

Supplemental Data for: Isolation of RNA from Acute Ischemic Stroke Clots Retrieved by Mechanical Thrombectomy

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Table S1. Primers used for qPCR.*.

<i>Transcript</i>	Primer Sequence	Avg. Annealing Temp. (°C)	Eff.	PCR Prod. Length (bp)
GAPDH	5'-CGCTCTCTGCTCCTCCTGTT-3'	59.8	1.1	81
<i>Housekeeping</i>	5'-CCATGGTGTCTGAGCGATGT-3'			
GPI	5'-AGGCTGCTGCCACATAAGGT-3'	61.7	0.95	240
<i>Housekeeping</i>	5'-AGCGTCGTGAGAGGTCACTTG-3'			
HPRT1	5'-TGGCGTCGTGATTAGTGATG-3'	57.4	0.82	131
<i>Housekeeping</i>	5'-CAAGACGTTCACTCCTGTCC-3'			

*Primers were selected using Primer3 and NCBI's Primer Blast. (Abbreviations: Avg.=average, bp=base pair, Eff.=efficiency, Prod.=product, qPCR=quantitative polymerase chain reaction, Temp.=temperature).

Table S2. Ct values for housekeeping genes from qPCR.*.

Sample ID	Sample Type	Ct (GAPDH)	Ct (GPI)	Ct (HPRT1)
C1	Clot	33.645	NR	37.800
C2	Clot	25.420	28.625	30.400
C3	Clot	24.795	28.220	30.550
C4	Clot	28.915	NR	32.790
C5	Clot	24.580	29.460	30.150
C6	Clot	31.235	35.705	35.790
C7	Clot	26.330	30.350	32.860
C9	Clot	23.490	27.965	29.860
C10	Clot	23.230	25.790	29.615
C11	Clot	25.840	29.615	31.265
C13	Clot	31.390	35.420	35.930
C14	Clot	28.310	30.445	33.240
C15	Clot	24.760	27.040	30.560
C16	Clot	27.145	30.180	33.140
C17	Clot	29.555	34.280	38.055
C18	Clot	26.155	30.275	30.895
C19	Clot	29.605	34.445	35.840
C20	Clot	34.005	NR	36.260
C21	Clot	28.130	32.375	35.630
C22	Clot	27.535	30.415	32.210
C23	Clot	27.920	30.115	32.340
C24	Clot	28.840	30.535	34.360
C25	Clot	26.920	29.765	34.235
C26	Clot	25.575	28.650	31.555
C27	Clot	25.270	29.080	31.725
C28	Clot	24.335	27.590	30.980

C29	Clot	26.995	30.505	33.010
C30	Clot	24.180	28.265	32.675
C31	Clot	22.115	28.000	28.600
C32	Clot	28.460	32.100	33.600
C33	Clot	26.280	29.965	32.490
C34	Clot	22.075	26.000	28.115
C35	Clot	25.305	30.210	32.050
C36	Clot	23.340	26.605	28.575
C37	Clot	22.655	25.140	27.770
C38	Clot	25.760	27.730	32.050
C39	Clot	23.710	26.660	31.145
C40	Clot	36.040	36.490	33.305
C41	Clot	21.890	26.270	31.325
C42	Clot	23.335	NR	31.670
C43	Clot	26.825	31.180	31.900
C44	Clot	23.680	27.245	30.080
C45	Clot	21.415	25.910	30.040
C46	Clot	25.435	27.895	32.915
C47	Clot	24.820	29.555	32.810
C48	Clot	26.075	30.400	33.690
C49	Clot	27.680	31.710	34.785
C50	Clot	25.290	28.285	32.825
C51	Clot	26.345	30.860	32.875
C52	Clot	25.240	28.890	32.625
C53	Clot	22.950	26.500	30.580
C54	Clot	29.915	33.745	32.010
C55	Clot	22.915	26.900	29.895
C56	Clot	24.155	NR	NR
C57	Clot	22.900	27.315	30.595
C58	Clot	28.145	34.230	35.630
C59	Clot	24.995	28.970	31.490
C60	Clot	29.270	33.090	36.295
C61	Clot	21.830	27.625	29.775
C62	Clot	22.090	27.735	31.885
C63	Clot	29.525	32.110	34.815
C64	Clot	23.995	26.815	28.830
C65	Clot	30.98	39.780	NR
C66	Clot	22.595	26.545	30.200
C67	Clot	27.110	32.720	34.000
C68	Clot	25.280	27.755	30.310
C69	Clot	23.590	26.830	30.315
C70	Clot	25.900	29.750	32.655
C71	Clot	23.450	27.635	32.035
C72	Clot	26.215	30.150	34.665
C73	Clot	20.220	22.760	27.325
B1	Blood	23.160	28.045	29.380
B2	Blood	23.260	26.095	27.655
B3	Blood	21.560	26.485	28.425

