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|           | Stop         | SEQ ID NO. | Hydrophilic   | SEQ ID NO. | Hydrophobic | SEQ ID NO. |
|-----------|--------------|------------|---------------|------------|-------------|------------|
| D1-1      | VQLER        | 8          | YNWND         | 45         | GTTGT       | 88         |
| HD1-1     | VPLAR        | 9          | YHWHN         | 46         | GTTGT       | 88         |
| D1-7      | V*LEL        | -          | YNWNY         | 47         | GTTGT       | 89         |
| HD1-7     | VSLAL        | 10         | YHWHY         | 48         | GTTGT       | 89         |
| D1-20     | V*LER        | -          | YNWND         | 45         | GTTGT       | 89         |
| HD1-20    | VSLAR        | 11         | YHWHN         | 46         | GTTGT       | 89         |
| D1-26     | V*WELL       | 12         | YSGSY         | 49         | GIVGAT      | 90         |
| HD1-26    | VSWEP        | 13         | YHGSY         | 50         | GIMGAT      | 91         |
| D2-2*02   | RIL**YQLLY   | 14         | GYCSSTSCYT    | 51         | DIVVPAAL    | 92         |
| HD2-2*02  | RTL*SYQLPY   | 15         | GHCSHTSOHT    | 52         | DIVVPAAL    | 93         |
| D2-8*01   | RILY*WCMLY   | 16, 17     | GYCTNGVCYT    | 53         | DIVLMVYAI   | 94         |
| HD2-8*01  | RTLYSWCMPY   | 18         | GHCTHGVCHT    | 54         | DIVLMVYAI   | 94         |
| D2-15     | RIL*WW*LLL   | -          | GYCSGGSCYS    | 55         | DIVVVAAT    | 95         |
| HD2-15    | RTL*SW*LPL   | -          | GHCSHGSCHS    | 56         | DIVVVAAT    | 96         |
| D2-21*02  | SILWW*LLF    | 19         | AYCGDCYS      | 57         | HIVVTAI     | 97         |
| HD2-21*02 | STLWWSLPL    | 20         | AHCGHCHS      | 58         | HIVVTAI     | 97         |
| D3-3*01   | VLRFLEWLLY   | 21         | YYDFWSGYT     | 59         | ITIFGWII    | 98         |
| HD3-3*01  | VSPFLEWSLY   | 22         | YHFWSGHYT     | 60         | ITIFGWII    | 98         |
| D3-9      | VLRYFDWLL*   | 23         | YYDILTGYN     | 61         | ITIF*LVII   | 99, 100    |
| HD3-9     | VSPYFDWSL*   | 24         | YHHILTGHYN    | 62         | ITIF*LVII   | 99, 100    |
| D3-10*01  | VLLWFGELL*   | 25         | YYGSGSYN      | 63         | ITMVRGVII   | 101        |
| HD3-10*01 | VSPWFGESL*   | 26         | YHGSAGSHYN    | 64         | ITMVRGVII   | 101        |
| D3-16*02  | VL*LRLGELSLY | 27         | YYDYVWGSYRYT  | 65         | IMITFGGVVI  | 102        |
| HD3-16*02 | VS*SRLGESSLY | 28         | YHDHVVWGSYRYT | 66         | IMITFGGVVI  | 102        |
| D3-22     | VLL***WLLL   | 29         | YYDSSGYY      | 67         | ITMIVVIT    | 103        |
| HD3-22    | VSLs**WSLL   | 30, 31     | YHYHSSGHYY    | 68         | ITIVVIT     | 104        |
| D4-4      | *LQ*L        | -          | DYSNY         | 69         | TTVT        | 105        |
| HD4-4     | *PQSL        | 32         | DHSY          | 70         | TTVT        | 105        |
| D4-11p    | *LQ*L        | -          | DYSNY         | 69         | TTVT        | 105        |

FIG. 1A

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|         | Stop    | SEQ ID NO. | Hydrophilic | SEQ ID NO. | Hydrophobic | SEQ ID NO. |
|---------|---------|------------|-------------|------------|-------------|------------|
| HD4-11p | *PQSL   | 32         | DHSY        | 70         | TTVT        | 105        |
| D4-17   | *LR*L   | -          | DYGDY       | 71         | TTVT        | 105        |
| HD4-17  | *PRSL   | 33         | DHGHY       | 72         | TTVT        | 105        |
| D4-23p  | *LRW*L  | -          | DYGGNS      | 73         | TTVT        | 106        |
| HD4-23p | *PRWSL  | 34         | DHGGHS      | 74         | TTVT        | 106        |
| D5-5    | WIQLWL  | 35         | GYSGY       | 75         | VDTAMV      | 107        |
| HD5-5   | WTQPWL  | 36         | GSHGY       | 76         | VDTAMV      | 107        |
| D5-12   | WI*WLRL | 37         | GYSGYDY     | 77         | VDIVATI     | 108        |
| HD5-12  | WT*WPPL | 38         | GSHGHY      | 78         | VDIVATI     | 108        |
| D5-18   | WIQLWL  | 35         | GYSGY       | 75         | VDTAMV      | 107        |
| HD5-18  | WTQPWL  | 36         | GSHGY       | 76         | VDTAMV      | 107        |
| D5-24p  | *RWLQL  | 39         | RDGYN       | 79         | VEMATI      | 109        |
| HD5-24p | *TWPL   | 40         | RHGHY       | 80         | VDMATI      | 110        |
| D6-6    | V*QLV   | -          | EYSSS       | 81         | SIAAR       | 111        |
| HD6-6   | A*PLV   | -          | ESHSS       | 82         | SIATR       | 112        |
| D6-13   | V*QQLV  | 41         | GYSSSWY     | 83         | GIAAG       | 113        |
| HD6-13  | A*PQLV  | 42         | GSHSWY      | 84         | GIATAG      | 114        |
| D6-19   | V*QWL   | 43         | GYSSGWY     | 85         | GIAVAG      | 115        |
| HD6-19  | A*PWL   | 44         | GSHGWY      | 86         | GIAAG       | 116        |
| D6-25   | V*QRL   | -          | GYSSGY      | 87         | GIAA        | 117        |
| HD6-25  | A*PRL   | -          | GSHGY       | 76         | GIATA       | 118        |

FIG. 1B

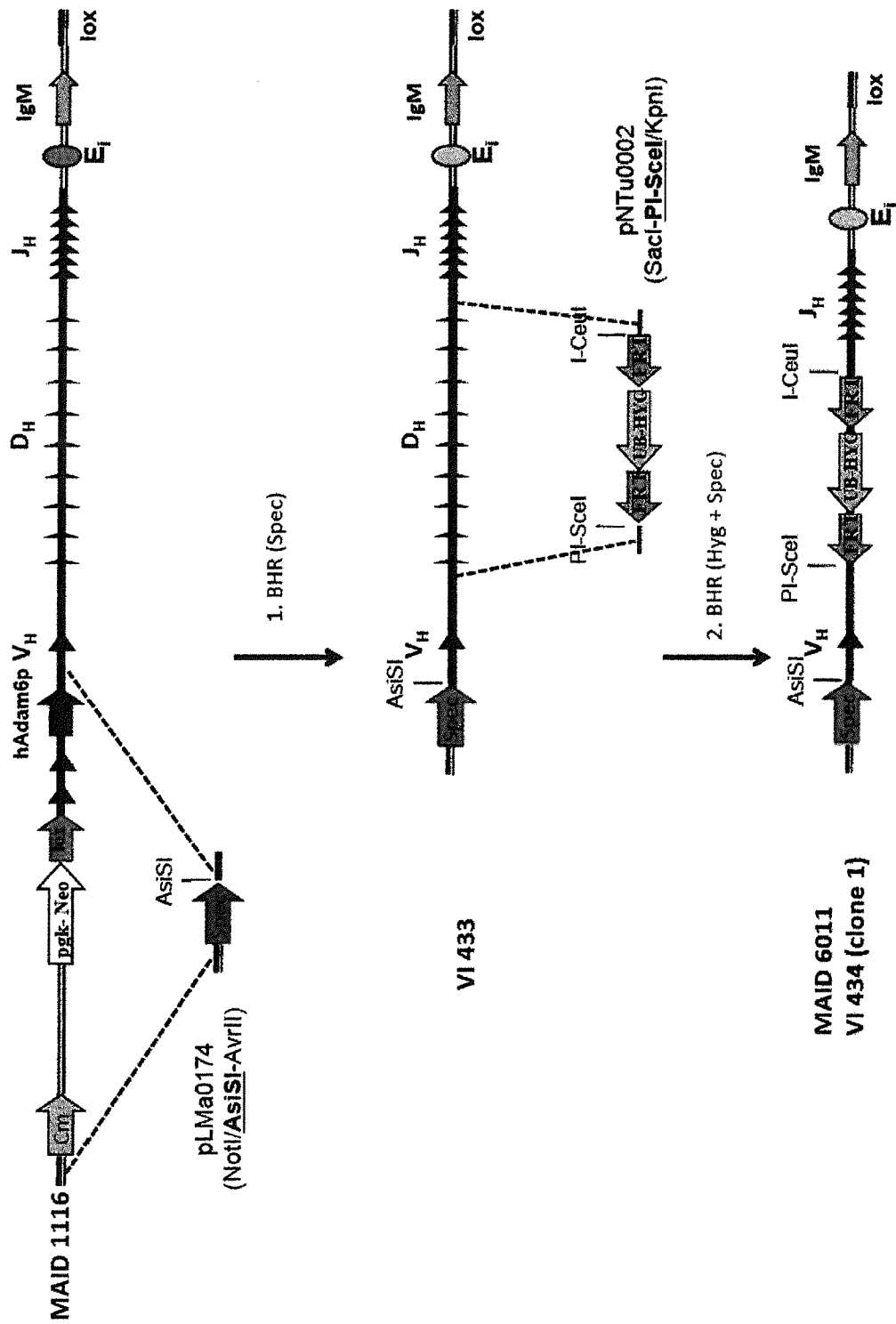


FIG. 2

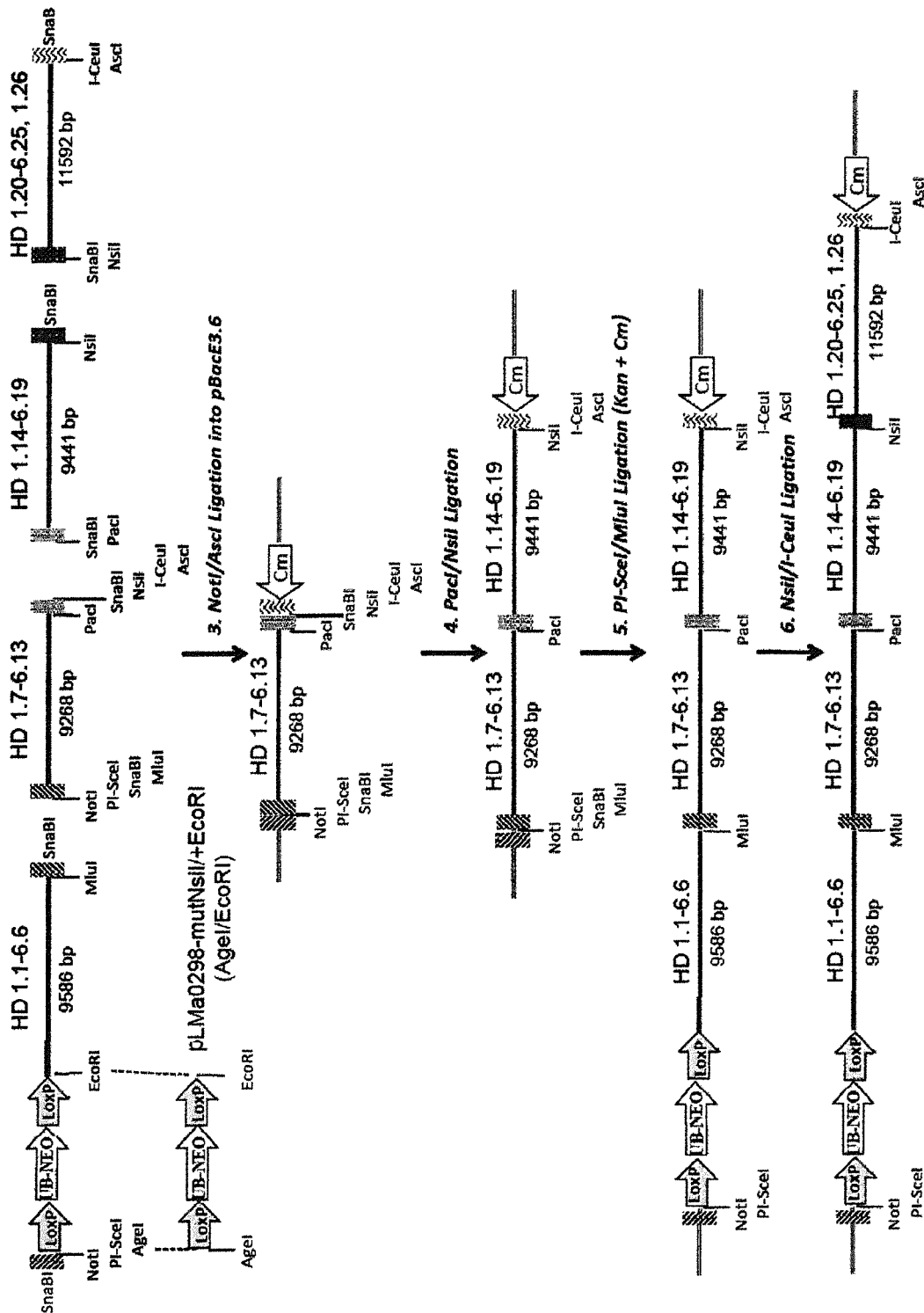


**FIG. 3**

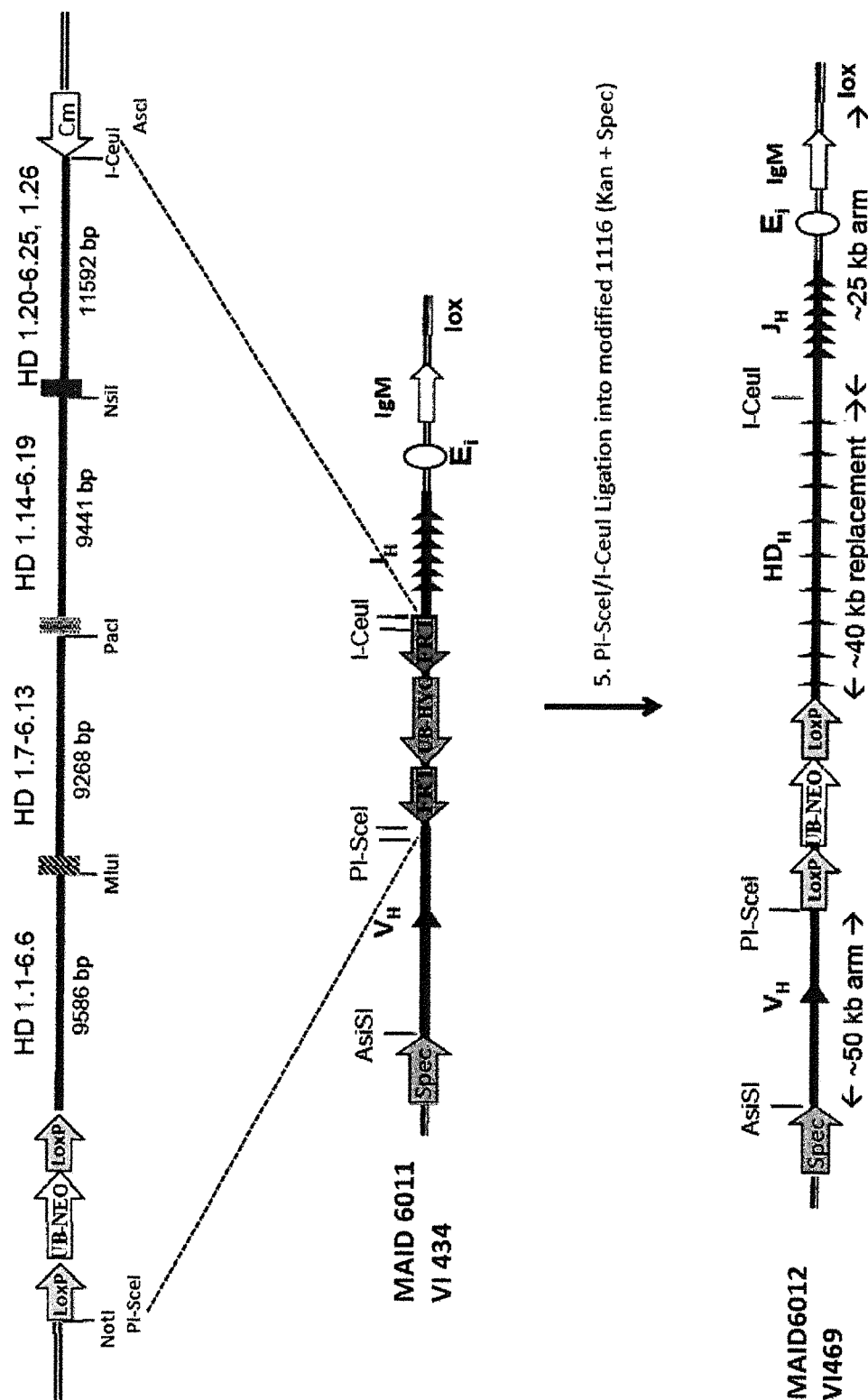


**FIG. 4**

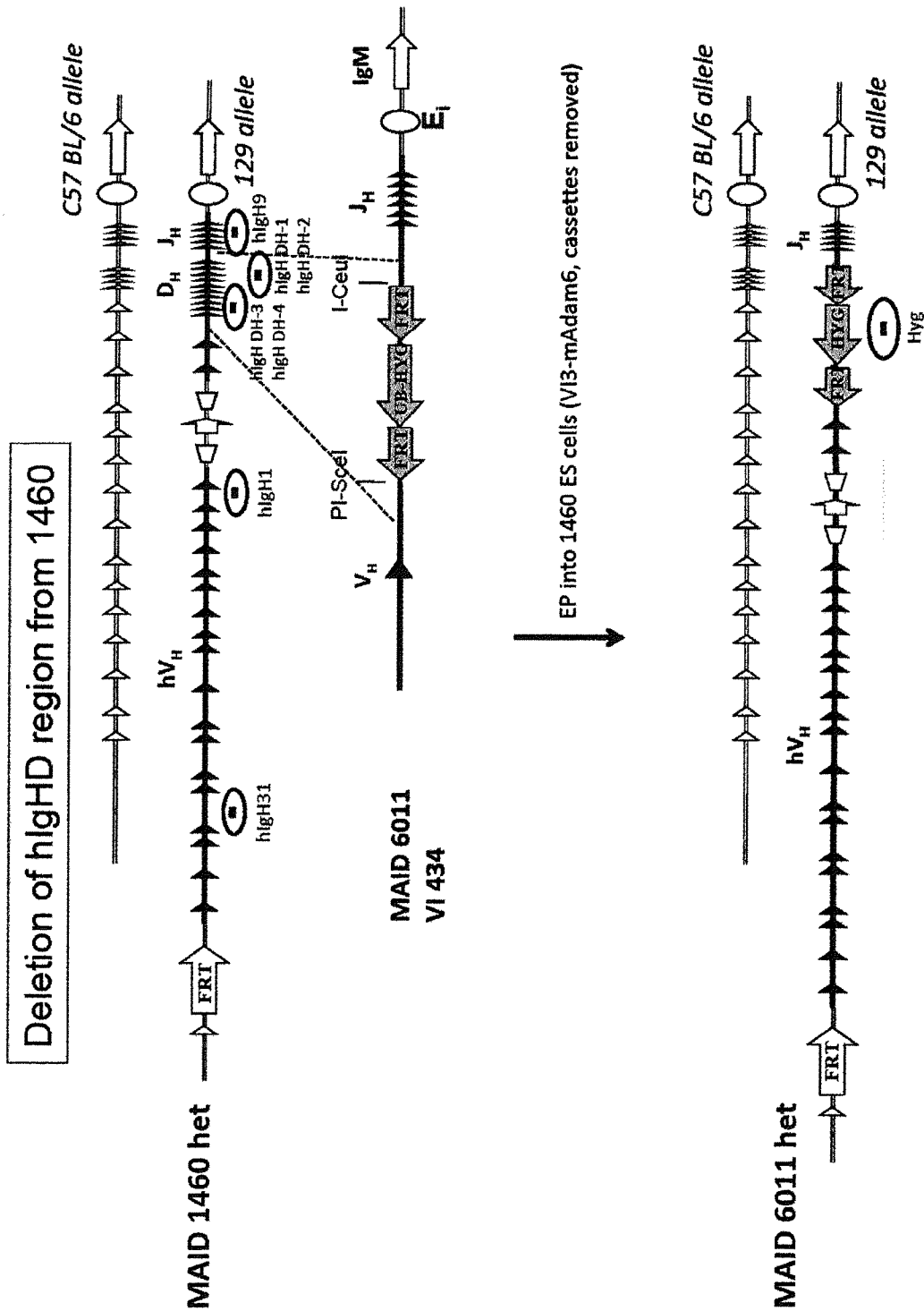


FIG. 5

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| Probes for MAID 6011 (deletion of hlgH DH segments in MAID1460 ) |                                           |                                                    |                                           |      |                  |                    |
|------------------------------------------------------------------|-------------------------------------------|----------------------------------------------------|-------------------------------------------|------|------------------|--------------------|
| Name                                                             | Forward Primer                            | Probe                                              | Reverse Primer                            | Type | Label            | Location           |
| hlgH<br>DH-1                                                     | CGGGTCACTGCCATTCTG<br>(SEQ ID NO: 119)    | TCTGCATTGCTCCAGCGC<br>(SEQ ID NO: 120)             | TCTGGCGCATGAACCCCAAT<br>(SEQ ID NO: 121)  | LOA  | FAM-<br>BHQ<br>1 | hlgH D<br>segments |
| hlgH<br>DH-2                                                     | GTGCAGGGGAGGACCTTCT<br>G (SEQ ID NO: 122) | AGTCACCAAGCACAGAGCCCTGAC<br>(SEQ ID NO: 123)       | GCCAGGGAGTTGCCCTAGTG<br>(SEQ ID NO: 124)  | LOA  | FAM-<br>BHQ<br>1 | hlgH D<br>segments |
| hlgH<br>DH-3                                                     | GTGGCCCACTTCCCTTCT<br>(SEQ ID NO: 125)    | CAGCTGGAACCCACCATGACCT<br>(SEQ ID NO: 126)         | GACCTGCCCTCGGATGACA<br>(SEQ ID NO: 127)   | LOA  | FAM-<br>BHQ<br>1 | hlgH D<br>segments |
| hlgH<br>DH-4                                                     | TGGCCAGAACTGACCTTAC<br>(SEQ ID NO: 128)   | ACCGACAAGAGTCCCTCAGG<br>(SEQ ID NO: 129)           | GGAGTCGGCTCTGGATGTG<br>(SEQ ID NO: 130)   | LOA  | BHQ-<br>plus     | hlgH D<br>segments |
| hyg                                                              | TGCGGCCGATCTTAGCC<br>(SEQ ID NO: 131)     | ACGAGCGGGTTCGGCCCATTC<br>(SEQ ID NO: 132)          | TTGACCGATTCTTGCGG<br>(SEQ ID NO: 133)     | GOA  | FA-<br>BHQ<br>1  |                    |
| hlgH1                                                            | CAGTCCCGTTGATCCAGCC<br>(SEQ ID NO: 134)   | CCCATCAGGGATTGTATCTCTGT<br>GGACG (SEQ ID NO: 135)  | GGATATGCAGCACTGTGCCAC<br>(SEQ ID NO: 136) | AR   |                  | hlgH               |
| hlgH9                                                            | TCCTCCAACGACAGGTCCC<br>(SEQ ID NO: 137)   | TCCCTGGAACCTCTGCCCGACACA<br>(SEQ ID NO: 138)       | GATGAACTGACGGGCACAGG<br>(SEQ ID NO: 139)  | AR   |                  | hlgH               |
| hlgH31                                                           | ATCACACTCATCCCATCCCC<br>(SEQ ID NO: 140)  | CCCTTCCCTAAGTACCACAGAGTGG<br>GCTC (SEQ ID NO: 141) | CACAGGGAAGCAGGAACTGC<br>(SEQ ID NO: 142)  | AR   |                  | hlgH               |

