

Sanger sequencing results

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Version 1.2 (29 March 2018)

Primer information

V1	QJL	1	2	3	4
E23	R	R	R	R	R
E27	F	F	F	F	F
E33	F	F	F	R	F
E39	F	F	F	F	F

```
## Warning: Setting row names on a tibble is deprecated.
```

```
## use default substitution matrix
## use default substitution matrix
## use default substitution matrix
## use default substitution matrix
```

MSA

```
## Warning in msaPrettyPrint(res.msa[[1]], output = "asis"): Cannot use
## default file name 'res.msa[[1]].asis' because it would contain invalid
## characters => resorting to 'msaPrettyPrintOutput.asis'!
```

logo

TAAAC TTT CAT GCACAC GTGTG CGAGT CAGTCC ATACCCA ACAACAC CTTT CTCT GCGC

	TAAACTTTTCATGCACACGTGTGCGAGTCAGTCCATACCCAACAACACCTTTTCTTGCCGC	
Father	0
Mother	0
Sister	TAAACTTTTCATGCACACGTGTGCGAGTCAGTCCATACCCAACAACACCTTTTCTTGCCGC	60
Brother	0
ProbandTCCTGCACTG	10
RefSeq	0
consensus	0

logo

C
G A A G G T C C T G C A A G C A G T C T A T T C T G T A T G C T C C T C C A A A

FatherCTTTGT.TGCCTTCTACAAAA	20
Mother	0
Sister	CTTTAGAGAGGAGGGAGGGAGGTTCTCTGCAAGCAGTCTTTTCGGTATGTCTCACTCCAAA	120
Brother	0
Proband	CAAAGAGCAATGGGAGAGCAGGTCCCTGCAAGCAGC..ATCCTGTATGGCTCCGTACAAA	68
RefSeq	0
consensus	0

logo

Father AAACAAAAAATATTTTTTTT.TGTGGGGAAGCCCCA...CGCACACTCCTCCCGGGGGG.. 74
 Mother 0
 Sister GAGCAATGAGTAGTTTCTTGCGTTGAGTAAACACAA.GCGCACATCTCTCCAGAAGATG 179
 Brother 0
 Proband AAGCGATGCTGAGTTATTCGTCTGAGTCAGCTGCAATGCCAGCTCACCTGCCGTGAGTTA 128
 RefSeq 0
 consensus

logo

Father .GCTA.CAGAACCTCAGGTTGGTTCCTTCCCTCCGG.GTGAAGTTCTGGACGTCAGTTCA 131
 MotherCGATGATGGTCTCTCTACGAGGGCGAGGGT...GAGGTAAGCTCC 44
 Sister AGCTAACGTAACGTCGGGTGGGTTCCTTCATCTCGGTGTGGGTTCGTGGTGG..AGTCCT 237
 Brother 0
 Proband CGCTAACG...TGCGAGTAGGTTCTTCATCAGAGG..TGAGGTGGGGTGAGTGAGTCAT 182
 RefSeq 0
 consensus * * ** ** * ** * **

logo

Father TTGTGGA.GGCATATCCA AAAATACCT.CCCAGGCAGGCACACTTTCTTTCTC..AGAG 187
 Mother TTTTGT..GACGCTGTTTATAAATTATCCCTGCGC.GGCCACATTCTTTCTCC..CTG 99
 Sister TTGTGGATGGCACATCCAACAATAACTACCCACGCGGCACACTTTCTTTCTCTCAGTG 297
 Brother 0
 Proband TTT.....ACGGAGCC.ATCATAACT.ACACACACAGCCACACACTCCTCC.....AG 228
 RefSeq 0
 consensus ** * ** ** * * * * * * * *

