Phylogenetic trees for 32 HPV genotypes

Figures S1-S32:

Phylogenetic trees constructed using maximum likelihood method (RAxML). Best trees were created from four multiple runs and 10 000 bootstraps. Trees are presented in ‘Fan’ mode. Each tree were color based on four variables; sample, site (vaginal or anal), cervical cytology outcome and HIV status. Cytology outcome were encoded; Negative = Negative for intra-epithelial lesions and malignancy (NILM), High grade = High grade squamous intra-epithelial lesions (HGSIL) and Atypical squamous cells, cannot exclude HGSIL (ASC-H), Low grade = Low-grade squamous intraepithelial lesion (LGSIL) and Atypical squamous cells of undetermined significance (ASC-US) and Unsatisfactory = slide was not satisfactory for evaluation ie had no distinct endothelial cells, poorly stained and/or smear poorly collected.

Fig S1: HPV 6b

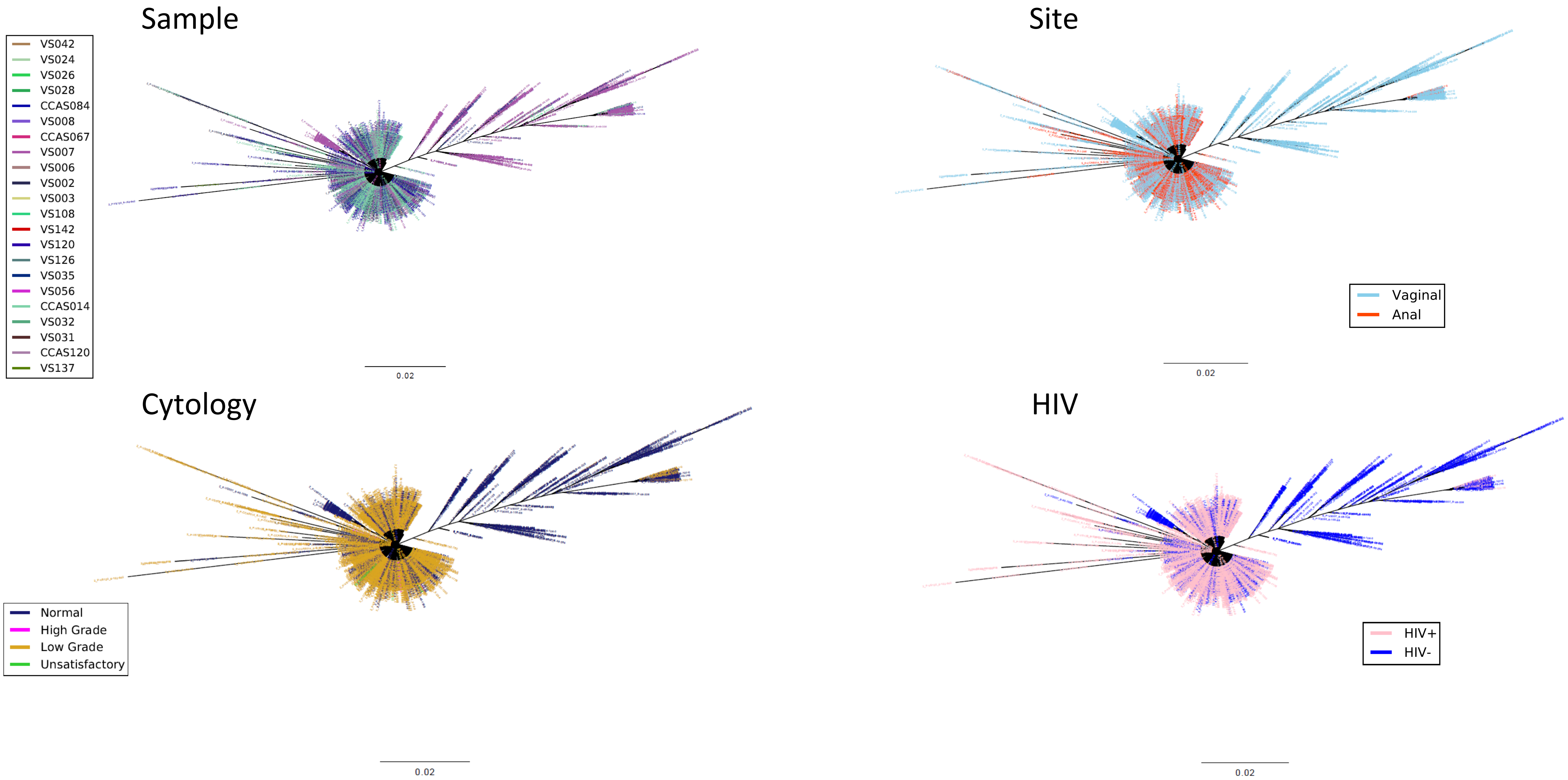

Sample
VS042
VS024
VS026
VS028
CCAS084
VS008
CCAS067
VS007
VS006
VS002
VS003
VS108
VS142
VS120
VS126
VS035
VS056
CCAS014
VS032
VS031
CCAS120
VS137
0.02
Site
Vaginal
Anal
0.02
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.02
HIV
HIV+
HIV-
0.02

Fig S2:HPV 11

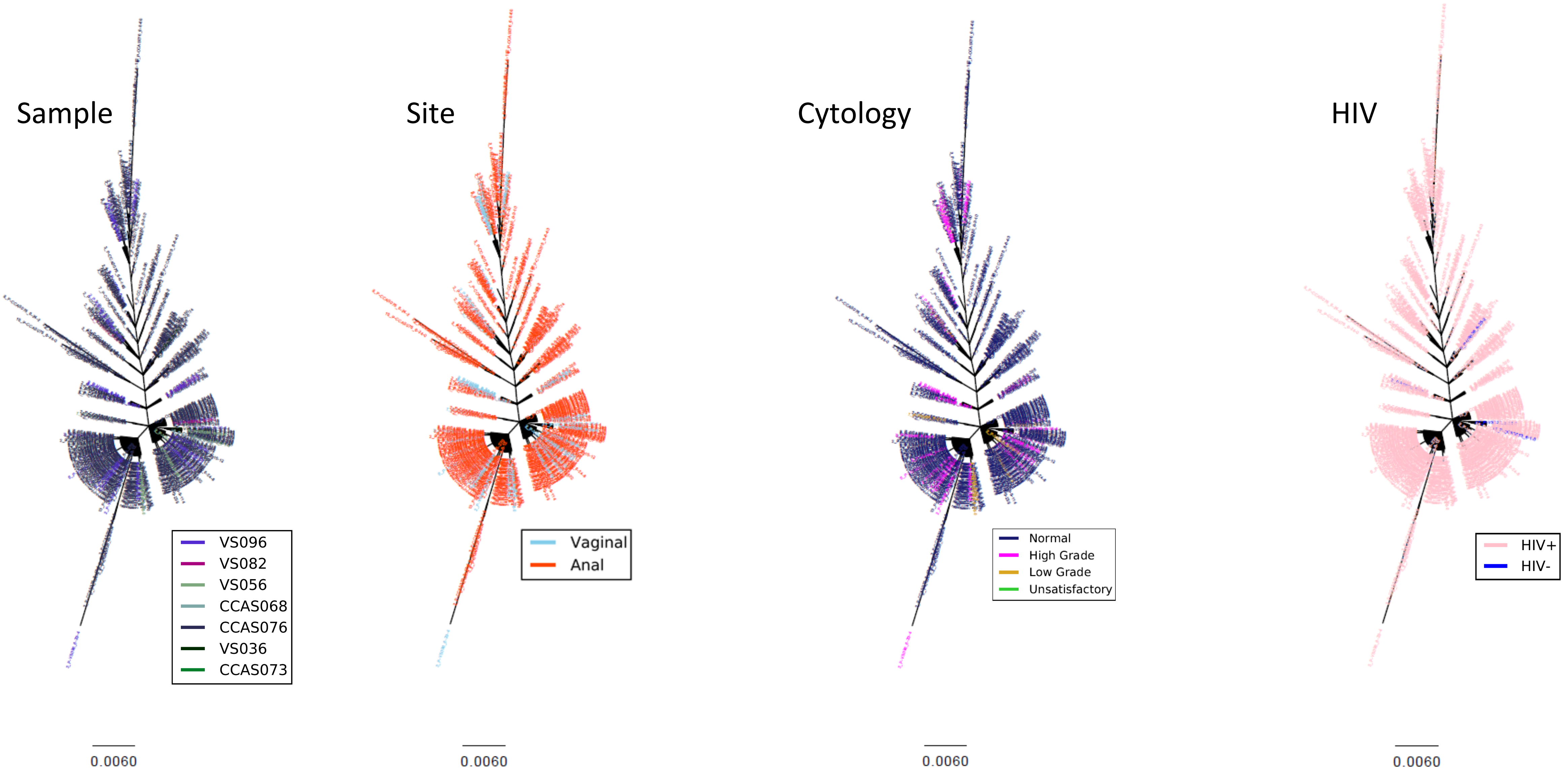

Sample
VS096
VS082
VS056
CCAS068
CCAS076
VS036
CCAS073
0.0060
Site
Vaginal
Anal
0.0060
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.0060
HIV
HIV+
HIV-
0.0060

Fig S3: HPV 26

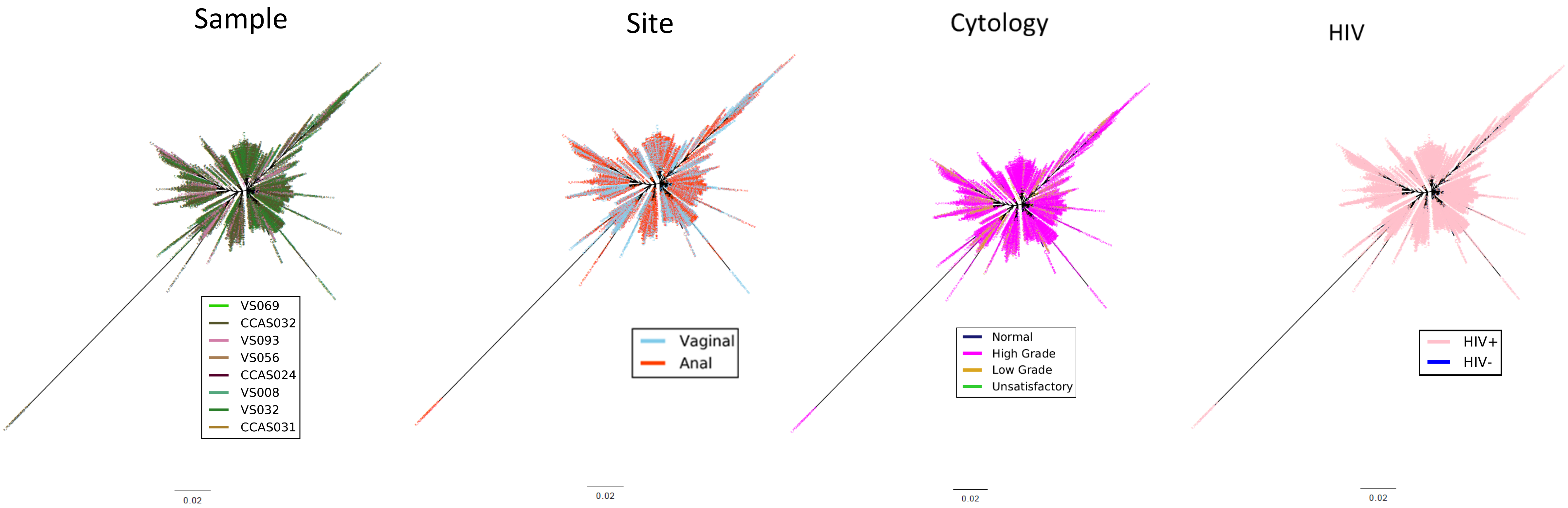

Sample
VS069
CCAS032
VS093
VS056
CCAS024
VS008
VS032
CCAS031
0.02
Site
Vaginal
Anal
0.02
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.02
HIV
HIV+
HIV-
0.02

Fig S4: HPV 31

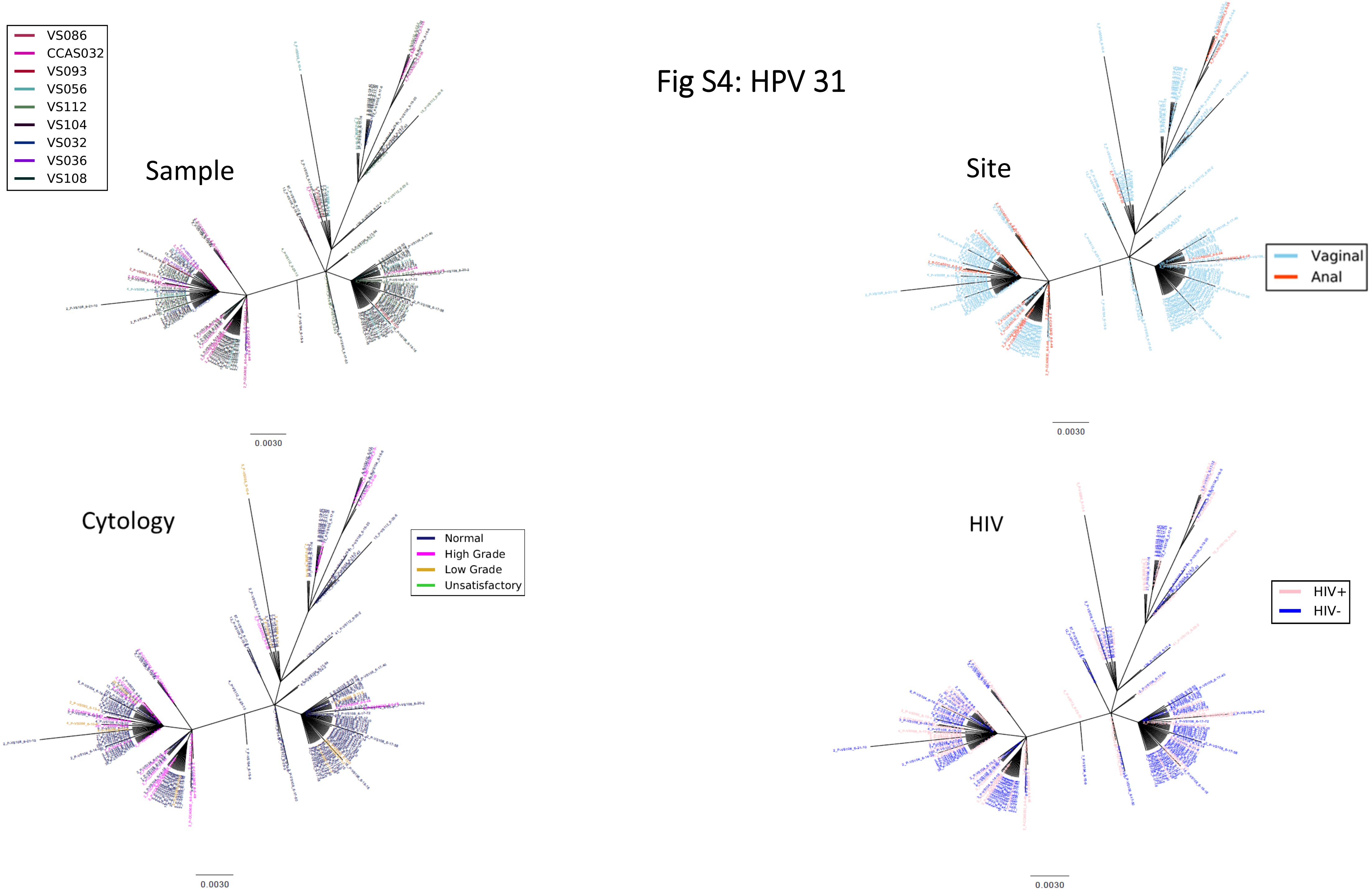

VS086
CCAS032
VS093
VS056
VS112
VS104
VS032
VS036
VS108
Sample
0.0030
Site
Vaginal
Anal
0.0030
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.0030
HIV
HIV+
HIV-
0.0030

