	Chronic SIV-infected (n=12)												Uninfected Controls (n=8)									
miRNA ID	**FE24**	**FT11**	**HN15**	**HI68**	**HG45**	**HB31**	**GA19**	**HD08-90D**	**HH07-180D**	**HF54-180D**	**HR42-180D**	**HV48**	**HD08-Pre**	**HH07-Pre**	**HF54-Pre**	**HR42-Pre**	**HT73**	**IH95**	**EJ34**	**IT05**	**Fold Change**	***P Value***
hsa-miR-194	15.4	15.8	16.9	17.7	17.5	16.8	17.4	15.8	14.3	16.3	15.8	40	15.9	15.0	13.8	13.6	15.4	14.4	13.3	13.8	-8.3	2.98E-03
hsa-miR-23b	21.4	21.0	21.3	21.9	22.0	22.2	40	21.2	20.6	21.0	20.5	19.6	20.3	19.5	19.8	19.0	19.4	19.6	18.6	18.0	-6.1	2.16E-03
hsa-miR-107	24.0	24.9	25.3	25.3	25.4	26.2	25.3	24.1	23.1	24.8	23.1	40	24.4	23.6	22.7	22.3	22.9	22.2	22.7	22.0	-4.8	9.56E-03
hsa-miR-28-3p	18.0	19.1	20.9	20.3	20.3	20.5	20.8	19.6	18.6	18.9	19.5	19.2	19.3	18.4	14.1	16.8	18.7	16.8	14.7	15.9	-3.8	2.98E-03
hsa-miR-10b	21.7	18.8	21.7	20.7	20.7	21.7	22.2	21.7	19.8	19.9	18.5	21.8	19.8	17.8	18.1	16.9	18.6	18.7	19.2	17.0	-3.2	5.49E-03
hsa-miR-342-3p	19.8	20.6	20.9	20.5	22.3	24.6	21.9	22.0	19.7	19.8	20.0	20.6	20.5	19.9	18.6	18.3	18.9	18.2	17.6	18.1	-2.7	7.30E-03
hsa-miR-181c	25.4	26.7	26.5	27.5	29.7	28.5	27.5	27.5	26.7	26.3	27.1	27.6	27.0	25.2	25.0	24.9	25.6	23.6	24.4	25.3	-2.4	7.30E-03
hsa-miR-28	19.6	19.6	21.2	21.4	21.0	20.8	21.0	19.6	18.5	19.8	18.9	22.2	19.6	18.4	17.8	17.8	19.2	18.0	17.5	17.2	-2.4	4.76E-04
hsa-miR-196b	20.8	19.8	21.8	22.0	21.4	21.6	21.3	19.6	17.7	20.8	19.9	24.2	20.7	19.5	18.1	18.5	19.8	17.8	17.7	18.8	-2.3	9.56E-03
hsa-miR-150	16.3	18.4	18.7	18.0	18.3	20.3	19.9	18.8	16.7	16.7	17.2	19.1	17.7	16.6	15.8	15.4	17.0	15.0	15.4	16.5	-2.3	9.56E-03
hsa-miR-328	25.6	26.2	25.6	24.8	25.7	26.8	27.8	25.3	24.8	24.0	25.3	23.6	24.6	24.3	23.7	23.8	23.4	22.6	22.8	22.4	-2.2	0.01586
hsa-miR-10a	18.2	17.4	18.8	18.7	19.2	18.8	19.8	16.8	16.0	18.1	16.9	18.8	17.3	16.5	15.4	15.7	16.8	16.1	15.4	15.8	-2.2	4.76E-04
hsa-miR-181a	20.2	21.6	22.0	22.0	21.3	22.7	22.7	21.1	19.7	20.5	20.2	21.8	20.8	19.8	18.8	19.4	20.5	18.5	18.8	18.7	-2.0	2.98E-03
hsa-miR-532-3p	21.4	22.1	23.0	23.2	22.6	23.6	24.1	22.0	21.6	22.6	21.9	23.1	22.0	21.2	20.5	19.9	21.5	21.0	19.9	19.8	-2.0	3.02E-04
