

## Supplemental Material for “Characterization of the platelet transcriptome by RNA sequencing in patients with acute myocardial infarction.”

**Supplemental Table 1:** Mitochondrial transcripts highly expressed in 32 MI platelet cells ( $\log\text{RPKM}>3$ )

**Supplemental Table 2:** Top KEGG pathways in MI cases ( $n=32$ ) with genes with expression  $\log\text{RPKM} \geq 3.0$

**Supplemental Table 3:** Top Pathway Commons Pathways in all MI Cases ( $n=32$ ) with genes with expression  $\log\text{RPKM} \geq 3.0$

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**Supplemental Table 6:** Genes looked with qPCR and mean expression levels

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**Supplemental Table 12:** Differentially expressed transcripts ( $p \leq 0.01$ ) of STEMI cases compared to NSTEMI cases with ANOVA, correcting for batch, age, gender, and body mass index (BMI).

**Supplemental Table 13:** Differentially expressed transcripts ( $p \leq 0.01$ ) of STEMI cases compared to NSTEMI cases with EdgeR, correcting for batch, age, gender, and body mass index (BMI).

**Supplemental Table 14:** Top KEGG pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using ANOVA

**Supplemental Table 15:** Top Pathway Commons pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using ANOVA

**Supplemental Table 16:** Top KEGG pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using EdgeR

**Supplemental Table 17:** Top Pathway Commons pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using EdgeR

**Supplemental Table 18:** Correlations of top differentially expressed transcripts from Supplemental Table 12 with platelet aggregation to collagen ( $10 \mu\text{g/mL}$ ) in washed platelets.

**Supplemental Table 19:** Correlations of top differentially expressed transcripts from Supplemental Table 12 with platelet aggregation to ADP ( $10 \mu\text{M}$ ) in platelet rich plasma.

**Supplemental Table 20:** Top correlated transcripts with platelet aggregation to TRAP ( $p < 0.01$ )

**Supplemental Table 21:** Top correlated transcripts with platelet aggregation to Collagen ( $p < 0.01$ )

**Supplemental Table 22:** Top correlated transcripts with platelet aggregation to ADP ( $p < 0.01$ )

**Supplemental Table 23:** Top correlated transcripts with platelet aggregation to ADP\_PRP ( $p < 0.01$ )

**Supplemental Figure 1:** Principal component analysis (PCA) of transcripts from RNA-seq (with  $\text{RPKM} \geq 0.3$ ) of 32 MI platelets samples grouped by (A) batch, (B) Gender, (C) Age, (D) Body Mass Index (BMI), and Time Interval from Event

**Supplemental Figure 2:** Top Gene Ontology (GO) pathways for all MI Cases ( $n=32$ ) with  $\log\text{RPKM} \geq 3.0$ .

**Supplemental Figure 3:** Top Gene Ontology (GO) pathways for all MI Cases ( $n=32$ ) with  $\log\text{RPKM} \geq 2.0$ .

**Supplemental Figure 4:** Top Gene Ontology (GO) pathways for differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases (ANOVA).

**Supplemental Figure 5:** Top Gene Ontology (GO) pathways for differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases (EdgeR).

**Supplemental Figure 6:** Principal component analysis (PCA) grouped by STEMI (n=16) and NSTEMI (n=16) case status

Supplemental Table 1: Mitochondrial transcripts highly expressed in 32 MI platelet cells ( $\log_{10}\text{RPKM}>3$ )

ID	Name	Average RPKM	Log RPKM	STEMI RPKM	STEMI logRPKM	NSTEMI RPKM	NSTEMI logRPKM
ENST00000387347	MT-RNR2	485620.25	5.69	484311.81	5.69	492015.19	5.69
ENST00000389680	MT-RNR1	227880.31	5.36	231766.39	5.37	216423.94	5.34
ENST00000387314	MT-TF	10010.99	4.00	9041.96	3.96	10914.90	4.04
ENST00000361335	MT-ND4L	6351.36	3.80	6211.30	3.79	6336.20	3.80
ENST00000387342	MT-TV	3885.42	3.59	3655.73	3.56	4164.53	3.62
ENST00000361624	MT-CO1	3807.99	3.58	3463.73	3.54	4062.49	3.61
ENST00000361739	MT-CO2	3541.47	3.55	3193.94	3.50	3802.27	3.58
ENST00000387377	MT-TM	3392.56	3.53	3132.88	3.50	3537.28	3.55
ENST00000361381	MT-ND4	2402.51	3.38	2269.06	3.36	2466.45	3.39
ENST00000386347	MT-TL1	2175.06	3.34	2071.45	3.32	2226.32	3.35
ENST00000361453	MT-ND2	2089.56	3.32	2002.05	3.30	2090.91	3.32
ENST00000362079	MT-CO3	1790.27	3.25	1664.61	3.22	1855.42	3.27
ENST00000361390	MT-ND1	1582.68	3.20	1549.35	3.19	1582.16	3.20
ENST00000387439	MT-TR	1448.16	3.16	1411.23	3.15	1458.07	3.16
ENST00000361789	MT-CYB	1357.63	3.13	1260.42	3.10	1400.00	3.15
ENST00000361899	MT-ATP6	1269.41	3.10	1173.93	3.07	1323.21	3.12
ENST00000361567	MT-ND5	1079.64	3.03	1005.94	3.00	1098.87	3.04

Supplemental Table 2: Top KEGG pathways in MI cases (n=32) with genes with expression logRPKM  $\geq$  3.0

Pathway Name	Obs/Ref	Transcript Names	P-value
Ribosome	6/92	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	$6.60 \times 10^{-8}$
Regulation of actin cytoskeleton	7/213	ACTB, RHOA, ARPC2, VCL, MYL12A, TMSB4X, ITGB3	$1.12 \times 10^{-7}$
Pathogenic E. coli infection	5/56	YWHAZ, ACTB, RHOA, ARPC2, TUBB1	$1.12 \times 10^{-7}$
Bacterial invasion of epithelial cells	4/70	ACTB, RHOA, ARPC2, VCL	$1.58 \times 10^{-5}$
Chemokine signaling pathway	5/189	PF4V1, RHOA, CCL5, PF4, PPBP	$2.77 \times 10^{-5}$
Focal adhesion	5/200	ACTB, RHOA, VCL, MYL12A, ITGB3	$3.04 \times 10^{-5}$
Leukocyte transendothelial migration	4/116	ACTB, RHOA, VCL, MYL12A	$6.73 \times 10^{-5}$
Shigellosis	3/61	ACTB, ARPC2, VCL	$2.00 \times 10^{-4}$
Phagosome	4/153	ACTB, HLA-E, ITGB3, TUBB1	$2.00 \times 10^{-4}$
Adherens junction	3/73	ACTB, RHOA, VCL	$3.00 \times 10^{-4}$

Obs = number of genes in category that were expressed at logRPKM  $\geq$  3.0; Ref = number of total genes in pathway

Supplemental Table 3: Top Pathway Commons Pathways in all MI Cases (n=32) with genes with expression logRPKM  $\geq$  3.0

Pathway Name	Obs/Ref	Transcript Names	P-value
Hemostasis	11/376	GNAS, PF4V1, HBB, RHOA, FCER1G, ITGB3, F13A1, YWHAZ, PRKAR2B, VCL, PF4	2.49x10 <sup>-10</sup>
Peptide chain elongation	6/83	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	3.56x10 <sup>-8</sup>
Viral mRNA translation	6/83	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	3.56x10 <sup>-8</sup>
Eukaryotic translation elongation	6/86	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	3.56x10 <sup>-8</sup>
Eukaryotic translation termination	6/83	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	3.56x10 <sup>-8</sup>
Nonsense mediated decay independent of exon junction complex	6/88	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	3.56x10 <sup>-8</sup>
Metabolism of proteins	8/261	RPS16, RPLP2, RPS11, RPL30, RPL37A, ACTB, RPL11, TUBB11	3.56x10 <sup>-8</sup>
Formation of a pool of free 40S subunits	6/93	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	4.37x10 <sup>-8</sup>
GTP hydrolysis and joining of the 60S ribosomal subunit	6/104	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	4.87x10 <sup>-8</sup>
Nonsense-Mediated Decay	6/105	RPL30, RPL37A, RPS16, RPLP2, RPS11, RPL11	4.87x10 <sup>-8</sup>

Obs = number of genes in category that were expressed at logRPKM  $\geq$  3.0; Ref = number of total genes in pathway

Supplemental Table 4: Top KEGG pathways in all MI Cases (n=32) with logRPKM  $\geq$  2.0

