

DsRed

CTTGA

ACTCC

ACCAG

G

GTAG

TGGCC

GCCG

T

CCTTC

AGCTT

CAGG

G

CCTT

GTGG

ATCT

CGCC

CTT

CAGC

ACG

CCG

T

CGCG

GG

3,200

3,208

3,216

3,224

3,232

3,240

3,248

3,256

3,264

3,272

3,280

DsRed

GGTAC

AGGCG

CTCG

GTGG

AGGC

CTCCC

AGCCC

ATGG

TCTT

CTTCT

GCATT

ACGGG

GCCG

T

CGG

AGGG

G

AAG

TT

CACG

CCG

3,280

3,288

3,296

3,304

3,312

3,320

3,328

3,336

3,344

3,352

3,360

DsRed

ATGAA

CTTCA

CCTTG

TAGAT

G

AAGC

AGCC

G

T

CCTG

CAGG

G

AGG

AGTCT

TGGG

T

CACG

G

T

CACC

ACG

CCG

CCG

T

CCTC

GAA

3,360

3,368

3,376

3,384

3,392

3,400

3,408

3,416

3,424

3,432

3,440

DsRed

GTTCA

T

CACG

C

GCTCC

CACTT

G

AAGC

CC

T

CGGG

G

AAG

G

ACAG

CTTCT

TGTAG

T

CGGG

G

ATGT

C

GGC

G

GGG

T

GCTT

CACG

T

3,440

3,448

3,456

3,464

3,472

3,480

3,488

3,496

3,504

3,512

3,520

DsRed

ACAC

CTTGG

AGCC

G

TACTG

GAACT

G

GGGG

G

ACAG

GATGT

CCCAG

G

G

CGA

AGGG

C

AGGG

G

G

CCG

CCCTT

GGTCA

CCTT

CAGC

3,520

3,528

3,536

3,544

3,552

3,560

3,568

3,576

3,584

3,592

3,600

DsRed

TTCAC

G

G

TGTT

GTGG

CCCTC

G

TAGG

G

G

CGGG

CCCTC

G

CCCTC

G

ATCTC

G

AACTC

G

TGGC

C

GTTCA

C

G

G

TG

CCCTC

3,600

3,608

3,616

3,624

3,632

3,640

3,648

3,656

3,664

3,672

3,680

DsRed

CATGC

G

CACCTT

G

AAGC

G

CATG

AACTC

CCTTG

ATG

ACG

TTCTT

G

GAGG

A

G

CGC

ACCAT

G

GGTGG

C

G

ACCTG