Fig S5:HPV 32

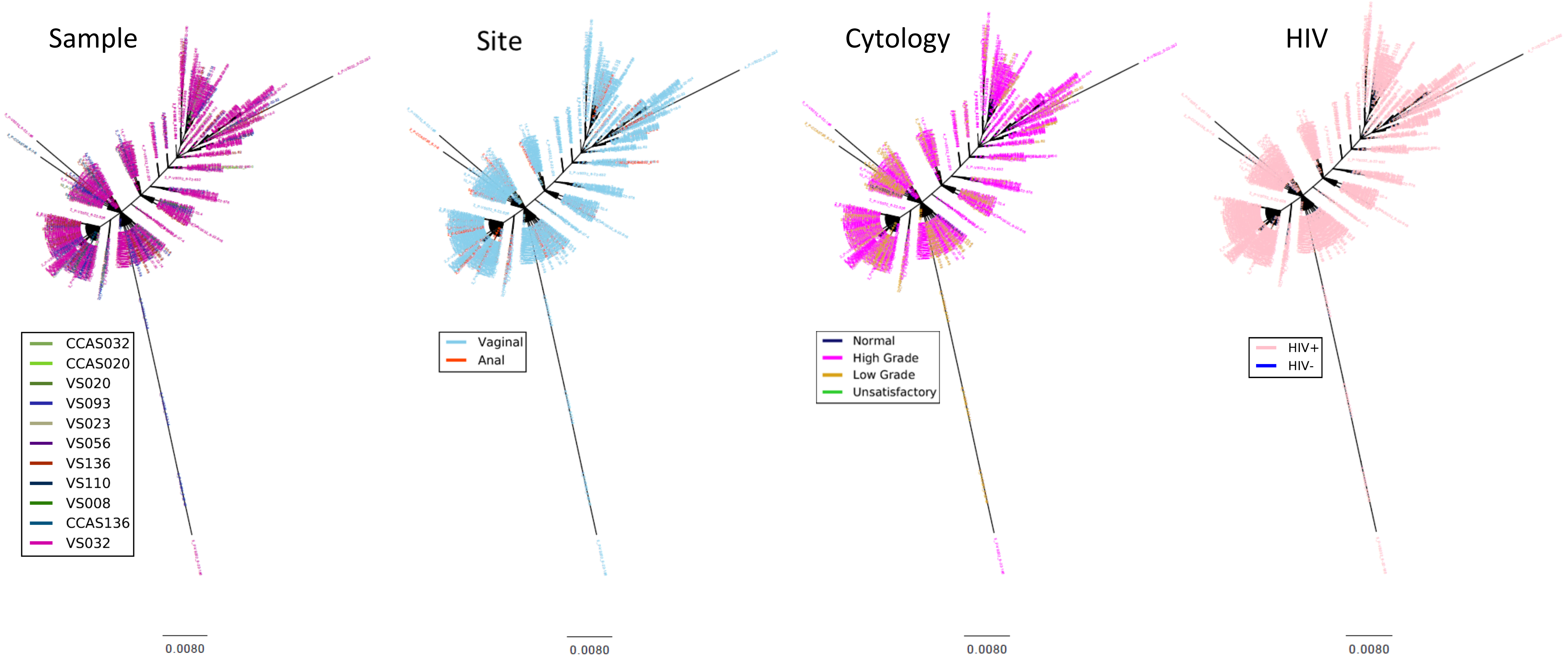

Sample
CCAS032
CCAS020
VS020
VS093
VS023
VS056
VS136
VS110
VS008
CCAS136
VS032
0.0080
Site
Vaginal
Anal
0.0080
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.0080
HIV
HIV+
HIV-
0.0080

Fig S6: HPV 35H

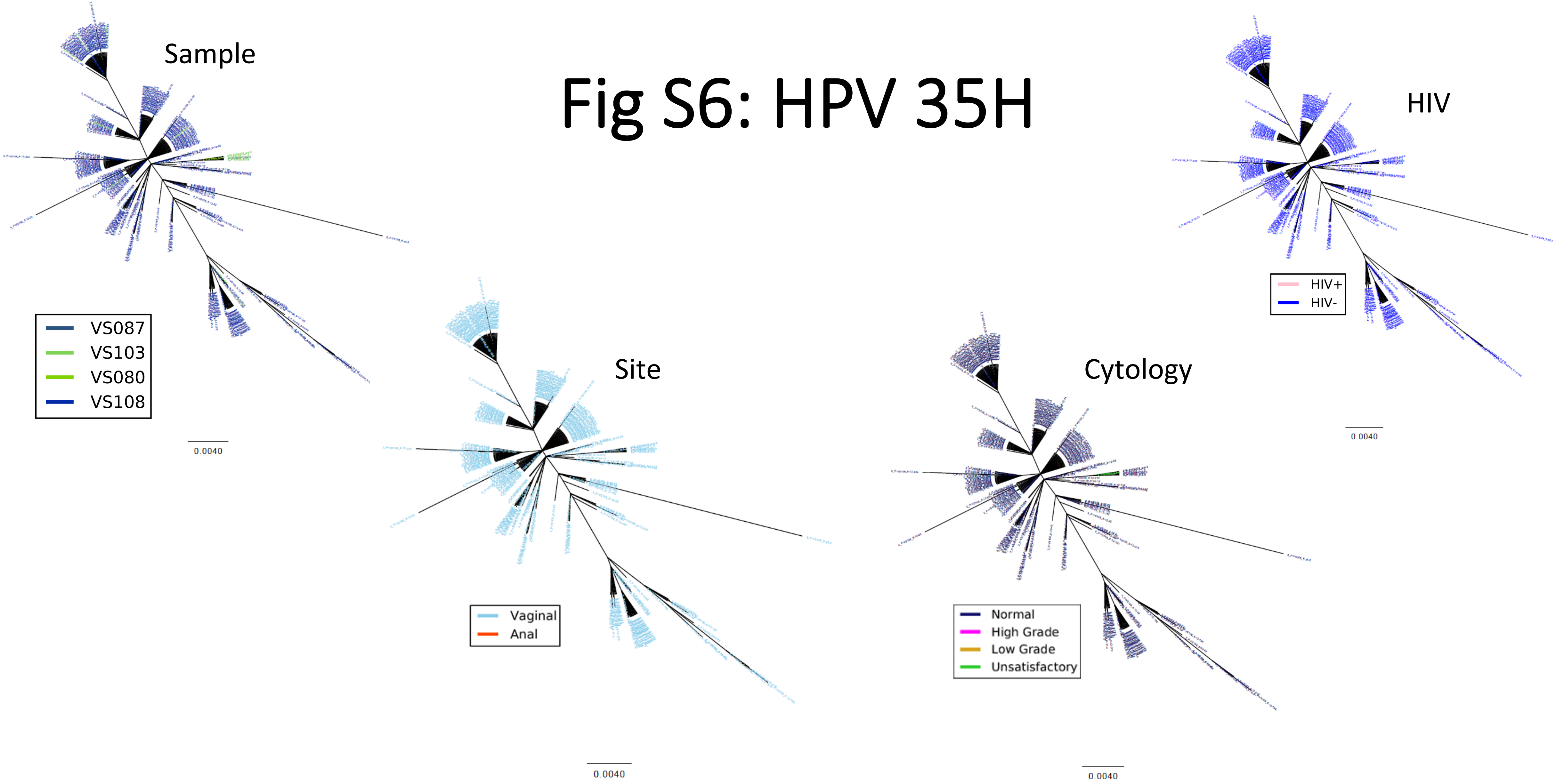


Fig S7: HPV 39

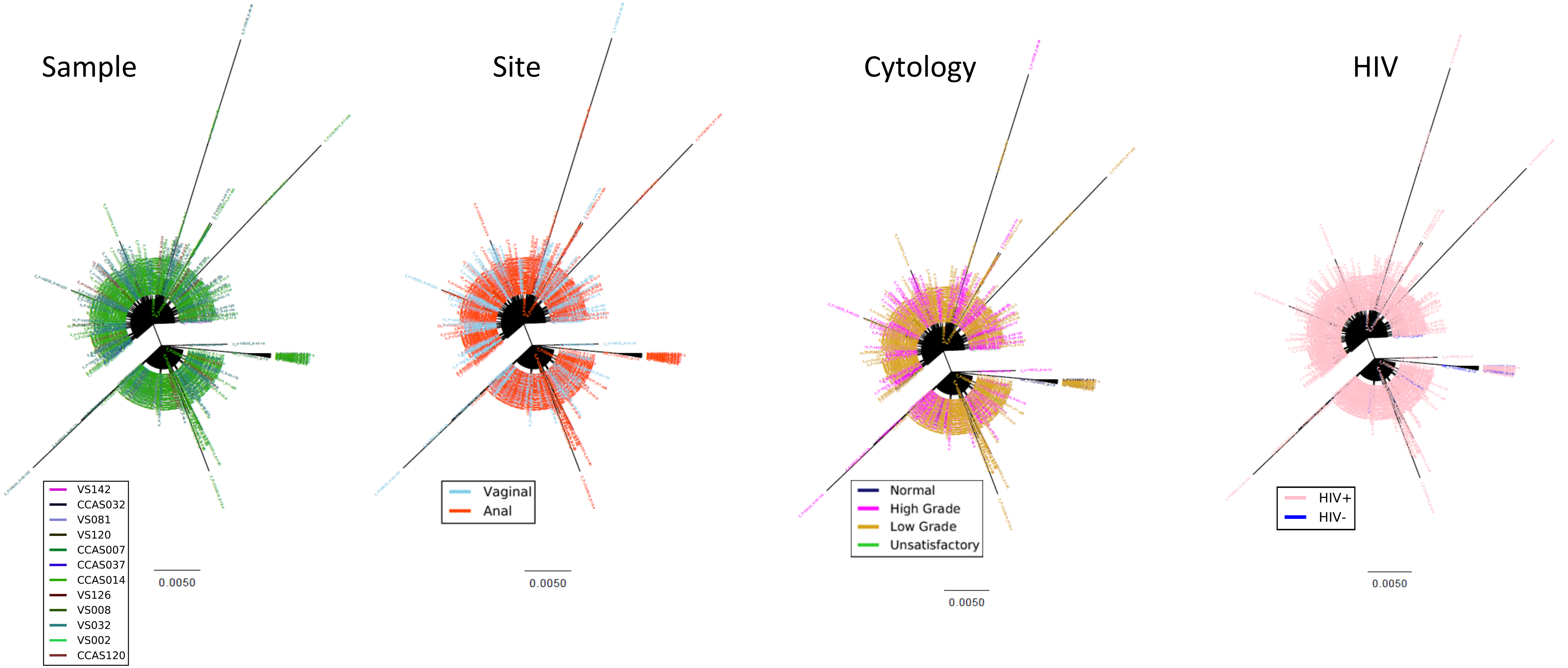
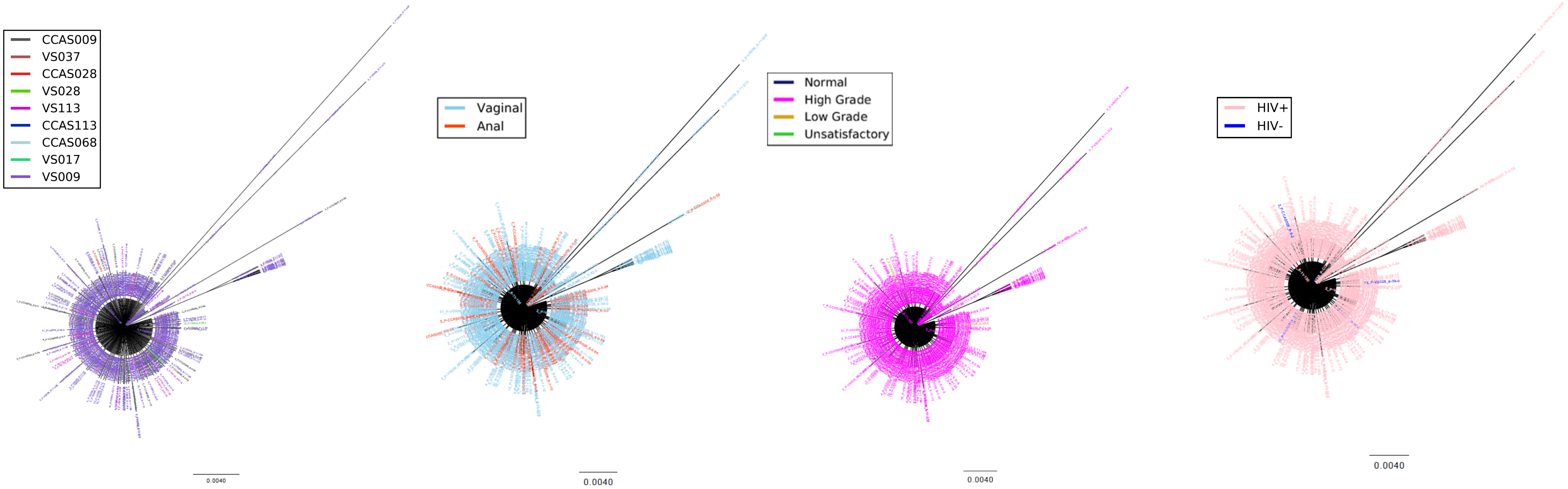

