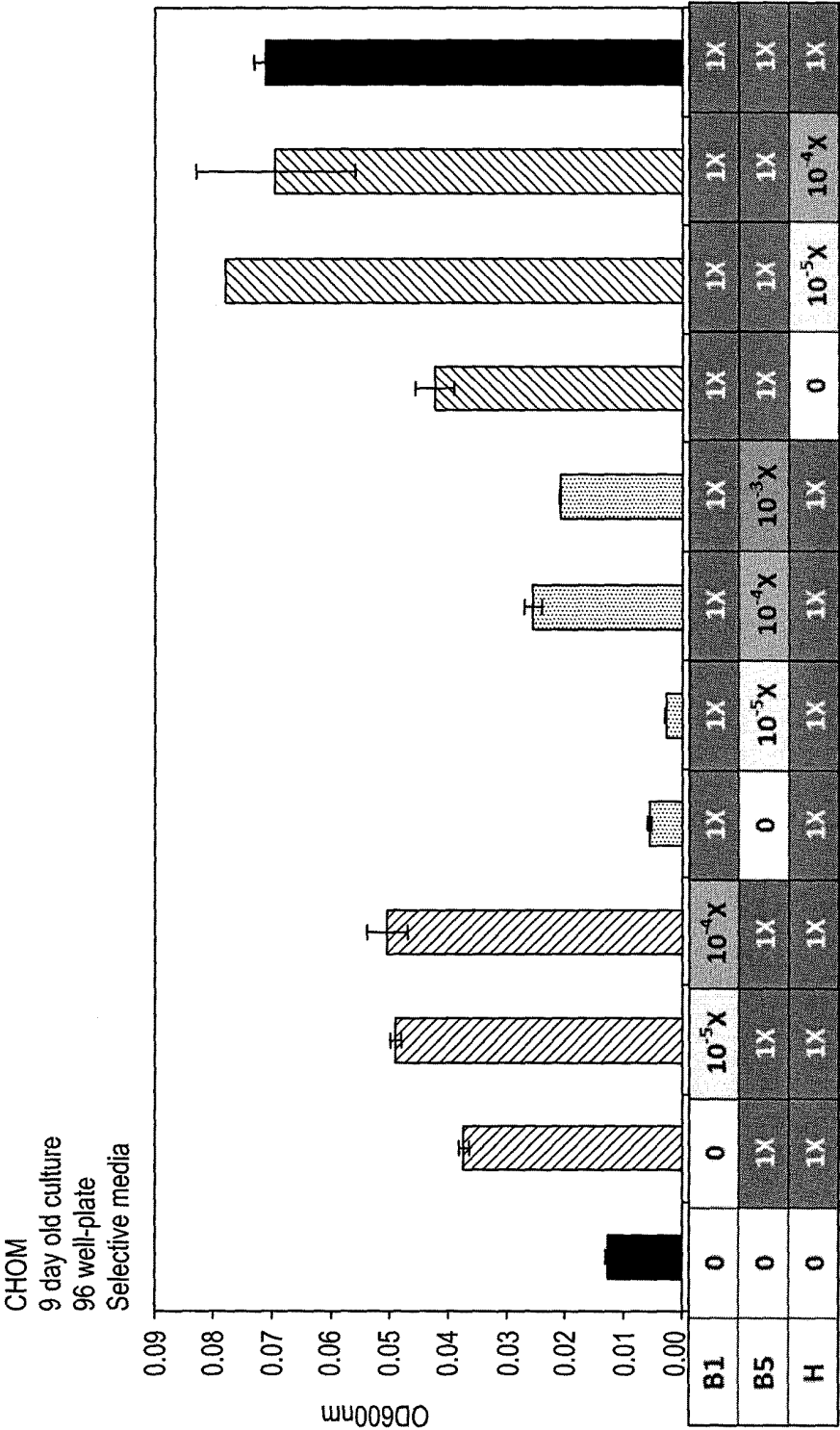


FIG. 3

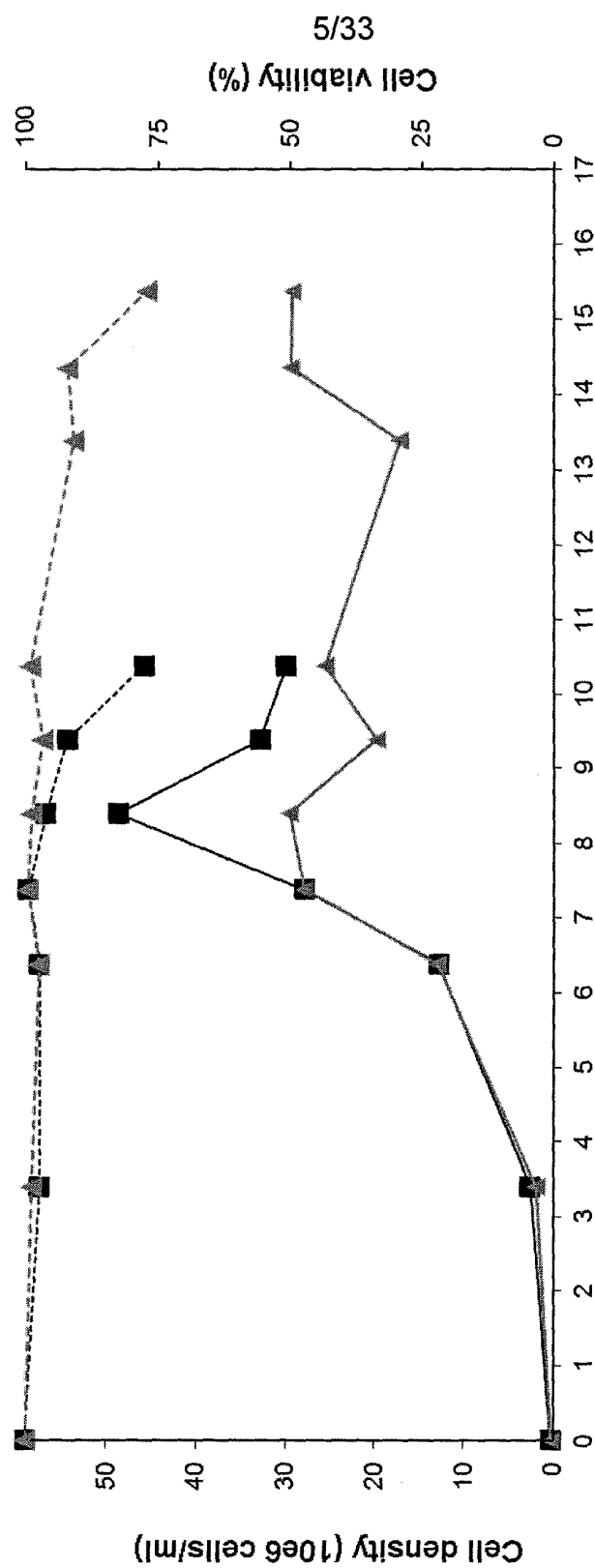


FIG. 4

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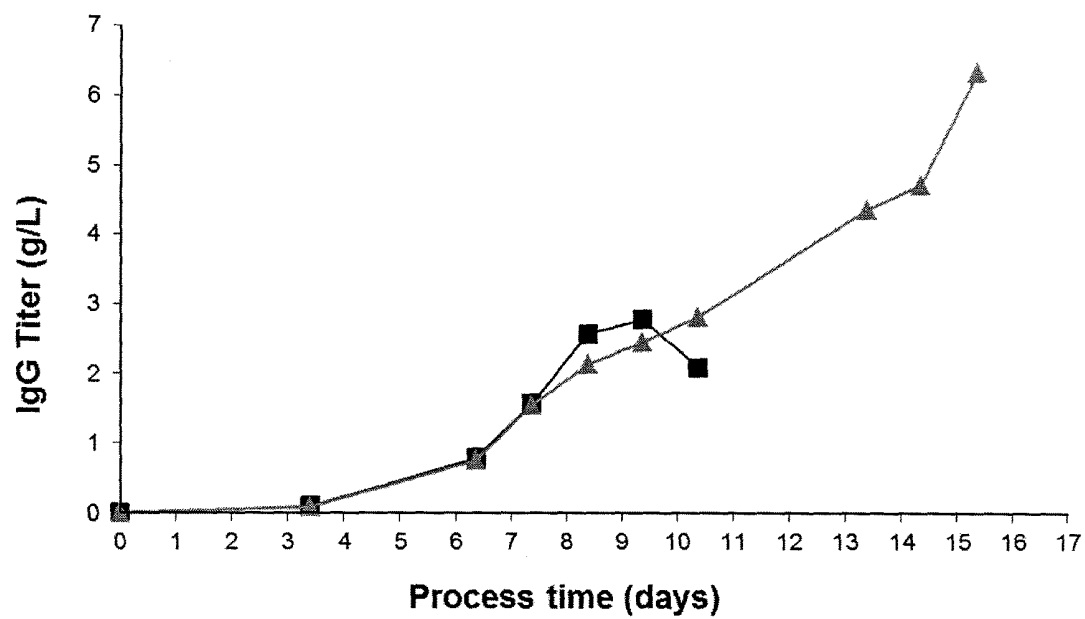


FIG. 5

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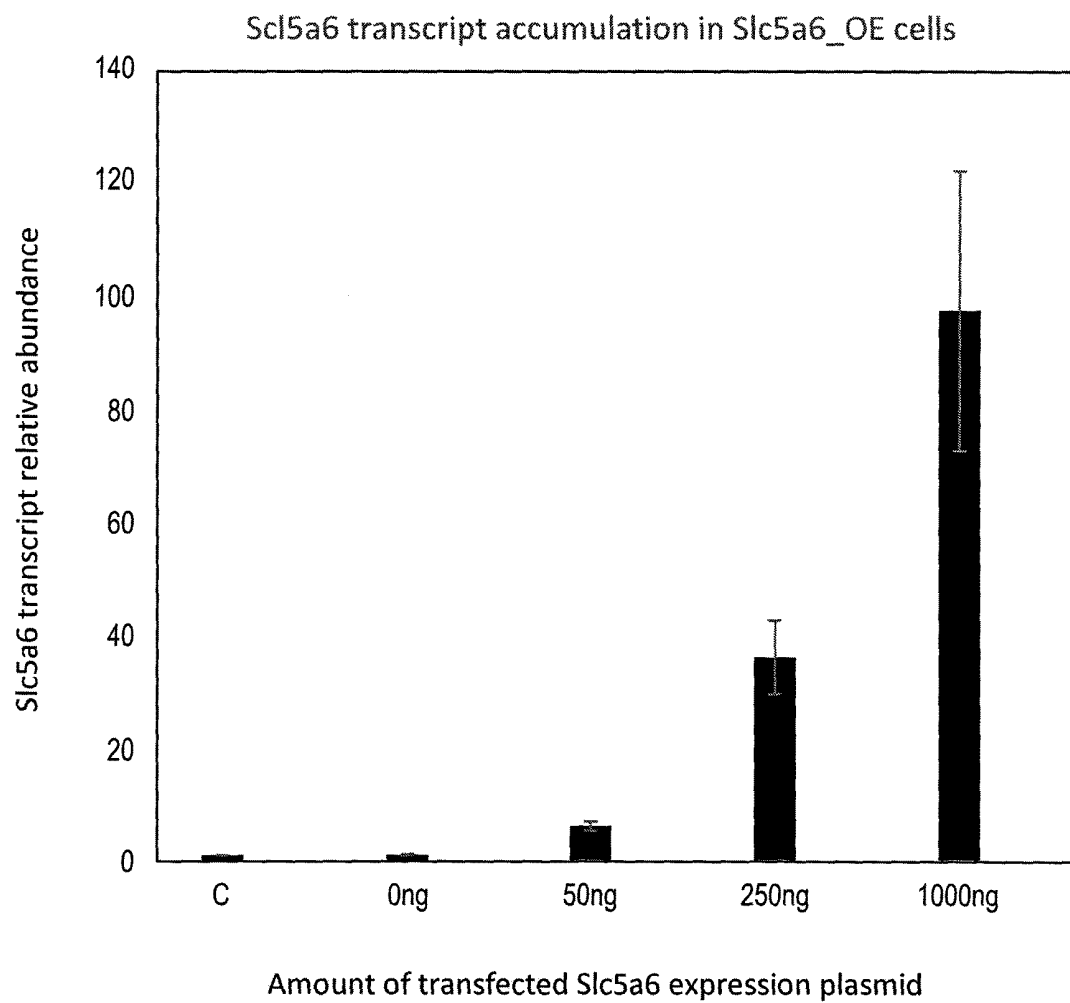
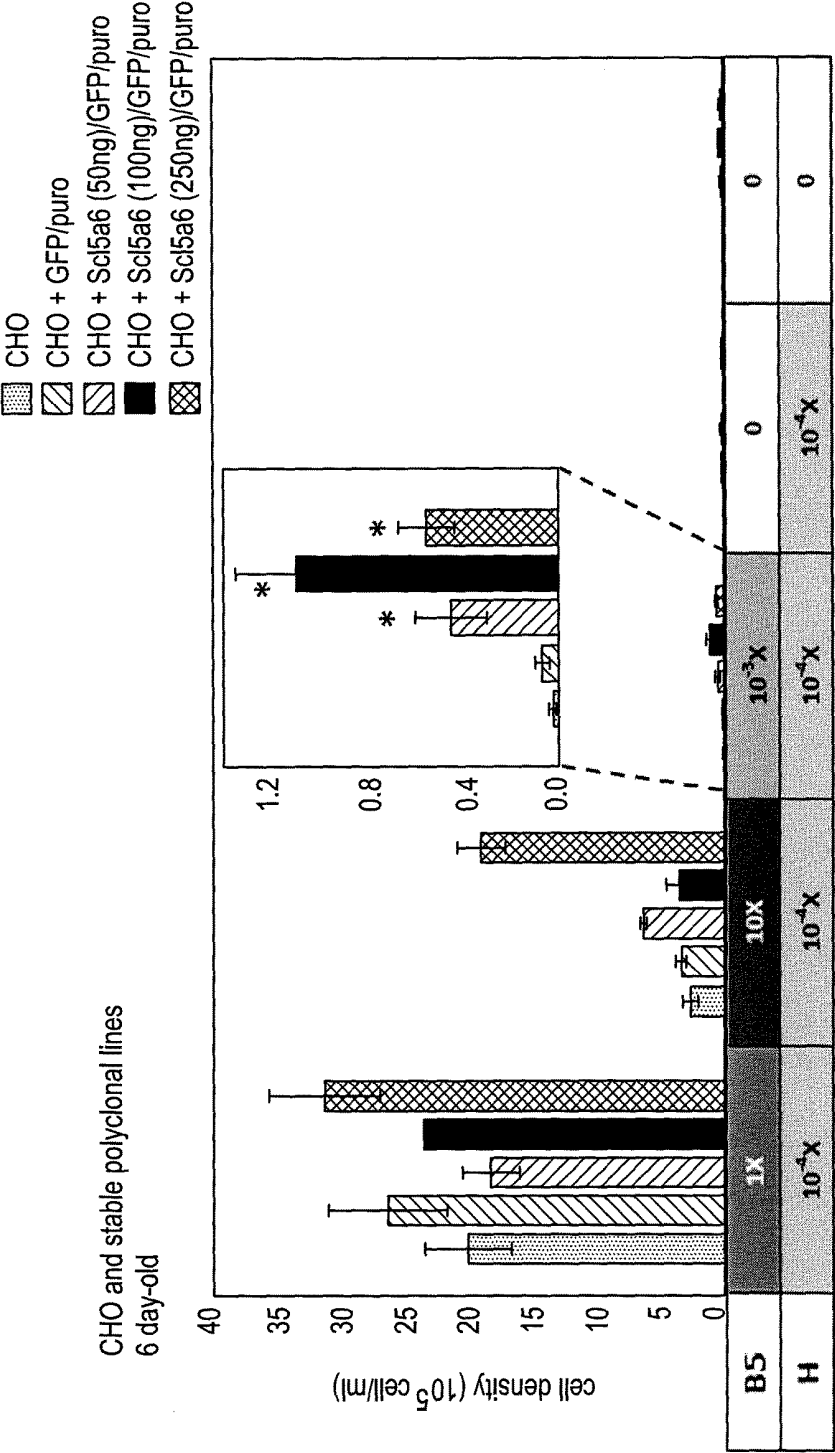


