

**M2: APPROXIMATE PATTERN MATCH**

MATCH_STARTS	AND_ENDS_AT	MATCH_RATING	MATCH_SPANS	MATCH_WEIGHT	COST_METRIC	COST_VECTOR
10095	11095	0.47058824	1001	1883.0	0	(2 7 5 1 1 1 7 0)

**FINEGRAIN ALIGNMENT WITHIN HPS INPUT SEQUENCE  
BETWEEN DNA SIGNATURE AND M2 [10095:11095] (47/100)**

DNA SEQUENCE	DESCRIPTION	SIGNATURE STARTS	MATCHING STARTS_AT	SIGNATURE ENDS	MATCH_ENDS_AT
HPS INPUT SEQUENCE	(SIGNATURE + TESTSEQUENCE)	SIGNATURE BP=0	TESTSEQUENCE BP=10100	SIGNATURE BP=1101	TESTSEQUENCE=11201
DNA SIGNATURE	---	BP-INDEX=0	---	BP- INDEX=1101	---
DNA TEST SEQUENCE	SUBSEQUENCE M2	----	BP- INDEX=8999	----	BP-INDEX=10100

**M2 ALIGNMENT AT GENOMIC ADDRESS [9001] FOR INPUT TEST  
SEQUENCE IN FILE [HPS\_1DNA\_INPUT\_SERIES\_BASES.DNA]**

(SIG:M2):	_0_	_1_	_2_	_3_	_4_	_5_	_6_	_7_	_8_	_9_	_10_	_11_	_12_	_13_	_14_	_15_	_16_	_17_	_18_	_19_
(SIG:M2): [9001]:	(G G)	(T T)	(C C)	(A A)	(G G)	(C C)	(G G)	(C C)	(T T)	(T A)	(T T)	(T T)	(G G)	(G G)	(T T)	(G T)	(C C)	(T T)	(G G)	(G G)
(SIG:M2): [9021]:	(A A)	(A A)	(G G)	(A A)	(C C)	(G G)	(G G)	(A A)	(A A)	(C C)	(C C)	(C C)	(C A)	(G G)	(T T)	(G T)	(T T)	(C C)	(A A)	(C C)
(SIG:M2): [9041]:	(G G)	(T G)	(T T)	(C C)	(G G)	(G G)	(G G)	(C C)	(A C)	(T A)	(T T)	(A A)	(G G)	(G G)	(G G)	(G G)	(C C)	(A A)	(A A)	(C C)
(SIG:M2): [9061]:	(A A)	(T G)	(G G)	(T T)	(T T)	(C C)	(G G)	(G G)	(A C)	(G G)	(G G)	(T T)	(T T)	(G G)	(G G)	(G G)	(G G)	(A A)	(A A)	(G G)
(SIG:M2): [9081]:	(T T)	(C C)	(G G)	(T T)	(T T)	(G T)	(T T)	(C C)	(A A)	(T A)	(T T)	(A A)	(C C)	(T T)	(T T)	(C C)	(A A)	(A A)	(T T)	(G G)
(SIG:M2): [9101]:	(A A)	(C C)	(C C)	(G G)	(G G)	(G T)	(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 C)	(T T)
