NCBI data base; control M/M, clone # 9

```
Score =  456 bits (237),  Expect = 2e-123 Identities = 237/237 (100%), Gaps = 0/237 (0%)
Strand=Plus/PlusQuery
10970       TAATCCCAGCACTTTGAGAGGCCGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCA  11029
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAATCCCAGCACTTTGAGAGGCCGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCA  60Query

11030       TCCTGGCTAACATGGTGAAACCCCGTCTCTACTAAAAACACAAAAAATTAGCCGGGTGTG  11089
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCTGGCTAACATGGTGAAACCCCGTCTCTACTAAAAACACAAAAAATTAGCCGGGTGTG  120Query

11090       GTGGCGGGCGCCTGTAGTCCCTGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAACC  11149
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTGGCGGGCGCCTGTAGTCCCTGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAACC  180

Query  11150 CGGGAGGTGGAGCTGGCAGTGAGCTGAGATCACACCACTGCAGTCCAGCCTGGGTGG   11206
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct  181  CGGGAGGTGGAGCTGGCAGTGAGCTGAGATCACACCACTGCAGTCCAGCCTGGGTGG  237
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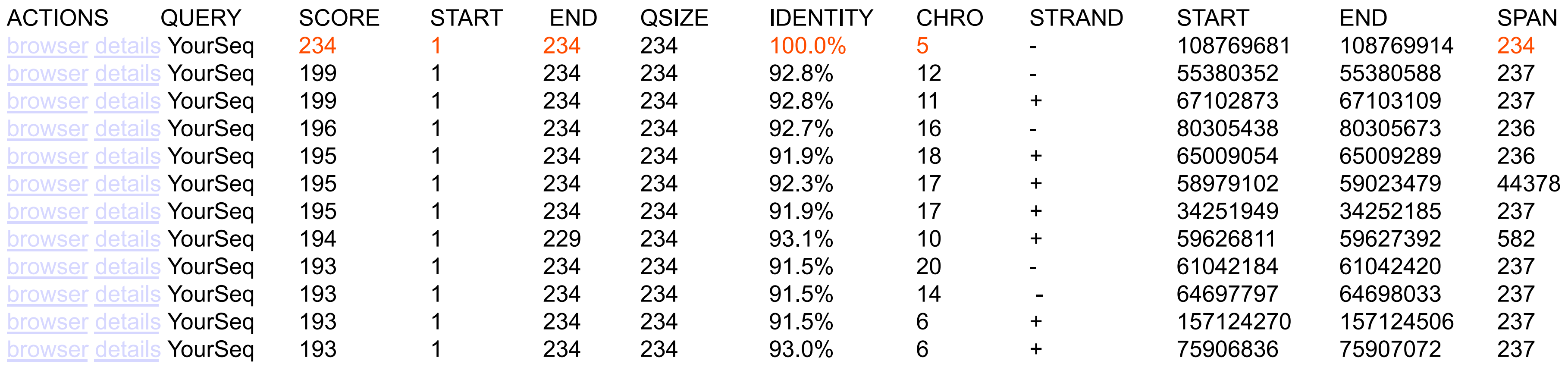
Fig. 1 supplem.



ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser details	YourSeq	234	1	234	234	100.0%	5	-	108769681	108769914	234
browser details	YourSeq	199	1	234	234	92.8%	12	-	55380352	55380588	237
browser details	YourSeq	199	1	234	234	92.8%	11	+	67102873	67103109	237
browser details	YourSeq	196	1	234	234	92.7%	16	-	80305438	80305673	236
browser details	YourSeq	195	1	234	234	91.9%	18	+	65009054	65009289	236
browser details	YourSeq	195	1	234	234	92.3%	17	+	58979102	59023479	44378
browser details	YourSeq	195	1	234	234	91.9%	17	+	34251949	34252185	237
browser details	YourSeq	194	1	229	234	93.1%	10	+	59626811	59627392	582
browser details	YourSeq	193	1	234	234	91.5%	20	-	61042184	61042420	237
browser details	YourSeq	193	1	234	234	91.5%	14	-	64697797	64698033	237
browser details	YourSeq	193	1	234	234	91.5%	6	+	157124270	157124506	237
browser details	YourSeq	193	1	234	234	93.0%	6	+	75906836	75907072	237

Fig. 2 supplem.