FIG. 6



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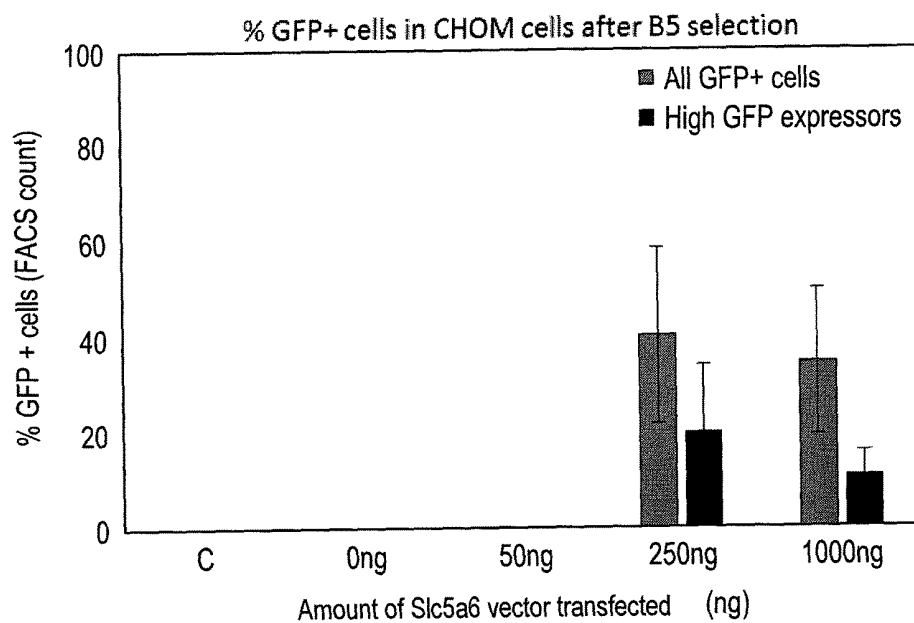


FIG. 8A

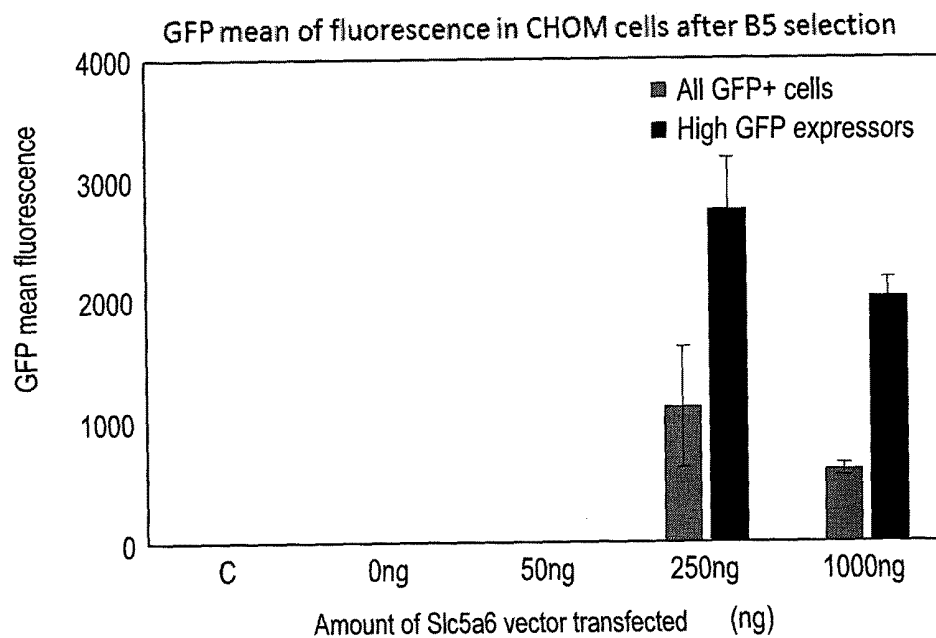


FIG. 8B

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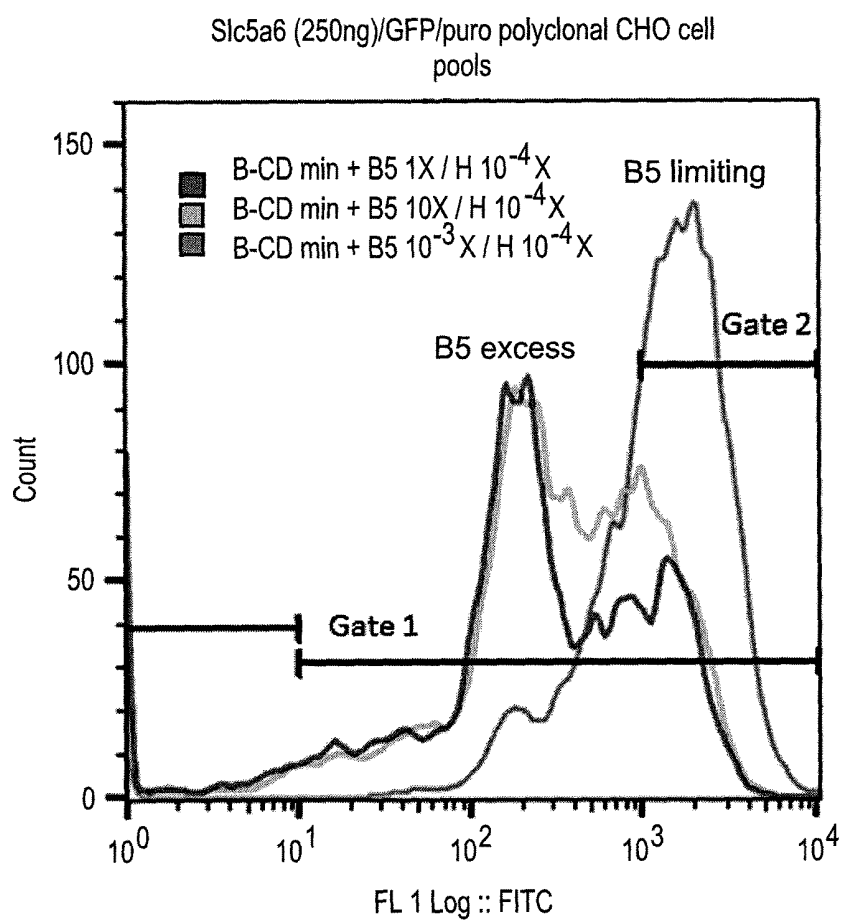