hsa-miR-148a	18.7	19.5	20.8	21.5	20.8	20.8	21.7	20.4	19.6	20.5	19.8	22.1	19.4	18.7	18.9	17.8	18.9	18.7	18.6	18.5	-2.0	5.49E-03
hsa-miR-339-5p	20.8	21.0	21.6	21.8	22.3	22.5	22.1	20.6	20.6	21.0	20.8	21.0	21.0	19.7	19.9	18.7	19.8	19.2	19.3	18.5	-2.0	2.98E-03
hsa-miR-378	25.7	24.6	26.7	26.1	26.4	26.3	27.8	24.8	23.9	26.6	25.0	24.7	23.9	24.4	23.7	23.8	24.5	23.9	23.5	23.4	-1.9	9.56E-03
hsa-miR-98	21.9	21.1	22.8	22.6	22.7	23.1	22.7	21.0	20.2	21.8	21.7	21.4	21.1	20.0	20.0	20.2	20.7	19.4	20.4	19.3	-1.9	2.98E-03
hsa-miR-365	25.8	25.1	24.4	25.2	25.0	25.4	24.6	23.9	23.5	23.7	23.1	24.1	23.1	22.6	22.7	23.2	23.9	22.9	21.3	22.6	-1.8	1.24E-02
hsa-miR-26a	15.9	16.8	18.5	17.8	17.7	18.3	17.8	16.7	15.8	16.9	16.5	18.4	17.4	15.8	15.3	15.1	16.3	15.1	14.4	15.3	-1.8	5.49E-03
hsa-miR-15b	17.3	18.8	19.0	19.5	18.4	19.5	20.5	18.2	17.3	18.7	17.5	20.6	18.2	17.4	16.8	16.8	18.0	16.8	16.6	16.3	-1.8	7.30E-03
hsa-let-7f	20.1	20.7	21.6	22.3	21.3	21.6	21.2	20.7	20.0	20.8	19.8	22.8	20.7	19.8	19.3	18.9	20.4	18.8	18.6	18.7	-1.7	7.30E-03
hsa-miR-30b	15.9	16.4	17.4	17.8	16.9	17.4	17.5	16.2	15.3	16.7	15.7	17.7	16.3	15.0	14.8	14.9	16.2	14.8	14.6	14.5	-1.7	3.02E-04
hsa-miR-26b	18.3	18.8	19.8	19.9	19.4	19.9	19.8	18.9	17.8	19.0	18.4	20.9	19.4	18.1	17.5	16.9	18.3	17.0	17.0	17.1	-1.6	0.01586
hsa-miR-30c	16.1	16.8	17.4	17.8	17.0	17.8	17.7	16.3	15.2	16.6	15.8	17.8	16.7	15.5	14.8	15.2	16.4	15.3	14.6	14.7	-1.5	4.10E-03
hsa-miR-324-5p	22.2	23.1	23.3	22.9	23.4	23.4	23.4	22.7	21.5	22.8	21.8	23.4	22.7	21.3	21.2	21.7	22.3	21.3	20.8	20.7	-1.4	5.49E-03
hsa-miR-185	22.7	24.0	22.8	23.9	23.0	24.1	23.1	22.9	21.8	23.0	22.8	23.8	24.5	22.4	22.0	23.4	24.5	23.2	22.0	23.8	1.9	2.98E-03
hsa-miR-127	23.6	24.9	22.8	23.8	24.3	24.8	22.8	23.8	23.3	22.7	23.6	24.8	24.8	23.8	24.2	24.0	24.2	23.4	22.1	24.7	2.0	0.01586
hsa-miR-337-5p	27.4	27.0	27.4	27.4	27.1	27.4	27.0	24.7	27.2	26.4	26.1	25.2	29.8	28.0	27.9	29.6	16.1	27.9	27.0	29.2	2.1	4.10E-03
hsa-miR-204	23.7	24.9	24.8	24.4	22.8	25.6	23.8	23.3	23.7	23.6	23.3	23.8	25.2	22.8	24.8	24.0	25.4	24.3	22.8	24.5	2.2	5.49E-03
hsa-miR-425*	24.7	25.6	24.9	23.8	24.4	24.3	24.9	24.7	23.4	26.5	24.6	22.9	25.5	24.2	24.7	25.6	25.1	25.7	23.6	25.7	2.4	7.30E-03