FIG. 6

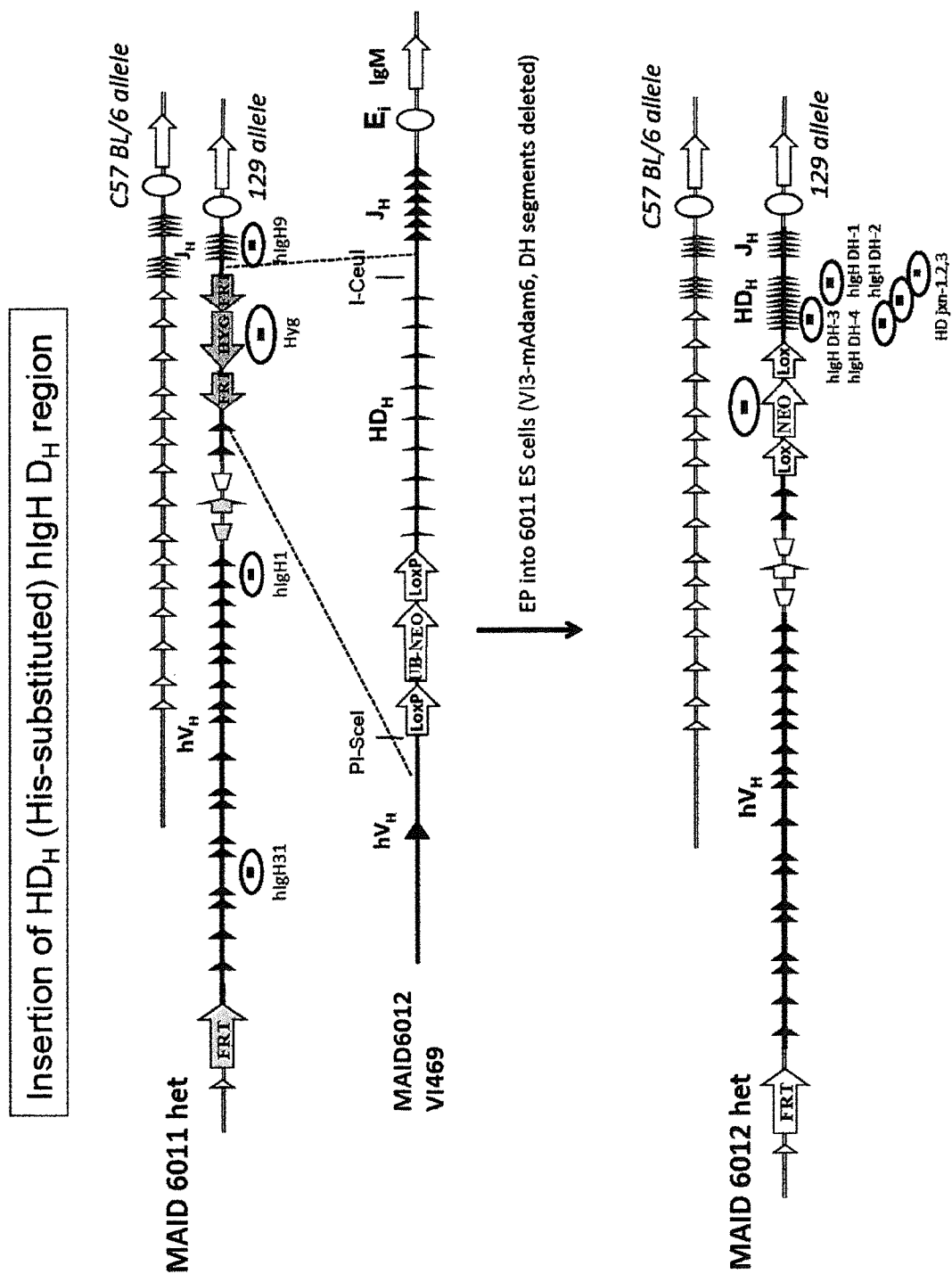


**FIG. 7**

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| Probes for MAID 6012 (insertion of HD, His-substituted high DH segments) |                                              |                                                    |                                             |      |              |                                         |
|--------------------------------------------------------------------------|----------------------------------------------|----------------------------------------------------|---------------------------------------------|------|--------------|-----------------------------------------|
| Name                                                                     | Forward Primer                               | Probe                                              | Reverse Primer                              | Type | Label        | Location                                |
| hys                                                                      | TGCGCCGATCTTAGCC<br>(SEQ ID NO: 131)         | ACGAGCGGTTCGGCCCATTC<br>(SEQ ID NO: 132)           | TTGACCGATTCTTGCGG<br>(SEQ ID NO: 133)       | LOA  | FAM-<br>BHQ1 |                                         |
| HD jxn-1                                                                 | GGAGCCAGGCAGGACACA<br>(SEQ ID NO: 143)       | TGGGCTCGTAGTTTGACGT<br>(SEQ ID NO: 144)            | GGGACTTCTTACCCACA<br>CTTCA (SEQ ID NO: 145) | GOA  | MGB          | Synthetic<br>linker-1 in HD<br>segments |
| HD jxn-2                                                                 | GGTCCCGAGCACTCTTAATAAA<br>C (SEQ ID NO: 146) | CCTCGAATGGAATAC<br>(SEQ ID NO: 147)                | GGGAGAGCAACCATTCG<br>TTGT (SEQ ID NO: 148)  | GOA  | MGB          | Synthetic<br>linker-2 in HD<br>segments |
| HD jxn-3                                                                 | CCGAGCACCGATGCATCTA<br>(SEQ ID NO: 149)      | CGCAGTCATGTAATGC<br>(SEQ ID NO: 150)               | GGGAGGCGAACTGACTG<br>TCA (SEQ ID NO: 151)   | GOA  | MGB          | Synthetic<br>linker-3 in HD<br>segments |
| high DH-1                                                                | CGGGTCACTGCCATTCTG<br>(SEQ ID NO: 119)       | TCTGCATTCGCTCCAGCGC<br>(SEQ ID NO: 120)            | TCTGCGGCATGAACCCAA<br>T (SEQ ID NO: 121)    | GOA  | FAM-<br>BHQ1 | high D<br>segments                      |
| high DH-2                                                                | GTGAGGGAGGACCTTCTG<br>(SEQ ID NO: 122)       | AGTACCAAGCACAGAGCCCTGA<br>C (SEQ ID NO: 123)       | GCCAGGGAGTTGCCTAG<br>TG (SEQ ID NO: 124)    | GOA  | FAM-<br>BHQ1 | high D<br>segments                      |
| high DH-3                                                                | GTGGCCCACTTCCCTTCCT<br>(SEQ ID NO: 125)      | CAGCTGGAACCCACCATGACCT<br>(SEQ ID NO: 126)         | GACCTGCTCGGATGACA<br>(SEQ ID NO: 127)       | GOA  | FAM-<br>BHQ1 | high D<br>segments                      |
| high DH-4                                                                | TGGCCAGAACTGACCCCTAC<br>(SEQ ID NO: 128)     | ACCGACAAGAGTCCCTCAGG<br>(SEQ ID NO: 129)           | GGAGTCGGCTCTGGATGTG<br>(SEQ ID NO: 130)     | GOA  | BHQ-<br>plus | high D<br>segments                      |
| neo                                                                      | GGTGGAGAGGCTATTGGC<br>(SEQ ID NO: 152)       | TGGGCACAACAGACAATCGGCTG<br>(SEQ ID NO: 153)        | GAACACGGCGCATCAG<br>(SEQ ID NO: 154)        | GOA  | FAM-<br>BHQ1 |                                         |
| highH1                                                                   | CAGTCCCCTTGATCCAGCC<br>(SEQ ID NO: 134)      | CCCATCAGGGATTTGTATCTC<br>TGTGGACG (SEQ ID NO: 135) | GGATATGCAGCACTGTGCC<br>AC (SEQ ID NO: 136)  | AR   |              | high                                    |
| highH9                                                                   | TCCTCCAACGACAGGTCCC<br>(SEQ ID NO: 137)      | TCCCTGGAACTCTGCCCCGACACA<br>(SEQ ID NO: 138)       | GATGAACTGACGGGCACA<br>GG (SEQ ID NO: 139)   | AR   |              | high                                    |
| highH31                                                                  | ATCACACTCATCCCATCCCC<br>(SEQ ID NO: 140)     | CCCTTCCCTAAGTACCACAGAGTG<br>GGCTC (SEQ ID NO: 141) | CACAGGGAAGCAGGAAGT<br>GC (SEQ ID NO: 142)   | AR   |              | high                                    |

FIG. 8

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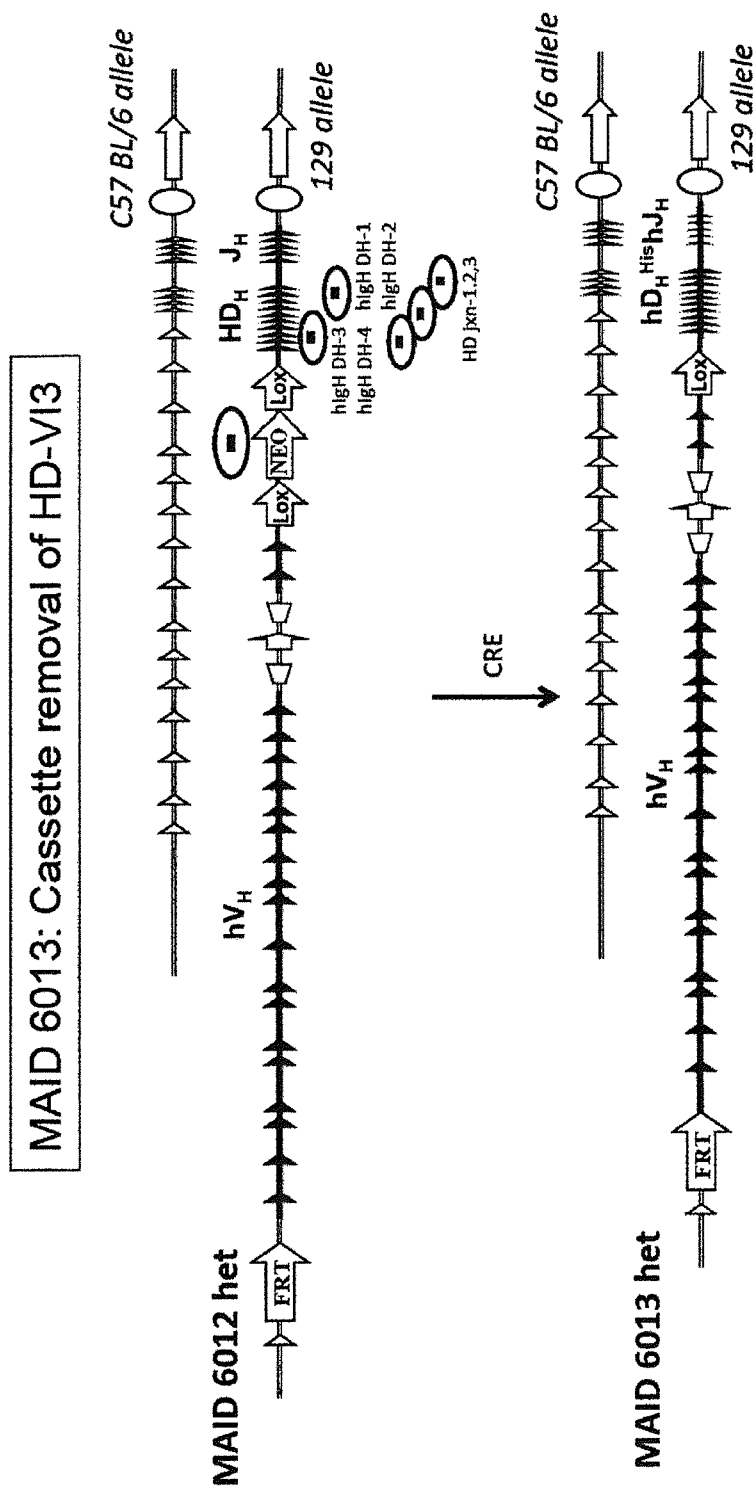


FIG. 9

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| Human D Gene Segment                    | Direct 5'-3' Orientation                                                                      | SEQ ID NO.               | Inverted Orientation                                                                            | SEQ ID NO.               |
|-----------------------------------------|-----------------------------------------------------------------------------------------------|--------------------------|-------------------------------------------------------------------------------------------------|--------------------------|
| IGHD1-1<br>X97051,<br>IGHD1-1*01        | ggtacaactggaacgac<br>G T T G T<br>V Q L E R<br>Y N W N D                                      | 155<br>88<br>8<br>45     | gtcgtccagttgtacc<br>V V P V V<br>S F Q L Y<br>R S S C T                                         | 206<br>207<br>208<br>209 |
| IGHD1-7<br>X13972,<br>IGHD1-7*01        | ggtataactggaactac<br>G I T G T<br>V * L E L<br>Y N W N Y                                      | 156<br>89<br>-<br>47     | gtagttccagttatacc<br>V V P V I<br>* F Q L Y<br>S S S Y T                                        | 210<br>211<br>212<br>213 |
| IGHD 1-20<br>X13972,<br>IGHD1-<br>14*01 | ggtataaccggaaccac<br>G I T G T<br>V * P E P<br>Y N R N H                                      | 157<br>89<br>-<br>158    | gtggtccggtatacc<br>V V P V I<br>W F R L Y<br>G S G Y T                                          | 214<br>211<br>215<br>216 |
| IGHD 1-20<br>X97501,<br>IGHD1-<br>20*01 | ggtataactggaacgac<br>G I T G T<br>V * L E R<br>Y N W N D                                      | 159<br>89<br>-<br>45     | gtcgtccagttatacc<br>V V P V I<br>S F Q L Y<br>R S S Y T                                         | 217<br>211<br>208<br>218 |
| IGHD1-26<br>X97501,<br>IGHD1-<br>26*01  | ggtatagtgaggagtactac<br>G I V G A T<br>V * W E L L<br>Y S G S Y Y                             | 160<br>90<br>12<br>49    | gtagtagctccactatacc<br>V V A P T I<br>* * L P L Y<br>S S S H Y T                                | 219<br>220<br>221<br>222 |
| IGHD2-2<br>J00232,<br>IGHD2-2*01        | aggatattgtagtaccagctgctatgcc<br>R I L * * Y Q L L C<br>G Y C S S T S C Y A<br>D I V V V P A M | 161<br>162<br>163<br>164 | ggcatagcagctggtactactacaatacct<br>G I A A G T T T I S<br>A * Q L V L L Q Y P<br>H S S W Y Y N I | 223<br>224<br>225<br>226 |

FIG. 10A

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| Human D Gene Segment   | Direct 5'-3' Orientation                                                                           | SEQ ID NO.                | Inverted Orientation                                                                                | SEQ ID NO.               |
|------------------------|----------------------------------------------------------------------------------------------------|---------------------------|-----------------------------------------------------------------------------------------------------|--------------------------|
| X97051,<br>IGHD2-2*02  | aggatattgtagtagtaccagctgctatacc<br>R I L * * Y Q L L Y<br>G Y C S S T S C Y T<br>D I V V V P A A I | 165<br>14<br>51<br>92     | ggatagcagctggtagtactacaataatcct<br>G I A A G T T T I S<br>V * Q L V L L Q Y P<br>Y S S W Y Y Y N I  | 227<br>224<br>225<br>226 |
|                        | tggaattgtagtagtaccagctgctatgcc<br>W I L * * Y Q L L C<br>G Y C S S T S C Y A<br>D I V V V P A A M  | 166<br>167<br>168<br>169  | ggcatagcagctggtagtactacaataatcca<br>G I A A G T T T I S<br>A * Q L V L L Q Y P<br>H S S W Y Y Y N I | 228<br>224<br>225<br>226 |
| X13972,<br>IGHD2-8*01  | aggatattgtagtagtggtagtactacc<br>R I L Y * W C M L Y<br>G Y C T N G V C Y T<br>D I V L M V Y A I    | 170<br>16, 17<br>53<br>94 | ggatagcatcacccattagtaacaatcct<br>G I A Y T I S T I S<br>V * H T P L V Q Y P<br>Y S I H H * Y N I    | 229<br>230<br>231<br>232 |
|                        | agcatattgtagtggtagtactacc<br>R I L Y W W C M L Y<br>G Y C T G G V C Y T<br>D I V L V V Y A I       | 171<br>172<br>173<br>174  | ggtagcatcacccagtagtaacaatcct<br>G I A Y T T S T I S<br>V * H T P P V Q Y L<br>Y S I H H Q Y N I     | 233<br>234<br>235<br>236 |
| J00234,<br>IGHD2-8*02  | aggatattgtagtggtagtactacc<br>R I L * W W * L L L<br>G Y C S G G S C Y S<br>D I V V V V A A T       | 175<br>-<br>55<br>95      | ggagtagcagctaccaccaciacaaatcct<br>G V A A T T T T I S<br>E * Q L P P L Q Y P<br>S S S Y H H Y N I   | 237<br>238<br>239<br>240 |
|                        | agcatattgtagtggtagtactacc<br>S I L W W * L L F<br>A Y C G G D C Y S<br>H I V V V I A I             | 176<br>19<br>57<br>177    | ggaatagcaatcacccacaaatgct<br>G I A I T T T I C<br>E * Q S P P Q Y A<br>N S N H H H N M              | 241<br>242<br>243<br>244 |
| X97051,<br>IGHD2-21*01 | agcatattgtagtggtagtactacc<br>S I L W W * L L F<br>A Y C G G D C Y S<br>H I V V V T A I             | 178<br>19<br>57<br>97     | ggatagcagctaccaccacaaatgct<br>G I A V T T T I C<br>E * Q S P P Q Y A<br>N S S H H H N M             | 245<br>246<br>247<br>248 |
|                        | agcatattgtagtggtagtactacc<br>S I L W W * L L F<br>A Y C G G D C Y S<br>H I V V V T A I             | 178<br>19<br>57<br>97     | ggatagcagctaccaccacaaatgct<br>G I A V T T T I C<br>E * Q S P P Q Y A<br>N S S H H H N M             | 245<br>246<br>247<br>248 |

FIG. 10B

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| Human D Gene Segment | Direct 5'-3' Orientation | SEQ ID NO. | Inverted Orientation               | SEQ ID NO. |
|----------------------|--------------------------|------------|------------------------------------|------------|
| IGHD3-3              | X13972,<br>IGHD3-3*01    | 179        | ggataataaccactccaaaatcgtaataac     | 249        |
|                      |                          | 21         | G I I T T P K I V I                | 250        |
|                      |                          | 59         | V * * P L Q K S * Y                | 251        |
|                      |                          | 98         | Y N N H S K N R N                  | 252        |
| IGHD3-9              | X93618,<br>IGHD3-3*02    | 180        | ggataataaccactccaaaatcgtaataac     | 253        |
|                      |                          | 181        | G I I T T P K M L I                | 254        |
|                      |                          | 182        | V * * P L Q K C * Y                | 255        |
|                      |                          | 183        | Y N N H S K N A N                  | 256        |
| IGHD3-10             | X13972,<br>IGHD3-9*01    | 184        | gtataataaccagtcacaaaatcgtaataac    | 257        |
|                      |                          | 23         | V I I T S Q N I V I                | 258        |
|                      |                          | 61         | L * * P V K I S * Y                | 259        |
|                      |                          | 99, 100    | Y N N Q S K Y R N                  | 260        |
| IGHD3-16             | X13972,<br>IGHD3-10*01   | 185        | gtataataacccccgaaccatagtaataac     | 261        |
|                      |                          | 25         | V I I T P R T I V I                | 262        |
|                      |                          | 63         | L * * L P E P * * Y                | 263        |
|                      |                          | 101        | Y N N S P N H S N                  | 264        |
| IGHD3-22             | X93615,<br>IGHD3-10*02   | 186        | gtataataacccccgaaccatagtaataac     | 265        |
|                      |                          | 187        | V I I T P R T * * Y                | 266        |
|                      |                          | 188        | L * * L P E H S N                  | 267        |
|                      |                          | 189        | Y N N S P N I V I                  | 268        |
| IGHD3-16             | X93614,<br>IGHD3-16*01   | 190        | ggataagcataactcccccaaacgtaataataac | 269        |
|                      |                          | 191        | G I S I T P P N V I I I            | 270        |
|                      |                          | 192        | V * A * L P Q T * S * Y            | 271        |
|                      |                          | 193        | Y K H N S P K R N H N              | 272        |
| IGHD3-22             | X93616,<br>IGHD3-22*01   | 194        | gtataataaccactacatagtaataac        | 273        |
|                      |                          | 29         | V V I T T T I I V I                | 274        |
|                      |                          | 67         | * * * P L L S * * Y                | 275        |
|                      |                          | 103        | S N N H Y Y H S N                  | 276        |