FIG. 9A

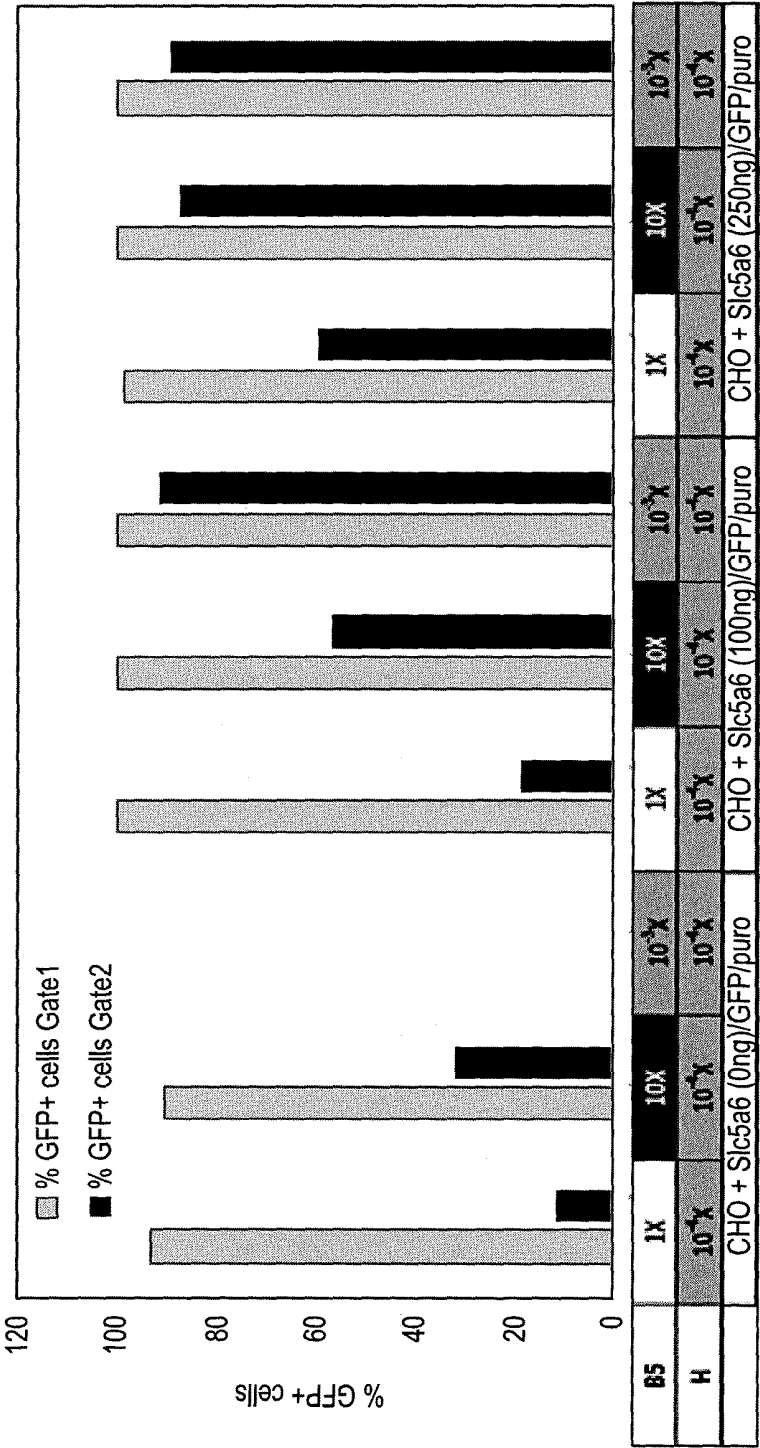
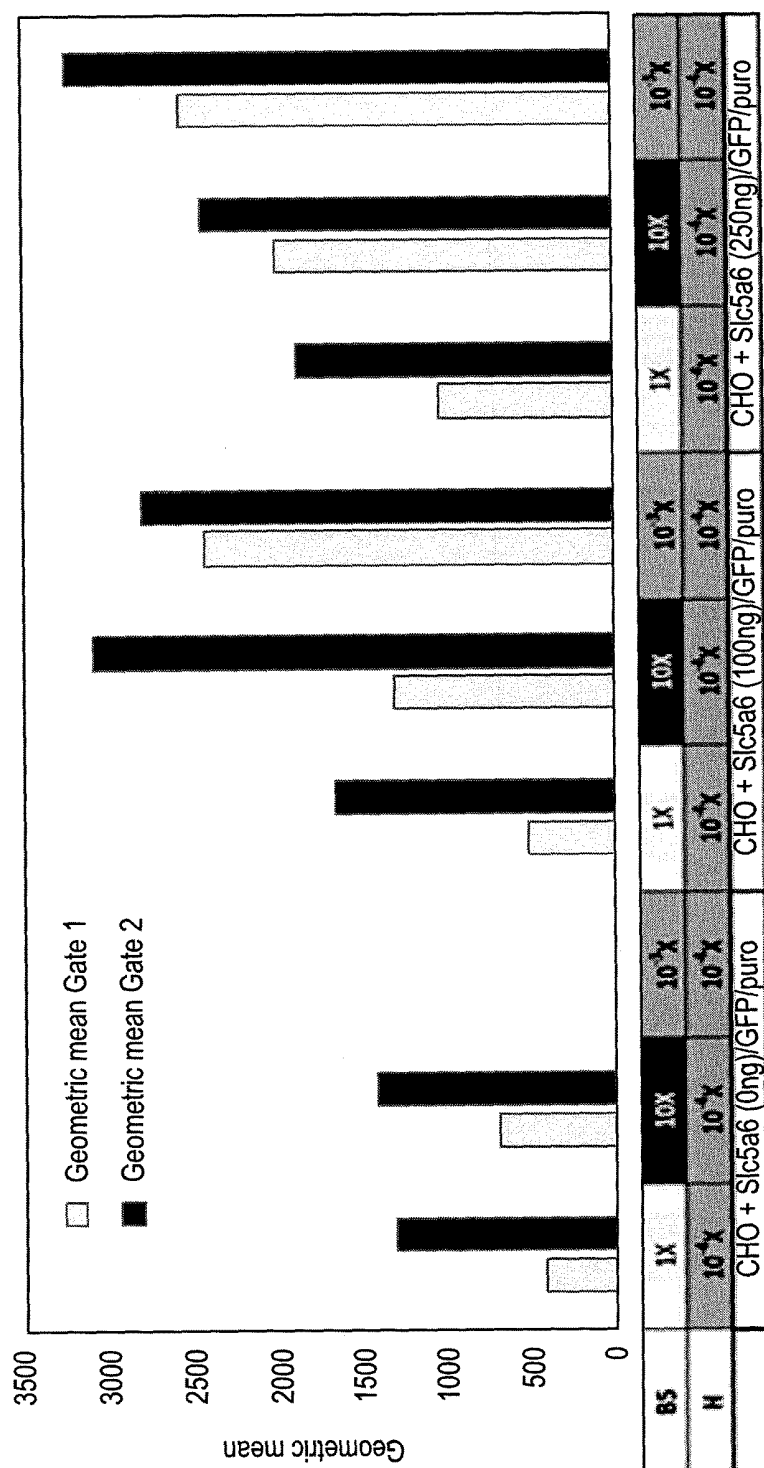


FIG. 9B



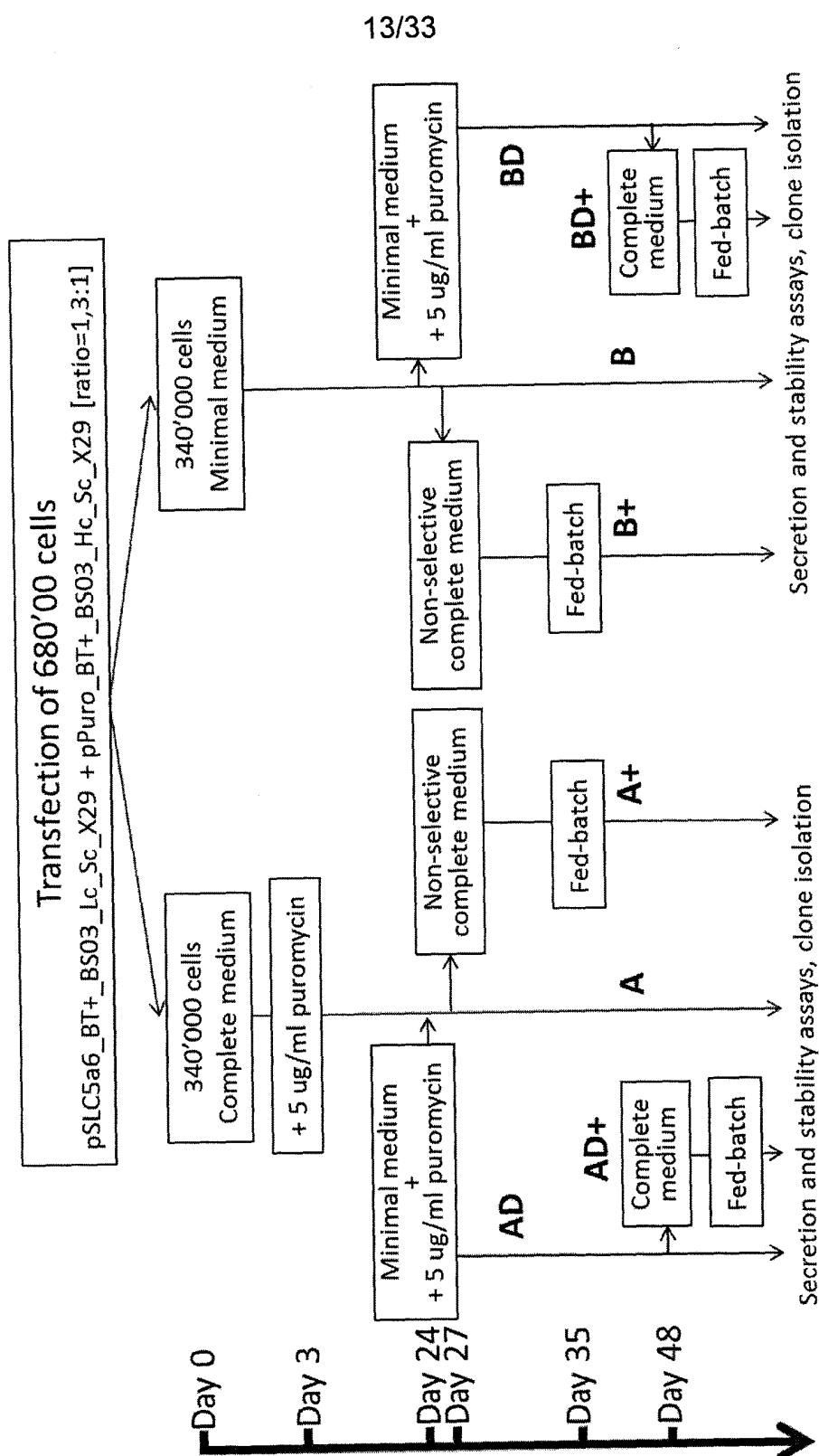


FIG. 10

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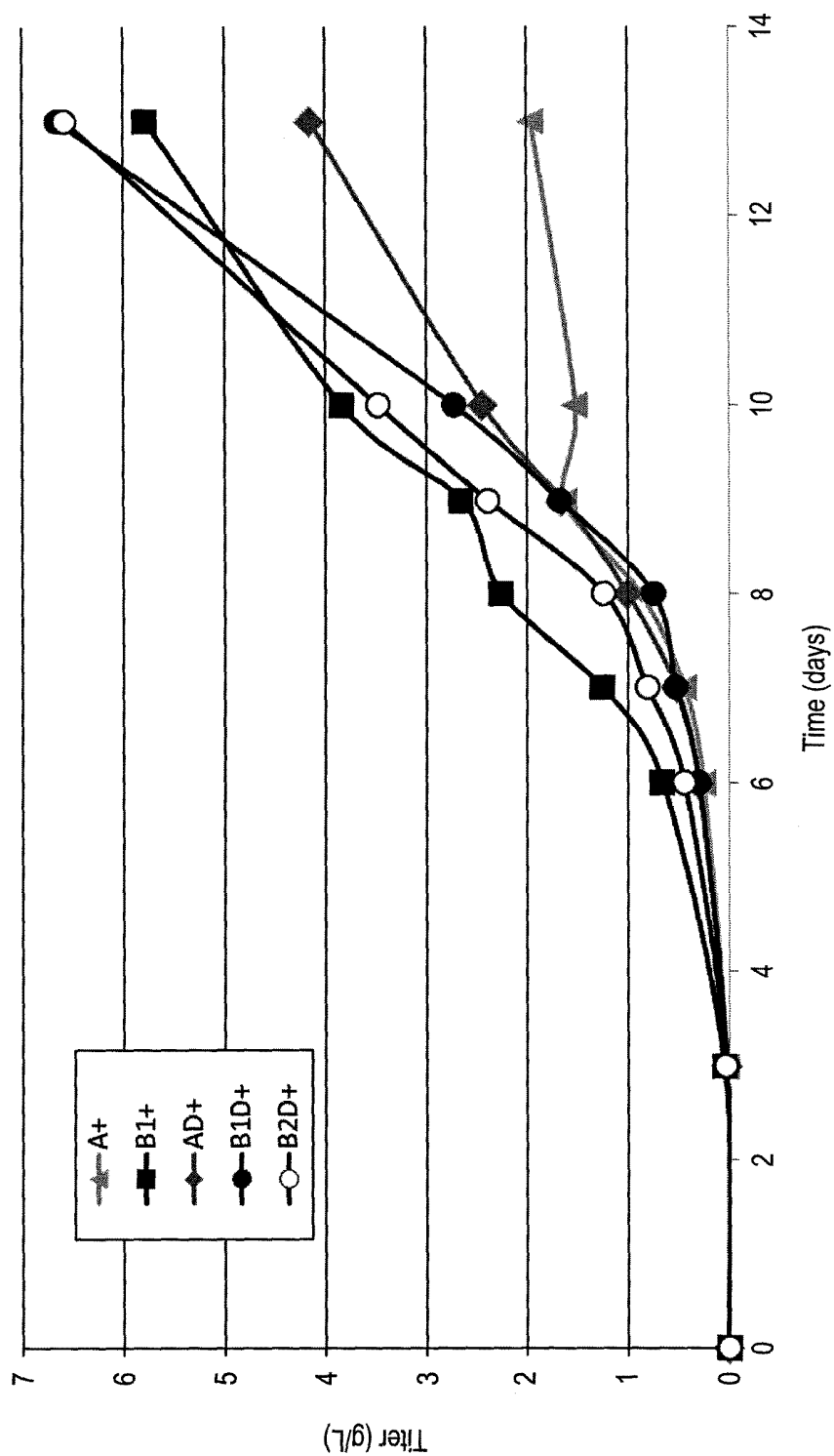


FIG. 11

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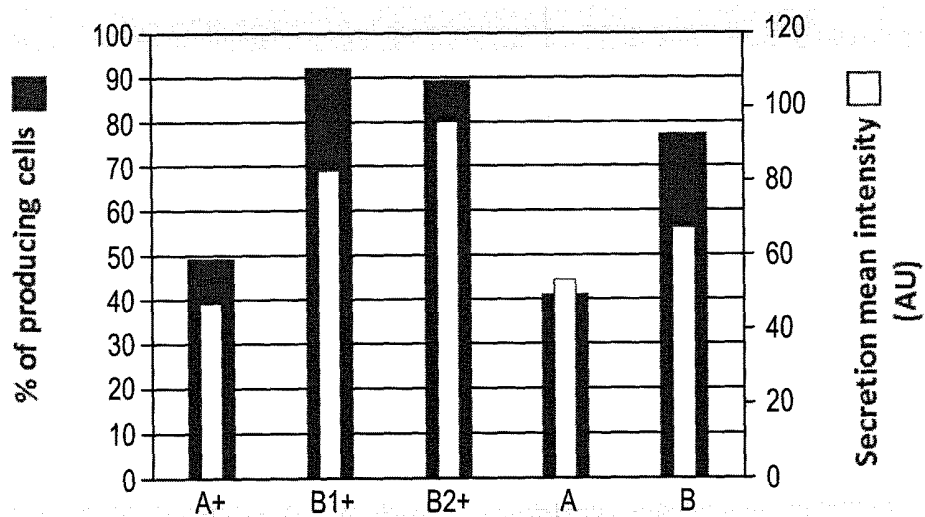