Pathway Name	Obs/Ref	Transcript Names	P-value
Ribosome	52/92	RPL3, RPS8, RPS20, RPS15, RPLP2, RPL30, RPS5, RPL15, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, RPS13, RPL26, RPL35, RPL36AL, RPS4Y1, RPS25, RPL31, RPL41, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, RPS3A, RPL36, RPL7A, RPS4X, RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	5.00x10 <sup>-71</sup>
Pathogenic E. Coli infection	20/56	RHOA, TUBA1A, ACTG1, YWHAQ, TUBA1C, ARPC4, TUBB1, ARPC3, TUBA1B, ARPC1B, CDC42, ARPC5, ITGB1, NCK2, ACTB, YWHAZ, CTTN, ARPC2, TUBB, TUBA4A	7.67x10 <sup>-22</sup>
Regulation of actin cytoskeleton	31/213	MYL9, RHOA, ACTG1, RAC1, MYH9, ARHGEF12, ACTN1, ARPC4, PIP4K2A, MYL12A, TMSB4X, ITGA2B, ARPC2, ITGB2, RAC2, BRK1, ARPC1B, CDC42, ARPC5, PFN1, ITGB3, MYLK, ITGB1, ACTB, ARPC2, F2R, VCL, MSN, GNA13, MYL12B, CFL1	2.97x10 <sup>-21</sup>
Phagosome	27/153	HLA-DRA, TUBA1A, ACTG1, RAB7A, HLA-E, RAC1, TUBA1C, CD36, FCGR3A, TUBB1, TUBA1B, THBS1, HLA-DPA1, ITGB2, HLA-B, CTSS, ITGB3, ITGB1, FCGR2A, ACTB, ATP6V0C, CORO1A, HLA-C, ATP6V0E1, TUBB, TUBA4A, CYBB,	7.15x10 <sup>-21</sup>
Leukocyte transendothelial migration	23/116	CD99, MYL9, RHOA, ACTG1, RAC1, RAP1B, ACTN1, JAM3, MYL12A, UTGB2, RAC2, ESAM, CXCR4, RAP1A, CDC42, PRKCB, ITGB1, ACTB, VCL, MSN, GNAI2, MYL12B, CYBB	4.68x10 <sup>-19</sup>
Focal adhesion	26/200	MYL9, RHOA, ACTG1, TLN1, RAC1, RAP1B, ACTN1, FLNA, ILK, MYL12A, ITGA2B, THBS1, CAPN2, ZYX, RAC2, RAP1A, CDC42, PRKCB, AKT3, ITGB3, MYLK, CCND3, ITGB1, ACTB, VCL, MYL12B	8.06x10 <sup>-17</sup>
Fc gamma R-mediated phagocytosis	17/94	PTPRC, RAC2, LAT, DNM3, CDC42, ARPC1B, PRKCB, ARPC5, AKT3, RAC1, FCGR2A, ARPC4, ARPC2, LYN, FCGR3A, CFL1, ARPC3	1.64x10 <sup>-13</sup>
Bacterial invasion of epithelial cells	15/70	RHOA, DNM3, CDC42, ARPC1B, ACTG1, ARPC5, RAC1, ITGB1, ACTB, ARPC4, CTTN, ILK, ARPC2, VCL, ARPC3	3.82x10 <sup>-13</sup>
Systemic lupus erythematosus	19/136	HLA-DRA, HIST2H2AA4, HIST1H2BK, HIST2H2BE, ACTN1, HIST1H2BJ, HIST1H3H, HIST1H2AG, HIST1H2BC, FCGR3A, HIST1H4H, HLA-DPA1, HIST1H2AC, FCGR2A, HIST2H2AA3, HIST1H2BH, HIST1H2BF, H3F3A, HIST1H2BO	4.69x10 <sup>-13</sup>
Shigellosis	14/61	CDC42, ARPC1B, ACTG1, ARPC5, PFN1, RAC1, ITGB1, ACTB, ARPC4, CTTN, CD44, ARPC2, VCL, ARPC3	8.09x10 <sup>-13</sup>

Obs = number of genes in category that were expressed at logRPKM  $\geq$  2.0; Ref = number of total genes in pathway

Supplemental Table 5: Top Pathway Commons pathways in all MI Cases (n=32) with logRPKM  $\geq$  2.0

Pathway Name	Obs/Ref	Transcript Names	P-value
Eukaryotic Translation Elongation	53/86	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EEF1G, RPL5, EEF1A1, RPL13A, EEF1B2, RPL11, RPL23, RPL18, RPS16, EEF2, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, RPS3A, RPL36, RPL7A, RPS4X, RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	$9.72 \times 10^{-75}$
Translation	58/118	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, EEF1G, RPL5, EEF1A1, RPL13A, EEF1B2, RPL11, RPL23, RPL18, RPS16, EEF2, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPS19, RPL14, RPLP1, RPL4, RPS12, RPL24, FAU, RPS3	$3.37 \times 10^{-74}$
Peptide chain elongation	51/83	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, RPL5, EEF1A1, RPL13A, RPL11, RPL23, RPL18, RPS16, EEF2, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, RPS3A, RPL36, RPL7A, RPS4X, RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	$3.28 \times 10^{-72}$
3'-UTR mediated translation regulation	54/103	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPS19, RPL14, RPLP1, RPL4, RPS12, RPL24, FAU, RPS3	$2.11 \times 10^{-71}$
L13a-mediated translational silencing of Ceruloplasmin expression	54/103	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPS19, RPL14, RPLP1, RPL4, RPS12, RPL24, FAU, RPS3	$2.11 \times 10^{-71}$
Formation of a pool of free 40S subunits	52/93	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K,	$7.93 \times 10^{-71}$

		RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	
GTP hydrolysis and joining of the 60S ribosomal subunit	53/104	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	2.66x10 <sup>-69</sup>
Eukaryotic translation initiation	54/111	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPS19, RPL14, RPLP1, RPL4, RPS12, RPL24, FAU, RPS3	2.84x10 <sup>-69</sup>
Cap-dependent translation initiation	54/111	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, EIF3E, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, EIF4A2, RPL6, RPL38, RPL7, RPL8, RPS24, RPL18A, RPS27, RPL10A, RPS9, EIF3H, RPS3A, RPL36, RPL7A, RPS4X, EIF3K, RPS15A, RPL28, RPS14, RPS19, RPL14, RPLP1, RPL4, RPS12, RPL24, FAU, RPS3	2.84x10 <sup>-69</sup>
Nonsense mediated decay independent of the exon junction complex	50/88	RPL3, RPS8, RPS20, RPLP2, RPL30, RPS5, RPL15, RPL5, RPL13A, RPL11, RPL23, RPL18, RPS16, RPS11, RPL27, RPS6, RPL37A, RPL19, RPS18, PABPC1, RPS13, RPL26, RPL35, RPS4Y1, RPS25, RPL31, RPL38, RPL7, RPL8, RPL6, RPS24, RPL18A, RPS27, RPL10A, RPS9, RPS3A, RPL36, RPL7A, RPS4X, RPS15A, RPL28, RPS14, RPLP1, RPS19, RPL14, RPL4, RPS12, RPL24, FAU, RPS3	9.00x10 <sup>-69</sup>

Obs = number of genes in category that were expressed at logRPKM  $\geq$  2.0; Ref = number of total genes in pathway



Supplemental Table 6: Genes measured by qPCR in FHS and their mean expression levels in FHS and distinct non-FHS UMass MI clinical samples ascertained by RNAseq. Inverse correlation is expected and observed between qPCR cycle threshold (Ct) and sequencing based RPKM (reads per kilobase mapped).

Transcript	FHS n	FHS Mean Ct	FHS SD Ct	MI RPKM	Transcript	FHS n	FHS Mean Ct	FHS SD Ct	MI RPKM
<i>B2M</i>	2239	7.558	3.273	3487.147	<i>SATB1</i>	2183	16.285	3.566	27.769
<i>PPBP</i>	2240	8.501	3.316	27505.520	<i>SVIL</i>	2161	16.300	3.079	9.687
<i>TUBB1</i>	2236	9.983	3.294	3223.008	<i>MEF2C</i>	2202	16.549	3.233	27.747
<i>TPM4</i>	2233	11.387	3.632	837.650	<i>TREML1</i>	2184	16.666	3.125	1002.136
<i>ACTB</i>	2235	11.758	3.522	11995.830	<i>SERPINE1</i>	2183	16.709	3.130	11.111
<i>GAPDH</i>	2234	12.830	3.482	1152.322	<i>STXBP5</i>	2156	16.739	3.277	9.405
<i>FURIN</i>	2222	13.556	3.440	44.765	<i>ATP6V1F</i>	2199	16.782	3.303	39.301
<i>TRIM58</i>	2222	13.680	3.536	302.160	<i>PTGES3</i>	2182	16.823	3.599	17.620
<i>CD68</i>	2225	14.376	3.295	187.535	<i>NRGN</i>	2192	16.919	3.129	1765.145
<i>TC2N</i>	2211	15.474	3.471	91.214	<i>ATP6V1B2</i>	2158	16.975	3.503	56.184
<i>VAMP8</i>	2212	15.623	3.375	57.779	<i>ITGA5</i>	2098	17.170	3.501	8.806
<i>MPL</i>	2209	15.761	3.274	94.342	<i>UBE2Z</i>	2155	17.486	3.398	22.383
<i>CTSZ</i>	2178	15.915	3.646	9.310	<i>BAZ2A</i>	2113	17.519	3.344	10.389
<i>ABCC4</i>	2207	16.141	3.353	139.266	<i>ANKS1A</i>	2111	17.605	3.005	5.807
<i>CBL</i>	2191	16.269	3.368	41.423	<i>ANKMY1</i>	2062	17.875	3.198	1.687
<i>ST3GAL4</i>	2163	16.276	3.057	7.675	<i>DOCK8</i>	2097	18.088	3.775	40.660
<i>KIF1B</i>	2109	18.116	3.112	5.075	<i>EXOC3L2</i>	2063	19.612	2.743	3.259
<i>VAMP5</i>	2128	18.136	3.264	13.179	<i>TPM1</i>	2051	19.686	2.910	567.970
<i>SORT1</i>	2146	18.292	3.212	26.154	<i>LRRC16A</i>	2067	19.726	2.938	5.678
<i>RCOR1</i>	2139	18.367	3.168	13.435	<i>ZC3HC1</i>	2032	19.821	3.010	3.082
<i>PTAFR</i>	2115	18.379	3.200	14.075	<i>RAD51B</i>	1953	19.971	3.433	2.816
<i>KIAA0232</i>	2121	18.535	3.162	6.362	<i>GGCX</i>	1833	20.082	3.103	2.278
<i>FAR2</i>	2079	18.636	2.984	1.283	<i>PDGFD</i>	1984	20.102	3.108	2.348
<i>AKAP10</i>	2099	18.823	3.403	10.279	<i>PDIA5</i>	2026	20.315	2.806	1.975
<i>THADA</i>	1957	18.960	3.390	6.095	<i>ARNTL</i>	1943	20.443	3.364	1.103
<i>STX2</i>	2026	18.977	3.378	5.560	<i>CABLES1</i>	2013	20.552	2.560	1.658
<i>BRF1</i>	1978	19.070	3.181	1.070	<i>KIAA1462</i>	1892	20.578	2.423	1.614
<i>HDAC9</i>	2110	19.14	3.151	12.153	<i>TRIB1</i>	1921	20.580	2.953	6.685
<i>PPAP2B</i>	2012	19.540	2.622	1.215	<i>PEMT</i>	1452	22.918	2.662	4.023
<i>SLC22A4</i>	1658	20.630	3.127	2.415	<i>FLT1</i>	1344	23.115	2.445	1.544
<i>GRTP1</i>	2007	20.665	2.616	4.404	<i>PPARG</i>	1251	23.166	2.620	2.326

