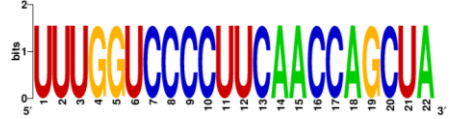
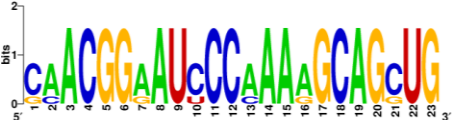
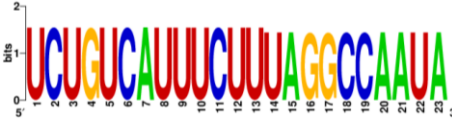
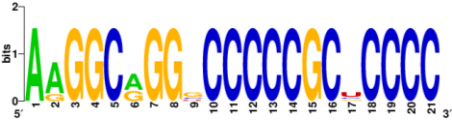


HG ¹	miRNAs IDENTIFIED IN HPV INTEGRATION SITES (Chromosomal location (Chain)) ²		
	hsa-mir-1-3p (18q11.2 (-))	hsa-mir-23a-3p (19p13.12 (-))	hsa-mir-23a-5p (19p13.12 (-))
CLM	UGGAAUGUAAAGAAGUAUGUAU	AUCACAUUGCCAGGGAUUUCC	GGGGUUCCUGGGGAUGGGAUUU
MXL	UGGAAUGUAAAGAAGUAUGUAU	AUCACAUUGCCAGGGAUUUCC	GGGGUUCCUGGGGAUGGGAUUU
PEL	UGGAAUGUAAAGAAGUAUGUAU	AUACA <u>A</u> UUGC <u>A</u> AGGGAUUUCC	GGGGUUCCUGGGGAUGGG <u>G</u> UUU
PUR	UGGAAUGUAAAGAAGUAUGUAU	AUCACAUUGCCAGGGAUUUCC	GGGGUUCCUGGGGA <u>G</u> GGGAUUU
BEB	UGGAAUGUAAAGAAGUAUGUAU	AUCACAU <u>C</u> GCCAGGGAUUUCC	GGGGUUCCUGGGGAUGGGAUUU
			
	hsa-mir-27a-3p (19p13.12 (-))	hsa-mir-27a-5p (19p13.12 (-))	hsa-mir-28 (3q28 (+))
CLM	UUCACAGUGGCUAAGUUCCGC	AGGGCUUAGCUGCUUGUGAGCA	CACUAGAUUGUGAGCUCCUGGA
MXL	UUCACAGUGGCUAAGUUCCGC	AGGGCUUAGCUGCUUGUGAGCA	CACUAGAUUGUGAGCUCCUGGA
PEL	UUCACAGUGGCUAAGU <u>U</u> CC	AGGGCUUAGCUGCUUGUGAGCA	CACUAGAUUGUGAGCUCCUGGA
PUR	UUCAC <u>C</u> GUGGCUAAG <u>C</u> UCCG	AGGGCUUAGCUGCUUGUG <u>G</u> GCA	CACUAGAUUGUGAGCUCCUGGA
BEB	UUCACAGUGGCUAAGU <u>C</u> CCCC	AGGGCUUAGCUG <u>A</u> UUGUGA <u>U</u> CA	CACUAGAUUGU <u>U</u> AGCUCCUGGA
			
	hsa-mir-31-3p (9p21.3 (-))	hsa-mir-31-5p (9p21.3 (-))	hsa-mir-103a-3p (20p13 (+))
CLM	UGCUAUGCCAACAUAUUGCCAU	AGGCAAGAUGCUGGCAUAGCU	AUUGUACAGGG <u>A</u> UAUGA
MXL	UGCUAUGCCAACAUAUUGCCAU	AGGCAAGAUGCUGGCAUAGCU	AGCAGCAUUGUACAGGGC <u>G</u> AUGA
PEL	UGCUAUGCCAACAUAUUGCCAU	AGGCAAGAUGCUGGCAU	AGCAGCAUUGUACAGGGCUAUGA
PUR	UGCUAUGCCAACAUAUUGCCAU	AGGCAAGAUGCUGGCAUAGCU	AGCAGCAUUGUACAGGGCUAUGA
BEB	UGCUAUGCCAACAUAUUGCCAU	AGGCAAGAUGCUGGCAUAGCU	AGCAGCAUUGUACAGGGCUAUGA
			

