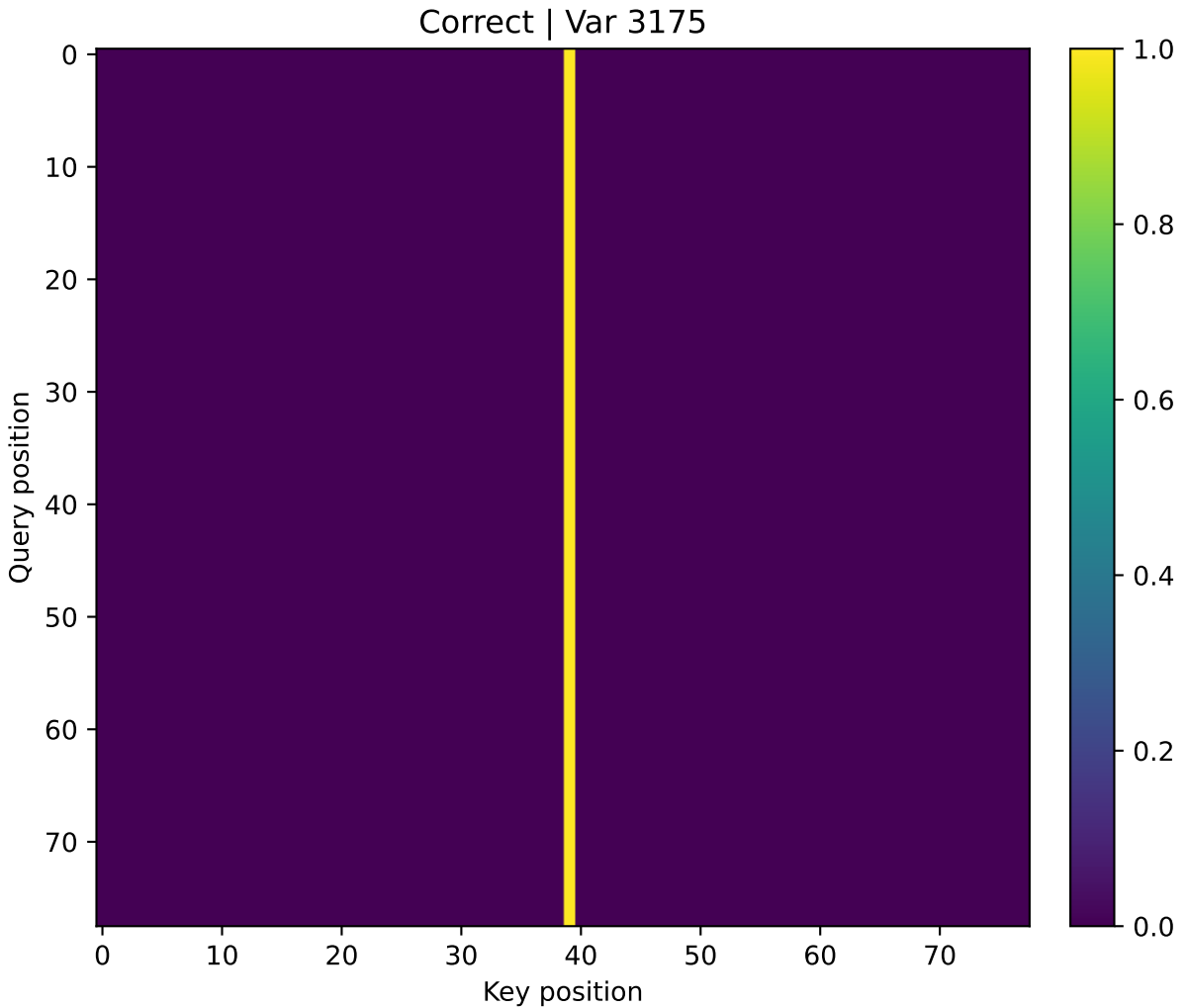
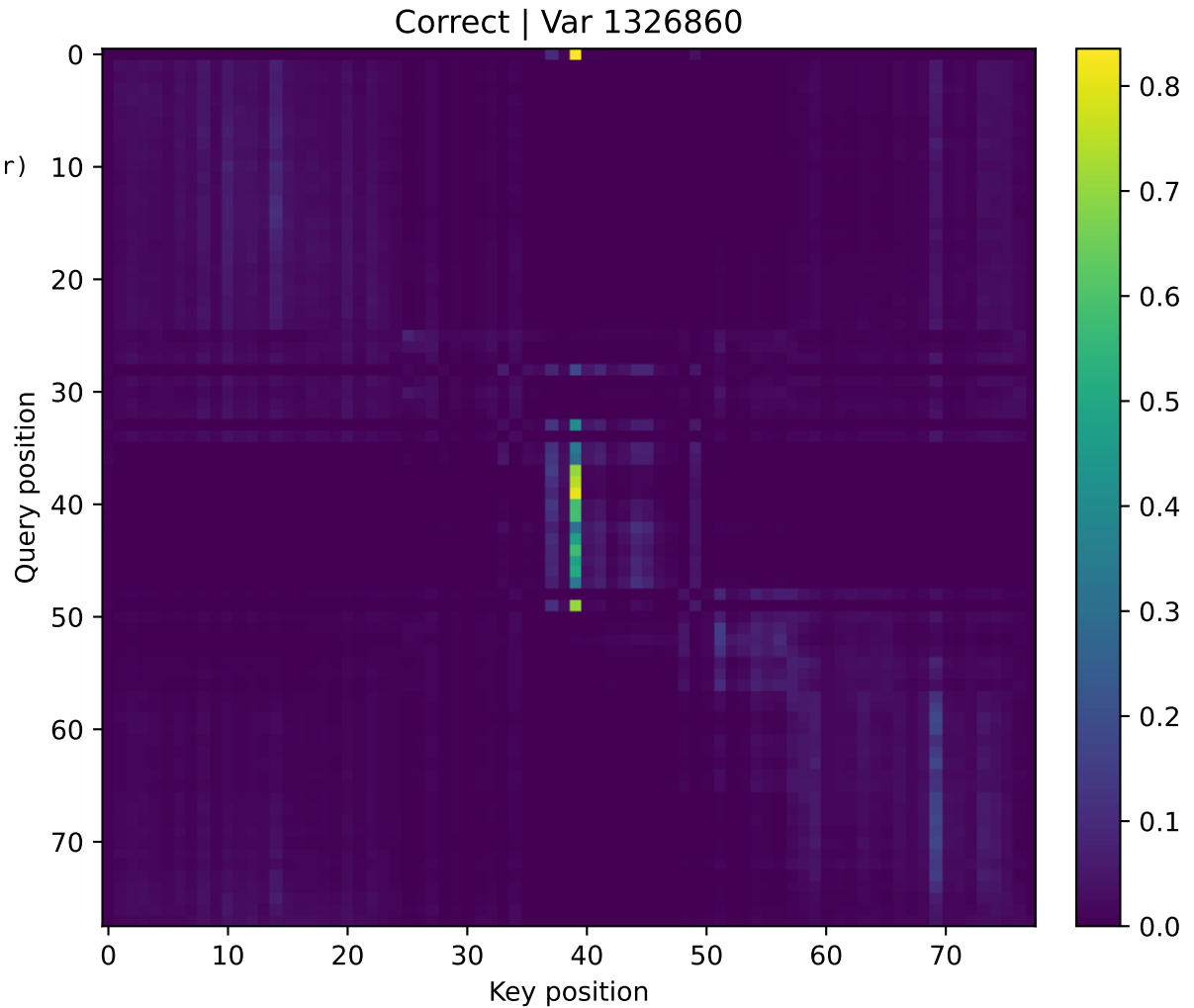
```
--- Correctly Predicted Variant ---
Top head → layer 4, head 15, score 1.0000

VariationID: 3175
VariationName: NM_000187.4(HGD):c.808G>A (p.Gly270Arg)
VariantType: single nucleotide variant
GeneSymbol: HGD
OMIM: 607474.0
AssemblyChr: 3
Start: 120641660
Stop: 120641660
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: G270R
HGVS_coding: NM_000187.4:c.808G>A
HGVS_protein: NP_000178.2:p.Gly270Arg
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 8
RecordType: classified
CLNSIG: Pathogenic/Likely_pathogenic
actual_label: 1
prediction: 1
```



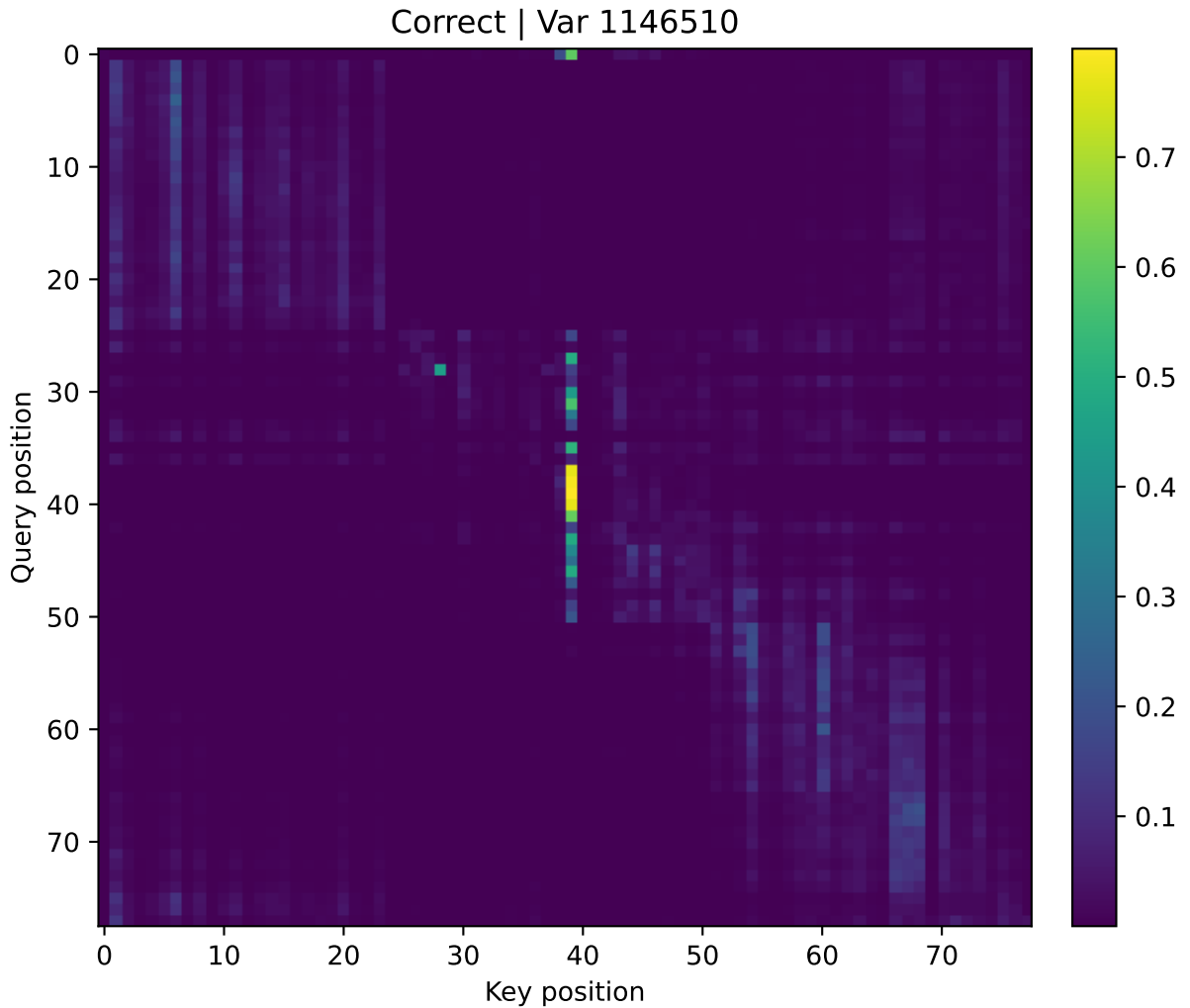
```
--- Correctly Predicted Variant ---
Top head → layer 14, head 18, score 0.8355

VariationID: 1326860
VariationName: NM_001204077.2(UBE4A):c.631C>T (p.Arg211Ter)
VariantType: single nucleotide variant
GeneSymbol: UBE4A
OMIM: 603753.0
AssemblyChr: 11
Start: 118372576
Stop: 118372576
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: R211*
HGVS_coding: NM_001204077.2:c.631C>T
HGVS_protein: NP_001191006.1:p.Arg211Ter
DateLastUpdated: 2023-12-25
NumberOfSubmitters: 2
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 1
```