*(Abbreviations: NR=not recorded, qPCR=quantitative polymerase chain reaction).

Table S3. Sequencing quality metrics.*.

Sample ID	Sample Type	R1, Total Seq.	R1, No. Poor Qual. Seq.	FastQC				MultiQC				
				R1, GC (%)	R1, Dup. (%)	R2, Total Seq.	R2, No. Poor Qual. Seq.	R2, GC (%)	R2, Dup. (%)	M Ass.	Ass. (%)	Alig. (%)
C3	Clot	35.2	0	41	33.7	35.2	0	40	37.7	8.9	21.5	95.3
C9	Clot	36.6	0	41	34.1	36.6	0	40	37.7	8.7	20.2	95.3
C10	Clot	41.6	0	47	39.4	41.6	0	46	43.6	20.1	39.4	96.7

C11	Clot	34.3	0	45	35.9	34.3	0	44	41.0	14.3	34.0	96.3
C13	Clot	22.4	0	47	55.6	22.4	0	46	61.8	10.8	37.3	92.5
C14	Clot	29.5	0	43	49.5	29.5	0	42	54.2	6.0	16.2	91.9
C15	Clot	33.6	0	46	41.6	33.6	0	45	47.2	16.0	38.3	95.8
C16	Clot	20.3	0	45	54.1	20.3	0	44	59.8	7.9	29.9	92.3
C17	Clot	33.8	0	41	27.6	33.8	0	37	30.2	2.0	4.7	94.3
C18	Clot	41.0	0	45	42.4	41.0	0	45	47.7	20.3	40.2	96.5
C19	Clot	41.8	0	46	37.3	41.8	0	44	41.9	6.2	11.0	94.9
C20	Clot	30.9	0	46	48.0	30.9	0	46	54.7	11.2	26.9	95.8
C21	Clot	31.2	0	43	51.5	31.2	0	41	54.5	6.8	18.2	93.1
C22	Clot	26.9	0	47	48.7	26.9	0	46	55.4	15.1	44.9	96.5
C23	Clot	32.1	0	44	50.7	32.1	0	42	56.2	11.1	27.6	94.6
C24	Clot	29.2	0	44	44.0	29.2	0	43	50.1	10.2	28.0	95.5
C25	Clot	34.1	0	41	30.7	34.1	0	40	33.2	4.4	10.7	94.8
C26	Clot	34.0	0	41	36.3	34.0	0	42	40.7	10.0	24.9	95.4
C27	Clot	42.4	0	49	51.5	42.4	0	48	56.3	14.0	17.1	97.0
C28	Clot	40.6	0	47	44.8	40.6	0	46	49.2	19.5	37.7	96.5
C31	Clot	37.7	0	46	55.1	37.7	0	47	62.9	27.0	61.4	97.0
C32	Clot	20.5	0	45	74.5	20.5	0	44	81.2	14.2	56.0	91.0
C33	Clot	31.3	0	46	65.8	31.3	0	46	73.6	23.3	63.3	96.2
C35	Clot	36.1	0	48	65.1	36.1	0	47	72.3	29.0	63.4	97.2
