MO: APPROXIMATE PATTERN MATCH

MATCH_STARTS AND_ENDS_AT MATCH_RATING MATCH_SPANS MATCH_WEIGHT COST_METRIC COST_VECTOR 23384 24440 0.98214287 1057 877.0 0 (2 1 51 0 0 1 0 0)

FINEGRAIN ALIGNMENT WITHIN HPS INPUT SEQUENCE BETWEEN DNA SIGNATURE AND M0 [23384:24440] (98/100)

DNA_	DESCRIPTION	SIGNATURE_	MATCHING_	SIGNATURE_	MATCH_ENDS_AT
SEOUENCE		STARTS	STARTS AT	ENDS	
SEQUENCE		STARTS		LIVES	
HPS INPUT	(SIGNATURE +	SIGNATURE	TESTSEOUENCE	SIGNATURE	TESTSEOUENCE=24470)
CECHENCE	TESTSEQUENCE)	BP= 0	BP= 23369)	BP= 1101)	,
SEQUENCE	TESTSEQUENCE)	DP=U	DP= 23309)	DP=IIUI)	
DNA		BP-INDFX=0		BP-	
DNA		BP-INDEX= 0			
DNA SIGNATURE		BP-INDEX= 0		BP- INDEX= 1101	
SIGNATURE		BP-INDEX= 0			
	SUBSEQUENCE M0		BP- INDEX= 22268		 BP-INDEX= 23369

MO ALIGNMENT AT GENOMIC ADDRESS [22270] FOR INPUT TEST SEQUENCE IN FILE [HPS_1DNA_INPUT_SERIES_BASES.DNA]

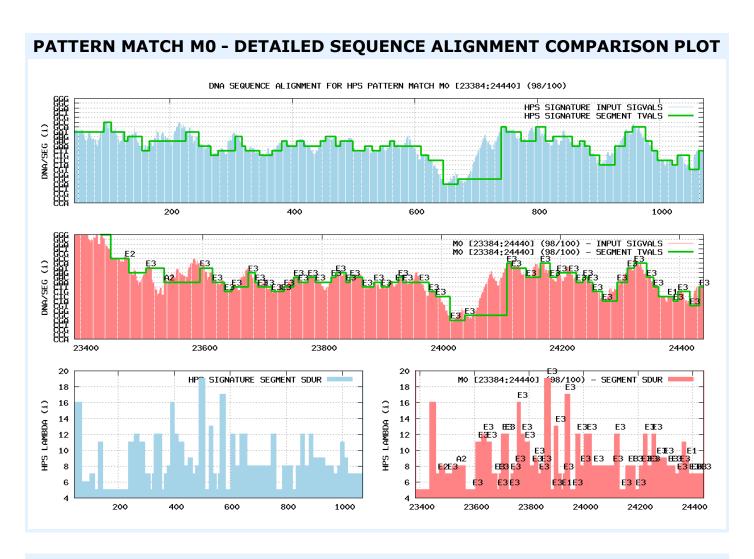
0 _1_ _2_ _3_ _4_ _5_ _6_ _7_ _8_ _9_ _10_ _11_ _12_ _13_ _14_ _15_ _16_ _17_ _18_ _19_ (SIG:M0): [22270]: (G G) (T T) (C C) (A A) (G G) (C C) (G G) (C C) (T T) (T T) (T T) (T T) (G G) (G G) (T T) (G G) (C C) (T T) (G G) (SIG:M0): [22290]: (A A) (A A) (G G) (A A) (C C) (G G) (G A) (C C) (SIG:M0): [22310]: (G G) (T T) (T T) (C C) (G G) (G G) (G G) (C C) (A A) (T T) (T T) (A A) (G G) (G G) (G G) (G G) (C C) (A A) (A A) (C C) (SIG:M0): [22330]: (A A) (T T) (G G) (T T) (T T) (C C) (G G) (G G) (A A) (G G) (G G) (T T) (T T) (G G) (G G) (G G) (G A) (A A) (G G) (SIG:M0): [22350]: (T T) (C C) (G G) (T T) (T T) (G G) (T T) (C C) (A A) (T T) (T T) (A A) (C C) (T T) (T T) (C C) (A A) (A A) (T T) (G G) (SIG:M0): [22370]: (A A) (C C) (C C) (G G) (G G) (G G) (T T) (A A) (T T) (C C) (A A) (A A) (G G) (A A) (A A) (A A) (T T) (C C) (A A) (T T) (SIG:MO): [22390]: (C C) (A A) (C C) (T T) (G G) (A A) (T T) (C C) (A A) (T T) (C C) (C C) (T T) (A A) (G G) (T T) (C C) (T T) (C C) (SIG:MO): [22410]: (G G) (T T) (C C) (A A) (A A) (A A) (T T) (C C) (G G) (T T) (T T) (A A) (C C) (T T) (C C) (G G) (T T) (A A) (T T) (SIG:MO): [22430]: (T T) (A A) (T T) (C C) (C C) (C C) (C C) (A A) (T T) (T T) (T T) (G G) (G G) (C C) (A A) (A A) (T T) (G