FIG. 12A

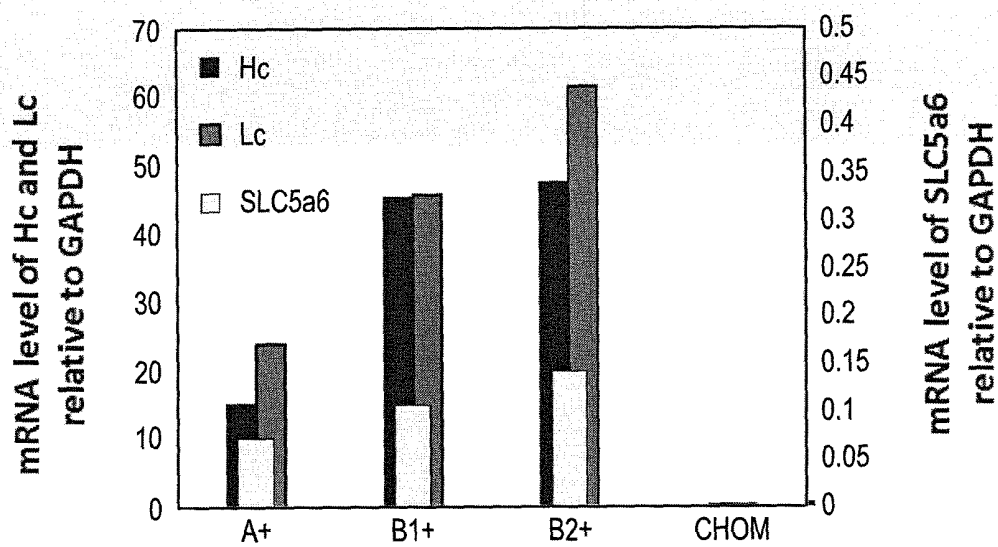


FIG. 12B

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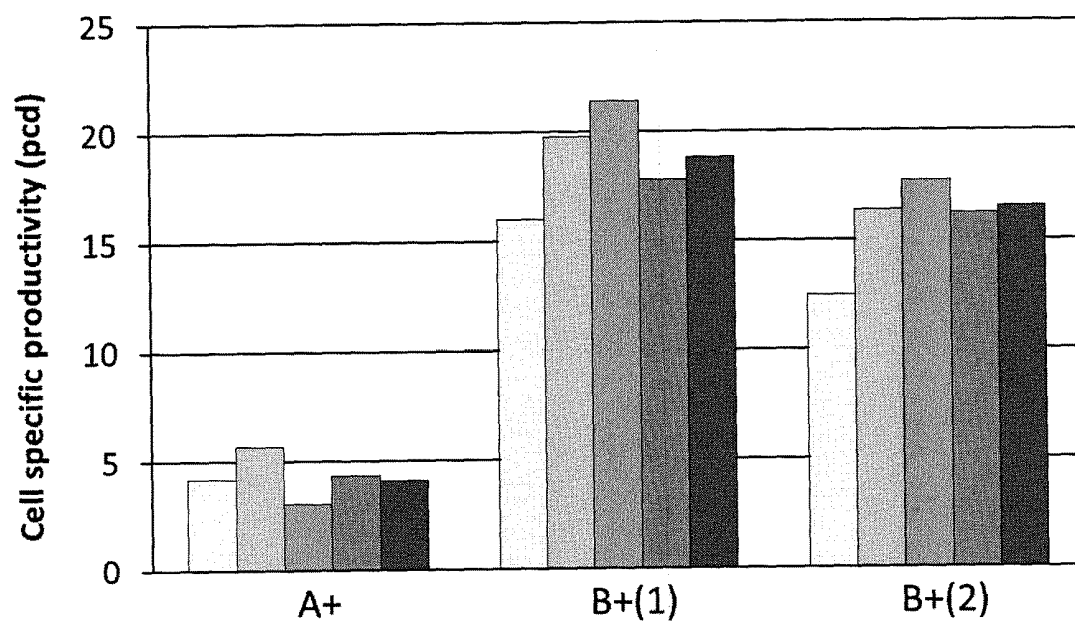


FIG. 13

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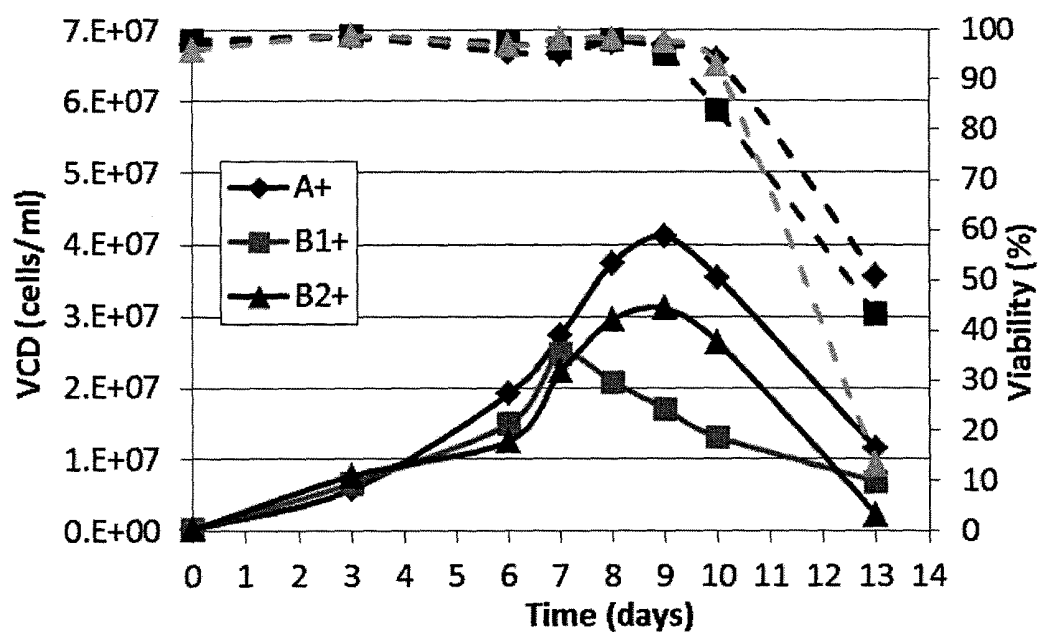


FIG. 14A

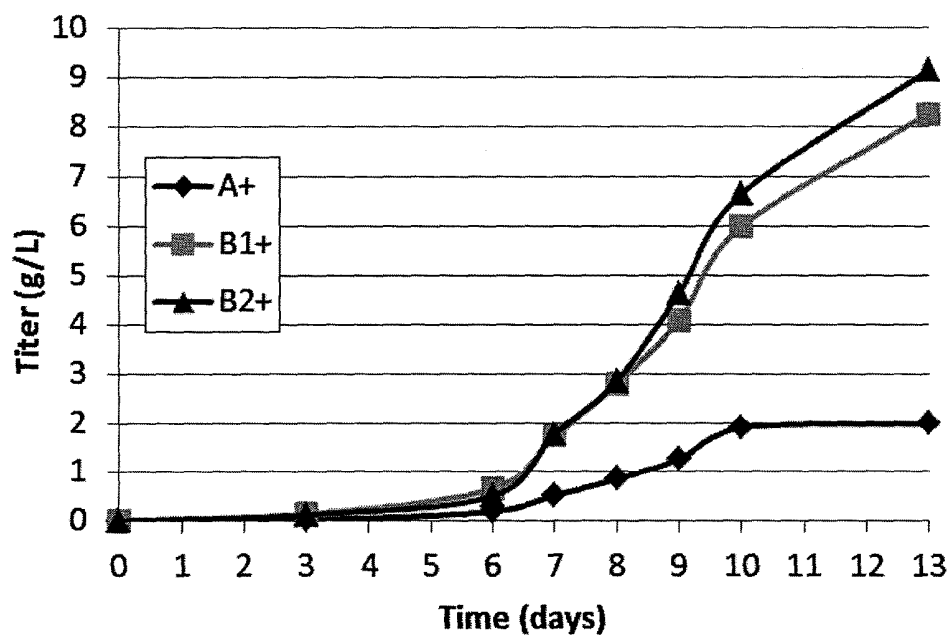


FIG. 14B

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FIG. 15

Coding sequences of the CHO-M vitamin genes

(SEQ ID NO. 21) >SLC5A6_CHO_CDS

ATGAGTGTGGAAGAGAGCACCTCAGCTCCCTTCTACACAACCTCAGATACCAACAAGGTTATTGCCA
CCTTTTCTGTTGTGGACTATGTGGTATTTGGCCTGTTGCTGGTTCTCTCCCTTGCCATTGGGCTCTAT
CATGCTTGCCGTGGATGGGGCCGGCATACTGTTGGTGAGCTGCTGCTGGCAGACCGAAAAATGGG
CTGCCTTCCTGTATCACTGTCCCTGCTGGCCACCTTCCAGTCAGCGGTAGCCATCCTGGGGGCACC
AGCTGAGATCTACCGATTTGGAACCCAGTATTGGTTCCTGGGATGCTCCTACTTTCTGGGGCTCCTG
ATCCCTGCTCACGTCTTCATCCCAGTCTTCTACCGCCTGCATCTTACCAGTGCCTATGAGTACCTGG
AGCTTCGCTTCAATAAAGCAGTGCGGATCCTGGGGACTGTGACCTTCATCTTTCAGATGGTGATCTA
CATGGGAGTTGCTCTCTATGCACCATCCTTGGCCCTCAATGCAGTGACTGGATTTGATCTGTGGCTG
TCAGTTCTGGCCCTGGGGATCGTCTGCAACATCTACACAGCACTGGGTGGGCTGAAGGCTGTCATC
TGGACAGATGTGTTCCAAACACTGGTCATGTTCTAGGGCAGCTGGTGGTTATCATTGTAGGCTCTG
CCAGAGTAGGCGGCTTGGGGCATGTATGGGATGTGGCCTCCAGCATAAACTCATCTCTGGGATTG
AGCTGGATCCTGACCCATTTGTGCGTCATACTTTCTGGACTTTGGCCTTTGGGGGTGTCTTCATGAT
GCTGTCTTTGTATGGTGTGAACCAGGCTCAGGTGCAGCGCTATCTCAGCTCCCGCTCAGAGAAGGC
TGCTGTGCTCTCCTGCTATGCCGTGTTCCCTGCCAGCAAGTGGCCCTCTGCATGAGCTCCCTCATT
GGTTTGGTCATGTTTGCCTATTATAAGAAATACACTATGAGCCCCAGCAAGAGCAAGCAGCACCTG
ACCAGTTAGTCCCTCTATTTTGTGATGGACCTTCTGAAGGACATGCCAGGGCTGCCTGGGCTCTTTGT
TGCCTGCCTCTTCAGTGGATCCCTCAGCACCATATCATCTGCATTCAATCACTGGCAACCGTCACC
ATGGAAGACCTCATTCAACCCTGGTTCCCTGAGCTGACCGAAACCCGGGCCATCATGCTTTCCCGAA
GCCTTGCCTTTGCCTATGGGCTGATTTGCCTGGGAATGGCCTATATTTCTCTCATCTGGGATCAGT
GCTCCAGGCAGCACTCAGCATCTTTGGCATGGTTGGAGGGCCACTGCTGGGACTCTTCTGCTTGGG
GATGTTCTTTCTTGTGCCAACCCCTCTTGGCGCCATCGTGGGCCTGTTGACTGGACTCACCATGGCT
TTCTGGATCGGCATTGGGAGCATAGTGAGCAGGATGAGTTCTGCCGTGGTGTCCCCTCCCATTAAC
GGGTCCAGCTCCTTCTGTCCAGCAACCTGACCATGGCCACTGTGACCACCCTGATGCCTTCCACC
ACCCAGTCCAAGCCCACAGGACTGCAGCGGTTCTACTCCCTGTCCTATTTATGGTACAGTGCACACA
ATTCCACCACAGTCATCGTTGTGGGCCTGATTGTGAGTCTGCTTACCGGGGAATGCGGGGCCGGA
CCCTGAACCCCGGCACCATTTATCCTGTGTTGCCAAAGCTCCTCTCACTCCTGCCCTTATCCTGCCA
GAAGCGGCTTTGCTGGAAGGCCACAGCCAGAATGCTCCAATGGTCCCCAACTGTGTCCAGAGAA
GATGAGGAATGGAGTGCTGCAGGACAGCAGGGACAAAGAGAGGATGGCTGAGGATGGCCTAGCCC
ACCAGCCATGCAGTCCTACCTATGTTGTCCAGGAGACCTCCCTGTGA

(SEQ ID NO. 22) >PANK1_CHO_CDS

ATGCAAATACCAGTGCGAAGTGAAGTTATCCAGTTACCGTTAGGAGCTCAAGGCAGTGCAGGCAGT
GGCTGTTACACGGGCACTGGAAGTCATGGCATCAGGTCTGCAGGCTTCTGGCTGTCTCGTGCCTAC
CTACCCAGTACCCTTTAGGCTCACTCTGCCACACAAAGCACGATCCGCCTATCTCCTCTTCGCAA
CCCTGAGAACTTCATTCTGCACGTTAAACTCGTCCGTGGCGGTGGCGGGCAGGACTGGGCATGCT
CAGTGGCGGGGACAGGTCTGGGAGGCGAGGAAGCCGCATTTGAACCTCTAGAGGCGCCGGGCGC
TGAAGGTGTTGGCCCGCGGTGGTTCCTGGCTAGTCCTATCCGCCTGACACTAGCTGTGGCTGCACC