TGG

ATCCC

G

T

3,680

3,688

3,696

3,704

3,712

3,720

3,728

3,736

3,744

3,752

3,760

3xP3

CCGGG

CCCCG

CGGTAC

CGT

CGACT

CTAG

CGGTAC

CCCCG

ATTG

TTTAG

CTTG

TTT

CAGCTG

CGCTT

G

TTT

ATTTG

CTTAG

CTT

3,760

3,768

3,776

3,784

3,792

3,800

3,808

3,816

3,824

3,832

3,840

3xP3

TCGCT

TAGCG

ACGTG

TTCA

CTTTG

CTTG

TTTGA

ATTGA

ATTG

TCGCTC

CGTAG

ACGA

AGCG

CCTCT

ATTTA

TA

CTCC

GGC

3,840

3,848

3,856

3,864

3,872

3,880

3,888

3,896

3,904

3,912

3,920

3xP3

GGTCG

AGGGT

TCGAA

ATCG

ATAAG

CTTGG

ATCCT

AATTG

AATTAG

CTCTA

AATTG

AATTAG

ATCC

3,920

3,928

3,936

3,944

3,952

3,960

3,968

3,976

3,984

3,992

4,000

3xP3

dsx homology arm

CCGGGCGAGCTCGAATTAACCATTTGTGGACCGGTCTTGTGTTTAGCAGGCAGGGGAGATGAGCGCAAACCTGTGCAAGAAG

4,0004,0084,0164,0244,0324,0404,0484,0564,0644,0724,080

dsx homology arm

AAGCATCACTGTGAAGACGGCAATGCAAAGATAGTGTGCTCAACTTCTCCGCGAAGATTGAAGCTAAATTAAGCACGAGA

4,0804,0884,0964,1044,1124,1204,1284,1364,1444,1524,160

dsx homology arm

TTAGCATGACTGAAGTGACTTTTCAAAGTGTCAGAATGGCTGCACTCGCAAACCTAGCTGGATGCAGCGCAATTTTGCCCC

4,1604,1684,1764,1844,1924,2004,2084,2164,2244,2324,240

dsx homology arm

GGTGTGTGCGCGCATGCAAACGAGCAACCGCAGAGGGCAAAGGAGAGGATGGGAAGGAGGGAGGGAGTGAAAGAGCAGGC

4,2404,2484,2564,2644,2724,2804,2884,2964,3044,3124,320

dsx homology arm

TTAAGGTTGCCCTCGGGCATTGAAGTCGATACAGCGGTTCTATTCCAGTGCCAGTAACGATGACGAAGACGATGTTGCTT