<i>SERPINI1</i>	2014	20.714	2.768	6.179	<i>KALRN</i>	704	23.453	2.237	3.281
<i>WDR12</i>	1918	20.976	3.049	4.879	<i>ATP6V0D2</i>	874	23.612	1.713	4.819
<i>WASL</i>	1981	20.987	2.957	3.436	<i>PLAT</i>	884	24.003	1.910	0.549
<i>RAI1</i>	1854	21.028	3.098	2.446	<i>TIMP4</i>	1101	24.151	1.713	0.715
<i>RASD1</i>	1582	21.318	2.713	0.953	<i>ZFPM2</i>	1220	24.231	1.740	1.467
<i>SLC22A5</i>	1692	21.426	3.054	1.207	<i>F2RL2</i>	650	24.303	2.487	1.779
<i>SMG6</i>	1757	21.922	2.997	3.661	<i>RNF145</i>	902	22.418	3.451	2.784
<i>TMPRSS6</i>	1099	22.096	2.268	0.391	<i>HSD17B13</i>	1187	22.453	2.734	1.182
<i>FEN1</i>	1737	22.380	2.793	2.084	<i>CXCL12</i>	1438	22.599	2.007	1.143

FHS, Framingham Heart Study; n, sample size; Ct, threshold cycle; MI, myocardial infarction; SD, standard deviation

Supplemental Table 7: Correlations between expression data from Londin et al. and the current study (n=4,533 transcripts) (Londin et al. 2014)

	EA1	EA2	EA3	EA4	EA5	EAavg
Current	0.556	0.610	0.633	0.606	0.616	0.617
	AA1	AA2	AA3	AA4	AA5	AAavg
Current	0.597	0.592	0.624	0.650	0.602	0.635
	Total Avg					
Current	0.629					

EA, European-American; AA, African-American

Supplemental Table 8: Summary of correlations within and between STEMI and NSTEMI groups\*

Group 1	Group 2	Average Correlation	Range of Correlations
STEMI	STEMI	0.752	0.664-0.807
NSTEMI	NSTEMI	0.770	0.683-0.831
STEMI	NSTEMI	0.758	0.675-0.830

\*Supplemental Tables S9-S11 contain full correlation results

Supplemental Table 9: Spearman correlations among expression among platelet samples from STEMI cases (n=16).

	<b>S1</b>	<b>S2</b>	<b>S3</b>	<b>S4</b>	<b>S5</b>	<b>S6</b>	<b>S7</b>	<b>S8</b>	<b>S9</b>	<b>S10</b>	<b>S11</b>	<b>S12</b>	<b>S13</b>	<b>S14</b>	<b>S15</b>	<b>S16</b>
<b>S1</b>	1															
<b>S2</b>	0.75	1														
<b>S3</b>	0.77	0.78	1													
<b>S4</b>	0.86	0.62	0.65	1												
<b>S5</b>	0.91	0.73	0.72	0.88	1											
<b>S6</b>	0.69	0.70	0.72	0.59	0.65	1										
<b>S7</b>	0.84	0.65	0.71	0.81	0.80	0.65	1									
<b>S8</b>	0.74	0.79	0.77	0.60	0.68	0.71	0.65	1								
<b>S9</b>	0.75	0.74	0.73	0.64	0.70	0.67	0.68	0.74	1							
<b>S10</b>	0.90	0.66	0.69	0.89	0.88	0.62	0.86	0.63	0.68	1						
<b>S11</b>	0.76	0.68	0.71	0.70	0.73	0.67	0.73	0.67	0.69	0.74	1					
<b>S12</b>	0.80	0.87	0.80	0.64	0.76	0.72	0.68	0.81	0.76	0.68	0.69	1				
<b>S13</b>	0.93	0.73	0.75	0.87	0.89	0.67	0.85	0.71	0.74	0.91	0.77	0.77	1			
<b>S14</b>	0.83	0.77	0.76	0.75	0.81	0.71	0.78	0.74	0.73	0.80	0.74	0.79	0.83	1		
<b>S15</b>	0.67	0.73	0.72	0.53	0.62	0.68	0.60	0.73	0.69	0.57	0.65	0.74	0.64	0.70	1	
<b>S16</b>	0.91	0.79	0.78	0.80	0.86	0.70	0.82	0.77	0.77	0.86	0.77	0.84	0.90	0.83	0.70	1
<b>Avg</b>	<b>0.81</b>	<b>0.73</b>	<b>0.74</b>	<b>0.72</b>	<b>0.78</b>	<b>0.68</b>	<b>0.74</b>	<b>0.72</b>	<b>0.71</b>	<b>0.76</b>	<b>0.71</b>	<b>0.76</b>	<b>0.80</b>	<b>0.77</b>	<b>0.66</b>	<b>0.81</b>

Supplemental Table 10: Spearman correlations among expression among platelet samples from NSTEMI cases (n=16).

	<b>N1</b>	<b>N2</b>	<b>N3</b>	<b>N4</b>	<b>N5</b>	<b>N6</b>	<b>N7</b>	<b>N8</b>	<b>N9</b>	<b>N10</b>	<b>N11</b>	<b>N12</b>	<b>N13</b>	<b>N14</b>	<b>N15</b>	<b>N16</b>
<b>N1</b>	1															
<b>N2</b>	0.76	1														
<b>N3</b>	0.83	0.69	1													
<b>N4</b>	0.73	0.74	0.66	1												
<b>N5</b>	0.90	0.71	0.82	0.68	1											
<b>N6</b>	0.87	0.69	0.83	0.65	0.86	1										
<b>N7</b>	0.88	0.69	0.86	0.64	0.87	0.88	1									
<b>N8</b>	0.80	0.61	0.78	0.59	0.82	0.79	0.82	1								
<b>N9</b>	0.79	0.78	0.69	0.77	0.71	0.69	0.68	0.61	1							
<b>N10</b>	0.78	0.70	0.75	0.67	0.74	0.75	0.76	0.68	0.71	1						
<b>N11</b>	0.80	0.74	0.78	0.71	0.77	0.77	0.79	0.70	0.74	0.75	1					
<b>N12</b>	0.85	0.74	0.79	0.70	0.82	0.82	0.83	0.72	0.75	0.77	0.79	1				
<b>N13</b>	0.87	0.64	0.85	0.60	0.87	0.89	0.91	0.84	0.64	0.74	0.75	0.81	1			
<b>N14</b>	0.82	0.74	0.78	0.71	0.79	0.78	0.79	0.73	0.75	0.73	0.78	0.77	0.76	1		
<b>N15</b>	0.89	0.69	0.84	0.65	0.89	0.88	0.89	0.82	0.68	0.75	0.76	0.82	0.91	0.78	1	
<b>N16</b>	0.89	0.78	0.80	0.75	0.83	0.81	0.82	0.73	0.80	0.76	0.79	0.83	0.80	0.81	0.82	1
<b>Avg</b>	<b>0.83</b>	<b>0.71</b>	<b>0.78</b>	<b>0.68</b>	<b>0.80</b>	<b>0.80</b>	<b>0.81</b>	<b>0.74</b>	<b>0.72</b>	<b>0.74</b>	<b>0.76</b>	<b>0.79</b>	<b>0.79</b>	<b>0.77</b>	<b>0.80</b>	<b>0.80</b>

Supplemental Table 11: Spearman correlations of expression in platelet samples between STEMI (n=16) and NSTEMI (n=16) cases.