HG ¹	miRNAs IDENTIFIED IN HPV INTEGRATION SITES (Chromosomal location (Chain)) ²		
	hsa-mir-107 (10q23.31 (-))	hsa-mir-133a-3p (18q11.2 (-))	hsa-mir-133a-5p (18q11.2 (-))
CLM	AGCAGCAUUGUACAGGGCUAUCA	UUUGGUCCCCUUCAACCAGCUG	AGCUGGUAAAAUGGAACCAAAU
MXL	AGCAGCAUUGUACAGGGCUAUCA	UUUGGUCCCCUUCAACCAGCUG	AGCUGGUAAAAUGGAACCAAAU
PEL	AGCAGCAUUGUACAGGGCUAUCA	UUUGGUCCCCUUCAACCAGCUG	AGCUGGUAAAAUGGAACCAAAU
PUR	AGCAGCAUUGUACAGGGCUAUCA	UUUGGUCCCCUUCAACCAGCUG	AGCUGGUAAAAUGGAACCAAAU
BEB	AGCAGCAUUGUACAGGGCUAUCA	UUUGGUCCCCUUCAACCAGCUG	AGCUGGUAAAAUGGAACCAAAU
			
	hsa-mir-133b (6p12.2 (+))	hsa-mir-152 (17q21.32 (-))	hsa-mir-181c-3p (19p13.12 (+))
CLM	UUUGGUCCCCUUCAACCAGCUA	CGGGUCUGUGCUACACUCCGACU	AACCAUCGACCGUUGAGUGGAC
MXL	UUUGGUCCCCUUCAACCAGCUA	UUUGGUCCCCUUCAACCAGCUA	AACCAUCGACCGUUGAGUGGAC
PEL	UUUGGUCCCCUUCAACCAGCUA	AGGUUCUGUGAUACACUACGACU	AACCAUCGACCGUUGAGUGGAC
PUR	UUUGGUCCCCUUCAACCAGCUA	UUUGGUCCCCUUCAACCAGCUA	AACCAUCGACCGUUGAGUGGAC
BEB	UUUGGUCCCCUUCAACCAGCUA	AGGUUCUGUGUGGACACUCUGACU	AACCAUCGACCGUUGAGGGGAC
			
	hsa-mir-181c-5p (19p13.12 (+))	hsa-mir-191-3p (3p21.31 (-))	hsa-mir-191-5p (3p21.31 (-))
CLM	AACAUUUAACCUUGUCGGUGAGU	GCUGCGCUUGGCUUUCGUCCCC	GAACGGGAUCCCAAAAGCAGCUG
MXL	AACAUUUAACCUUGUCGGUGAGU	GCUGCGCUUGGAUUUCGUCCCC	CAACGGAAUCCCAAAAGCAGCUG
PEL	AACAUGCAACCUUGUCGGAAGAGU	GCUGCGCUUGGAUUUCGUCCCC	CCACGGAAUCCCAAAAGCAGCUG
PUR	AACAUUUAACCUUGUCGUUGAGU	GCUGCGCUUGGAUUUCGUCCCC	CAACGGAAUCCCAAAAGCAGCUG
BEB	AACCUUCAACCUUGUGGGUGAGU	GCUGCGCCUGCAUUUCGUGCCC	CAACGGAAUCCCAAAAGCAGGUG
			

HG ¹	miRNAs IDENTIFIED IN HPV INTEGRATION SITES (Chromosomal location (Chain)) ²		
	hsa-mir-194-1 (1q41 (-))	hsa-mir-215-3p (1q41 (-))	hsa-mir-215-5p (1q41 (-))
CLM	UGUAACAGCAACUCG AUGUGGA	UCUGUCAUUUCUUUAGGCCAAUA	AUGACCUAUGAAUUGACAGAC
MXL	UGUAACAGCAACUCCAUGUGGA	UCUGUCAUUUCUUUAGGCCAAUA	AUGACCUAUGAAUUGACAGAC
PEL	UGUAACAGCAACUCCAUGUGGA	UCUGUCAUUUCUU	AUGACCUAUGAAUUGACAGAC
PUR	UGUAACAGCAACUCCAUGUGGA	UCUGUCAUUUCUUUAGGCCAAUA	AUGACCUAUGAAUUGACAGAC
BEB	UGUAACAGCAACUCCAUGUGGA	UCUGUCAUUUCUUUAGGCCAAUA	AUGACCUAUGAAUUGACAGAC
			