4,3204,3284,3364,3444,3524,3604,3684,3764,3844,3924,400

dsx homology arm

CTGCTGCTGTTGCTGCTGTTGTTGTTGATGATGATGATGATAATAGTGCAAATATAAAATAAATCTTCCGTAAGCTTTGT

4,4004,4084,4164,4244,4324,4404,4484,4564,4644,4724,480

dsx homology arm

GTAGTGGTGCGTGGCTACTATAAGCCCGTCTGGAAGCAAGGAAGCTAGTCGGGCAGGGTCATGCAAAAGGGAGACACCTT

4,4804,4884,4964,5044,5124,5204,5284,5364,5444,5524,560

dsx homology arm

CGGAGCTCCGGAGCTCCCGCCGGCACTCTCGGGGGGACGTCGGTTATGCGTTGTGATTTATTATGGAATATTTATTATAG

4,5604,5684,5764,5844,5924,6004,6084,6164,6244,6324,640

dsx homology arm

TGTCTTGTTTTGAAAAAATAACTTCAACGGTTTCAATTTCTTACACCTCGAGATCGGGGCTGGAGTGGCAACGTGGTACG

4,6404,6484,6564,6644,6724,6804,6884,6964,7044,7124,720

dsx homology arm

GAACGGTACAGCGGTTTGAAGCCGTTTCGGTCTTGGGACTCACGGATCGCAGAATGTTATTGTGCGCGCACTGATGGGAAAG

4,7204,7284,7364,7444,7524,7604,7684,7764,7844,7924,800

dsx homology arm

TCATTTTTCACCGAGTGGTCAGGGCGCGTAGTCCAGTTCGTTTCTGGCTGCTGTTGCTGATGCTACGATCCTCAGGAATG

4,8004,8084,8164,8244,8324,8404,8484,8564,8644,8724,880

dsx homology arm

ATTGGAAACGCCTGGAGATGGTGGGAAAAAATCAAACACAAAAACGATCCTAATGAACATCGTGTGTTCTCATTTCGCTGC

4,8804,8884,8964,9044,9124,9204,9284,9364,9444,9524,960

dsx homology arm

CACGATTGACACCTTCGATAAGACGCACATAATGAGCTAAAGGAGAGGGGACAGGGTCTTGTCTTTGCCACGAGCGATAA

4,9604,9684,9764,9844,9925,0005,0085,0165,0245,0325,040

dsx homology arm

GATTGCAATCACTCGTGAGCGTGTGCTGCTGGGCTGAAGAAGAAACGCTTTCCACAGCAGTAGGTGGGAAGTGGGATTGT