	<b>N1</b>	<b>N2</b>	<b>N3</b>	<b>N4</b>	<b>N5</b>	<b>N6</b>	<b>N7</b>	<b>N8</b>	<b>N9</b>	<b>N10</b>	<b>N11</b>	<b>N12</b>	<b>N13</b>	<b>N14</b>	<b>N15</b>	<b>N16</b>	<b>Avg</b>
<b>S1</b>	0.93	0.71	0.85	0.66	0.91	0.89	0.90	0.84	0.70	0.77	0.79	0.84	0.92	0.80	0.92	0.85	0.83
<b>S2</b>	0.83	0.80	0.72	0.77	0.75	0.73	0.73	0.64	0.82	0.73	0.76	0.77	0.68	0.77	0.73	0.83	0.75
<b>S3</b>	0.80	0.76	0.75	0.73	0.75	0.74	0.75	0.69	0.76	0.72	0.77	0.76	0.71	0.77	0.74	0.79	0.75
<b>S4</b>	0.80	0.58	0.80	0.53	0.80	0.83	0.86	0.78	0.57	0.70	0.70	0.79	0.88	0.69	0.85	0.73	0.74
<b>S5</b>	0.89	0.68	0.82	0.63	0.85	0.86	0.89	0.77	0.69	0.75	0.75	0.86	0.89	0.75	0.88	0.81	0.80
<b>S6</b>	0.71	0.71	0.69	0.68	0.69	0.67	0.68	0.63	0.70	0.67	0.71	0.71	0.64	0.70	0.66	0.72	0.69
<b>S7</b>	0.80	0.63	0.82	0.58	0.81	0.81	0.85	0.81	0.61	0.69	0.74	0.75	0.85	0.74	0.83	0.75	0.75
<b>S8</b>	0.79	0.77	0.71	0.74	0.74	0.71	0.72	0.65	0.78	0.72	0.75	0.76	0.67	0.76	0.71	0.79	0.74
<b>S9</b>	0.78	0.72	0.72	0.71	0.75	0.73	0.73	0.68	0.73	0.69	0.74	0.74	0.70	0.74	0.73	0.77	0.73
<b>S10</b>	0.85	0.62	0.83	0.58	0.86	0.87	0.90	0.83	0.60	0.70	0.72	0.79	0.91	0.73	0.89	0.76	0.78
<b>S11</b>	0.75	0.68	0.74	0.65	0.74	0.74	0.77	0.70	0.67	0.70	0.73	0.73	0.73	0.72	0.75	0.74	0.72
<b>S12</b>	0.88	0.80	0.73	0.77	0.79	0.75	0.75	0.67	0.83	0.72	0.77	0.79	0.71	0.79	0.76	0.87	0.77
<b>S13</b>	0.91	0.68	0.85	0.65	0.90	0.89	0.91	0.85	0.68	0.75	0.78	0.83	0.92	0.79	0.91	0.83	0.82
<b>S14</b>	0.85	0.74	0.80	0.70	0.82	0.80	0.82	0.75	0.74	0.74	0.78	0.79	0.80	0.77	0.81	0.82	0.78
<b>S15</b>	0.71	0.73	0.67	0.71	0.66	0.65	0.64	0.60	0.73	0.67	0.73	0.70	0.60	0.72	0.64	0.73	0.68
<b>S16</b>	0.92	0.74	0.83	0.72	0.88	0.86	0.88	0.81	0.75	0.77	0.79	0.83	0.87	0.81	0.88	0.86	0.83
<b>Avg</b>	<b>0.82</b>	<b>0.71</b>	<b>0.77</b>	<b>0.67</b>	<b>0.79</b>	<b>0.78</b>	<b>0.80</b>	<b>0.73</b>	<b>0.71</b>	<b>0.72</b>	<b>0.75</b>	<b>0.78</b>	<b>0.78</b>	<b>0.75</b>	<b>0.79</b>	<b>0.79</b>	<b>0.76</b>

Supplemental Table 12: Differentially expressed transcripts ( $p \leq 0.01$ ) of STEMI cases compared to NSTEMI cases with ANOVA, correcting for batch, age, gender, and body mass index (BMI).

RefSeq ID	Transcript	p-value	Fold Change	Up/Down in STEMI
NM_014165	NDUFAF4	0.000392262	2.02493	Up
NM_015480	PVRL3	0.000416549	8.36565	Down
NM_001243286	PVRL3	0.000496408	8.21475	Down
NM_000156	GAMT	0.000889981	5.25155	Up
NM_012160	FBXL4	0.000906727	1.97553	Up
NM_001039960	SLC4A8	0.000974241	1.34155	Up
NM_017647	FTSJ3	0.00153179	2.49921	Up
NM_001204376	NPR3	0.00158298	4.12875	Up
NR_103728	PVRIG2P	0.00177534	5.19159	Down
NM_032936	TMEM60	0.00177637	2.27392	Down
NM_018335	ZNF839	0.00187377	2.0383	Up
NM_001256435	PCYT2	0.00192273	2.87624	Down
NM_001252043	TAOK2	0.00196462	2.19191	Up
NM_002864	PZP	0.00213302	3.37876	Down
NM_001258401	SLC4A8	0.00234573	1.33228	Up
NM_024886	C10orf95	0.00242163	35.2985	Down
NM_002861	PCYT2	0.00242636	2.74355	Down
NM_001184917	PCYT2	0.00243006	2.74387	Down
NM_001256434	PCYT2	0.00243549	2.74296	Down
NM_004783	TAOK2	0.00271827	1.86546	Up
NM_014165	TAOK2	0.00273379	2.10828	Up
NM_015480	SERPINF1	0.00275318	3.9477	Down
NM_001243286	ATP1A1OS	0.00305853	2.34952	Down
NM_000156	ATP6V0E2	0.00305934	2.66498	Down
NM_012160	RNF146	0.0031064	2.89745	Up
NR_033685	PCYT2	0.00365601	2.54661	Down
NM_005614	RHEB	0.00372166	1.79189	Down
NR_045103	RNF146	0.00379536	2.87205	Up
NM_001007248	ZNF599	0.0039227	1.32751	Down
NM_001100592	ATP6V0E2	0.00396277	2.53638	Down
NM_006231	POLE	0.0043521	2.23394	Up
NM_001195218	DCXR	0.00436834	2.31456	Down



NM_016286	DCXR	0.0044085	2.31861	Down
NM_001271696	ABCB7	0.00440945	2.7362	Up
NM_004299	ABCB7	0.00441073	2.7358	Up
NM_174928	N6AMT2	0.00442505	13.292	Down
NM_001134415	TBCCD1	0.00454263	2.99604	Down
NM_138431	MFSD3	0.00457049	2.74936	Up
NM_018138	TBCCD1	0.00462213	2.98283	Down
NM_001144931	LOC391322	0.00464975	3.03933	Down
NM_001130859	PPIP5K1	0.00466149	2.29325	Up
NM_001242851	RNF146	0.00480221	2.71445	Up
NM_145326	ZNF493	0.00485534	7.11043	Down
NM_001037866	RGPD6	0.00494965	1.89954	Down
NM_032260	RGPD5	0.00494965	1.89954	Down
NM_001258	CDK3	0.00504156	11.2208	Down
NM_024594	PANK3	0.00530938	1.39072	Up
NM_001128214	KCTD6	0.00531617	2.64179	Down
NM_001197131	PPP1R12B	0.00533946	1.68048	Down
NM_001145672	SORBS2	0.00537173	1.95189	Up
NR_029701	MIR146A	0.00546303	9.57002	Up
NM_033343	LHX4	0.00547565	3.29556	Up
NM_005708	GPC6	0.00584506	2.03236	Down
NM_021217	ZNF77	0.00586863	9.09125	Down
NM_001146683	TMEM253	0.00591763	2.46675	Up
NM_001136109	CASP5	0.0060823	3.23435	Down
NR_033399	DDX12P	0.00609666	2.7806	Down
NM_014264	PLK4	0.00609748	3.50259	Down
NM_004347	CASP5	0.00614646	3.19557	Down
NM_001136112	CASP5	0.00614978	3.19378	Down
NR_015341	LRRC37BP1	0.00646203	2.35459	Down
NM_001190801	PLK4	0.00659981	4.12555	Down
NM_001114331	CLCN7	0.00660373	2.99449	Up
NM_001033050	MTERFD3	0.00665667	2.20711	Down
NM_001145073	USP27X	0.00667021	12.7654	Down
NM_001287	CLCN7	0.00672071	3.12589	Up
NR_027786	SERHL	0.00673115	2.86351	Down
NM_153812	PHF13	0.00678717	2.00558	Up

NR_003135	CEP170P1	0.00734926	2.13891	Up
NM_012276	LILRA4	0.00736992	5.87899	Down
NR_002222	ARGFXP2	0.00737225	3.11142	Up
NR_015353	LOC92249	0.00747305	2.53449	Up
NM_001242850	RNF146	0.00753448	2.68285	Up
NR_028330	C15orf37	0.00758658	2.18044	Down
NM_022078	GPATCH3	0.00759901	3.2445	Down
NM_025198	MTERFD3	0.00759963	2.15758	Down
NM_003440	ZNF140	0.00762146	3.07993	Up
NM_002481	PPP1R12B	0.00777174	1.84058	Down
NM_001242844	RNF146	0.00785005	2.61504	Up
NM_014037	SLC6A16	0.00793351	3.2534	Down
NM_001127670	KCNE1	0.0079339	1.64548	Up
NR_045102	RNF146	0.0080964	2.57515	Up
NM_001190799	PLK4	0.00809978	3.71103	Down
NM_001242845	RNF146	0.00831127	2.59982	Up
NR_046465	MEG3	0.00856136	2.37099	Up
NM_001242852	RNF146	0.0086168	2.62107	Up
NM_138353	DCAF15	0.00892753	2.37104	Down
NM_001184766	ODF2L	0.00895868	2.16625	Up
NM_032738	FCRLA	0.00899248	5.24679	Up
NM_001184866	FCRLA	0.00899559	5.24572	Up
NM_001184765	ODF2L	0.00902355	2.16522	Up
NM_030963	RNF146	0.00912692	2.58227	Up
NM_194279	ISCA2	0.00923271	1.91203	Down
NR_026722	SARNP	0.00930273	2.86162	Up
NM_020713	ZNF512B	0.00934355	1.51049	Down
NR_027382	RDH13	0.00953155	2.28287	Down
NR_038381	TSC22D1-AS1	0.00966185	2.12231	Down
NR_002746	SNORD47	0.00974039	2.9189	Down
NM_001256067	NOXA1	0.00994943	1.81243	Up
NR_038164	NSFL1C	0.00997664	2.1948	Up

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Supplemental Table 13: Differentially expressed transcripts ( $p \leq 0.01$ ) of STEMI cases compared to NSTEMI cases with EdgeR, correcting for batch, age, gender, and body mass index (BMI).