C36	Clot	70.8	0	47	52.8	70.8	0	47	58.9	46.2	52.3	97.1
C37	Clot	41.8	0	47	49.5	41.8	0	48	55.8	28.8	54.2	97.5
C39	Clot	33.9	0	47	55.3	33.9	0	47	63.2	23.8	56.8	96.9
C40	Clot	47.9	0	49	61.5	47.9	0	49	68.0	33.2	49.5	95.7
C41	Clot	43.5	0	49	48.7	43.5	0	49	54.3	30.9	58.9	97.5
C43	Clot	27.3	0	47	61.5	27.3	0	46	70.5	19.1	54.0	95.3
C44	Clot	41.5	0	50	56.4	41.5	0	50	63.4	29.2	53.1	97.3
C45	Clot	41.2	0	50	58.2	41.2	0	50	65.4	29.5	52.8	97.4
C46	Clot	30.3	0	48	56.3	30.3	0	48	64.7	21.0	52.9	95.5
C47	Clot	27.9	0	49	60.8	27.9	0	49	69.2	18.9	51.5	92.3
C48	Clot	20.7	0	48	66.3	20.7	0	47	73.7	12.9	44.2	89.4
C51	Clot	36.3	0	44	40.5	36.3	0	42	45.9	11.9	25.5	95.2
C52	Clot	30.1	0	46	63.4	30.1	0	46	72.3	23.0	63.0	96.0
C54	Clot	40.8	0	49	58.1	40.8	0	49	65.4	22.6	30.4	97.0
C55	Clot	35.0	0	47	55.2	35.0	0	47	63.2	25.6	58.1	97.0
C57	Clot	31.5	0	42	29.0	31.5	0	40	32.7	7.1	18.7	94.8
C63	Clot	42.7	0	48	52.2	42.7	0	48	58.4	30.4	58.3	97.3
C65	Clot	42.4	0	50	59.5	42.4	0	50	65.1	22.9	29.1	97.4
C66	Clot	20.3	0	48	66.6	20.3	0	48	74.1	13.7	57.8	89.3
C67	Clot	39.4	0	47	60.3	39.4	0	47	68.3	30.4	66.4	97.5
C69	Clot	27.0	0	46	56.6	27.0	0	47	61.4	17.6	51.7	96.0
C70	Clot	28.6	0	46	50.2	28.6	0	47	58.0	15.1	43.3	95.6
C72	Clot	34.7	0	46	59.3	34.7	0	47	66.7	20.7	48.4	95.2
C73	Clot	42.8	0	46	49.4	42.8	0	46	55.4	27.9	52.1	97.1
B1	Blood	39.5	0	53	66.7	39.5	0	54	71.1	21.6	35.3	97.8
B2	Blood	37.6	0	55	65.0	37.6	0	54	76.0	27.2	40.3	98.2
B3	Blood	42.4	0	54	69.4	42.4	0	54	72.7	26.4	45.3	97.7

*(Abbreviations: Alig.=aligned, Ass.=assigned, Dup.=duplicate, M=million, No.=number, Qual.=quality, R1=strand 1, R2=strand 2, Seq.=sequences).