(SIG:M2): [9121]:	(C C)	(A A)	(C C)	(T T)	(G G)	(A A)	(T T)	(C C)	(A C)	(T T)	(T T)	(C C)	(C C)	(T T)	(A A)	(G T)	(T T)	(C C)	(T T)	(C C)
(SIG:M2): [9141]:	(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 T)	(T T)	(A A)	(A C)	(T T)
(SIG:M2): [9161]:	(T T)	(A A)	(T T)	(C C)	(C C)	(C C)	(C C)	(A A)	(T T)	(T A)	(T T)	(T T)	(G G)	(G G)	(C C)	(A A)	(A A)	(T T)	(G G)	(T T)
(SIG:M2): [9181]:	(C C)	(T G)	(G G)	(C C)	(A A)	(C C)	(C C)	(A A)	(A A)	(T T)	(G G)	(A A)	(C C)	(G G)	(C C)	(C C)	(G G)	(A A)	(T T)	(G G)
(SIG:M2): [9201]:	(A A)	(A A)	(G G)	(A A)	(A A)	(G T)	(C C)	(T T)	(T T)	(C C)	(T T)	(C C)	(C A)	(G G)	(G G)	(G T)	(A A)	(C C)	(A A)	(T T)
(SIG:M2): [9221]:	(G G)	(C C)	(C A)	(C C)	(A A)	(A A)	(G G)	(G G)	(T T)	(C C)	(T T)	(T G)	(G G)	(T T)	(G G)	(A A)	(T T)	(T T)	(A C)	(G G)
(SIG:M2): [9241]:	(C C)	(T G)	(C A)	(C C)	(C C)	(G T)	(G G)	(C C)	(A C)	(G G)	(C C)	(T T)	(G G)	(A A)	(T T)	(G T)	(G G)	(C C)	(A C)	(T A)
(SIG:M2): [9261]:	(G G)	(C C)	(C A)	(A A)	(C C)	(G T)	(T T)	(C C)	(A C)	(G G)	(T T)	(A A)	(C A)	(T T)	(A A)	(C C)	(C C)	(G G)	(A A)	(T A)
(SIG:M2): [9281]:	(G G)	(A A)	(C C)	(C C)	(T T)	(C C)	(T T)	(C C)	(T T)	(T T)	(C C)	(T T)	(T T)	(A A)	(C C)	(C C)	(T T)	(G G)	(A A)	(T A)
(SIG:M2): [9301]:	(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 A)
(SIG:M2): [9321]:	(T T)	(T T)	(G G)	(C C)	(C C)	(G G)	(A A)	(T T)	(A A)	(T T)	(C C)	(T G)	(C A)	(T T)	(A A)	(C C)	(C C)	(C C)	(G G)	(T T)
(SIG:M2): [9341]:	(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 C)	(G G)
(SIG:M2): [9361]:	(C C)	(T G)	(C A)	(G G)	(A A)	(A A)	(A A)	(G G)	(G G)	(C C)	(G G)	(C C)	(C A)	(C C)	(A A)	(G G)	(A A)	(A A)	(T T)	(G G)