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FIG. 15 (cont'd)

CACCTGTGCCATGCACATGTTTCATCCAGATGGGCGAGGAGAAGAACTTCTCCAGCCTCCACACCAC
CCTCTGTGCCACGGGAGGTGGGGCTTTCAAGTTTGAGGAGGACTTCAGAATGATAGCAGACCTACA
GCTGCATAAACTGGACGAACTGGACTGCTTGATACAGGGCCTGCTTTACGTTGACTCAGTTGGCTTC
AACGGCAAGCCAGAATGTTACTATTTTGAACCCCAAAATCCTGAATTGTGTCAAAAGAAGCCATA
CTGCCTTGATAACCCATACCCTATGCTGCTGGTTAACATGGGCTCAGGTGTCAGCATTCTAGCAGTG
TACTCCAAGGACAACCTACAAAAGAGTTACTGGGACCAGTCTTGGAGGCGGGACATTCTAGGCCTGT
GTTGCTTGCTGACTGGTTGTGAGACCTTTGAAGAAGCTCTGGAGATGGCAGCTAAAGGCGACAGCA
CCAATGTTGATAAGCTGGTGAAGGACATTTACGGAGGAGACTATGAACGATTTGGCCTTCAAGGATC
TGCTGTAGCATCAAGCTTTGGCAACATGATGAGTAAAGAAAAGAGAGAGGCCATCAGCAAAAGAAGAC
CTCGCCCGTGCCACATTGGTCACCATCACCAACAACATTGGCTCCATTGCTCGGATGTGTGCTCTAG
AGGAGAAATATTGACCGAGTTGTATTCGTTGGGAACCTTTCTCAGAATCAACATGGTCTCAATGAAGTTG
CTCGCATATGCCATGGACTTTTGGTCTAAAGGACAGCTGAAAGCACTGTTTTTGAACATGAGGGTT
ATTTTGGAGCTGTTGGGGCCCTGTTGGAACCTGTTCAAAATGACTGATGCGCAGTAG

(SEQ ID NO. 23) >PANK2_CHO_CDS

ATGTCTGGTGGCTTCCCTAAGGCTAGCCCCCTCCTTGAGAAGCCATGTGCAGTTAGGGCAGCATTGC
ATACAGGTGACTGGAGGAGTGGTTGGATACTCAGTTTTTCCATGGTTTGGCTTGGATATTGGTGGAA
CCCTAGTTAAGCTGGTTTATTTTGAACCTAAAGACATCACTGCTGAAGAAGAAAAGGAGGAAGTGA
GAGTCTGAAAAGTATTCGCAAGTACCTGACCTCCAATGTGGCTTATGGATCCACAGGAATTCGGGAC
GTGCACCTTGAGCTGAAGGACCTGACTCTGTGTGGACGCAAAAGGCAATCTGCACCTTATACGCTTTC
CCACTCATGACATGCCTGCTTTTATTCAAATGGGCAAGATAAAAACCTTCTCGAGTCTCCACACTGTC
TTTTGTGCCACTGGAGGTGGATCATACAAATTTGAGCAGGATTTTCTCACAATAGGTGACCTTCAGCT
TCACAACTGGATGAAGTGGATTGCTTAATAAAAGGAATTTGTACATTGATTCAGTTGGATTTAATGG
ACGGTCACAGTGCTATTATTTTGAATCCTGCTGATTCTGAAAATGTCAGAAGTTACCATTTGATTT
GAAAAATCCATACCCTCTGCTTCTGGTGAACATCGGCTCAGGGGTTAGCATCTTAGCAGTGTATTCC
AAAGATAATTATAAGAGGGTCCACAGGCACCACTTGGAGGAGGAACCTTTTGGTCTCTGCTGTC
TTCTTACTGGCTGAGCACTTTTGAAGAAGCTCTTGAATGGCATCTCGTGGGGATAGCACCAAAGT
GGACAAATTAGTTCGAGACATTTATGGAGGAGACTATGAACGGTTTGGATTGCCAGGCTGGGCTGTG
GCTTCAAGTTTTGAAACATGATGAGCAAGGAGAAGAGAGAGGCTGCCAGTAAGGAGGACCTTGCC
AGAGCAACTTTGATCACCATCACCAACAACATTGGCTCCATAGCAAGAATGTGTGCCCTTAATGAAAA
CATTAAACAGGTTGTATTTGTCGGCAATTTCTGAGAGTCAACACAATCGCCATGCGACTTCTGGCAT
ATGCTCTGGATTACTGGTCCAAGGGGCGAGCTAAAAGCACTGTTTTCAGAGCACGAGTACCAGGAAAT
TTTTCCATTTGGGGCAGGGTTCTACTTCACCCTACCCTTGTGTGACTCCTGTGAACCTAACACTGCCT
TGGGGCTGGCTGACCGGTTGTGA

(SEQ ID NO. 24) >SLC19A2_CHO_CDS

ATGCATGGATTATGCAGCCATGCTGCGCAAGCTCGCAAGCTCGTAAGGCTCTGGGATGACTATGCAT
TTTGCCTGAATGCAGATGGCCATGTGGGTGGCTATGGAACCCCGGAAATGACAACACAGAATATGC
CTTTCCAACCTGCTCTAGACCAAGTGTTAAAAATGTTTGACATGTCCACGCTTTTATAGTCACTGCTT
GCTCATTTAGCTGCCTTTAAGGTCTTCAATGAAATTTACCCCGTCTGGACGTACTCTTACTTGGTGTG
CCTCTTTCCTGTGTTCCCTTGCCACAGACTACCTCCGTACAAAGCCTGTCACTTCTGCTTCAGGGACTCA
GCCTTATTGTTACATGGTTCATGCTGCTCTATGCCCAAGGATTGCTGGCTATTAGTTCTTGAATTC
TTCTATGGCATTGCCACAGCCACTGAAATTCCTATTACTCCTATATCTACAGTGTGGTGCACCTGGG
CATGTACCAGAAAGTCACAAGTTACTGTAGAAGTGCCACCTTGGTAGGCTTCACAGTGGGCTCTGTC
TTAGGGCAAATCCTTGTGTCAGTGGCTCACTGGCCACTGTTTCAGCTTGAACGTCTCTCCCTCACCT
GTGTTTCTGTTGCTTTTGTGTTGGCCTGGTTTCTGCCATGCCACAGAAGAGTCTTCTTTACCAC
ATTCCTGCCTCCTGTCATGGAGTGAATGGCATCAAGGTACAAAATGGTGGCATCGTTACTGAAAACC

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FIG. 15 (cont'd)

CAGCATCTAACCACCTTCCTGGATGGGAGGACATTGAGTCAAAAATTCCTCTAAATTTAGATGAACCT
CCTGTGGAGGAACCGGAGCCCAAGCCAGACCGGCTGCGTGTGCTGAAAGTCCTGTGGAATGACTTC
TTGATCTGTTACTCTTCCCGCCCTCTGCTCTGCTGGTCCGTGTGGTGGGCCCTCTCCACCTGCGGCT
ATTTTCAAGTGGTGAACACACCCAGGGATTGTGGGAGAAGGTGATGCCTTCTCAAAGTGCCGTTAT
CTACAATGGTGGTGTGGAGGCTGTGTCAACCTTGTGGGTGCAAGCGCTGTATTTGCAGTTGGTTAT
ATAAAAATATCCTGGTCAACTTGGGGAGAAATGACGCTATTCCTCTGTTCTCTCTGATTGCTGCTGC
AGTGTATACCATGGACACTGTGAATAACATTTGGGTGTGCTATACATCCTATGTTGTCTTCAGAATCA
TCTACATGGTACTCATCACCATAGCAACTTTTCAGATTGCTGCAAACTCAGCATGGAACGTTACGCC
CTTGTTGGTGTAAACACTTTTCATTGCCCTGGCATTGCAGACCCTGCTCACTCTAATTGTGGTTGA
TAACAAGGGCCTTGGCTTAGAGATTACCACACAGTTCTGATTTATGCCAGTTACTTTGCGGTCTCT
CTGTAGTTTTCTGGCTAACGGTGCACTAGTGTCTAAAGAAATGCAGAAAGCAGGAGGATCCAG
CTCCAGCCCTCAAGCAACTACTCCCTAA

(SEQ ID NO. 25) >SLC19A3_CHO_CDS

ATGGAAACCATAATGAAGATACAGGGAAAGTCAGCCAAAACATCTTTCACCTTGATGGAGACAGAAA
ATGCCTTTGTTTCATAGTCGCTCATGTCTCGGGAAGAGACAAGAGCTCTGGTCTCGGGAGGAGACAG
AGTGTGCTTGGGAGATCACCAACTGCCACCTGGAAGACGTTCCAGGAAGTCTGTGGGAACCTCAGG
GACGCTTGGGAGATTCCCGTCGGGGAGCCGGTGACACCATAGCCGGCTGCATTTGCCAGACTTTGG
ACTGCTGTGACAAAATATCTGATCCGAAGAATCACAGATTTCCAGACACAGTATCAGACAGCAGG
ACTCACCAACAAACCGGTCCTGGCAGCACCTGCCAGAGGCCAGCAGTCATCCTAGCAGCAGCAT
GCTTCTGGCAGCAGCACTTCTGCTGACAACAGCCCTTCCCACAGCCACATCCACAGCCACAGCCAC
AGGAGCCACAGCCGCGAGGAGCGGCAGGGGGAGAGGGGGGGGGGGACGGCCACCGCCACAGCC
GCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCC
CCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCC
CACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCC
ACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCATGT
TGTCAGTAGAGAGGACTCAGGGTGACTGTGTTGCTGAGGCTAATCTTGAACCTCCTGGGCTCCTGTGA
TCTCCCCAGCGAGGGTGACTGTGTTGCTGAGGCTAATCTTGAACCTCCTGGGCTCCTGTGATCTCCCC
ACGCAGCCACCACAGCCGCCACAGCCGCCACAGCCGCCACAGCCGCCACAGCTGCCACAGCCTCC
ACAGCCACCGCAGCCACCACAACCACAGCAACCCATGATGTCAGTAAAGAGGACTCGGGTGAAGAC
TTTGTGCTCCATTGCTGTGGGAAGGGCTGTGGCTGTGGCTGTGGCTGTGGGAAGGGCTGTTGCCAG
CAGAAGTGTGCTGCCAGCAGAAGTGTGGCTGCAAGAAGTGTGCTGCTAGGATGGCTGTTGTCTC
TGCTTCTAACTAAGTACAGCTTGGAGCCTTGTGGCTGCATTTGGACCGTCATGACCTGAAACTG
AACAACTCTGGAGTATTGGACAGCCACACCTACTGCCACCAACGCCAGCAAGTGGTGATGAGT
GCCATATTAGCCCAGGAACCTGAAGTCACCTGCTTCTCTGAGGGCTATCTTGGAGGACGGGTGCG
GGGTGGGAGACTGCAGAGGAGTGTGCCTTAGGCATGCACCACGCCAGCGAACAGAGCAGCTGGCT
TCCGCGCCTGGGGCCTTCTGTGATCTGCTGTGTTCTTGTGCTGGAACCCACCCAAGTTGGTCTA
GCCAGGATTCTGTACCGCCCTCCGCAAGAGTAAAGGCCATTGAGTGGGCCCAATTCACACCTTTT
TACGCTGTGCGAATGCTTCTTCAAACCGCTGCGGTTGGGGAGTTGGCATGAAGCTTACCAGCGAG
TTTGGATAAACCCAACTCAAAGACAGTGTTGAGTTTGCCTCGTGCGAATTGGAATTACCGCAGTCA
CTGTACCTATACGCTGTGCTTCTGGTCACCCCTACATATCTACTCCACAGATGACAAATGAGGTCTC
TCCTGTTTGGACATACTCCTACCTGGCGATGCTGCCCCCTGTGTTGCTCCTCACTGATTACCTGCGC
TACAAACAGTCATCATATTACACATCATGGCCTTCATCGTTTGTACCTGATTCTTTTGTGGCCAG
GGTGTGATGCTCATGCAGGTGGCTGAGTTCTTTTTGGGGTTGTCTCAGCTACGGAGATAGGCTACT
ATTCTACATATACAGCATGGTCAGCCAGAACTACCAGAAAGTGAGCAGCTACTGTGCGAGTGT
CACTCTTGTGGCCTACACAGTAGGCTCGGTGCTGGCCAGCTCCTGGTATCCCTGGCAGCTCTGCC
ATACTCTTCTCTTTTACACAACCTTGGCCTGTGCTCTGTGGCTTTCTTTTCTCGCTTTTCTTTTACCA
ATGCCTAAGAAGAGCATGTTTTTTCATACAAATGATGACAGAGAAGCCCATCAAAGCCACTGGGAC
AAGATACTGTCTTGGAGGAAGCTCAGAAGAACAAGACAGCTCAGCCAGAAATGCTGCTGCTTCTTCTC
AGGGAAGTCCAGGGAACATCAAGCCAAGGGGCCAGAGCCAGAAACGTTGGCTTTGAGAGTCTTTGT
GCATTGGTTCCAAGACCTGAAGGAGTGCTACTCTCCAAGCACCTTTTGTACTGGTCCCTGTGGTGG

