

**A rhesus macaque model of congenital cytomegalovirus infection reveals a spectrum of
vertical transmission outcomes**

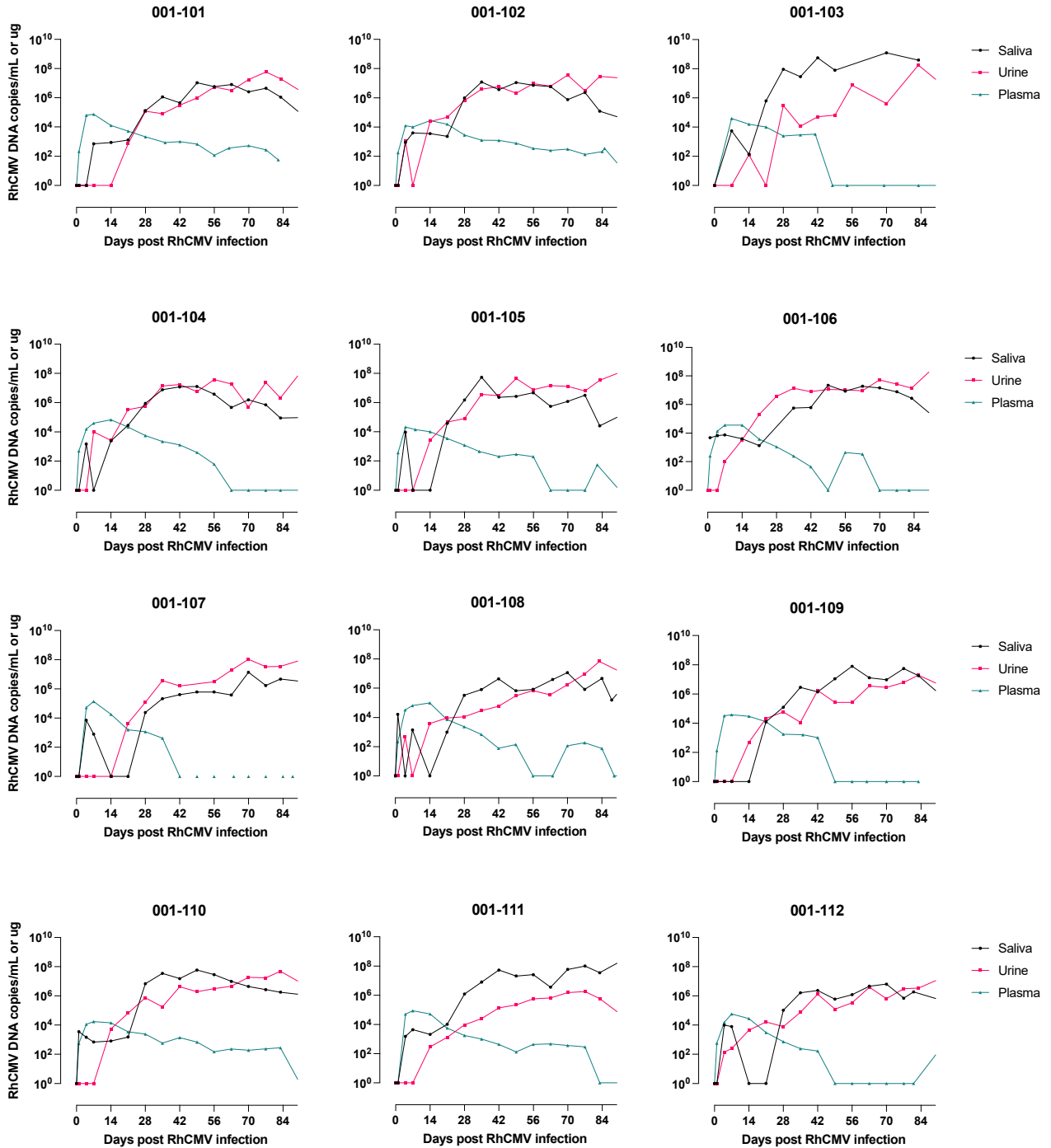
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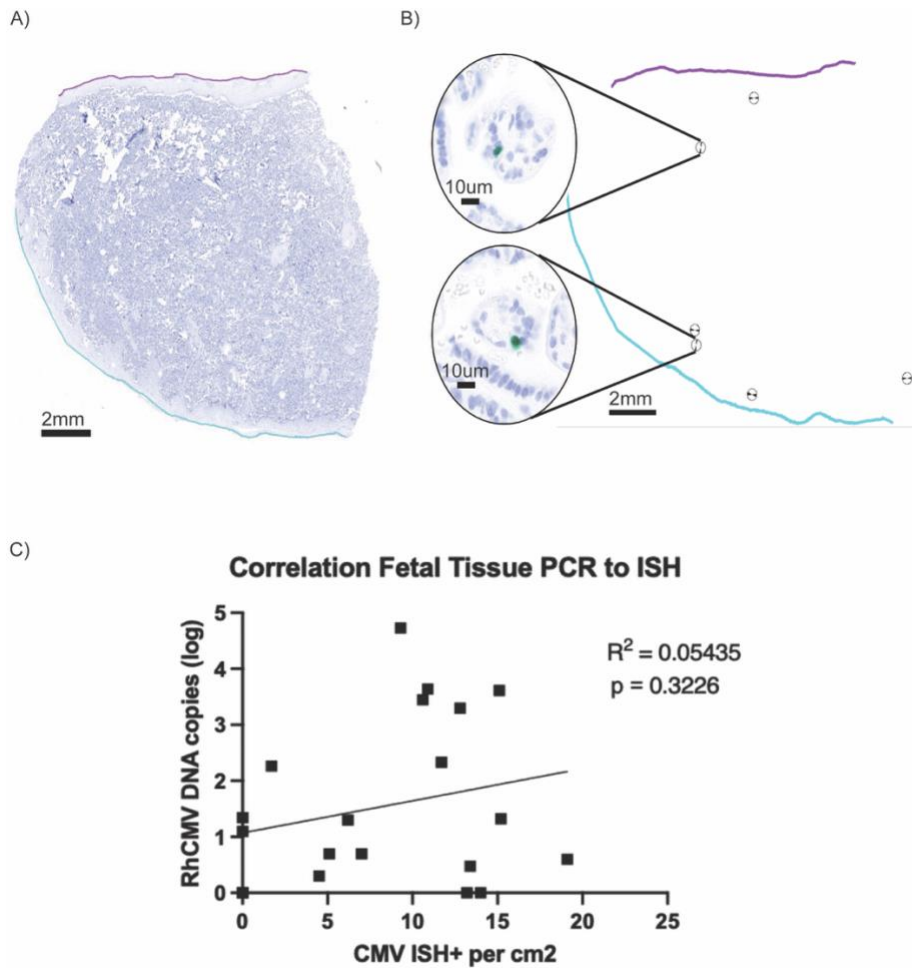
Supplementary Figures 1-8