5,0405,0485,0565,0645,0725,0805,0885,0965,1045,1125,120

dsx homology arm

GGAACGTGGCATTGAAAAGAACCTATTTTCTAAAGCCCGAGAGCCCGTTCTCGAACTGGAAAACCAGATGCAGAAGTTTT

5,1205,1285,1365,1445,1525,1605,1685,1765,1845,1925,200

dsx homology arm

TTATTGTCCCCCGCCAGGAAAACAAATGTATTTAATGCTTTCTTTGCCTTTTCCGCCCCGTTTCAGACGACGAGCTAGTG

5,2005,2085,2165,2245,2325,2405,2485,2565,2645,2725,280

dsx homology arm

AAGCGAGCCCAATGGCTGTTGGAGAAACTCGGCTACCCGTGGGAGATGATGCCCCTGATGTACGTCATACTAAAGAGCGC

5,2805,2885,2965,3045,3125,3205,3285,3365,3445,3525,360

dsx homology arm

CGATGGCGATGTACAAAAAGCACACCAGCGGATCGACGAAGGTAAGCTGGCGATGATGGTGTCGTTTCGACATCACTTTCA

5,3605,3685,3765,3845,3925,4005,4085,4165,4245,4325,440

dsx homology arm

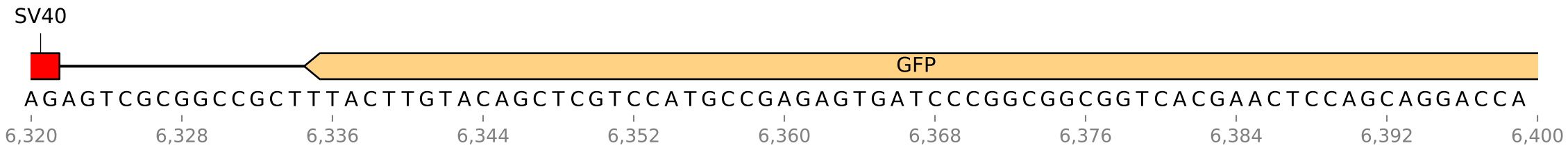
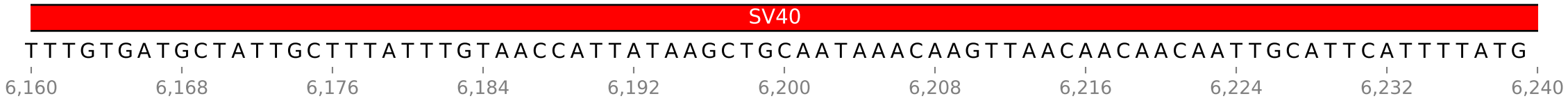
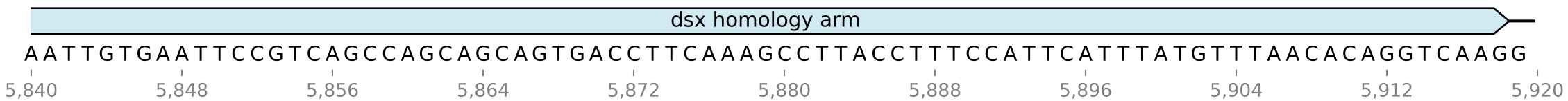
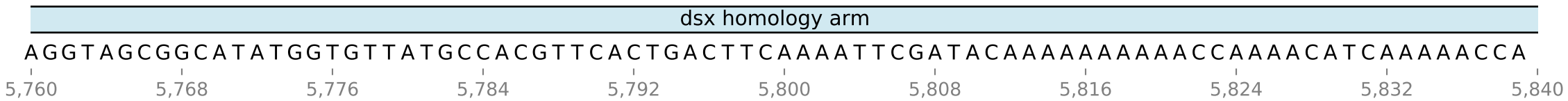
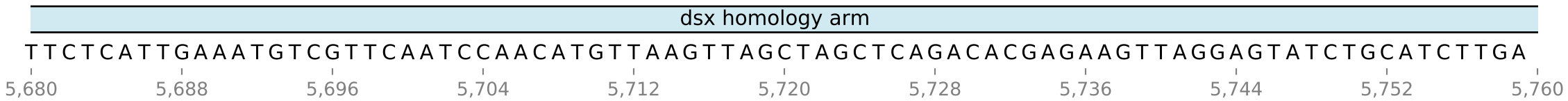
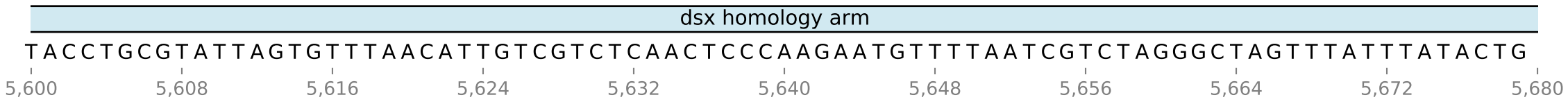
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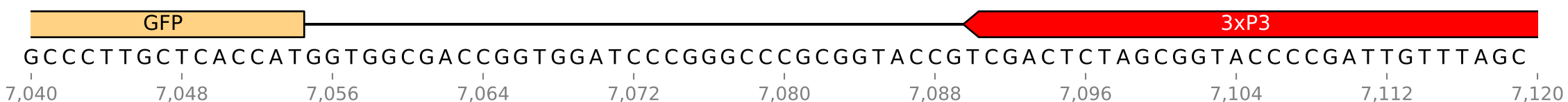
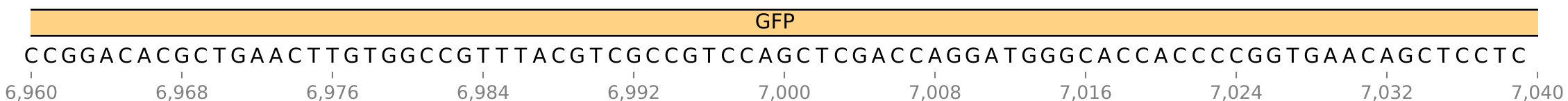
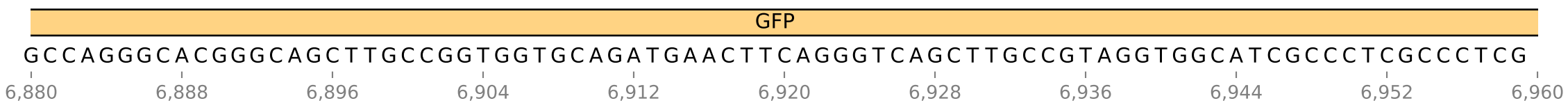
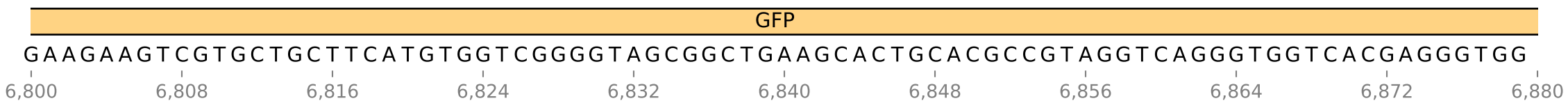
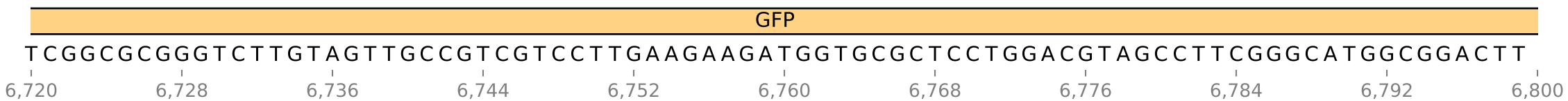
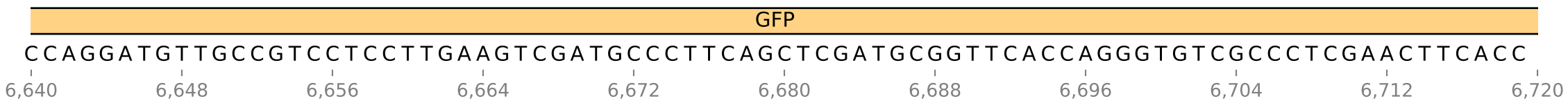
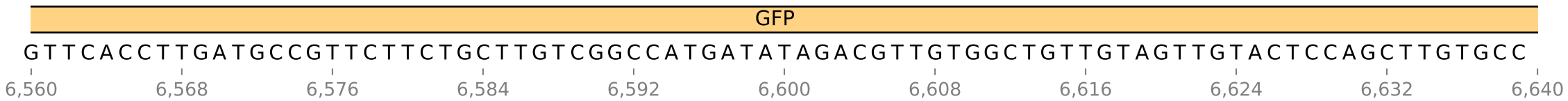
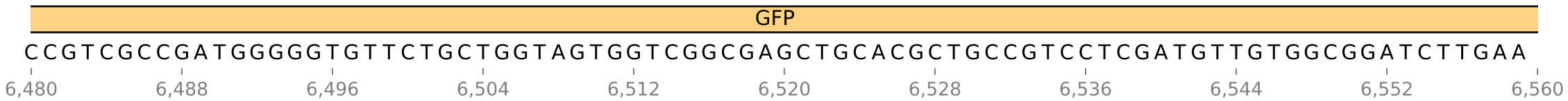
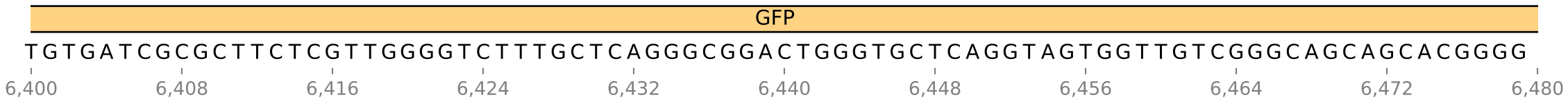
dsx homology arm