Sample
VS142
CCAS032
VS081
VS120
CCAS007
CCAS037
CCAS014
VS126
VS008
VS032
VS002
CCAS120
0.0050
Site
Vaginal
Anal
0.0050
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.0050
HIV
HIV+
HIV-
0.0050

Fig S8: HPV 40


Sample
CCAS004
VS114
VS004
CCAS144
VS144
Site
Vaginal
Anal
0.08
Cytology
Normal
High Grade
Low Grade
Unsatisfactory
0.08
HIV
HIV+
HIV-
0.08

Fig S9: HPV 42A



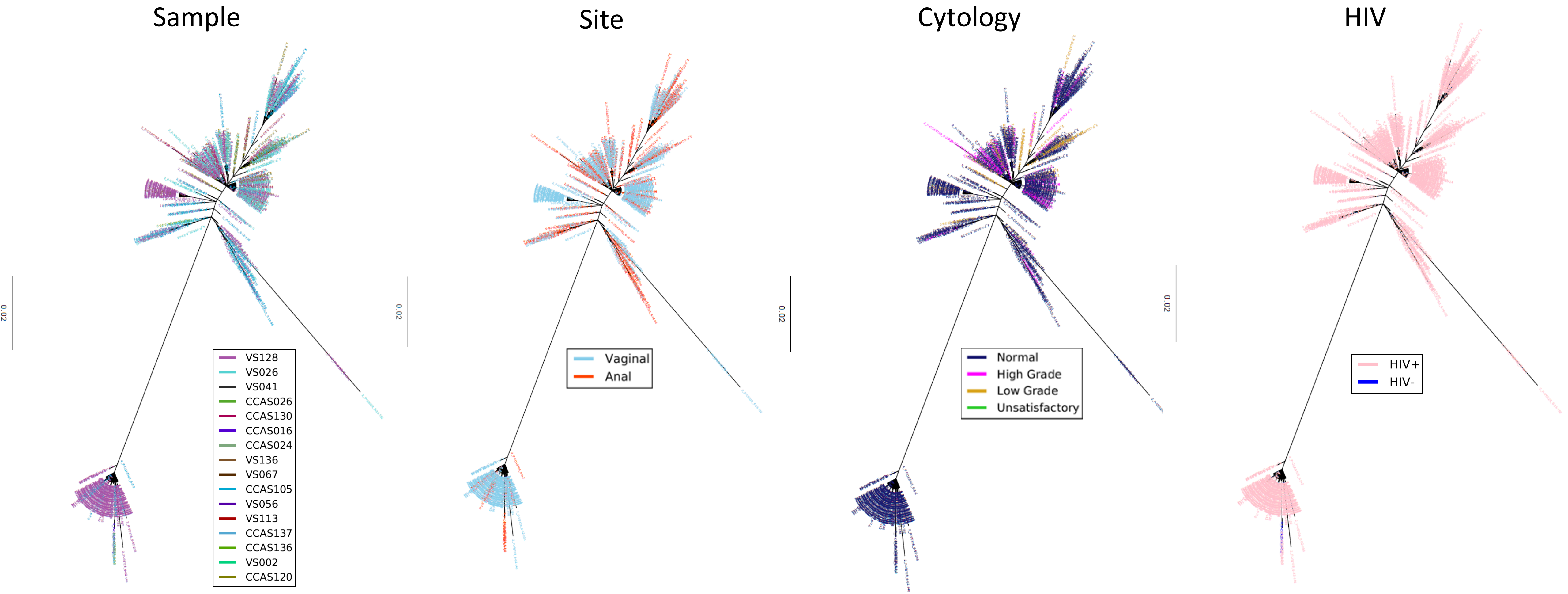
Sample

Site

Cytology

HIV

Fig S10: HPV 44



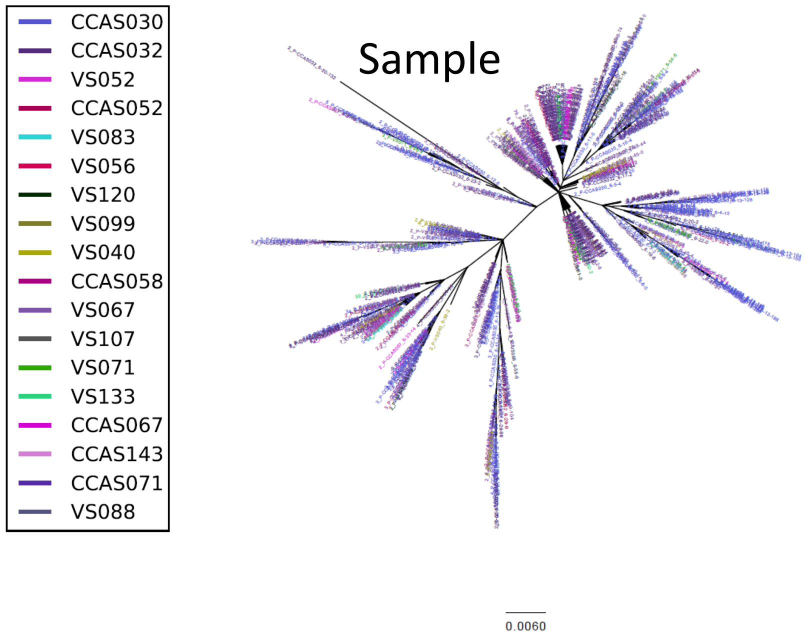