FIG. 10C

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| Human D Gene Segment | Direct 5'-3' Orientation | SEQ ID NO. | Inverted Orientation                                                     | SEQ ID NO. |
|----------------------|--------------------------|------------|--------------------------------------------------------------------------|------------|
| IGHD4-4              | X13972,<br>IGHD4-4*01    | 195        | gtagtactgtagtca<br>V V T V V<br>* L L * S<br>S Y C S                     | 277        |
|                      |                          | -          |                                                                          | 278        |
|                      |                          | 69         |                                                                          | -          |
|                      |                          | 105        |                                                                          | 279        |
| IGHD4-11             | X13972,<br>IGHD4-11*01   | 195        | gtagtactgtagtca<br>V V T V V<br>* L L * S<br>S Y C S                     | 277        |
|                      |                          | -          |                                                                          | 278        |
|                      |                          | 69         |                                                                          | -          |
|                      |                          | 105        |                                                                          | 279        |
| IGHD4-17             | X97501,<br>IGHD4-17*01   | 196        | gtagtaccgtagtca<br>V V T V V<br>* S P * S<br>S H R S                     | 280        |
|                      |                          | -          |                                                                          | 278        |
|                      |                          | 71         |                                                                          | -          |
|                      |                          | 105        |                                                                          | 281        |
| IGHD4-23             | X97051,<br>IGHD4-23*01   | 197        | ggagtaccaccgtagtca<br>G V T T V V<br>E L P P * S<br>S Y H R S            | 282        |
|                      |                          | -          |                                                                          | 283        |
|                      |                          | 73         |                                                                          | 284        |
|                      |                          | 106        |                                                                          | 285        |
| IGHD5-5              | X13972,<br>IGHD5-5*01    | 198        | gtaaccatagctgtagccac<br>V T I A V S<br>* P * L Y P<br>N H S C I H        | 286        |
|                      |                          | 107        |                                                                          | 287        |
|                      |                          | 35         |                                                                          | -          |
|                      |                          | 75         |                                                                          | 288        |
| IGHD5-12             | X13972,<br>IGHD5-12*01   | 199        | gtaatcgtagccactatccac<br>V I V A T I S<br>* S * P L Y P<br>N R S H Y I H | 289        |
|                      |                          | 108        |                                                                          | 290        |
|                      |                          | 37         |                                                                          | 291        |
|                      |                          | 77         |                                                                          | 292        |
| IGHD5-18             | X97051,<br>IGHD5-18*01   | 198        | gtaaccatagctgtagccac<br>V T I A V S<br>* P * L Y P<br>N H S C I H        | 286        |
|                      |                          | 107        |                                                                          | 287        |
|                      |                          | 35         |                                                                          | -          |
|                      |                          | 75         |                                                                          | 288        |

FIG. 10D

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| Human D Gene Segment | Direct 5'-3' Orientation                                                                           | SEQ ID NO. | Inverted Orientation                                                  | SEQ ID NO. |
|----------------------|----------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------------|------------|
| IGHD5-24             | X97051,<br>IGHD5-<br>24*01<br>gtagataggctacaattac<br>V E M A T I<br>* R W L Q L<br>R D G Y N Y     | 200        | gtaattgtagccatctctac<br>V I V A I S<br>* L * P S L<br>N C S H L Y     | 293        |
|                      |                                                                                                    | 110        |                                                                       | 294        |
|                      |                                                                                                    | 39         |                                                                       | -          |
|                      |                                                                                                    | 79         |                                                                       | 295        |
| IGHD6-6              | X13972,<br>IGHD6-6*01<br>gagtatagcagctgtctc<br>E Y S S S S<br>S I A A R<br>V * Q L V               | 201        | ggacgagctgtctactc<br>G R A A I L<br>D E L L Y<br>T S C Y T            | 296        |
|                      |                                                                                                    | 81         |                                                                       | 297        |
|                      |                                                                                                    | 112        |                                                                       | 298        |
|                      |                                                                                                    | -          |                                                                       | 299        |
| IGHD6-13             | X13972,<br>IGHD6-<br>13*01<br>gggtatagcagcagctgttac<br>G Y S S S W Y<br>G I A A A G<br>V * Q Q L V | 202        | gtaccagctgtgtctataccc<br>V P A A A I P<br>Y Q L L L Y<br>T S C C Y T  | 300        |
|                      |                                                                                                    | 83         |                                                                       | 301        |
|                      |                                                                                                    | 114        |                                                                       | 302        |
|                      |                                                                                                    | 41         |                                                                       | 303        |
| IGHD6-19             | X97051,<br>IGHD6-<br>19*01<br>gggtatagcagtggtgttac<br>G Y S S G W Y<br>G I A V A G<br>V * Q W L V  | 203        | gtaccagccactgtctataccc<br>V P A T A I P<br>Y Q P L L Y<br>T S H C Y T | 304        |
|                      |                                                                                                    | 85         |                                                                       | 305        |
|                      |                                                                                                    | 116        |                                                                       | 306        |
|                      |                                                                                                    | 44         |                                                                       | 307        |
| IGHD6-25             | X97051,<br>IGHD6-<br>25*01<br>gggtatagcagcgggttac<br>G Y S S G Y<br>G I A A A<br>V * Q R L         | 204        | gtagccgctgtctataccc<br>V A A A I P<br>* P L L Y<br>S R C Y T          | 308        |
|                      |                                                                                                    | 87         |                                                                       | 309        |
|                      |                                                                                                    | 116        |                                                                       | 310        |
|                      |                                                                                                    | -          |                                                                       | 311        |
| IGHD7-27             | J00256,<br>IGHD7-<br>27*01<br>ctaactgggga<br>L T G<br>* L G<br>N W G                               | 205        | tccccagttag<br>S P V<br>P Q L<br>P S *                                | 312        |
|                      |                                                                                                    | -          |                                                                       | -          |
|                      |                                                                                                    | -          |                                                                       | -          |
|                      |                                                                                                    | -          |                                                                       | -          |

FIG. 10E

Antibody Sequence 1

1c1|Query\_1\_reversed  
IGHV4-34\*01

<-----FWR1-----><-----CDR1  
Q V Q L Q Q W G A G L L K P S D T L S L T C A V Y G G S F S  
CAGTGCAGTACAGCAGTGGGGCAGAGACTGTTGAGCTTCGGATACCTGTCCCTCACCGCGCTCTATGGTGGGTCCCTTCAGT  
.....G.....  
Q V Q L Q Q W G A G L L K P S E T L S L T C A V Y G G S F S  
-----FWR2-----><-----CDR2-----><  
G Y Y W S W I R Q P P G K G L E W I G E I N H S G S T N Y N  
GGTTACTGAGCTGGATCCCGCAGCCGCCAGGGAGGGCTGGAGTGGGAAATCAATCATAGTGGAAAGCAACCACTACAC  
.....G.....  
G Y Y W S W I R Q P P G K G L E W I G E I N H S G S T N Y N  
-----FWR3-----  
P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T  
CCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCTCCAGACCCAGTCTCTCCCTGAGCTGAGCTCTGTGACCCGCCGGGACACG  
.....  
P S L K S R V T I S V D T S K N Q F S L K L S S V T A A D T  
----->  
A V Y Y C A G H S H G W Y Y Y Y Y G M D V W G Q G T T V T V  
CCTGTGATTACTGTCCGGGCATATCCATGGCTGGTACTACTACTACGGTATGGAGCTCTGGGGCCAGGCAACCGGTCCACCGTC  
.....  
A V Y Y C A (SEQ ID NO:314)  
----->  
S S (SEQ ID NO:313)  
TCCTCA 473 (SEQ ID NO:312)  
..... 62

1c1|Query\_1\_reversed  
IGHV4-34\*01

1c1|Query\_1\_reversed  
IGHV4-34\*01

1c1|Query\_1\_reversed  
IGHV4-34\*01

IGHHD6-19, RUC1  
IGHJ6\*02

1c1|Query\_1\_reversed  
IGHJ6\*02

| D gene segment | Hydrophilic | SEQ ID NO. |
|----------------|-------------|------------|
| D6-19          | GYSSGWY     | 85         |
| HD6-19         | GSHGWY      | 86         |

FIG. 11

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| D gene segment | Hydrophilic | SEQ ID NO. |
|----------------|-------------|------------|
| D4-17          | DYGDY       | 71         |
| HD4-17         | DHGHY       | 72         |

**FIG. 12**

| D gene segment | Hydrophilic | SEQ ID NO. |
|----------------|-------------|------------|
| D6-13          | GYSSSWY     | 83         |
| HD6-13         | GHSHSWY     | 84         |

**FIG. 13**

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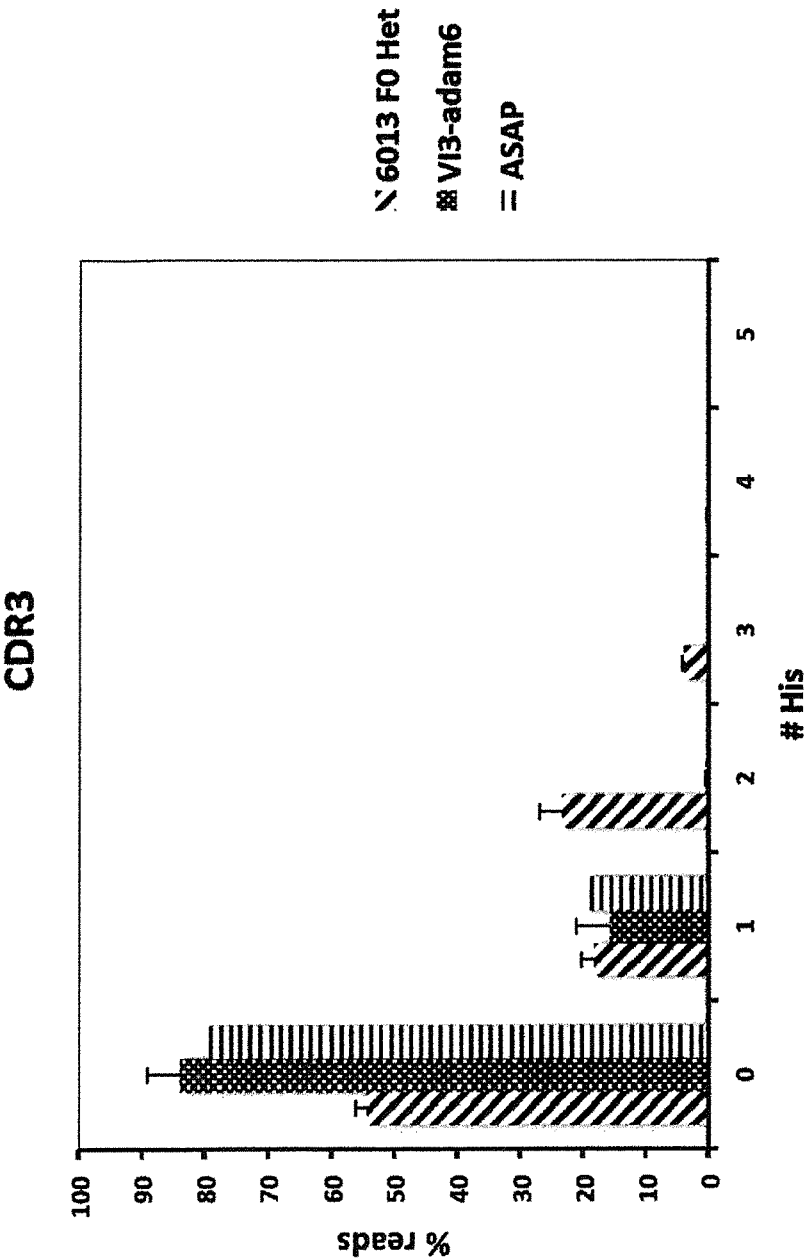


FIG. 14

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|             |                                                             |               |
|-------------|-------------------------------------------------------------|---------------|
| IGKV1-39*01 | -----FR1-IMGT----- CDR1  -----FR2-IMGT----- C -----         | SEQ ID NO:325 |
| A           | DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPS |               |
| B           | .....F...T <b>H</b> .....I....V...YT....                    |               |
| C           | A.....I.NF.....G.YN.....                                    |               |
| D           | ..... <b>HN</b> NN.....H.....N.....                         |               |
| E           | .....A.....T.N.....                                         |               |
| F           | .....N.D.....                                               |               |
| G           | A.L.....N.N.....N.D.....                                    |               |
| H           | A.....N.N.. <b>H</b> .....D.F.....                          |               |
| I           | A.L.....                                                    |               |
| J           | A.....                                                      |               |
| K           | A.L.....M.....                                              |               |
| IGKV1-39*01 | -----FR3-IMGT----- CDR3-                                    |               |
| A           | RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST-P-----                   |               |
| B           | ...A.....T....NI..FTFGPGTKVDIKR                             |               |
| C           | .....Y...T.H...GN.....SMYTFGQGTQLEIKR                       |               |
| D           | ..... <b>H</b> .....I..ITFGQGTRLEIKR                        |               |
| E           | ..... <b>H</b> .....I..ITFGQGTRLEIKR                        |               |
| F           | .....T.H..... <b>H</b> .....ITFGQGTRLEIKR                   |               |
| G           | .....T..... <b>H</b> .....ITFGQGTRLEIKR                     |               |
| H           | .....P.ITFGQGTRVEIKR                                        |               |
| I           | ...K..... <b>I</b> H.ITFGQGTKEIKR                           |               |
| J           | ..... <b>H</b> .IP.ITFGQGTRLEIK.                            |               |
| K           | .....T.....R..... <b>H</b> ..P.ITFGQGTKEIKR                 |               |

FIG. 15



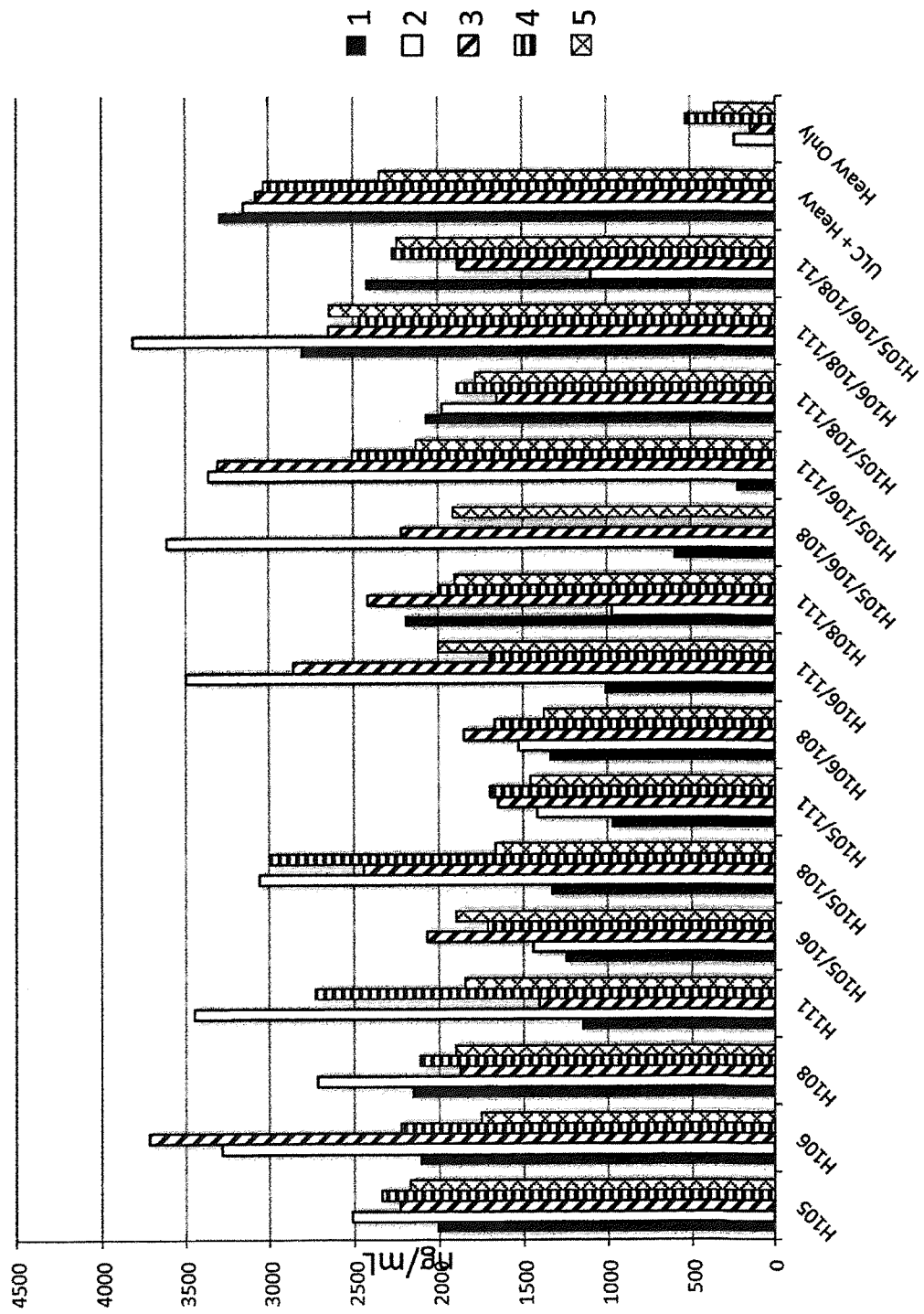


FIG. 17

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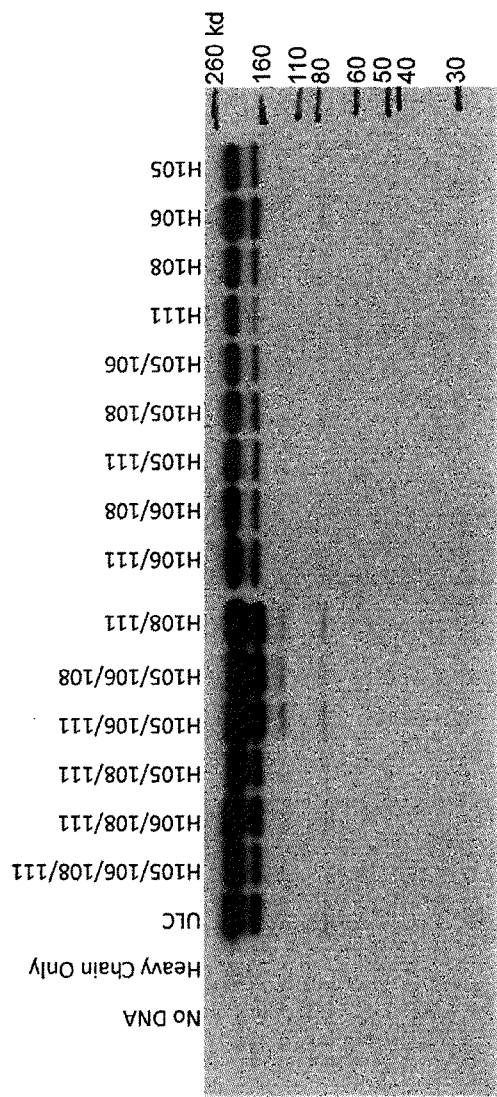


FIG. 18

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| HC      | Vk<br>mut   | Kinetics at pH 7.2        |                                |           |          |          | Kinetics at pH 5.75 |                           |                                |           |          | low/neutral pH |         |     |     |     |
|---------|-------------|---------------------------|--------------------------------|-----------|----------|----------|---------------------|---------------------------|--------------------------------|-----------|----------|----------------|---------|-----|-----|-----|
|         |             | mAb capture<br>level (RU) | 100nM<br>Antigen<br>bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | % (min)             | mAb capture<br>level (RU) | 100nM<br>antigen<br>bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)         | % (min) | ka  | kd  | KD  |
| H4H6006 | H105        | 44                        | 11                             | 4.25E+05  | 1.18E-03 | 2.77E-09 | 10                  | 32                        | 5                              | 1.27E+06  | 2.05E-03 | 1.61E-09       | 6       | 3.0 | 1.7 | 0.6 |
|         | H106        | 46                        | 12                             | 4.42E+05  | 9.32E-04 | 2.11E-09 | 12                  | 27                        | 4                              | 1.56E+06  | 1.72E-03 | 1.10E-09       | 7       | 3.5 | 1.8 | 0.5 |
|         | H108        | 46                        | 12                             | 4.51E+05  | 9.02E-04 | 2.00E-09 | 13                  | 33                        | 5                              | 1.15E+06  | 1.47E-03 | 1.28E-09       | 8       | 2.5 | 1.6 | 0.6 |
|         | H111        | 47                        | 13                             | 3.86E+05  | 9.54E-04 | 2.47E-09 | 12                  | 36                        | 5                              | 8.81E+05  | 1.52E-03 | 1.73E-09       | 8       | 2.3 | 1.6 | 0.7 |
|         | H105        | 16                        | 1                              | NB        | NB       | NB       | NB                  | 6                         | -4                             | NB        | NB       | NB             | NB      |     |     |     |
|         | H105        | 40                        | 11                             | 4.83E+05  | 8.73E-04 | 1.81E-09 | 13                  | 30                        | 4                              | 1.54E+06  | 1.26E-03 | 8.20E-10       | 9       | 3.2 | 1.4 | 0.5 |
|         | H105        | 22                        | 4                              | 3.81E+05  | 1.32E-03 | 3.45E-09 | 9                   | 16                        | -2                             | NB        | NB       | NB             | NB      |     |     |     |
|         | H106        | 51                        | 15                             | 4.87E+05  | 7.60E-04 | 1.56E-09 | 15                  | 40                        | 8                              | 1.16E+06  | 1.04E-03 | 8.96E-10       | 11      | 2.4 | 1.4 | 0.6 |
|         | H106        | 38                        | 9                              | 3.94E+05  | 9.00E-04 | 2.28E-09 | 13                  | 29                        | 2                              | 1.55E+06  | 1.60E-03 | 1.03E-09       | 7       | 3.9 | 1.8 | 0.5 |
|         | H108        | 51                        | 14                             | 3.98E+05  | 8.29E-04 | 2.08E-09 | 14                  | 40                        | 6                              | 8.42E+05  | 1.19E-03 | 1.42E-09       | 10      | 2.1 | 1.4 | 0.7 |
|         | H105        | 14                        | 1                              | NB        | NB       | NB       | NB                  | 9                         | -5                             | NB        | NB       | NB             | NB      |     |     |     |
|         | H105        | 15                        | 1                              | NB        | NB       | NB       | NB                  | 10                        | -5                             | NB        | NB       | NB             | NB      |     |     |     |
|         | H105        | 17                        | 2                              | 4.38E+05  | 9.60E-04 | 2.19E-09 | 12                  | 12                        | -5                             | NB        | NB       | NB             | NB      |     |     |     |
|         | H10         | 40                        | 10                             | 3.72E+05  | 7.42E-04 | 2.00E-09 | 16                  | 30                        | 2                              | NB        | NB       | NB             | NB      |     |     |     |
|         | H105        | 15                        | 1                              | NB        | NB       | NB       | NB                  | 9                         | -6                             | NB        | NB       | NB             | NB      |     |     |     |
|         | L-39<br>UIC | 72                        | 22                             | 3.90E+05  | 1.18E-03 | 3.03E-09 | 10                  | 56                        | 11                             | 7.89E+05  | 1.84E-03 | 2.39E-09       | 6       | 2.0 | 1.6 | 0.8 |