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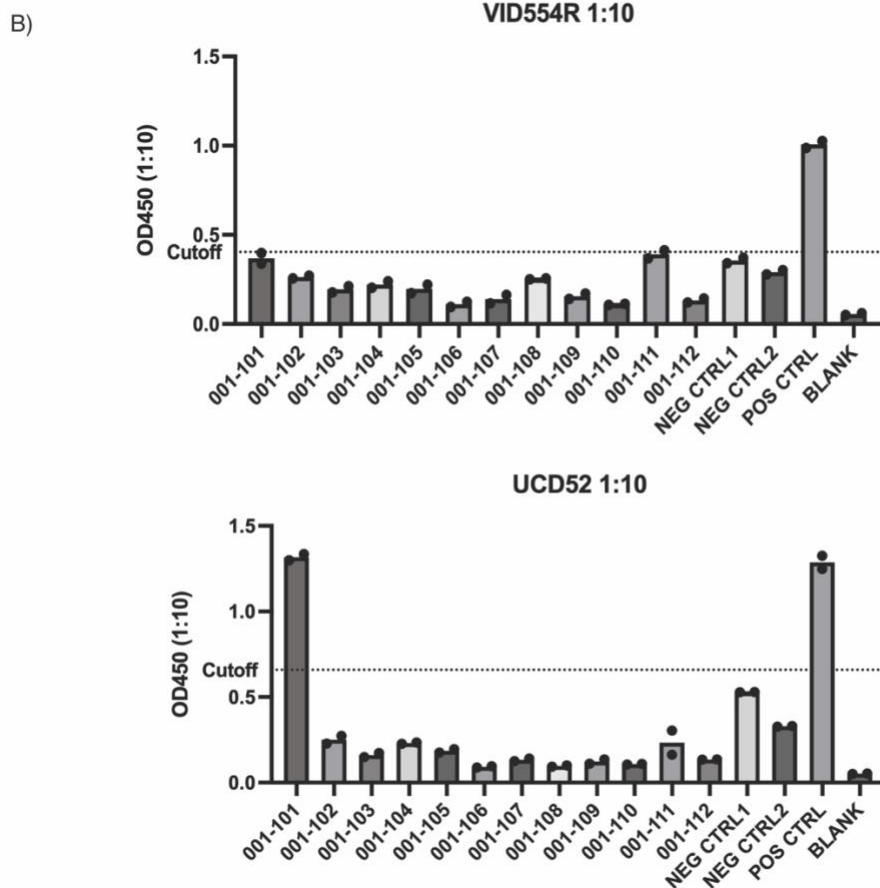
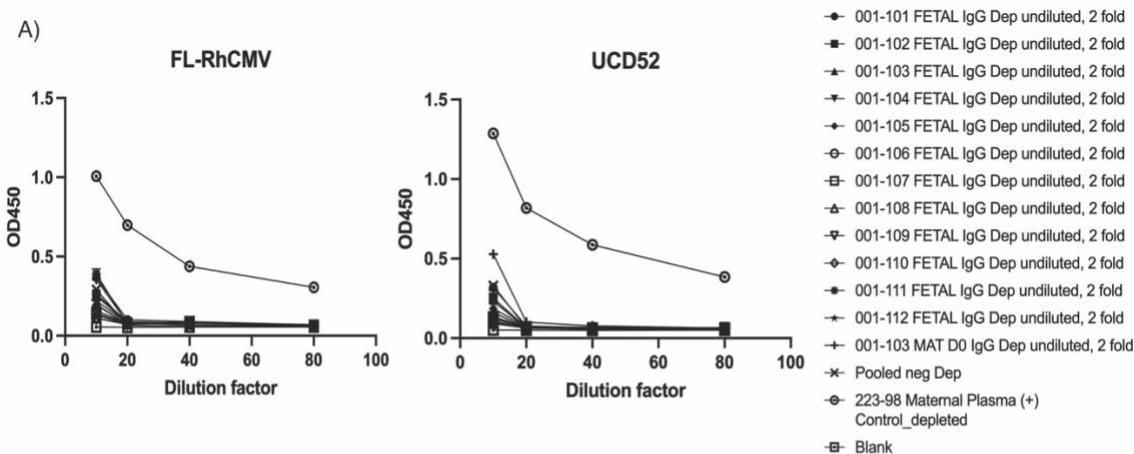
Supplementary Figure 1. Viral Loads in Maternal Fluids of Individual Dams.

Plasma, saliva, and urine viral loads of individual dams. Viral loads expressed as mean copies of input RhCMV DNA per mL of plasma, and per ug of input DNA in saliva or urine.



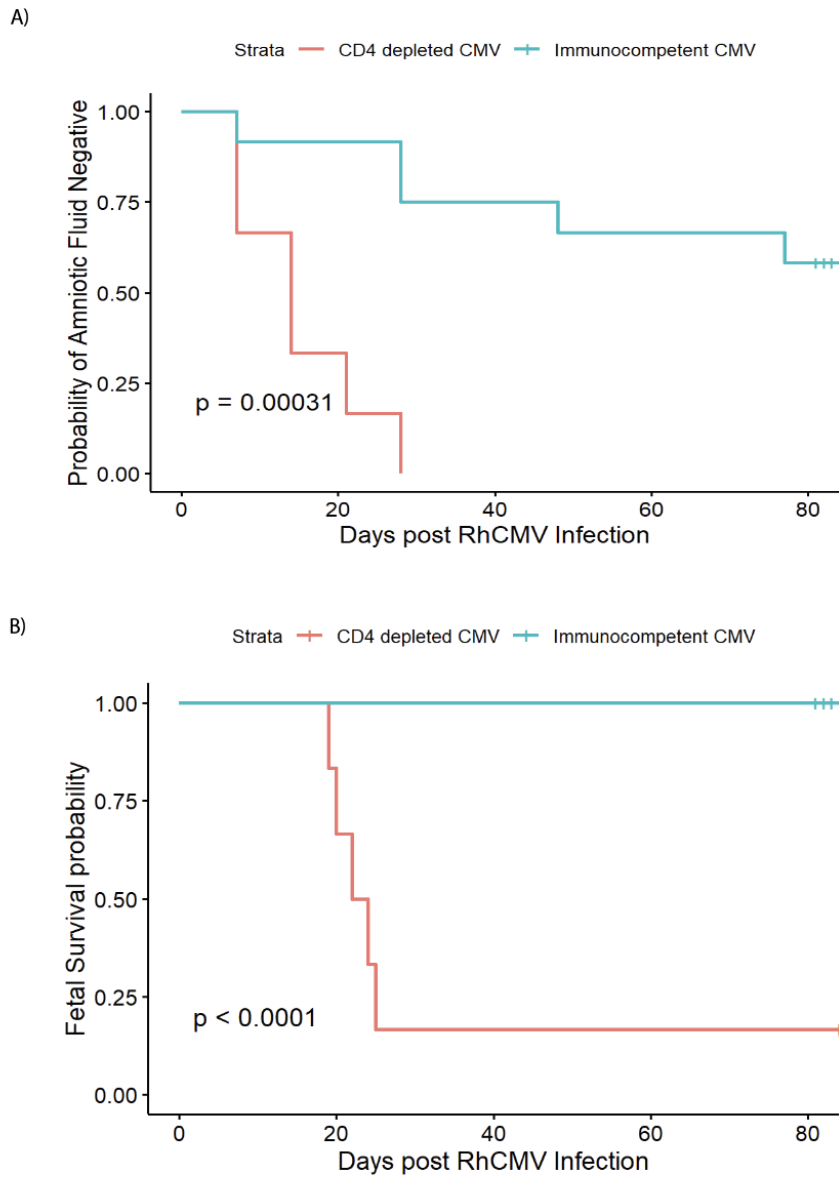
Supplementary Figure 2. M-F Interface and Fetal Tissue ISH.