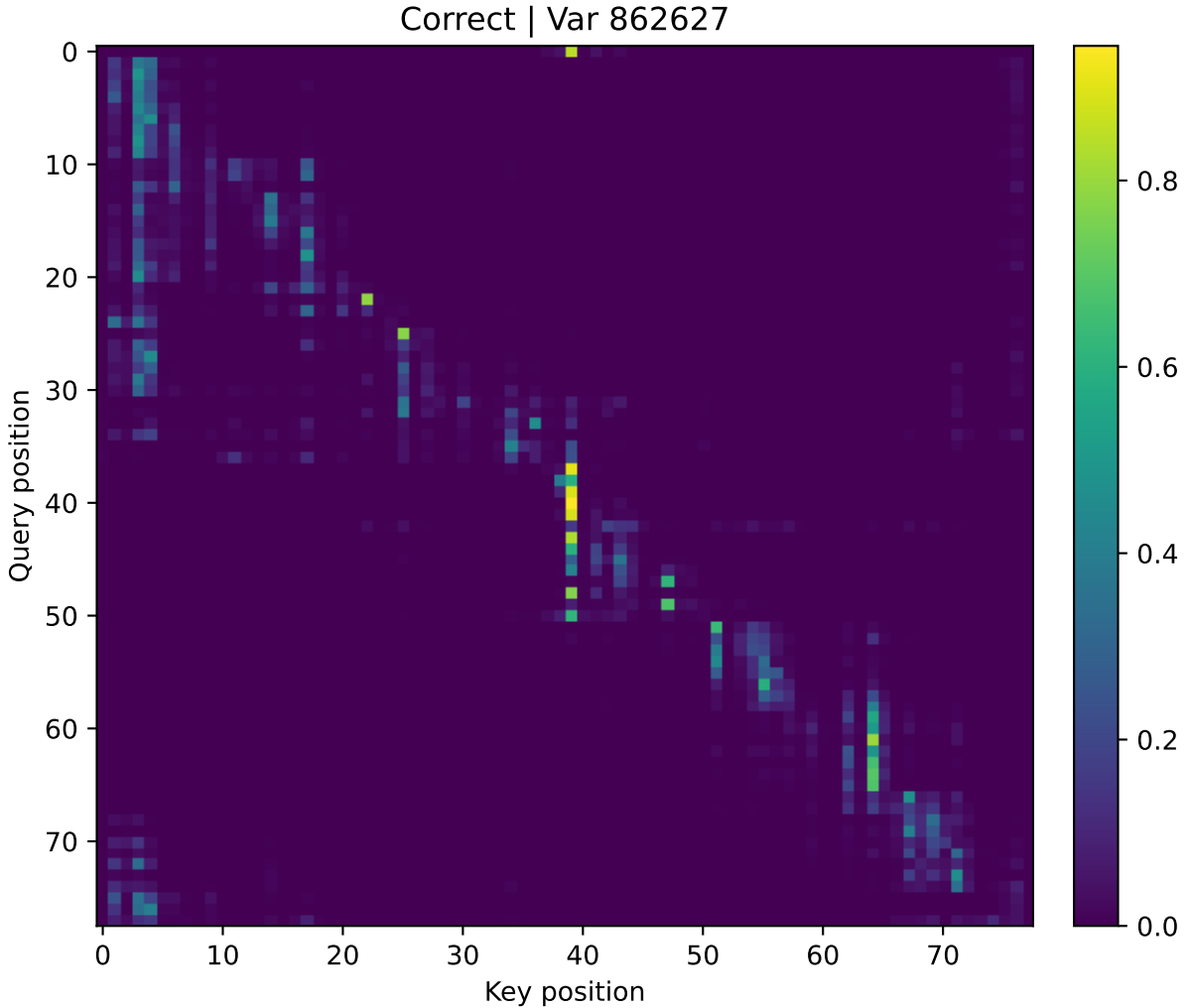
--- Correctly Predicted Variant ---
Top head → layer 11, head 16, score 0.5990

VariationID: 1146510
VariationName: NM_006846.4(SPINK5):c.2526C>T (p.Ser842=)
VariantType: single nucleotide variant
GeneSymbol: SPINK5
OMIM: 605010.0
AssemblyChr: 5
Start: 148120379
Stop: 148120379
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_001127698.2:c.2526C>T
HGVS_protein: NP_001121170.1:p.Ser842=
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 0



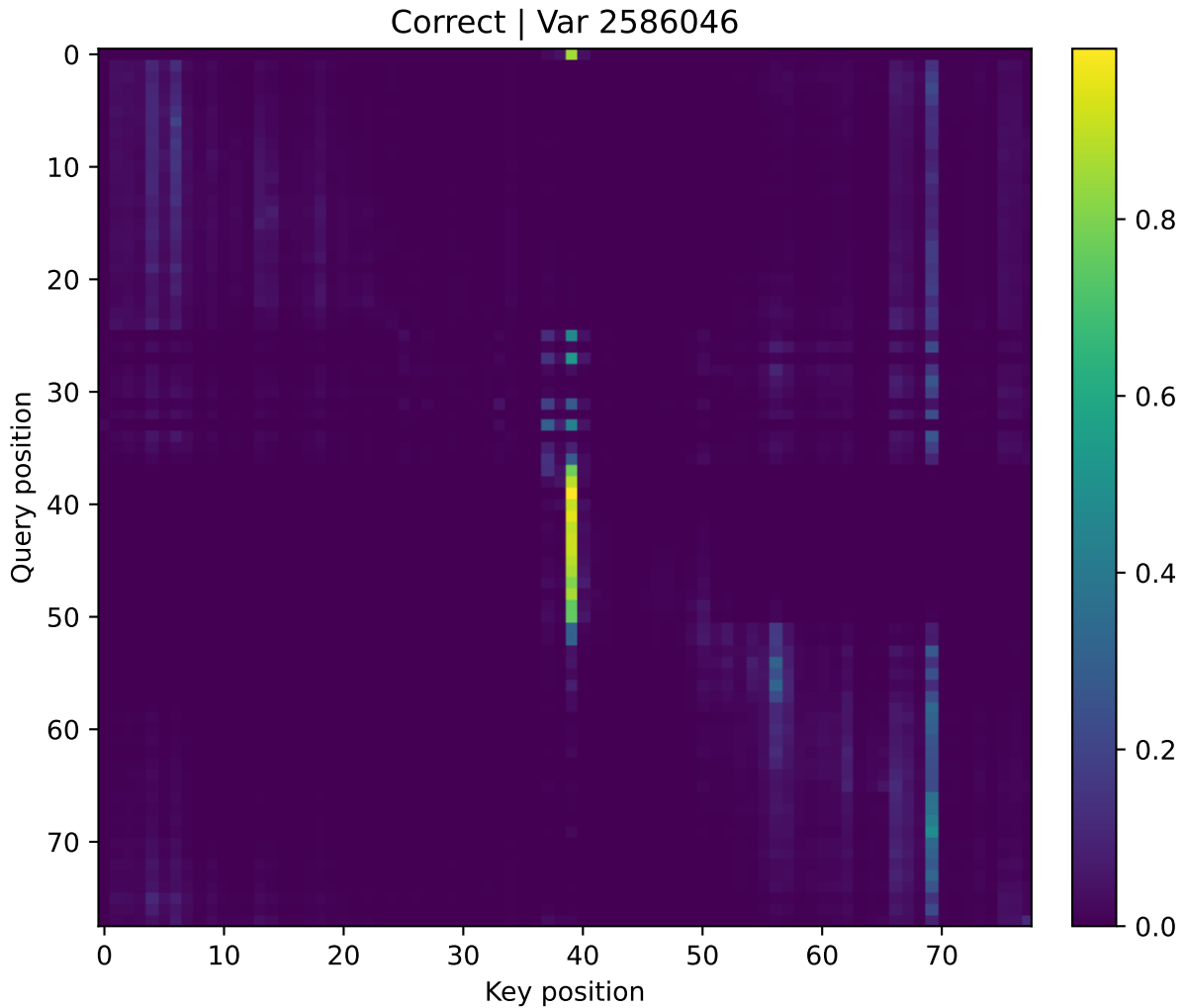
```
--- Correctly Predicted Variant ---
Top head → layer 6, head 11, score 0.8463

VariationID: 862627
VariationName: NM_000393.5(COL5A2):c.3147+1G>A
VariantType: single nucleotide variant
GeneSymbol: COL5A2
OMIM: 120190.0
AssemblyChr: 2
Start: 189049346
Stop: 189049346
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_000393.5:c.3147+1G>A
HGVS_protein: nan
DateLastUpdated: 2025-02-26
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 1
```