FIG. 19A

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| HC      | V <sub>k</sub><br>mut | Kinetics at pH 7.2        |                                |                       |                      |          |         | Kinetics at pH 5.75       |                                |                       |                      |          |         | low/neutral pH |                |     |
|---------|-----------------------|---------------------------|--------------------------------|-----------------------|----------------------|----------|---------|---------------------------|--------------------------------|-----------------------|----------------------|----------|---------|----------------|----------------|-----|
|         |                       | mAb capture<br>level (RU) | 100nM<br>Antigen<br>bound (RU) | k <sub>a</sub> (1/Ms) | k <sub>d</sub> (1/s) | KD (nM)  | % (min) | mAb capture<br>level (RU) | 100nM<br>antigen<br>bound (RU) | k <sub>a</sub> (1/Ms) | k <sub>d</sub> (1/s) | KD (nM)  | % (min) | k <sub>a</sub> | k <sub>d</sub> | KD  |
| H4H6008 | H105                  | 79                        | 21                             | 3.47E+05              | 1.09E-03             | 3.15E-09 | 11      | 62                        | 8                              | 5.15E+05              | 3.54E-03             | 6.87E-09 | 3       | 1.5            | 3.2            | 2.2 |
|         | H106                  | 60                        | 13                             | 3.19E+05              | 1.92E-03             | 6.02E-09 | 6       | 48                        | 2                              | 1.92E+06              | 2.48E-02             | 1.29E-08 | 0       | 6.0            | 12.9           | 2.1 |
|         | H108                  | 84                        | 20                             | 2.89E+05              | 2.66E-03             | 9.17E-09 | 4       | 1                         | -5                             | NB                    | NB                   | NB       | NB      | 1.5            | 5.1            | 3.4 |
|         | H111                  | 77                        | 19                             | 3.28E+05              | 1.54E-03             | 4.69E-09 | 8       | 60                        | 5                              | 4.96E+05              | 7.85E-03             | 1.58E-08 | 1       | 1.5            | 5.1            | 3.4 |
|         | H105                  | 30                        | 4                              | 3.39E+05              | 9.91E-04             | 2.92E-09 | 12      | -1                        | -7                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H105                  | 77                        | 20                             | 3.16E+05              | 1.40E-03             | 4.45E-09 | 8       | 62                        | 6                              | 4.76E+05              | 5.41E-03             | 1.14E-08 | 2       | 1.5            | 3.9            | 2.6 |
|         | H105                  | 44                        | 11                             | 3.51E+05              | 4.10E-04             | 1.17E-09 | 28      | 34                        | 0                              | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H106                  | 81                        | 18                             | 2.99E+05              | 2.20E-03             | 7.34E-09 | 5       | 66                        | 4                              | 3.87E+05              | 1.16E-02             | 3.01E-08 | 1       | 1.3            | 5.3            | 4.1 |
|         | H106                  | 87                        | 19                             | 3.05E+05              | 1.64E-03             | 5.38E-09 | 7       | 73                        | 5                              | 4.34E+05              | 6.96E-03             | 1.60E-08 | 2       | 1.4            | 4.2            | 3.0 |
|         | H108                  | 85                        | 22                             | 3.42E+05              | 1.63E-03             | 4.76E-09 | 7       | 70                        | 5                              | 3.94E+05              | 8.00E-03             | 2.03E-08 | 1       | 1.2            | 4.9            | 4.3 |
|         | H105                  | 29                        | 4                              | 3.53E+05              | 9.63E-04             | 2.73E-09 | 12      | 24                        | -5                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H105                  | 32                        | 5                              | 2.87E+05              | 9.83E-04             | 3.43E-09 | 12      | 26                        | -5                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H105                  | 39                        | 9                              | 3.47E+05              | 3.26E-04             | 9.38E-10 | 35      | 32                        | -2                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H106                  | 57                        | 11                             | 2.72E+05              | 1.63E-03             | 5.99E-09 | 7       | 46                        | -1                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H105                  | 36                        | 6                              | 2.93E+05              | 1.05E-03             | 3.58E-09 | 11      | 29                        | -5                             | NB                    | NB                   | NB       | NB      |                |                |     |
|         | H105                  | 128                       | 33                             | 3.02E+05              | 1.86E-03             | 6.15E-09 | 6       | 103                       | 13                             | 3.24E+05              | 5.67E-03             | 1.75E-08 | 2       | 1.1            | 3.1            | 2.8 |
|         | UIC                   |                           |                                |                       |                      |          |         |                           |                                |                       |                      |          |         |                |                |     |

FIG. 19B

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| HC      | Vk mut   | Kinetics at pH 7.2     |                          |           |          |        |          | Kinetics at pH 5.75    |                          |           |          |        |          | low/neutral pH |    |    |
|---------|----------|------------------------|--------------------------|-----------|----------|--------|----------|------------------------|--------------------------|-----------|----------|--------|----------|----------------|----|----|
|         |          | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M) | t½ (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M) | t½ (min) | ka             | kd | KD |
| H4H3046 | H105     | 73                     | 0                        | NB        | NB       | NB     | NB       | 62                     | -8                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H106     | 64                     | 0                        | NB        | NB       | NB     | NB       | 54                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H108     | 75                     | 1                        | NB        | NB       | NB     | NB       | 64                     | -8                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H111     | 73                     | 0                        | NB        | NB       | NB     | NB       | 62                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H105     | 45                     | 0                        | NB        | NB       | NB     | NB       | 38                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H106     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H105     | 65                     | 0                        | NB        | NB       | NB     | NB       | 56                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H108     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H105     | 34                     | 0                        | NB        | NB       | NB     | NB       | 27                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H106     | 77                     | 0                        | NB        | NB       | NB     | NB       | 67                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H108     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H106     | 75                     | 0                        | NB        | NB       | NB     | NB       | 67                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H108     | 66                     | 0                        | NB        | NB       | NB     | NB       | 56                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H105     | 54                     | 0                        | NB        | NB       | NB     | NB       | 46                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H106     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H108     | 47                     | 0                        | NB        | NB       | NB     | NB       | 41                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H105     | 37                     | 0                        | NB        | NB       | NB     | NB       | 31                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H108     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H106     | 69                     | 0                        | NB        | NB       | NB     | NB       | 59                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H108     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H105     | 54                     | 0                        | NB        | NB       | NB     | NB       | 49                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |
|         | H106     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H108     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | H111     |                        |                          |           |          |        |          |                        |                          |           |          |        |          |                |    |    |
|         | 1-39 ULC | 97                     | 0                        | NB        | NB       | NB     | NB       | 88                     | -9                       | NB        | NB       | NB     | NB       |                |    |    |

FIG. 19C

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| HC      | Vk mut   | Kinetics at pH 7.2     |                          |           |          |          |          | Kinetics at pH 5.75    |                          |           |          |          |          | low/neutral pH |     |     |
|---------|----------|------------------------|--------------------------|-----------|----------|----------|----------|------------------------|--------------------------|-----------|----------|----------|----------|----------------|-----|-----|
|         |          | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t½ (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t½ (min) | ka             | kd  | KD  |
| HAH2964 | H105     | 327                    | 23                       | 1.43E+05  | 8.40E-03 | 5.89E-08 | 1        | 318                    | 2                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H106     | 303                    | 26                       | 9.67E+04  | 3.40E-03 | 3.52E-08 | 3        | 289                    | 11                       | 9.46E+04  | 2.08E-02 | 2.20E-07 | 1        | 1.0            | 6.1 | 6.3 |
|         | H108     | 287                    | 29                       | 1.37E+05  | 2.46E-03 | 1.80E-08 | 5        | 268                    | 12                       | 7.69E+04  | 1.32E-02 | 1.71E-07 | 1        | 0.6            | 5.4 | 9.5 |
|         | H111     | 311                    | 21                       | 1.31E+05  | 6.83E-03 | 5.20E-08 | 2        | 292                    | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 285                    | 17                       | 9.65E+04  | 6.20E-03 | 6.43E-08 | 2        | 262                    | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |
|         | H108     | 271                    | 21                       | 1.23E+05  | 9.82E-03 | 7.99E-08 | 1        | 262                    | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 221                    | 11                       | 2.37E+05  | 2.11E-02 | 8.88E-08 | 1        | 216                    | -6                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     | 344                    | 28                       | 1.04E+05  | 6.66E-03 | 6.38E-08 | 2        | 316                    | 3                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H108     | 341                    | 25                       | 1.16E+05  | 9.09E-03 | 7.81E-08 | 1        | 321                    | 2                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H111     | 300                    | 20                       | 9.64E+04  | 1.01E-02 | 1.05E-07 | 1        | 274                    | -4                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 269                    | 10                       | 1.31E+05  | 2.52E-02 | 1.93E-07 | 0        | 243                    | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     | 286                    | 5                        | 6.34E+04  | 5.06E-02 | 7.99E-07 | 0        | 265                    | -9                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108     | 309                    | 13                       | 3.26E+05  | 3.47E-02 | 1.06E-07 | 0        | 279                    | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111     |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |
|         | H105     | 315                    | 9                        | 1.55E+05  | 5.89E-02 | 3.81E-07 | 0        | 279                    | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |
|         | H108     | 260                    | 0                        | NB        | NB       | NB       | NB       | 238                    | -10                      | NB        | NB       | NB       | NB       |                |     |     |
|         | H111     |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |
|         | 1-39 ULC | 386                    | 32                       | 1.30E+05  | 2.05E-03 | 1.58E-08 | 6        | 362                    | 17                       | 7.58E+04  | 7.97E-03 | 1.05E-07 | 1        | 0.6            | 3.9 | 6.6 |

FIG. 19D

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| HC      | V <sub>k</sub> mut | Kinetics at pH 7.2     |                          |           |          |          |          | Kinetics at pH 5.75    |                          |           |          |          |          | low/neutral pH |     |     |
|---------|--------------------|------------------------|--------------------------|-----------|----------|----------|----------|------------------------|--------------------------|-----------|----------|----------|----------|----------------|-----|-----|
|         |                    | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t% (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t% (min) | ka             | kd  | KD  |
| H4H3010 | H105               | 52                     | 8                        | 1.06E+05  | 7.43E-04 | 7.04E-09 | 16       | 43                     | -1                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106               | 50                     | 9                        | 1.26E+05  | 3.54E-04 | 2.82E-09 | 33       | 40                     | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H108               | 50                     | 8                        | 9.29E+04  | 2.43E-04 | 2.62E-09 | 48       | 42                     | -1                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111               | 55                     | 11                       | 1.53E+05  | 1.66E-04 | 1.09E-09 | 69       | 48                     | 2                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H105               | 55                     | 10                       | 1.31E+05  | 5.18E-04 | 3.94E-09 | 22       | 45                     | 1                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H106               | 48                     | 8                        | 8.96E+04  | 4.58E-04 | 5.12E-09 | 25       | 41                     | -1                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108               | 38                     | 6                        | 8.85E+04  | 1.64E-04 | 1.85E-09 | 70       | 32                     | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111               | 59                     | 11                       | 1.06E+05  | 1.61E-04 | 1.52E-09 | 72       | 52                     | 2                        | 4.79E+05  | 1.00E-06 | 2.09E-12 | 11550    | 4.5            | 0.0 | 0.0 |
|         | H106               | 76                     | 7                        | 6.81E+04  | 5.23E-04 | 7.68E-09 | 22       | 72                     | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H108               | 58                     | 11                       | 1.17E+05  | 9.26E-05 | 7.92E-10 | 125      | 52                     | 2                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H111               | 67                     | 13                       | 1.11E+05  | 3.17E-04 | 2.86E-09 | 36       | 58                     | 4                        | IC        | IC       | IC       | IC       |                |     |     |
|         | H105               | 70                     | 8                        | 6.45E+04  | 9.94E-04 | 1.54E-08 | 12       | 57                     | -1                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106               | 49                     | 8                        | 8.52E+04  | 1.10E-04 | 1.29E-09 | 105      | 44                     | -1                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108               | 54                     | 3                        | 1.02E+04  | 1.46E-03 | 1.44E-07 | 8        | 46                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111               | 70                     | 6                        | 7.28E+04  | 5.55E-03 | 7.61E-08 | 2        | 62                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105               | 83                     | 15                       | 1.02E+05  | 1.79E-04 | 1.77E-09 | 64       | 77                     | 7                        | 2.11E+05  | 1.00E-06 | 4.74E-12 | 11550    | 2.1            | 0.0 | 0.0 |
|         | 1-39               |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |
|         | ULC                |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |

FIG. 19E

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| HC      | Vk mut   | Kinetics at pH 7.2     |                          |           |          |          |                        | Kinetics at pH 5.75      |           |        |          |    |    | low/neutral pH |  |  |
|---------|----------|------------------------|--------------------------|-----------|----------|----------|------------------------|--------------------------|-----------|--------|----------|----|----|----------------|--|--|
|         |          | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | Kd (M)   | t½ (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | Kd (M) | t½ (min) | ka | Kd |                |  |  |
| H4H3029 | H105     | 71                     | 8                        | 1.41E+05  | 2.96E-04 | 39       | 60                     | -3                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     | 72                     | 8                        | 1.50E+05  | 2.39E-04 | 48       | 64                     | -2                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H108     | 68                     | 7                        | 1.19E+05  | 7.97E-05 | 145      | 61                     | -2                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H111     | 69                     | 8                        | 1.50E+05  | 1.78E-04 | 65       | 63                     | -2                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H105     | 88                     | 10                       | 1.60E+05  | 2.45E-04 | 47       | 77                     | 0                        | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H105     | 67                     | 8                        | 1.45E+05  | 1.14E-04 | 102      | 59                     | -3                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H108     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H105     | 13                     | 0                        | NB        | NB       | NB       | 14                     | -11                      | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H108     | 92                     | 10                       | 1.34E+05  | 1.34E-04 | 86       | 82                     | 0                        | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H108     | 85                     | 5                        | 5.82E+04  | 1.10E-03 | 10       | 78                     | -4                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H105     | 62                     | 7                        | 1.48E+05  | 1.73E-04 | 67       | 55                     | -4                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H108     | 85                     | 10                       | 1.36E+05  | 1.97E-04 | 59       | 75                     | 0                        | NB        | NB     | NB       |    |    |                |  |  |
|         | H105     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H106     | 78                     | 6                        | 1.35E+05  | 2.18E-03 | 5        | 70                     | -4                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H108     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H105     | 55                     | 6                        | 1.50E+05  | 2.48E-04 | 47       | 48                     | -5                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H106     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H108     | 73                     | 4                        | 8.60E+04  | 1.59E-03 | 7        | 66                     | -6                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H105     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H106     | 95                     | 7                        | 1.19E+05  | 6.71E-03 | 2        | 85                     | -6                       | NB        | NB     | NB       |    |    |                |  |  |
|         | H108     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H105     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | H106     | 108                    | 12                       | 1.34E+05  | 1.65E-04 | 70       | 98                     | 2                        | IC        | IC     | IC       |    |    |                |  |  |
|         | H108     |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |
|         | 1-39 ULC |                        |                          |           |          |          |                        |                          |           |        |          |    |    |                |  |  |

FIG. 19F

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| HC      | Vk mut | Kinetics at pH 7.2     |                          |           |          |          |          | Kinetics at pH 5.75    |                          |           |          |          |          | low/neutral pH |     |     |
|---------|--------|------------------------|--------------------------|-----------|----------|----------|----------|------------------------|--------------------------|-----------|----------|----------|----------|----------------|-----|-----|
|         |        | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t% (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t% (min) | ka             | kd  | KD  |
| H4HS978 | H105   | 44                     | 7                        | 3.88E+05  | 5.73E-03 | 1.48E-08 | 2        | 41                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106   | 36                     | 7                        | 3.15E+05  | 3.03E-03 | 9.62E-09 | 4        | 34                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108   | 38                     | 8                        | 3.18E+05  | 9.61E-04 | 3.02E-09 | 12       | 32                     | -4                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111   | 43                     | 8                        | 3.13E+05  | 2.32E-03 | 7.40E-09 | 5        | 40                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 33                     | 4                        | 2.69E+05  | 5.41E-03 | 2.01E-08 | 2        | 29                     | -9                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 34                     | 7                        | 2.13E+05  | 2.15E-03 | 1.01E-08 | 5        | 30                     | -7                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 32                     | 5                        | 3.47E+05  | 6.27E-03 | 1.81E-08 | 2        | 30                     | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106   | 50                     | 10                       | 3.67E+05  | 3.09E-03 | 8.42E-09 | 4        | 46                     | -4                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106   | 62                     | 12                       | 2.88E+05  | 4.47E-03 | 1.55E-08 | 3        | 56                     | -2                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108   | 45                     | 9                        | 3.22E+05  | 2.05E-03 | 6.37E-09 | 6        | 43                     | -4                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 36                     | 5                        | 3.57E+05  | 7.48E-03 | 2.10E-08 | 2        | 35                     | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 39                     | 7                        | 3.37E+05  | 8.35E-03 | 2.48E-08 | 1        | 35                     | -6                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 29                     | 4                        | 2.94E+05  | 4.52E-03 | 1.54E-08 | 3        | 28                     | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106   | 41                     | 7                        | 3.12E+05  | 6.37E-03 | 2.04E-08 | 2        | 39                     | -6                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105   | 50                     | 9                        | 2.97E+05  | 6.83E-03 | 2.30E-08 | 2        | 45                     | -5                       | NB        | NB       | NB       | NB       |                |     |     |
|         | 1-39   | 74                     | 16                       | 2.92E+05  | 1.73E-03 | 5.91E-09 | 7        | 67                     | 3                        | 1.20E+06  | 9.67E-03 | 8.05E-09 | 1        | 4.1            | 5.6 | 1.4 |
|         | ULC    |                        |                          |           |          |          |          |                        |                          |           |          |          |          |                |     |     |

FIG. 19G

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| HC      | Vk mut   | Kinetics at pH 7.2     |                          |           |          |          |         | Kinetics at pH 5.75    |                          |           |          |          |         | low/neutral pH |      |      |
|---------|----------|------------------------|--------------------------|-----------|----------|----------|---------|------------------------|--------------------------|-----------|----------|----------|---------|----------------|------|------|
|         |          | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | % (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | % (min) | ka             | kd   | KD   |
| H4H5981 | H105     | 121                    | 24                       | 3.04E+05  | 8.81E-03 | 2.90E-08 | 1       | 112                    | 7                        | 4.47E+05  | 6.21E-02 | 1.39E-07 | 0       | 1.5            | 7.1  | 4.8  |
|         | H106     | 113                    | 29                       | 2.41E+05  | 2.99E-03 | 1.24E-08 | 4       | 103                    | 10                       | 6.84E+05  | 1.89E-02 | 2.76E-08 | 1       | 2.8            | 6.3  | 2.2  |
|         | H108     | 114                    | 31                       | 3.09E+05  | 2.83E-03 | 9.16E-09 | 4       | 104                    | 11                       | 5.06E+05  | 1.33E-02 | 2.63E-08 | 1       | 1.6            | 4.7  | 2.9  |
|         | H111     | 104                    | 26                       | 3.45E+05  | 3.98E-03 | 1.15E-08 | 3       | 96                     | 4                        | 4.54E+05  | 6.26E-02 | 1.38E-07 | 0       | 1.3            | 15.8 | 12.0 |
|         | H105     | 109                    | 26                       | 2.39E+05  | 3.10E-03 | 1.29E-08 | 4       | 103                    | 9                        | 5.00E+05  | 1.77E-02 | 3.53E-08 | 1       | 2.1            | 5.7  | 2.7  |
|         | H105     | 109                    | 27                       | 2.91E+05  | 4.48E-03 | 1.54E-08 | 3       | 97                     | 7                        | 1.00E+06  | 9.77E-02 | 9.76E-08 | 0       | 3.4            | 21.8 | 6.3  |
|         | H105     | 85                     | 16                       | 2.62E+05  | 7.59E-03 | 2.90E-08 | 2       | 80                     | -1                       | NB        | NB       | NB       | NB      |                |      |      |
|         | H106     | 121                    | 33                       | 2.33E+05  | 2.71E-03 | 1.16E-08 | 4       | 115                    | 14                       | 3.88E+05  | 1.19E-02 | 3.07E-08 | 1       | 1.7            | 4.4  | 2.6  |
|         | H106     | 117                    | 32                       | 2.29E+05  | 2.28E-03 | 9.97E-09 | 5       | 113                    | 13                       | 3.71E+05  | 8.88E-03 | 2.40E-08 | 1       | 1.6            | 3.9  | 2.4  |
|         | H108     | 93                     | 24                       | 3.39E+05  | 4.04E-03 | 1.19E-08 | 3       | 87                     | 3                        | 4.54E+05  | 5.11E-02 | 1.12E-07 | 0       | 1.3            | 12.7 | 9.4  |
|         | H105     | 94                     | 25                       | 2.24E+05  | 1.23E-03 | 5.47E-09 | 9       | 85                     | 8                        | 4.94E+05  | 3.02E-03 | 6.12E-09 | 4       | 2.2            | 2.5  | 1.1  |
|         | H105     | 111                    | 24                       | 2.31E+05  | 4.65E-03 | 2.01E-08 | 2       | 100                    | 4                        | 1.94E+05  | 8.05E-02 | 4.15E-07 | 0       | 0.8            | 17.3 | 20.6 |
|         | H105     | 83                     | 21                       | 2.60E+05  | 5.20E-03 | 2.00E-08 | 2       | 79                     | 1                        | NB        | NB       | NB       | NB      |                |      |      |
|         | H106     | 100                    | 28                       | 2.11E+05  | 2.23E-03 | 1.05E-08 | 5       | 93                     | 6                        | 4.26E+05  | 1.83E-02 | 4.29E-08 | 1       | 2.0            | 8.2  | 4.1  |
|         | H105     | 104                    | 24                       | 2.46E+05  | 5.05E-03 | 2.05E-08 | 2       | 98                     | 2                        | IC        | IC       | IC       | IC      |                |      |      |
|         | H105     | 133                    | 34                       | 2.80E+05  | 3.40E-03 | 1.22E-08 | 3       | 124                    | 13                       | 4.29E+05  | 1.42E-02 | 3.30E-08 | 1       | 1.5            | 4.2  | 2.7  |
|         | 1-39 ULC |                        |                          |           |          |          |         |                        |                          |           |          |          |         |                |      |      |