	hsa-mir-378a-3p (5q32 (+))	hsa-mir-425-3p (3p21.31 (-))	hsa-mir-425-5p (3p21.31 (-))
CLM	CCUGGCCUGGGAGUCAAGAGGC	AUCGGGAAUGUCGUGUCAGCCC	AAUGACACGAUCACUCCCGUUGA
MXL	ACUGGACUUGGAGUCAGAAGGC	AUCGGGAAUGUNGUGUCCGCC	AAUGACACGAUCACUCCCGUUGA
PEL	ACUGGACUUGGAGUCAGAAGGA	AUCGGGAAUGUCGUGUCCGCC	AAUGACACGAUCACUCCCGUUGA
PUR	ACUGGACUUGGAGUCAGAAGGC	AUCGGGAAUGUCGUGUCCGCC	ACUGACACGUCACUCCCGUUGA
BEB	ACUGGACUUGGAGUCAGAAGGC	AUCGGGAAUUCGUGUCCGCC	AAUGACACGAUCACUCCCGUUGA
			
	hsa-mir-449a (5q11.2 (-))	hsa-mir-449b-3p (5q11.2 (-))	hsa-mir-449b-5p (5q11.2 (-))
CLM	UGGCAGGGUAUUGUUAGCUGGU	AAGCCA A A A C C A C C C U G C C A C U	AGCCAGUGUAU C A U U A G C U G G C
MXL	UGGCAGUGUAUUGUUAGCUGGU	CAGCCACCACUACCCUGCCACU	AGGCAGUGUAUUGUUAGCUGGC
PEL	UGGCAGUGUAUUGUUAGCUGGU	CAGCCACAACUACCCUGCCACU	AGGCAGUGUAUUGUUAGCUGGC
PUR	AGGCAGUGUAUUGUUAGCUGGU	CAGCCACAACUACCCUGCCACC	AGGCAGUGUAUUGUUAGCUGGC
BEB	UGGCAGUGUAUUGUUAGCUGGU	CAGCCACAACUACCCUGCCACU	AGGCAGUGUAUUGUUAGCUGGC
			

HG ¹	miRNAs IDENTIFIED IN HPV INTEGRATION SITES (Chromosomal location (Chain)) ²		
	hsa-mir-491-3p (9p21.3 (+))	hsa-mir-491-5p (9p21.3 (+))	hsa-mir-548b (6q22.31 (-))
CLM	CUUAUGCAAGAUUCCCUUCUAC	AGUGGGGAACCCUUCCAUGAGG	AAAAGUAAUUGUGGUUUUGGCC
MXL	CUUAUGCAAGAUUCCCUUCUAC	AGUGGGGAACCCUUCCAUGAGG	AAAAGUAAUUGUGGUAGUCGCC
PEL	CUUAUGCAAGAUUCCCUUCUAC	CGUGGGGAACACUUCCAUGAGG	AAAAGUAAUUGUGGUUUUGGCC
PUR	CUUAUGCAAGAUUCCCUUCUAC	AGUGGGGAACCCUUCCAUGAGG	AAAAGUAAUUGUGGUUUUGGCC
BEB	CUUAUGCAAGAUUCCCUUCUAC	AGUGGGGAACCCUUCCAUGAGG	AAAAGUAAUUGUGGUUUUGGCC
			