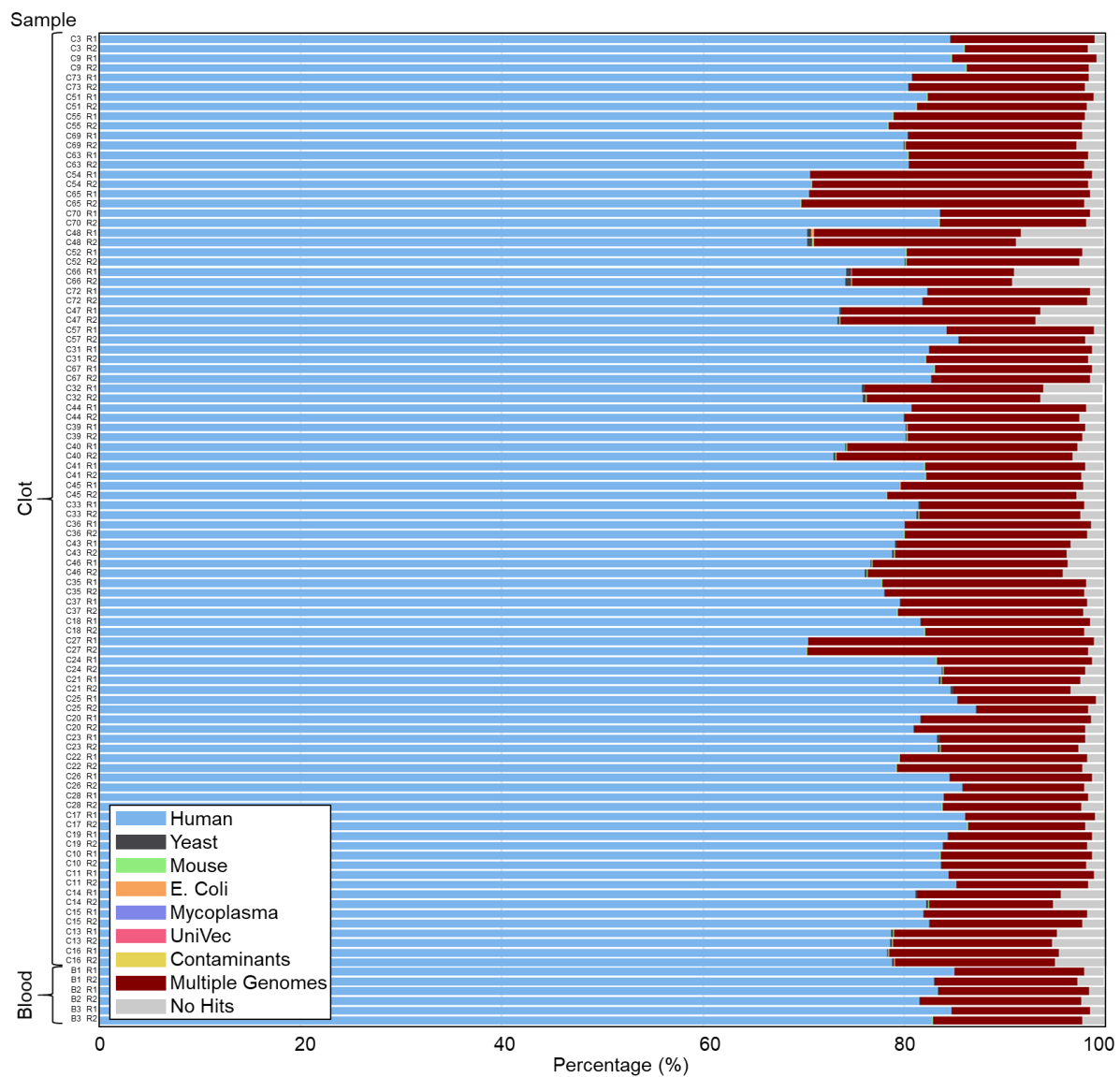


Figure S1. FastQC Screen results. Percentages of reads show mapping predominantly to the human genome or multiple genomes.