RefSeq ID	Transcript	p-value	Fold Change	Up/Down in STEMI
NM_004217	AURKB	0.000258745	-8.63222	Up
NM_001256834	AURKB	0.000265651	-8.60529	Up
NM_001145522	RAI14	0.000273142	-7.99413	Up
NM_001145523	RAI14	0.000291714	-7.87419	Up
NM_015577	RAI14	0.000303989	-7.86752	Up
NM_001145525	RAI14	0.000304039	-7.8675	Up
NM_001145521	RAI14	0.00030416	-7.86746	Up
NM_001145520	RAI14	0.000304296	-7.86742	Up
NM_001243432	ERG	0.000454806	-5.96683	Up
NM_017752	TBC1D8B	0.000590775	-3.67223	Up
NM_001725	BPI	0.000601125	-7.51393	Up
NM_004117	FKBP5	0.000694276	-1.22312	Up
NM_001145776	FKBP5	0.000694319	-1.22314	Up
NM_001145775	FKBP5	0.000696828	-1.22403	Up
NM_002875	RAD51	0.00080064	-5.65137	Up
NM_133487	RAD51	0.000816366	-5.66684	Up
NM_001164270	RAD51	0.000908018	-4.98943	Up
NM_001164269	RAD51	0.00101681	-5.54055	Up
NM_012160	FBXL4	0.00127392	-1.19725	Up
NM_203416	CD163	0.00132158	-1.87938	Up
NM_173636	WDR62	0.00135242	5.37939	Down
NM_001083961	WDR62	0.00135259	5.3794	Down
NM_004244	CD163	0.00142484	-1.86957	Up
NM_001128147	NF1	0.00234323	-2.05213	Up
NR_027051	THAP7-AS1	0.00251142	4.4435	Down
NM_002476	MYL4	0.00268304	8.71989	Down
NM_001002841	MYL4	0.00282648	8.79471	Down
NM_001134745	LRRTM4	0.00317153	6.34266	Down
NM_153321	PMP22	0.00322031	-5.58221	Up
NM_153322	PMP22	0.00345516	-5.51741	Up
NM_000304	PMP22	0.0034853	-5.51328	Up
NM_025165	ELL3	0.00414341	-3.27744	Up

NM_005809	PRDX2	0.0041565	-1.54987	Up
NM_019058	DDIT4	0.00457318	-1.37996	Up
NR_045862	ARMCX4	0.00469939	4.06405	Down
NM_021150	GRIP1	0.00479163	-3.22397	Up
NM_000441	SLC26A4	0.00525217	-6.22997	Up
NM_001178074	GRIP1	0.00530423	-3.2005	Up
NM_153367	ZCCHC24	0.00563344	-2.05342	Up
NM_080676	MACROD2	0.00605811	-7.37403	Up
NM_133443	GPT2	0.00631755	-6.15874	Up
NM_001142466	GPT2	0.00632925	-6.15566	Up
NM_174942	GAS2L3	0.00649871	-3.99996	Up
NM_144590	ANKRD22	0.00658536	-5.48371	Up
NM_001033087	MACROD2	0.00671053	-7.23178	Up
NR_024278	LOC646762	0.00673582	-3.16438	Up
NM_031439	SOX7	0.00703777	-7.2502	Up
NM_002099	GYPA	0.00709452	-5.90543	Up
NM_001099286	MTRF2	0.00717788	-6.3069	Up
NM_016608	ARMCX1	0.00750741	5.09213	Down
NM_138419	MTRF2	0.00775542	-6.17775	Up
NM_001184830	VSIG4	0.00781655	-3.58648	Up
NM_007268	VSIG4	0.00792187	-3.58249	Up
NM_005729	PPIF	0.0087726	-1.00646	Up
NM_001171174	CX3CR1	0.00888666	0.909068	Down
NM_001171171	CX3CR1	0.00901238	0.907279	Down
NM_001171172	CX3CR1	0.0090138	0.907273	Down
NR_033841	LOC200772	0.00913289	3.01578	Down
NM_001337	CX3CR1	0.00943372	0.905793	Down
NM_001184831	VSIG4	0.00971727	-3.46875	Up
NM_138639	BCL2L12	0.00973952	-4.39955	Up
NM_001040668	BCL2L12	0.00974173	-4.39957	Up
NM_147184	TP53I3	0.00979279	-2.9722	Up
NM_001257403	VSIG4	0.00979799	-3.5502	Up
NM_000851	GSTM5	0.00985795	-3.24171	Up
NM_001100431	VSIG4	0.00988212	-3.46363	Up

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Supplemental Table 14: Top KEGG pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using ANOVA.

Pathway Name	Obs/Ref	Transcript Names	P-value
Metabolic Pathways	32/1130	PCCB, COQ7, AGPAT4, GAMT, GALT, POLR1A, SMPD1, UGDH, ETNK1, ATP6V0A1, AGPAT3, HYI, DCT, ST3GAL6, POLR3A, BCAT2, FLAD1, LSS, POLE, ACADSB, ALAD, DCXR, POLR2E, PPCDC, PAFAH1B2, BPNT1, PCYT2, IDH3B, ZNRD1, PANK3, ATP6V0E2, ACSM3	$3.33 \times 10^{-5}$
RNA polymerase	4/29	ZNRD1, POLR1A, POLR3A, POLR2E	0.0055
Pyrimidine metabolism	6/99	AK3, POLE, ZNRD1, POLR1A, POLR3A, POLR2E	0.0096
Panthothenate and CoA biosynthesis	3/16	PANK3, PPCDC, BCAT2	0.0096
Valine, leucine, and isoleucine degradation	4/44	PCCB, ACADSB, OXCT1, BCAT2	0.0132
Glycerophospholipid metabolism	5/80	LCAT, AGPAT3, PCYT2, AGPAT4, ETNK1	0.0147
Cytokine-cytokine receptor interaction	8/265	XCL2, CXCR7, IL18RAP, HGF, TNFRSF25, PDGFB, TNFSF9, IL3RA	0.0597
Hepatitis C	5/134	PIAS3, PPP2R2B, NR1H3, LDLR, PPP2CB	0.0765
Glyoxylate and dicarboxylate metabolism	2/18	PCCB, HYI	0.0765
Amino sugar and nucleotide sugar metabolism	3/48	GALT, UGDH, RENBP	0.0765

Obs = number of genes in category that were differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases; Ref = number of total genes in pathway

Supplemental Table 15: Top Pathway Commons pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using ANOVA

Pathway Name	Obs/Ref	Transcript Names	P-value
Proteoglycan syndecan-mediated signaling events	30/1345	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, NUDT16L1, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
Arf6 signaling events	29/1288	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
Sphingosine 1-phosphate (S1P) pathway	30/1311	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, SMPD1, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
ErbB1 downstream signaling	29/1288	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
Transmembrane transport of small molecules	14/379	SLC9A9, RHAG, SLC4A5, SLC46A1, SLC7A5, SLC26A6, SLC16A3, ATP8B1, ATP6V0A1, SLC5A6, STEAP3, SLC35B2, ATP6V0E2	0.0008
Glypican pathway	30/1338	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, IGFBP4, PERP, MYB, TAGLN	0.0008
Signaling events mediated by focal adhesion kinase	29/1288	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
Arf6 trafficking events	29/1288	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
IL3-mediated signaling events	30/1295	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, IL3RA, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008
IGF1 pathway	29/1291	MMP9, SNIP1, TAOK2, RUNX2, NKX3-1, SNURF, PARD6A, TXLNG, RPS27L, JDP2, PPP2CB, YES1, PDGFB, ERC1, RHEB, EGR2, DDIT4, PIAS3, COPS5, NFYC, STEAP3, HGF, TAF12, PPP2R2B, GTF2H2, TAB1, PERP, MYB, TAGLN	0.0008

Obs = number of genes in category that were differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases; Ref = number of total genes in pathway

Supplemental Table 16: Top KEGG pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using EdgeR

Pathway Name	Obs/Ref	Transcript Names	P-value
Metabolic pathways	17/1130	GPT2, CYP19A1, ACSL1, NMNAT1, GAMT, UGDH, ATP6V0A1, ST6GALNAC3, PLCD3, CHKA, IDI1, ALAD, ALPL, DGK1, DGAT2, PCYT2, ALOX15B	0.0006
Progesterone-mediated oocyte maturation	3/86	ADCY3, BUB1, CDK1	0.0640
Glycerolipid metabolism	2/50	DGK1, DGAT2	0.0640
Oocyte meiosis	3/112	ADCY3, BUB1, CDK1	0.0640
Rheumatoid arthritis	3/91	ATP6V0A1, HLA-DQA1, FLT1	0.0640
mTOR signaling pathway	2/54	RHEB, DDIT4	0.0640
Cell adhesion molecules (CAMs)	3/133	HLA-DQA1, PVRL3, OCLN	0.0640
Glycerophospholipid metabolism	3/80	PCYT2, DGK1, CHKA	0.0640
Cell Cycle	3/124	BUB1, CDK1, ORC6	0.0640
Vibrio cholera infection	2/54	ATP6V0A1, ADCY3	0.0640



Supplemental Table 17: Top Pathway Commons pathways of differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases identified using EdgeR

Pathway Name	Obs/Ref	Transcript Names	P-value
Beta1 integrin cell surface interactions	16/1351	TAOK2, NF1, AKAP5, NR4A1, ADAM12, CDK1, TP53I3, TCF7L2, RHEB, GPLD1, CREM, FKBP5, TGM2, BAG1, OCLN	0.0084
CDC42 signaling events	11/757	TAOK2, NF1, AKAP5, NR4A1, NET1, FKBP5, CDK1, OCLN, TCF7L2, BAG1, CREM	0.0084
Transmission across chemical synapses	5/121	GRIP1, ADCY3, ALC6A12, SYT1, AKAP5	0.0084
Sphingosine 1-phosphate (S1P) pathway	15/1311	TAOK2, NF1, AKAP5, NR4A1, FLT1, FKBP5, CDK1, TP53I3, OCLN, TCF7L2, RHEB, BAG1, GPLD1, DDIT4, CREM	0.0084
Glypican 1 network	15/1299	TAOK2, NF1, AKAP5, NR4A1, FLT1, FKBP5, CDK1, TP53I3, OCLN, TCF7L2, RHEB, BAG1, GPLD1, DDIT4, CREM	0.0084
Cyclin A: Cdk2-associated events at S phase entry	4/90	PSMD10, PSMF1, CDK1, ORC6	0.0084
P73 transcription factor network	4/78	BUB1, RAD51, TP53I3, CDK1	0.0084
Integrin-linked kinase signaling	11/656	TAOK2, NF1, AKAP5, NR4A1, PPP1R14A, FKBP5, CDK1, OCLN, TCF7L2, BAG1, CREM	0.0084
Mitotic M-M/G1 phases	6/242	PSMD10, BUB1, AURKB, PSMF1, CDK1, ORC6	0.0084
VEGF and VEGFR signaling network	16/1304	TAOK2, MYOF, NF1, NR4A1, CDK1, TP53I3, TCF7L2, RHEB, GPLD1, DDIT4, CREM, FLT1, FKBP5, BAG1, OCLN	0.0084

Supplemental Table 18: Correlations of top differentially expressed transcripts from Supplemental Table 12 with platelet aggregation to collagen (10  $\mu$ g/mL) in washed platelets.