A) In situ hybridization for detection of RhCMV-positive cells in full thickness placental sections (sub-gross view) obtained from dam 001-110. Annotations were used to delineate the maternal (blue) from fetal (purple) side of the placenta. B) Spatial plots for visualization of the distribution of RhCMV positive cells within the placenta. Insets: RhCMV+ cells (green) within villi near the fetal (top) and maternal (bottom) interfaces. No correlation between PCR DNA copies and ISH+ cells in fetal tissues (C) of dam 001-101.



Supplementary Figure 3. Fetal IgM

A) Graph demonstrating FL-RhCMV and UCD52 IgG depletion from fetal plasma of all 12 dams. B) IgM ELISA results.



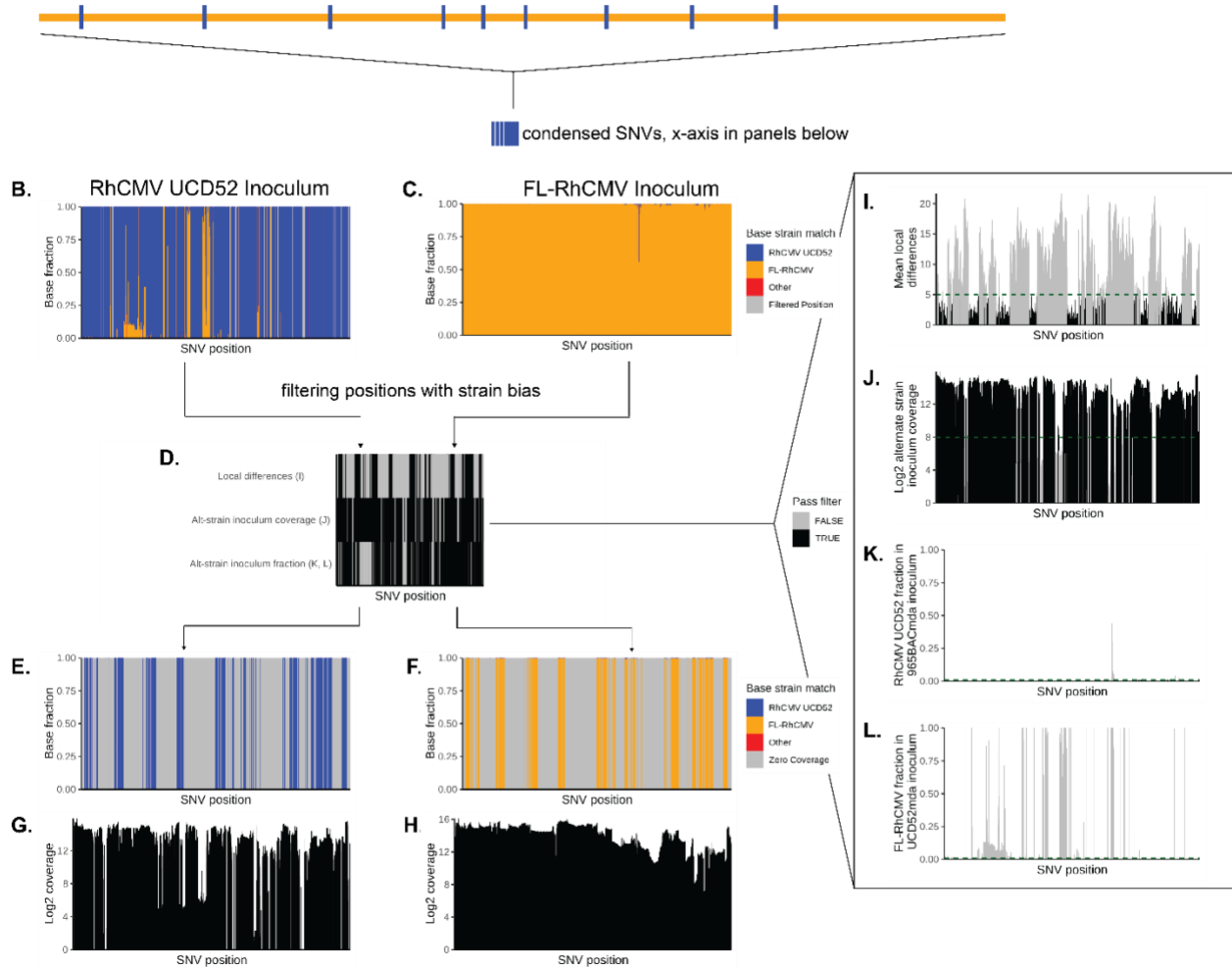
Supplementary Figure 4. Probability of amniotic fluid transmission and fetal survival.

A) Kaplan-Meier curve showing probability of amniotic fluid transmission for the study cohort (blue) (n=12) and the CD4⁺ T cell-depleted rhesus macaque cohort (n=6) (gray)

described in Bialas et al (n=4) and Nelson et al (n=2). B) Kaplan-Meier curve showing probability of fetal survival for the study cohort (blue) (n=12) and the CD4+ T cell-depleted rhesus macaque cohort (n=6) (gray) described in Bialas et al and Nelson et al.