hsa-miR-486	21.8	27.6	22.6	24.0	21.7	22.8	24.6	23.3	22.2	21.8	22.0	23.4	23.1	23.6	23.1	24.3	24.0	24.9	22.7	23.4	2.6	4.10E-03
hsa-miR-212	24.3	24.6	23.3	23.4	24.0	22.8	23.8	23.3	23.1	24.3	24.5	23.0	23.8	25.1	22.2	24.8	24.1	24.1	25.5	24.8	2.7	1.24E-02
hsa-miR-143	18.6	21.0	19.2	19.6	18.5	19.6	16.8	18.9	18.9	17.3	19.5	17.8	19.4	17.0	19.1	21.3	21.3	18.9	19.0	20.2	3.0	0.01586
hsa-miR-19b	14.5	16.7	14.0	14.7	13.8	14.9	14.6	13.9	12.8	14.1	13.5	15.8	14.6	13.2	13.1	17.7	18.2	15.9	13.4	15.3	3.0	1.24E-02
hsa-miR-200a*	21.8	21.8	22.2	21.9	22.8	22.3	23.6	22.2	20.9	22.8	21.9	20.6	22.8	21.2	21.2	23.8	23.5	24.6	22.3	23.2	3.1	2.98E-03
hsa-miR-886-5p	24.8	23.8	24.7	22.7	24.5	23.0	22.7	22.4	22.3	26.0	24.9	26.1	25.5	25.1	25.7	23.6	24.7	23.7	26.7	23.7	3.2	0.01586
hsa-miR-455	24.8	24.9	25.9	26.9	25.5	27.1	24.5	25.8	28.2	24.4	27.3	26.8	27.5	25.8	27.9	26.7	27.9	25.1	26.6	27.7	3.3	1.24E-02
hsa-miR-130a	21.7	22.9	22.7	22.3	21.8	23.5	20.8	21.8	22.6	21.7	22.6	21.6	23.1	21.4	23.2	24.3	24.6	23.0	22.0	23.5	3.6	4.76E-04
hsa-miR-24	15.7	18.7	15.7	15.1	15.3	16.0	15.7	15.4	14.8	14.7	14.9	15.8	15.8	14.5	14.0	19.8	19.8	18.4	14.5	16.9	3.8	0.01586
hsa-miR-106a	14.7	17.8	15.3	15.2	14.8	14.8	15.5	14.5	13.7	15.6	14.1	16.7	15.6	14.3	13.9	19.9	19.6	17.9	14.5	16.5	4.5	1.52E-03
hsa-miR-1255B	27.5	26.7	26.3	24.1	25.4	27.2	25.6	25.9	24.5	40	25.5	28.0	26.7	27.1	27.1	27.0	27.8	40	27.3	26.2	4.9	7.30E-03
hsa-miR-1274A	18.4	16.8	16.4	15.9	17.9	16.7	15.1	15.3	15.6	21.6	16.3	17.2	18.2	16.3	16.7	21.4	19.4	20.9	16.2	18.1	5.0	2.98E-03
hsa-miR-31	18.0	27.0	24.0	25.5	24.6	23.8	23.1	25.3	24.0	23.4	22.2	25.8	28.2	24.8	25.8	25.0	24.6	25.4	24.0	25.6	5.2	2.98E-03
hsa-miR-452	26.6	26.6	24.8	26.7	24.6	26.8	25.0	25.8	26.8	24.8	26.8	27.0	29.2	25.5	29.1	28.6	28.3	26.4	26.1	28.1	5.6	7.14E-04
hsa-miR-224	26.1	28.0	26.3	28.6	26.5	28.4	26.0	26.1	27.5	25.7	28.2	25.5	28.9	25.6	27.9	28.7	40	26.6	26.6	27.1	7.3	0.01586

MiRNA species originating from the opposite arm of the precursor are denoted with an asterisk (*). Pre- Preinfection

Downregulated miRNAs, Upregulated miRNAs

Supplemental Table 1. Raw C_T, fold change and P values for all differentially expressed miRNAs in Colonic Epithelium of Chronically SIV-infected rhesus macaques.