Sample

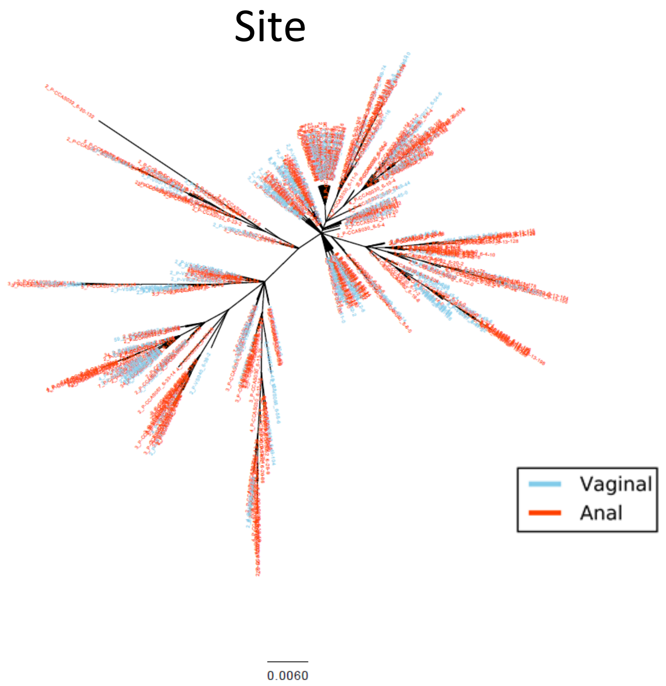
Site

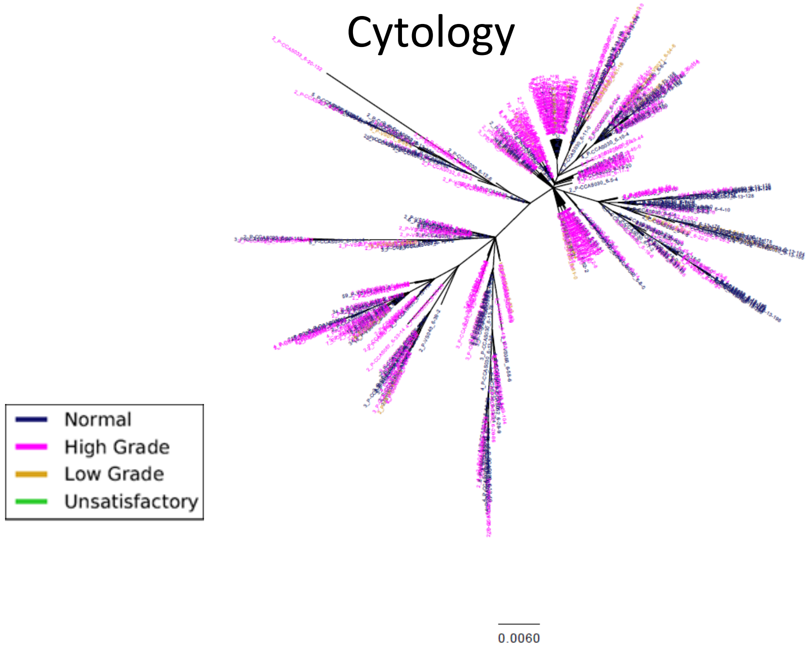
Cytology

HIV

Fig S11: HPV 45


Sample


Site


Cytology

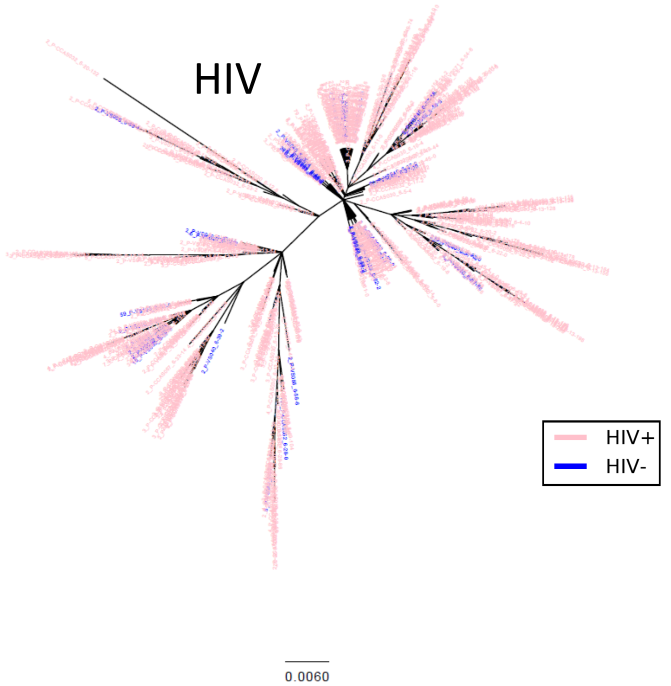

HIV

Fig S12: HPV 51

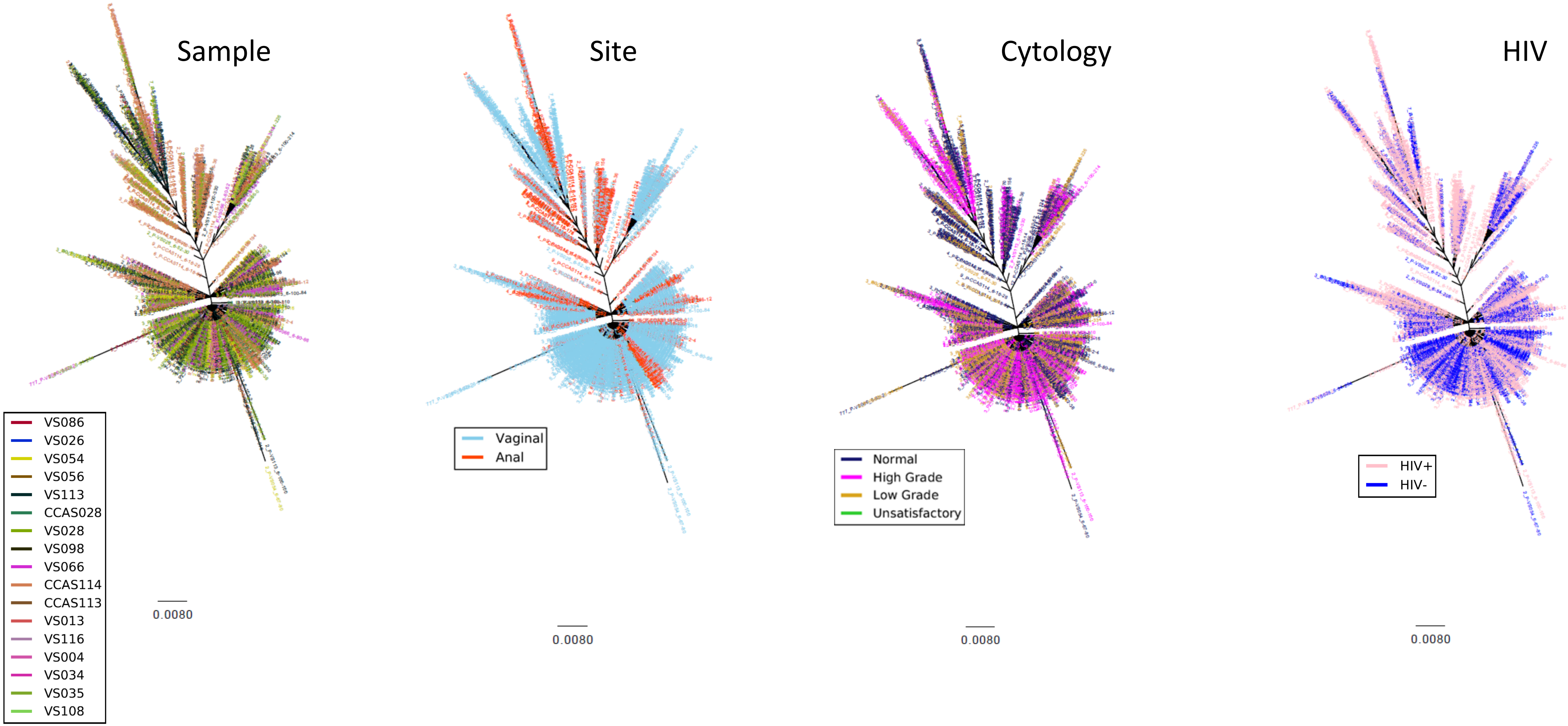


Fig S13: HPV 53

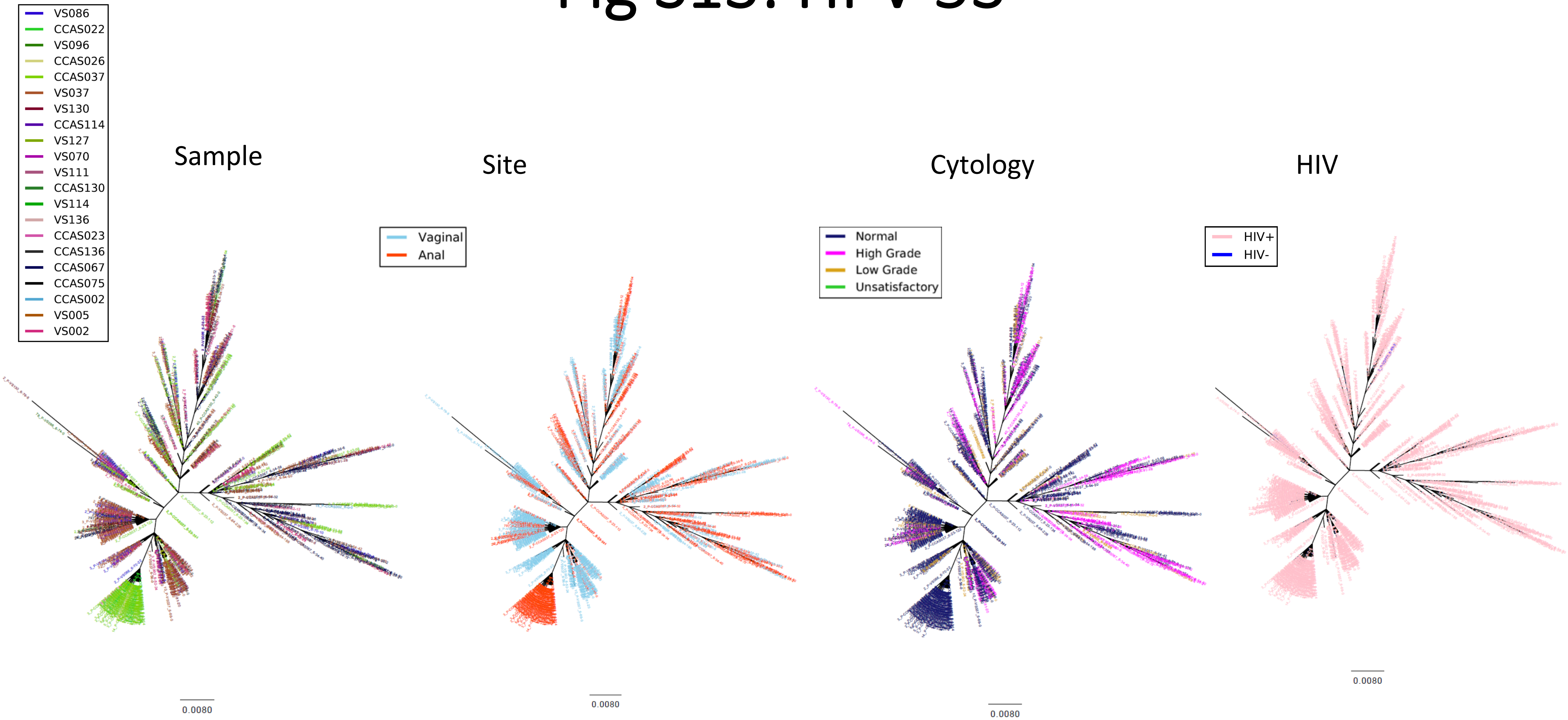


Fig S14: HPV 58

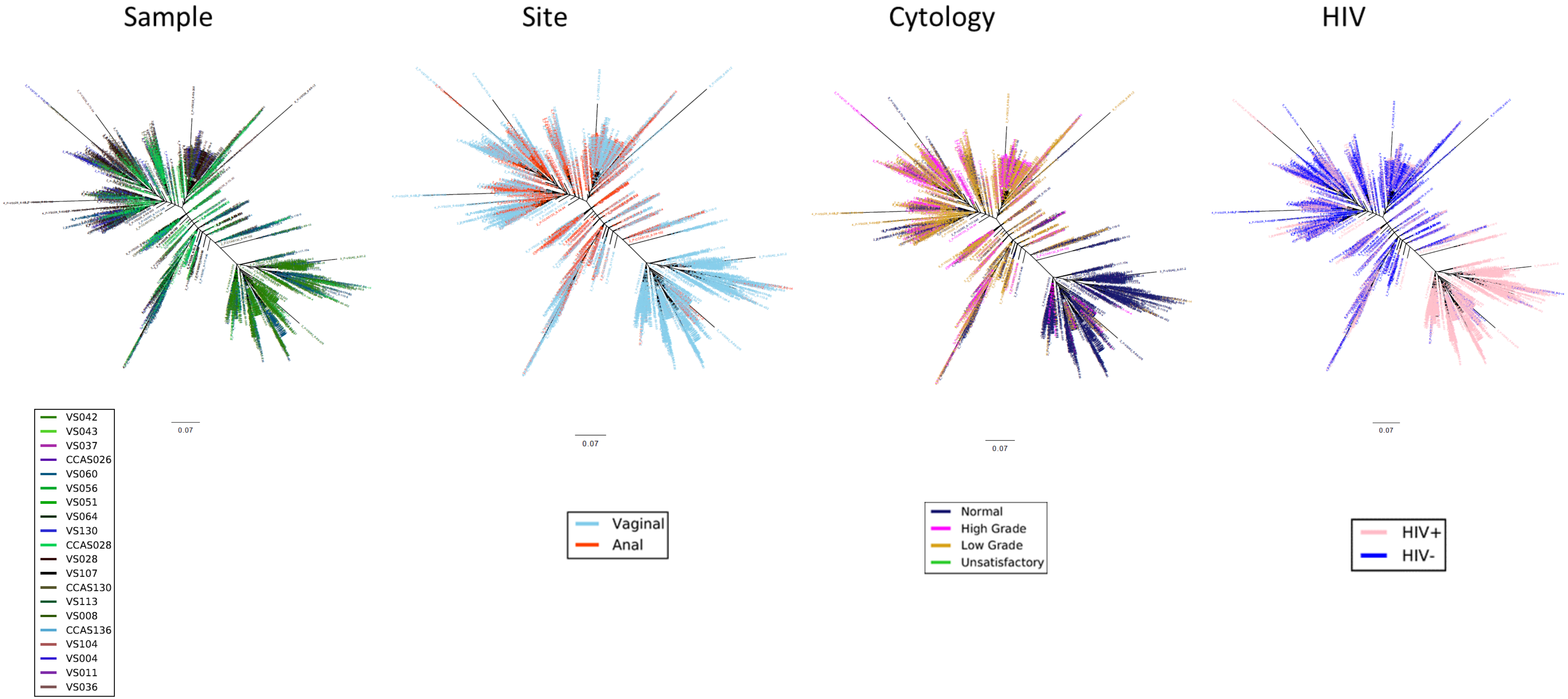


Fig S15: HPV 59

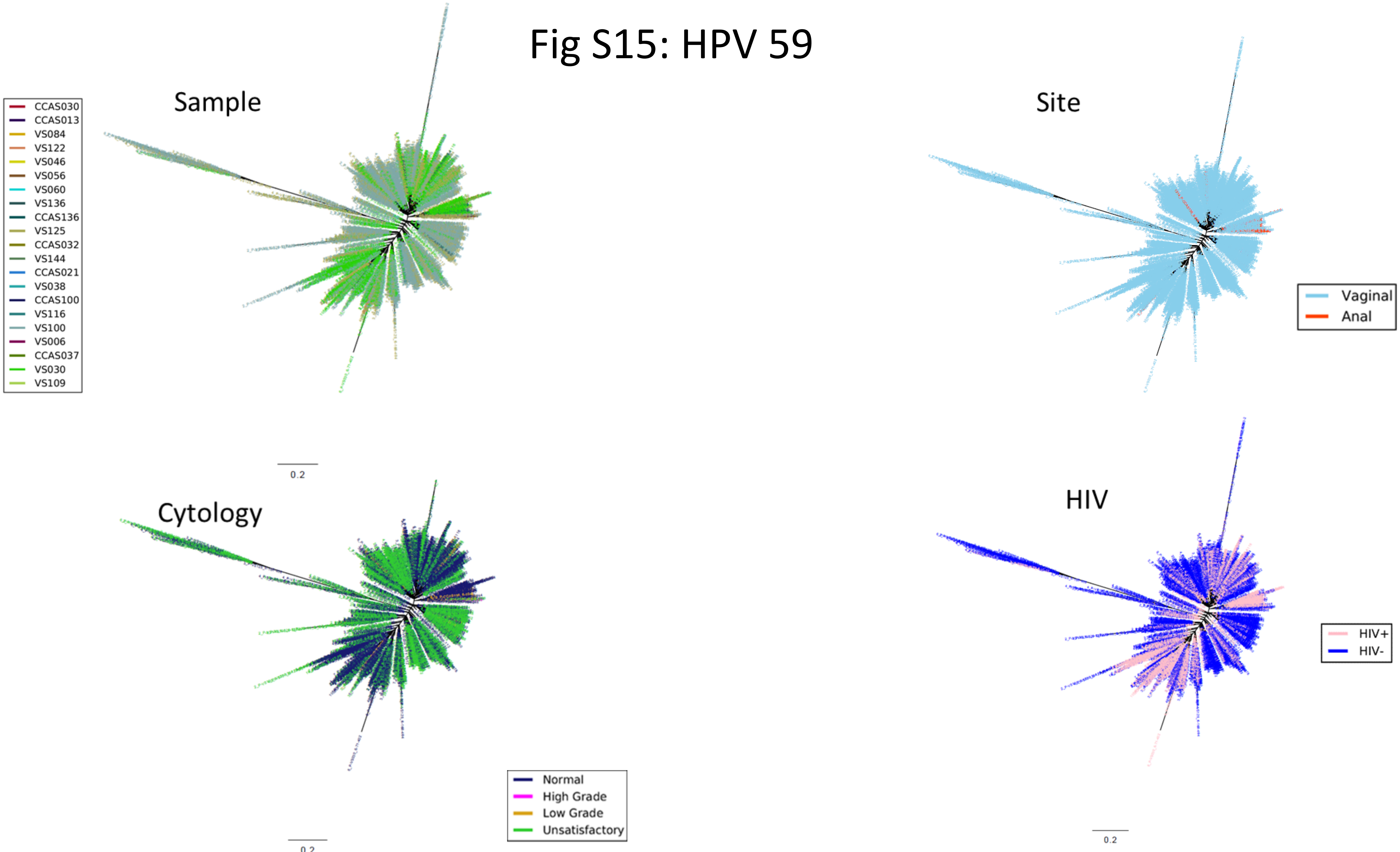
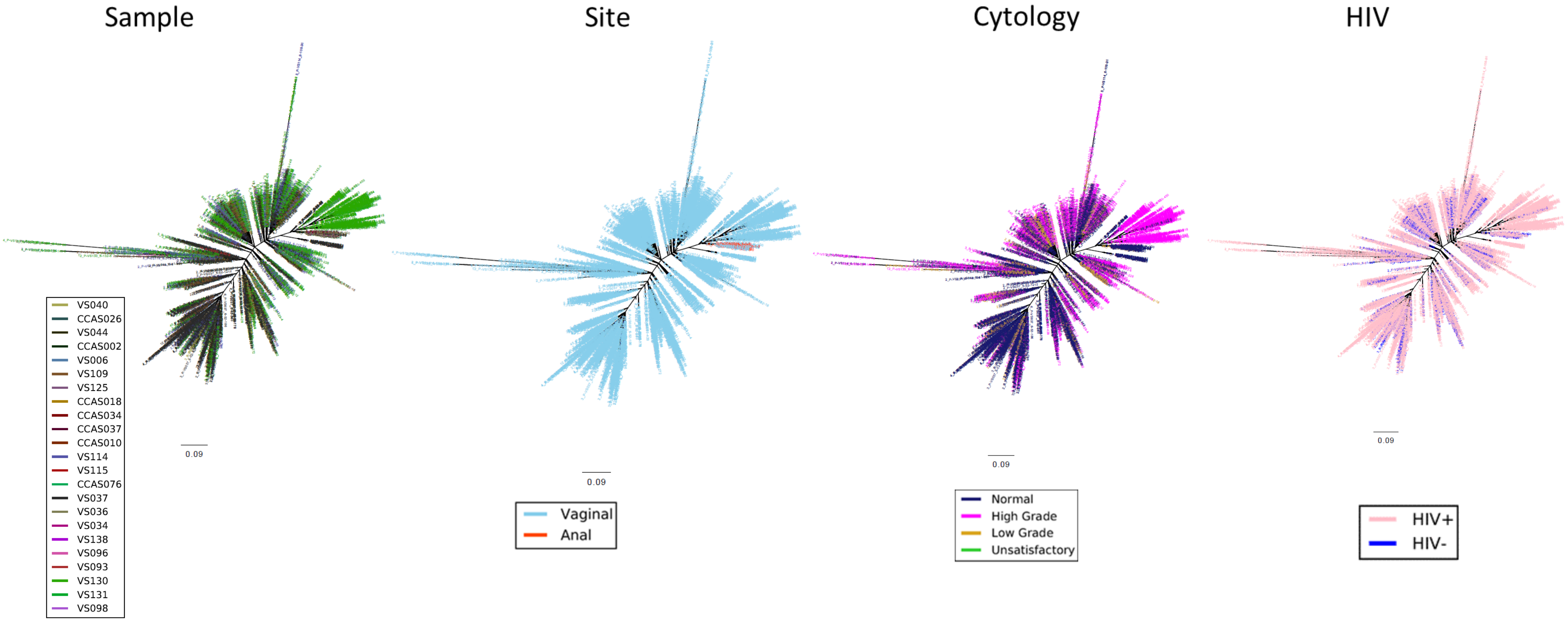