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FIG. 15 (cont'd)

GCTTTCGCTACGTCGGGTTATAACCAAGTCTTGAACATGTTCAAGTCTTATGGGAACACAAGGCAC
CCTCCCAAGACTCTTCTATTTATAATGGAGCAGTAGAGGCTGCTGCCACATTTGGAGGAGCTTTGGC
TGCTTCTCTGTGGGCTACGTGAAGGTCAACTGGGACCTCCTAGGAGAACTGGGTCTGGCCATCTTC
TCAGCTGTCATTGCCGGCGCTCTGTTTCTCATGAATTACACGCTCAGCATCTGGGTGTGCTATGCCG
GCTATTTGCTGGTCAAGTCTAGCTATATGTTTCTTATAACCATAGCAGTGTTTCAGATTGCTGTAAAC
TGAGCGTAGAACGTTATGCCCTGGTGTGGCATAGACACTTTTCATTGCCTTGGTGATTCAAGGCCAT
CATGACTGTGATTGTGGCTGATCAAAGAGGACTCCACTTGCCAGTCACCACTCAGTTTTTGGTTTATG
GAAGTACTTTGCTGTCAATTGCTGTGGTCTTCTAATGAGAAAGCACATATATTATCTACTCAGCCAAG
TGCCAAAAGGAAGTAGAGAGCCTTGCTGTCTGTGAGAGTCCCAATGAGCCACACCCACAACAGCCG
AGAGATGTGTCAACCAAGTTCTGA

(SEQ ID NO. 26) >TPK1_CHO_CDS

ATGGAGCATGCGTTTACCCCGCTGGAGCCCCTGCTACCCACGGGAAATTTGAAATATTGCCTCATGG
TTCTTAATCAGCCTTTGGACACACGCTTTCGTATCTTTGAAAAAAGCTCTTTTCAGAGCCTGTGGC
GACGGTGGTGCCAACCTGCTTGATGACCTCACCGAAGGAGAGAGAGAAAGATTCTTGCTGAATTCA
TCAGTGGGGACTTTGATTCTATTAGGCCTGAAGTCAGAGAGTACTACACTGAAAAGGGCTGTGATCT
TATTTCAACTCCTGACCAAGACCACACTGATTTTACCAAGTGCCTTAAAGTGCTCCAAAGGAAGATAG
AAGAGAAAGAGCTGCAGGTGGACGTGATTGTGACCTGGGAGGACTTGGTGGGCGTTTTGACCAGA
TCATGGCATCGGTGAACACCCTTTTCCAAGCCCCCTCACATCACTCCTGTGCCAATTATAATAATCCAA
GGGAATCTCTCATCTACCTCCTCCAACCGGGAAAGCACAGGCTCCATGTGGACACTGGAATGGAA
GGCAGCTGGTGTGGTCTTATCCCTGTTGGACAGCGTTGCAGCCAGGTGACAACAACGGGCCTGAAA
TGGAACCTGACAAATGATGTGCTTGCCTTTGGAACACTGGTCAGTACTTCTAACACCTACGATGGGT
CTGGGGTGGTGAAGTGTGGAGACTGACCACCCGCTTCTCTGGACCATGGCCGTCAAAAGCTAA

(SEQ ID NO. 27) >SLC25A19_CHO_CDS

ATGGTCGGCTATGACGCCAAAGCAGATATCAGGAGTAAGTCCAAGTTGGAGGTGGCGGTGGCAGGA
TCAGTGTCTGGATTTGTCACTCGTGCCCTGATCAGCCCTTTGGACGTCATCAAGATCCGTTTCCAGC
TTCAGATTGAACGGCTGTGTCCAAGTGACCCCAAAGCCAAATACCACGGGATCTTGACGGCAATCAA
GCAGATTCTGCAGGAGGAGGGACCAGCGCTTTCTGGAAAGGGCACGTTCCAGCCCAGATCCTGTC
CGTAGGCTATGGAGCTGTCCAATTTCTGACGTTTGAAGAGCTGACTGAACTGCTCCATAGAATCAAC
TTGTATGAAACCCGCCAGTTCTCAGCACACTTCGTATGTGGCGGCCTGTCTGCTGGTGCAGCCACC
CTTGCTGTGCACCCTGTGGATGTCTGCGCACCCGCTCGCGGCTCAGGGGGAGCCCAAGATCTAT
AGCAACCTCCGAGACGCCGTGTGACCATGTACAGGACCGAGGGCCCTTGGTCTTCTACAAAGGC
TTGACTCCCACCGTGATAGCCATCTTCCCTACGCGGGCCTGCAGTTCTCCTGCTACCGGTCTTTGA
AGCAAGTCTACGACTGGGTACATCTCCAGATGGAAAGCAAACAGGGAACCTGAAAACTGCTCTG
TGGATGTGGGTCTGGAGTCATCAGCAAGACCCTCACATATCCCCTGGACCTCTCAAGAAGCGTCTG
CAGGTGGGAGGGTTTGAGCGTGCCGATCCGCTTTGGCGAGGTGCGTAGCTACAGGGGCCTCCT
GGACCTACCAAGCAGGTGCTACAAGATGAAGGCACCCAGGGCCTCTTCAAGGGCCTGTCCCCCAG
CCTGCTGAAGGCGGCCCTCTCCACCGGCTTCATGTTCTTCTGGTACGAGCTCTTCTGTAACCTCTT
CACTGCATAAGGAGTGAAGACAGATAG

(SEQ ID NO. 35) >PANK3-isoform X1_CHO_CDS

ATGCCAAAAAACCTCTTTCCCATGGTTTGAATGGACATTGGGGGAACTCTAGTAAAGCTCTCATATTTGAAC
CTATCGATATCACAGCAGAGGAAGAACAAGAGGAAGTTGAGAGCTTAAAAAGCATTGGGAAATATTTGACTTCTA
ATGTAGCATATGGATCTACTGGCATTGCGGATGTACACCTTGAAGTGAAGGACTTAACCTTTTTGGACGAAGAGG
GAACTTGCATTTATCAGATTTCCAACCCAGGACCTGCCTACTTTTATCCAAATGGGAAGAGATAAAAACTTCTCAA
CCTTACAAACGGTGCTGAGTGCTACAGGAGGTGGTGTACAAGTTTGAAGAAATTTTCGCACAATTGGAAACC

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FIG. 15 (cont'd)

TCCACCTGCACAACTGGATGAACTTGACTGCCTTGTAAGGGCTTGCTGTATATAGATTCTGTCAGTTTCAATGGA
CAAGCAGAATGCTATTATTTTGCTAATGCCTCAGAACCTGAGCGATGCCAAAAGATGCCTTTTAACCTGGATGATC
CTTATCCACTGCTGGTAGTGAATATTGGCTCAGGAGTCAGTATTTTAGCAGTTCATTCCAAAGACAACCTATAAAAG
AGTGACTGGAACAAGCCTTGGAGGGGTACCTTTCTTGATTTATGCAGTTTATTGACTGGCTGTGAAAGTTTGA
GAGGCTCTTGAAATGGCATCCAAAGGTGACAGCACCCAAGCTGATAGGCTGGTCCGTGATTTATGGAGGAGAT
TATGAAAGATTTGGTCTGCCAGGTTGGGCTGTGGCATCTAGTTTGGGAATATGATTTATAAGGAGAAGCGAGAA
ACTGTTAGTAAAGAGGATCTGGCAAGAGCTACTTTAGTTACTATCACTAATAACATTGGTTCCGTGGCCCGGATGT
GTGCTGTTAACGAGAAAATTAACAGAGTTGTCTTCGTTGGAACTTTTACGTGTTAATACTCTCTATGAACTT
CTGGCATATGCTTTGGATTACTGGTCAAAGGTCAATTGAAAGCATTGTTCTAGAACATGAGGGATACTTTGGAG
CTGTTGGTGCACCTTCTGGATTGCCAAATTCAGCTGA

(SEQ ID NO. 36) >PANK3-isoform X2_CHO_CDS

ATGAAGATCAAGGATGCCAAAAACCTCTTTCCCATGGTTTGAATGGACATTGGGGGAACTCTAGTAAAGCTCT
CATATTTTGAACCTATCGATATCACAGCAGAGGAAGAACAAGAGGAAGTTGAGAGCTTAAAAAGCATTGCGAAAT
ATTTGACTTCTAATGTAGCATATGGATCTACTGGCATTGCGGATGTACACCTTGAAGTGAAGGACTTAACCTTTT
GGACGAAGAGGGAACCTTGCACCTTTATCAGATTTCCAACCCAGGACCTGCCTACTTTTATCCAAATGGGAAGAGATA
AAAACCTCTCAACCTTACAAACGGTGCTGAGTGCTACAGGAGGTGGTGCTTACAAGTTTGAGAAAGATTTTCGCAC
AATTGGAAACCTCCACCTGCACAACTGGATGAACTTGACTGCCTTGTAAGGGCTTGCTGTATATAGATTCTGTC
AGTTTCAATGGACAAGCAGAATGCTATTATTTTGCTAATGCCTCAGAACCTGAGCGATGCCAAAAGATGCCTTTTA
ACCTGGATGATCCTTATCCACTGCTGGTAGTGAATATTGGCTCAGGAGTCAGTATTTAGCAGTTCATTCCAAAGAC
AACTATAAAAGAGTGACTGGAACAAGCCTTGGAGGGGTACCTTTCTTGGTTTATGCAGTTTATTGACTGGCTGTG
AAAGTTTGAAGAGGCTCTTGAAATGGCATCCAAAGGTGACAGCACCCAAGCTGATAGGCTGGTCCGTGATTTT
ATGGAGGAGATTATGAAAGATTTGGTCTGCCAGGTTGGGCTGTGGCATCTAGTTTGGGAATATGATTTATAAGG
AGAAGCGAGAACTGTTAGTAAAGAGGATCTGGCAAGAGCTACTTTAGTTACTATCACTAATAACATTGGTTCCGT
GGCCCGGATGTGTGCTGTTAACGAGAAAATTAACAGAGTTGTCTTCGTTGGAACTTTTACGTGTTAATACTCTCT
CTATGAACTTCTGGCATATGCTTTGGATTACTGGTCAAAGGTCAATTGAAAGCATTGTTCTAGAACATGAGGG
ATACTTTGGAGCTGTTGGTGCACCTTCTGGATTGCCAAATTCAGCTGA

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FIG. 16

Amino Acid sequences of the CHO-M vitamin genes

(SEQ ID NO. 28) >SLC5A6_CHO_PROT

MSVEESTSAPFYTTSDTNKVIATFSVVDYVVFGLLLVLSLAIGLYHACRGWGRHTVGELLADRKMGCPL
VLSLLATFQSAVAILGAPAEIYRFGTQYWFLGCSYFLGLLIPAHVFIPVFYRLHLTSAYEYLELRFNKAVRIL
GTVTFIFQMVIYMGVALYAPSLALNAVTFGDLWLSVLALGIVCNITYTALGGLKAVIWTDFQTLVMFLGQLV
VIIVGSARVGGGLGHVWDVASQHKLSGIELDPDPFVRHTFWTLAFGGVFMMLSLYGVNQAAQVQRYLSSR
SEKAAVLSCYAVFPCQQVALCMSSILGLVMFAYYKKYTMSPQQEQAAPDQLVLYFVMDLLKDMPLPGL
FVACLFSGSLSTISSAFNSLATVTMEDLIQPWFPPELTETRAIMLSRSLAFAYGLICLGMAYISSHLGSVLQAA
LSIFGMVGGPLLGLFCLGMFFPCANPLGAIVGLLTGLTMAFWIGIGSIVSRMSSAVVSPPINGSSSFLSSNL
TMAVTTLMPSTTQSKPTGLQRFYSLSYLWYSAHNSTTVIVVGLIVSLLTGGMRGRTLNPGTIYPVLPKLL
SLLPLSCQKRCLCWKSHSQNAPMVPKLCPEKMRNGVLQDSRDKERMAEDGLAHQPCSPTYVYVQETSL*