FIG. 19H

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| HC         | Vk<br>mut   | Kinetics at pH 7.2           |                                |           |          |          |          | Kinetics at pH 5.75          |                                |           |          |        |          | low/neutral pH |    |    |
|------------|-------------|------------------------------|--------------------------------|-----------|----------|----------|----------|------------------------------|--------------------------------|-----------|----------|--------|----------|----------------|----|----|
|            |             | mAb<br>capture<br>level (RU) | 100nM<br>Antigen<br>bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t% (min) | mAb<br>capture<br>level (RU) | 100nM<br>antigen<br>bound (RU) | ka (1/Ms) | kd (1/s) | KD (M) | t% (min) | ka             | kd | KD |
| 669999H4H5 | H105        | 87                           | 8                              | 5.04E+04  | 1.18E-03 | 2.34E-08 | 10       | 78                           | -5                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        | 72                           | 7                              | 1.04E+05  | 6.40E-04 | 6.17E-09 | 18       | 66                           | -7                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H108        | 77                           | 6                              | 3.47E+04  | 1.47E-03 | 4.23E-08 | 8        | 72                           | -8                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        | 77                           | 6                              | 1.39E+05  | 4.59E-03 | 3.31E-08 | 3        | 71                           | -8                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H105        | 85                           | 8                              | 9.95E+04  | 3.69E-04 | 3.71E-09 | 31       | 77                           | -6                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H108        | 71                           | 6                              | 2.60E+03  | 8.63E-04 | 3.32E-07 | 13       | 63                           | -7                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        | 51                           | 3                              | 9.81E+03  | 7.03E-03 | 7.16E-07 | 2        | 47                           | -10                            | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        | 80                           | 6                              | 4.81E+04  | 4.78E-04 | 9.94E-09 | 24       | 71                           | -10                            | NB        | NB       | NB     | NB       |                |    |    |
|            | H108        | 91                           | 9                              | 3.28E+04  | 6.44E-04 | 1.96E-08 | 18       | 85                           | -6                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        | 70                           | 6                              | 3.98E+04  | 2.01E-03 | 5.05E-08 | 6        | 65                           | -9                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H105        | 79                           | 5                              | 4.95E+04  | 5.53E-04 | 1.12E-08 | 21       | 74                           | -10                            | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H108        | 74                           | 8                              | 1.92E+04  | 4.59E-04 | 2.39E-08 | 25       | 68                           | -6                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H105        | 56                           | 4                              | 1.03E+03  | 4.18E-03 | 4.04E-06 | 3        | 52                           | -10                            | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H108        | 74                           | 5                              | 8.96E+03  | 1.66E-03 | 1.86E-07 | 7        | 66                           | -9                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H105        | 79                           | 7                              | 1.73E+04  | 9.49E-04 | 5.50E-08 | 12       | 75                           | -9                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H106        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | H108        | 110                          | 10                             | 5.01E+05  | 4.02E-03 | 8.02E-09 | 3        | 100                          | -5                             | NB        | NB       | NB     | NB       |                |    |    |
|            | H111        |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |
|            | 1-39<br>ULC |                              |                                |           |          |          |          |                              |                                |           |          |        |          |                |    |    |

FIG. 19I

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| HC      | Vk mut   | Kinetics at pH 7.2     |                          |           |          |          |          | Kinetics at pH 5.75    |                          |           |          |          |          | low/neutral pH |     |     |
|---------|----------|------------------------|--------------------------|-----------|----------|----------|----------|------------------------|--------------------------|-----------|----------|----------|----------|----------------|-----|-----|
|         |          | mAb capture level (RU) | 100nM Antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t½ (min) | mAb capture level (RU) | 100nM antigen bound (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t½ (min) | ka             | kd  | KD  |
| H4H6011 | H105     | 150                    | 22                       | 1.15E+05  | 3.17E-04 | 2.77E-09 | 36       | 147                    | 6                        | 7.61E+04  | 1.00E-06 | 1.31E-11 | 11550    | 0.7            | 0.0 | 0.0 |
|         | H106     | 127                    | 17                       | 8.73E+04  | 3.46E-04 | 3.96E-09 | 33       | 119                    | 2                        | 4.89E+04  | 1.00E-06 | 2.05E-11 | 11550    | 0.6            | 0.0 | 0.0 |
|         | H108     | 124                    | 15                       | 7.56E+04  | 5.90E-04 | 7.80E-09 | 20       | 112                    | -4                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111     | 135                    | 17                       | 1.08E+05  | 5.59E-04 | 5.19E-09 | 21       | 128                    | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 130                    | 18                       | 1.03E+05  | 3.91E-04 | 3.81E-09 | 30       | 123                    | 3                        | 1.89E+05  | 2.33E-04 | 1.23E-09 | 49       | 1.8            | 0.6 | 0.3 |
|         | H106     | 117                    | 16                       | 9.29E+04  | 5.24E-04 | 5.64E-09 | 22       | 110                    | -2                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108     | 109                    | 16                       | 1.06E+05  | 4.39E-04 | 4.15E-09 | 26       | 105                    | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 111                    | 16                       | 1.06E+05  | 4.39E-04 | 4.15E-09 | 26       | 105                    | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     | 105                    | 8                        | 6.95E+04  | 4.86E-04 | 7.00E-09 | 24       | 100                    | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108     | 171                    | 16                       | 3.07E+05  | 1.44E-03 | 4.69E-09 | 8        | 163                    | 0                        | NB        | NB       | NB       | NB       |                |     |     |
|         | H111     | 133                    | 16                       | 9.17E+04  | 6.20E-04 | 6.76E-09 | 19       | 126                    | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 135                    | 10                       | 6.11E+04  | 6.93E-04 | 1.13E-08 | 17       | 132                    | -8                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     | 117                    | 12                       | 6.52E+04  | 8.99E-04 | 1.38E-08 | 13       | 111                    | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H108     | 129                    | 16                       | 9.95E+04  | 5.82E-04 | 5.85E-09 | 20       | 121                    | -3                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H111     | 124                    | 11                       | 2.36E+04  | 8.53E-04 | 3.62E-08 | 14       | 118                    | -6                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H105     | 144                    | 14                       | 3.65E+04  | 9.51E-04 | 2.60E-08 | 12       | 140                    | -6                       | NB        | NB       | NB       | NB       |                |     |     |
|         | H106     | 198                    | 25                       | 1.13E+05  | 4.36E-04 | 3.85E-09 | 27       | 181                    | 6                        | 6.02E+04  | 2.02E-04 | 3.36E-09 | 57       | 0.5            | 0.5 | 0.9 |
|         | 1-39 ULC | 2                      | 1                        | NB        | NB       | NB       | NB       | -2                     | -11                      | NB        | NB       | NB       | NB       |                |     |     |
|         | Buffer   | 3                      | 1                        | NB        | NB       | NB       | NB       | 0                      | -10                      | NB        | NB       | NB       | NB       |                |     |     |

FIG. 19J

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| Heavy Chain | Light Chain Mutant | Kinetics at pH 7.4 |                           |           |          |          |                        | Kinetics at pH 5.75 |                           |           |          |          |                        | Ratio of low pH / neutral pH |     |     |
|-------------|--------------------|--------------------|---------------------------|-----------|----------|----------|------------------------|---------------------|---------------------------|-----------|----------|----------|------------------------|------------------------------|-----|-----|
|             |                    | mAb captured (RU)  | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | mAb captured (RU)   | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | ka                           | kd  | KD  |
| 1           | H105               | 488                | 47.2                      | 3.52E+05  | 9.30E-03 | 2.64E-08 | 1.2                    | 378                 | 37.8                      | 4.24E+05  | 1.38E-02 | 3.24E-08 | 0.8                    | 1.2                          | 1.5 | 1.2 |
|             | H106               | 620                | 73.7                      | 3.22E+05  | 3.67E-03 | 1.14E-08 | 3.1                    | 505                 | 65.4                      | 3.66E+05  | 4.86E-03 | 1.33E-08 | 2.4                    | 1.1                          | 1.3 | 1.2 |
|             | H108               | 648                | 99.0                      | 3.17E+05  | 2.07E-03 | 6.54E-09 | 5.6                    | 496                 | 80.7                      | 3.59E+05  | 3.02E-03 | 8.41E-09 | 3.8                    | 1.1                          | 1.5 | 1.3 |
|             | H111               | 669                | 81.0                      | 3.01E+05  | 3.81E-03 | 1.27E-08 | 3.0                    | 536                 | 62.8                      | 3.32E+05  | 5.41E-03 | 1.63E-08 | 2.1                    | 1.1                          | 1.4 | 1.3 |
|             | H105/106           | 492                | 55.6                      | 3.74E+05  | 6.44E-03 | 1.72E-08 | 1.8                    | 404                 | 45.7                      | 4.30E+05  | 1.01E-02 | 2.34E-08 | 1.1                    | 1.2                          | 1.6 | 1.4 |
|             | H105/108           | 538                | 75.2                      | 3.28E+05  | 4.17E-03 | 1.27E-08 | 2.8                    | 416                 | 56.3                      | 3.87E+05  | 7.43E-03 | 1.92E-08 | 1.6                    | 1.2                          | 1.8 | 1.5 |
|             | H105/111           | 501                | 44.6                      | 3.44E+05  | 9.77E-03 | 2.84E-08 | 1.2                    | 402                 | 31.9                      | 4.06E+05  | 1.70E-02 | 4.19E-08 | 0.7                    | 1.2                          | 1.7 | 1.5 |
|             | H106/108           | 494                | 64.9                      | 3.36E+05  | 4.14E-03 | 1.23E-08 | 2.8                    | 407                 | 43.0                      | 4.07E+05  | 1.17E-02 | 2.86E-08 | 1.0                    | 1.2                          | 2.8 | 2.3 |
|             | H106/111           | 536                | 78.2                      | 3.09E+05  | 3.10E-03 | 1.00E-08 | 3.7                    | 423                 | 61.4                      | 3.62E+05  | 4.68E-03 | 1.29E-08 | 2.5                    | 1.2                          | 1.5 | 1.3 |
|             | H108/111           | 584                | 78.5                      | 3.11E+05  | 3.80E-03 | 1.22E-08 | 3.0                    | 473                 | 59.0                      | 3.50E+05  | 6.13E-03 | 1.75E-08 | 1.9                    | 1.1                          | 1.6 | 1.4 |
|             | H105/106/108       | 442                | 51.2                      | 3.72E+05  | 6.38E-03 | 1.71E-08 | 1.8                    | 370                 | 28.4                      | 4.26E+05  | 2.13E-02 | 5.00E-08 | 0.5                    | 1.1                          | 3.3 | 2.9 |
|             | H105/106/111       | 473                | 62.8                      | 3.40E+05  | 4.55E-03 | 1.34E-08 | 2.5                    | 378                 | 47.6                      | 4.07E+05  | 7.42E-03 | 1.82E-08 | 1.6                    | 1.2                          | 1.6 | 1.4 |
|             | H105/108/111       | 433                | 49.5                      | 3.57E+05  | 7.42E-03 | 2.08E-08 | 1.6                    | 354                 | 31.3                      | 4.09E+05  | 1.73E-02 | 4.23E-08 | 0.7                    | 1.1                          | 2.3 | 2.0 |
|             | H106/108/111       | 491                | 66.6                      | 3.44E+05  | 3.82E-03 | 1.11E-08 | 3.0                    | 415                 | 43.3                      | 3.91E+05  | 1.06E-02 | 2.72E-08 | 1.1                    | 1.1                          | 2.8 | 2.5 |
|             | H105/106/108/111   | 454                | 57.9                      | 3.51E+05  | 5.77E-03 | 1.64E-08 | 2.0                    | 368                 | 36.8                      | 4.06E+05  | 1.35E-02 | 3.32E-08 | 0.9                    | 1.2                          | 2.3 | 2.0 |
|             | ULC + Heavy        | 586                | 76.0                      | 3.16E+05  | 3.85E-03 | 1.22E-08 | 3.0                    | 483                 | 66.5                      | 3.45E+05  | 4.58E-03 | 1.33E-08 | 2.5                    | 1.1                          | 1.2 | 1.1 |
| Heavy only  |                    | 141                | -1.3                      | NB        | NB       | NB       | NB                     | 107                 | -6.7                      | NB        | NB       | NB       | NB                     | Negative Control             |     |     |
| No DNA      |                    | 60                 | -1.5                      | NB        | NB       | NB       | NB                     | 26                  | -7.2                      | NB        | NB       | NB       | NB                     |                              |     |     |

FIG. 20A

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| Heavy Chain | Light Chain Mutant | Kinetics at pH 7.4 |                           |           |          |          |                        | Kinetics at pH 5.75 |                           |           |          |          |                        | Ratio of low pH / neutral pH   |      |       |
|-------------|--------------------|--------------------|---------------------------|-----------|----------|----------|------------------------|---------------------|---------------------------|-----------|----------|----------|------------------------|--------------------------------|------|-------|
|             |                    | mAb capture d (RU) | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | mAb capture d (RU)  | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | ka                             | kd   | KD    |
|             | H105               | 720                | 33.7                      | 1.02E+05  | 9.10E-04 | 8.89E-09 | 12.7                   | 595                 | 0.3                       | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H106               | 735                | 32.9                      | 9.11E+04  | 4.47E-04 | 4.91E-09 | 25.8                   | 623                 | 4.3                       | 2.27E+04  | 6.41E-03 | 2.82E-07 | 1.8                    | 0.2                            | 14.3 | 57.4  |
|             | H108               | 728                | 32.2                      | 8.48E+04  | 2.67E-04 | 3.14E-09 | 43.3                   | 598                 | 3.6                       | 1.16E+03  | 3.41E-03 | 2.93E-06 | 3.4                    | 0.0                            | 12.8 | 933.1 |
|             | H111               | 802                | 42.4                      | 1.17E+05  | 1.15E-04 | 9.88E-10 | 100.3                  | 670                 | 14.1                      | 3.01E+04  | 7.08E-04 | 2.35E-08 | 16.3                   | 0.3                            | 6.1  | 23.8  |
|             | H105/106           | 570                | 24.9                      | 8.51E+04  | 2.92E-04 | 3.43E-09 | 39.5                   | 484                 | 2.4                       | 1.14E+04  | 6.47E-03 | 5.69E-07 | 1.8                    | 0.1                            | 22.1 | 165.9 |
|             | H105/108           | 723                | 28.4                      | 8.73E+04  | 1.30E-03 | 1.49E-08 | 8.9                    | 603                 | -2.6                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H105/111           | 627                | 28.5                      | 8.82E+04  | 3.60E-04 | 4.08E-09 | 32.1                   | 519                 | 2.3                       | 1.02E+04  | 1.30E-02 | 1.27E-06 | 0.9                    | 0.1                            | 36.2 | 311.3 |
|             | H106/108           | 550                | 21.1                      | 6.75E+04  | 9.12E-04 | 1.35E-08 | 12.7                   | 470                 | -1.9                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H106/111           | 808                | 32.7                      | 9.01E+04  | 6.78E-04 | 7.52E-09 | 17.0                   | 678                 | 0.9                       | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H108/111           | 801                | 40.5                      | 1.17E+05  | 9.80E-05 | 8.40E-10 | 117.8                  | 676                 | 10.6                      | 1.87E+04  | 5.84E-04 | 3.12E-08 | 19.8                   | 0.2                            | 6.0  | 37.1  |
|             | H105/106/108       | 409                | 13.0                      | 8.21E+04  | 4.29E-04 | 5.22E-09 | 26.9                   | 345                 | -4.4                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H105/106/111       | 767                | 9.3                       | 4.84E+04  | 1.25E-03 | 2.58E-08 | 9.3                    | 645                 | -6.1                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H105/108/111       | 578                | 24.5                      | 8.99E+04  | 2.87E-04 | 3.19E-09 | 40.2                   | 479                 | -0.7                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H106/108/111       | 765                | 15.1                      | 5.04E+04  | 1.65E-03 | 3.27E-08 | 7.0                    | 661                 | -5.9                      | NB        | NB       | NB       | NB                     | No binding at Low pH           |      |       |
|             | H105/106/108/111   | 723                | 0.3                       | NB        | NB       | NB       | NB                     | 611                 | -7.0                      | NB        | NB       | NB       | NB                     | No binding at either pH tested |      |       |
|             | ULC + Heavy only   | 781                | 39.8                      | 1.13E+05  | 1.78E-04 | 1.57E-09 | 64.9                   | 665                 | 11.7                      | 2.04E+04  | 1.22E-03 | 6.00E-08 | 9.4                    | 0.2                            | 6.9  | 38.2  |
|             | No DNA             | 63                 | -2.1                      | NB        | NB       | NB       | NB                     | 35                  | -6.4                      | NB        | NB       | NB       | NB                     | Negative Control               |      |       |

FIG. 20B

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| Heavy Chain | Light Chain Mutant | Kinetics at pH 7.4 |                           |           |          |          |                        | Kinetics at pH 5.75 |                           |           |          |          |                        | Ratio of low pH / neutral pH                  |            |        |
|-------------|--------------------|--------------------|---------------------------|-----------|----------|----------|------------------------|---------------------|---------------------------|-----------|----------|----------|------------------------|-----------------------------------------------|------------|--------|
|             |                    | mAb captured (RU)  | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | mAb captured (RU)   | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | ka                                            | kd         | KD     |
| 3           | H105               | 574                | 12.4                      | 5.64E+04  | 1.21E-03 | 2.15E-08 | 9.5                    | 496                 | 0.1                       | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H106               | 662                | 16.1                      | 7.37E+04  | 5.36E-04 | 7.27E-09 | 21.5                   | 584                 | 3.0                       | 3.00E+04  | 4.79E-03 | 1.58E-07 | 2.4                    | 0.4                                           | 8.9        | 21.7   |
|             | H108               | 518                | 12.3                      | 4.82E+04  | 2.15E-04 | 4.46E-09 | 53.7                   | 440                 | 2.2                       | 3.70E+04  | 1.25E-03 | 3.40E-08 | 9.3                    | 0.8                                           | 5.8        | 7.6    |
|             | H111               | 480                | 9.1                       | 1.82E+04  | 4.16E-04 | 2.28E-08 | 27.7                   | 406                 | 0.4                       | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H105/106           | 487                | 7.4                       | 1.82E+04  | 7.45E-03 | 4.10E-07 | 1.6                    | 423                 | -4.1                      | NB        | NB       | NB       | NB                     | Poor binding at Neutral, No binding at Low pH | No binding | Low pH |
|             | H105/108           | 548                | 11.8                      | 3.25E+04  | 5.25E-04 | 1.62E-08 | 22.0                   | 468                 | 0.0                       | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H105/111           | 504                | 7.9                       | 1.06E+04  | 1.66E-03 | 1.57E-07 | 7.0                    | 430                 | -1.6                      | NB        | NB       | NB       | NB                     | Poor binding at Neutral, No binding at Low pH | No binding | Low pH |
|             | H106/108           | 487                | 10.7                      | 6.64E+04  | 2.91E-04 | 4.38E-09 | 39.7                   | 424                 | -4.2                      | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H106/111           | 563                | 10.5                      | 2.75E+04  | 3.71E-04 | 1.35E-08 | 31.2                   | 482                 | -1.9                      | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H108/111           | 528                | 10.1                      | 1.10E+04  | 8.01E-05 | 7.27E-09 | 144.2                  | 449                 | -0.5                      | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H105/106/108       | 470                | 6.4                       | 2.64E+04  | 5.40E-03 | 2.04E-07 | 2.1                    | 412                 | -5.3                      | NB        | NB       | NB       | NB                     | Poor binding at Neutral, No binding at Low pH | No binding | Low pH |
|             | H105/106/111       | 539                | 0.8                       | NB        | NB       | NB       | NB                     | 462                 | -5.6                      | NB        | NB       | NB       | NB                     | No binding at either pH tested                | No binding | Low pH |
|             | H105/108/111       | 419                | 6.5                       | 1.76E+04  | 4.01E-04 | 2.27E-08 | 28.8                   | 354                 | -3.8                      | NB        | NB       | NB       | NB                     | No binding                                    | No binding | Low pH |
|             | H106/108/111       | 509                | 3.3                       | 5.47E+04  | 9.07E-04 | 1.66E-08 | 12.7                   | 443                 | -5.9                      | NB        | NB       | NB       | NB                     | Poor binding at Neutral, No binding at Low pH | No binding | Low pH |
|             | H105/106/108/111   | 450                | -1.1                      | NB        | NB       | NB       | NB                     | 382                 | -6.4                      | NB        | NB       | NB       | NB                     | No binding at either pH tested                | No binding | Low pH |
|             | ULC + Heavy        | 688                | 16.9                      | 3.54E+04  | 3.57E-04 | 1.01E-08 | 32.3                   | 598                 | 5.0                       | 1.16E+04  | 1.76E-03 | 1.52E-07 | 6.6                    | 0.3                                           | 4.9        | 15.0   |
|             | Heavy only         | 152                | -1.6                      | NB        | NB       | NB       | NB                     | 127                 | -5.4                      | NB        | NB       | NB       | NB                     | Negative Control                              |            |        |
|             | No DNA             | 54                 | -1.7                      | NB        | NB       | NB       | NB                     | 30                  | -5.6                      | NB        | NB       | NB       | NB                     |                                               |            |        |