G) (T T) (SIG:MO): [22450]: (C C) (T T) (G G) (C C) (A A) (C C) (C C) (A A) (A A) (T T) (G G) (A A) (C C) (C C) (C C) (G G) (A A) (T T) (G G) (SIG:MO): [22470]: (A A) (A A) (G G) (A A) (A A) (G G) (C C) (T T) (T T) (C C) (T T) (C C) (C C) (G G) (G G) (A A) (C C) (A A) (T T) (SIG:MO): [22490]: (G G) (C C) (C C) (C C) (A A) (A A) (G G) (G G) (T T) (C C) (T T) (T T) (G G) (T T) (G G) (T T) (T T) (A A) (G G) (SIG:MO): [22510]: (C C) (T T) (C C) (C C) (C C) (G G) (G G) (C C) (A A) (G G) (C C) (T T) (G G) (A A) (T T) (G G) (G G) (C C) (A A) (T T) (SIG:M0): [22530]: (G G) (C C) (C C) (A A) (C C) (G G) (T T) (C C) (A A) (G G) (T T) (A A) (C C) (T T) (A A) (C C) (C C) (G G) (A A) (T T) (SIG:M0): [22550]: (G G) (A A) (C C) (C C) (T T) (C C) (T T) (C C) (T T) (C C) (T T) (T T) (A A) (C C) (C C) (T T) (G G) (A A) (T T) (SIG:M0): [22570]: (A A) (C C) (G G) (C C) (C C) (A A) (T T) (A A) (A A) (C C) (A A) (T T) (C C) (G G) (T T) (G G) (G G) (C C) (G G) (T T) (SIG:M0): [22590]: (T T) (T T) (G G) (C C) (C C) (G G) (A A) (T T) (A A) (T T) (C C) (T T) (C C) (T T) (A A) (C C) (C C) (C C) (G G) (T T) (SIG:M0): [22610]: (A A) (A A) (G G) (C C) (T T) (G G) (A A) (C C) (G G) (C C) (G G) (T T) (T T) (T T) (A A) (C C) (T T) (G G) (A A) (G G) (SIG:M0): [22630]: (C C) (T T) (C C) (G G) (A A) (A A) (A A) (G G) (G C) (C C) (G G) (C C) (C C) (C A) (G G) (A A) (A A) (T T) (G G) (SIG:MO): [22650]: (G G) (C C) (T T) (G G) (C C) (A A) (T T) (T T) (A A) (T T) (C C) (T T) (C G) (G G) (G G) (C C) (G G) (A A) (T T) (SIG:MO): [22670]: (A A) (A A) (C C) (C C) (C C) (G G) (G G) (A A) (T T) (G G) (C C) (T T) (G G) (C C) (T T) (G G) (C C) (SIG:MO): [22690]: (G G) (T T) (T T) (A A) (G G) (A A) (A A) (A A) (A A) (T T) (G G) (C C) (C C) (C C) (G G) (C C) (G G) (C C) (G G) (C T) (SIG:MO): [22710]: (T T) (C C) (C C) (C C) (A A) (G G) (G G) (T T) (A A) (T T) (G G) (A A) (C C) (T T) (G G) (G G) (C C) (A A) (T T) (G G) (SIG:MO): [22730]: (G G) (A A) (T T) (C C) (T T) (G G) (G G) (C C) (A A) (T T) (A A) (A A) (G G) (A A) (A A) (G G) (T T) (G G) (A A) (C C) (SIG:M0): [22750]: (C C) (A A) (C C) (C C) (G G) (C C) (A A) (G G) (A A) (T