(SIG:M2): [9381]:	(G G)	(C C)	(T T)	(G G)	(C C)	(A A)	(T T)	(T T)	(A A)	(T T)	(C C)	(T G)	(C C)	(G G)	(G G)	(G G)	(C C)	(G G)	(A A)	(T T)
(SIG:M2): [9401]:	(A A)	(A A)	(C C)	(C C)	(C C)	(G G)	(G G)	(A A)	(T T)	(G G)	(C C)	(T G)	(G G)	(C C)	(G G)	(C C)	(T T)	(G G)	(G G)	(C C)
(SIG:M2): [9421]:	(G G)	(T T)	(T T)	(A A)	(G G)	(A A)	(A A)	(A A)	(A A)	(T A)	(G G)	(C C)	(C C)	(C C)	(G G)	(C C)	(G G)	(C C)	(G G)	(T T)
(SIG:M2): [9441]:	(T T)	(C C)	(C C)	(C C)	(A A)	(G G)	(G G)	(T T)	(A C)	(T T)	(G G)	(A A)	(C A)	(T T)	(G G)	(G G)	(C C)	(A A)	(T T)	(G G)
(SIG:M2): [9461]:	(G G)	(A A)	(T T)	(C C)	(T T)	(G G)	(G G)	(C C)	(A A)	(T A)	(A A)	(A A)	(G G)	(A A)	(A A)	(G G)	(T T)	(G G)	(A A)	(C C)
(SIG:M2): [9481]:	(C C)	(A A)	(C C)	(C C)	(G G)	(C C)	(A A)	(G G)	(A A)	(T A)	(G G)	(C C)	(C C)	(T T)	(A A)	(G T)	(A A)	(G G)	(A C)	(T T)
(SIG:M2): [9501]:	(C G)	(C G)	(C A)	(C C)	(C A)	(C C)	(C A)	(C A)	(C G)	(C G)	(C G)	(C G)	(C A)	(C G)	(C C)	(C T)	(C G)	(C G)	(C A)	(C C)
(SIG:M2): [9521]:	(C T)	(C T)	(C G)	(C A)	(C C)	(C C)	(C G)	(C T)	(G G)	(G G)	(C C)	(C C)	(T T)	(G G)	(C C)	(C C)	(A A)	(G G)	(T A)	
(SIG:M2): [9541]:	(A A)	(T G)	(C C)	(G G)	(A A)	(A A)	(A A)	(A A)	(T A)	(G G)	(A A)	(C A)	(G G)	(A A)	(C C)	(G G)	(A A)	(G G)	(C C)	
(SIG:M2): [9561]:	(T T)	(T G)	(C C)	(C C)	(G G)	(G T)	(T T)	(C C)	(A C)	(T A)	(C C)	(T G)	(T T)	(C C)	(G G)	(G T)	(G G)	(G G)	(A C)	(T T)
(SIG:M2): [9581]:	(T T)	(A A)	(T T)	(G G)	(A A)	(G T)	(T T)	(T T)	(T T)	(G G)	(G G)	(T T)	(G G)	(C C)	(C C)	(A A)	(A A)	(G G)	(A C)	(G G)
(SIG:M2): [9601]:	(C C)	(A A)	(C A)	(C C)	(A A)	(G T)	(C C)	(C C)	(T T)	(G G)	(C C)	(T G)	(G G)	(A A)	(T T)	(G G)	(C C)	(T T)	(G G)	(G G)