logo

Father ACAGACAGAGGGATGAG.TGAGCTCAGTC AAGCGGGCGTGCTTTCTGTCTCAGGGGAGGG 246
 Mother AGAAGCT.ATGGATGTC.GACCCTCAGTCACA CCGAGGAGCTTTCTGTCTGAG.GGAGGG 156
 Sister AGAGGCTGAGGATGAGATGAGCTCAGTC AAGCGGGCGTGCTTTCTGTCTCAGTGAGGG 357
 Brother 0
 Proband ACAGACAGAGTATGAGG.TAAGGTCAGTC CAGCGGGCGAGCTT.CTGTCTGGGTGAGGG 286
 RefSeq 0
 consensus * * * * * * * * * * * * * * *

logo

Father GGAAGGG.TTCA TTCCGGCAAGCAAGGCAGGCAGCGTTCTTGGAGGGGGGGGGGAGG 305
 Mother GGAAGAGGATCTTTCCGGGCAGTCAAGGAGGCGCGTTTATTGGAGAAAAAGGGAGGCG 216
 Sister GGGGAGGGGTTTCA TTCCGGCAATCAAGGCAGAGA CCGTTTATTGGAGAGAGGGGGGAGG 417
 Brother 0
 Proband AGAAGGGAAACC..TTCCGGCAGGCGAGGAGGGGCGGTGCGTTTCTGAGGGAGGGGAGAGG 344
 RefSeq 0
 consensus * * * * * * * * * * * * * *

logo

Father	AGCGGAGA. GTGAGTGG. GGGAGGCGTGAG. CAACCAACCCAGCCCTGCCACAAACCCATA	362
Mother	AGCGAAAATAATAGAGG. GACGCCCCGAAG. TGACAAAGCAAGCCCATCCACTATCGAGA	274
Sister	AGCGGACA. GTCAGTGG. GGGGCGCG. GAG. CAGCCAGCCATCCCTAGTCACTAGCCATA	473
Brother	0
Proband	AGCAGAGA. GTGAGTGGAGGCACGCGCGAGGTGAGAAAGCCCTGCCCTATCGACAGCCAGA	403
RefSeq	0
consensus	*** * * * * * * * * * * * * *	

logo

Father	CTCATTCC. TGACCTTGCTGGCTGCTCCATTTTATATAA. .AGCTATGGAAAAAGAGGG	419
Mother	GTCATTCCGTTCAAGCCCGAGCTGCAACCAGATTGAAAAT. .ACCTATAGAAAATGAGGG	332
Sister	CTCATTCC. TGAGCTTGCTGGCCGCGATCCAAATTTAAATAT. .AGGTATGGAAAAAGAGGG	530
Brother	0
Proband	CTCATTCC. TGAGCTTCCGGGCCGCGCTCCCTTTTATTGATAGGGTAAGCAAAAGAGGG	462
RefSeq	0
consensus	***** * * * * * * * * * * * *	

logo

Father	GCCA.CA. TGTGCCCTTGGGC. .TGATATGTCACATGCAATGTCCTCTCTTGTTTCC	475
Mother	GTCACCA. TGTGCCCTGGGCA. .GAATATGACACAGGGCATGTCGCTCTCTGTTTCC	388
Sister	AAAAACA. TGTTCCTTGGGGGCGTATATGACACATGCAATGTCCTCTCTTGTTTCC	589
Brother	18
Proband	GGGCA.CA. TGGTCCCTCGGGGGCGTATATGACACATGCGCATGTCGCTCTCTGTTTCC	522
RefSeq	0
consensus	* * * * * * * * * * * * * * * * *	

logo

Father	ATAGCTTTAAATAAAATGGGGCCAGCAAGGAAGCTCAGGAATGGGTCTTGGCAATGGCAA	535
Mother	ATAGCTTTAAATAAAATGGGGCCAGCAAGGAAGCTCAGGAATGGGTCTTGGCAATGGCAA	448
Sister	ATAGCTTTAAATAAAATGGGGCCAGCAAGGAAGCTCAGGAATGGGTCTTGGCAATGGCAA	649
Brother	ATAGCTTTAAATAAAATGGGGCCAGCAAGGAAGCTCAGGAATGGGTCTTGGCAATGGCAA	78
Proband	ATAGCTTTAAATAAAATGGGGCCAGCAAGGAAGCTCAGGAATGGGTCTTGGCAATGGCAA	582
RefSeq	0
consensus	*****	