Reference = FL-RhCMV

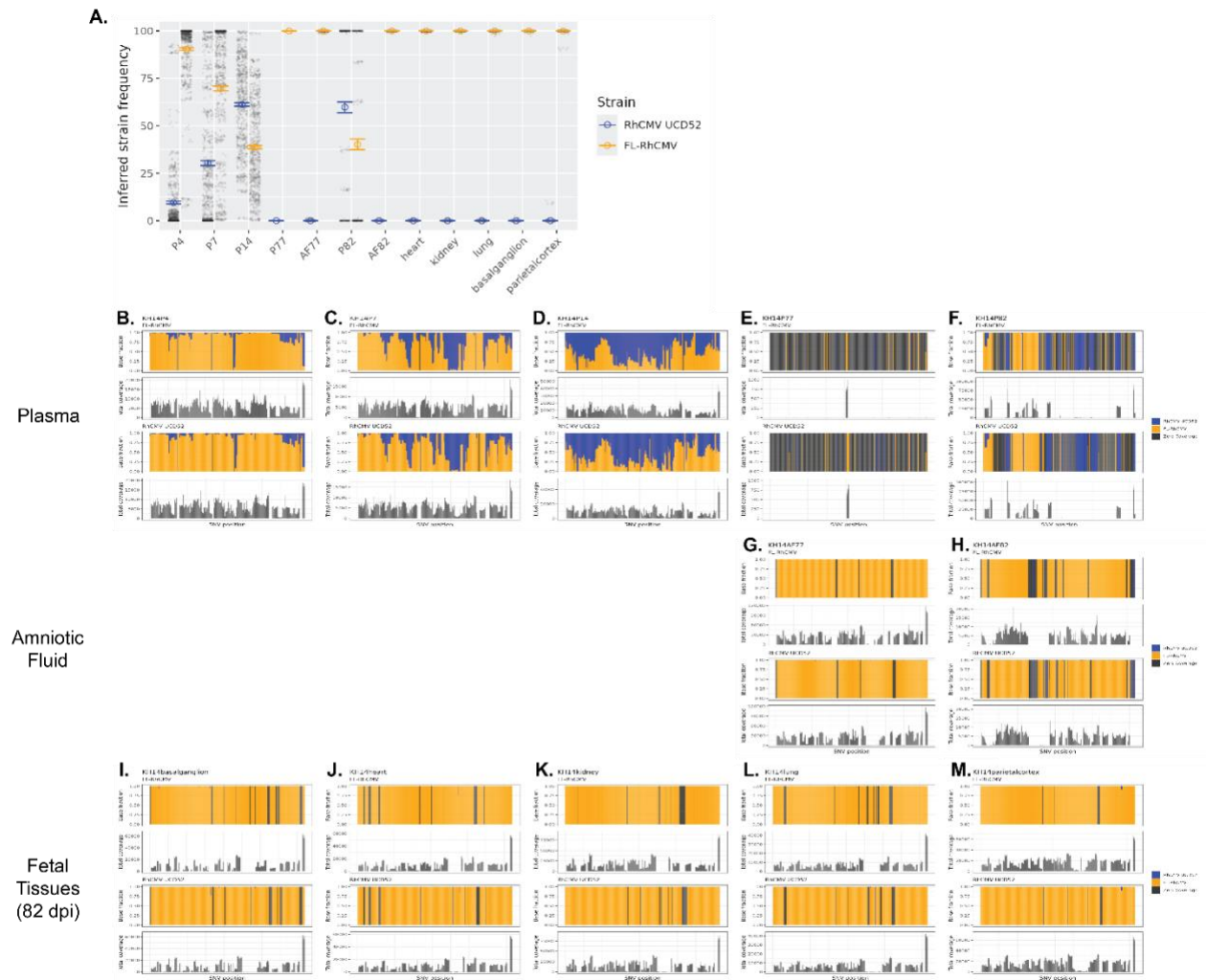
A. single nucleotide variants where **RhCMV UCD52** differs from **FL-RhCMV**



Supplementary Figure 5. Filtering schema for removing strain biased segregating SNVs using FL-RhCMV as the reference.

A) SNVs positions determined by nucdiff to differ between FL-RhCMV and RhCMV UCD52 are used as the x-axis for the remaining figures. In B and C, the estimated base fraction at every SNV for each viral inoculum (when mapped to FL-RhCMV) is shown. Each of the SNV

positions were put through three filters (I-L, summarized in D) to identify high-confidence segregating SNVs (E, F). Total read coverage for each inoculum is shown in G and H. Right panels show the positions that pass (black) or fail (gray) each of the three filters with threshold shown by the green dashed line: removal of SNVs in hypervariable regions with more than 5 local differences (I), removal of SNVs with fewer than 250 reads when mapped to alternate reference (J), and removal of SNVs with $>1\%$ alternate strain frequency in FL-RhCMV (K) or RhCMV UCD52 (L) inoculum. This process was repeated with RhCMV UCD52 as the reference to check for reference strain bias.

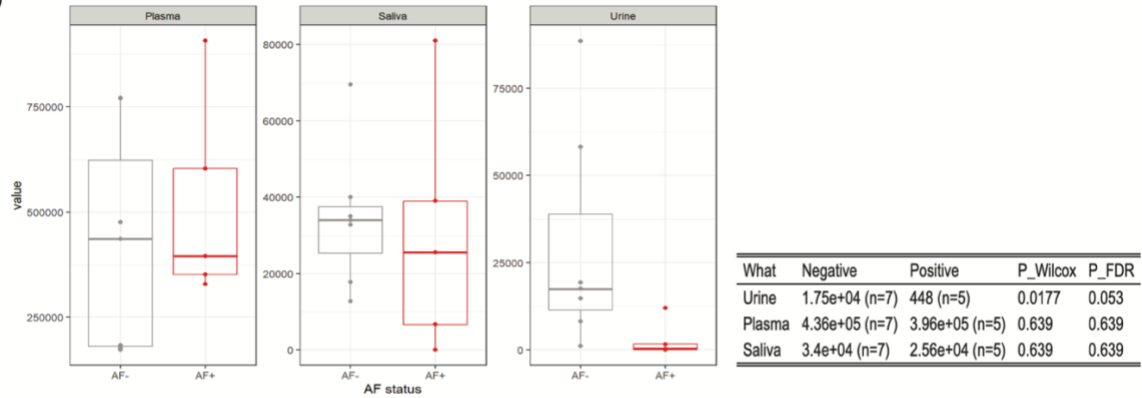


Supplementary Figure 6. Inferred RhCMV strain frequency in 001-101 with RhCMV UCD52 as mapping reference and sample level strain frequencies.

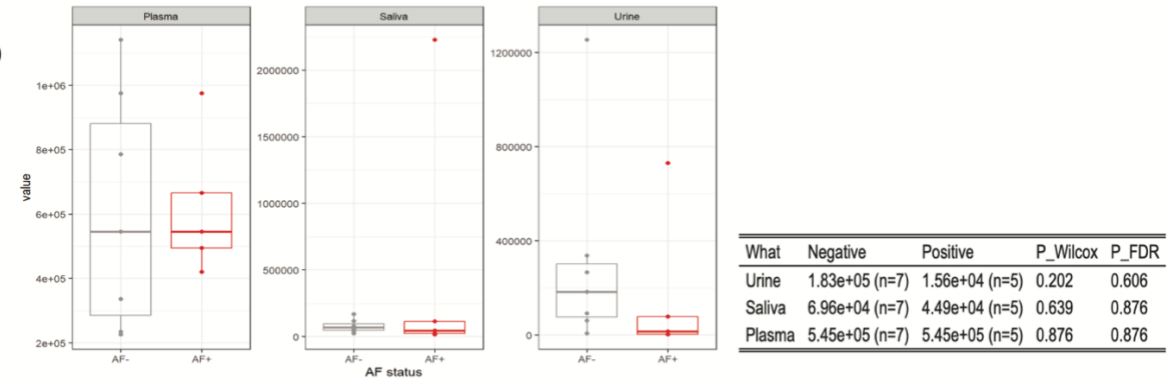
A) For each sample (x axis, “P” = plasma, “AF” = amniotic fluid, # = days post infection, M = maternal, F = fetal the inferred strain frequency (blue = RhCMV UCD52, orange = FL-RhCMV) was determined by taking the mean of the percent of reads with the nucleotide corresponding to each strain at the positions where the two inoculating strains differ. Mean indicated by the open circle with error bars corresponding to the standard error. Black dots represent frequencies at a

single SNV. B-M) For each, the top panel is the strain frequency calculated with FL-RhCMV as the reference (862 SNVs); the third panel is the strain frequency calculated with UCD52 as the reference (850 SNVs); the second and fourth panels are the read coverage at each position. For each sample, the coloring of each vertical line corresponds to the proportion of reads with the nucleotide that corresponds to either FL-RhCMV (orange) or RhCMV UCD52 (blue). Positions that were excluded from samples due to insufficient coverage (<100 reads) are in grey.