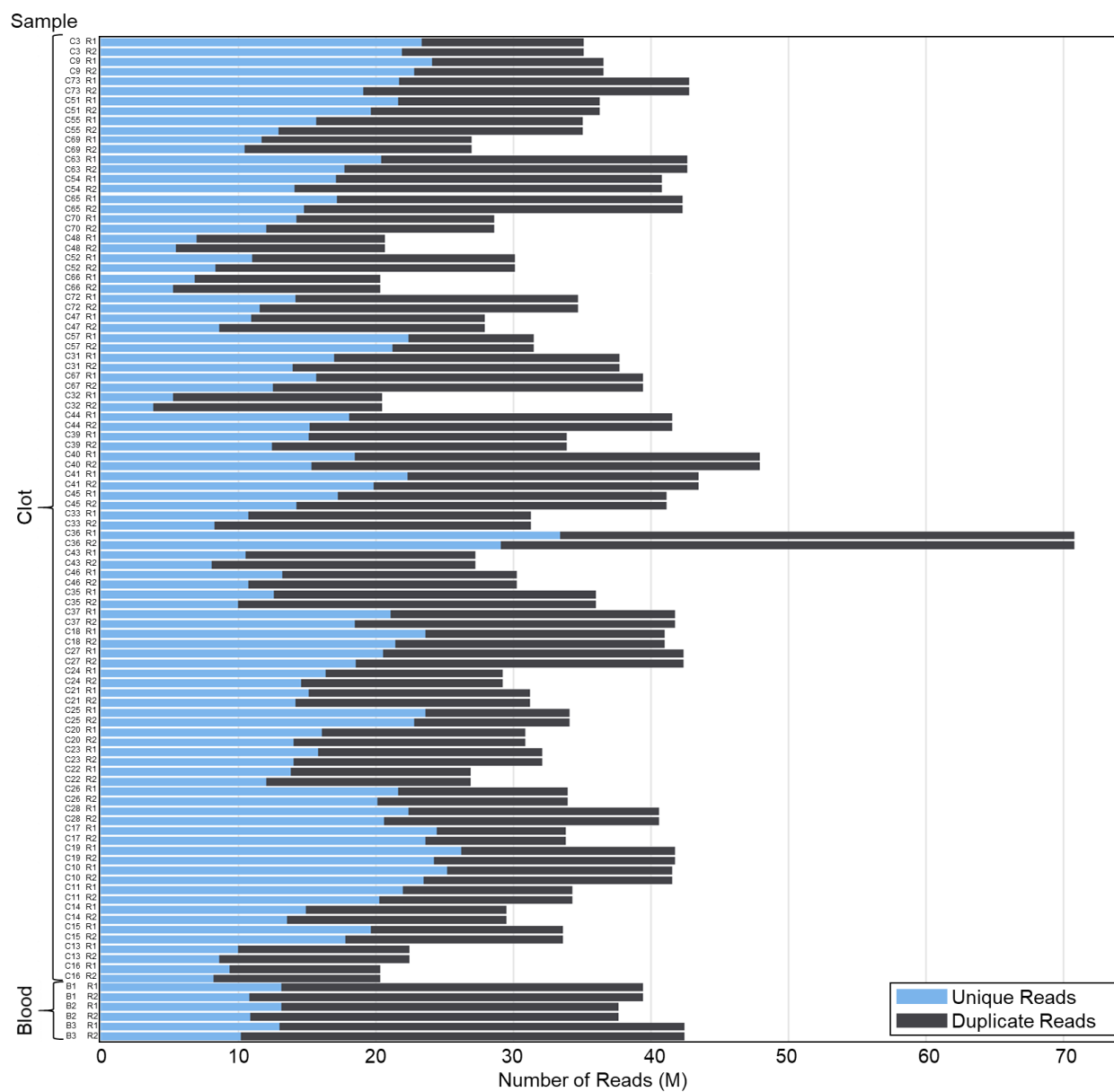


Figure S2. FastQC results. Number of unique and duplicate reads for each transcriptome.