Gene Symbol	Gene Name	Fold Change	P value	Predicted Targeting miRNA (Upregulated)
	Epithelial barrier function			
NT5E	5'-nucleotidase, ecto (CD73)	-8.3	0.0014	miR-185, -212, -204, -224
ABCB1	ATP-binding cassette, sub-family B, member 1	-8.2	0.0219	miR-224
OCLN	Occludin	-2.6	0.0021	miR-212, -455, -486, -204, -224, -24
PPARG	Peroxisome proliferator-activated receptor gamma	-2.3	0.0293	miR-130a, -24
PPARGC1A	Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	-4.1	0.0144	miR-130a , -204, -19b, -452
PARD3	Par-3 family cell polarity regulator	-2.3	0.0092	miR-212, -130a, -143, -185
CFTR	Cystic fibrosis transmembrane conductance regulator	-3.6	0.0001	miR-212
ADORA3	Adenosine A3 receptor	-1.8	0.0029	miR-204, -185, -143
EDNRA	Endothelin receptor type A	-6.4	0.0011	miR-212, -24, -224, -455
EDNRB	Endothelin receptor type B	-3.1	0.0043	miR-455, -19b, -212, -24, -486
TFF2	Trefoil factor 2	-3.0	0.0162	
HNF4G	Hepatocyte nuclear factor 4, gamma	-1.8	0.0191	miR-106a, -204, -224
HBP1	High Mobility Group box transcription factor 1	-3.3	0.0032	miR-130a, -106a, -19b
ARNT2	Aryl hydrocarbon receptor nuclear translocator 2	-5.2	0.0035	miR-24, -455, -185, -224
FN1	Fibronectin 1	-5.8	0.0410	miR-486, -130a
ITGA8	Integrin, alpha 8	-2.2	0.0267	miR-455, -24, -224
TGFBR3	Transforming growth factor, beta receptor III	-2.2	0.0115	miR-106a, -455, -19b, -24
	Oxidative injury/inflammation			
OXR1	Oxidation resistance 1	-2.4	0.0027	miR-106a, -19b, -224
MEF2C	Myocyte enhancer factor 2C	-3.1	0.0234	miR-212, -455, -19b, -204, -106a, -452
	Intestinal stem cell growth/maintenance			
PROM1	Prominin 1	-6.9	0.0083	miR-486, -19b
RICTOR	RPTOR independent companion of MTOR, complex 2	-3.0	0.0261	miR-212, -19b, -204, -452
SOX6	SRY (sex determining region Y)-box 6	-2.9	0.012	miR-212, -455, -19b, -204, -452, -143, -24
	DNA damage repair			
RAD17	RAD17 homolog (S. pombe)	-2.8	0.0042	miR-130a
RAD50	RAD50 homolog (S. cerevisiae)	-2.2	0.0277	miR-212, -106a, -185, -452, -24, -143
	Wnt Signaling			
APC	Adenomatous polyposis coli	-2.1	0.0333	miR-24, -212
TNIK	TRAF2 and NCK interacting kinase	-3.4	0.0003	miR-31, -106a, -130a, -24, -452, -143, -204, -486
DKK3	Dickkopf 3	-2.0	0.0481	-212, -130a, -19b, -224, -185
	Ion/water transport			
CA1	Carbonic anhydrase 1	-37.7	0.0029	
AQP8	Aquaporin 8	-19.4	0.0363	
BEST2	Bestrophin 2	-6.6	0.0250	
	Cell Survival			
FASLG	Fas ligand (TNF superfamily, member 6)	-4.2	0.0219	miR-130a, -106a, -455, -24
AKT3	v-akt murine thymoma viral oncogene homolog 3	-4.3	0.0006	miR-212, -106a, -224, -455
	Miscellaneous Genes			
TNFAIP3	Tumor necrosis factor, alpha-induced protein 3	-2.9	0.011	miR-106a, -204

Supplemental Table 2. List of downregulated genes and their targeting miRNA/s in colonic epithelium of chronically SIV-infected rhesus macaques

Gene Symbol	Gene Name	Fold Change	P value	Predicted Targeting miRNA/s (Downregulated miRNAs)
	Interferon response genes			
MX1	Myxovirus resistance 1, interferon-inducible protein p78	9.7	0.0011	miR-26a/26b, -342-3p
MX2	Myxovirus (influenza virus) resistance 2	1.7	0.0249	miR-15b, miR-107
IFI6	Interferon, alpha-inducible protein 6	8.8	0.015	
IFI27	ISG12(c) protein-like	5.4	0.0100	
