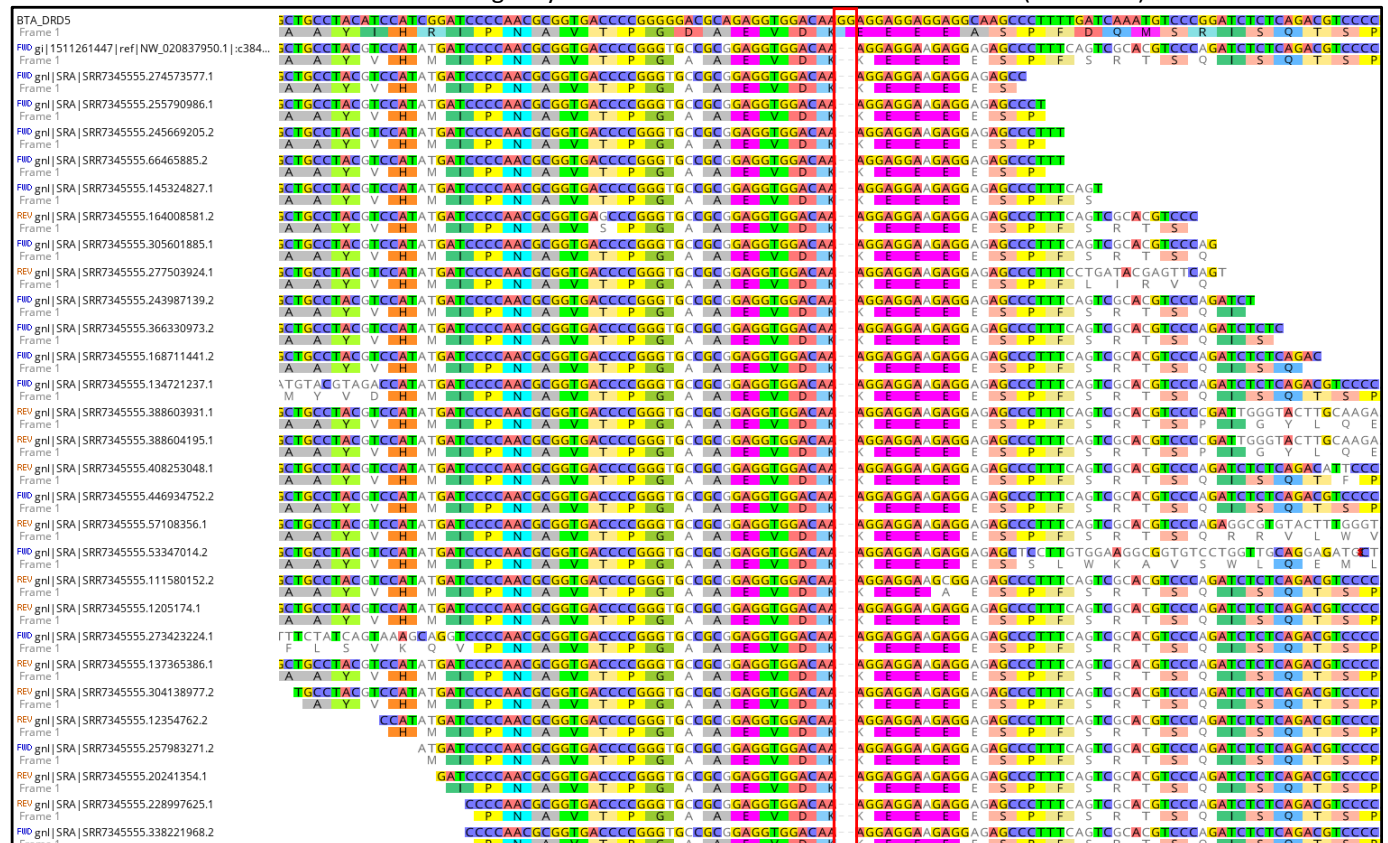


SRX466994 - PRJNA236163 - University of Durham



SRX200685 - PRJNA20367 - Baylor College of Medicine (BCM)