Fig S16: HPV 61



Sample

Site

Cytology

HIV

Fig S17: HPV 62

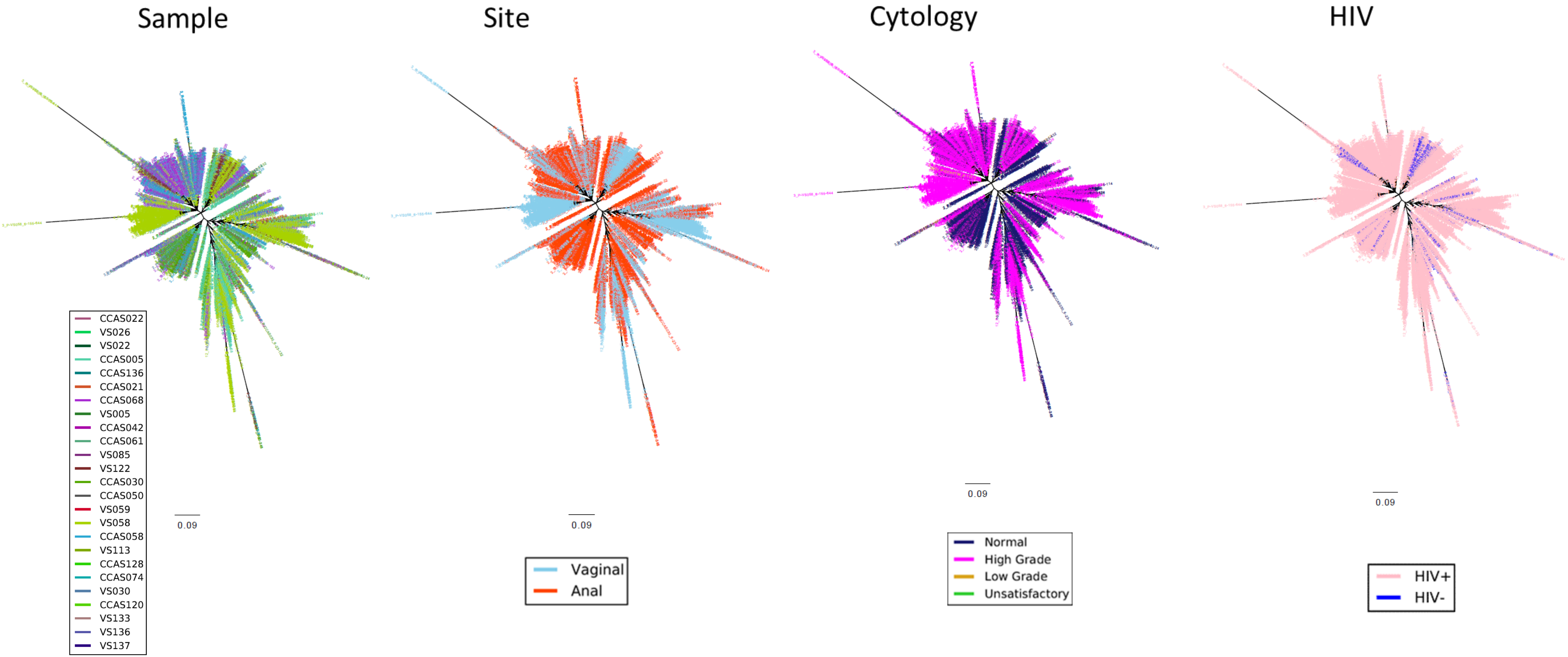


Fig S18:HPV 66

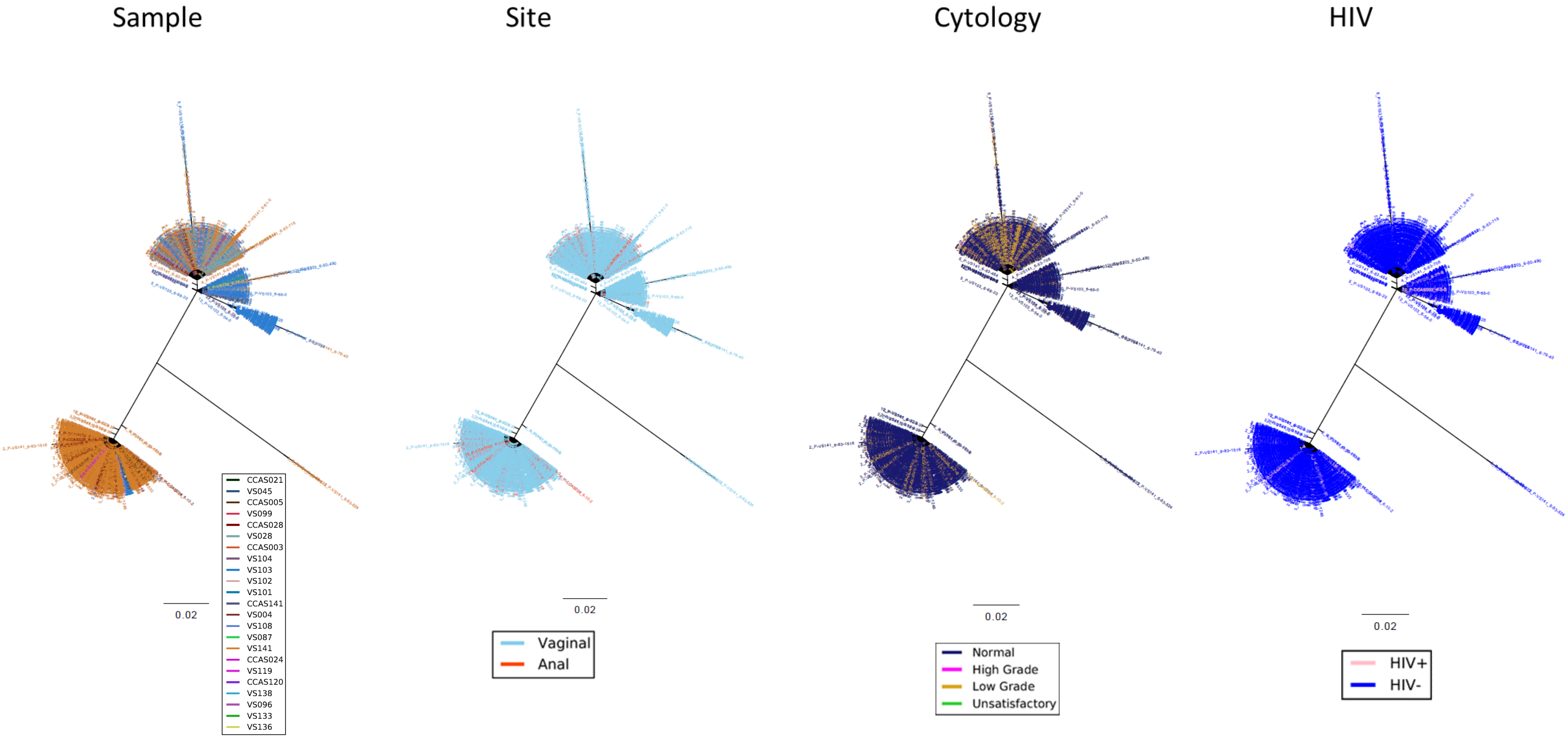


Fig S19: HPV 68

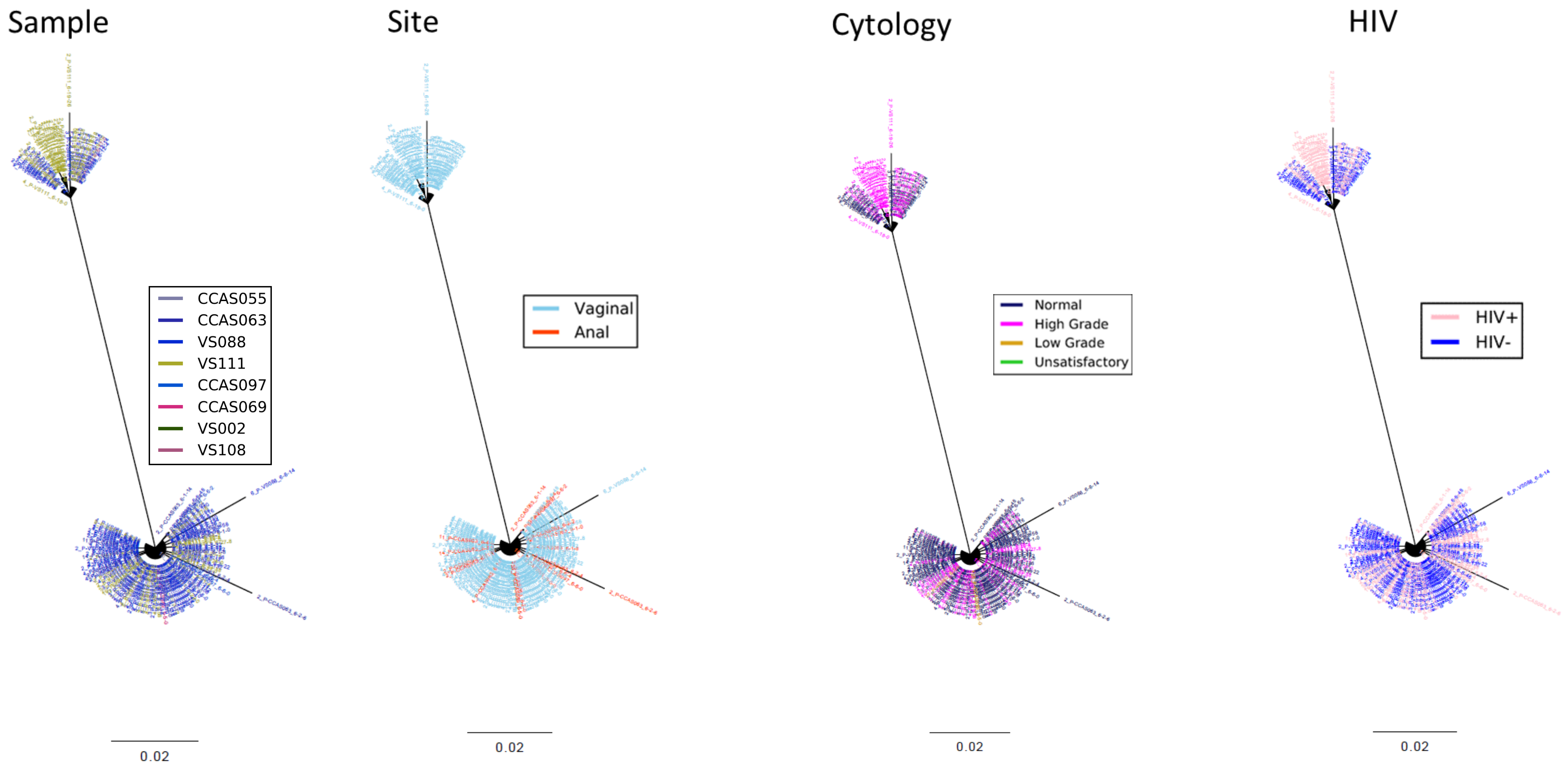


Fig S20: HPV 69