Transcript	Refseq ID	Up/Down in STEMI	Spearman Corr	Corr p-value	N
RDH13	NR_027382	Down	0.60	0.0089	18
SNORD47	NR_002746	Down	0.54	0.0114	21
SERHL	NR_027786	Down	0.59	0.0218	15
PHF13	NM_153812	Up	-0.46	0.0354	21
DDX12P	NR_033399	Down	0.49	0.0469	17
ABCB7	NM_001271696	Up	-0.36	0.0537	29
ABCB7	NM_004299	Up	-0.36	0.0537	29
ZNF77	NM_021217	Down	-0.53	0.0788	12
PZP	NM_002864	Down	0.44	0.0807	17
TSC22D1-AS1	NR_038381	Down	0.38	0.0815	22
KCNE1	NM_001127670	Up	0.58	0.0816	10

Supplemental Table 19: Correlations of top differentially expressed transcripts from Supplemental Table 12 with platelet aggregation to ADP (10  $\mu$ M) in platelet rich plasma.

Transcript	Refseq ID	Up/Down in STEMI	Spearman Corr	Corr p-value	N
NPR3	NM_001204376	Up	0.81	0.0079	9
LINC01278	NR_015353	Up	0.43	0.01867	29
USP27X	NM_001145073	Down	-0.55	0.05177	13
RHEB	NM_005614	Down	-0.34	0.06298	30
CASP5	NM_001136109	Down	-0.44	0.08663	16
CASP5	NM_004347	Down	-0.44	0.08663	16
CASP5	NM_001136112	Down	-0.44	0.08663	16
LHX4	NM_033343	Up	0.64	0.1194	7
PANK3	NM_024594	Up	0.28	0.1308	30
FCRLA	NM_032738	Up	0.30	0.1663	23

Supplement Table 20: Top correlated transcripts with platelet aggregation to TRAP (p&lt;0.01)

RefSeqID	Gene	Spearman Coeff	p-value	N
NM_001204078	ATP6V1G2	0.907182	4.63E-05	12
NR_027083	AFMID	-0.964286	0.000454149	7
NM_025261	LY6G6C	-0.733746	0.000528393	18
NM_001127670	KCNE1	0.890909	0.000542144	10
NM_001145248	FAM157A	0.664524	0.000542885	23
NR_046723	SGOL1-AS1	0.75791	0.000669784	16
NM_001128160	UBP1	-0.563854	0.000777111	32
NM_001144900	MIEF2	-0.878788	0.000813862	10
NM_031954	KCTD10	-0.555597	0.000962914	32
NM_014517	UBP1	-0.554679	0.00098579	32
NM_001128161	UBP1	-0.549909	0.0011126	32
NM_015662	IFT172	0.791209	0.00127502	13
NM_032118	WDR54	-0.650605	0.00140527	21
NM_001160418	ZBP1	-0.618542	0.00165435	23
NM_001127669	KCNE1	0.818182	0.00208314	11
NM_001270404	KCNE1	0.842424	0.00222003	10
NR_002605	DLEU1	0.544334	0.00226796	29
NM_022903	CCDC71	0.743675	0.00229591	14
NM_198141	GANC	-0.525838	0.00238061	31
NM_001160417	ZBP1	-0.599753	0.00248669	23
NM_030776	ZBP1	-0.599753	0.00248669	23
NM_001394	DUSP4	0.928571	0.00251947	7
NM_206914	METTL21B	0.574014	0.00269605	25
NM_001168485	ARMCX5	0.545056	0.00270544	28
NM_032294	CAMKK1	-0.695141	0.00279609	16
NM_172206	CAMKK1	-0.695141	0.00279609	16
NM_015433	METTL21B	0.569394	0.00297022	25
NM_001270405	KCNE1	0.8	0.00311043	11
NM_001127668	KCNE1	0.8	0.00311043	11
NM_006931	SLC2A3	0.506239	0.00311392	32
NM_145243	OMA1	-0.521265	0.00313888	30
NM_001168480	ARMCX5	0.534648	0.00337791	28
NM_001168479	ARMCX5	0.534648	0.00337791	28

NR_001587	AURKAPS1	0.682353	0.00358797	16
NM_148886	MIEF2	-0.85	0.00370478	9
NM_139162	MIEF2	-0.85	0.00370478	9
NM_080668	CDCA5	-0.740343	0.00380289	13
NM_014057	OGN	-0.880952	0.00385032	8
NM_139006	HFE	-0.546637	0.00385868	26
NM_000410	HFE	-0.545953	0.00391234	26
NR_046311	NEIL1	0.788157	0.00395619	11
NR_003228	AFG3L1P	0.714286	0.00410441	14
NR_002812	HCG26	0.598246	0.00417338	21
NM_001168482	ARMCX5	0.521227	0.00445217	28
NM_022838	ARMCX5	0.521227	0.00445217	28
NM_183373	PXDC1	0.581614	0.00452194	22
NM_031412	GABARAPL1	0.48789	0.00461613	32
NR_102760	TRIM52-AS1	-0.486606	0.00474134	32
NM_001190182	CCDC17	0.942857	0.00480466	6
NM_001114938	CCDC17	0.942857	0.00480466	6
NR_046734	PRRT3-AS1	0.942857	0.00480466	6
NM_001099777	C3orf55	0.974679	0.00481823	5
NM_001243729	C3orf55	0.974679	0.00481823	5
NM_005386	NNAT	-0.974679	0.00481823	5
NM_003733	OASL	0.55558	0.00482407	24
NM_001271022	ATRIP	0.565142	0.00495425	23
NM_020745	AARS2	-0.62984	0.00508942	18
NM_032534	KRBA1	-0.774489	0.00513118	11
NR_027286	FLVCR1-AS1	-0.833333	0.00526569	9
NR_102761	TRIM52-AS1	-0.480367	0.00539186	32
NM_001113536	FOLR2	0.675	0.0057635	15
NM_001113535	FOLR2	0.675	0.0057635	15
NM_001113534	FOLR2	0.675	0.0057635	15
NM_001165994	GDPD1	-0.828459	0.00579537	9
NM_032166	ATRIP	0.555254	0.00595311	23
NM_001144940	VMO1	-0.620868	0.00596504	18
NM_021196	SLC4A5	0.765378	0.00604554	11
NM_000803	FOLR2	0.671429	0.00612777	15
NM_001142555	ADCK4	0.588856	0.00630144	20

NR_003022	SNORA59B	-0.857143	0.00653002	8
NR_003025	SNORA59A	-0.857143	0.00653002	8
NM_032088	PCDHGA8	0.760822	0.00654508	11
NR_102759	TRIM52-AS1	-0.469725	0.00667826	32
NM_020980	AQP9	0.476537	0.00672428	31
NM_015680	CNPPD1	-0.476335	0.00675088	31
NM_001159995	NRG1	0.547973	0.00679138	23
NM_002060	GJA4	0.892857	0.00680719	7
NM_002178	IGFBP6	-0.892857	0.00680719	7
NM_024876	ADCK4	0.584338	0.00681819	20
NR_002208	MRPL42P5	-0.816667	0.00722479	9
NM_001184904	CARD8	-0.465688	0.00723038	32
NM_017670	OTUB1	-0.472096	0.00733052	31
NR_003089	OTUB1	-0.472096	0.00733052	31
NM_012415	RAD54B	-0.727273	0.00735503	12
NM_139003	HFE	-0.520986	0.00757655	25
NM_003532	HIST1H3E	0.622086	0.00766515	17
NM_181689	NNAT	-0.927634	0.00766584	6
NM_001190977	YAF2	0.477114	0.00767736	30
NM_001160001	NRG1	0.53907	0.00794743	23
NM_181313	TAZ	-0.482742	0.00799245	29
NM_181311	TAZ	-0.481263	0.00821549	29
NR_027072	LINC00189	0.653571	0.00823037	15
NM_024821	CCDC134	0.617647	0.00824233	17
NM_181312	TAZ	-0.481016	0.00825317	29
NM_001261825	OASL	0.547047	0.00841897	22
NM_001270403	KCNE1	0.745455	0.00845473	11
NR_024048	TAZ	-0.479044	0.00855987	29
NR_004859	SCAND2P	0.545763	0.00860506	22
NM_139004	HFE	-0.513285	0.00868764	25
NM_022044	SDF2L1	-0.597832	0.00878342	18
NM_080829	FAM65C	-0.502824	0.00884176	26
NM_020675	SPC25	-0.711034	0.00952876	12
NM_001040078	LGALS9C	-0.457968	0.00957745	31
NM_000116	TAZ	-0.472633	0.0096238	29
NM_002854	PVALB	0.464982	0.00962563	30