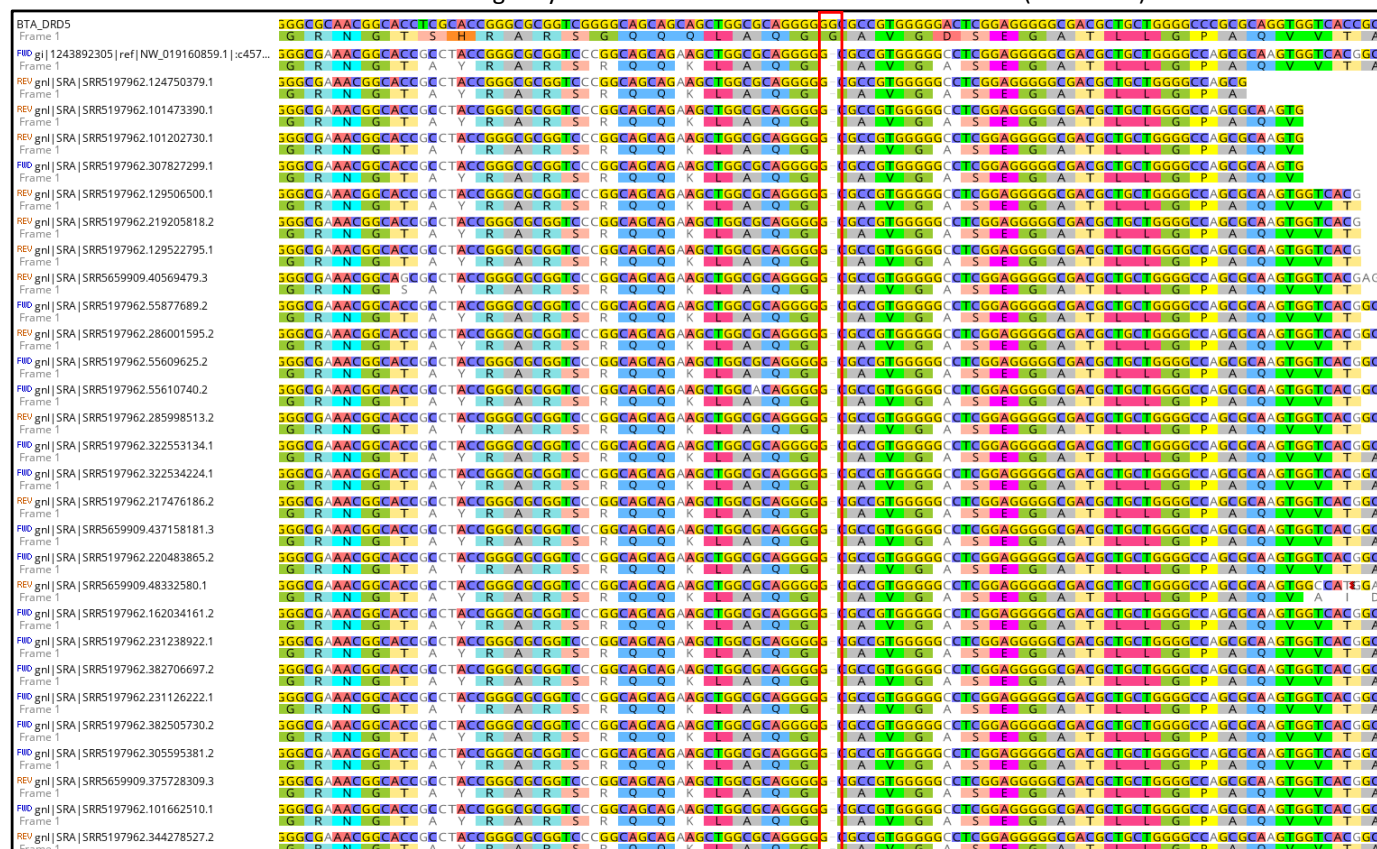
The figure displays a genomic alignment visualization. The top track, labeled 'BTA_DRS', shows a reference sequence. Below it, the 'REV_gb|QXD02011962.1' track shows the alignment of a specific genomic region. The bottom track, labeled 'FMD_gnl|SRA|SRR606322.7102008.2', shows the alignment of a specific genomic region. The tracks are color-coded by base pair: A (green), C (blue), G (red), and T (yellow). Gaps are indicated by 'N', 'H', 'M', 'L', 'P', 'V', 'D', 'I', 'S', 'Q', 'L', 'R', 'F', 'E', 'S', 'P', 'F', 'S', 'R', 'T', 'S', 'Q', 'L', 'S'. A red vertical line highlights a specific genomic position across all tracks.