logo

Father	GGCTTTGCTGCTCACCTCGGGCCTCCTCTGAGTCTCTGTCCCGCTCCTCCTCCTCTTCCT	595
Mother	GGCTTTGCTGCTCACCTCGGGCCTCCTCTGAGTCTCTGTCCCGCTCCTCCTCCTCTTCCT	508
Sister	GGCTTTGCTGCTCACCTCGGGCCTCCTCTGAGTCTCTGTCCCGCTCCTCCTCCTCTTCCT	709
Brother	GGCTTTGCTGCTCACCTCGGGCCTCCTCTGAGTCTCTGTCCCGCTCCTCCTCCTCTTCCT	138
Proband	GGCTTTGCTGCTCACCTCGGGCCTCCTCTGAGTCTCTGTCCCGCTCCTCCTCCTCTTCCT	642
RefSeq	0
consensus	*****	

logo
 CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCGAGAGC
 Father CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCGGAGAGC 655
 Mother CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCGGAGAGC 568
 Sister CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCGGAGAGC 769
 Brother CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCAGAGAGC 198
 Proband CGAATGCCCTCTGCCTCCATTGCCGCCAGGAATGTTCCCTTTCCCTGAGCCGGAGAGC 702
 RefSeq 0
 consensus *****



logo
 ATGCGCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG
 Father ATGCCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG 715
 Mother ATGCCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG 628
 Sister ATGCCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG 829
 Brother ATGCTCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG 258
 Proband ATGCCCTGGGCTTGACGGTGCTCATCCCTCAACTTGTCTCTCAAGGAGAAAGTGTGTGG 762
 RefSeqGAGAAAGTGTGTGG 14
 consensus *****!!!!!!!!!!!!!!

logo
 CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT
 Father CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 775
 Mother CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 688
 Sister CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 889
 Brother CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 318
 Proband CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 822
 RefSeq CCTGTGTGGGAATTTTGATGGCATCCAGAACAAATGACCTCACCAGCAGCAACCTCCAAGT 74
 consensus !!!

logo
 GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC
 Father GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 835
 Mother GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 748
 Sister GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 949
 Brother GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 378
 Proband GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 882
 RefSeq GGAGGAAGACCTGTGGACTTTGGGAACCTCTGGAAAGTGAGCTCGCAGTGTGCTGACAC 134
 consensus !!!

logo
 CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCAGAGCTTGCTTCCTGGAATGT
 Father CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCAGAGCTTGCTTCCTGGAATGT 895
 Mother CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCAGAGCTTGCTTCCTGGAATGT 808
 Sister CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCAGAGCTTGCTTCCTGGAATGT 1009
 Brother CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCTAGAGCTTGCTTCCTGGAATGT 438
 Proband CAGAAAAGTACGTCTGGGTCTCTGTGTGGACAGAGCCCAGAGCTTGCTTCCTGGAATGT 942
 RefSeq CAGAAAA..... 141
 consensus !!!!!!!!!*****

logo	CCCTCTGTCCCCATGTCATGGGCTGAAAGGGT	
Father	CCCTCTGTCCCCATGTCATGGGCTGAAAGGGAGTG	931
Mother	CCCTCTGTCCCCATGTCATGGGACTGAAGCTA....	840
Sister	CCCTCTGTCCCCATGTCATGGGACTGAAGGGG.GTA	1044
Brother	CCCTCTGTCCCCATGTCATGGGCTGAATGGGGTTA	474
Proband	CCCTCTGTCCCCATGTCATGGGTCTGAACGGGCGT	978
RefSeq	141
consensus	*****	

 non conserved
 ≥ 50% conserved