	hsa-mir-548c-3p (12q14.2 (+))	hsa-mir-548c-5p (12q14.2 (+))	hsa-mir-548d-5p (8q24.13 (+))
CLM	AAAAAAUCUCAAUUACUUUUGC	AAAAGUAAUUGCGGUUUUUGCC	AAAAGUAAUUGUGGUUUUUGCC
MXL	CAAAAAACUCAUUUUUUUUGCC	AAAAGUAAUUGCGGUUUUUGCC	AAAAGUAAUUGUGGUUUUUGCC
PEL	CAAAAAUCUCAAUUACUUUUGC	AAAAGUAAUUGCGGUUUUUGCC	AAAAGUAAUUGUGGUUUUUGCC
PUR	CAAAAAUCUCAAUUACUUUUGC	AAAAGUAAUUGCGGUUUUUGCC	AAAAGUAAUUGUGGUUUUUGCC
BEB	CAAAAACUCUAAUUUCUUUGCC	AAAAAAAUUAAAGGUUUUUGCC	AAAAGUAAUUGUGGUUUUUGCC
			
	hsa-mir-572 (4p15.33 (+))	hsa-mir-574 (4p14 (+))	hsa-mir-576 (4q25 (+))
CLM	GUCCGCUCGGCGGGGGGCCA	UGAGGGGGUGUGUGUGAGUGUGG	AAGAUGUGGAAAAAUUGGAAUC
MXL	GUCCGCUCGGCGGGGGGCCA	UGAGUGUGUGUGUGUGAGUGUGU	AAGAUGUGGAAAAAUUGGAAUC
PEL	GUCCGCUCGGCGGUGGCCCC	UGCGUGUGUGUGUUUGAGGGUGU	AAGAUGUGGAAAAAUUGGAAUC
PUR	GUCCGCUCGGCGGUGGCCCA	UGAGUGUGUGUGUGUGAGUGUGU	AAGAUGUGGAAAAAUUGGAAUC
BEB	GUCCGCCCGGCGGUGGCACA	GGAGGGUGUGUGUGUGAGUGUGU	AAGAUGAGGAAAAAUUGGAAUC
			

HG ¹	miRNAs IDENTIFIED IN HPV INTEGRATION SITES (Chromosomal location (Chain)) ²		
	hsa-mir-581 (5q11.2 (-))	hsa-mir-584 (5q32 (-))	hsa-mir-940 (16p13.3 (+))
CLM	UCUUGUGUUCUCUAGAUCAGU	UUAUGGUUUGCCUGGGG CUGAG	A G G G C G G G C C C C C G C C C C C
MXL	UCUUGUGUUCUCUAGAUCAGU	UUAUGGUUUGCCUGGGACUGAG	A A G G C A G G G C C C C C G C U C C C C
PEL	U U U U U U U C U C U A G A U C A G U	UUAUGGUUUGCCUGGGACUGAG	A A G G C G G G U C C C C C G C U C C C C
PUR	UCUUGUGUUCUCUAGAUCAGU	UUAUGGUUUGCCUGGGACUGAG	A A G G C A G G G C C C C C G C G C C C C
BEB	UCUUGUGUUCUCUAGAUCAGU	UUAUGGUUUGCCUGGGACUGAG	A A G G C A G G G C C C C C G C U C C C C
			
	hsa-mir-944 (3q28 (+))	hsa-mir-1287-5p (10q24.2 (-))	hsa-mir-5095 (1p32.3 (-))
CLM	AAAUAUUGUACAUCGGAUGAG	UGCUGGAUCAGUGGUUCG C GUC	UUACAGGCGUGAACCACCGCG
MXL	AAAUAUUGUACAUCGGAUGAG	UGCUGGAUCAGUGGUUCGAGUC	UUACAGGCGUGAACCACCGCG
PEL	AAAUAUUGUACAUCGGAUGAG	UGCUGGAUCAGUGG GUCGAGAC	UUACAGGCGUGAACCACCGCG
PUR	AAAUAUUGUACAUCGGAUGAG	UGCUGG CUCACUGGUUCGAGUC	UUACAGGCG GGAACCACCCCG
BEB	AAAUAUUGUACAUCGGAUGAG	UGCUGGAUCAGUGGUUCGAGUC	UUACAGGCG GGAACCACCCCG
			

Key:

¹ HG: Human genome; CLM: variant of Medellin, Colombia; MXL: Los Angeles with Mexican ancestry; PEL: Lima, Peru; PUR: of Puerto Rico; BEB: Bengali, Bangladesh.

² The size of each letter indicates the enrichment of each nucleotide in Latin American variants of the human genome, displayed through WebLogo.