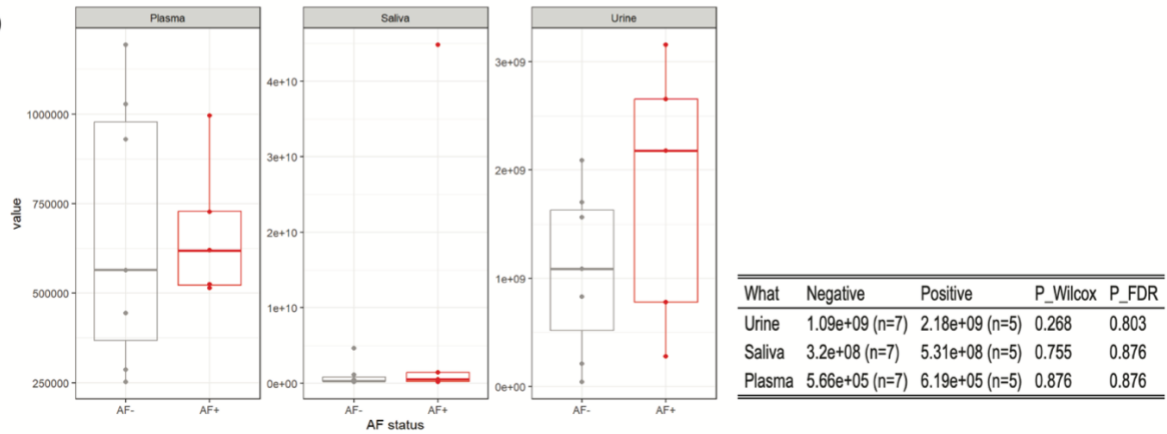
A)



B)

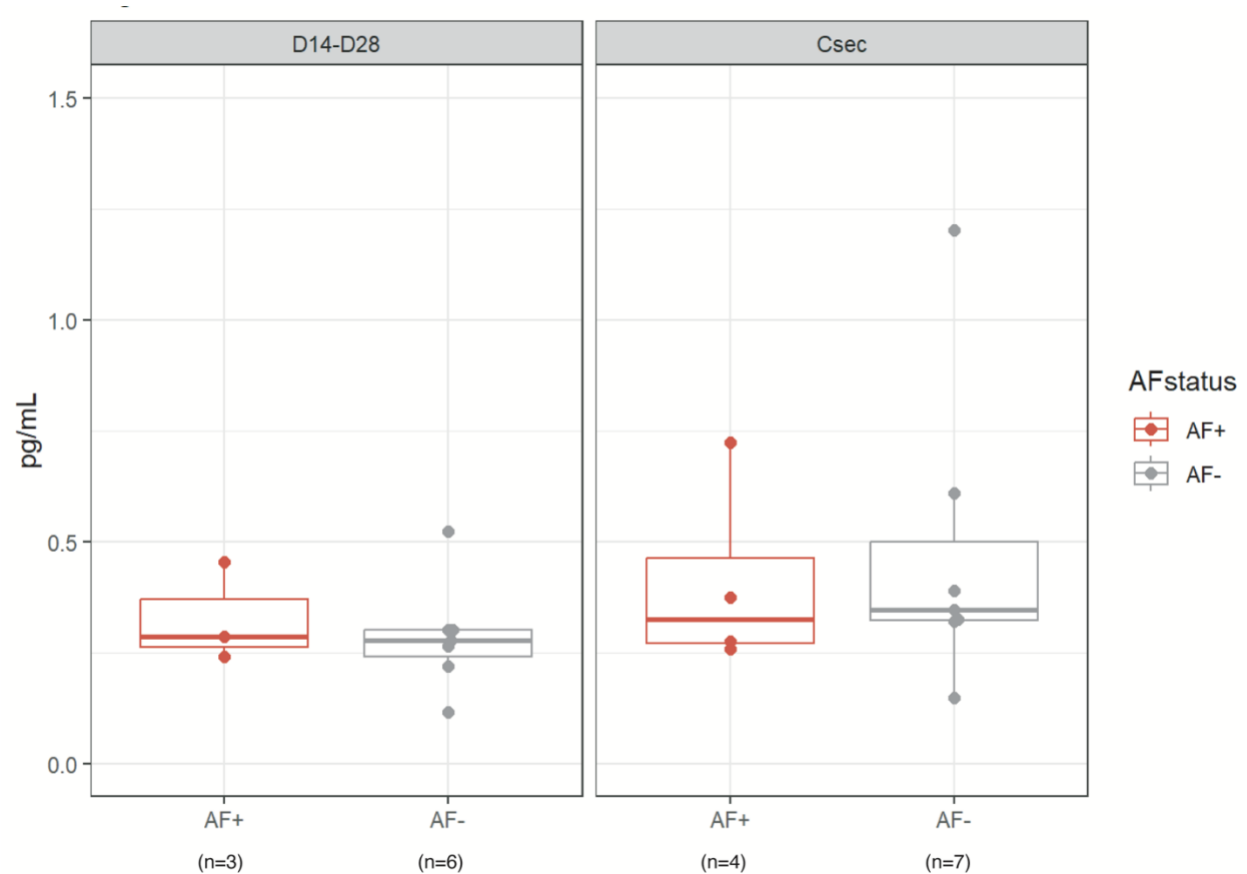


C)



Supplementary Figure 7. AUC of Viral Loads in Maternal Fluids

A) AUC of viral loads in plasma, saliva, and urine of AF+ and AF- dams during the first two weeks PI. B) AUC of viral loads in plasma, saliva, and urine of AF+ and AF- dams during the first three weeks PI. C) AUC of viral loads in plasma, saliva, and urine of AF+ and AF- dams during the whole study time course. Error bars denote minimum and maximum measurements.



Supplementary Figure 8. Chemerin Concentrations in Amniotic Fluid

Chemerin concentrations in the amniotic fluid taking during the 2nd trimester (between days 14 PI and 28 PI; GD 70-98) and at C-section during the 3rd trimester (GD 136-154). Error bars denote minimum and maximum measurements.

Animal ID	Dam Age (Yrs)	Number of Prior Pregnancies	GD at RhCMV Infection	GD at C-section	Weeks PI at C-section	Sex of Fetus
001-101	9.6	3	67	149	11	F
001-102	8.7	1	69	154	12	F
001-103	6.6	1	56	139	11	F
001-104	7.4	3	67	138	11	F
001-105	8.5	3	67	149	11	M
001-106	5.7	1	60	142	11	F
001-107	6.5	2	65	153	12	F
001-108	6.4	1	57	146	12	M
001-109	5.6	1	60	143	11	F
001-110	3.9	1	57	140	11	F
001-111	3.9	0	59	142	11	F
001-112	2.8	0	55	136	11	M

Supplementary Table 1. Characteristics of RhCMV-Seronegative Female Macaques

Enrolled in Study

*Gestation day (GD)

*Post-infection (PI)

Animal ID	Placentitis	Chorioamnionitis	Placental Infarct
001-102	X		
001-104		X	
001-106	X		
001-110	X		
001-111	X		X
001-112			X

Supplementary Table 2. Placental lesions found in dams at the time of C-section.