FIG. 20C

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| Heavy Chain | Light Chain Mutant | Kinetics at pH 7.4 |                           |           |          |          |                        | Kinetics at pH 5.75 |                           |           |          |        |                        | Ratio of low pH / neutral pH                  |    |    |
|-------------|--------------------|--------------------|---------------------------|-----------|----------|----------|------------------------|---------------------|---------------------------|-----------|----------|--------|------------------------|-----------------------------------------------|----|----|
|             |                    | mAb captured (RU)  | 50nM Antigen Binding (RU) | ka (1/MS) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | mAb captured (RU)   | 50nM Antigen Binding (RU) | ka (1/MS) | kd (1/s) | KD (M) | t <sub>1/2</sub> (min) | ka                                            | kd | KD |
| 4           | H105               | 598                | 4.9                       | 2.80E+04  | 1.38E-03 | 4.91E-08 | 8.4                    | 512                 | -0.2                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H106               | 569                | 7.1                       | 1.49E+04  | 9.67E-04 | 6.49E-08 | 11.9                   | 494                 | 1.2                       | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H108               | 587                | 6.3                       | 2.25E+04  | 2.02E-03 | 8.96E-08 | 5.7                    | 500                 | -0.9                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H111               | 606                | 5.6                       | 3.46E+04  | 2.19E-03 | 6.33E-08 | 5.3                    | 521                 | -0.9                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/106           | 517                | 3.1                       | 2.00E+04  | 2.05E-03 | 1.03E-07 | 5.6                    | 460                 | -1.1                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/108           | 581                | 2.5                       | 1.61E+05  | 2.30E-03 | 1.43E-08 | 5.0                    | 506                 | -2.7                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/111           | 575                | 3.8                       | 1.01E+04  | 1.70E-03 | 1.68E-07 | 6.8                    | 504                 | -2.0                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H106/108           | 498                | 2.5                       | 4.01E+04  | 6.07E-04 | 1.51E-08 | 19.0                   | 447                 | -3.9                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H106/111           | 587                | 3.0                       | 7.85E+04  | 9.20E-04 | 1.17E-08 | 12.6                   | 509                 | -2.6                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H108/111           | 599                | 4.0                       | 9.68E+04  | 2.02E-03 | 2.09E-08 | 5.7                    | 528                 | -2.6                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/106/108       | 64                 | -1.7                      | NB        | NB       | NB       | NB                     | 46                  | -5.4                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/106/111       | 561                | 1.1                       | NB        | NB       | NB       | NB                     | 493                 | -2.8                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/108/111       | 521                | 2.7                       | 7.66E+04  | 1.29E-03 | 1.68E-08 | 9.0                    | 461                 | -3.2                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H106/108/111       | 577                | 1.3                       | NB        | NB       | NB       | NB                     | 514                 | -4.2                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/106/108/111   | 554                | 0.6                       | NB        | NB       | NB       | NB                     | 495                 | -4.8                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | ULC + Heavy        | 585                | 7.4                       | 5.69E+04  | 2.01E-03 | 3.53E-08 | 5.7                    | 527                 | 1.9                       | NB        | NB       | NB     | NB                     | No binding at Low pH                          |    |    |
|             | Heavy only         | 187                | -2.4                      | NB        | NB       | NB       | NB                     | 161                 | -5.4                      | NB        | NB       | NB     | NB                     | No binding at Low pH                          |    |    |
|             | No DNA             | 49                 | -2.6                      | NB        | NB       | NB       | NB                     | 25                  | -5.6                      | NB        | NB       | NB     | NB                     | Negative Control                              |    |    |

FIG. 20D

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| Heavy Chain | Light Chain Mutant | Kinetics at pH 7.4 |                           |           |          |          |                        | Kinetics at pH 5.75 |                           |           |          |        |                        | Ratio of low pH / neutral pH                  |    |    |
|-------------|--------------------|--------------------|---------------------------|-----------|----------|----------|------------------------|---------------------|---------------------------|-----------|----------|--------|------------------------|-----------------------------------------------|----|----|
|             |                    | mAb captured (RU)  | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M)   | t <sub>1/2</sub> (min) | mAb captured (RU)   | 50nM Antigen Binding (RU) | ka (1/Ms) | kd (1/s) | KD (M) | t <sub>1/2</sub> (min) | ka                                            | kd | KD |
| 5           | H105               | 522                | 3.2                       | 5.05E+04  | 9.48E-03 | 1.88E-07 | 1.2                    | 463                 | -4.3                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H106               | 496                | 0.3                       | NB        | NB       | NB       | NB                     | 437                 | -5.2                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H108               | 475                | -0.1                      | NB        | NB       | NB       | NB                     | 415                 | -5.7                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H111               | 523                | 1.6                       | NB        | NB       | NB       | NB                     | 463                 | -4.7                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/106           | 534                | -0.6                      | NB        | NB       | NB       | NB                     | 472                 | -5.5                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/108           | 499                | 2.0                       | 5.80E+04  | 1.16E-02 | 1.99E-07 | 1.0                    | 433                 | -5.5                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/111           | 489                | 0.1                       | NB        | NB       | NB       | NB                     | 426                 | -4.7                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H106/108           | 441                | -0.5                      | NB        | NB       | NB       | NB                     | 386                 | -4.2                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H106/111           | 529                | -0.8                      | NB        | NB       | NB       | NB                     | 461                 | -6.3                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H108/111           | 495                | 4.1                       | 1.73E+05  | 1.06E-02 | 6.11E-08 | 1.1                    | 435                 | -4.0                      | NB        | NB       | NB     | NB                     | Poor binding at Neutral, No binding at Low pH |    |    |
|             | H105/106/108       | 505                | -1.1                      | NB        | NB       | NB       | NB                     | 444                 | -5.5                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/106/111       | 499                | -1.7                      | NB        | NB       | NB       | NB                     | 438                 | -5.8                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/108/111       | 436                | 0.8                       | NB        | NB       | NB       | NB                     | 388                 | -3.7                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H106/108/111       | 539                | -1.4                      | NB        | NB       | NB       | NB                     | 477                 | -4.0                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | H105/106/108/111   | 556                | -1.6                      | NB        | NB       | NB       | NB                     | 490                 | -4.4                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | ULC + Heavy        | 516                | 0.6                       | NB        | NB       | NB       | NB                     | 451                 | -5.0                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | Heavy only         | 144                | -1.3                      | NB        | NB       | NB       | NB                     | 122                 | -5.7                      | NB        | NB       | NB     | NB                     | No binding at either pH tested                |    |    |
|             | No DNA             | 47                 | -1.4                      | NB        | NB       | NB       | NB                     | 25                  | -5.8                      | NB        | NB       | NB     | NB                     | Negative Control                              |    |    |

FIG. 20E

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| $V_H$ | $V_K$                 | $K_D$ at pH7.4<br>(nM) | $K_D$ at pH5.75<br>(nM) | $T_{1/2}$ at pH7.4<br>(min) | $T_{1/2}$ at pH5.75<br>(min) |
|-------|-----------------------|------------------------|-------------------------|-----------------------------|------------------------------|
| 2     | Parental ULC          | 1.6                    | 60                      | 65                          | 9.4                          |
| 2     | ULC (His105,106)      | 3.4                    | 570                     | 39                          | 1.8                          |
| 2     | ULC (His105,111)      | 4.1                    | 1270                    | 32                          | 0.9                          |
| 2     | ULC (His105,108,111)  | 3.2                    | NB                      | 40                          | NB                           |
| 2     | ULC (His105,106,108)  | 5.2                    | NB                      | 27                          | NB                           |
| 3     | Parental ULC          | 10.1                   | 152                     | 32                          | 6.6                          |
| 3     | ULC (His106,108)      | 4.4                    | NB                      | 40                          | NB                           |
| 3     | ULC (His108,111)      | 7.3                    | NB                      | 144                         | NB                           |
| 6     | Parental ULC          | 3.0                    | 2.4                     | 10                          | 6                            |
| 6     | ULC (His105,111)      | 3.5                    | NB                      | 9                           | NB                           |
| 6     | ULC (His106, 108,111) | 2.0                    | NB                      | 16                          | NB                           |

FIG. 21

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of Universal Light Chain of hVK1-39JK5

| Primer name             | Sequence                                                                               | %GC  | N  | %mismatch | Tm   |
|-------------------------|----------------------------------------------------------------------------------------|------|----|-----------|------|
| GERMLINE hVH1-39/JK5    | CAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGC                                     |      |    |           |      |
| 1633-H106/108/111 F     | CCTTACTACTGTCAACATAGT <b>C</b> ACAGTACCC <b>A</b> TCCGATCACCTTCG                       | 47.0 | 45 | 6.7       | 79.0 |
| 1633-H105/106/108/111 F | CAACTTACTACTGTCA <b>C</b> CA <b>T</b> AGT <b>C</b> ACAGTACCC <b>A</b> TCCGATCACCTTCGGC | 50.0 | 50 | 8.0       | 80.5 |
| 1633-H106/108/111 R     | CGAAGGTGATCGGA <b>T</b> GGGTACTGT <b>G</b> ACT <b>A</b> TATGTTGACAGTAGTAAG             | 47.0 | 45 | 6.7       | 79.0 |
| 1633-H105/106/108/111 R | GCCGAAGGTGATCGGA <b>T</b> GGGTACTGT <b>G</b> ACT <b>A</b> TATGTTGACAGTAGTAAGTTG        | 50.0 | 50 | 8.0       | 80.5 |

| Primer                  | SEQ ID NO |
|-------------------------|-----------|
| GERMLINE hVK1-39/JK5    | 405       |
| 1633-H106/108/111 F     | 358       |
| 1633-H105/106/108/111 F | 359       |
| 1633-H106/108/111 R     | 360       |
| 1633-H105/106/108/111 R | 361       |

FIG. 22

Construction of VK1-39 HULC LTVECs

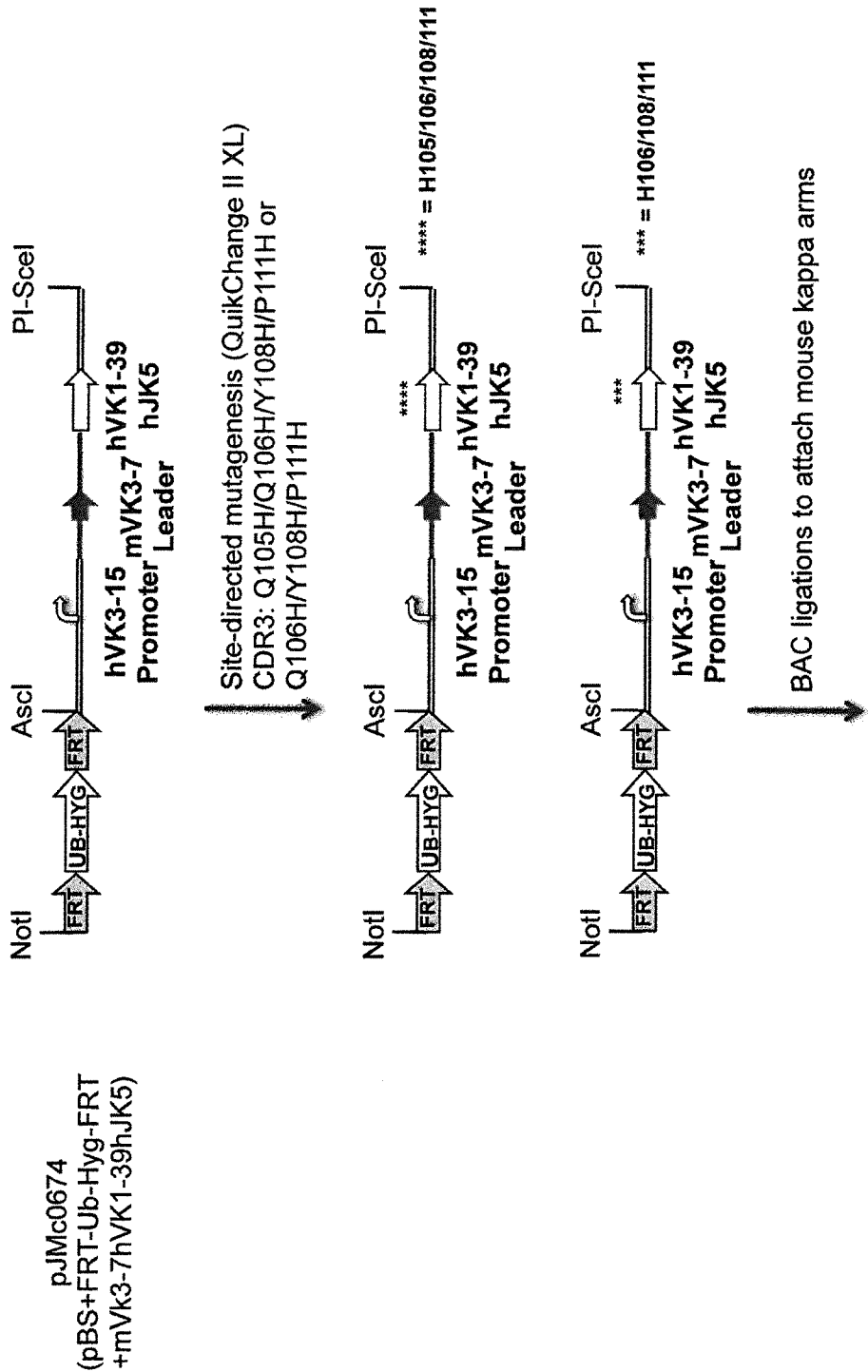
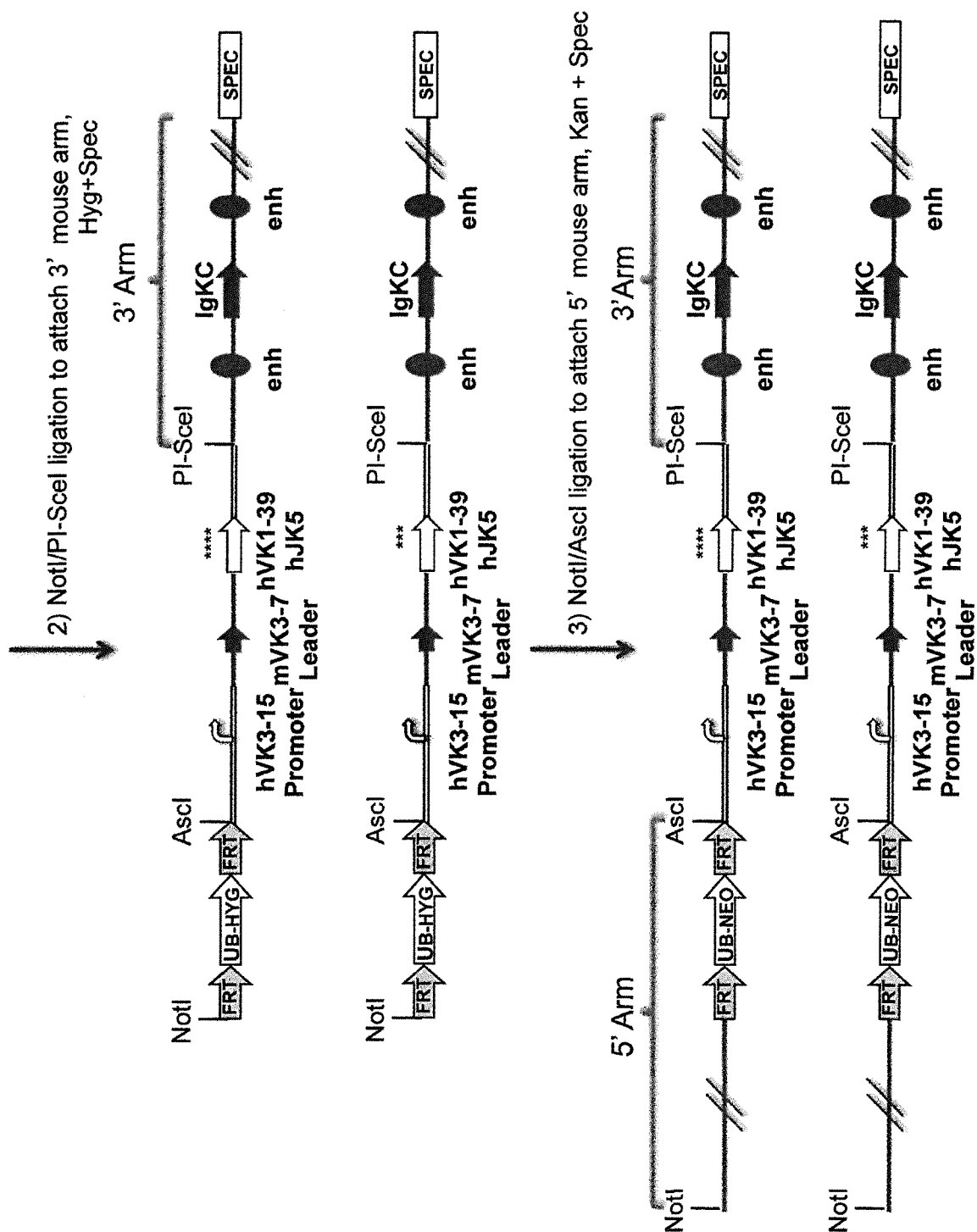


FIG. 23A

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(ULC-H105/106/108/111)

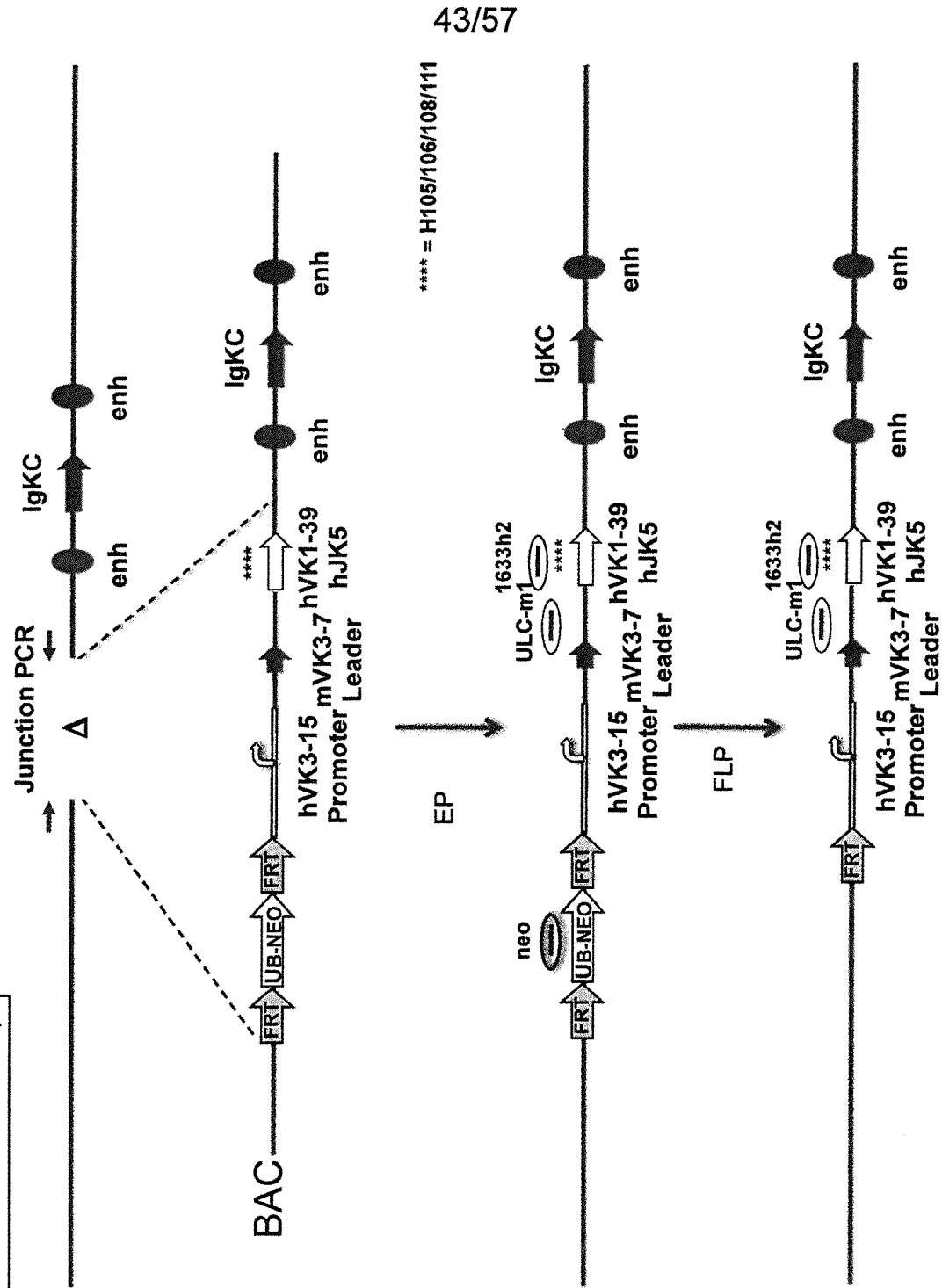
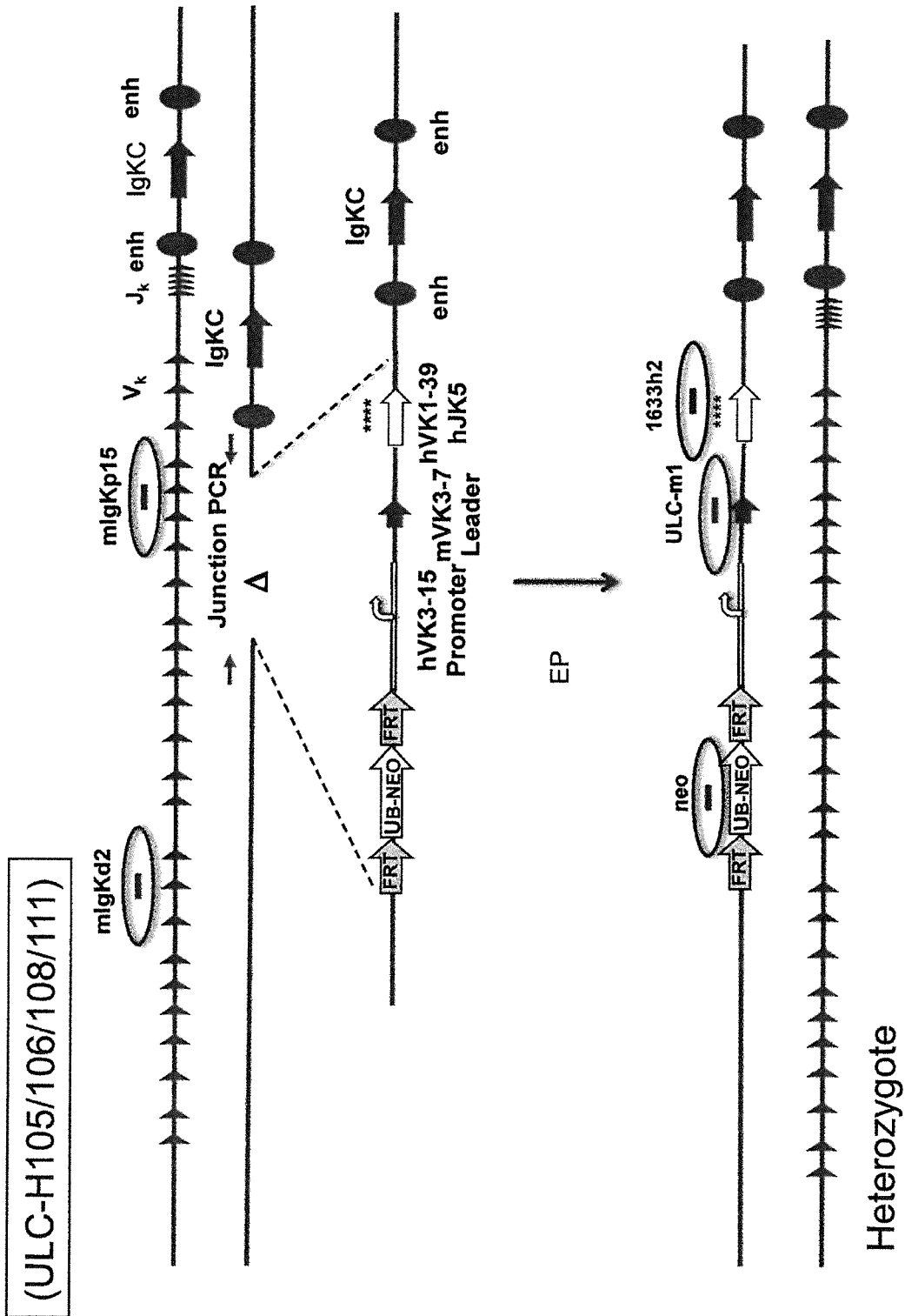