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser details	YourSeq	237	1	237	237	100.0%	8	-	142008284	142008520	237
browser details	YourSeq	237	1	237	237	100.0%	8	-	63092748	63092984	237
browser details	YourSeq	237	1	237	237	100.0%	6	-	47454630	47454866	237
browser details	YourSeq	237	1	237	237	100.0%	3	-	194223385	194223621	237
browser details	YourSeq	237	1	237	237	100.0%	3	-	119153906	119154142	237
browser details	YourSeq	237	1	237	237	100.0%	3	-	101268103	101268339	237
browser details	YourSeq	237	1	237	237	100.0%	2	-	179496114	179496350	237
browser details	YourSeq	237	1	237	237	100.0%	2	-	38468039	38468275	237
browser details	YourSeq	237	1	237	237	100.0%	13	-	58555819	58556055	237
browser details	YourSeq	237	1	237	237	100.0%	13	-	56145920	56146156	237
browser details	YourSeq	237	1	237	237	100.0%	11	-	124418361	124418597	237
browser details	YourSeq	237	1	237	237	100.0%	10	-	132748550	132748786	237
browser details	YourSeq	237	1	237	237	100.0%	10	-	54677732	54677968	237
browser details	YourSeq	237	1	237	237	100.0%	1	-	105706004	105706240	237
browser details	YourSeq	237	1	237	237	100.0%	9	+	108063976	108064212	237
browser details	YourSeq	237	1	237	237	100.0%	8	+	72713998	72714234	237
browser details	YourSeq	237	1	237	237	100.0%	7	+	86453425	86453661	237
browser details	YourSeq	237	1	237	237	100.0%	6	+	17580288	17580524	237
browser details	YourSeq	237	1	237	237	100.0%	5	+	172822360	172822596	237
browser details	YourSeq	237	1	237	237	100.0%	5	+	121322642	121322878	237
browser details	YourSeq	237	1	237	237	100.0%	5	+	94135413	94135649	237
browser details	YourSeq	237	1	237	237	100.0%	4	+	177409451	177409687	237
browser details	YourSeq	237	1	237	237	100.0%	4	+	135304612	135304848	237
browser details	YourSeq	237	1	237	237	100.0%	3	+	120056392	120056628	237
browser details	YourSeq	237	1	237	237	100.0%	2	+	233303596	233303832	237
browser details	YourSeq	237	1	237	237	100.0%	2	+	81556351	81556587	237
browser details	YourSeq	237	1	237	237	100.0%	19	+	33811653	33811889	237
browser details	YourSeq	237	1	237	237	100.0%	15	+	81072366	81072602	237
browser details	YourSeq	237	1	237	237	100.0%	13	+	45617789	45618025	237
browser details	YourSeq	237	1	237	237	100.0%	11	+	6228494	6228730	237
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Fig. 3 supplem.

control M/V, clone # 2

NCBI database

intergenic

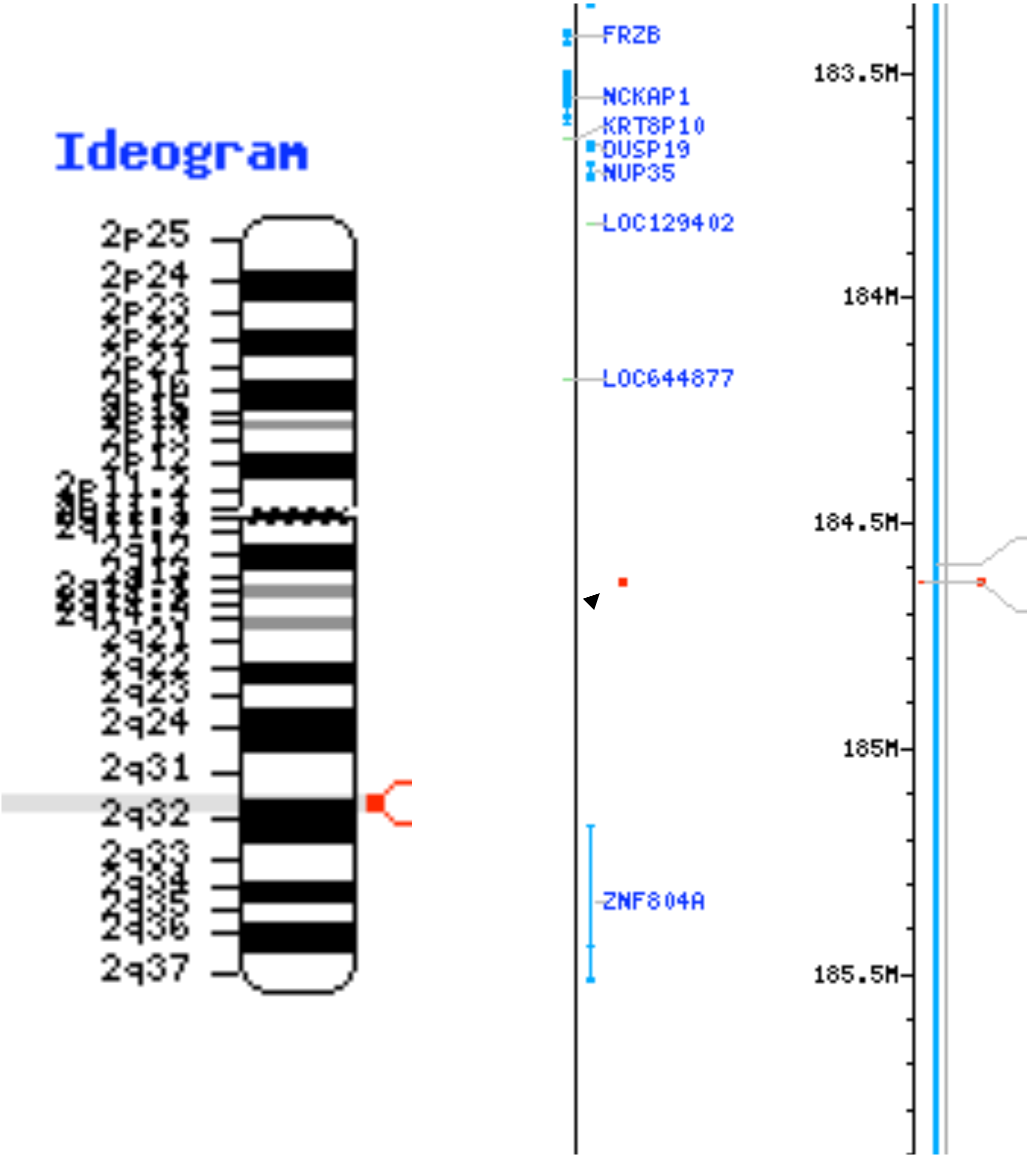

Fig. 4 supplem.