(SEQ ID NO. 29) >PANK1_CHO_PROT

MQIPVRSEVIQLPLGAQGSAGSGCYTGTGSHGIRSAGFWLSRAYLTQYPLGSLCHTKHDPPISSSQTLR
SFCTKLVLGGGGGGQDWACSVAGTGLGGEEAAFELEAPGAEGVGPWFPLASPIRLTLAVAAPSVTVEKR
RTLCLLLVAGSMHPTDLGSGTRHKADCHSPGSLPSPNTSFGVCISGYQGCPLNRRVTAILMKQTDEE
SYQEAVRCVLGTAMSADRSQCVALSCQPAAGLCSQRCRKKQLAFPWFMDIGGTLVKLVYFEPKDITA
EEEQEEVENLKSIRKYLTSTNTAYGKTGIRDVHLELKNLTMCGRKGNLHFIRFPTCAMHMFQMGSEKNFS
SLHTTLCATGGGAFFKFEEDFRMIADLQLHKLDELDCLIQGLLYVDSVGFNGKPECYFFENPTNPELCQKK
PYCLDNYPYMLLVNMGSGVSILAVYSKDNKYKRVGTGSLGGGTFFGLCCLLTGCETFEAALEMAAKGDST
NVDKLVKDIYGGDYERFGLQGSAVASSFGNMMMSKEKREASKEDLARATLVTITNNGSIARMCALLENID
RVVVFVGNFLRINMVMKLLAYAMDFWSKGQLKALFLEHEGYFGAVGALLELFKMTDAQ*

(SEQ ID NO. 30) >PANK2_CHO_PROT

MSGGFPKASPSLRSHVQLGQHCIQVTGGVVGYSVFPWFGLDIGGTLVKLVYFEPKDITAEKEEVEESLK
SIRKYLTSTNAVYGSTGIRDVHLELKDLTLCGRKGNLHFIRFPTHDMPAFIQMGKDNFSSLHTVFCATGGG
SYKFEQDFLTIGDLQLHKLDELDCIKGILYIDSVGFNGRSQCYYFENPADSEKQKLPFDLKNPYPLLVN
IGSGVSILAVYSKDNKYKRVGTGSLGGGTFFGLCCLLTGCSTFEAALEMASRGDSTKVDKLVVDIYGGDY
RFGLPGWAVASSFGNMMMSKEKREASKEDLARATLITITNNGSIARMCALNENINQVVFVGNFLRVNTIA
MRLLAYALDYWSKGQLKALFSEHEYQEIPFGAGFYFTLPLCDSCELNTALGLADRL*

(SEQ ID NO. 31) >SLC19A2_CHO_PROT

MHGLCSHAAQARKLVRLWDDYAFCLNADGHVGGYGTPEMTTQNMFPQPALDQVLKMFDMSTLFRSLL
AHLAAFKVFNEIYPVWTYSYLVLLFPVFLATDYLRYPVILLQGLSLIVTWFMMLYAQGLLAIQFLEFFYGIAT
ATEIAYYSYIYSVDLGMVQKVTSCRSATLVGFTVGSVLGQILVSAHWPLFSLNVISLTCVSVAFVAW
FLPMPQKSLFFHHIPASCHGVNGIKVQNGGIVTENPASNHLPGWEDIESKIPLNLDEPPVEEPEPKPDLR
VLKVLWNDFLICYSSRPLCWSVWWALSTCGYFQVVNYTQGLWEKVMPSQSASVIYNGGVEAVSTLLGA
SAVFAVGYIKISWSTWGEMTLFLCSLLIAAAVYTMDTVNNIWWCYTSYVVFRIIYMLITIAFQIAANLSME
RYALVFGVNTFIALALQTLTLIVVDNKGLGLEITTQFLIYASYFAVISVWFLANGAFSVLKKCRKQEDPSSSP
QATTP*

FIG. 16(cont'd)

[illegible]

MEHAFTPLELLPTGNLKYCLMVLNQPLDTRFRHLWKKALFRACADGGANCLYDLTEGERERFLPEFISG
DFDSIRPEVREYYTEKGC DLISTPDQDHTDFTKCLKVLQRKIEEKELQVDVIVTLGGLGGRFDQIMASVNT
LFQAPHITVPVPIIIQGESLIYLLQPGKHRLHVD TGMEGSWCGLIPVGQRCSQVTTTGLKWNLTNDVLAFT
LVSTSN TYDGSGVVTVEDHPLLW TMAVKS*

MVGYDAKADIRSNSKLEAVAGSVSGFVTRALISPLDVIKIRFQLQIERLCPSPDKAKYHGILQAIKQILQEE
 GPAAFWKGHVPAQILSVGYGAVQFLTFEELTELLHRINLYETRQFSAHFVCGGLSAGAATLAVHPVDVLR
 TRLAAQGEPKIYSNLRDAVSTMRYTEGPLVFYKGLTPTVIAIFPYAGLQFSCYRSLKQVYDWVIPPDGKQT
 GNLNLLCGCGSGVISKLTYPDLDFKKRLQVGGFERARSAFGEVRSYRGLLDLTKVLQDEGTQGLFK
 GLSPSLLKAALSTGFMFFWYELFCNLFHCIRSEDR*

MPKKPSFPWFGM DIGGTLVKLSYFEPIDITAE EEEQEEVESLKSIRKYLTSNVAYGSTGIRDVHLELKD LTLFGRRGNLHFIR
FPTQDLPTFIQMGRDKNFSTLQTVLSATGGGAYKFEKDFRTIGNLHLHLKLDCLVKGLLYIDSVSFGNQAECYFANA
SEPERCQKMPFNLDPPYLLVNVIGSGVSILAVHSDNYKRVGTSLGGGTFLDCLSLTTGCESFEEALEMASKGDSTQA
DRLVRDIYGGDYERFGLPGWAVASSFGNMIYKEKRETVSKEDLARATLVITNNIGSVARMCAVNEKINRVVFGVGNFLR
VNTLSMKLLAYALDYWSKGQLKALFLEHEGYFGAVGALLGLPNFS

MKIKDAKKPSFPWFGMDIGGTLVKLSYFEPIDITAEQEEVESLSKIRKYLTSNVAYGSTGIRDVHLELKDLTLFGRRGNL
 HFIRFPTQDLPTFIQMGDKNFSTLQTVLSATGGGAYKFEKDFRTIGNLHLHKLDELDCLVKGLLYIDSVSFNGQAEYYF
 ANASEPERCQKMPENLDDPYPLLWNIGSGVSLAVHSDKNYKRVGTSLGGGTFLGLCSLLTGCESFEEALEMASKGDS

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FIG. 16(cont'd)

TQADRLVRDIYGGDYERFGLPGWAVASSFGNMIYKEKRETVSKEDLARATLVTITNNIGSVARMCAVNEKINRVFVG
NFLRVNTLSMKLLAYALDYWSKGQLKALFLEHEGYFGAVGALLGLPNFS

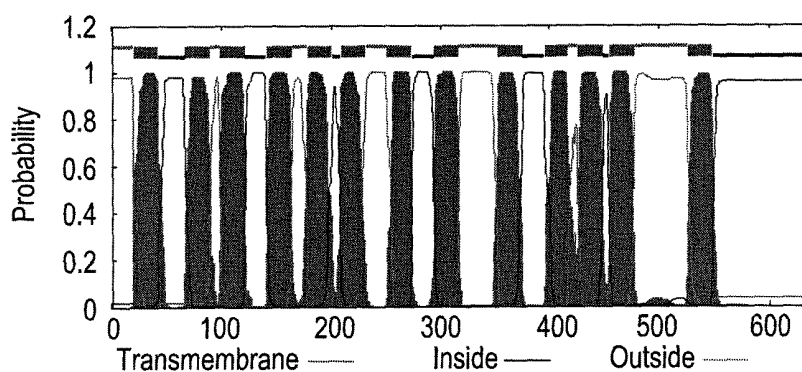
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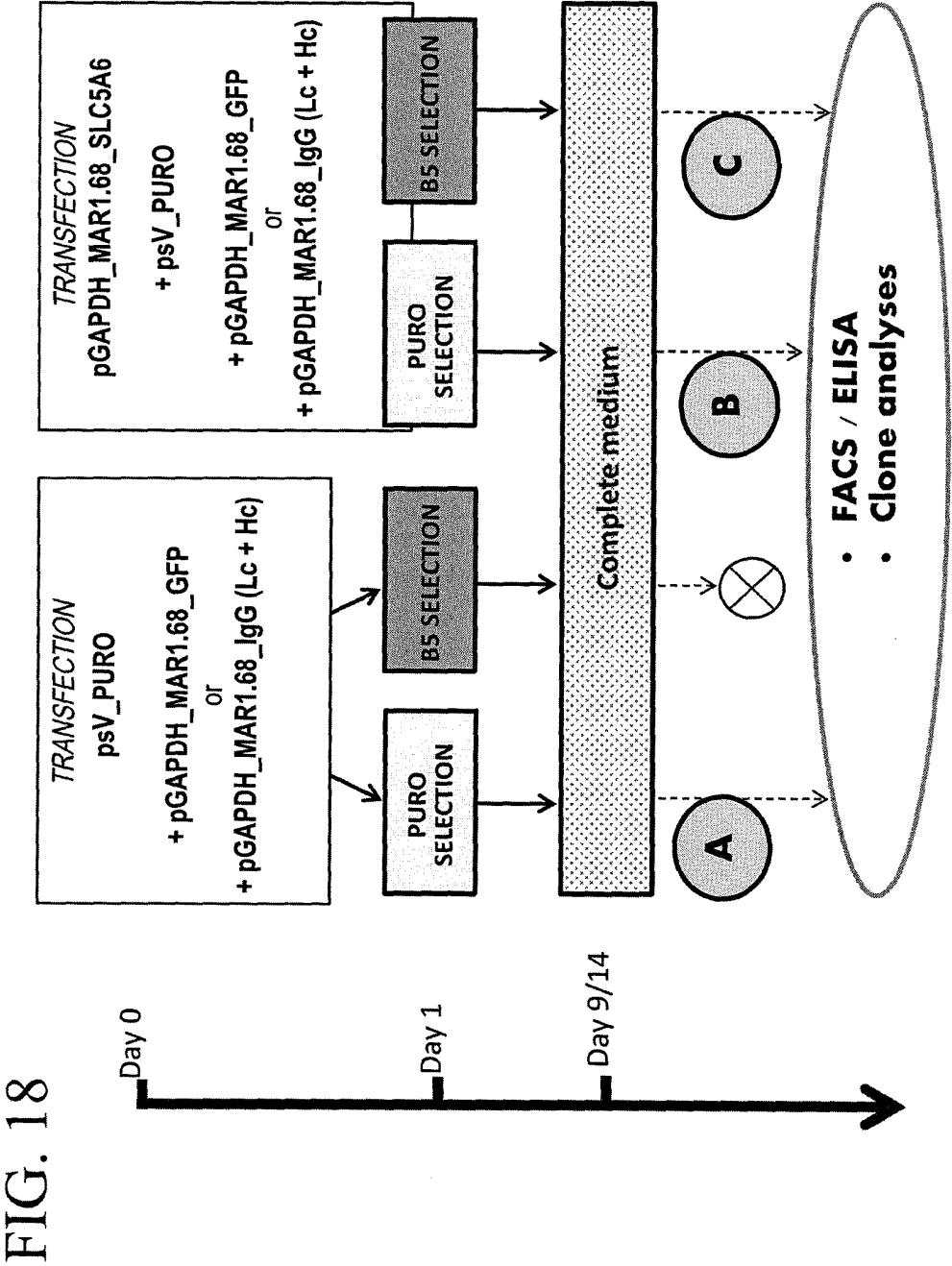
FIG. 17

5a6 Length: 636
 # 5a6 Number of predicted TMHs: 13
 # 5a6 Exp number of AAs in TMHs: 288.7242
 # 5a6 Exp number, first 60 AAs: 23.19072
 # 5a6 Total prob of N-in: 0.01766
 # 5a6 POSSIBLE N-term signal sequence

5a6	TMHMM2.0	outside	1	19
5a6	TMHMM2.0	TMhelix	20	42
5a6	TMHMM2.0	inside	43	66
5a6	TMHMM2.0	TMhelix	67	89
5a6	TMHMM2.0	outside	90	98
5a6	TMHMM2.0	TMhelix	99	121
5a6	TMHMM2.0	inside	122	140
5a6	TMHMM2.0	TMhelix	141	163
5a6	TMHMM2.0	outside	164	177
5a6	TMHMM2.0	TMhelix	178	200
5a6	TMHMM2.0	inside	201	208
5a6	TMHMM2.0	TMhelix	209	231
5a6	TMHMM2.0	outside	232	250
5a6	TMHMM2.0	TMhelix	251	273
5a6	TMHMM2.0	inside	274	293
5a6	TMHMM2.0	TMhelix	294	316
5a6	TMHMM2.0	outside	317	352
5a6	TMHMM2.0	TMhelix	353	375
5a6	TMHMM2.0	inside	376	395
5a6	TMHMM2.0	TMhelix	396	416
5a6	TMHMM2.0	outside	417	425
5a6	TMHMM2.0	TMhelix	426	448
5a6	TMHMM2.0	inside	449	454
5a6	TMHMM2.0	TMhelix	455	477
5a6	TMHMM2.0	outside	478	525
5a6	TMHMM2.0	TMhelix	526	548
5a6	TMHMM2.0	inside	549	636