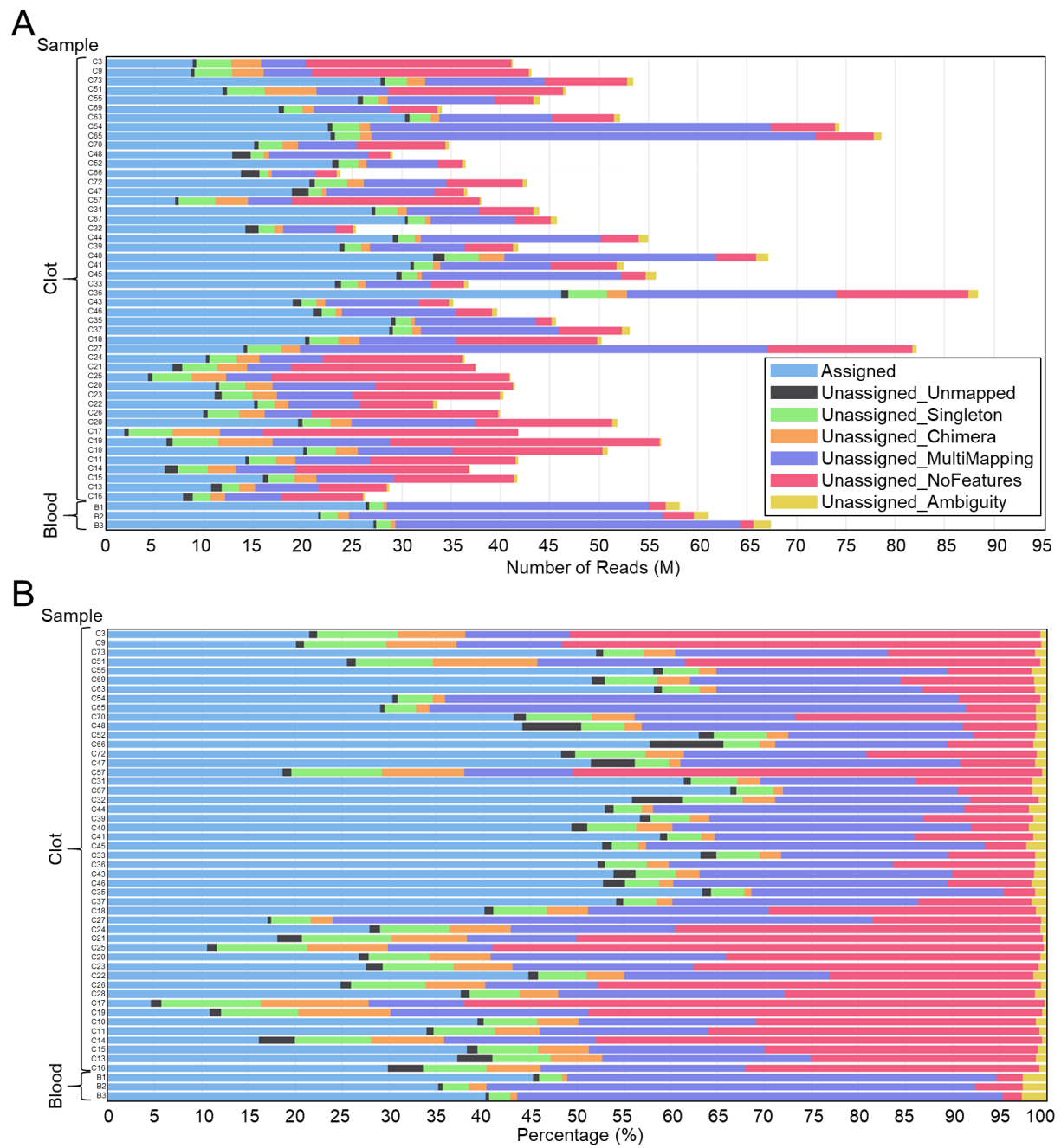


Figure S3. MultiQC read results. The A). number and B). percentage of reads for each transcriptome.