A) **Median (IQR)**

Groups	Strata	n	Abdominal circumference (cm)	Crown-rump length (cm)	Fetal weight (g)	Head circumference (cm)	Right foot (cm)	Right hand (cm)	Thoracic circumference (cm)	Total Placenta weight (g)	Trans-temporal (cm)
Amniotic Fluid	PCR Negative	7	-0.7 (-0.7, 0.2)	-0.8 (-1.7, 0.0)	-0.2 (-0.7, 0.2)	-0.5 (-0.9, 0.1)	-0.6 (-0.9, 0.1)	-1.3 (-1.9, 0.0)	-0.6 (-1.7, 0.3)	0.8 (0.4, 1.3)	-0.5 (-0.9, 0.7)
	PCR Positive	5	-0.3 (-0.4, 0.0)	-1.7 (-3.2, -0.6)	-0.8 (-1.3, -0.1)	0.1 (-0.2, 0.2)	-0.4 (-0.4, -0.3)	-0.9 (-1.3, -0.6)	-0.1 (-0.3, 0.1)	0.6 (0.1, 0.9)	-0.8 (-1.5, -0.6)
Fetal Tissue	PCR Negative	9	-0.5 (-0.7, 0.6)	-0.8 (-2.8, 0.7)	-0.1 (-0.7, 0.4)	-0.3 (-0.6, 0.1)	-0.3 (-1.0, 0.4)	-1.3 (-1.7, 0.0)	-0.1 (-1.1, 0.3)	0.8 (0.1, 1.2)	-0.6 (-1.5, 0.4)
	PCR Positive	3	-0.2 (-0.4, -0.2)	-1.4 (-1.6, -1.0)	-1.0 (-1.1, -0.7)	0.2 (-0.3, 0.4)	-0.4 (-0.5, -0.4)	-0.9 (-1.5, -0.7)	-0.3 (-0.5, 0.1)	0.6 (0.3, 0.9)	-0.8 (-0.9, -0.3)
Maternal-Fetal Interface	PCR Lo	6	-0.4 (-0.7, 0.5)	-0.6 (-1.2, 0.3)	-0.3 (-0.4, 0.2)	0.1 (-0.7, 0.3)	-0.4 (-0.5, 0.2)	-0.3 (-1.1, 0.0)	0.1 (-0.5, 0.4)	1.0 (0.3, 1.2)	-0.7 (-0.8, 0.2)
	PCR Hi	6	-0.4 (-0.7, -0.2)	-2.3 (-3.1, -1.0)	-1.2 (-1.3, -0.1)	-0.3 (-0.6, -0.2)	-0.7 (-1.1, -0.3)	-1.5 (-2.1, -1.0)	-0.3 (-0.6, -0.3)	0.7 (-0.1, 0.8)	-1.0 (-1.5, 0.0)

B)

Groupings	Abdominal circumference (cm)	Crown-rump length (cm)	Fetal weight (g)	Head circumference (cm)	Right foot (cm)	Right hand (cm)	Thoracic circumference (cm)	Total Placenta weight (g)	Transtemporal (cm)
AF PCR	0.807	0.370	0.570	0.167	0.684	0.935	0.744	0.416	0.328

Groupings	Abdominal circumference (cm)	Crown-rump length (cm)	Fetal weight (g)	Head circumference (cm)	Right foot (cm)	Right hand (cm)	Thoracic circumference (cm)	Total Placenta weight (g)	Transtemporal (cm)
Fetus PCR	0.517	>0.999	0.229	0.309	0.643	0.711	0.781	0.643	0.853
Placenta PCR	0.297	0.092	0.337	0.337	0.378	0.297	0.377	0.336	0.422

Supplementary Table 3. Fetal Morphometric Comparisons in RhCMV-Infected Dams.

Sample	Mapping reference	SNPs used for analysis	UCD52 mean strain frequency (SE)	FL mean strain frequency (SE)	Other mean strain frequency (SE)
965BACmda	FL-RhCMV	862	0.09321 (0.005581)	99.88 (0.005627)	0.02423 (0.001002)
965BACmda	UCD52	850	0.1115 (0.005846)	99.86 (0.005992)	0.02685 (0.001453)
Dam 001-101 AF77	FL-RhCMV	775	0.02026 (0.002829)	99.96 (0.0038)	0.02013 (0.002621)
Dam 001-101 AF77	UCD52	764	0.04041 (0.005267)	99.94 (0.00624)	0.0221 (0.003469)
Dam 001-101 AF82	FL-RhCMV	575	0.0214 (0.002817)	99.96 (0.004068)	0.02204 (0.002369)
Dam 001-101 AF82	UCD52	565	0.03156 (0.003407)	99.94 (0.004217)	0.0235 (0.002651)
Dam 001-101 fetal basal ganglion	FL-RhCMV	602	0.01563 (0.002518)	99.97 (0.00263)	0.0113 (0.0008016)
Dam 001-101 fetal basal ganglion	UCD52	591	0.03065 (0.005965)	99.96 (0.00599)	0.01153 (0.00083)
Dam 001-101 fetal heart	FL-RhCMV	669	0.03007 (0.003826)	99.95 (0.004236)	0.01645 (0.001626)
Dam 001-101 fetal heart	UCD52	660	0.04444 (0.004658)	99.94 (0.005171)	0.01807 (0.002142)
Dam 001-101 fetal kidney	FL-RhCMV	664	0.01373 (0.001487)	99.97 (0.001823)	0.01431 (0.001148)
Dam 001-101 fetal kidney	UCD52	656	0.02765 (0.003205)	99.96 (0.003746)	0.01683 (0.001978)
Dam 001-101 fetal lung	FL-RhCMV	661	0.01924 (0.002428)	99.96 (0.006714)	0.02522 (0.00633)
Dam 001-101 fetal lung	UCD52	647	0.03987 (0.005094)	99.93 (0.008116)	0.02705 (0.006492)
Dam 001-101 P14	FL-RhCMV	793	60.17 (0.857)	39.81 (0.8571)	0.02391 (0.001184)
Dam 001-101 P14	UCD52	780	61.23 (0.8503)	38.74 (0.8504)	0.02409 (0.001479)
Dam 001-101 P4	FL-RhCMV	794	9.272 (0.637)	90.71 (0.637)	0.01991 (0.001724)
Dam 001-101 P4	UCD52	782	9.612 (0.6555)	90.37 (0.6555)	0.01946 (0.001292)
Dam 001-101 P7	FL-RhCMV	760	29.33 (1.201)	70.65 (1.201)	0.01967 (0.001358)
Dam 001-101 P7	UCD52	751	30.34 (1.221)	69.64 (1.221)	0.01839 (0.0009919)
Dam 001-101 P77	FL-RhCMV	14	0.03547 (0.03547)	99.94 (0.04298)	0.02716 (0.02716)
Dam 001-101 P77	UCD52	14	0.07392 (0.03901)	99.87 (0.05566)	0.05794 (0.03945)
Dam 001-101 P82	FL-RhCMV	273	59.08 (2.857)	40.9 (2.856)	0.01419 (0.001392)
Dam 001-101 P82	UCD52	275	59.8 (2.84)	40.19 (2.84)	0.01386 (0.001381)
Dam 001-101 fetal parietal cortex	FL-RhCMV	779	0.08491 (0.02818)	99.9 (0.02823)	0.01442 (0.001013)
Dam 001-101 fetal parietal cortex	UCD52	767	0.1034 (0.03004)	99.88 (0.03009)	0.01638 (0.001385)
UCD52mda	FL-RhCMV	862	99.93 (0.003923)	0.04987 (0.003876)	0.01896 (0.0007992)
UCD52mda	UCD52	850	99.94 (0.003651)	0.04014 (0.003608)	0.01782 (0.0006893)