GAGACTCTACCTCATGATGCAGCTGTTAAGGAAAGGTTTCAGATGAAGGCAATTTTTCTAGGATAAGATGATCTTAAGT

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3xP3

CCGTAGACGAAGCGCCTCTATTTATACTCCGGCGGTCGAGGGTTCGAAATCGATAAGCTTGGATCCTAATTGAATTAGCT

7,2007,2087,2167,2247,2327,2407,2487,2567,2647,2727,280

3xP3

CTAATTGAATTAGTCTCTAATTGAATTAGATCCCCGGGCGAGCTCGAATTAACCATTTGTGGTTAATTAACCCCCAACTGA

7,2807,2887,2967,3047,3127,3207,3287,3367,3447,3527,360

AttP

GAGAACTCAAAGGTTACCCCACTTTGGGGGGCGCGCCCACTTTGTATAGAAAAGTTGGGTGAGTGAGGAGGAGGGTGGTA

7,3607,3687,3767,3847,3927,4007,4087,4167,4247,4327,440

dsx homology arm

GTGCCACACAGAGAGCTTCGCGGTGGTCAACGAATACTCACGATTGCATAATCTGAACATGTTTGATGGCGTGGAGTTGC

7,4407,4487,4567,4647,4727,4807,4887,4967,5047,5127,520

dsx homology arm

GCAATACCACCCGTCAGAGTGGATGATAAACTTTCCGCACCACTGTAAGTGTCCGTATCTTTGTATGTGGGTGTGTGTAT

7,5207,5287,5367,5447,5527,5607,5687,5767,5847,5927,600

dsx homology arm

GTGTGTTTGGTGAAACGAATTCAATAGTTCTGTGCTATTTTAAATCAAGCCGCGTGCGCAACTGATGCCGATAAGTTCAA

7,6007,6087,6167,6247,6327,6407,6487,6567,6647,6727,680

dsx homology arm

ACTAGTGTTTAAGGAGTGGAGCGAGAGAGCCGCACCACGGTACAGAAGGGCAGCAGAATGGGTCTGGCAGCCTAGCTGCAC

7,6807,6887,6967,7047,7127,7207,7287,7367,7447,7527,760

dsx homology arm

TGGTGCGGTGCGTCCGGCGTCTCGGGGGGAGGGCGAGGAAATTCTAGTGTTAAATCGGAGCAGCAAAAACAAAACAGTGG

7,7607,7687,7767,7847,7927,8007,8087,8167,8247,8327,840

dsx homology arm

TCGTCCCGTTCAAGAAACGGCCTGTACACACACACAGAAAACACTGCAGCATGTTTGTACATAGTAGATCCTAGAGCAGG

7,8407,8487,8567,8647,8727,8807,8887,8967,9047,9127,920

dsx homology arm

TGGTCGTTGCTCCTCGAACGCTCTGGACGCACGGCTTCGCGCGTATTTGCGTAGCGTTCCGCCGATCGTGGGTATTCGTA

7,9207,9287,9367,9447,9527,9607,9687,9767,9847,9928,000

dsx homology arm

CTGCCACAAGCCCGCTTTCTCCCATGCAATCTCTGCAACCAAACCAACAACAACAAAAACCAATCGACAAAATGA

8,0008,0088,0168,0248,0328,0408,0488,0568,0648,0728,080

dsx homology arm

ATCACACCCCTTTTGTATCATCTGTATATTCTTGTTCTTTGCGTTCTTTTCTATGTGGCCACGCCCCGGCGGGTACGTA

8,0808,0888,0968,1048,1128,1208,1288,1368,1448,1528,160

dsx homology arm