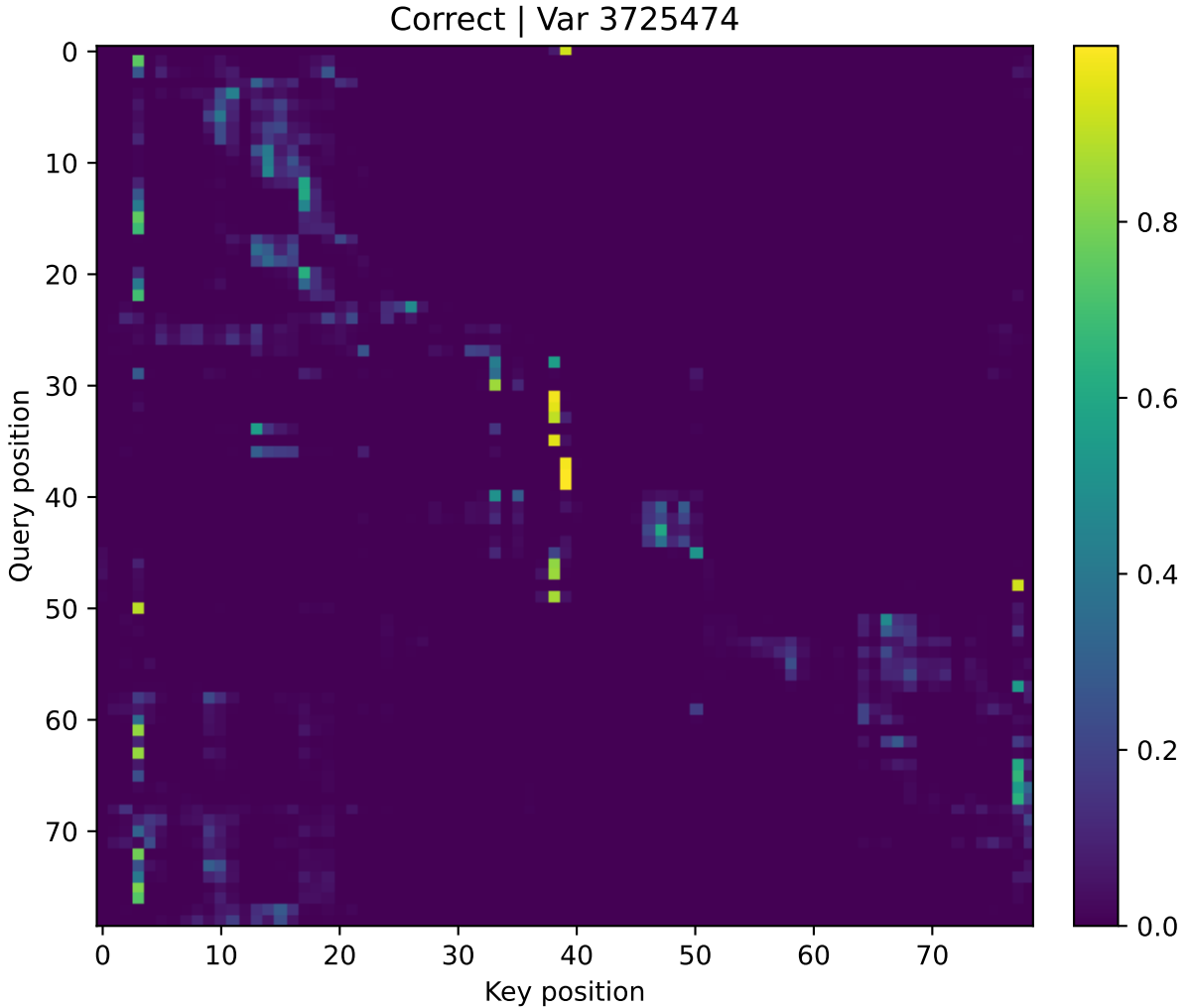
```
--- Correctly Predicted Variant ---
Top head → layer 13, head 16, score 0.8555

VariationID: 2586046
VariationName: NM_014000.3(VCL):c.875-4T>G
VariantType: single nucleotide variant
GeneSymbol: VCL
OMIM: 193065.0
AssemblyChr: 10
Start: 74083362
Stop: 74083362
RefAlleleVCF: T
AltAlleleVCF: G
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_003373.4:c.875-4T>G
HGVS_protein: nan
DateLastUpdated: 2025-05-19
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 0
```



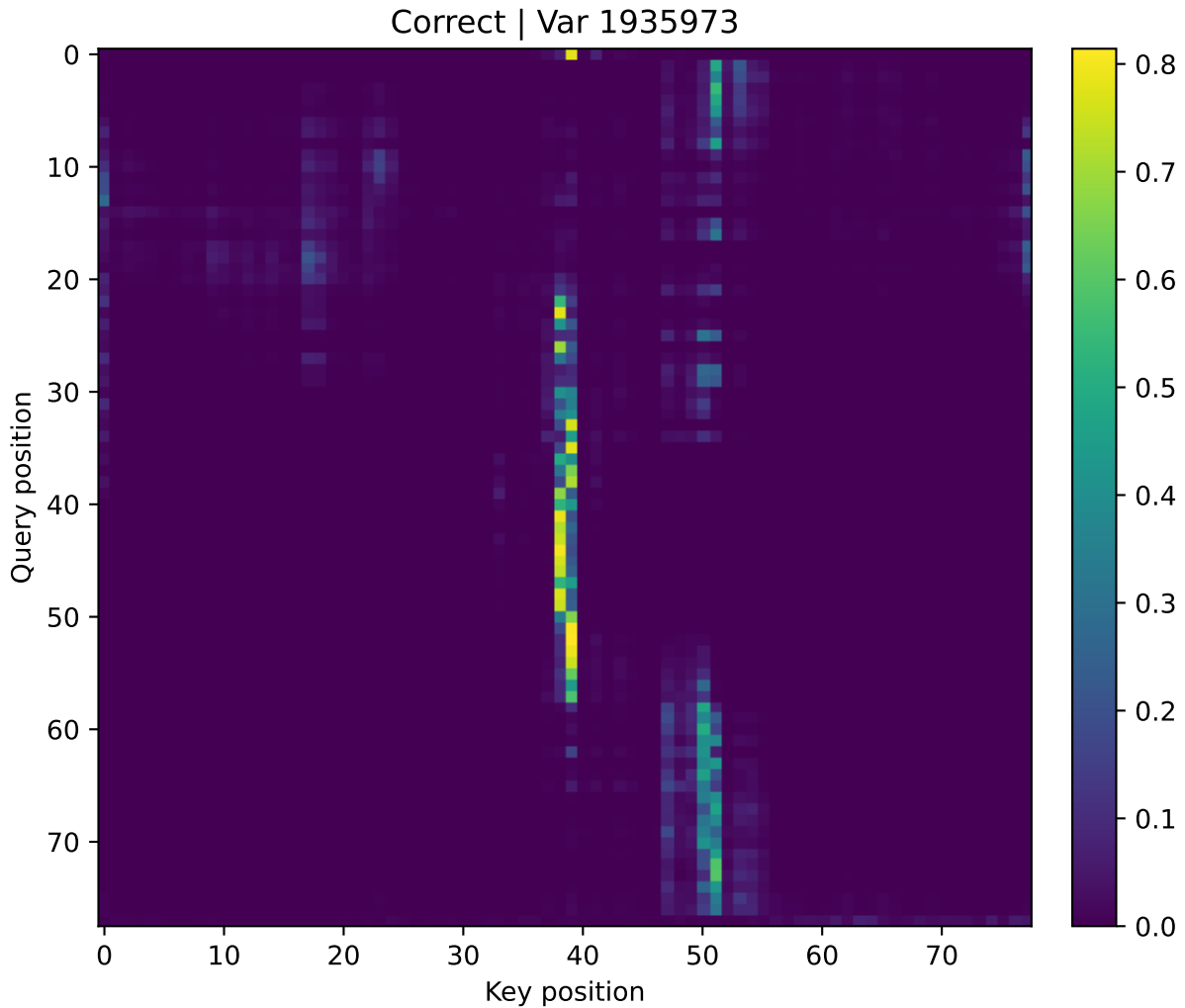
```
--- Correctly Predicted Variant ---
Top head → layer 9, head 14, score 0.9269

VariationID: 3725474
VariationName: NM_000426.4(LAMA2):c.101dup (p.His34fs)
VariantType: Duplication
GeneSymbol: LAMA2
OMIM: 156225.0
AssemblyChr: 6
Start: 128883345
Stop: 128883346
RefAlleleVCF: C
AltAlleleVCF: CA
VariantLength: 1
ProteinChange: H34fs
HGVS_coding: NM_000426.4:c.101dup
HGVS_protein: NP_000417.3:p.His34fs
DateLastUpdated: 2025-04-08
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 1
```