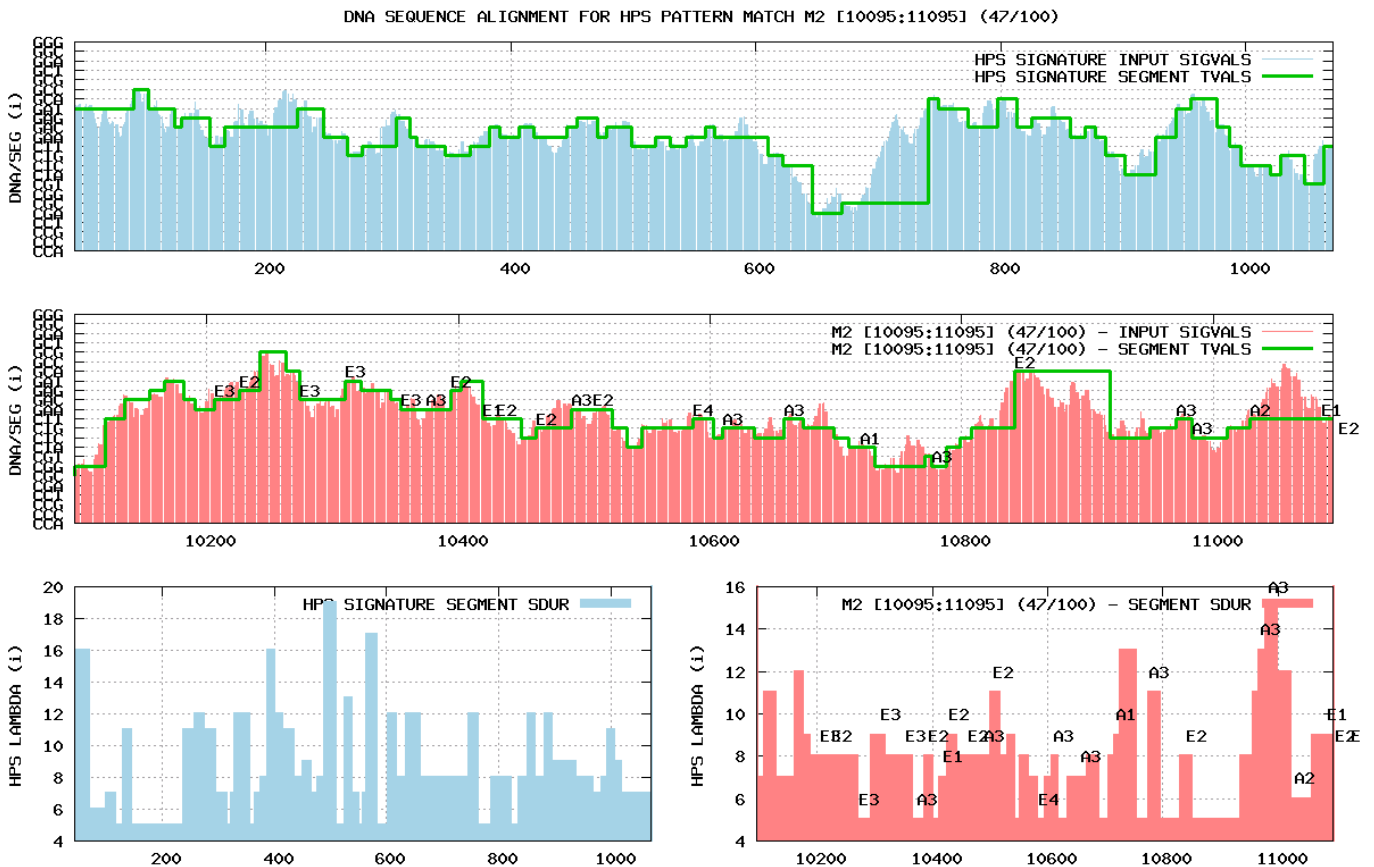
(SIG:M2): [9621]: (T T) ( **T G** ) (G G) (A A) (T T) (A A) (G G) (A A) (G G) (G G) (C C) (T T) (G G) (T T) (C C) (G G) (C C) (C C) (T T) (G G)  
(SIG:M2): [9641]: (A A) (C C) (C C) (A A) (T T) (C C) (G G) (T T) (T T) (C C) (C C) ( **T G** ) (G G) (C C) (G G) (C C) (A A) (A A) (A A) (C C)  
(SIG:M2): [9661]: (T T) (T T) (C C) (T T) (G G) (C C) (G G) (G G) (A A) ( **T A** ) (G G) (A A) (T T) (G G) (T T) (G G) (C C) (T T) (G G) ( **T A** )  
(SIG:M2): [9681]: (A A) (A A) ( **C A** ) (T T) (G G) (A A) (A A) (T T) ( **A C** ) (C C) (A A) ( **T G** ) ( **C A** ) (C C) (G G) (G G) (C C) (A A) (T T) (C C)  
(SIG:M2): [9701]: (T T) (T T) (C C) (C C) (T T) (C C) (T T) (C C) ( **A C** ) ( **T A** ) (A A) (C C) (G G) (G G) (T T) (C C) (C C) (T T) (G G) (G G)  
(SIG:M2): [9721]: (C C) ( **T G** ) ( **C A** ) (C C) (C C) (C C) (G G) (G G) ( **A C** ) (C C) (C C) (C C) (G G) (T T) (G G) (C C) (G G) (A A) (T T) (T T)  
(SIG:M2): [9741]: (A A) (C C) (G G) (C C) (C C) (A A) (T T) (T T) (A A) (C C) (C C) ( **T G** ) (C C) (C C) (A A) ( **G T** ) (C C) (C C) (A A) (G G)  
(SIG:M2): [9761]: (A A) (A A) ( **C A** ) (T T) (T T) (C C) (C C) (T T) ( **A C** ) (G G) (A A) (A A) ( **C A** ) (C C) (C C) (G G) (A A) (T T) (A A) (T T)  
(SIG:M2): [9781]: (T T) (C C) (C C) (G G) (G G) ( **G T** ) (A A) (T T) (T T) (C C) (G G) ( **T G** ) (C C) (A A) (T T) (C C) (T T) (G G) (T T) (C C)  
(SIG:M2): [9801]: (T T) (C C) (G G) (G G) (T T) (C C) (A A) (T T) ( **A C** ) ( **T A** ) (G G) (C C) (T T) (G G) (C C) ( **G T** ) (G G) (G G) ( **A C** ) (G G)  