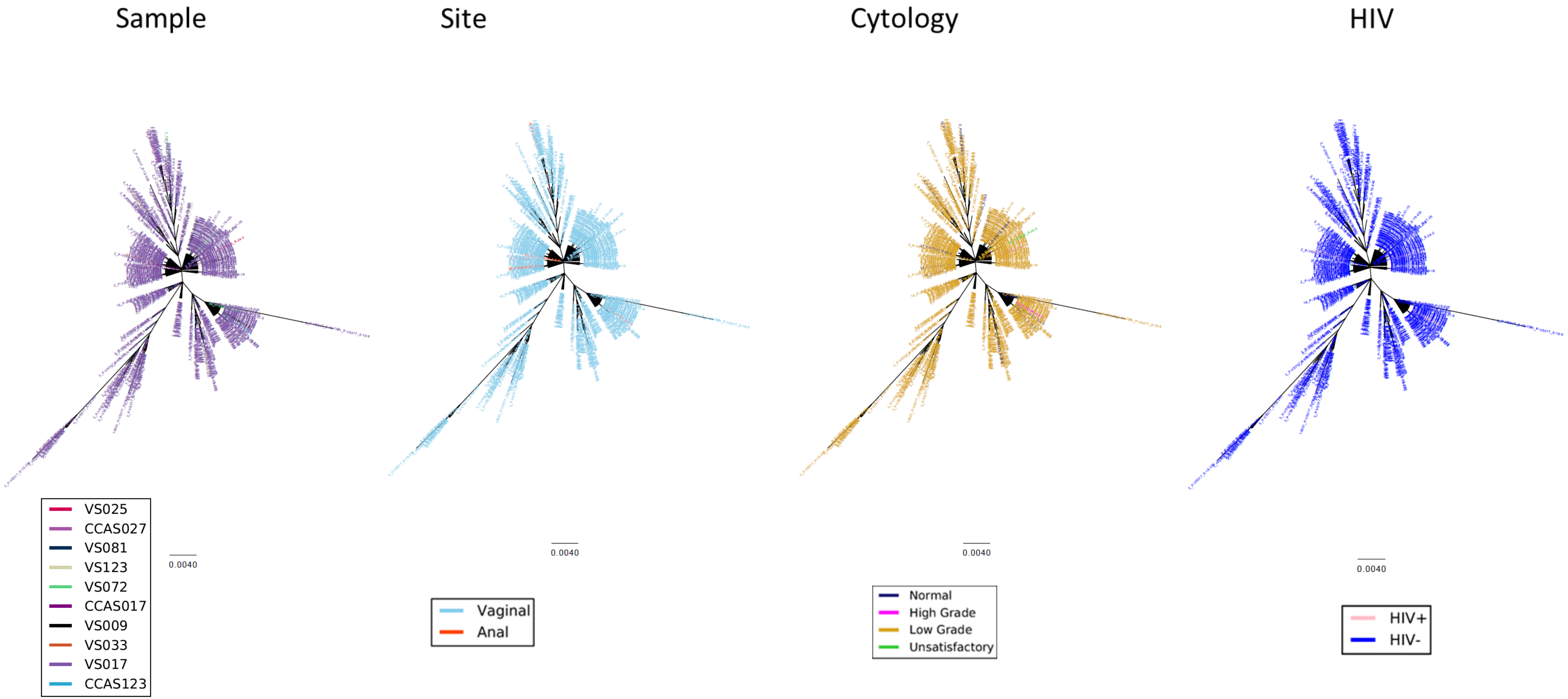


Fig S21: HPV 70

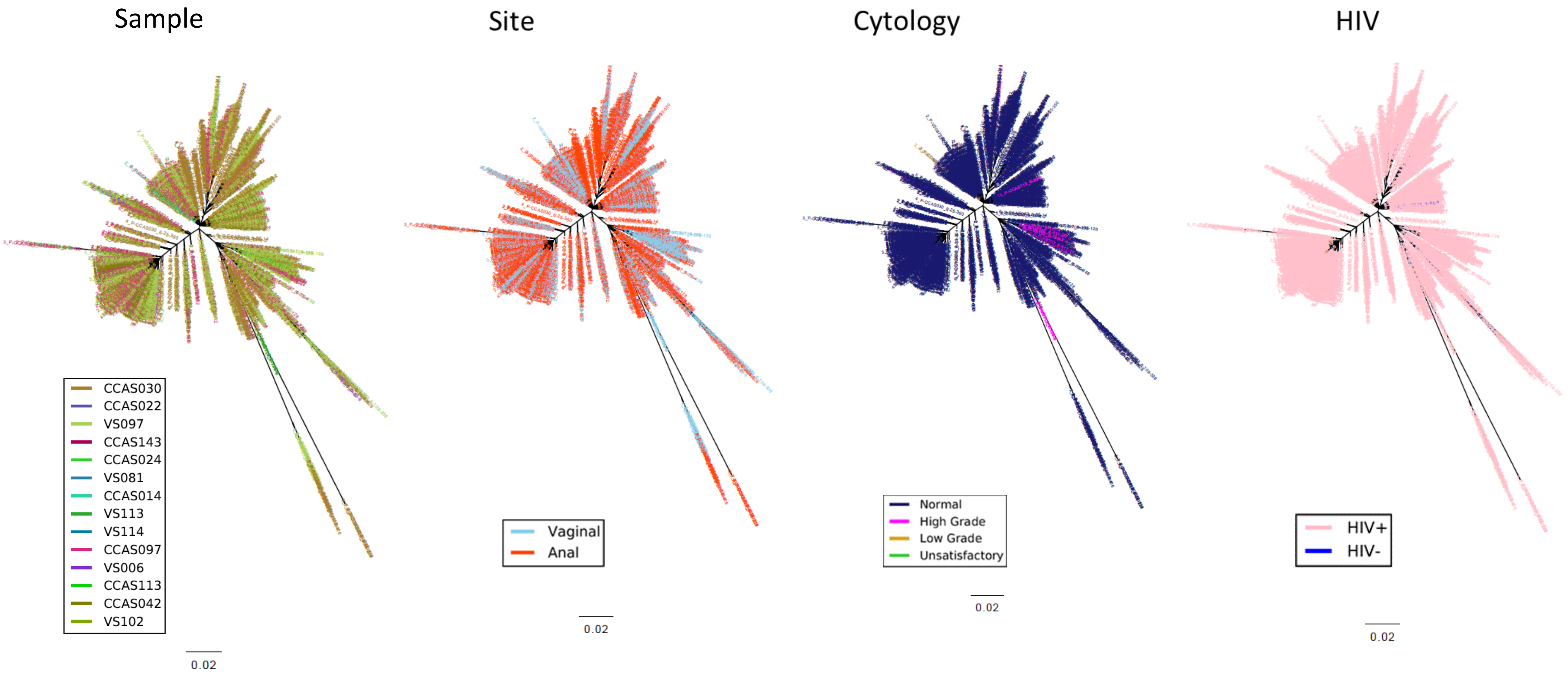


Fig S22: HPV 71

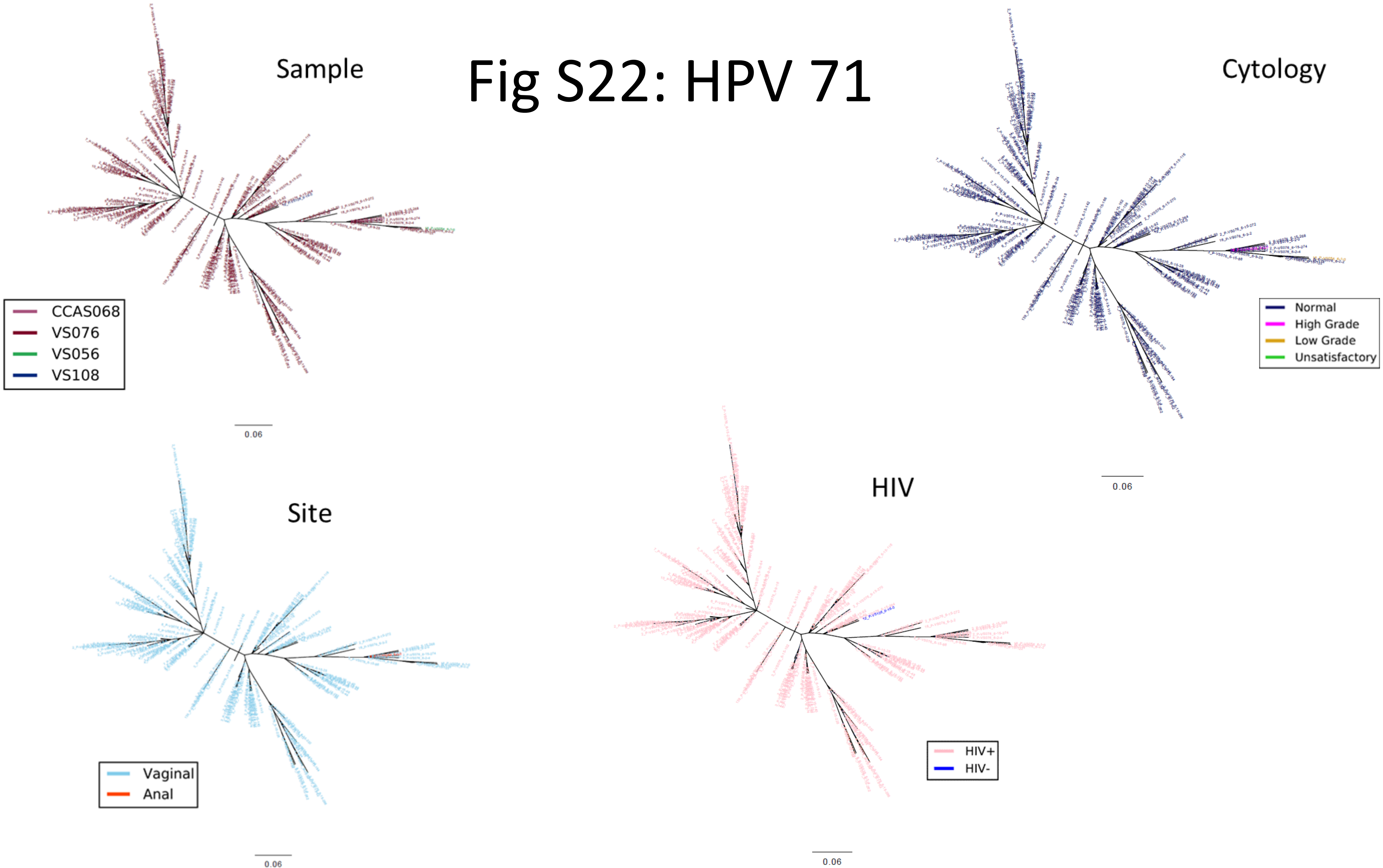


Fig S23: HPV 72

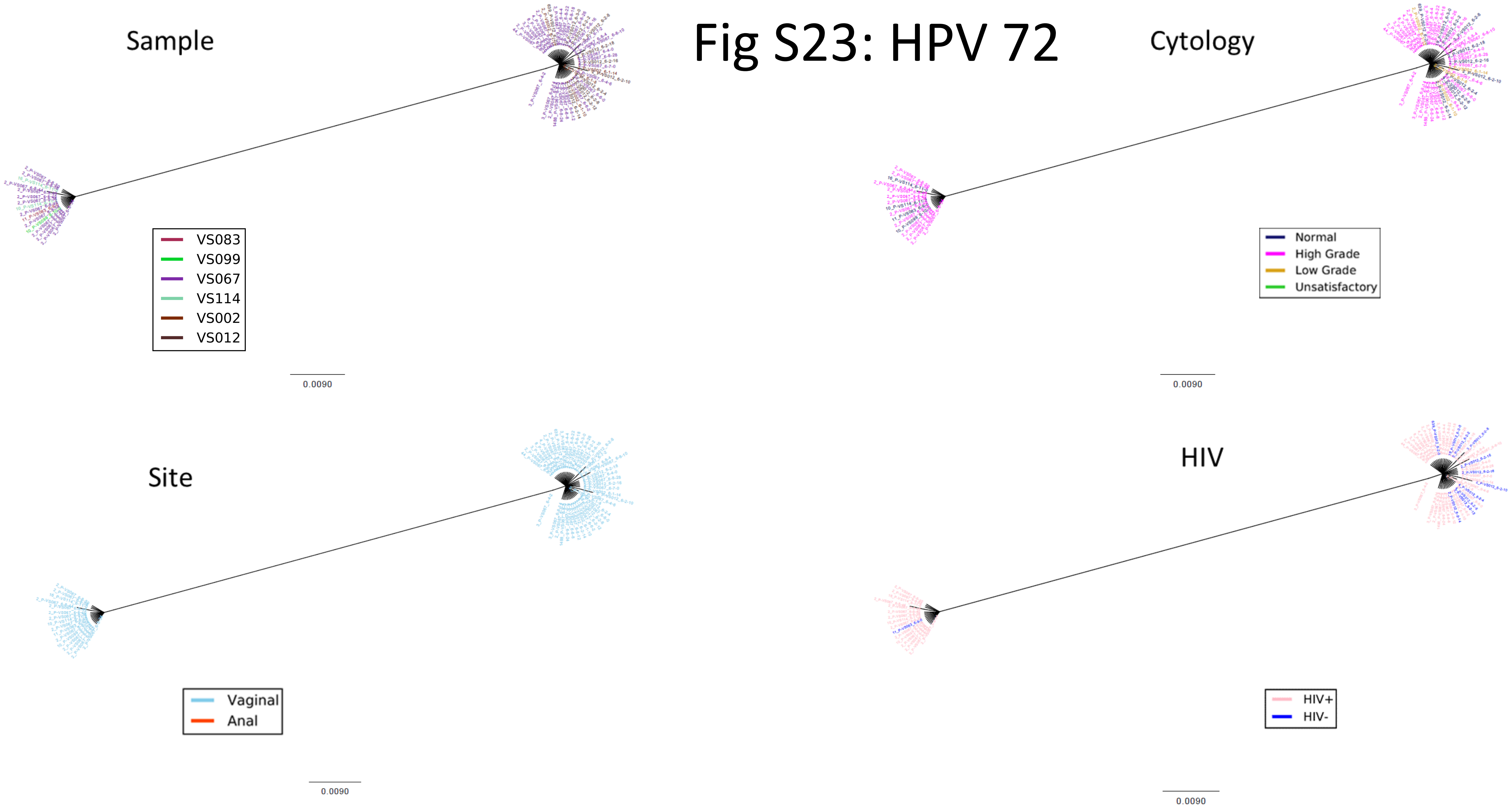
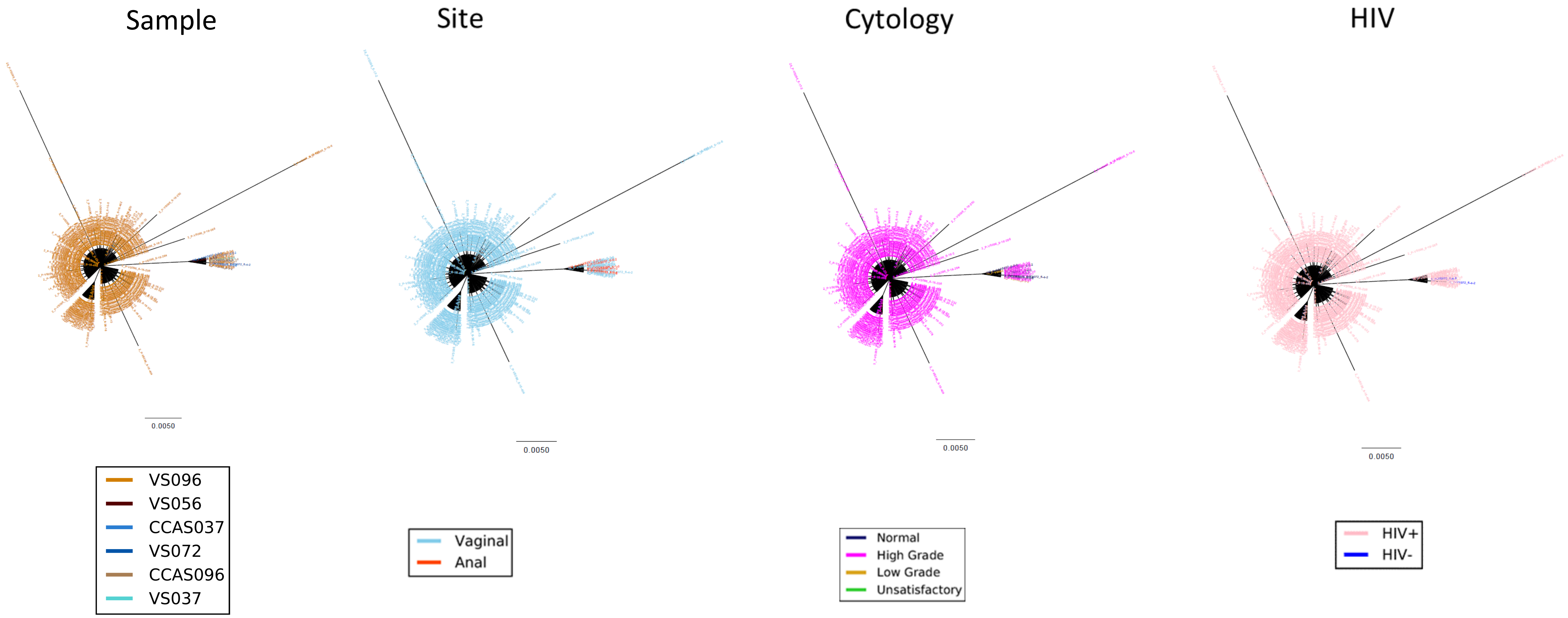