Supplementary Table 4. Single Nucleotide Polymorphisms (SNPs) in Sequenced Samples.

Analyte	AUC (D1-14 PI) P value	AUC (D1-14 PI) Adjusted P value	Day 1	Day 4	Day 7	Day 14
IL-15	<1e-4	<1e-4	0.00781	0.00391	0.00781	0.00391
PD-L1	<1e-4	<1e-4	0.0156	0.00586	0.0312	0.00391
IP-10	<1e-4	<1e-4	0.0391	0.00293	0.0156	0.00195
VEGF	<1e-4	<1e-4	0.359	0.00781	0.0234	0.203
MIP-3 alpha	0.0042	0.007412	0.492	0.0483	0.297	0.0371
PDGF-AA	<1e-4	<1e-4	0.496	0.00293	0.0781	0.00195
IL-6	<1e-4	<1e-4	0.875	0.00781	0.0234	0.875
IFN-alpha	0.0007	0.0015	1	0.0156	1	0.938
IFN-gamma	<1e-4	<1e-4	1	0.0156	0.375	0.5
I-TAC	<1e-4	<1e-4	0.75	0.0156	0.0938	0.75
IL-10	<1e-4	<1e-4	0.75	0.00781	0.25	0.0938
GM-CSF	<1e-4	<1e-4	0.875	0.00391	0.188	0.406
Granzyme B	0.0232	0.03867	0.945	0.117	0.875	0.0156
CXCL13 / BLC	0.0003	0.00075	1	1	1	0.25
CXCL2 / GRO beta	0.0004	0.0009231	1	0.0625	0.656	0.656
Eotaxin	0.0001	0.0002727	1	0.168	0.938	1
IFN-beta	0.0339	0.05085	1	0.25	1	1

Analyte	AUC (D1-14 PI) P value	AUC (D1-14 PI) Adjusted P value	Day 1	Day 4	Day 7	Day 14
CD40 Ligand	0.003	0.005625	0.695	0.109	0.388	0.388
BDNF	0.0337	0.05085	0.835	0.835	0.438	0.835
TNF-alpha	0.0016	0.0032	0.875	0.0938	0.375	0.906
G-CSF	0.866	0.8959				
IL-12 p70	0.1838	0.2297				
IL-13	1	1				
IL-17 / IL-17A	0.4226	0.4876				
IL-2	0.0832	0.1135				
IL-21	0.4752	0.528				
IL-4	0.3782	0.4538				
IL-7	0.0605	0.08643				
IL-8	0.6858	0.7348				
PDGF-BB	0.1414	0.1844				

Supplementary Table 5. Change from baseline for individual analytes.

Bold represents significant unadjusted P values.

Analyte	AF- Dams	AF+ Dams	P value	FDR
IL-10	39.5 (n=7)	6.48 (n=5)	0.0455	0.502
BDNF	2.88e+03 (n=7)	1.61e+03 (n=5)	0.048	0.502
IP-10	198 (n=6)	123 (n=5)	0.0519	0.502
IL-8	2.04e+03 (n=7)	1.65e+03 (n=5)	0.106	0.604
IL-7	6.26 (n=6)	1.41 (n=5)	0.119	0.604
TNF-alpha	0.13 (n=7)	2.66 (n=5)	0.125	0.604
IL-17 / IL-17A	0.395 (n=7)	0.395 (n=5)	0.311	1.00
G-CSF	3.52 (n=7)	3.52 (n=4)	0.321	1.00
Eotaxin	327 (n=7)	190 (n=5)	0.323	1.00
IL-6	0.875 (n=7)	6.39 (n=5)	0.413	1.00
IFN-gamma	2.15 (n=7)	2.15 (n=5)	0.417	1.00
VEGF	30.8 (n=7)	25.9 (n=5)	0.432	1.00
IL-2	6.41 (n=7)	6.36 (n=5)	0.61	1.00
IFN-beta	3.25 (n=7)	3.25 (n=5)	0.691	1.00
CXCL2 / GRO beta	1.26e+03 (n=6)	917 (n=4)	0.762	1.00
CD40 Ligand	1.89e+03 (n=6)	1.38e+03 (n=5)	0.792	1.00
PDGF-BB	1.54e+03 (n=7)	902 (n=3)	0.833	1.00
MIP-3 alpha	35.7 (n=7)	35.7 (n=5)	0.876	1.00
PDGF-AA	55.3 (n=7)	55.7 (n=5)	0.876	1.00
IFN-alpha	0.01 (n=5)	0.525 (n=4)	0.905	1.00
IL-15	3.76 (n=7)	3.93 (n=5)	0.912	1.00
PD-L1	419 (n=6)	477 (n=5)	0.931	1.00
GM-CSF	8.22 (n=7)	8.22 (n=5)	0.965	1.00
I-TAC	1.18 (n=7)	1.18 (n=5)	1.00	1.00
Granzyme B	12.8 (n=7)	11.1 (n=5)	1.00	1.00

IL-4	0 (n=7)	0 (n=5)	1.00	1.00
IL-12 p70	0.7 (n=7)	0.7 (n=5)	1.00	1.00
IL-21	0.37 (n=7)	0.37 (n=5)	1.00	1.00
CXCL13 / BLC	11.9 (n=7)	11.9 (n=5)	1.00	1.00

Supplementary Table 6. Luminex assay on maternal plasma at C-section.