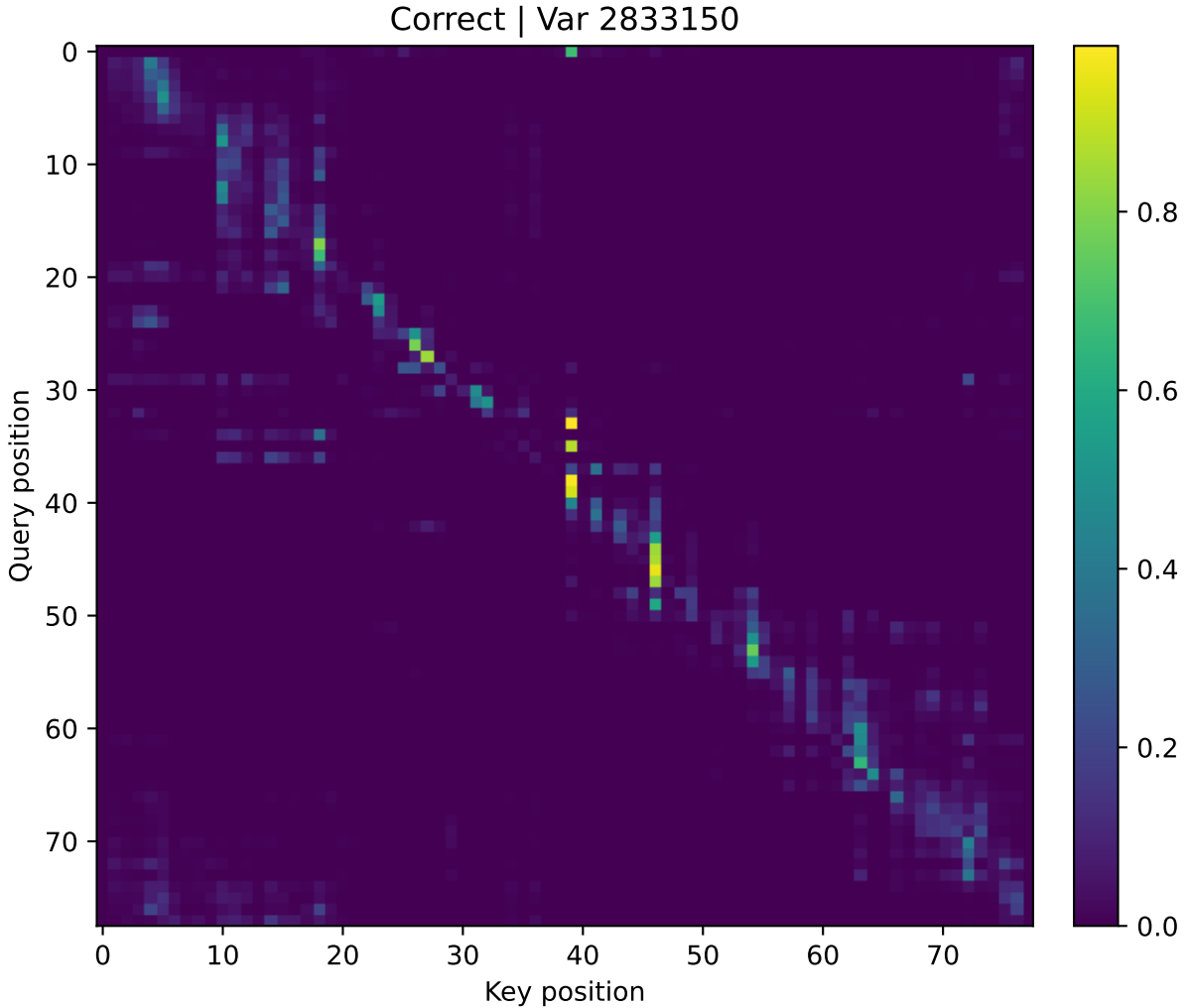
```
--- Correctly Predicted Variant ---
Top head → layer 10, head 13, score 0.7816

VariationID: 1935973
VariationName: NM_006766.5(KAT6A):c.5667C>T (p.Arg1889=)
VariantType: single nucleotide variant
GeneSymbol: KAT6A
OMIM: 601408.0
AssemblyChr: 8
Start: 41932553
Stop: 41932553
RefAlleleVCF: G
AltAlleleVCF: A
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_006766.5:c.5667C>T
HGVS_protein: NP_006757.2:p.Arg1889=
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Benign
actual_label: 0
prediction: 0
```



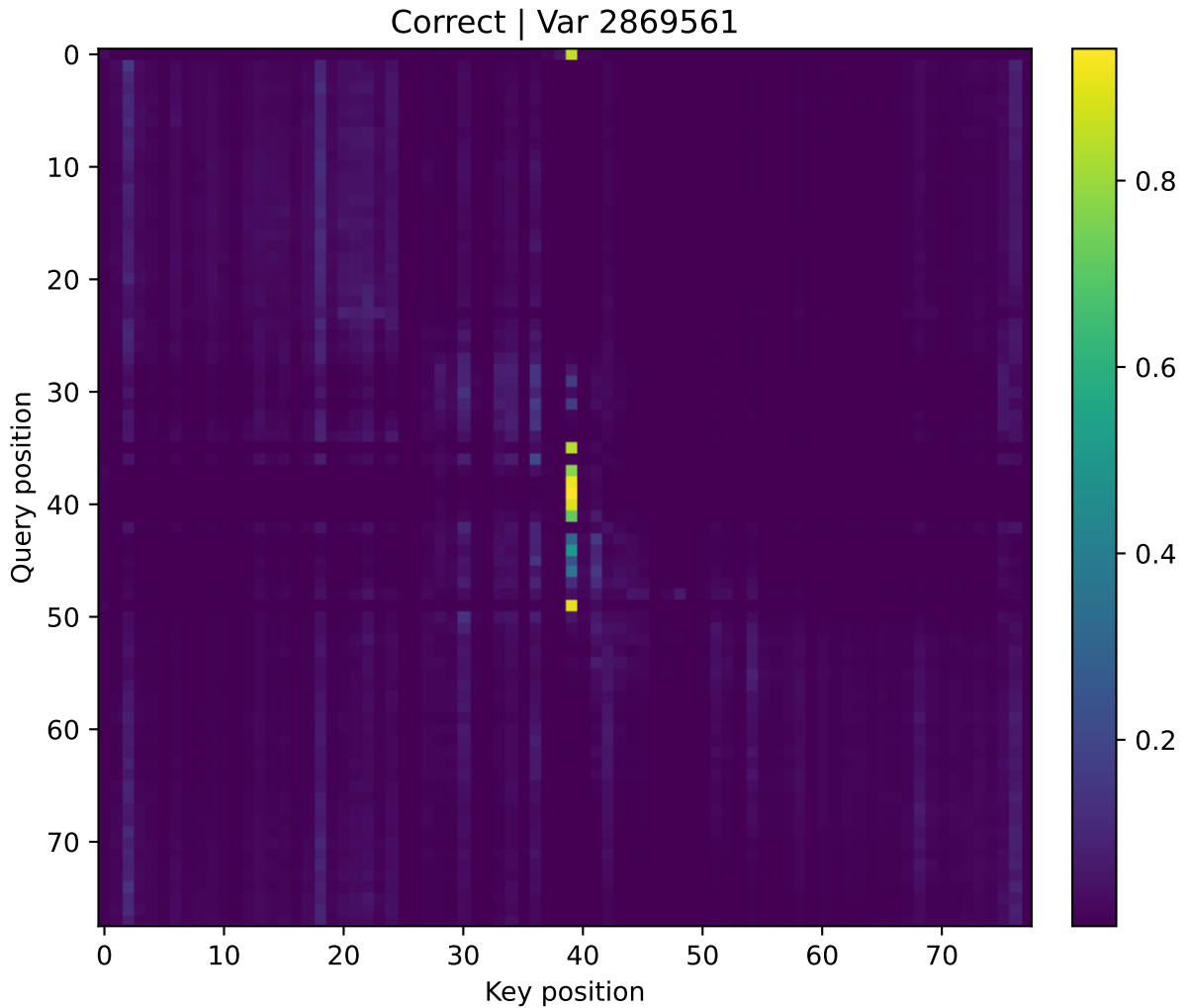
```
--- Correctly Predicted Variant ---
Top head → layer 7, head 11, score 0.6800

VariationID: 2833150
VariationName: NM_005908.4(MANBA):c.2244C>A (p.Cys748Ter)
VariantType: single nucleotide variant
GeneSymbol: MANBA
OMIM: 609489.0
AssemblyChr: 4
Start: 102634959
Stop: 102634959
RefAlleleVCF: G
AltAlleleVCF: T
VariantLength: 1
ProteinChange: C748*
HGVS_coding: NM_005908.4:c.2244C>A
HGVS_protein: NP_005899.3:p.Cys748Ter
DateLastUpdated: 2025-05-19
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 1
```



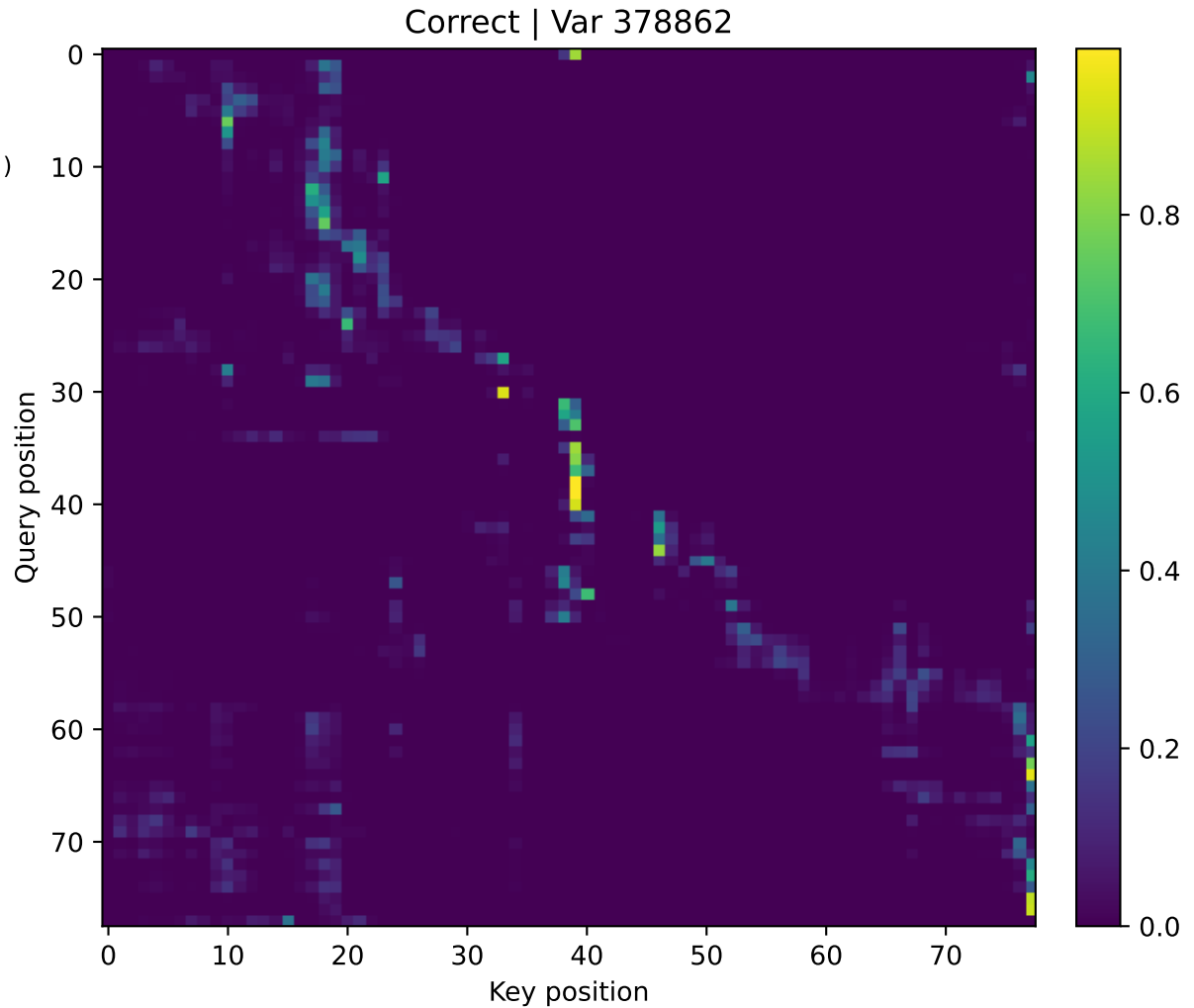
```
--- Correctly Predicted Variant ---
Top head → layer 12, head 11, score 0.8508

VariationID: 2869561
VariationName: NM_000732.6(CD3D):c.271C>T (p.Arg91Ter)
VariantType: single nucleotide variant
GeneSymbol: CD3D
OMIM: 186790.0
AssemblyChr: 11
Start: 118340378
Stop: 118340378
RefAlleleVCF: G
AltAlleleVCF: A
VariantLength: 1
ProteinChange: R91*
HGVS_coding: NM_000732.6:c.271C>T
HGVS_protein: NP_000723.1:p.Arg91Ter
DateLastUpdated: 2025-05-19
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 1
```