T) (G G) (C C) (C C) (T T) (A A) (G G) (A A) (G G) (A A) (T T) (SIG:M0): [22770]: (C C) (SIG:MO): [22790]: (C C) (C G) (C C) (C G) (C C) (G G) (C C) (C G) (C C) (C C) (C C) (C C) (C C) (A A) (G G) (T T) (SIG:M0): [22810]: (A A) (T T) (C C) (G G) (A A) (A A) (A A) (A A) (A A) (T T) (G G) (A A) (C C) (G G) (A A) (C C) (G G) (A A) (C C) (SIG:MO): [22830]: (T T) (T T) (C C) (C C) (G G) (G G) (T T) (C C) (A A) (T T) (C C) (T T) (T T) (C C) (G G) (G G) (G G) (G A) (T T) $(SIG:MO): [22850]: (T\ T) \ (A\ A) \ (T\ T) \ (G\ G) \ (A\ A) \ (G\ G) \ (T\ T) \ (T\ T) \ (G\ G) \ (G\ G) \ (T\ T) \ (G\ G) \ (C\ C) \ (C\ C) \ (A\ A) \ (A\ A) \ (G\ G) \ (A\ A) \ (G\ G) \$ (SIG:M0): [22870]: (C C) (A A) (C C) (C C) (A A) (G G) (C C) (C C) (T T) (G G) (C C) (T T) (G G) (A A) (T T) (G G) (C C) (T T) (G G) (SIG:M0): [22890]: (T T) (T T) (G G) (A A) (T T) (A A) (G G) (A A) (G G) (C C) (T T) (G G) (T T) (C C) (G G) (C C) (C C) (T T) (G G) (SIG:MO): [22910]: (A A) (C C) (C C) (A A) (T T) (C C) (G G) (T T) (T T) (C C) (C C) (T T) (G G) (C C) (G G) (C C) (A A) (A A) (A A) (C C) (SIG:MO): [22930]: (T T) (T T) (C C) (T T) (G G) (C C) (G G) (G G) (A A) (T T) (G G) (A A) (T T) (G G) (T T) (G G) (C C) (T T) (G G) (T T) (SIG:MO): [22950]: (A A) (A A) (C C) (T T) (G G) (A A) (A A) (T T) (A A) (C C) (A A) (T T) (C C) (C C) (G G) (G G) (C C) (A A) (T T) (C C) (SIG:MO): [22970]: (T T) (T T) (C C) (C C) (T T) (C C) (T T) (C C) (A A) (T T) (A A) (C C) (G G) (G G) (T T) (C C) (C C) (T T) (G G) (G G) (SIG:MO): [22990]: (C C) (T T) (C C) (C C) (C C) (C C) (G G) (G A) (C C) (C C) (C C) (G G) (T T) (G G) (C C) (G G) (A A) (T T) (T T)

(SIG:MO): [23010]: (A A) (C C) (G G) (C C) (C C) (A A) (T T) (T T) (A A) (C C) (C C) (T T) (C C) (C C) (A A) (G G) (C C) (C C) (A A) (G G) (SIG:MO): [23030]: (A A) (A A) (C C) (T T) (T T) (C C) (C C) (T T) (A A) (G G) (A A) (A A) (C C) (C C) (G G) (A A) (T T) (A A) (T T) (SIG:MO): [23050]: (T T) (C C) (C C) (G G) (G G) (G G) (A A) (T T) (T T) (C C) (G G) (T T) (C C) (A A) (T T) (C C) (T T) (G G) (T T) (C C) (SIG:MO): [23070]: (T T) (C C) (G G) (G G) (T T) (C C) (A A) (T T) (A A) (T T) (G G) (C