**S10. Correlated Phylogenetic Independent Contrasts of DNA Sequence Motifs\*.**

***Alphapapillomavirus***

CpG R Q

G duplexes 0.700 <0.001

Inverted repeats -0.343 0.004

Inverted repeats + palindromes -0.378 0.001

TLR9 0.396 0.001

**Low Risk 1**

CpG

G duplexes 0.750 0.007

**Low Risk 2**

CpG

G duplexes 0.600 0.004

APOBEC3 on + strand 0.546 0.008

% APOBEC3 on – strand -0.636 0.001

TLR9

APOBEC3 0.643 0.003

APOBEC3 on + strand 0.688 0.001

APOBEC3 on + strand

APOBEC3 on – strand 0.696 <0.001

Inverted repeats + palindromes

APOBEC3 on – strand -0.534 0.023

**High Risk Human**

CpG

APOBEC3­ -0.644 0.001

***Alphapapillomavirus 5 + Alphapapillomavirus 6***

G quadruplexes

E2 sites 0.521 0.006

APOBEC3 on + strand 0.658 <0.001

***Alphapapillomavirus 7***

APOBEC3

CpG -0.593 <0.001

TLR9 0.560 0.001

Non-canonical E2 sites - 0.583 <0.001

G duplexes -0.703 <0.001

***Alphapapillomavirus 9***

TLR9

E2 sites 0.540 0.001

APOBEC3 -0.489 0.003

Inverted repeats 0.428 0.003

G quadruplexes -0.465 0.003

\*excluding autocorrelated pairs (e.g., G duplexes/G quadruplexes).