TMHMM posterior probabilities for 5a6





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FIG. 19A

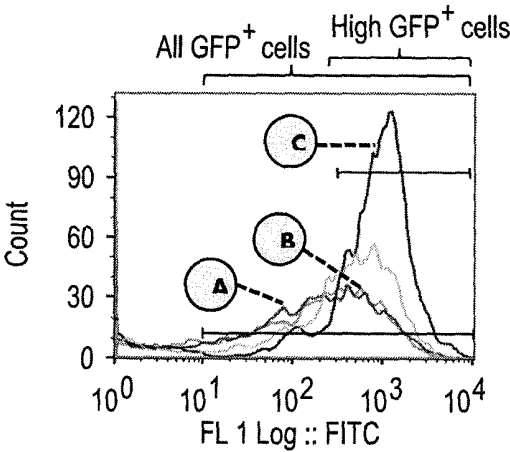


FIG. 19B

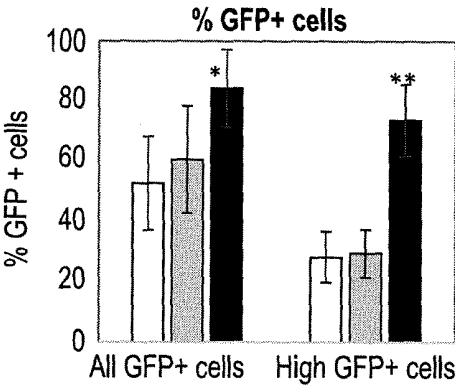
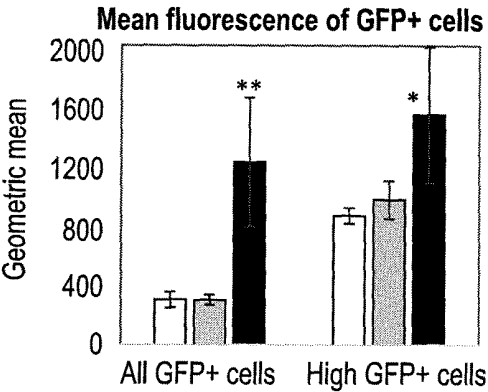


FIG. 19C



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FIG. 20A

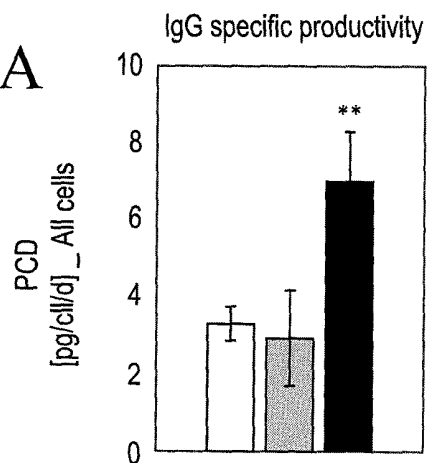
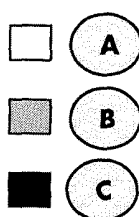
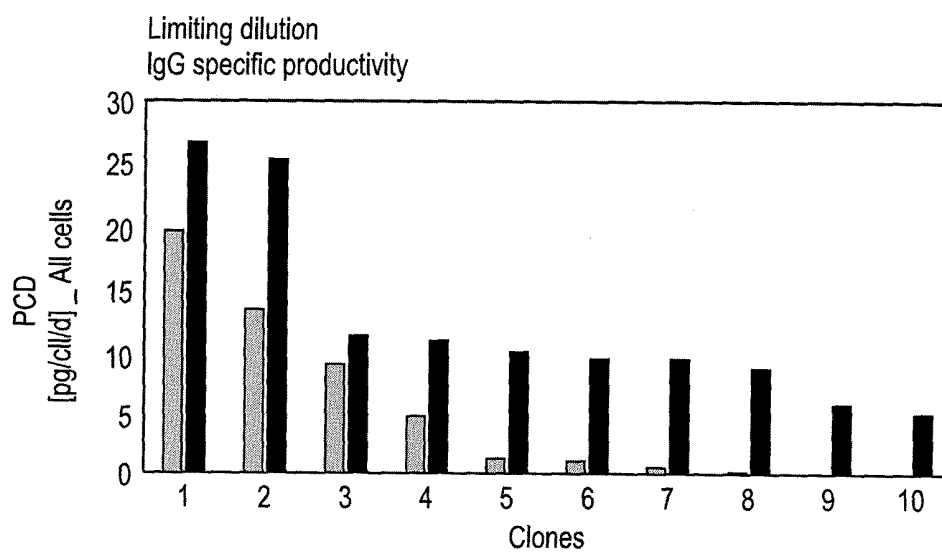


FIG. 20B



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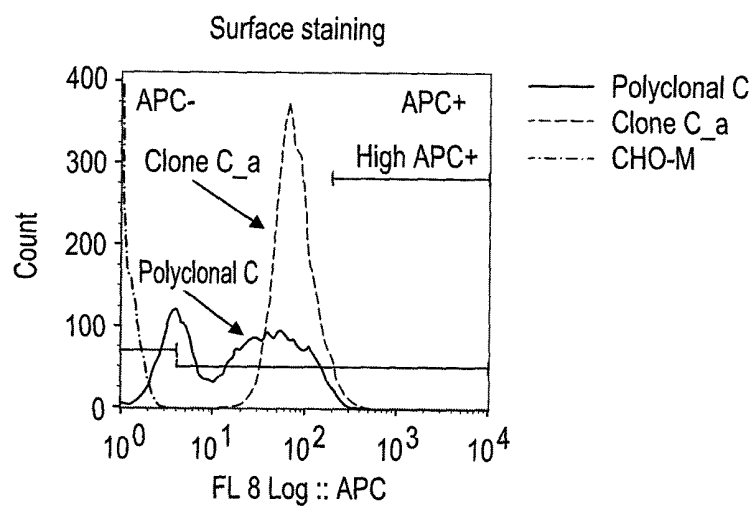


FIG. 21A

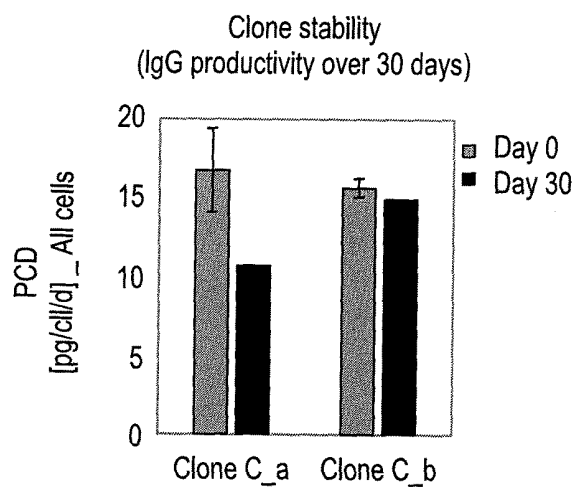


FIG. 21B

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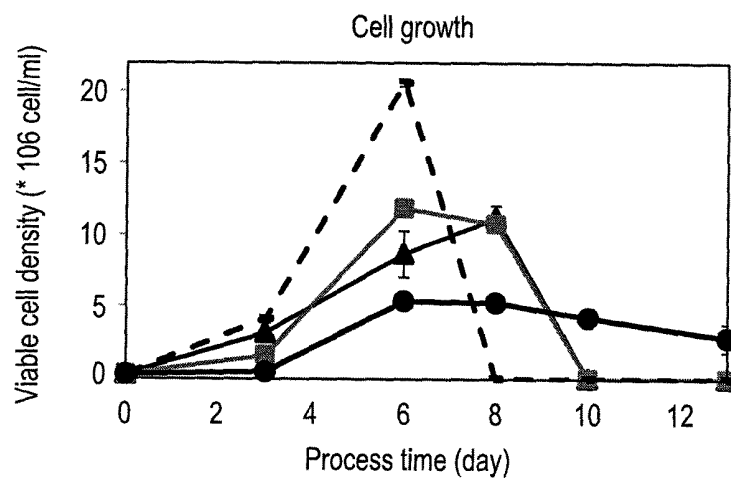


FIG. 21C

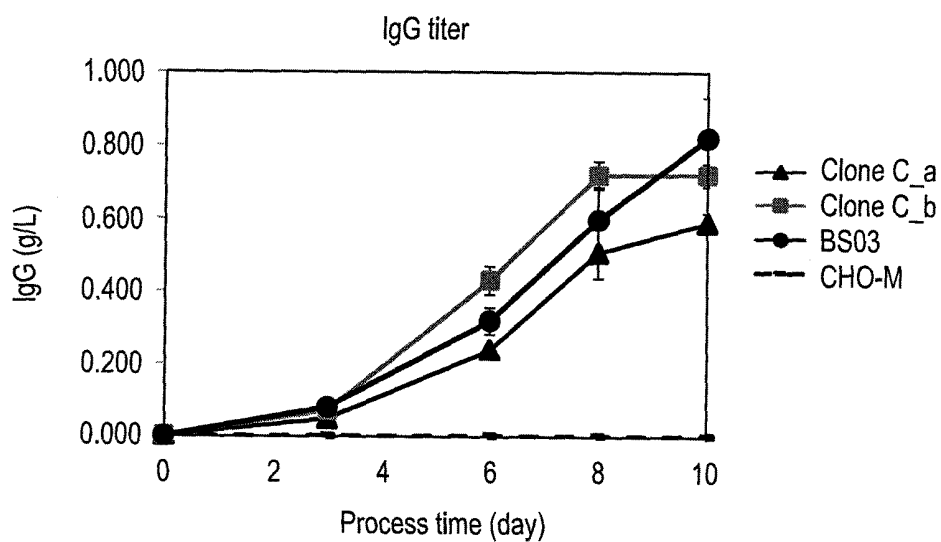


FIG. 21D

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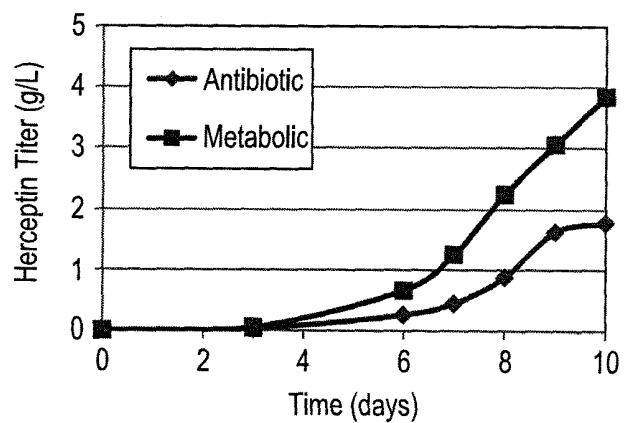


FIG. 22A

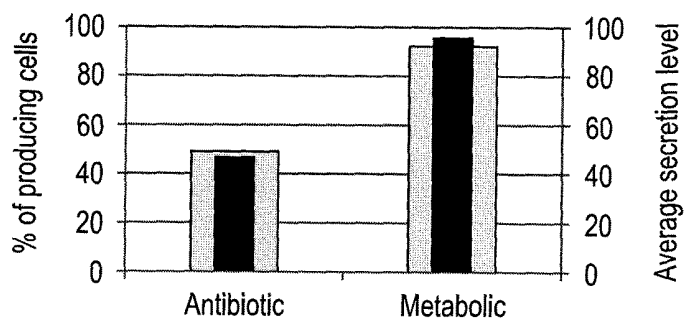


FIG. 22B

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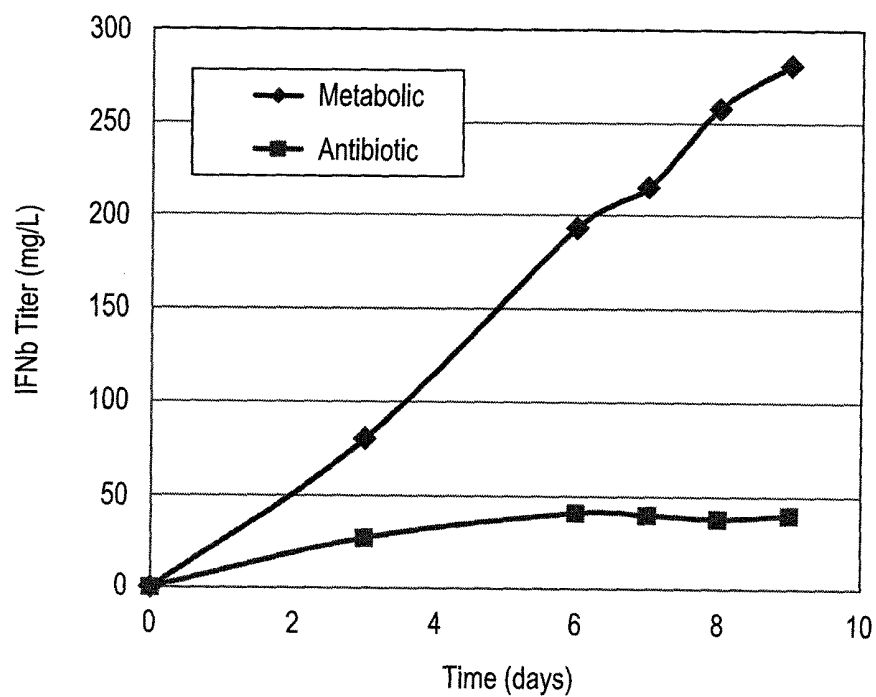


FIG. 22C