C) (T T) (G G) (C C) (G G) (G G) (G A) (G G) (SIG:MO): [23090]: (C C) (T T) (G G) (G G) (C C) (G G) (A A) (G G) (A A) (G G) (G G) (T T) (G G) (C C) (G G) (A A) (A A) (G G) (A A) (C C) (SIG:MO): [23110]: (T T) (T T) (T T) (C C) (A A) (A A) (A A) (A A) (T T) (G G) (A A) (A A) (C C) (T T) (T T) (G G) (G G) (G T) (C C) (SIG:M0): [23130]: (A A) (C C) (C C) (A A) (C C) (G G) (G G) (C C) (G G) (C C) (A A) (C C) (C C) (C C) (A A) (T T) (C C) (A A) (G G) (SIG:M0): [23150]: (G G) (T T) (T T) (A A) (A A) (A A) (G G) (A A) (T T) (G G) (T T) (T T) (G G) (A A) (G G) (A A) (A A) (A A) (A A) (T T) (SIG:M0): [23170]: (C C) (T T) (T T) (G G) (G G) (G G) (A A) (A A) (T T) (G G) (A A) (T T) (C C) (A A) (C C) (C C) (G G) (C C) (A A) (C C) (SIG:M0): [23190]: (A A) (T T) (C C) (A A) (C C) (C C) (A A) (C C) (G G) (G G) (T T) (T T) (T T) (T T) (G G) (C C) (G G) (T T) (G G) (SIG:M0): [23210]: (G G) (A A) (C C) (G G) (A A) (A A) (G G) (C C) (A A) (T T) (C C) (A A) (T T) (T T) (A A) (C C) (C C) (T T) (G G) (C C) (SIG:M0): [23230]: (A A) (A A) (C C) (C C) (C C) (G G) (G G) (C C) (G G) (T T) (G G) (T T) (C C) (A A) (C C) (G G) (C C) (A A) (T T) (T T) (SIG:MO): [23250]: (A A) (A A) (T T) (C C) (C C) (C C) (T T) (G G) (T T) (T T) (C C) (T T) (C C) (C C) (G G) (G G) (T T) (A A) (A A) (G G) (SIG:M0): [23270]: (T T) (T T) (C C) (C C) (A A) (G G) (G G) (G G) (A A) (T T) (T T) (T T) (C C) (A A) (T T) (C C) (A A) (C C) (SIG:MO): [23290]: (C C) (T T) (C C) (T T) (A A) (A A) (A A) (C C) (A A) (G G) (G G) (C C) (C C) (T T) (T T) (C C) (A A) (G G) (A A) (T T) (SIG:MO): [23310]: (T T) (C C) (C C) (A A) (G G) (G G) (G G) (G G) (G A) (T T) (C C) (C C) (C C) (T T) (G G) (A A) (A A) (G G) (A A) (C C) (SIG:MO): [23330]: (A A) (T T) (C C) (C C) (C C) (G G) (G G) (G G) (T T) (C C) (C C) (A A) (C C) (G A) (C C) (G A) (C C) (SIG:M0): [23350]: (C C) (T T) (C C) (G G) (C C) (C C) (G G) (T T) (T T) (G G) (T T) (T T) (C C) (G G) (A A) (C C) (C C) (A A) (A A) (T T) (SIG:M0): [23370]: (T T)

DETAILED PATTERN MATCHING SUMMARY FOR MO

ORIG-SEG	OTVAL	MAPS?	MATCH-SEG	MTVAL	MATCH-QUALITY	WEIGTH
(44 60 16 35 MS)	(GAT)	***	n/a	- n/a -	NOTFOUND_WARNG	49
