

The benchmark dataset S containing 550 RNA samples, of which 176 RNA sequence samples belong to the positive subset S^+ and 374 RNA sequence samples belong to the negative subset S^- .

Note that each sequence samples that we considered is 23 nt long with U at the center along the RNA sequences given below.

Positive subset S^+

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>positive_Human_1
UUCGGCUGUUAACUGAAAGGUUGGUGGUUCGAGCCCACCCA
>positive_Human_2
UGUCUCUGUGGCGCAAUCGGUUAGCGCGUUCGGCUGUUAAC
>positive_Human_3
CGCCGUGAUCGUUAGUGGUUAGUACUCUGCGUUGUGGCCG
>positive_Human_4
CUUCCCUGGUGGUCUAGUGGUUAGGAUUCGGCGCUCUCACC
>positive_Human_5
UUCGCCUCACACGCGAAAGGUCCCCGGUUCGAAACUGGGCG
>positive_Human_6
GGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUCACACGC
>positive_Human_7
CUGGGCCAUAAACCCAGAGGUCCAUGGAUCGAAACCAUCCU
>positive_Human_8
UGUCAGUCUCUGUGGCGCAAUCGGUUAGCGCGUUCGGCUGU
>positive_Human_9
UAGCAUUGGUGGUUCAGUGGUAGAAUUCUGCCUGCCACGC
>positive_Human_10
GUGUCAGGAUGGCCGAGUGGUCUAAGGCGCCAGACUCAAGG
>positive_Human_11
UUAGACUGAAGAUCUAAAGGUCCCUGGUUCGAUCCCGGGUU
>positive_Human_12
CUUCGCCGAAAUAGCUCAGUUGGGAGAGCGUUAGACUGAAG
>positive_Human_13
CGGCAGCCGAAAUAGCUCAGUUGGGAGAGCGUUAGACUGAA
>positive_Human_14
AACGUGCCGAAAUAGCUCAGUUGGGAGAGCGUUAGACUGAA
>positive_Human_15
CAGCGCCGUCUGGUGUAGUGGUUAUCAUGCAAGAUUCCAUUC
>positive_Human_16
CGUAGUCGUGGCCGAGUGGUUAAGGCGAUGGACUAGAAAUC
>positive_Human_17
CAGGUCCAUUGGUGUAAUGGUUAGCACUCUGGACUUUGAAU
>positive_Human_18
CGGAGCCUUCGAUAGCUCAGUUGGUAGAGCGGAGGACUGUA
>positive_Human_19
AGGGCGUGGCAAUCCUUAAGGUCGUGGUUCGAUUCGGGCUC
>positive_Human_20
AGGCGGGGGAUUAGCUCAAAUGGUAGAGCGCUCGCUUAGCA
>positive_Human_21
GUGGGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAC
>positive_Human_22
UGCAAGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAC
>positive_Human_23
CAUCUGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAC
>positive_Human_24
GGUACGUAGUCGUGGCCGAGUGGUUAAGGCGAUGGACUUGA
>positive_Human_25
UAUCUGUAGUCGUGGCCGAGUGGUUAAGGCGAUGGACUAGA
>positive_Human_26
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GGCGUGCCGUGAUCGUUAUAGUGGUUAGUACUCUGCGUUGUG
>positive_Human_27
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>positive_Human_28
UGCCUCGUUAGCGCAGUAGGUAGCGCGUCAGUCUCAAAUC
>positive_Human_29
GUUAAGAUGGCAGAGCCCGUAAUCGCAUAAAACUAAAAAC
>positive_Mus_1
UGAGACUCUAAUCUCAGGGUCGUGGGUUCGAGCCCCACGU
>positive_Mus_2
CGCCCCGUAGCUCAGUCGGUAGAGCAUGAGACUCUAAUC
>positive_Mus_3
CAGCUGGCCGGUUAAGCUCAGUUGGUUAGAGCGUGGUGCUAA
>positive_Mus_4
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>positive_Mus_5
UGGUGCUAAUAACGCCAAGGUCGCGGGUUCGAUCCCCGUAC
>positive_Mus_6
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>positive_Mus_8
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>positive_Mus_13
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>positive_Sac.cer_3
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>positive_Sac.cer_4
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>positive_Sac.cer_5
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>positive_Sac.cer_8
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>positive_Sac.cer_9
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>positive_Sac.cer_10
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>positive_Sac.cer_11
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>positive_Sac.cer_12
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>positive_Sac.cer_13
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>positive_Sac.cer_14
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>positive_Sac.cer_15
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>positive_Sac.cer_16
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>positive_Sac.cer_17
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 >positive_Drosophila_melanogaster_6
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 >positive_Drosophila_melanogaster_8
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Negative subset S⁻

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 >negative_Homo_3
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>negative_E.coli_112
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