

1

ALIGNMENT LENGTH

Number of residues in each sequence

1350

DOWNLOAD RESULTS

Download DiMA results

JSON XLSX HCS

SAMPLE NAME

Name of the sample being analysed

MERS-CoV surface glycoprotein

SUPPORT THRESHOLD

Minumum support required per position to be analysed

30

POSITION SUPPORT

Support at the selected k-mer position

171

DISTINCT VARIANTS

Distinct k-mers at the position, sans the index

2

POSITION ENTROPY

Shannon's entropy for the selected position

0.09

SELECTED POSITION

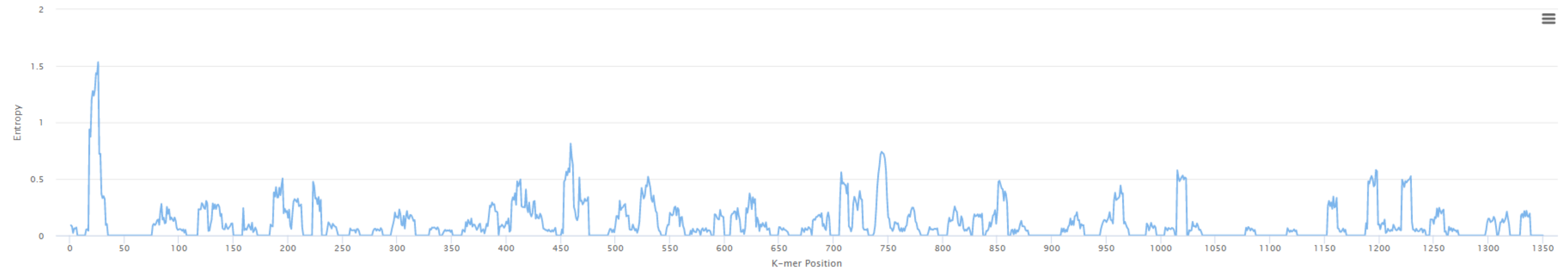
Currently selected k-mer position

< 1 >

K-MER POSITION ENTROPY

Shannon's entropy of the overlapping k-mer positions

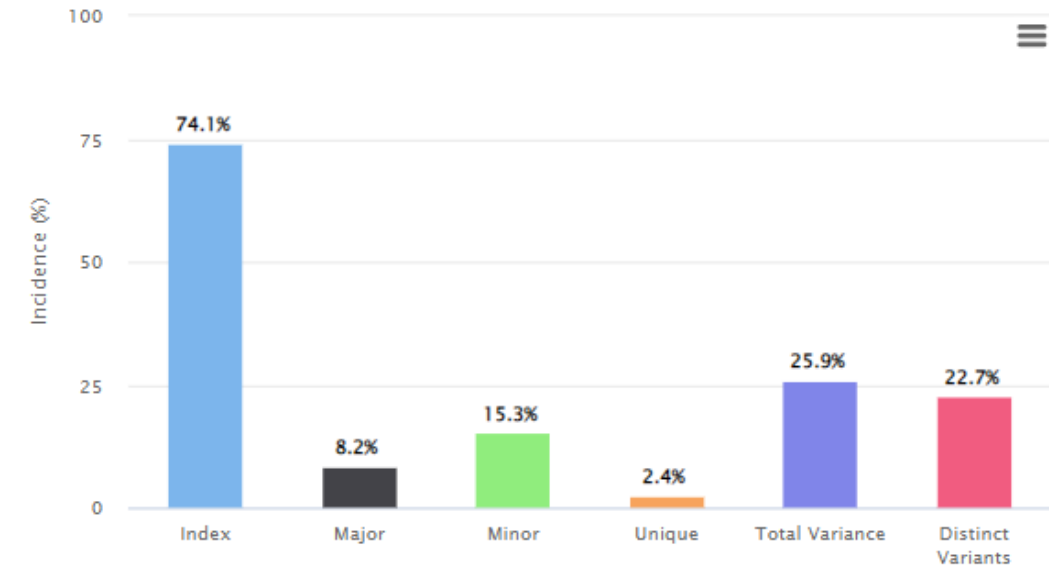
Click & Drag to zoom in



3

MOTIF DISTRIBUTION

The distribution of motifs at k-mer position 26



K-MER POSITION SEQUENCES

Distinct sequences observed at the k-mer position 26

Select to view metadata

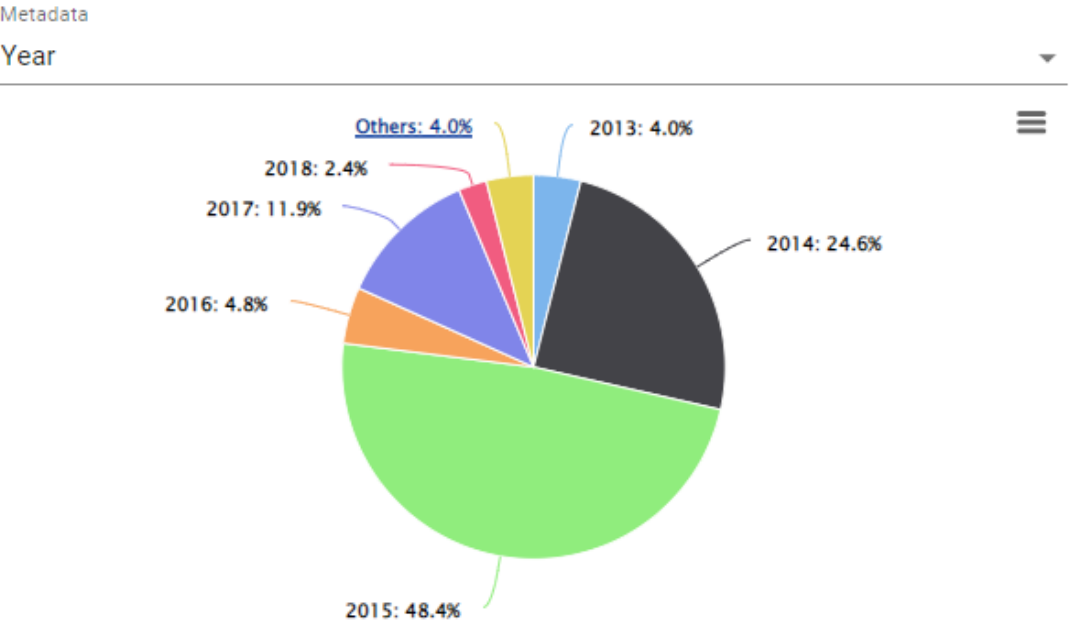
| Sequence | ↓ Frequency | Incidence | Motif Class |
|-----------|-------------|-----------|-------------|
| VKSACIEVD | 126 | 74.12 | Index |
| FKSACIEVD | 14 | 8.24 | Major |
| VKPACIEVD | 9 | 5.29 | Minor |
| AKSACIEVD | 6 | 3.53 | Minor |
| VKSACIAVD | 4 | 2.35 | Minor |
| LKSACIEVD | 4 | 2.35 | Minor |
| VKSACIEVH | 3 | 1.76 | Minor |

1 row selected 1-11 of 11

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SEQUENCE METADATA

Metadata of the selected distinct sequence



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