(92 98 6 37 MS)	(G C C)	>	(23469 23476 7 37 MS)	(G C C)	APPROX32_MATCH	11
(104 111 7 35 MS)	(GAT)	>	(23504 23511 7 35 MS)	(GAT)	APPROX64_MATCH	16
(154 159 5 31 MS)	(CTT)	>	(23535 23543 8 32 MS)	(G A A)	APPROX32_MISPL	31
(226 231 5 35 MS)	(G A T)	>	(23595 23600 5 35 MS)	(GAT)	APPROX64_MATCH	15
(247 258 11 32 MS)	(G A A)	>	(23616 23627 11 32 MS)	(G A A)	APPROX64_MATCH	15
(267 279 12 30 MS)	(CTG)	>	(23636 23648 12 30 MS)	(CTG)	APPROX64_MATCH	15
(279 290 11 31 MS)	(CTT)	>	(23648 23659 11 31 MS)	(CTT)	APPROX64_MATCH	15
(307 314 7 34 MS)	(G A G)	>	(23676 23683 7 34 MS)	(G A G)	APPROX64_MATCH	15
(318 323 5 32 MS)	(G A A)	>	(23687 23692 5 32 MS)	(G A A)	APPROX64_MATCH	15
(323 330 7 31 MS)	(CTT)	>	(23692 23699 7 31 MS)	(CTT)	APPROX64_MATCH	15
(334 346 12 31 MS)	(CTT)	>	(23703 23715 12 31 MS)	(CTT)	APPROX64_MATCH	15
(346 358 12 30 MS)	(CTG)	>	(23715 23727 12 30 MS)	(CTG)	APPROX64_MATCH	15
(362 367 5 30 MS)	(CTG)	>	(23731 23736 5 30 MS)	(CTG)	APPROX64_MATCH	15
(367 374 7 31 MS)	(CTT)	>	(23736 23743 7 31 MS)	(CTT)	APPROX64_MATCH	15
(383 391 8 33 MS)	(G A C)	>	(23752 23760 8 33 MS)	(G A C)	APPROX64_MATCH	15
(391 407 16 32 MS)	(G A A)	>	(23760 23776 16 32 MS)	(G A A)	APPROX64_MATCH	15
(407 419 12 33 MS)	(G A C)	>	(23776 23788 12 33 MS)	(G A C)	APPROX64_MATCH	15
(419 430 11 32 MS)	(G A A)	>	(23788 23799 11 32 MS)	(G A A)	APPROX64_MATCH	15
(446 454 8 33 MS)	(G A C)	>	(23815 23823 8 33 MS)	(G A C)	APPROX64_MATCH	15
(454 463 9 34 MS)	(G A G)	>	(23823 23832 9 34 MS)	(G A G)	APPROX64_MATCH	15
(471 478 7 32 MS)	(G A A)	>	(23840 23847 7 32 MS)	(G A A)	APPROX64_MATCH	15
(478 486 8 33 MS)	(G A C)	>	(23847 23855 8 33 MS)	(G A C)	APPROX64_MATCH	15
(499 518 19 31 MS)	(CTT)	>	(23868 23887 19 31 MS)	(CTT)	APPROX64_MATCH	15
(518 523 5 32 MS)	(G A A)	>	(23887 23892 5 32 MS)	(G A A)	APPROX64_MATCH	15
(530 543 13 31 MS)	(CTT)	>	(23899 23912 13 31 MS)	(CTT)	APPROX64_MATCH	15
(543 550 7 32 MS)	(G A A)	>	(23923 23928 5 32 MS)	(G A A)	EXACTING_MATCH	12
(559 566 7 33 MS)	(G A C)	>	(23928 23935 7 33 MS)	(G A C)	APPROX64_MATCH	15
(566 583 17 32 MS)	(G A A)	>	(23935 23952 17 32 MS)	(G A A)	APPROX64_MATCH	15