ATTGCGTCGAAAACCCCGAAAACCCCGGCACATACAGTGTACATACGGTTTGAGGACAACCTTTGACCTGCAGCCCTTCTG

8,1608,1688,1768,1848,1928,2008,2088,2168,2248,2328,240

dsx homology arm

GGGTTGCCACGTGTAGCTATACTTGTGAGATCGGGCGCCGACGGTGTAAGCGCGAATGGCCGCCACACAGTGTGTCCAC

8,2408,2488,2568,2648,2728,2808,2888,2968,3048,3128,320

dsx homology arm

TCCAACACTACCCCTCTGGAACTACCCCGTCCAGGGATGCACCGGCTCGGCTCATGCCCTTGCAAAACAGTCCGGGGCTCC

8,3208,3288,3368,3448,3528,3608,3688,3768,3848,3928,400

dsx homology arm

ACTGTAGTAGCTCCGGCGTTGCTCTGAGAGAAGGATGCCCTTCGAAGTGTCGAAAGCGTGCAATTGGGCGTTCAAGTGTGT

8,4008,4088,4168,4248,4328,4408,4488,4568,4648,4728,480

dsx homology arm

GTGTGTGTGTTAGGTTTAGCGAGAAACAGCAGCAGTTGCGTGCTGAAAAGCGAAGGAGTAATAGAGTGCATAATGAAA

8,4808,4888,4968,5048,5128,5208,5288,5368,5448,5528,560

dsx homology arm

ATGAAAATGAAAATGAAGCAAAAGTAGAAGGCGGAGGAGAGCAACCTGTGTTCCACTAGTAGCGAATAGTTTAGTCTAGT

8,5608,5688,5768,5848,5928,6008,6088,6168,6248,6328,640

dsx homology arm

TTCGTCACCAATCAACCTTCCAACCATCGTTCAACCAATACCTGAGTCAACATCGTCATCGTTATCGTGCCACAACCTTA

8,6408,6488,6568,6648,6728,6808,6888,6968,7048,7128,720

dsx homology arm

TTAAAAATGAACCTTGTCCGCGCCACCGTAGGGTGATCTAAGGCGACCTTTCTTACGGGCGCGACCCACATGCCATCGTC

8,7208,7288,7368,7448,7528,7608,7688,7768,7848,7928,800

dsx homology arm

ACCTTCTCCAATCAAAACCAACAGCCTGTACCGATGGTGTGCAATTGTGCGTGCGTGTGTGTTATTAGCAAAAAAAGAGA

8,8008,8088,8168,8248,8328,8408,8488,8568,8648,8728,880

dsx homology arm

AAGAGTCGACGAGAGAGAGATAGATCGAGATCGAGAGTACAAAAGAGCAGTAGAAATGTTTCGTTGTTTGTTTTTTCGTAAC

8,8808,8888,8968,9048,9128,9208,9288,9368,9448,9528,960

dsx homology arm

ACAGTTGTTTAGCCAAAATGGGAATTTCCAATAATCCCGGGGGCGGGGAAATGCGGGAATACTGCGTACACACATACATC

8,9608,9688,9768,9848,9929,0009,0089,0169,0249,0329,040

dsx homology arm

AATCAAAAAGAAAAATCCTTGCGCTACATCACTACCGTTTGCGCGGTGCTGATCTAGAGCAGACCACTTTCCACTCCACT

9,0409,0489,0569,0649,0729,0809,0889,0969,1049,1129,120

dsx homology arm

CTACAATCAATCAATCTGTGCAGAAGGTATGGTAAGACGGCCTTTGAGCGAGTCACGGTCGCCACCATAACGCCGTCCGA

9,1209,1289,1369,1449,1529,1609,1689,1769,1849,1929,200