NM_033014	OGN	-0.8	0.00962792	9
NM_001167935	CCM2	0.480416	0.00966588	28
NM_130384	ATRIP	0.527071	0.00975953	23
NM_001722	POLR3D	0.562829	0.00977701	20

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Supplement Table 21: Top correlated transcripts with platelet aggregation to Collagen (p&lt;0.01)

RefSeqID	Gene	Spearman Coeff	p-value	N
NM_001184813	CEACAM1	-0.779985	0.000365569	16
NM_001184815	CEACAM1	-0.772627	0.000450582	16
NM_001184816	CEACAM1	-0.771155	0.000469399	16
NM_000696	ALDH9A1	-0.581988	0.0004756	32
NM_148672	CCL28	-0.817057	0.000650041	13
NR_038278	LINC00665	-0.878788	0.000813862	10
NR_001566	TERC	-0.807692	0.00083916	13
NR_027489	MTHFSD	-0.685972	0.000840285	20
NM_001177479	HDX	-0.851938	0.000870365	11
NM_144657	HDX	-0.851938	0.000870365	11
NM_173551	ANKS6	-0.869305	0.00108699	10
NM_001102371	FOXRED2	-0.698709	0.00125608	18
NM_024955	FOXRED2	-0.698709	0.00125608	18
NM_001159380	MTHFSD	-0.665664	0.00135755	20
NM_001159379	MTHFSD	-0.665664	0.00135755	20
NM_001159378	MTHFSD	-0.665664	0.00135755	20
NM_001159377	MTHFSD	-0.665664	0.00135755	20
NR_027490	MTHFSD	-0.665664	0.00135755	20
NM_022764	MTHFSD	-0.665664	0.00135755	20
NM_000290	PGAM2	-0.587873	0.00199899	25
NM_006563	KLF1	-0.904762	0.00200828	8
NM_002827	PTPN1	-0.531168	0.0021078	31
NR_027402	FAM223B	-0.765843	0.00227236	13
NR_027401	FAM223A	-0.765843	0.00227236	13
NM_024648	OGFOD3	-0.686695	0.00232872	17
NM_152496	MANEAL	0.928571	0.00251947	7
NM_001199978	PLSCR2	-0.68179	0.0025747	17
NM_030906	STK33	-0.832831	0.00277789	10
NM_000098	CPT2	-0.571099	0.0028664	25
NM_001145248	FAM157A	0.589516	0.00307332	23
NM_021818	SAV1	0.50564	0.00315529	32
NM_182541	TMEM31	0.796357	0.00335464	11
NM_001205344	CEACAM1	-0.668302	0.00336244	17



NM_001024912	CEACAM1	-0.668302	0.00336244	17
NM_001145636	C1orf228	-0.609091	0.00338229	21
NM_018092	NETO2	-0.590396	0.00381951	22
NM_006418	OLFM4	-0.880952	0.00385032	8
NM_080759	DACH1	-0.527584	0.00391178	28
NM_203344	SERTAD3	-0.575241	0.00408293	23
NM_001712	CEACAM1	-0.656039	0.0042389	17
NM_004219	PTTG1	-0.639463	0.00426956	18
NM_016073	HDGFRP3	-0.523145	0.00428286	28
NM_030935	TSC22D4	0.49773	0.00438367	31
NM_052945	TNFRSF13C	-0.755245	0.00450844	12
NR_002571	SNORD58A	0.730769	0.00454773	13
NM_032138	KBTBD7	-0.606243	0.0046031	20
NM_016529	ATP8A2	0.942857	0.00480466	6
NR_036487	FGF14-AS2	-0.942857	0.00480466	6
NM_001198940	DTNA	-0.942857	0.00480466	6
NM_001198939	DTNA	-0.942857	0.00480466	6
NR_030784	MIR155	0.942857	0.00480466	6
NR_031706	MIR1306	-0.942857	0.00480466	6
NM_018649	H2AFY2	-0.704071	0.004944	14
NM_005304	FFAR3	-0.833333	0.00526569	9
NM_014762	DHCR24	-0.582657	0.00557542	21
NM_003836	DLK1	0.639706	0.00568479	17
NR_073107	ITGA2	0.476295	0.00585646	32
NM_016044	FAHD2A	-0.566743	0.00595622	22
NM_001171930	CDH23	-0.63681	0.00597828	17
NM_031940	TM2D2	0.474645	0.00605432	32
NM_004336	BUB1	-0.533205	0.00605833	25
NM_014673	EMC2	-0.488869	0.00611891	30
NM_138442	CCDC124	-0.601141	0.00648323	19
NM_001278324	TROAP	0.857143	0.00653002	8
NM_001242534	MFSD11	-0.48553	0.00653145	30
NM_172232	ABCA5	0.734266	0.00654349	12
NM_001145000	ITGAV	-0.508708	0.00673584	27
NM_146421	GSTM1	-0.483473	0.00679721	30
NM_001007544	C1orf186	0.892857	0.00680719	7

NM_001013619	HYKK	0.892857	0.00680719	7
NM_194436	LDHD	-0.892857	0.00680719	7
NM_153486	LDHD	-0.892857	0.00680719	7
NM_138393	REEP6	0.892857	0.00680719	7
NM_002203	ITGA2	0.468226	0.00687898	32
NR_073106	ITGA2	0.468226	0.00687898	32
NR_073105	ITGA2	0.468226	0.00687898	32
NM_001242533	MFSD11	-0.498494	0.00693549	28
NM_001242532	MFSD11	-0.498494	0.00693549	28
NM_001144999	ITGAV	-0.506875	0.0069705	27
NM_032957	RTEL1	-0.627451	0.00701135	17
NR_073103	ITGA2	0.466758	0.00708036	32
NM_032890	DISP1	0.728548	0.00720175	12
NR_038883	LINC00649	-0.578631	0.00752009	20
NM_003863	DPM2	-0.463457	0.00755189	32
NM_000454	SOD1	-0.46309	0.00760589	32
NM_002210	ITGAV	-0.501986	0.00763014	27
NM_080661	GLYATL1	0.477293	0.00765126	30
NM_001002901	FCRLB	-0.927634	0.00766584	6
NM_001164496	WDR52	0.564186	0.00771955	21
NM_001220494	GLYATL1	0.475957	0.00784735	30
NM_001177478	HDX	-0.811723	0.0078893	9
NM_001012755	SLC25A53	-0.655943	0.00792251	15
NM_001220496	GLYATL1	0.47529	0.00794697	30
NR_073104	ITGA2	0.460523	0.00799318	32
NM_005886	KATNB1	-0.496946	0.00836444	27
NM_024311	MFSD11	-0.484799	0.00893276	28
NR_027382	RDH13	0.596692	0.00894665	18
NM_007189	ABCF2	-0.468663	0.00899477	30
NM_001161476	WDR25	-0.581467	0.00902	19
NM_001242535	MFSD11	-0.483703	0.00911151	28
NM_005733	KIF20A	-0.769697	0.00922195	10
NM_001136203	CCDC124	-0.580079	0.00922566	19
NM_025010	KLHL18	-0.509819	0.00923017	25
NM_018025	GPATCH1	-0.519373	0.00929728	24
NM_013987	PARK2	-0.838338	0.00932312	8

NM_004562	PARK2	-0.838338	0.00932312	8
NM_152753	SCUBE3	-0.838338	0.00932312	8
NR_024271	SEPT7P2	-0.466607	0.00934261	30
NM_024515	WDR25	-0.576197	0.00982093	19
NR_048575	GLUD1P3	0.641645	0.00992355	15

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Supplement Table 22: Top correlated transcripts with platelet aggregation to ADP (p&lt;0.01)

RefSeqID	Gene	Spearman Coeff	p-value	N
NM_001024939	SLC2A11	0.70908	0.000104843	24
NM_030807	SLC2A11	0.665002	0.000287068	25
NM_001191015	GSTO2	-0.985611	0.000309086	6
NM_001024938	SLC2A11	0.654556	0.000385247	25
NM_001039888	ANKRD34A	0.963624	0.000475304	7
NM_152470	RNF165	-0.963624	0.000475304	7
NM_001256758	RNF165	-0.963624	0.000475304	7
NM_032139	ANKRD27	0.58058	0.000616694	31
NM_031491	RBP5	0.954994	0.000805535	7
NM_152361	EID2B	-0.87395	0.000946026	10
NM_138929	DIABLO	0.56738	0.00107628	30
NM_001278342	DIABLO	0.56738	0.00107628	30
NM_001001660	LYRM5	-0.547235	0.00118976	32
NR_103725	RCHY1	-0.543736	0.00129776	32
NM_172341	PSENN	-0.862422	0.00132317	10
NM_001009922	RCHY1	-0.542079	0.00135185	32
NM_145062	ZUFSP	0.651445	0.0013787	21
NM_052998	ADC	0.915729	0.00140317	8
NM_001278537	RCHY1	-0.538949	0.00145941	32
NR_103724	RCHY1	-0.538028	0.00149243	32
NM_001278303	DIABLO	0.547492	0.00173989	30
NM_198881	TBC1D8B	0.753068	0.00187653	14
NM_001278539	RCHY1	-0.524034	0.00208112	32
NR_037914	RCHY1	-0.524034	0.00208112	32
NM_021572	ENPP5	0.709017	0.00210307	16
NM_001008925	RCHY1	-0.523114	0.0021261	32
NM_015436	RCHY1	-0.523114	0.0021261	32
NR_103723	RCHY1	-0.523114	0.0021261	32
NR_037913	RCHY1	-0.523114	0.0021261	32
NM_001278538	RCHY1	-0.522561	0.00215349	32
NM_000614	CNTF	0.721734	0.00238377	15
NM_001271147	ST3GAL6	-0.522803	0.00254922	31
NM_019887	DIABLO	0.530061	0.00258878	30