(SIG:M2): [9821]: (C C) (T T) (G G) (G G) (C C) (G G) (A A) (G G) ( **A C** ) (G G) (G G) (T T) (G G) (C C) (G G) (A A) (A A) (G G) (A A) (C C)  
(SIG:M2): [9841]: (T T) ( **T G** ) (T T) (C C) (A A) (A A) (A A) (A A) (T T) (G G) (A A) (A A) ( **C A** ) (T T) (T T) ( **G T** ) (G G) (G G) (T T) (C C)  
(SIG:M2): [9861]: (A A) (C C) (C C) (A A) (C C) (G G) (G G) (C C) (G G) (G G) (C C) (A A) ( **C A** ) (C C) (C C) (A A) (T T) (C C) ( **A C** ) (G G)  
(SIG:M2): [9881]: (G G) (T T) (T T) (A A) (A A) (A A) (G G) (A A) (T T) (G G) (T T) ( **T G** ) (G G) (A A) (G G) (A A) (A A) (A A) (A A) ( **T A** )  
(SIG:M2): [9901]: (C C) ( **T G** ) (T T) (G G) (G G) ( **G T** ) (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 C** ) (C C)  
(SIG:M2): [9921]: (A A) ( **T G** ) ( **C A** ) (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) (G G) (T T) (G G)  
(SIG:M2): [9941]: (G G) (A A) (C C) (G G) (A A) (A A) (G G) (C C) (A A) ( **T A** ) (C C) (A A) (T T) (T T) (A A) (C C) (C C) (T T) (G G) (C C)  
(SIG:M2): [9961]: (A A) (A A) ( **C A** ) (C C) (C C) ( **G T** ) (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 A** )  
(SIG:M2): [9981]: (A A) (A A) (T T) (C C) (C C) (C C) (T T) (G G) (T T) (T T) (C C) ( **T G** ) ( **C A** ) (C C) (G G) (G G) (T T) (A A) ( **A C** ) (G G)  
(SIG:M2): [10001] (T T) (T T) ( **C A** ) (C C) (A A) (G G) (G G) (G G) ( **A C** ) ( **T A** ) (T T) (T T) (C C) (A A) (T T) (C C) (G G) (C C) (A A) (C C)  
:  
(SIG:M2): [10021] (C C) ( **T G** ) ( **C A** ) (T T) (A A)  
:

## DETAILED PATTERN MATCHING SUMMARY FOR M2

ORIG-SEG	OTVAL	MAPS?	MATCH-SEG	MTVAL	MATCH-QUALITY	WEIGHT
(44 60 16 35 MS)	(G A T)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	43
(92 98 6 37 MS)	(G C C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	77
(104 111 7 35 MS)	(G A T)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	43
(126 131 5 33 MS)	(G A C)	-->	(10206 10214 8 33 MS)	(G A C)	APPROX64_MATCH	27
(131 142 11 34 MS)	(G A G)	-->	(10226 10234 8 34 MS)	(G A G)	APPROX32_MATCH	12
(154 159 5 31 MS)	(C T T)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	57
(166 171 5 33 MS)	(G A C)	-->	(10274 10279 5 33 MS)	(G A C)	APPROX64_MATCH	13
(226 231 5 35 MS)	(G A T)	-->	(10310 10319 9 35 MS)	(G A T)	APPROX64_MATCH	27
(247 258 11 32 MS)	(G A A)	-->	(10354 10362 8 32 MS)	(G A A)	APPROX64_MATCH	24
(279 290 11 31 MS)	(C T T)	-->	(10374 10379 5 32 MS)	(G A A)	APPROX64_MISPL	40
(307 314 7 34 MS)	(G A G)	-->	(10394 10402 8 34 MS)	(G A G)	APPROX32_MATCH	12
(318 323 5 32 MS)	(G A A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	NIL
(323 330 7 31 MS)	(C T T)	-->	(10419 10426 7 31 MS)	(C T T)	EXACTING_MATCH	1
(334 346 12 31 MS)	(C T T)	-->	(10430 10439 9 31 MS)	(C T T)	APPROX32_MATCH	13
(346 358 12 30 MS)	(C T G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	37
(362 367 5 30 MS)	(C T G)	-->	(10462 10470 8 30 MS)	(C T G)	APPROX32_MATCH	17
(383 391 8 33 MS)	(G A C)	-->	(10490 10498 8 32 MS)	(G A A)	APPROX64_MISPL	28
(407 419 12 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	NIL
(419 430 11 32 MS)	(G A A)	-->	(10507 10518 11 32 MS)	(G A A)	APPROX32_MATCH	7
(446 454 8 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	61
(454 463 9 34 MS)	(G A G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	73
(471 478 7 32 MS)	(G A A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	41
(478 486 8 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	54
(499 518 19 31 MS)	(C T T)	-->	(10586 10591 5 31 MS)	(C T T)	SPANNING_MATCH	64
(518 523 5 32 MS)	(G A A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	41
(530 543 13 31 MS)	(C T T)	-->	(10610 10618 8 30 MS)	(C T G)	APPROX64_MISPL	51
(543 550 7 32 MS)	(G A A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	37
(554 559 5 32 MS)	(G A A)	-->	(10659 10666 7 31 MS)	(C T T)	APPROX64_MISPL	34
(610 622 12 30 MS)	(C T G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	47
(622 630 8 29 MS)	(C T C)	-->	(10719 10728 9 28 MS)	(C T A)	EXACTING_MISPL	22
(646 658 12 24 MS)	(C G A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	46
(670 678 8 25 MS)	(C G C)	-->	(10776 10787 11 26 MS)	(C G G)	APPROX64_MISPL	39
(741 749 8 36 MS)	(G C A)	-->	(10842 10850 8 36 MS)	(G C A)	APPROX32_MATCH	6
(773 778 5 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	62
(797 805 8 36 MS)	(G C A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	50
(813 821 8 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	86
(825 830 5 34 MS)	(G A G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	98
(845 853 8 34 MS)	(G A G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	74
(857 869 12 32 MS)	(G A A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	38
(869 877 8 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	58

(877 885 8 32 MS)	(G A A)	-->	(10970 10983 13 31 MS)	(C T T)	APPROX64_MISPL	38
(885 897 12 30 MS)	(C T G)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	25
(901 910 9 28 MS)	(C T A)	-->	(10983 10998 15 29 MS)	(C T C)	APPROX64_MISPL	53
(926 935 9 32 MS)	(G A A)	-->	(11029 11035 6 31 MS)	(C T T)	APPROX32_MISPL	36
(955 963 8 36 MS)	(G C A)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	NIL
(976 983 7 33 MS)	(G A C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	55
(987 995 8 31 MS)	(C T T)	-->	(11086 11095 9 31 MS)	(C T T)	EXACTING_MATCH	8
(996 1007 11 29 MS)	(C T C)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	NIL
(1011 1020 9 29 MS)	(C T C)	-->	(11099 11107 8 29 MS)	(C T C)	APPROX32_MATCH	11
(1020 1027 7 28 MS)	(C T A)	-->	(11127 11135 8 28 MS)	(C T A)	APPROX64_MATCH	16
(1064 1071 7 31 MS)	(C T T)	***	----- n/a -----	- n/a -	NOTFOUND_WARNG	81

## PATTERN MATCH M2 - DETAILED SEQUENCE ALIGNMENT COMPARISON PLOT



## PATTERN MATCH M2 - PAIRWISE SEQUENCE ALIGNMENT PLOT AND HISTOGRAMS