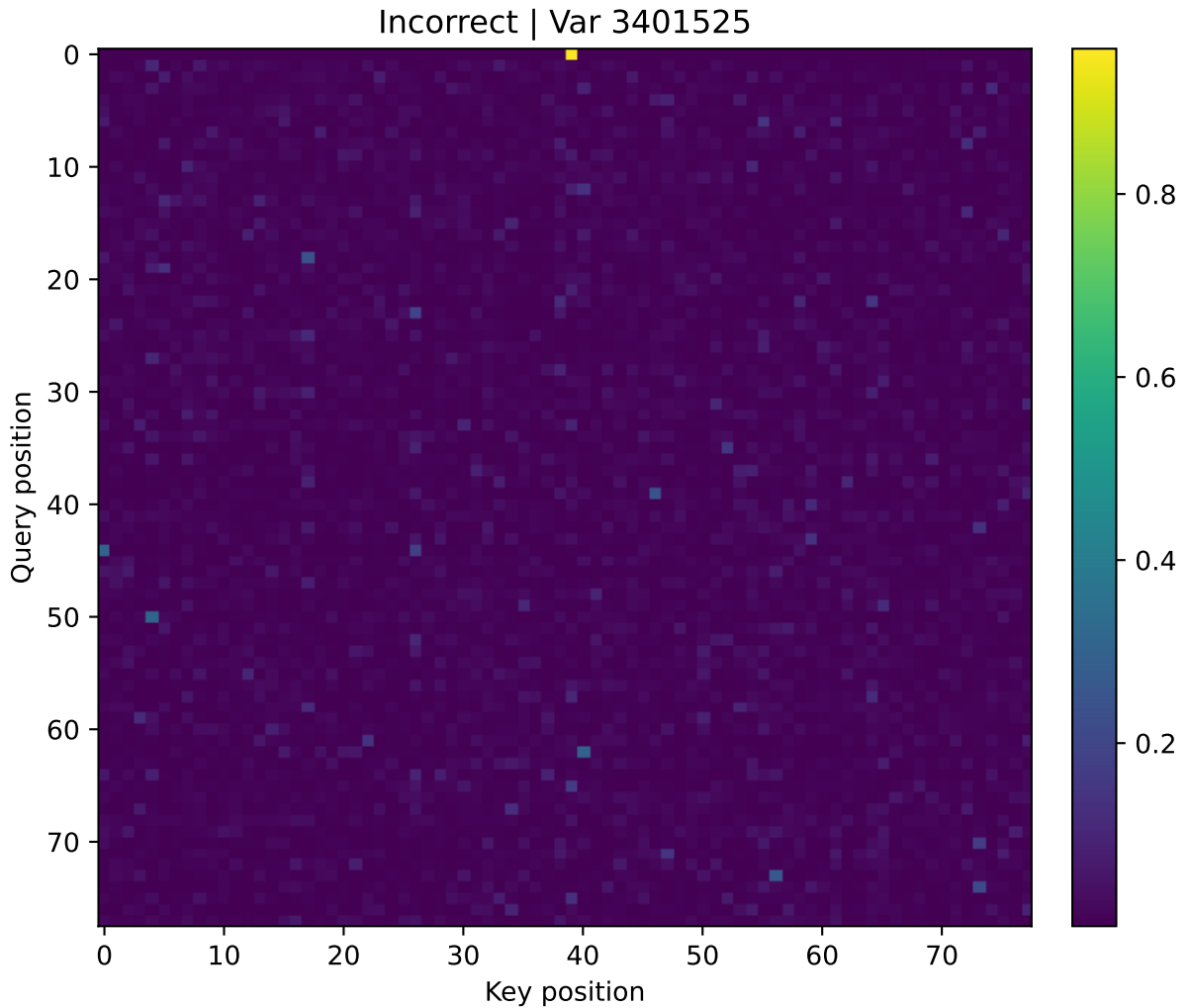
```
--- Correctly Predicted Variant ---
Top head → layer 9, head 14, score 0.8459

VariationID: 378862
VariationName: NM_025216.3(WNT10A):c.1168G>T (p.Glu390Ter)
VariantType: single nucleotide variant
GeneSymbol: WNT10A
OMIM: 606268.0
AssemblyChr: 2
Start: 218893185
Stop: 218893185
RefAlleleVCF: G
AltAlleleVCF: T
VariantLength: 1
ProteinChange: E390*
HGVS_coding: NM_025216.3:c.1168G>T
HGVS_protein: NP_079492.2:p.Glu390Ter
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 3
RecordType: classified
CLNSIG: Pathogenic/Likely_pathogenic
actual_label: 1
prediction: 1
```



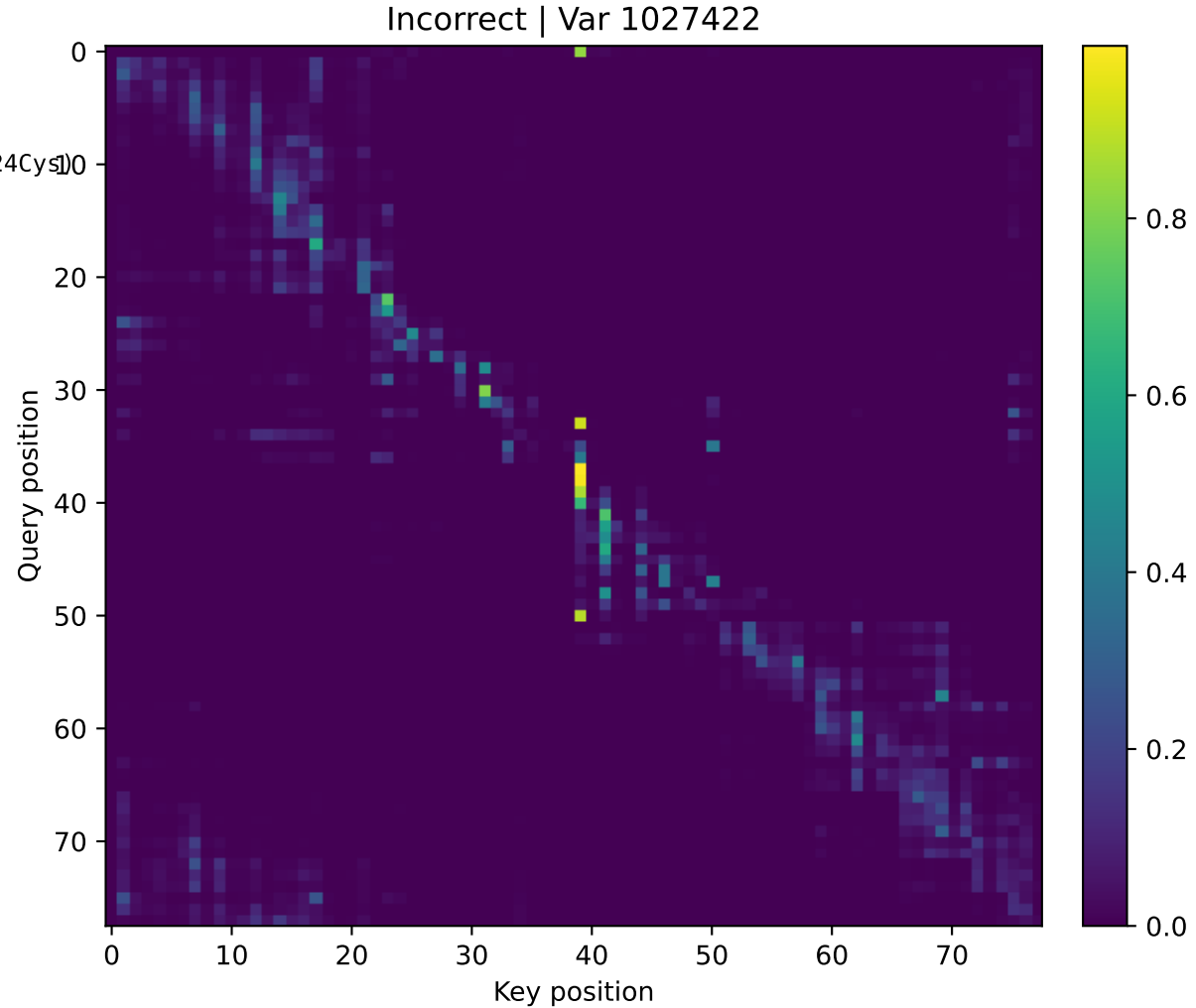
```
--- Incorrectly Predicted Variant ---
Top head → layer 0, head 7, score 0.9588

VariationID: 3401525
VariationName: NM_001150.3(ANPEP):c.1775G>A (p.Arg592Lys)
VariantType: single nucleotide variant
GeneSymbol: ANPEP
OMIM: 151530.0
AssemblyChr: 15
Start: 89801155
Stop: 89801155
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: R592K
HGVS_coding: NM_001150.3:c.1775G>A
HGVS_protein: NP_001141.2:p.Arg592Lys
DateLastUpdated: 2025-01-19
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



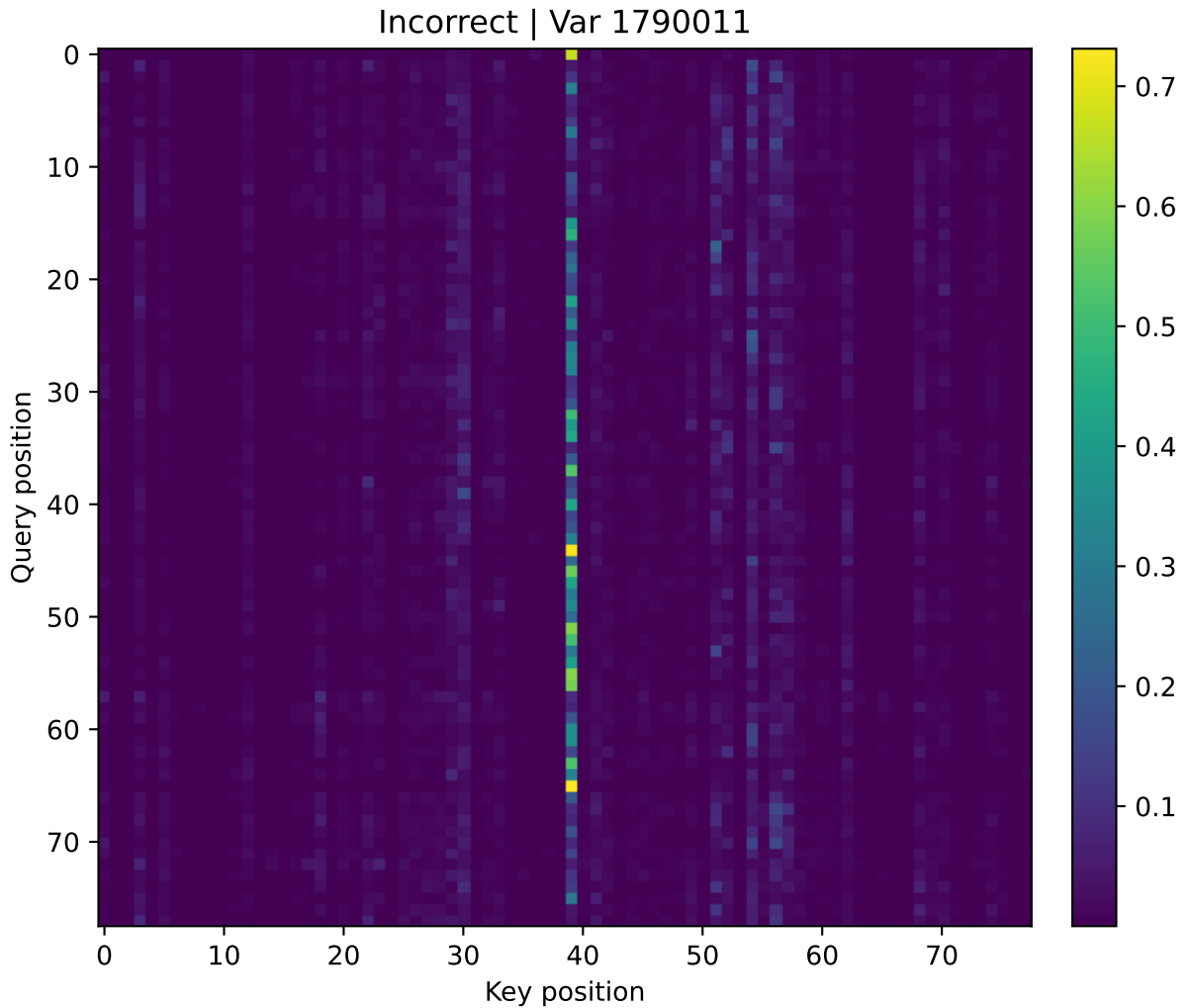
```
--- Incorrectly Predicted Variant ---
Top head → layer 7, head 11, score 0.8344