Fig S24: HPV 73


Sample

Site

Cytology

HIV

Fig S25: HPV 81

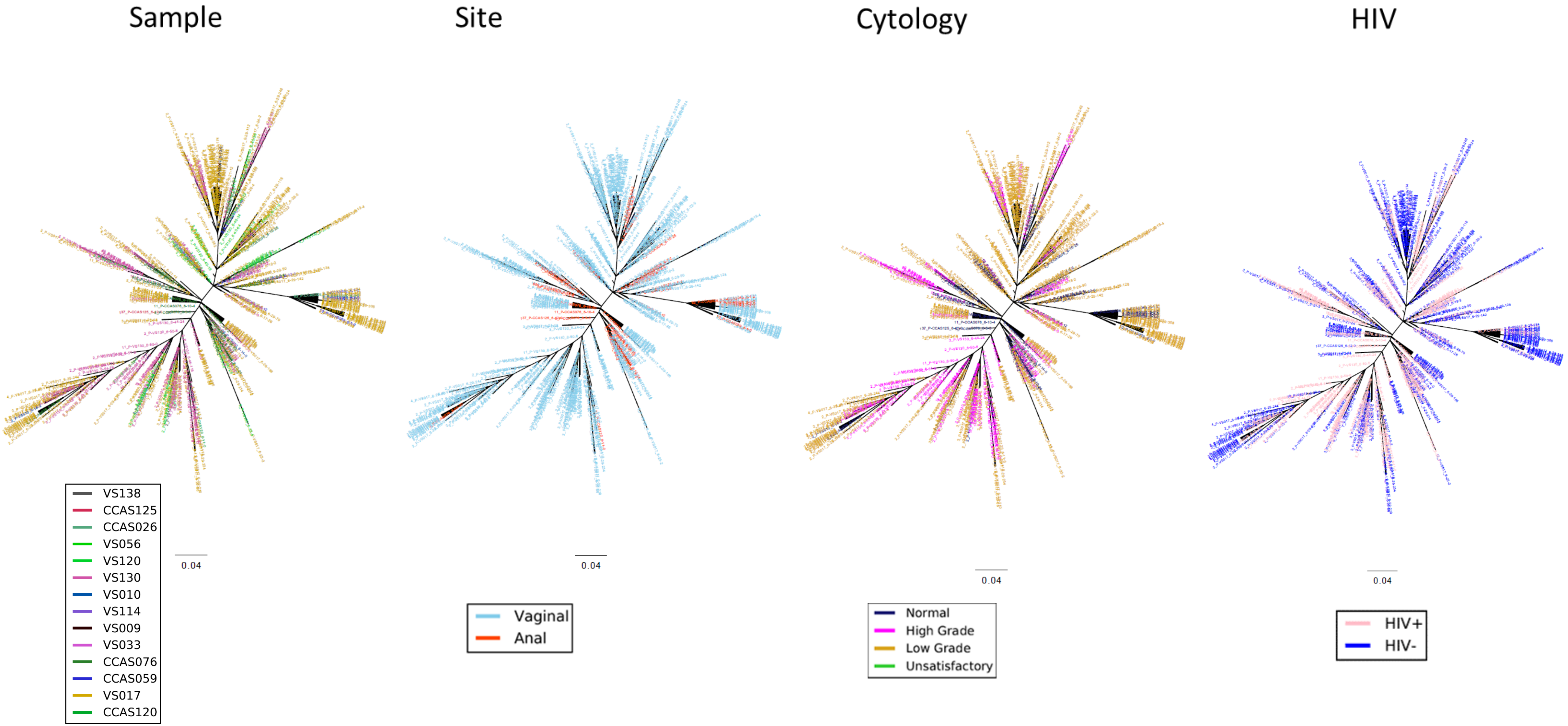


Fig S26: HPV 82

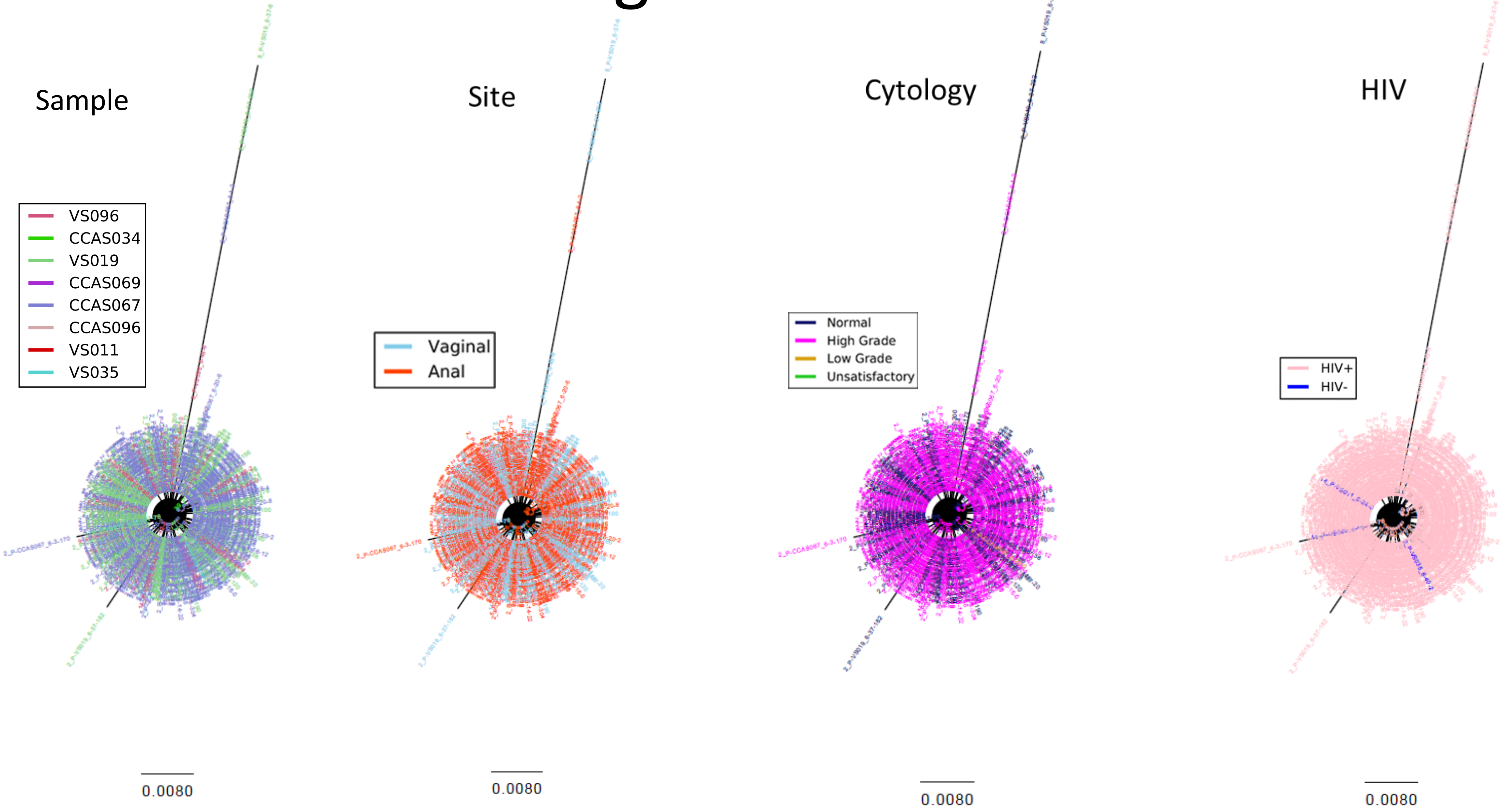


Fig S27: HPV 83

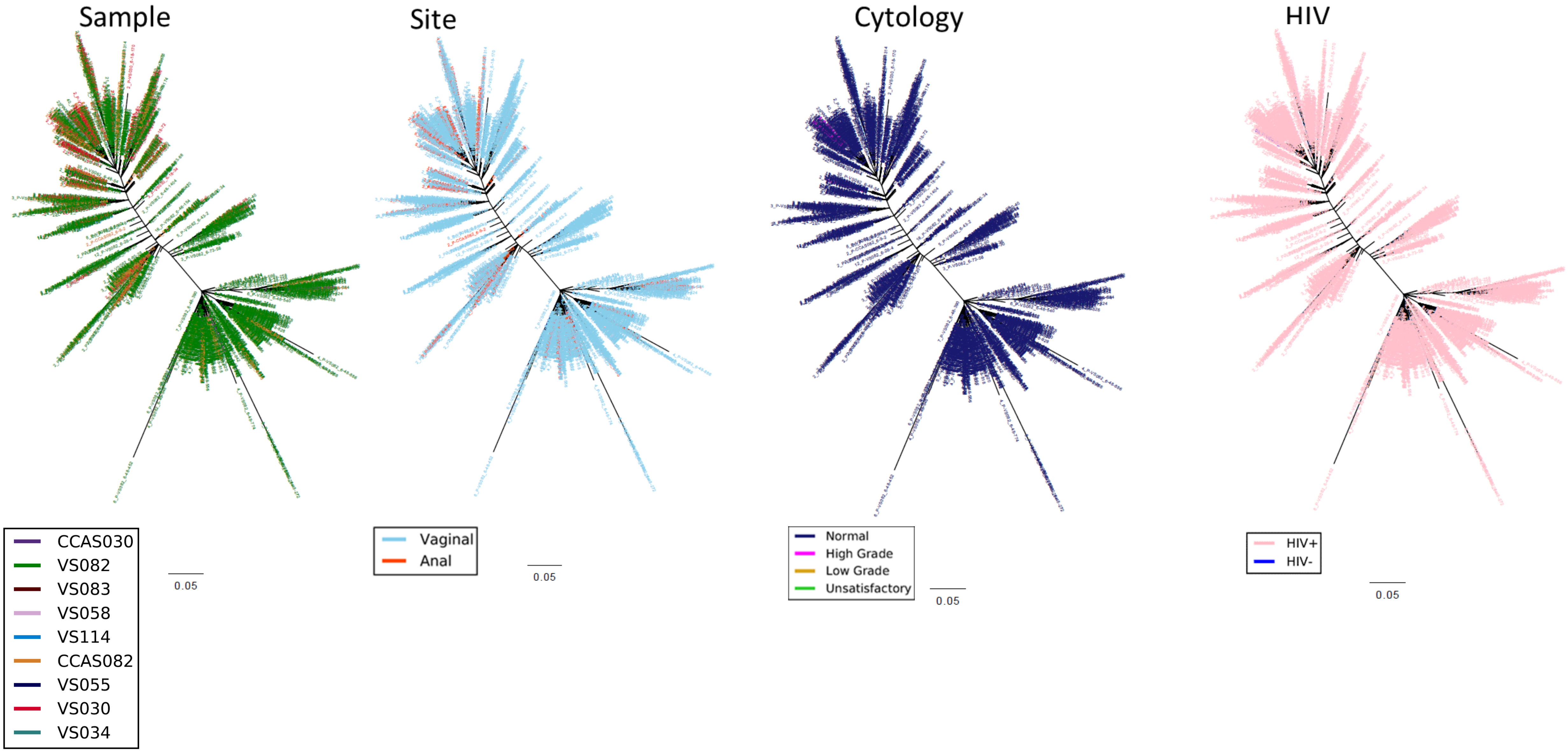


Fig S28: HPV 84

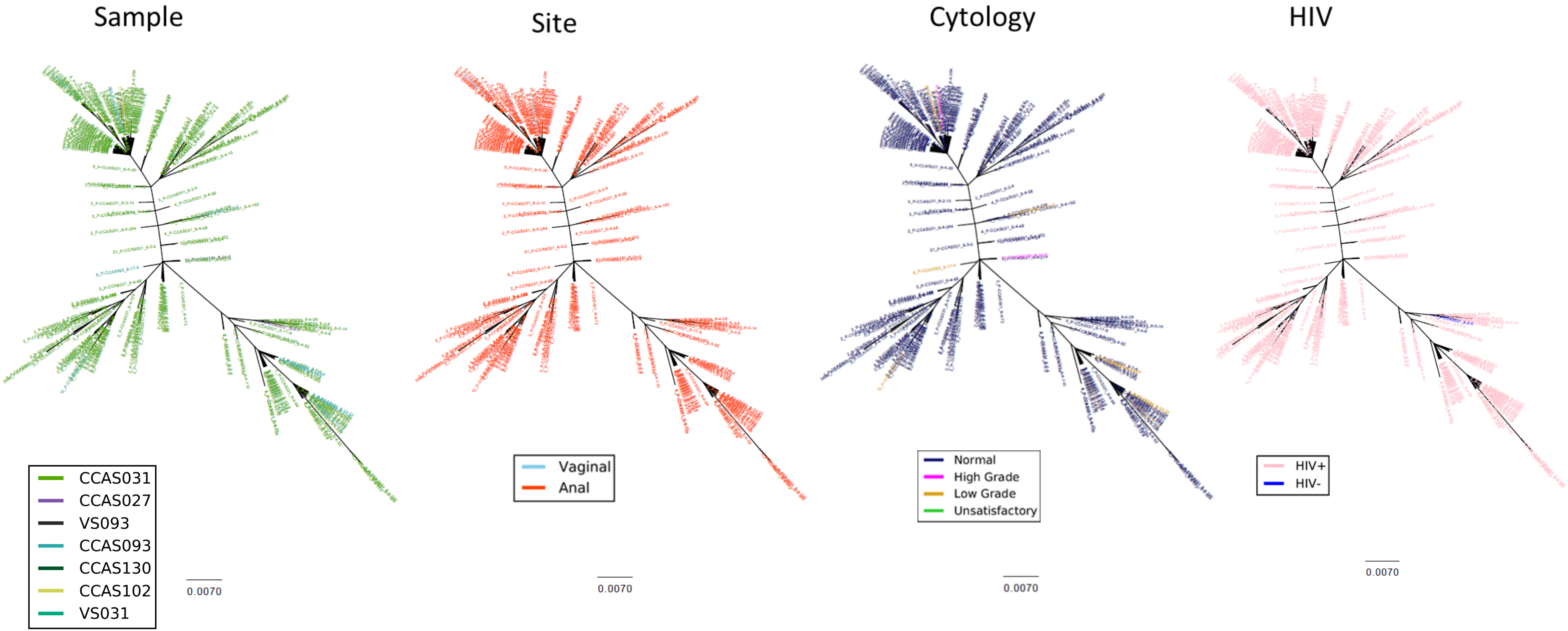


Fig S29: HPV 86

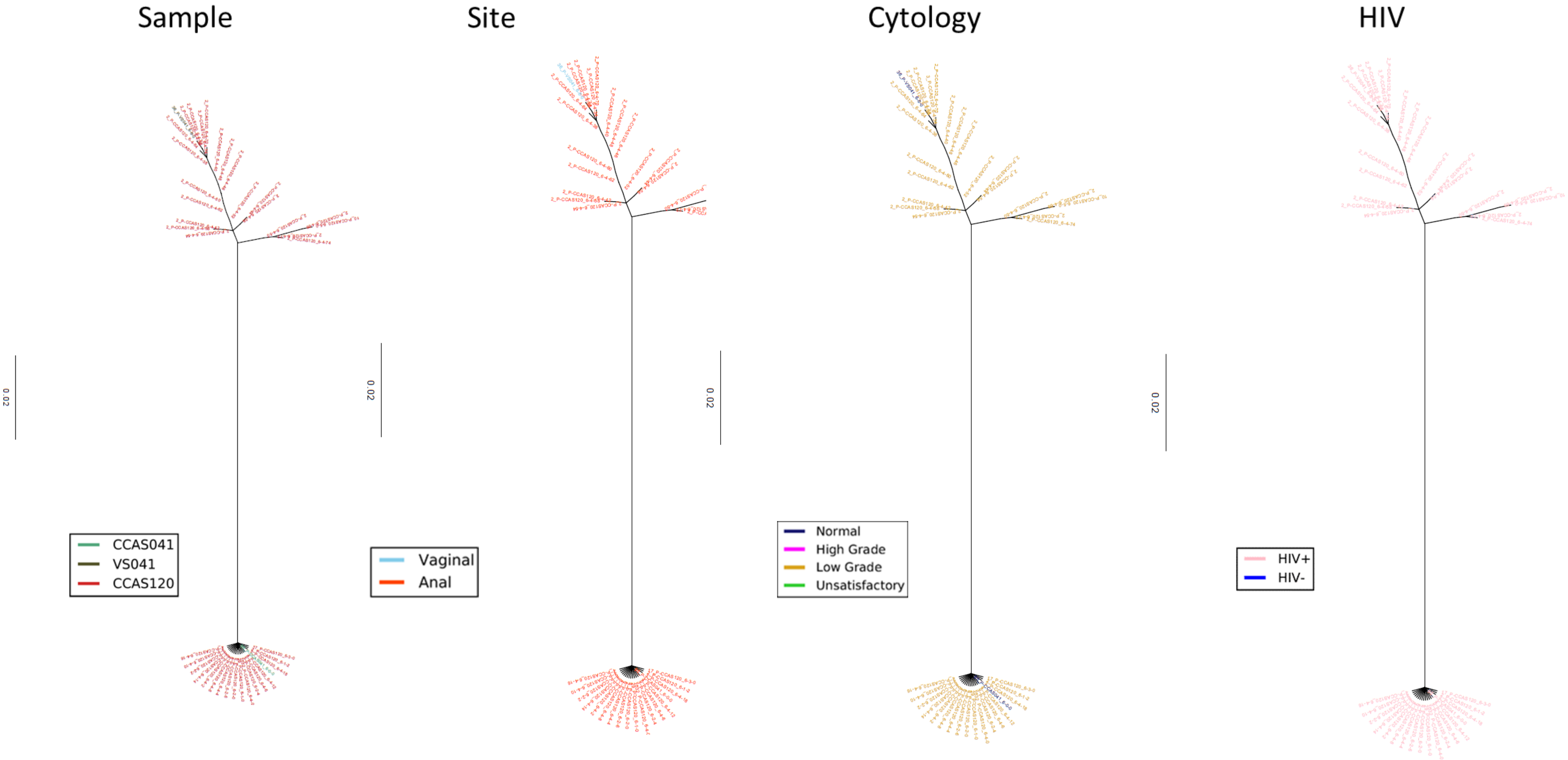


Fig S30: HPV 89

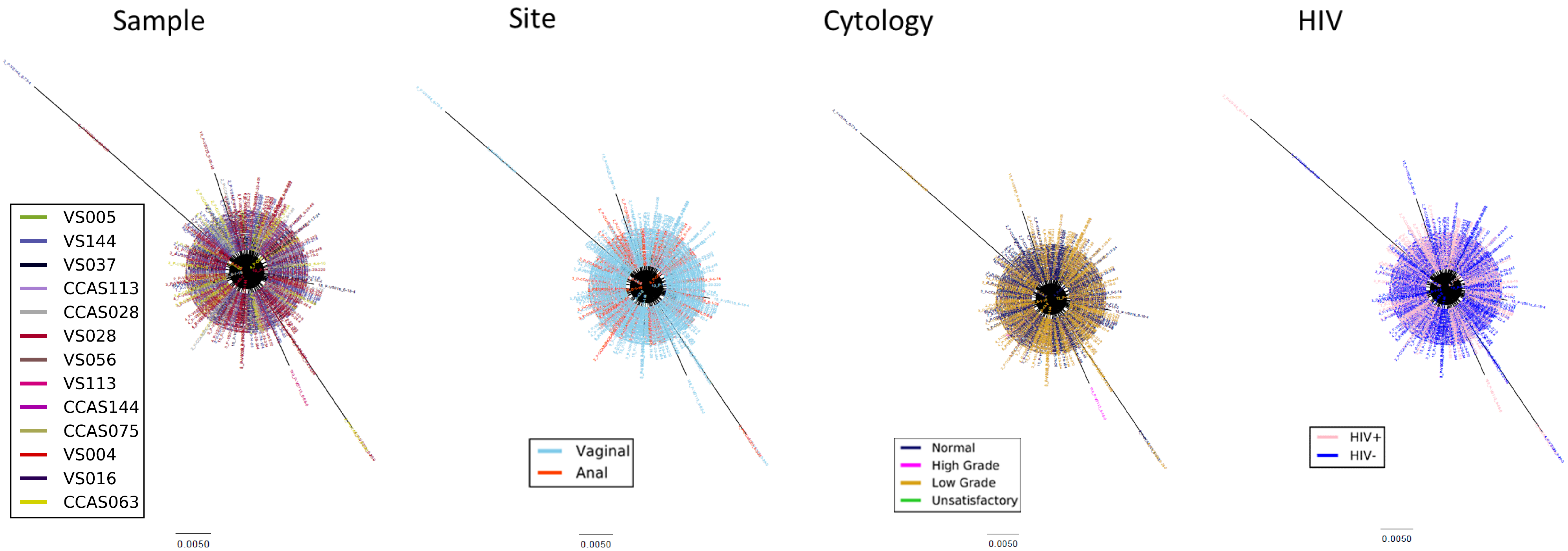


Fig S31: HPV 91

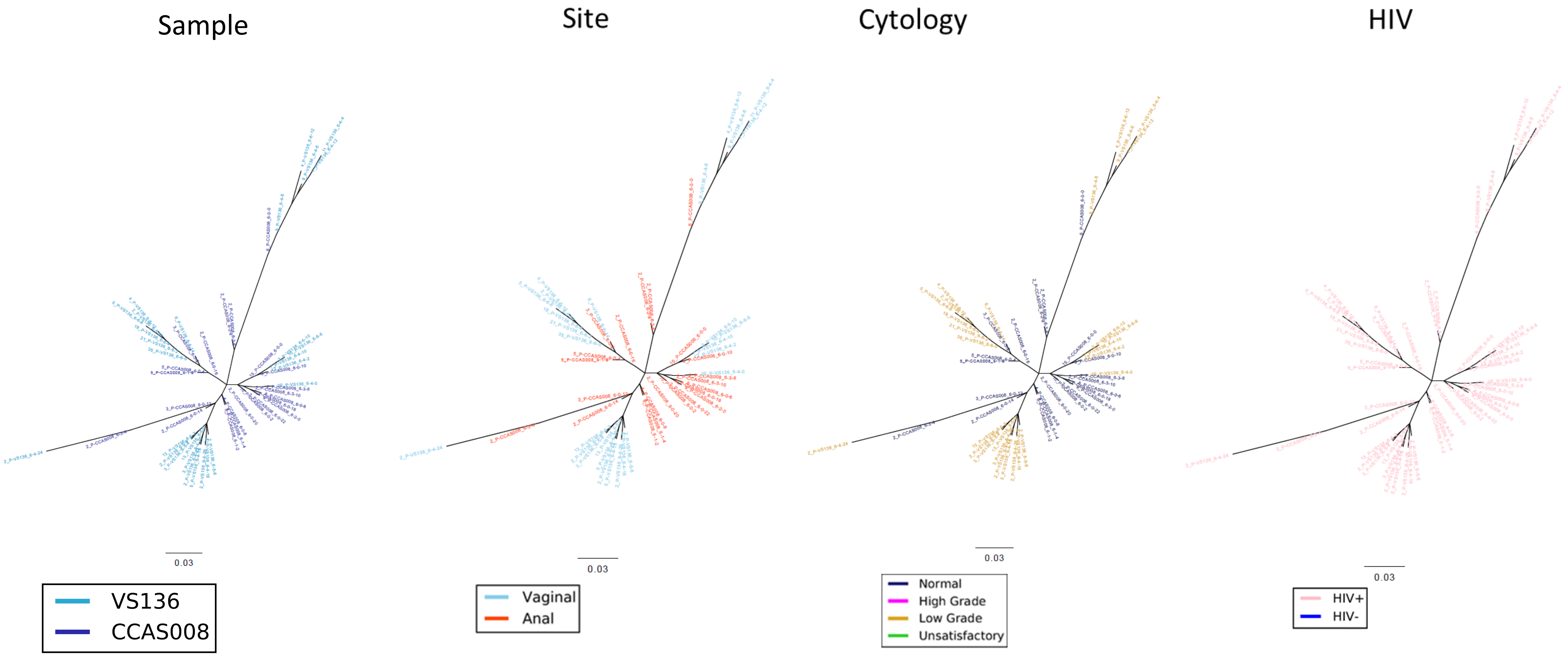
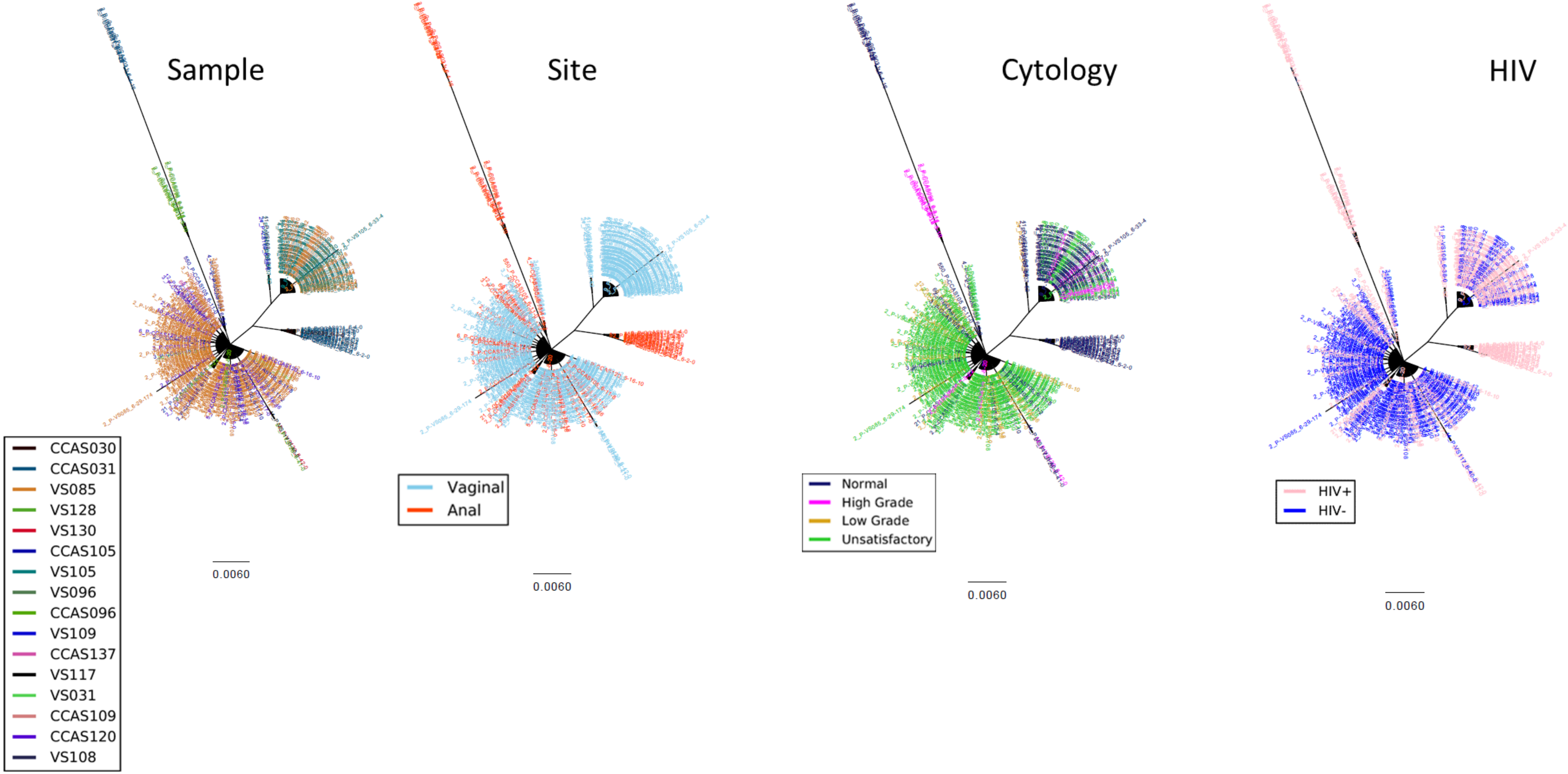


Fig S32:HPV 114



Summary of results

The total number of samples for each genotype ranged from 1-25. Genotypes with at least five samples were HPVs 35, 40, 71, 86 and 91. HPV 35 had a typical ‘fishbone’ phylogenetic tree. Although the phylogenetic distance was short, there were 3 distinct lineages and numerous intermediate variants. HPV 40 and 71 had 3 lineages. They had 195 and 183 sequence counts and numerous variants signified by the typical fishbone branching of the phylogenetic trees. HPV 91 phylogenetic tree was drawn from 2 samples with sequence count of 57. A fishbone pattern of 4 lineages and numerous variants was observed.