Analyte	AF- Dams	AF+ Dams	P value	FDR
IFN-alpha	5.62 (n=7)	13.3 (n=5)	0.0265	0.342
IL-21	88.4 (n=7)	132 (n=5)	0.0467	0.342
BDNF	49.9 (n=7)	37.8 (n=5)	0.0732	0.342
IFN-beta	3.64e+03 (n=7)	5.23e+03 (n=5)	0.0732	0.342
IFN-gamma	357 (n=7)	696 (n=5)	0.0732	0.342
VEGF	660 (n=7)	919 (n=5)	0.0732	0.342
MIP-3 alpha	821 (n=7)	936 (n=5)	0.106	0.371
CXCL13 / BLC	127 (n=7)	218 (n=5)	0.106	0.371
IL-17	3.49 (n=7)	2.53 (n=5)	0.138	0.417
CD40 Ligand	4.71e+04 (n=7)	5.77e+04 (n=5)	0.149	0.417
IL-7	3.75 (n=7)	2.65 (n=5)	0.21	0.534
TNF-alpha	103 (n=7)	148 (n=4)	0.23	0.535
Granzyme B	28.2 (n=7)	53.4 (n=5)	0.268	0.535
IP-10	675 (n=7)	1.42e+03 (n=5)	0.268	0.535
GM-CSF	39.6 (n=7)	31.3 (n=5)	0.322	0.601
PD-L1	1.58e+03 (n=7)	1.14e+03 (n=5)	0.343	0.601
IL-4	0.34 (n=7)	0.29 (n=5)	0.365	0.601
IL-13	71.9 (n=7)	64.7 (n=5)	0.492	0.707
IL-12	16.4 (n=7)	16.4 (n=5)	0.497	0.707
IL-2	2 (n=7)	4.09 (n=5)	0.505	0.707
CXCL2 / GRO beta	434 (n=7)	384 (n=5)	0.639	0.813
IL-8	1.12e+03 (n=7)	1.82e+03 (n=5)	0.639	0.813
IL-6	4.59e+03 (n=7)	4.03e+03 (n=5)	0.755	0.842
IL-15	52.7 (n=7)	58.5 (n=5)	0.755	0.842

PDGF-BB	11.1 (n=7)	8.98 (n=5)	0.755	0.842
Eotaxin	144 (n=7)	93.5 (n=5)	0.782	0.842
PDGF-AA	1.07e+03 (n=7)	963 (n=5)	0.876	0.909
G-CSF	34.9 (n=7)	36.1 (n=5)	0.975	0.975

Supplementary Table 7. Luminex assay on amniotic fluid at C-section.

Analyte	AF- Dams	AF+ Dams	P value	FDR
TNF-alpha	0.13 (n=7)	4.49 (n=5)	0.00126	0.0379
CXCL2 / GRO beta	838 (n=5)	263 (n=5)	0.0794	0.758
I-TAC	1.18 (n=7)	1.18 (n=5)	0.152	0.758
IFN-beta	3.25 (n=7)	3.25 (n=5)	0.152	0.758
IL-21	0.37 (n=7)	0.37 (n=5)	0.152	0.758
CXCL13 / BLC	11.9 (n=7)	11.9 (n=5)	0.152	0.758
IL-17 / IL-17A	0.395 (n=7)	2.98 (n=5)	0.187	0.801
IL-8	772 (n=7)	450 (n=4)	0.23	0.808
IFN-alpha	0.01 (n=7)	1.44 (n=5)	0.242	0.808
GM-CSF	0.03 (n=7)	6.49 (n=5)	0.311	0.828
PDGF-BB	2.59e+03 (n=7)	977 (n=5)	0.343	0.828
CD40 Ligand	1.01e+03 (n=7)	514 (n=5)	0.404	0.828
IL-2	3.32 (n=7)	2.28 (n=5)	0.407	0.828
IL-10	6.48 (n=7)	6.48 (n=5)	0.417	0.828
Granzyme B	0.45 (n=7)	0.45 (n=5)	0.47	0.828
G-CSF	3.52 (n=7)	3.52 (n=5)	0.47	0.828
MIP-3 alpha	0.515 (n=7)	0.515 (n=5)	0.523	0.828
IL-12 p70	0.7 (n=7)	0.7 (n=5)	0.523	0.828
PDGF-AA	148 (n=7)	165 (n=4)	0.527	0.828
VEGF	134 (n=7)	109 (n=5)	0.602	0.828
Eotaxin	217 (n=7)	432 (n=5)	0.612	0.828
IL-15	6.33 (n=7)	5.52 (n=5)	0.639	0.828
IL-7	0.48 (n=7)	0.065 (n=5)	0.659	0.828
PD-L1	128 (n=6)	139 (n=5)	0.662	0.828

IL-6	0.875 (n=7)	1.75 (n=5)	0.817	0.98
IP-10	46.1 (n=7)	45.8 (n=5)	0.876	1.00
BDNF	3.83e+03 (n=7)	4.19e+03 (n=4)	0.927	1.00
IL-4	0 (n=7)	0 (n=5)	1.00	1.00
IFN-gamma	2.15 (n=7)	2.15 (n=5)	1.00	1.00
IL-13	22.4 (n=7)	22.4 (n=5)	1.00	1.00

Supplementary Table 8. Luminex assay on fetal plasma.

Analyte	AF– Dams	AF+ Dams	P value	FDR
Granzyme B	0.45 (n=7)	4.38 (n=5)	0.0568	0.795
IL-7	0.13 (n=7)	0.065 (n=5)	0.0808	0.795
CXCL2 / GRO beta	242 (n=6)	143 (n=5)	0.0823	0.795
G-CSF	3.52 (n=7)	3.52 (n=5)	0.205	1.00
VEGF	142 (n=6)	120 (n=4)	0.257	1.00
IFN-alpha	0.01 (n=7)	1.54 (n=5)	0.323	1.00
IL-6	3.66 (n=7)	20.8 (n=5)	0.357	1.00
I-TAC	1.18 (n=7)	1.18 (n=5)	0.417	1.00
IFN-beta	3.25 (n=7)	3.25 (n=5)	0.417	1.00
IL-15	6.15 (n=7)	5.79 (n=5)	0.496	1.00
GM-CSF	0.03 (n=7)	3.74 (n=5)	0.52	1.00
IL-21	0.37 (n=7)	0.37 (n=5)	0.523	1.00
TNF-alpha	0.13 (n=7)	0.13 (n=5)	0.523	1.00
IL-8	467 (n=7)	355 (n=4)	0.527	1.00
CD40 Ligand	1e+03 (n=7)	757 (n=5)	0.639	1.00
IP-10	41.7 (n=7)	47.8 (n=5)	0.639	1.00
BDNF	3.18e+03 (n=7)	4.15e+03 (n=4)	0.648	1.00
IL-2	2.82 (n=7)	2.03 (n=5)	0.755	1.00
PDGF-AA	156 (n=7)	163 (n=4)	0.788	1.00
PD-L1	139 (n=6)	130 (n=5)	0.792	1.00
PDGF-BB	1.83e+03 (n=7)	1.78e+03 (n=4)	0.927	1.00
Eotaxin	277 (n=7)	279 (n=5)	0.96	1.00
MIP-3 alpha	0.515 (n=7)	0.515 (n=5)	1.00	1.00
IL-4	0 (n=7)	0 (n=5)	1.00	1.00

IL-12 p70	0.7 (n=7)	0.7 (n=5)	1.00	1.00
IFN-gamma	2.15 (n=7)	2.15 (n=5)	1.00	1.00
IL-10	6.48 (n=7)	6.48 (n=5)	1.00	1.00
IL-13	22.4 (n=7)	22.4 (n=5)	1.00	1.00
IL-17 / IL-17A	0.395 (n=7)	0.79 (n=5)	1.00	1.00

Supplementary Table 9. Luminex assay on umbilical cord plasma.