VariationID: 1027422
VariationName: NM_001130438.3(SPTAN1):c.4870C>T (p.Arg1624Cys)
VariantType: single nucleotide variant
GeneSymbol: SPTAN1
OMIM: 182810.0
AssemblyChr: 9
Start: 128611810
Stop: 128611810
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: R1599C
HGVS_coding: NM_001130438.3:c.4870C>T
HGVS_protein: NP_001123910.1:p.Arg1624Cys
DateLastUpdated: 2023-12-25
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_pathogenic
actual_label: 1
prediction: 0
```



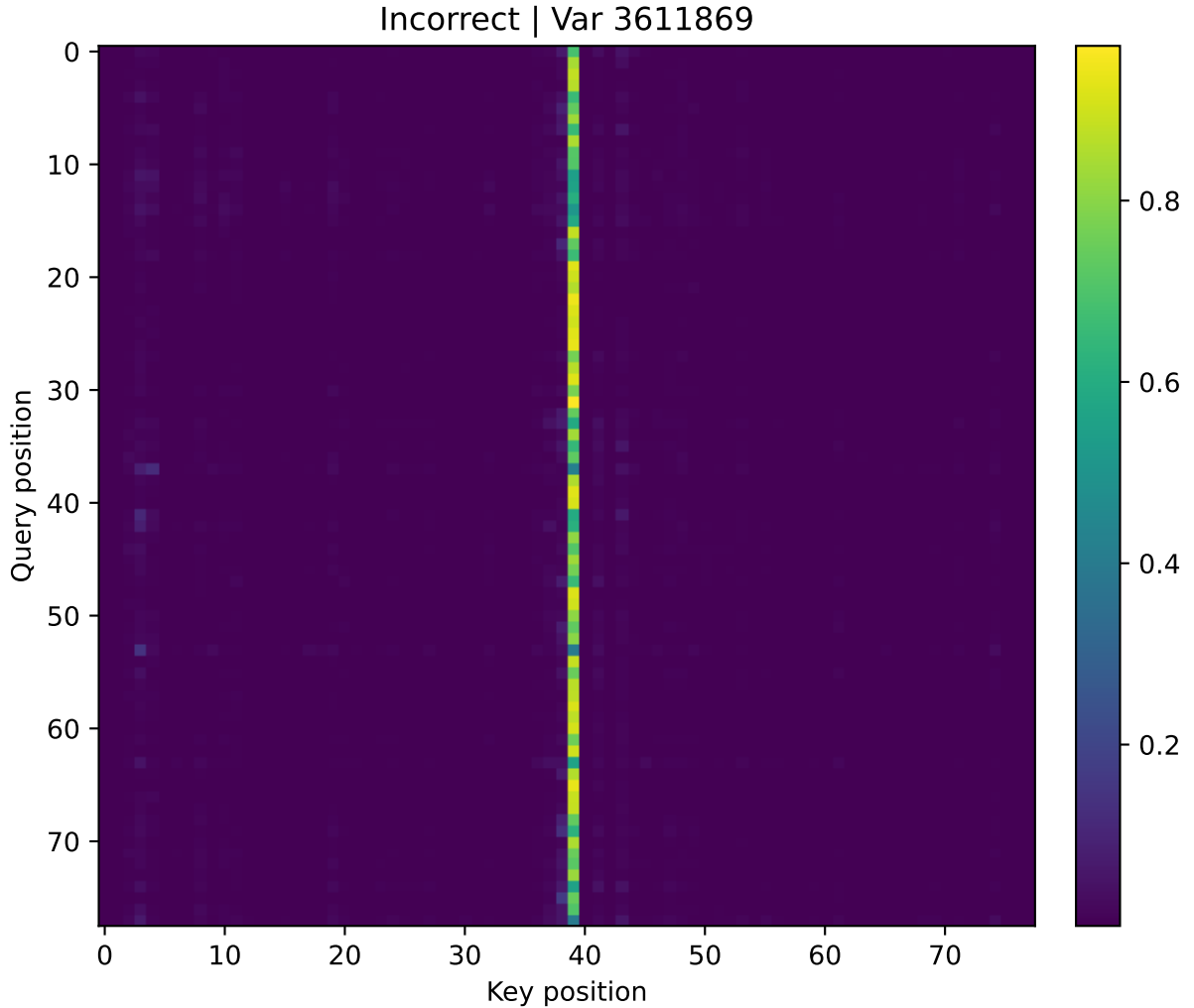
```
--- Incorrectly Predicted Variant ---
Top head → layer 1, head 6, score 0.6653

VariationID: 1790011
VariationName: NM_020774.4(MIB1):c.2351A>G (p.Asn784Ser)
VariantType: single nucleotide variant
GeneSymbol: MIB1
OMIM: 608677.0
AssemblyChr: 18
Start: 21847083
Stop: 21847083
RefAlleleVCF: A
AltAlleleVCF: G
VariantLength: 1
ProteinChange: N784S
HGVS_coding: NM_020774.4:c.2351A>G
HGVS_protein: NP_065825.1:p.Asn784Ser
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