Delphinapterus leucas SRA confirmation of 1-nucleotide deletion

SRA experiments searched:

SRX2513439 - PRJNA360851 - BC Cancer Agency Michael Smith Genome Sciences Centre (BCCAGSC)

SRX2896241 - PRJNA360851 - BC Cancer Agency Michael Smith Genome Sciences Centre (BCCAGSC)

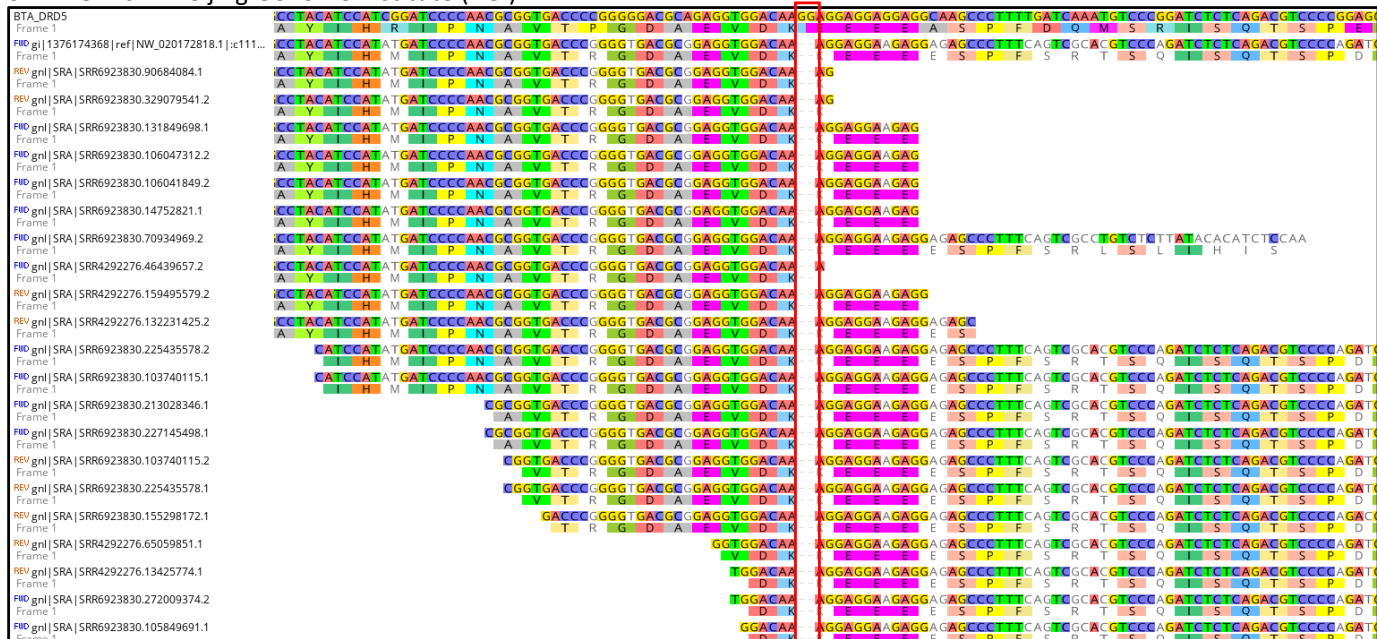


Neophocaena asieorientalis asiaeorientalis SRA confirmation of 2-nucleotide deletion

SRA experiments searched:

SRX3870625 - PRJNA433603 - Northwestern Polytechnical University

SRX2187761 - Beijing Genome Institute (BGI)



SRX3230023 - PRJNA411766 - Beijing Genome Institute (BGI)
ERX2601910 - PRJEB24146 - CNGB



Eschrichtius robustus SRA confirmation of 1-nucleotide deletion

SRA experiments searched:

SRX2901264 - PRJNA389516 - Senckenberg Gesellschaft fuer Naturforschung

SRX2776065 - PRJNA384396 - Purdue University

BTA_DRD5	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.144818446.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.56023424.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.101602106.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.142311965.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.304508258.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.78360400.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.44506126.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.15207391.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.410208718.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.404940377.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.162994286.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.46570186.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.359228677.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5495108.423852781.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.406413442.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.33829924.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.26216578.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.51790908.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.86439176.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.164135914.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.60137980.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.54718455.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.324348094.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.90280098.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.70642975.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.336251711.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR5665641.84835822.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5495108.351997023.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR5665641.52014476.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA

Balaena mysticetus SRA confirmation of 1-nucleotide deletion

SRA experiments searched:

SRX790318 - PRJNA194091 - University of Liverpool

SRX790317 - PRJNA194091 - University of Liverpool

BTA_DRD5	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl BL_ORD_ID 3417	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685385.269280738.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.98012068.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.76142596.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.63536902.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.29514256.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.10263345.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.297040727.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.239979482.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.213955026.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.41364351.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.425653884.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.396274396.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.333293940.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.335489092.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.44353086.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685385.149969940.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.267980314.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.297562912.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685386.422785349.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685385.320646821.2	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685386.1696186.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685386.374168648.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685385.49289746.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
FIND gnl SRA SRR1685385.14966504.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.231509377.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.291177678.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA
REV gnl SRA SRR1685385.166653611.1	Frame 1	CCACCTGGAACCGACCTACGCCATCTCCCTCAGTCATCAGCTCTCA