HPVs 42, 54, 73, 82 and 89 had unresolved evolution, with all the variants emanating from one node, as observed by the ‘dandelion’ shape of the phylogenetic tree. HPVs 39, 66, 68 and 72 had 2 distinct lineages emanating from one node, with each lineage showing no evolution. Numerous variants were observed in HPVs 11, 32, 44, 45, 53, 58, 61, 71, 81, 83, 84 and 91 phylogenetic trees, characterized by the typical ‘fishbone’ outlook of the tree.

HPVs 31, 32, 35, 40, 58, 59, 69, 71, 72, 73, 81 and 83 were predominantly of vaginal origin. HPV 84 was purely of anal origin and HPVs 11, 45 and 70 were predominantly of anal origin with a few variants of vaginal origin. Based on cervical cytology outcome HPVs 69 and 86 were predominantly from low-grade lesions. HPVs 26, 32, 33, 42 and 72 were predominantly from high-grade lesions. HPVs 35, 40, 66, 70, 71, 83 and 84 were predominantly from normal cytology.

Based on HIV status, phylogenetic trees for HPVs 31, 35, 58, 66 and 69 were predominantly from HIV negative samples. Nineteen HPV genotypes were predominantly from HIV positive samples; these included HPVs 11 and 33.

Summary of discussion

HPVs 11, 32, 44, 45, 53, 58, 61, 71, 81, 83, 84 and 91 from the 32 trees in the supplementary section had typical ‘fish-bone’ phylogenetic trees. HPVs 26, 32, 42, 66, 69, 71, 73, 83, 84 and 86 had some lineages predominantly from normal cervical cytology, High-grade and Low-grade lesions. These findings are in line with the HPV16,18 and 52 trees.