(594 599 5 32 MS)	(G A A)	>	(23963 23968 5 32 MS)	(G A A)	APPROX64_MATCH	15
(610 622 12 30 MS)	(CTG)	>	(23979 23991 12 30 MS)	(CTG)	APPROX64_MATCH	15
(622 630 8 29 MS)	(C T C)	>	(23991 23999 8 29 MS)	(CTC)	APPROX64_MATCH	15
(646 658 12 24 MS)	(C G A)	>	(24015 24027 12 24 MS)	(C G A)	APPROX64_MATCH	15
(670 678 8 25 MS)	(C G C)	>	(24039 24047 8 25 MS)	(C G C)	APPROX64_MATCH	15
(741 749 8 36 MS)	(G C A)	>	(24110 24118 8 36 MS)	(G C A)	APPROX64_MATCH	15
(749 761 12 35 MS)	(G A T)	>	(24118 24130 12 35 MS)	(G A T)	APPROX64_MATCH	15
(773 778 5 33 MS)	(G A C)	>	(24142 24147 5 33 MS)	(G A C)	APPROX64_MATCH	15
(797 805 8 36 MS)	(G C A)	>	(24166 24174 8 36 MS)	(G C A)	APPROX64_MATCH	15
(813 821 8 33 MS)	(G A C)	>	(24182 24190 8 33 MS)	(G A C)	APPROX64_MATCH	15
(825 830 5 34 MS)	(G A G)	>	(24194 24199 5 34 MS)	(G A G)	APPROX64_MATCH	15
(845 853 8 34 MS)	(G A G)	>	(24214 24222 8 34 MS)	(G A G)	APPROX64_MATCH	15
(857 869 12 32 MS)	(G A A)	>	(24226 24238 12 32 MS)	(G A A)	APPROX64_MATCH	15
(869 877 8 33 MS)	(G A C)	>	(24238 24246 8 33 MS)	(G A C)	APPROX64_MATCH	15
(877 885 8 32 MS)	(G A A)	>	(24246 24254 8 32 MS)	(G A A)	APPROX64_MATCH	15
(885 897 12 30 MS)	(CTG)	>	(24254 24266 12 30 MS)	(CTG)	APPROX64_MATCH	15
(901 910 9 28 MS)	(C T A)	>	(24270 24279 9 28 MS)	(CTA)	APPROX64_MATCH	15

(926 935 9 32 MS)	(G A A)	>	(24295 24304 9 32 MS)	(G A A)	APPROX64_MATCH	15
(943 951 8 35 MS)	(G A T)	>	(24312 24320 8 35 MS)	(G A T)	APPROX64_MATCH	15
(955 963 8 36 MS)	(G C A)	>	(24324 24332 8 36 MS)	(G C A)	APPROX64_MATCH	15
(976 983 7 33 MS)	(G A C)	>	(24345 24352 7 33 MS)	(G A C)	APPROX64_MATCH	15
(987 995 8 31 MS)	(CTT)	>	(24356 24364 8 31 MS)	(CTT)	APPROX64_MATCH	15
(996 1007 11 29 MS)	(C T C)	>	(24380 24389 9 29 MS)	(CTC)	EXACTING_MATCH	8
(1020 1027 7 28 MS)	(C T A)	>	(24389 24396 7 28 MS)	(CTA)	APPROX64_MATCH	15
(1028 1035 7 30 MS)	(C T G)	>	(24397 24404 7 30 MS)	(C T G)	APPROX64_MATCH	15
(1048 1055 7 27 MS)	(C G T)	>	(24417 24424 7 27 MS)	(C G T)	APPROX64_MATCH	15
(1064 1071 7 31 MS)	(CTT)	>	(24433 24440 7 31 MS)	(CTT)	APPROX64_MATCH	15



PATTERN MATCH MO - PAIRWISE SEQUENCE ALIGNMENT PLOT AND HISTOGRAMS