FIG. 23C



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(ULC-H106/108/111)

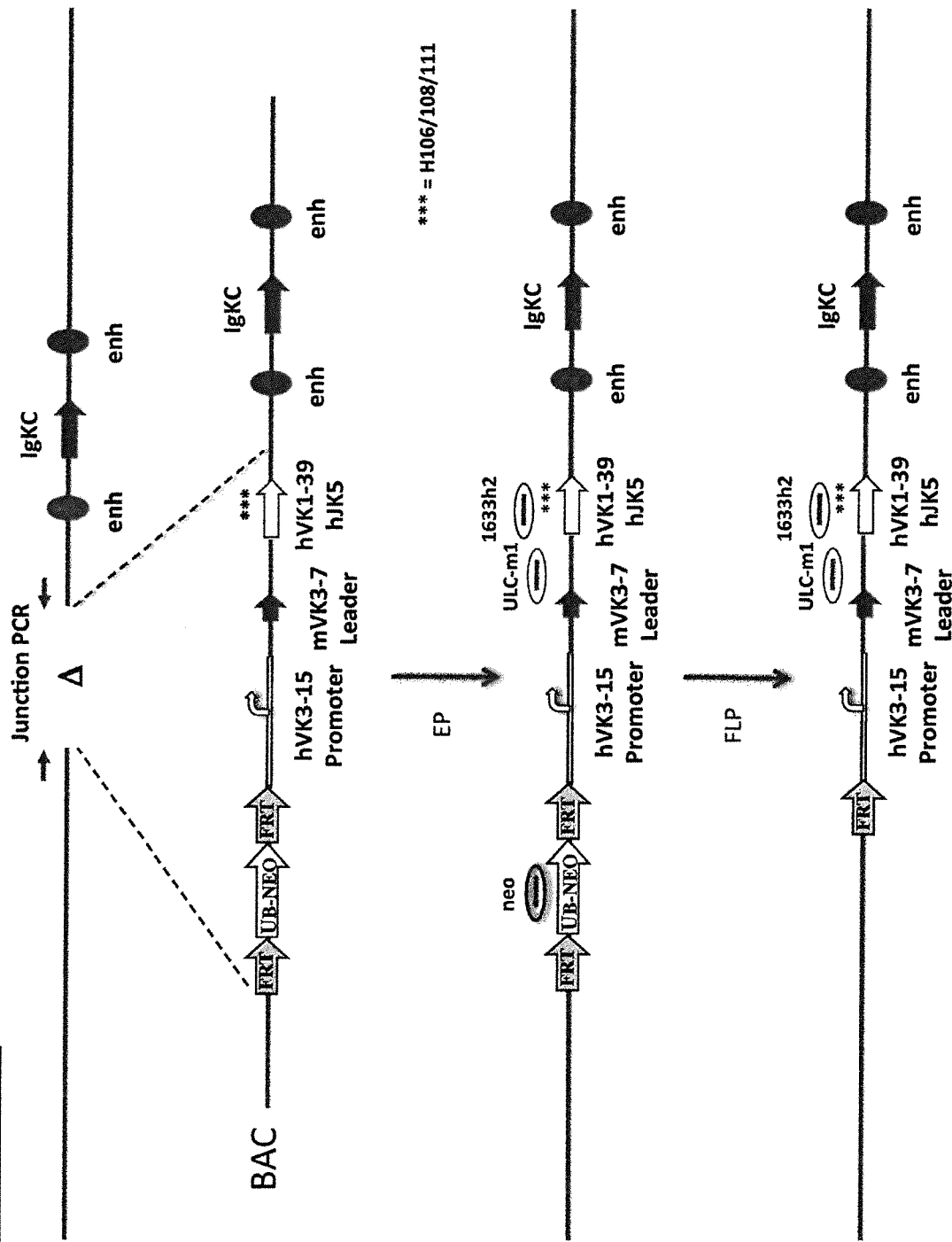


FIG. 23E

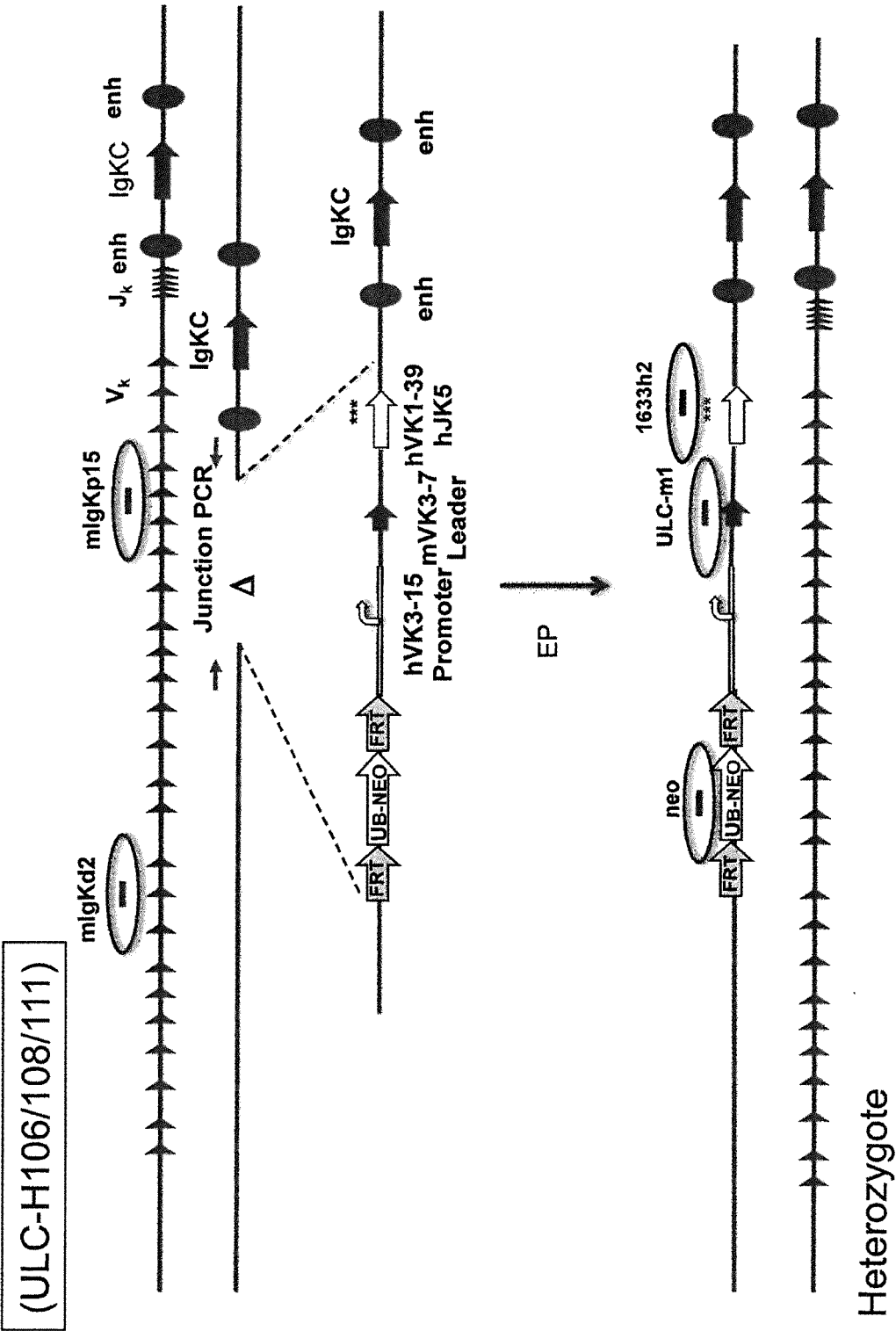


FIG. 23F

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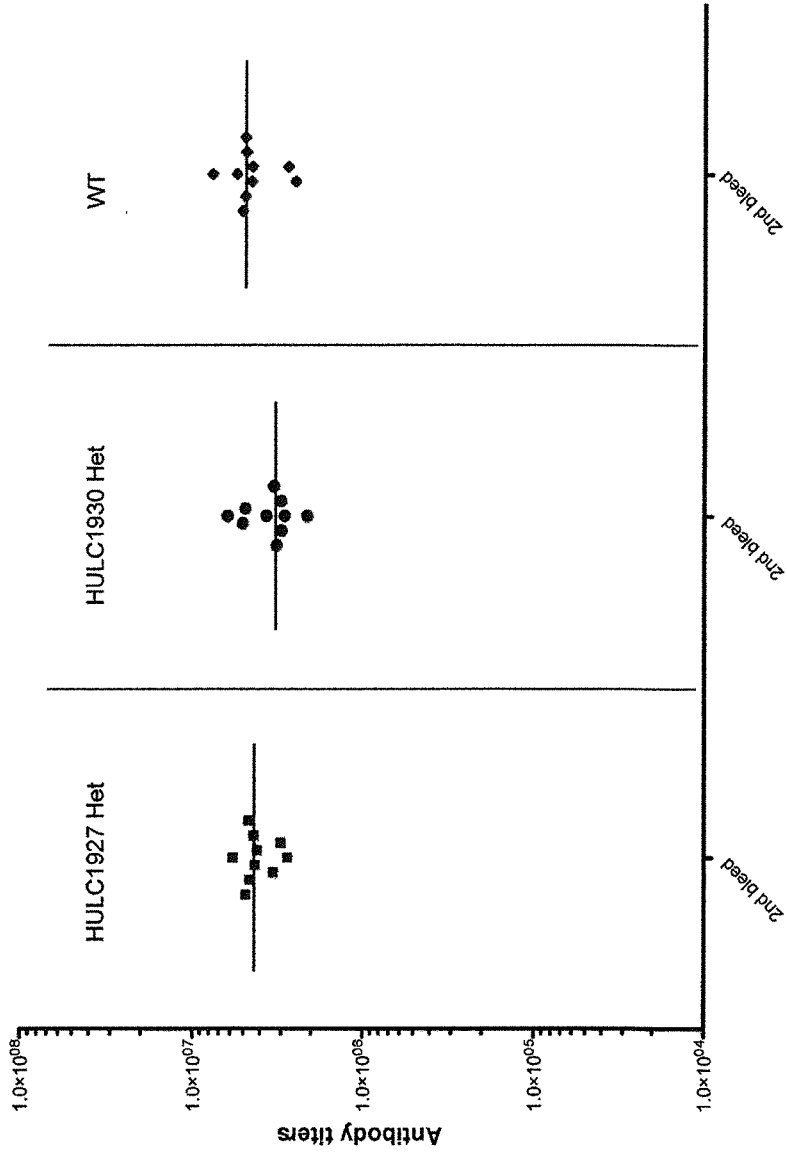


FIG. 24

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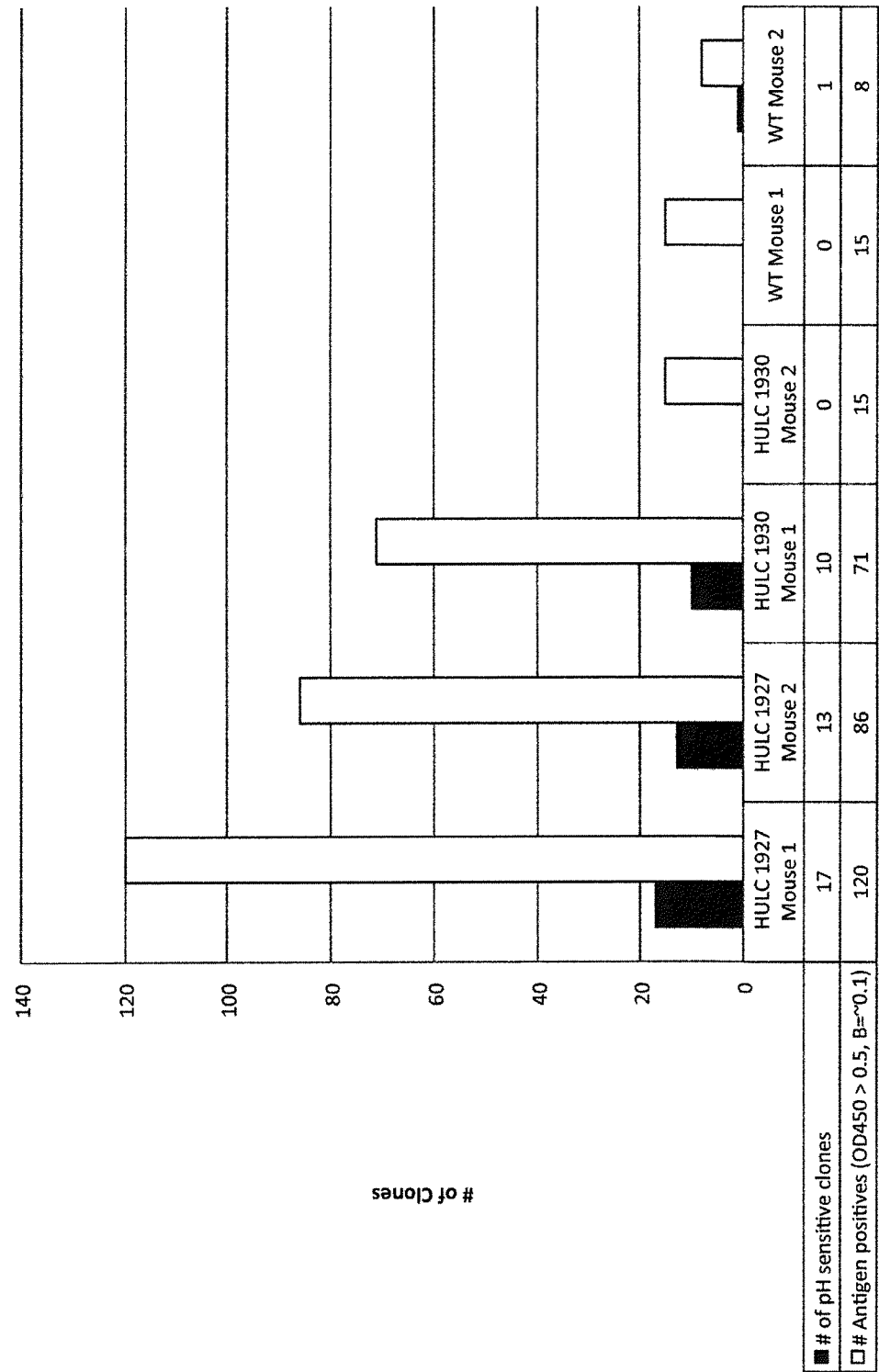