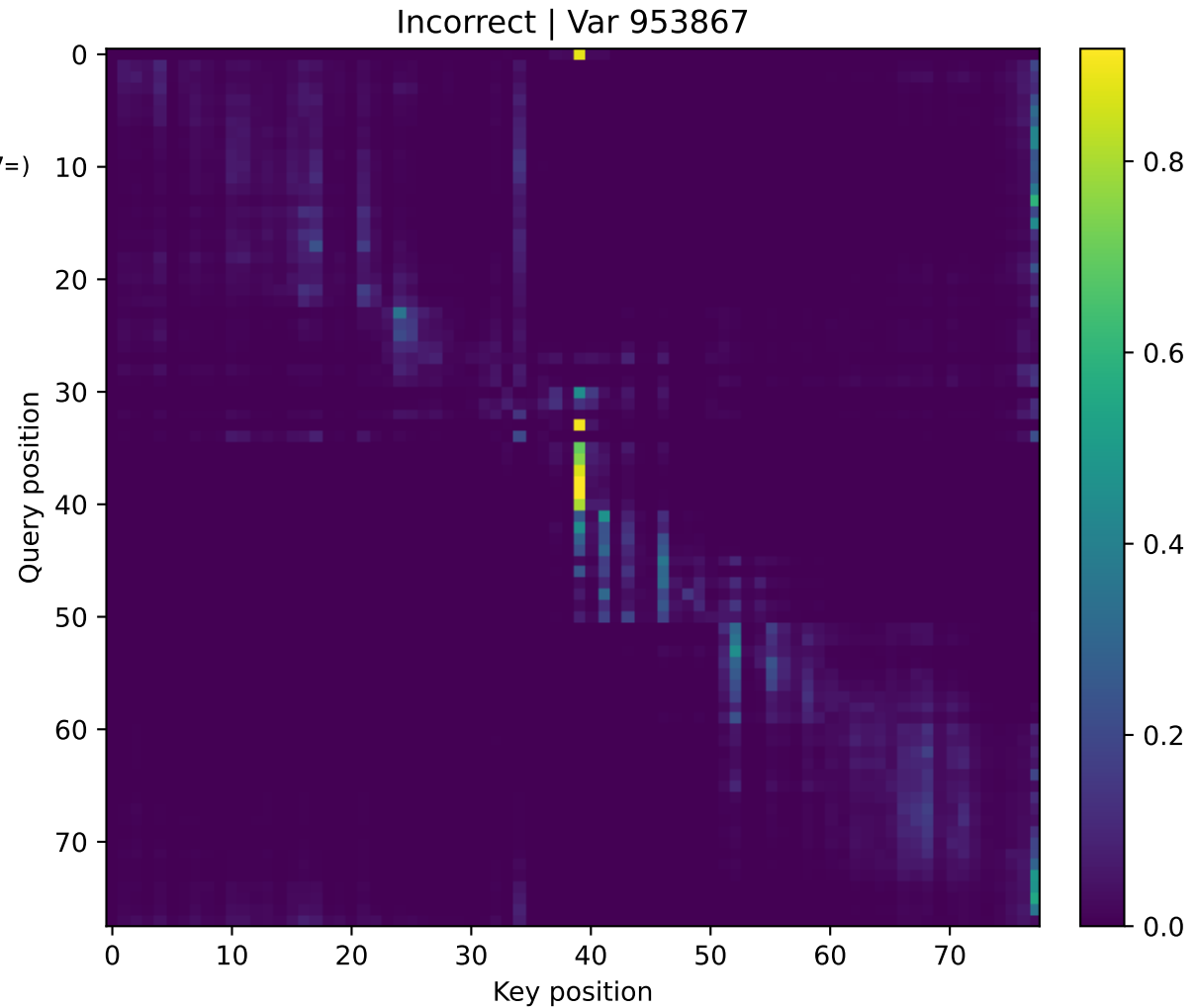
```
--- Incorrectly Predicted Variant ---
Top head → layer 1, head 3, score 0.6875

VariationID: 3611869
VariationName: NM_001039141.3(TRIOBP):c.5380-12T>C
VariantType: single nucleotide variant
GeneSymbol: LOC126863145
OMIM: 609761.0
AssemblyChr: 22
Start: 37754865
Stop: 37754865
RefAlleleVCF: T
AltAlleleVCF: C
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_001039141.3:c.5380-12T>C
HGVS_protein: nan
DateLastUpdated: 2025-04-08
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



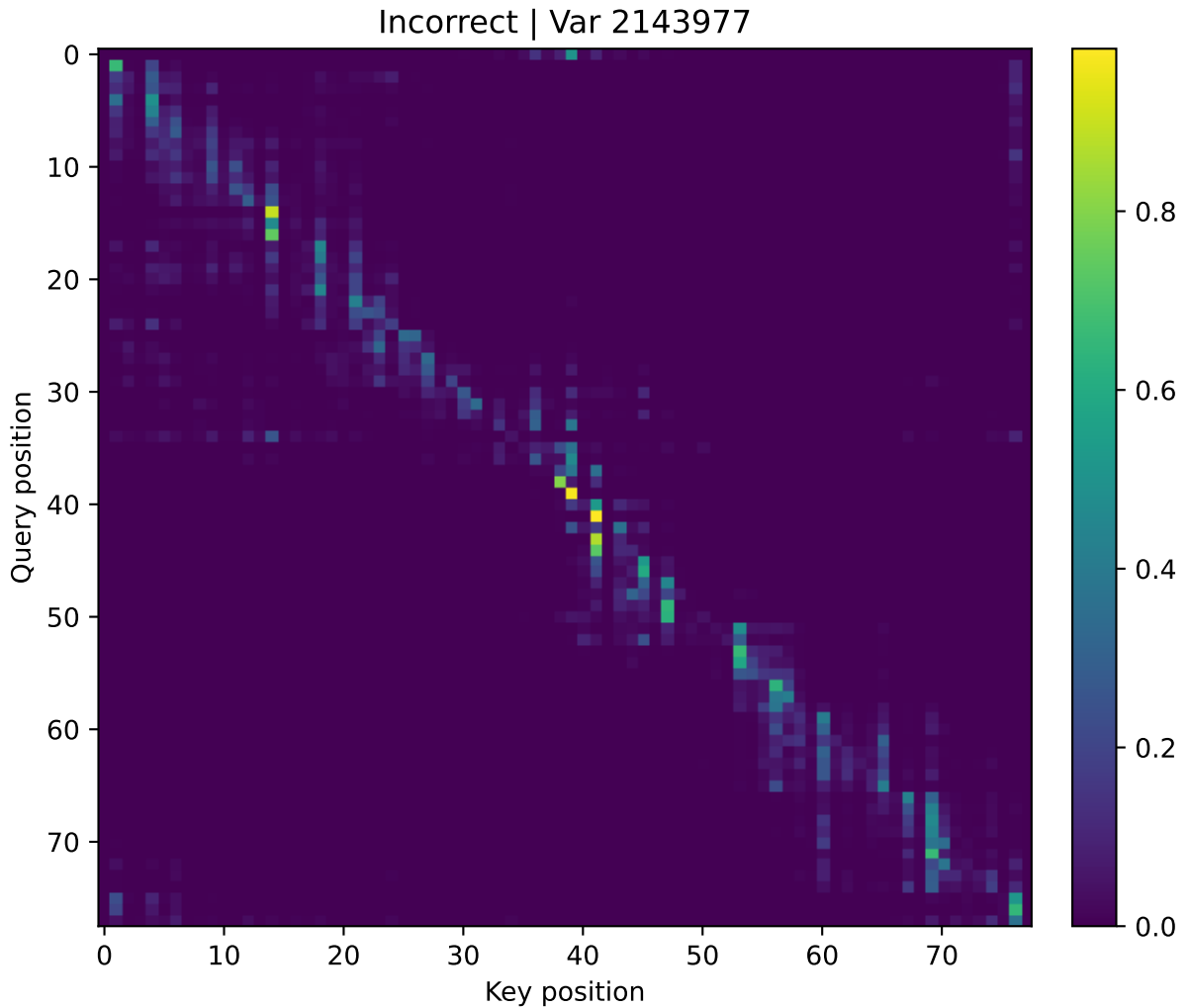
```
--- Incorrectly Predicted Variant ---
Top head → layer 11, head 17, score 0.8835

VariationID: 953867
VariationName: NM_001113378.2(FANCI):c.3171G>A (p.Leu1057=)
VariantType: single nucleotide variant
GeneSymbol: FANCI
OMIM: 611360.0
AssemblyChr: 15
Start: 89305227
Stop: 89305227
RefAlleleVCF: G
AltAlleleVCF: A
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_001113378.2:c.3171G>A
HGVS_protein: NP_001106849.1:p.Leu1057=
DateLastUpdated: 2025-03-22
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