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	3.4	0.011	miR-28, -339-5p, -26a/26b , -107
LOC720763	Interferon-induced transmembrane protein 3-like	3.1	0.0018	
IRF9	Interferon regulatory factor 9	2.9	0.0001	
	Anti-microbial response			
ROAD-1	Oral alpha defensin 1	8.5	0.0164	
MNP2	Alpha-defensin 2	8.9	0.0091	
DEFA4	Defensin, alpha 4, corticostatin	10.5	0.0107	miR-342-3p
LOC574309	Alpha-defensin 2 precursor	9.0	0.0230	
DEFB122	Beta defensin 122	2.2	0.0018	
MUC2	Mucin 2, oligomeric mucus/gel-forming	2.2	0.0061	miR-342-3p, -150, -15b
	Proinflammatory cytokine and chemokine signaling			
NLRP1	NLR family, pyrin domain containing 1	2.3	0.0340	miR-15b, -107, -181a/181c, -532-3p, -342-3p
NLRP7	NLR family, pyrin domain containing 7	2.6	0.0154	miR-532-3p, -150, -339-5p
IL18BP	interleukin 18 binding protein	1.7	0.0498	miR-150, -148a, -532-3p, -342-3p
TNF	Tumor necrosis factor	2.6	0.0044	miR-150, -532-3p
IL23R	Interleukin 23 receptor	2.1	0.0002	miR-150, -23b, -28
CCL24	Chemokine (C-C motif) ligand 24	1.7	0.0431	miR-342-3p
CX3CR1	C-X3-C Motif Chemokine Receptor 1	1.9	0.0029	miR-15b, -28
SOCS1	Suppressor of cytokine signaling 1	2.5	0.0009	let-7f, -98-5p, -30b/30c,
PIAS3	Protein inhibitor of activated STAT3	2.0	0.0078	miR-150, -532-3p, -181a/181c
FKBP4	FK506 binding protein 4, 59kDa	3.9	0.0040	miR-181a/181c, -150, -532-3p, -342-3p, miR-98, -324-5p, -23b
AHR	Aryl hydrocarbon receptor	1.9	0.0077	miR-196b, miR-23b
TIMP3	TIMP metallopeptidase inhibitor 3	1.9	0.0003	miR-181a/181c, -30b/30c, -10a/10b, -342-3p, -196b, -194
S100B	S100 calcium binding protein B	2.5	0.0441	miR-324-5p, -148a
	Cellular apoptosis			
BAK1	BCL2-antagonist/killer 1	1.6	0.0152	miR-150, -107, -23b, -28, -532-3p, -342-3p
BCL2L11	BCL2-like 11 (apoptosis facilitator)	1.8	0.0121	miR-181a/181c, -30b/30c, -148a, -107, -339-5p, -324-5p, -10a/10b, -15b , -23b
	Intestinal stem cell growth/maintenance			
BCL9	B-cell CLL/lymphoma 9	2.5	0.0016	miR-181a/181c, -30b/30c, -532-3p, -324-5p
WISP1	WNT1 inducible signaling pathway protein 1	3.0	0.02	miR-26a/26b, -23b, -181a/181c, -28, -532-3p, -339-5p
SMAD3	SMAD family member 3	4.5	0.0148	miR-181a/181c, -150, -23b, -28, -342-3p
SNAI1	Snail homolog 1 (Drosophila)	5.4	0.0223	miR-30b/30c, -339-5p
	DNA damage response			
OGG1	8-oxoguanine DNA glycosylase	1.9	0.0270	miR-150, -532-3p, -98, let-7f, -15b
FANCG	Fanconi anemia, complementation group G	2.3	0.0000	miR-23b
RAD23B	RAD23 homolog B (S. cerevisiae)	1.7	0.0140	miR-181a/181c, -30b/30c, -150, -532-3p ,-342-3p, -196b, -23b
GADD45G	Growth arrest and DNA-damage-inducible, gamma	3.9	0.0112	miR-26a/26b, -107, -15b, -28, -181a/181c
	Cellular/Oxidative stress protection			
CLU	Clusterin	5.1	0.0295	miR-532-3p, -194
HMOX1	Heme oxygenase (decycling) 1	3.6	0.0035	miR-26a/26b
DDIT3	DNA-damage-inducible transcript 3	2.9	0.0033	
SRXN1	Sulforedoxin 1	2.3	0.0091	miR-532-3p, -148a, -28-3p, -107, -181a/181c
	Microbial Translocation			
DUOX1	Dual oxidase 1	4.3	0.0151	
LCN2	Lipocalin 2	8.7	0.0100	miR-150, -28-5p
	Miscellaneous genes			
AIPL1	Aryl hydrocarbon receptor interacting protein-like 1	2.2	0.0100	miR-150, let-7f, -98

Supplemental Table 3. List of Upregulated genes and their targeting miRNA/s in colonic epithelium of chronically SIV-infected rhesus macaques.