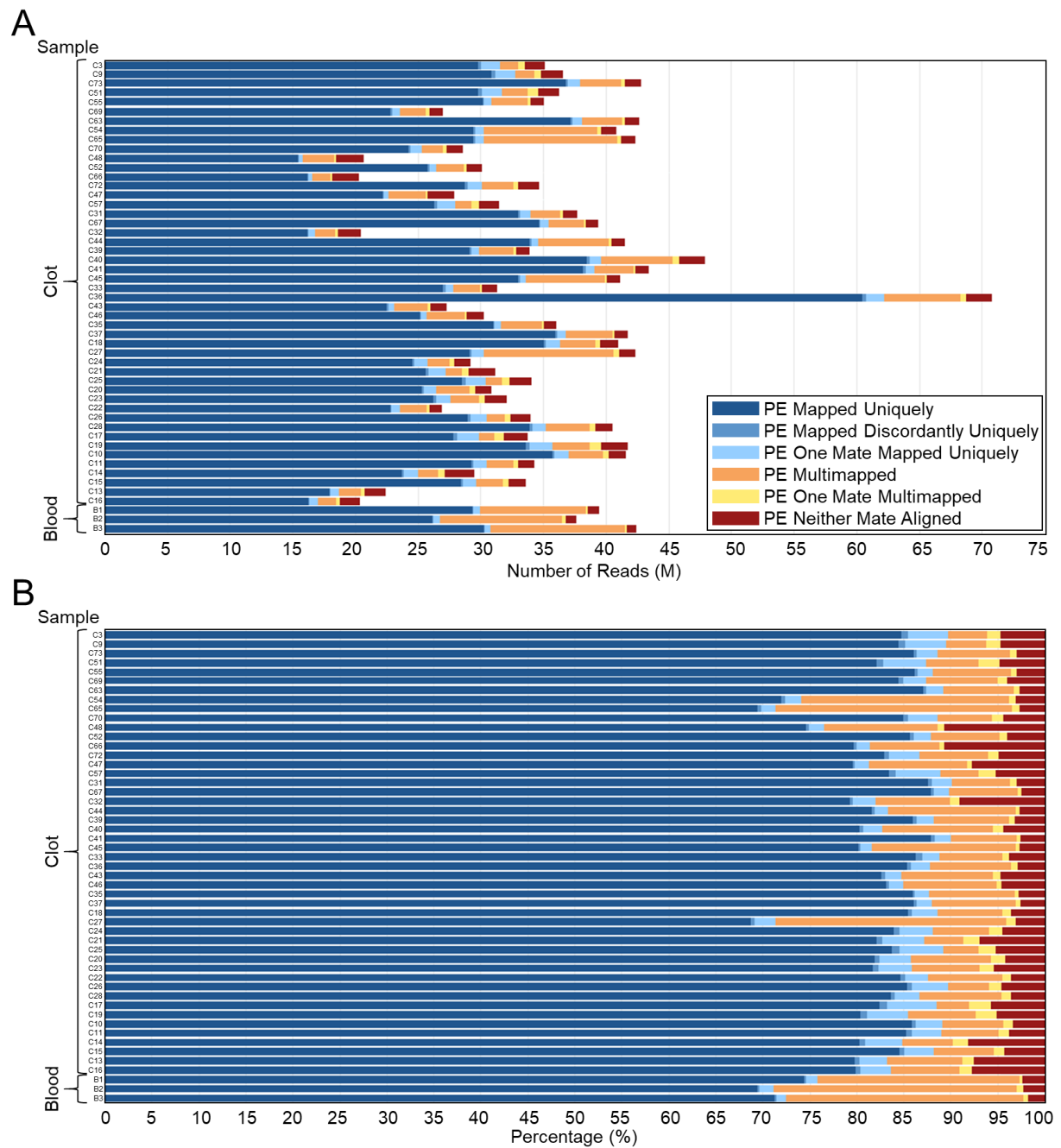


Figure S4. MultiQC mapping results. The **A**). number and **B**). percentage of read mapping for each transcriptome.

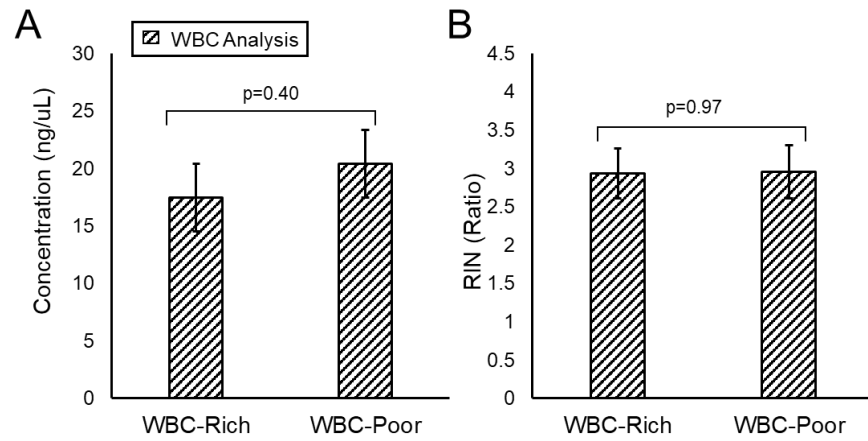


Figure S5. Histologic analysis of clots. A). Average concentration in WBC-rich (\geq median WBC %) vs. WBC-poor ($<$ median WBC %) clots. **B).** Average RIN in WBC-rich vs. WBC-poor clots. Values are averages, and error bars represent standard error. (Abbreviations: RIN=RNA integrity number, WBC=white blood cell).