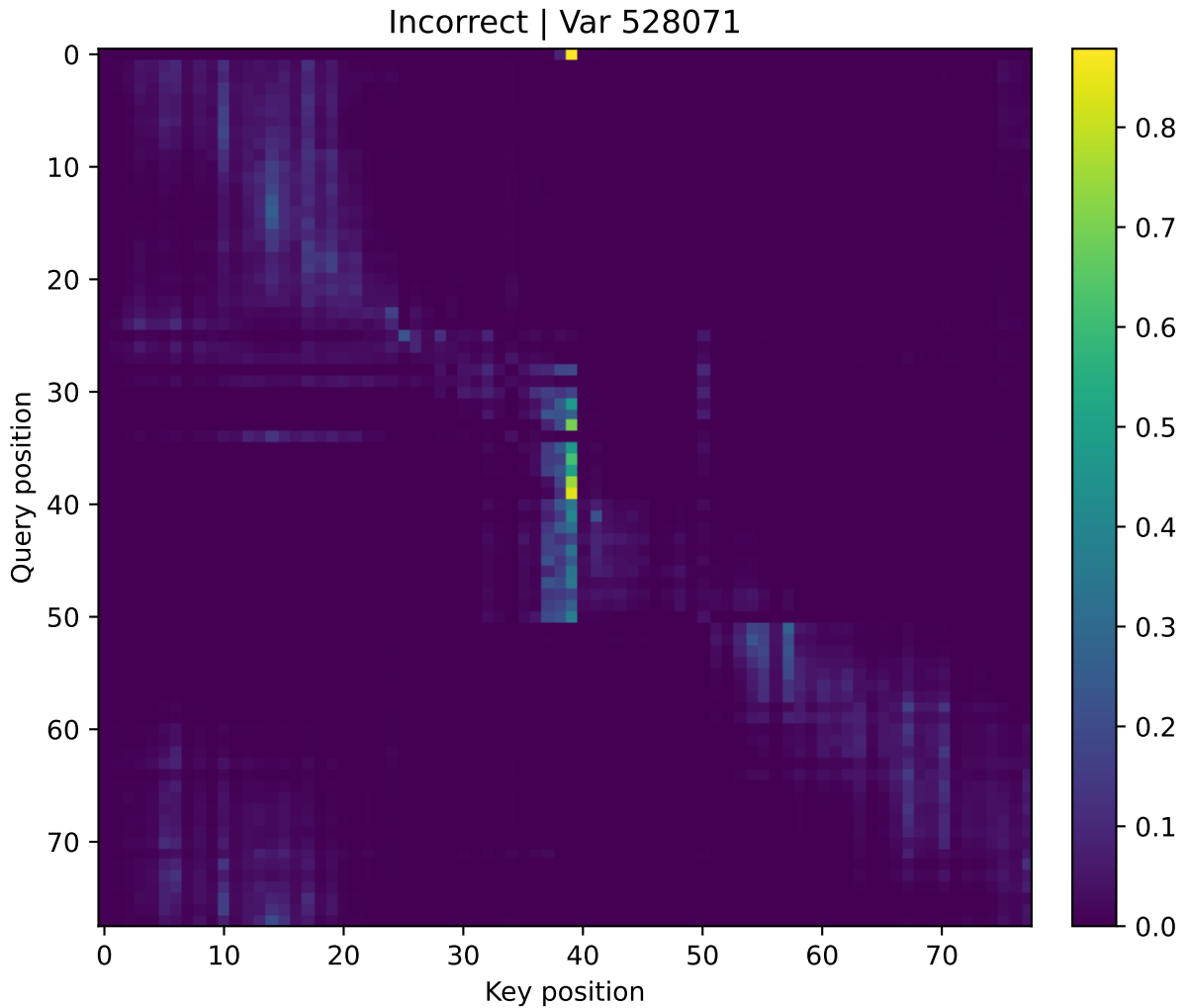
```
--- Incorrectly Predicted Variant ---
Top head → layer 6, head 14, score 0.5040

VariationID: 2143977
VariationName: NM_000245.4(MET):c.3633-13G>A
VariantType: single nucleotide variant
GeneSymbol: MET
OMIM: 164860.0
AssemblyChr: 7
Start: 116783291
Stop: 116783291
RefAlleleVCF: G
AltAlleleVCF: A
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_001127500.3:c.3687-13G>A
HGVS_protein: nan
DateLastUpdated: 2025-05-19
NumberOfSubmitters: 2
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



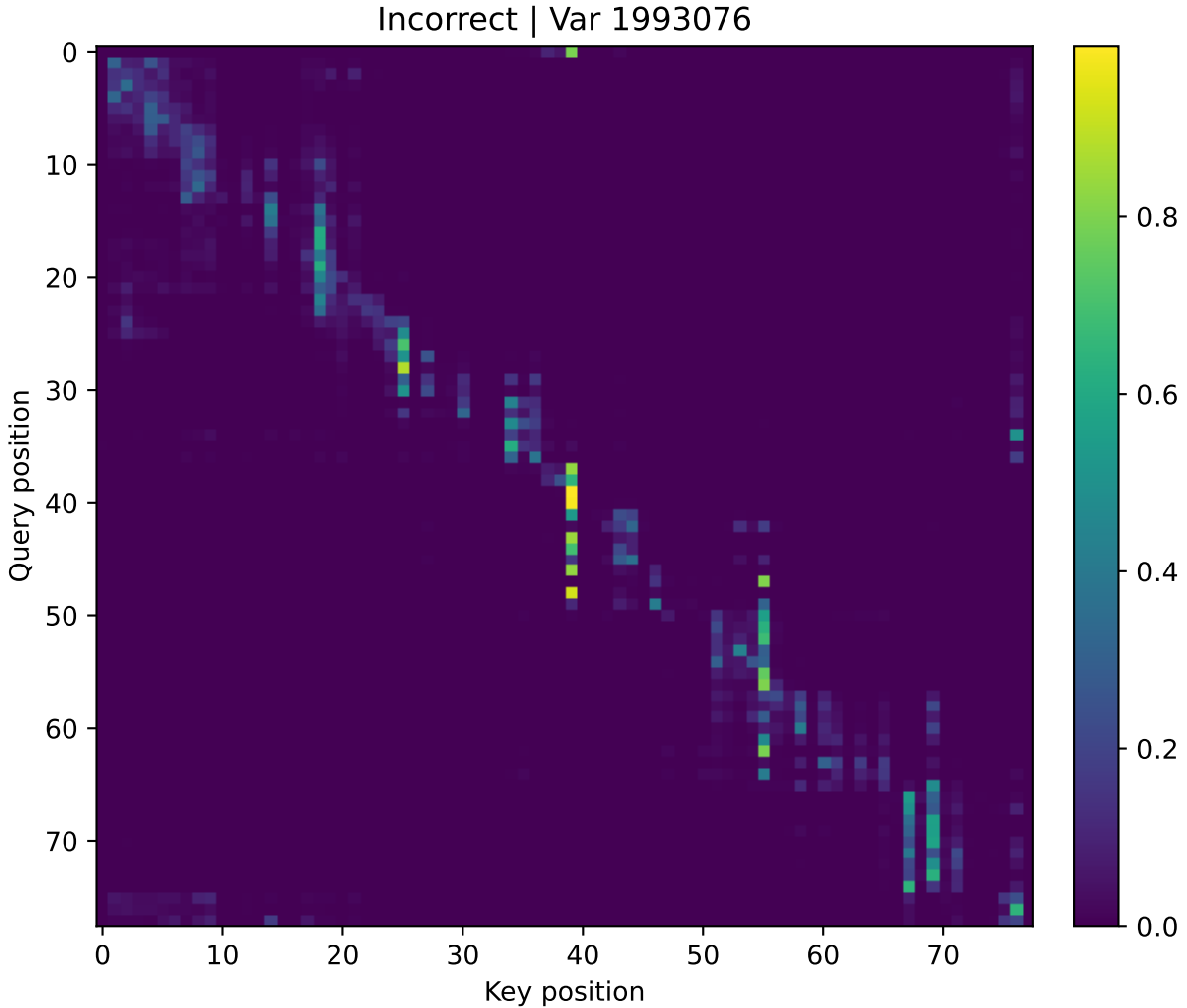
```
--- Incorrectly Predicted Variant ---
Top head → layer 11, head 18, score 0.8786

VariationID: 528071
VariationName: NM_001114753.3(ENG):c.683C>A (p.Ser228Ter)
VariantType: single nucleotide variant
GeneSymbol: ENG
OMIM: 131195.0
AssemblyChr: 9
Start: 127825701
Stop: 127825701
RefAlleleVCF: G
AltAlleleVCF: T
VariantLength: 1
ProteinChange: S228*
HGVS_coding: NM_000118.4:c.683C>A
HGVS_protein: NP_000109.1:p.Ser228Ter
DateLastUpdated: 2025-02-26
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 0
```



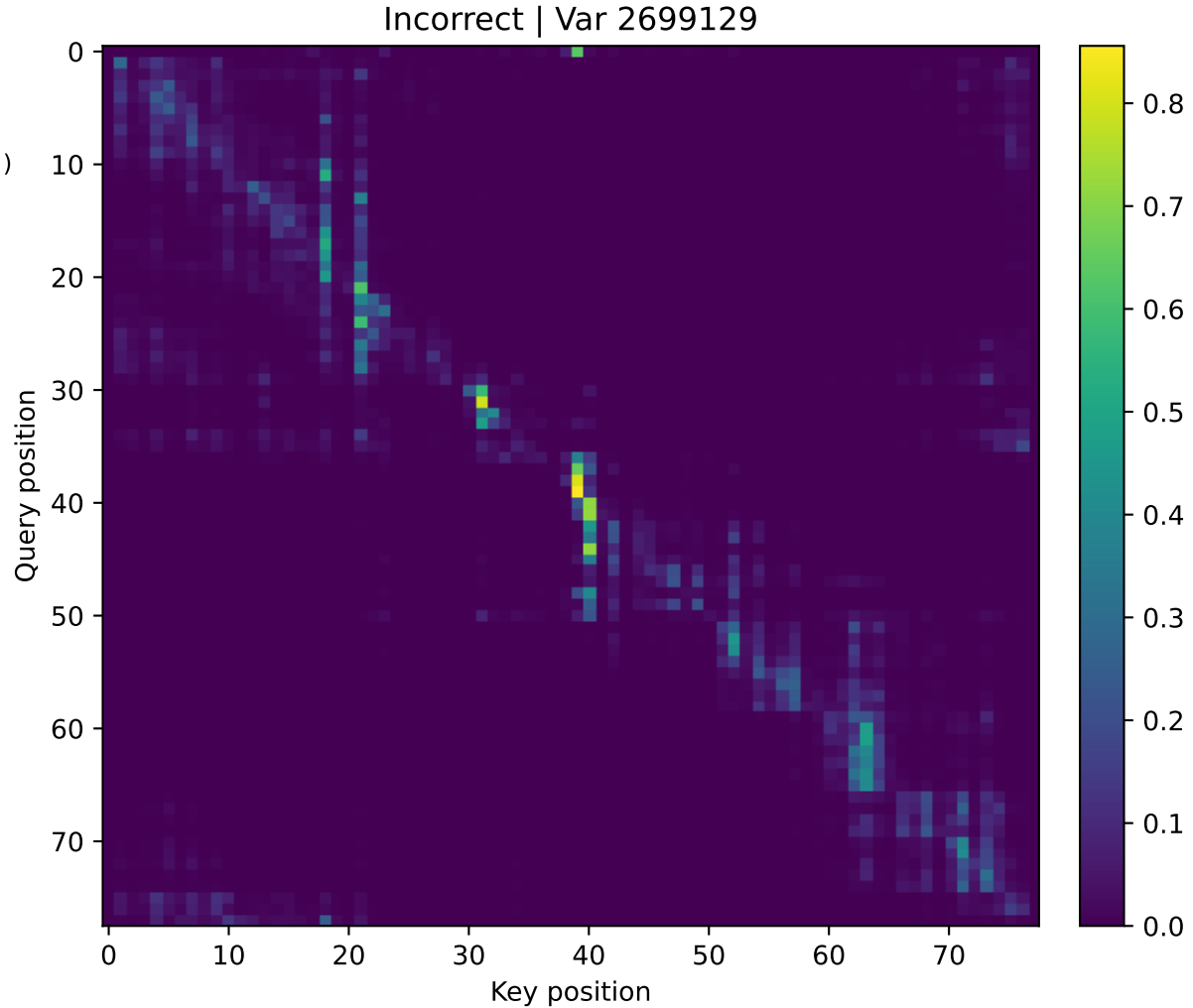
```
--- Incorrectly Predicted Variant ---
Top head → layer 6, head 11, score 0.7928

VariationID: 1993076
VariationName: NM_205768.3(ZBTB18):c.362T>G (p.Val121Gly)
VariantType: single nucleotide variant
GeneSymbol: ZBTB18
OMIM: 608433.0
AssemblyChr: 1
Start: 244054136
Stop: 244054136
RefAlleleVCF: T
AltAlleleVCF: G
VariantLength: 1
ProteinChange: V121G
HGVS_coding: NM_001278196.2:c.335T>G
HGVS_protein: NP_001265125.1:p.Val112Gly
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```



```
--- Incorrectly Predicted Variant ---
Top head → layer 7, head 4, score 0.6365

VariationID: 2699129
VariationName: NM_005559.4(LAMA1):c.3888T>A (p.Tyr1296Ter)
VariantType: single nucleotide variant
GeneSymbol: LAMA1
OMIM: 150320.0
AssemblyChr: 18
Start: 7009352
Stop: 7009352
RefAlleleVCF: A
AltAlleleVCF: T
VariantLength: 1
ProteinChange: Y1296*
HGVS_coding: NM_005559.4:c.3888T>A
HGVS_protein: NP_005550.2:p.Tyr1296Ter
DateLastUpdated: 2025-05-19
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Pathogenic
actual_label: 1
prediction: 0
```



```
--- Incorrectly Predicted Variant ---
Top head → layer 12, head 11, score 0.8014

VariationID: 1921276
VariationName: NM_024580.6(EFL1):c.1444+16G>A
VariantType: single nucleotide variant
GeneSymbol: EFL1
OMIM: 617538.0
AssemblyChr: 15
Start: 82220062
Stop: 82220062
RefAlleleVCF: C
AltAlleleVCF: T
VariantLength: 1
ProteinChange: nan
HGVS_coding: NM_001040610.3:c.1291+16G>A
HGVS_protein: nan
DateLastUpdated: 2025-05-17
NumberOfSubmitters: 1
RecordType: classified
CLNSIG: Likely_benign
actual_label: 0
prediction: 1
```