dsx homology arm

CGAGGGCTGAATGCGAACTTTGCTAATCGATTTTCCGCTTTCTTTTTATCCCACCTCCTTTTCTCTCCCTCTCTCTCTTT

9,2009,2089,2169,2249,2329,2409,2489,2569,2649,2729,280

dsx homology arm

TGCACTGCCCCTTGTAACCCCCAAAAAGGTAAACGACACATTAAGACCTACGAAGCGTTGGTGAAGTCATCGCTCGATCC

9,2809,2889,2969,3049,3129,3209,3289,3369,3449,3529,360

dsx homology armAttB

GAACAGCGACCGGCTGACGGAGGACGACGACGAGGACGAGAACATCTCGGTGACCCGCACCACGCGTGGGTCCCATGGGT

9,3609,3689,3769,3849,3929,4009,4089,4169,4249,4329,440

AttBpiggyBac

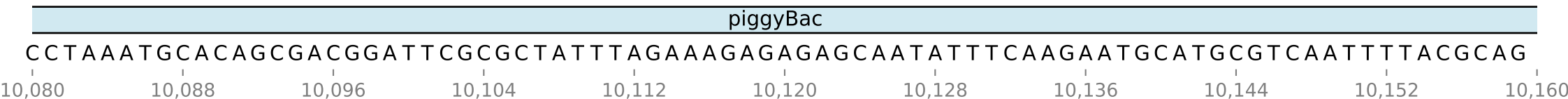
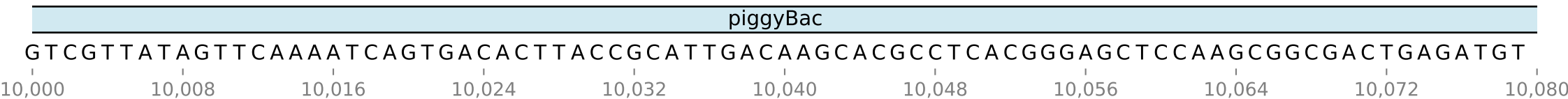
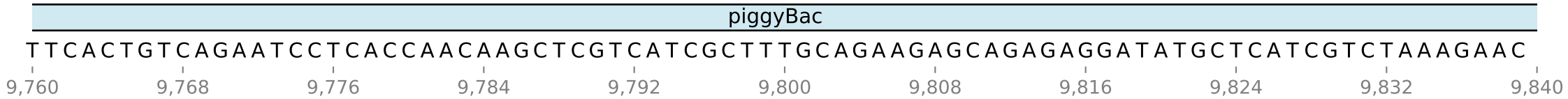
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piggyBac

GACTCGGCTACGCCTCGTGGACTTTGAAGTTGACCAACAATGTTTATTCTTACCTCTAATAGTCCTCTGTGGCAAGGTCA

9,5209,5289,5369,5449,5529,5609,5689,5769,5849,5929,600



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CTCTTTAACAAACTAGAAATATTGTATATACAAAAAATCATAAATAATAGATGAATAGTTTAATTATAGGTGTTTCATCAA

10,400 10,408 10,416 10,424 10,432 10,440 10,448 10,456 10,464 10,472 10,480

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TCGAAAAAGCAACGTATCTTATTTAAAGTGCGTTGCTTTTTTCTCATTTATAAGGTTAAATAATTCTCATATATCAAGCA

10,480 10,488 10,496 10,504 10,512 10,520 10,528 10,536 10,544 10,552 10,560

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AAGTGACAGGCGCCCTTAAATATTCTGACAAATGCTCTTTCCTAAACTCCCCCATAAAAAAACCCGCCGAAGCGGGTT

10,560 10,568 10,576 10,584 10,592 10,600 10,608 10,616 10,624 10,632 10,640

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TTTACGTTATTTGCGGATTAACGATTACTCGTTATCAGAACCGCCCAGGGGGCCCGAGCTTAAGACTGGCCGTCGTTTTA

10,640 10,648 10,656 10,664 10,672 10,680 10,688 10,696 10,704 10,712 10,720

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CAACACAGAAAGAGTTTGTAGAAACGCAAAAAGGCCATCCGTCAGGGGCCTTCTGCTTAGTTTGATGCCTGGCAGTTCCC

10,720 10,728 10,736 10,744 10,752 10,760 10,768 10,776 10,784 10,792 10,800

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TACTCTCGCCTTCCGCTTCCTCGCTCACTGACTCG

10,800 10,808 10,816 10,824 10,832