FIG. 25

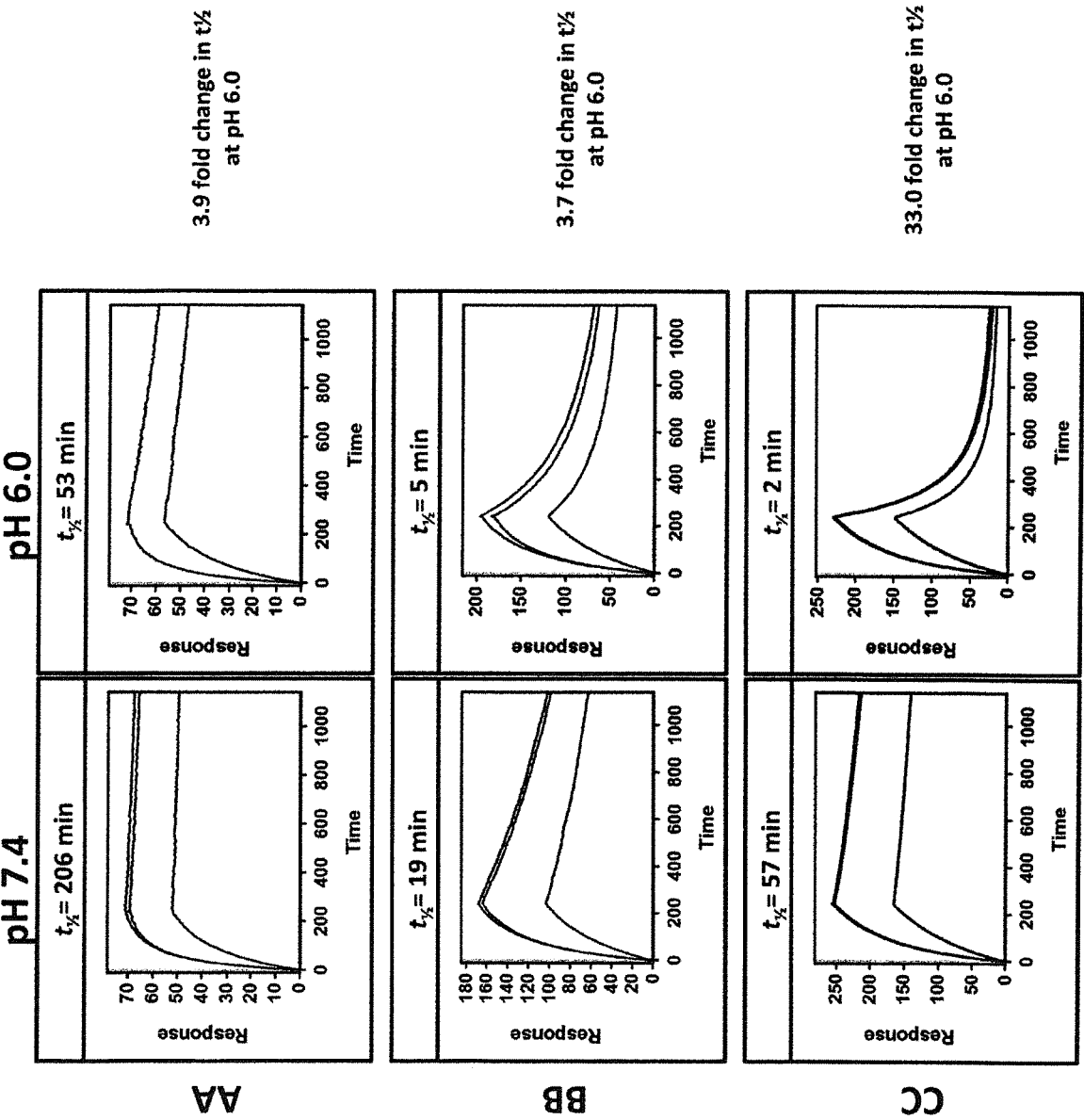


FIG. 26A

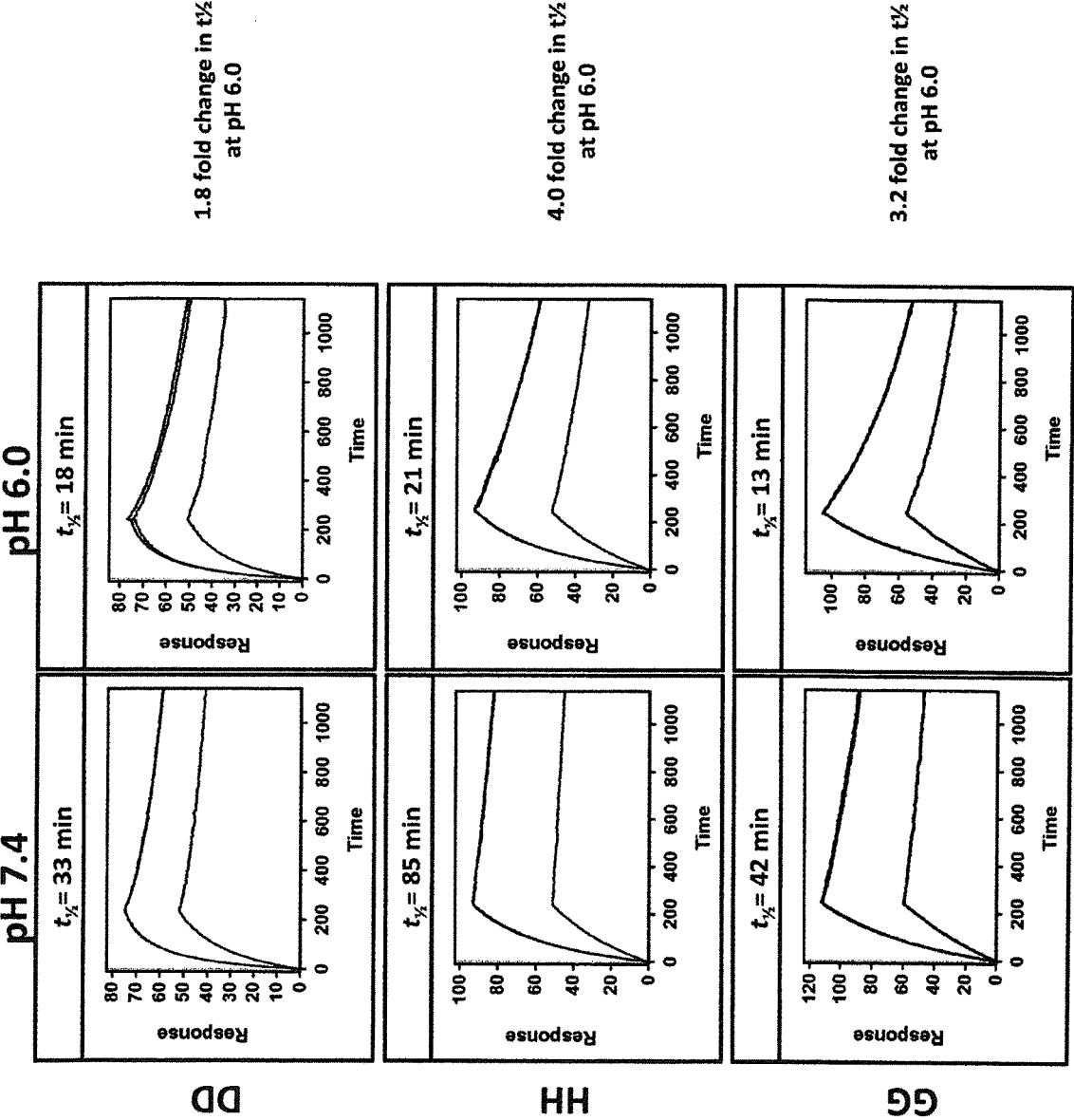


FIG. 26B

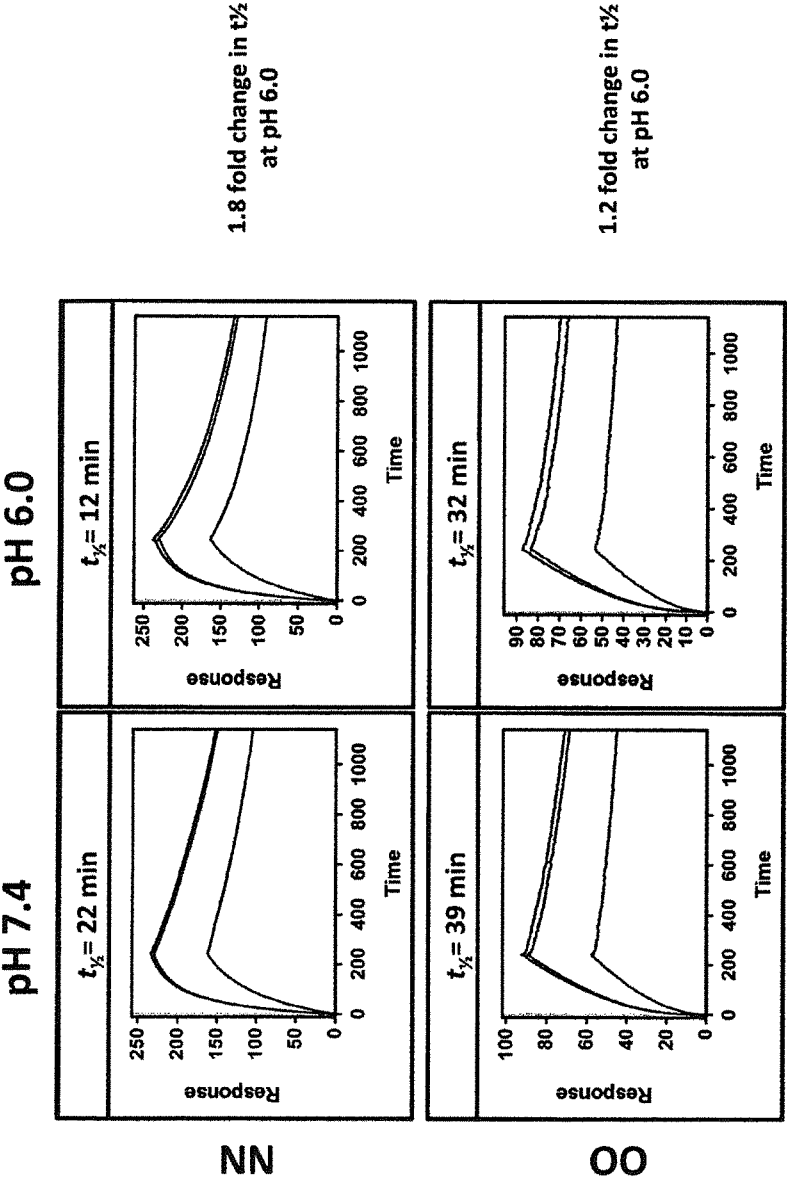


FIG. 26C

|                  |     |     |     |     |     |     |     |                |
|------------------|-----|-----|-----|-----|-----|-----|-----|----------------|
|                  | 105 | 106 | 107 | 108 | 109 | 110 | 111 |                |
| WT               | Q   | Q   | Y   | G   | S   | S   | P   | SEQ. ID NO:399 |
|                  | CAG | CAG | TAT | GGT | AGC | TCA | CCT | SEQ. ID NO:398 |
| H105/106/107/109 | H   | H   | H   | G   | H   | S   | P   | SEQ. ID NO:401 |
|                  | CAT | CAC | CAT | GGT | CAC | TCA | CCT | SEQ. ID NO:400 |
| H105/106/109     | H   | H   | Y   | G   | H   | S   | P   | SEQ. ID NO:403 |
|                  | CAT | CAC | TAT | GGT | CAC | TCA | CCT | SEQ. ID NO:402 |

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FIG. 27

Site-directed mutagenesis primers for Histidine substitutions in CDR3 of VK3-20JK1 ULC plasmid

| Primer name                  | Sequence                                               | %GC | N  | mismatches | Tm   |
|------------------------------|--------------------------------------------------------|-----|----|------------|------|
| GERMLINE hVK3-20             | GATTTTCAGTGTATTACTCTCAGCAGTATGGTAGCTCACCTTGGACGTTCCGGC |     |    |            |      |
| hVK3-20 (H105/106/107/109) F | GATTTTCAGTGTATTACTCTCAGCAGTATGGTAGCTCACCTTGGACGTTCCGGC | 48  | 54 | 5          | 79.5 |
| hVK3-20 (H105/106/107/109) R | GCCGAACGTCCAAAGTGAGTGACCATGGTGATGACAGTAATACACTGCAAAATC | 48  | 54 | 5          | 79.5 |
| hVK3-20 (H105/106/109) F     | GCAGTGTATTACTCTCAGTCACTATGGTCACTCACCTTGGACGTTCCGG      | 49  | 47 | 4          | 78.7 |
| hVK3-20 (H105/106/109) R     | CCGAACGTCCAAAGTGAGTGACCATAGTGATGACAGTAATACACTGC        | 49  | 47 | 4          | 79.7 |

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| Primer                     | SEQ ID NO |
|----------------------------|-----------|
| GERMLINE hVK3-20/JK1       | 384       |
| hVK3-20 H105/106/107/109 F | 385       |
| hVK3-20 H105/106/107/109 R | 386       |
| hVK3-20 H105/106/109 F     | 387       |
| hVK3-20 H105/106/109 R     | 388       |

FIG. 28

Construction of VK3-20 HULC LTVECs

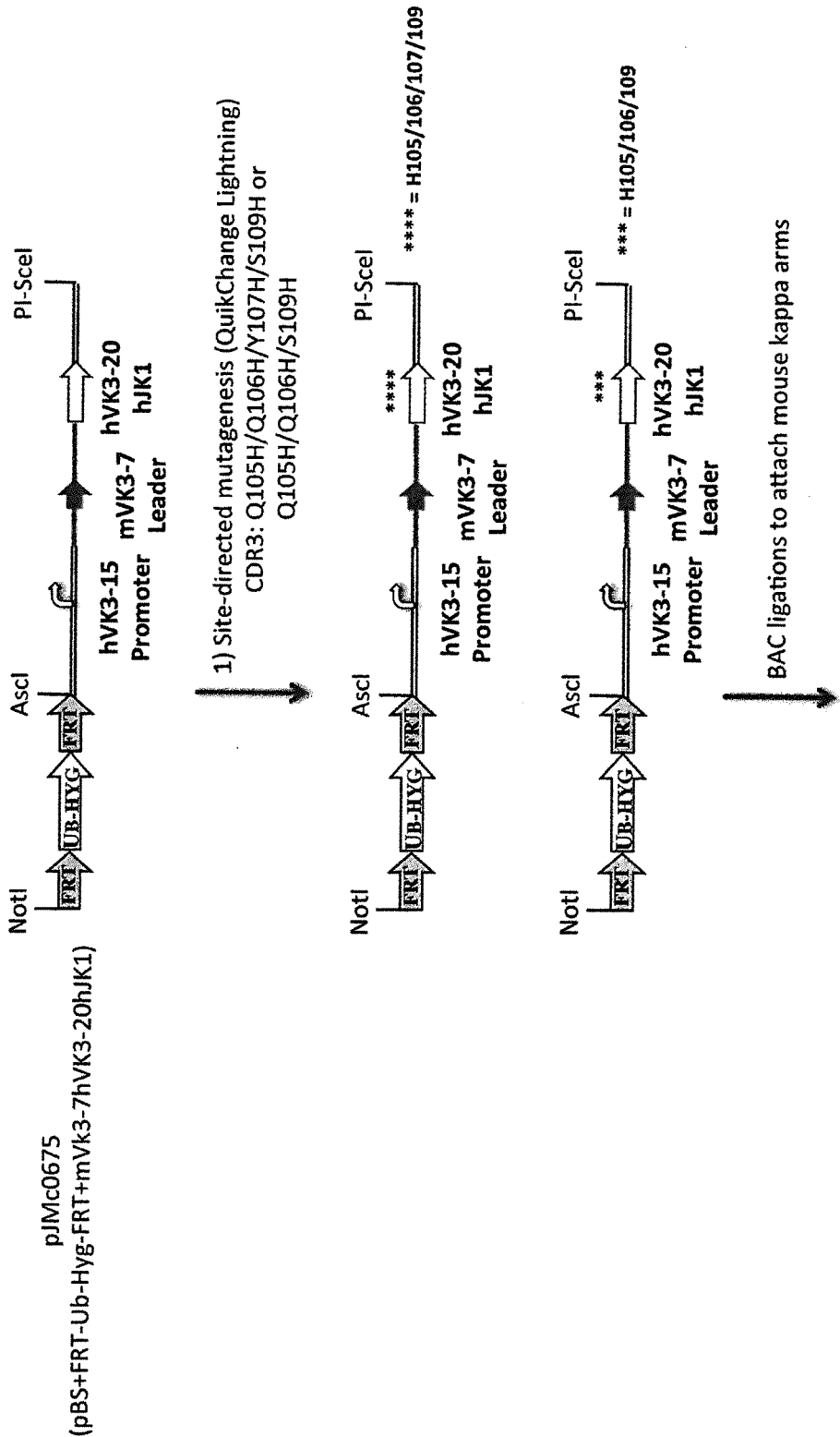
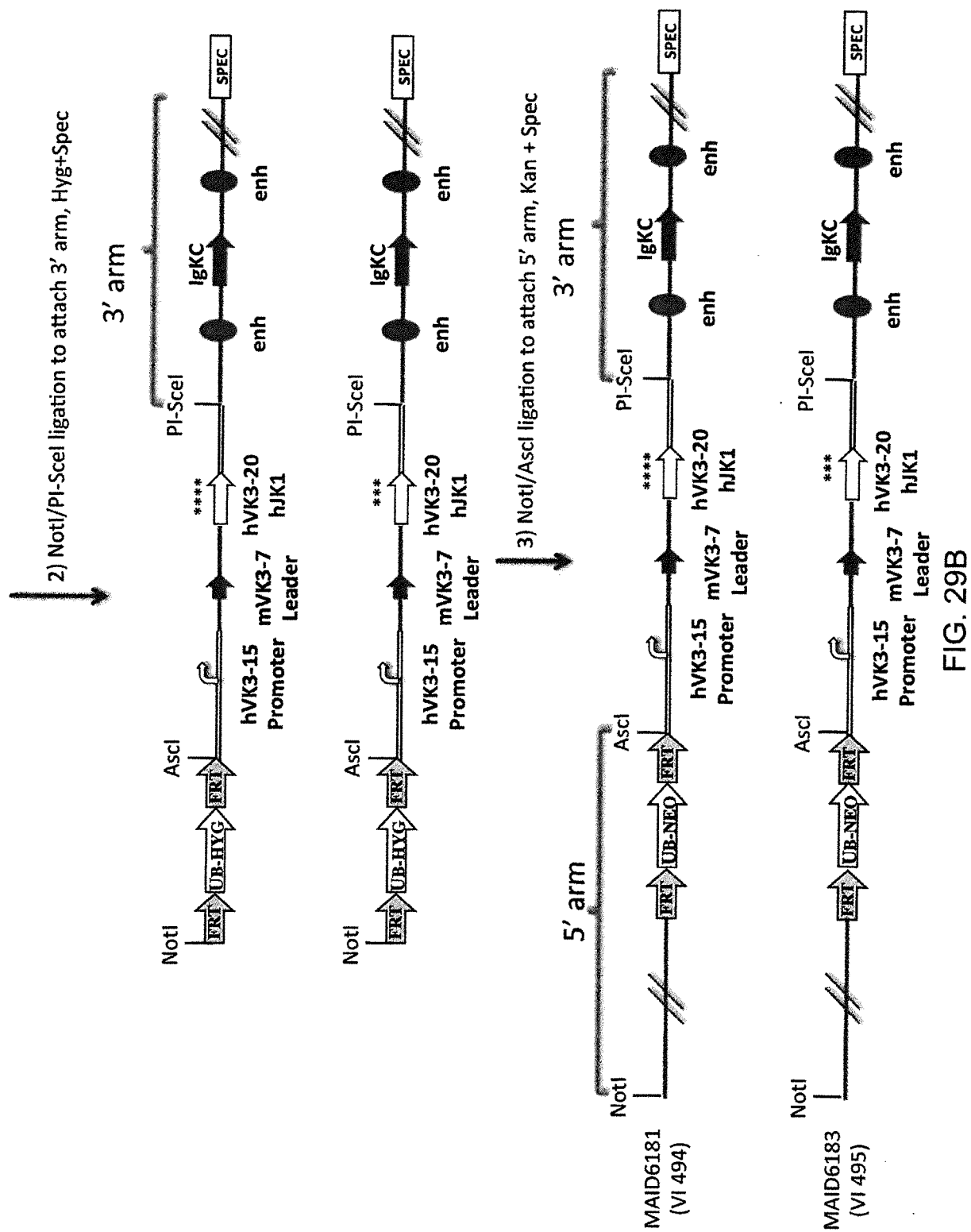


FIG. 29A



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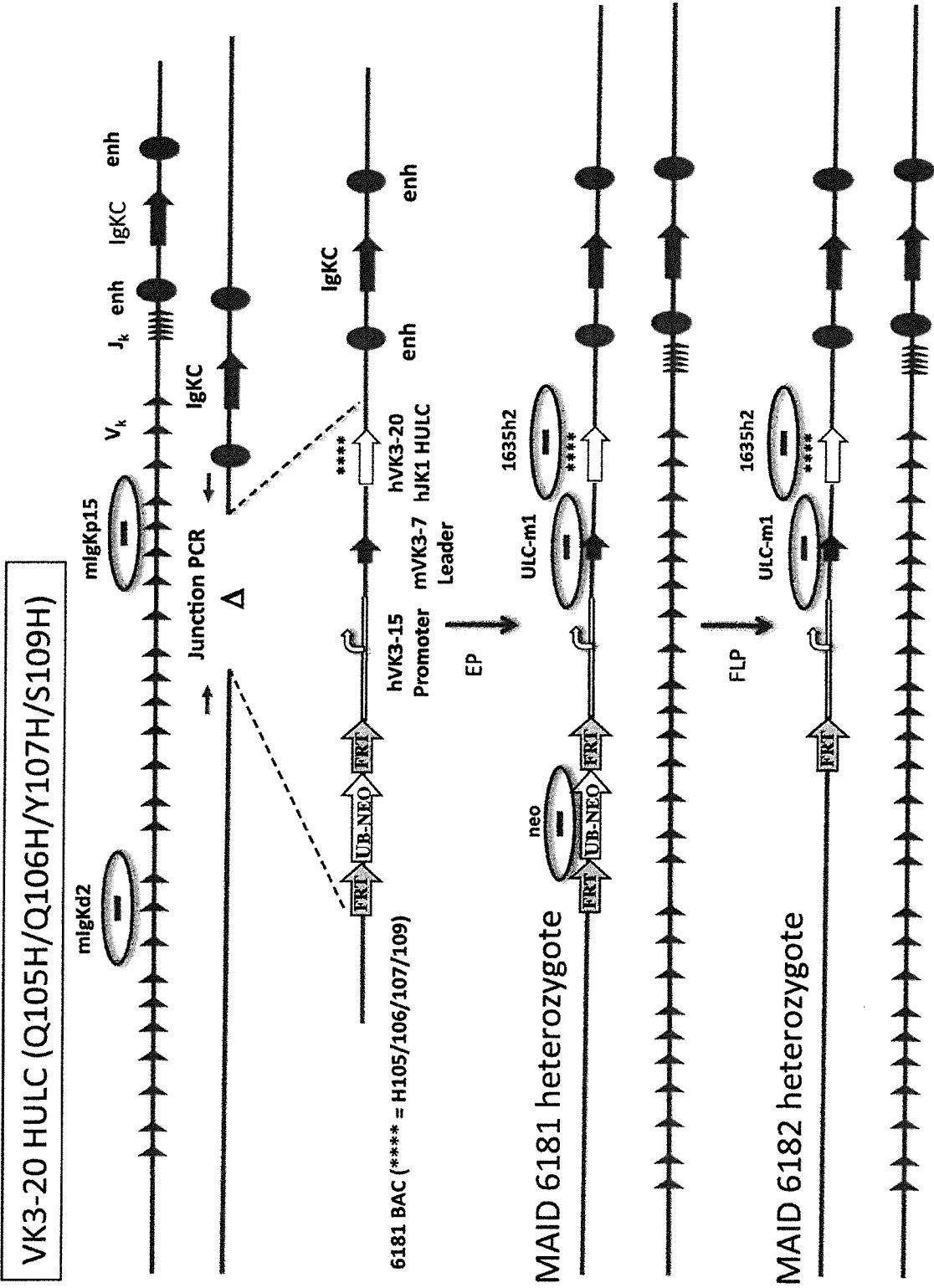


FIG. 29C

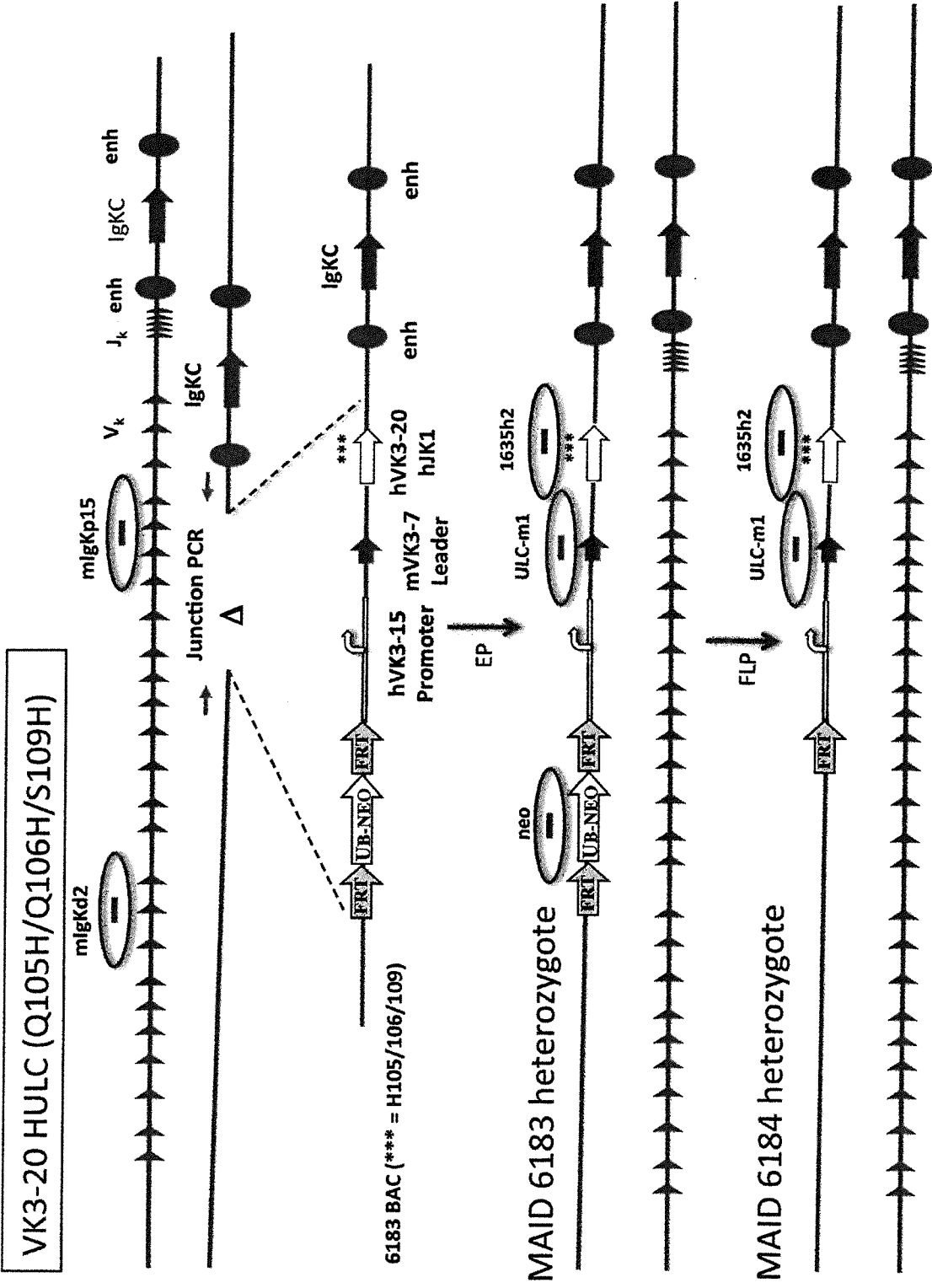


FIG. 29D