NM_024671	ZNF768	0.649555	0.00261355	19
NM_173631	ZNF547	-0.716995	0.00262677	15
NR_074080	MAZ	0.513171	0.00266838	32
NM_004854	CHST10	0.679877	0.00267623	17
NM_138794	LYPLAL1	-0.512618	0.00270174	32
NM_001278536	RCHY1	-0.511882	0.00274677	32
NM_018708	FEM1A	0.55321	0.00276208	27
NM_012301	MAGI2	-0.695723	0.0027637	16
NM_017439	GSAP	-0.510225	0.00285049	32
NM_001276276	MAZ	0.51004	0.00286222	32
NM_001278302	DIABLO	0.524921	0.00289908	30
NR_024601	DIABLO	0.524921	0.00289908	30
NM_001042539	MAZ	0.508751	0.00294551	32
NM_001080511	CLEC2L	0.532119	0.00296687	29
NM_018984	SSH1	0.507831	0.00300628	32
NM_018365	MNS1	0.724871	0.00335679	14
NM_138930	DIABLO	0.517994	0.00336768	30
NR_024600	DIABLO	0.517994	0.00336768	30
NR_036211	MIR4257	0.886243	0.00337334	8
NM_001160030	FLT1	0.852389	0.00351094	9
NR_027508	FAM133CP	0.683444	0.00351408	16
NM_003441	ZNF141	0.560671	0.00355285	25
NR_003655	POLR2J4	0.522584	0.00363419	29
NM_019105	TNXB	-0.698394	0.00377908	15
NR_047558	ZNF32-AS2	-0.678501	0.00385892	16
NM_003878	GGH	0.629081	0.00390754	19
NR_003602	LOC541473	0.785396	0.00417558	11
NM_002383	MAZ	0.491996	0.00423474	32
NR_024497	LINC00999	-0.842744	0.00433838	9
NM_001143682	CALCOCO1	0.48997	0.00441937	32
NM_001258448	PKD2L2	0.52098	0.00447437	28
NM_025163	PIGZ	0.731327	0.00450146	13
NR_026554	CALCOCO1	0.488865	0.00452296	32
NM_014386	PKD2L2	0.51988	0.0045745	28
NM_080631	VPS41	-0.488313	0.00457553	32
NM_001109903	RNFT2	-0.708304	0.0045812	14

NM_018688	BIN3	0.568173	0.00467784	23
NR_036573	LOC155060	-0.778876	0.00472932	11
NM_018184	ARL8B	-0.485919	0.00480945	32
NM_001161342	TMEM171	-0.974679	0.00481823	5
NM_173490	TMEM171	-0.974679	0.00481823	5
NM_031461	CRISPLD1	0.974679	0.00481823	5
NM_000260	MYO7A	0.974679	0.00481823	5
NM_001127180	MYO7A	0.974679	0.00481823	5
NR_073496	ESR2	-0.974679	0.00481823	5
NR_073505	ESR2	-0.974679	0.00481823	5
NM_001271142	ST3GAL6	-0.492813	0.00485276	31
NM_001276275	MAZ	0.484262	0.00497735	32
NM_178427	ARNT	0.48371	0.00503442	32
NM_001197325	ARNT	0.48371	0.00503442	32
NM_181809	BMP8A	-0.83551	0.00504022	9
NM_002483	CEACAM6	0.941124	0.00509754	6
NM_001017981	RNF215	0.834231	0.00517185	9
NM_001130483	VRK2	-0.4815	0.00526834	32
NR_002604	SNORD10	0.625587	0.00549046	18
NM_020898	CALCOCO1	0.478554	0.00559468	32
NR_026873	LINC00174	-0.696806	0.00561861	14
NR_036498	LOC388906	-0.900937	0.00562059	7
NM_001836	CMA1	0.718243	0.00568656	13
NR_036441	VRK2	-0.477265	0.00574281	32
NM_014234	HSD17B8	-0.67513	0.00575059	15
NM_001260	CDK8	-0.476345	0.00585065	32
NM_022817	PER2	0.567544	0.00587033	22
NM_017681	NUP62CL	-0.862291	0.00587299	8
NM_001668	ARNT	0.475792	0.00591618	32
NM_001128302	LYRM1	-0.490508	0.00592473	30
NR_046163	MIRLET7DHG	-0.715706	0.00594165	13
NM_006296	VRK2	-0.473583	0.00618463	32
NM_001130480	VRK2	-0.473583	0.00618463	32
NM_017850	C1orf109	0.634191	0.00625415	17
NM_017673	SWT1	-0.471189	0.00648712	32
NM_031910	C1QTNF6	0.790277	0.00651422	10

NM_001277325	NPIPA5	0.517471	0.00678157	26
NM_198488	FAM83H	0.820091	0.00678753	9
NM_003356	UCP3	0.787786	0.00680728	10
NM_017503	SURF2	0.584286	0.00682429	20
NM_024043	DBNDD1	0.757999	0.00686945	11
NM_001271146	ST3GAL6	-0.475386	0.00687714	31
NM_020424	LYRM1	-0.482016	0.00699085	30
NM_001071775	MZT1	-0.498013	0.00699852	28
NM_001105518	SWT1	-0.467322	0.0070024	32
NM_152312	GYLTL1B	0.785936	0.00703074	10
NM_001130482	VRK2	-0.466954	0.00705325	32
NM_024658	IPO4	0.569293	0.0070684	21
NR_051979	IPO4	0.569293	0.0070684	21
NM_144612	LOXHD1	0.505445	0.00715825	27
NM_022117	TSPYL2	0.480606	0.00718275	30
NM_001278393	USP44	-0.704009	0.00723344	13
NM_013305	ST8SIA5	0.680673	0.00737329	14
NM_032788	ZNF514	0.554715	0.00737592	22
NM_001271145	ST3GAL6	-0.471333	0.00743924	31
NM_021270	LAIR2	0.554213	0.0074408	22
NM_006100	ST3GAL6	-0.471131	0.00746834	31
NM_001130481	VRK2	-0.463271	0.00757921	32
NM_138281	DLX4	-0.927634	0.00766584	6
NM_152720	NEK3	0.519494	0.00778205	25
NM_002498	NEK3	0.519494	0.00778205	25
NR_027415	NEK3	0.519494	0.00778205	25
NM_001184938	EPB41L5	0.723132	0.00786978	12
NM_002288	LAIR2	0.55023	0.00797223	22
NM_001029998	SLC10A7	-0.474951	0.0079978	30
NM_012227	GTPBP6	0.499012	0.00805652	27
NM_018487	TMEM176A	0.549373	0.00809053	22
NM_020357	PCNP	-0.4583	0.00834188	32
NM_001214902	ESR2	-0.775476	0.00839373	10
NM_001191014	GSTO2	-0.882919	0.00845034	7
NM_002606	PDE9A	0.843435	0.00850323	8
NM_001001583	PDE9A	0.843435	0.00850323	8

NM_001001582	PDE9A	0.843435	0.00850323	8
NM_001001581	PDE9A	0.843435	0.00850323	8
NR_049781	VRK2	-0.456827	0.00857999	32
NM_003618	MAP4K3	-0.478155	0.00870122	29
NM_007279	U2AF2	0.47003	0.00876964	30
NM_001012478	U2AF2	0.47003	0.00876964	30
NM_001129889	DCT	0.743151	0.00877259	11
NM_001922	DCT	0.743151	0.00877259	11
NM_001146099	NEK3	0.512547	0.00880095	25
NM_001278304	DIABLO	0.469725	0.00881936	30
NR_024486	LOC100130093	-0.715794	0.00884773	12
NM_001277145	ZBTB10	0.502246	0.0089328	26
NR_038236	LINC00968	0.687004	0.00948153	13
NM_032840	SPRYD3	-0.516843	0.00970842	24
NM_001099403	PRDM8	-0.591407	0.00973575	18
NR_046165	MIRLET7DHG	-0.685192	0.00974921	13
NM_002569	FURIN	0.448725	0.00999511	32

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Supplement Table 23: Top correlated transcripts with platelet aggregation to ADP in platelet-rich plasma (p&lt;0.01)

RefSeqID	Gene	Spearman Coeff	p-value	N
NM_004060	CCNG1	-0.631649	0.000181444	30
NM_199246	CCNG1	-0.630091	0.000190337	30
NM_001080449	DNA2	0.666553	0.000200756	26
NR_102264	DNA2	0.660739	0.000238669	26
NM_024840	ZNF613	-0.840224	0.000323614	13
NM_173517	VKORC1L1	-0.61095	0.000335707	30
NM_001031721	ZNF613	-0.826449	0.000495889	13
NM_030809	CSRNP2	0.630859	0.000549735	26
NR_045072	CSRNP2	0.630859	0.000549735	26
NM_001270519	LATS1	0.590919	0.00058544	30
NM_002608	PDGFB	-0.616963	0.000787564	26
NM_001171931	CDH23	0.765654	0.000876758	15
NM_005688	ABCC5	0.629541	0.000980063	24
NM_138690	GRIN3B	0.779736	0.00100657	14
NR_003046	SNORD59B	0.75782	0.00106356	15
NM_018269	ADI1	-0.564211	0.00116423	30
NM_024705	DHRS12	-0.668924	0.00125995	20
NM_002107	H3F3A	-0.557089	0.00138508	30
NR_002315	H3F3AP4	-0.557089	0.00138508	30
NM_001664	RHOA	-0.549967	0.00164157	30
NR_072981	LINC00957	0.686629	0.00164804	18
NR_072982	LINC00957	0.686629	0.00164804	18
NM_001193331	C9orf3	-0.778543	0.00171706	13
NR_038387	LINC00886	-0.824604	0.00178946	11
NR_036211	MIR4257	0.936975	0.00185103	7
NM_001991	EZH1	0.55175	0.00191714	29
NM_014709	USP34	0.541064	0.00201945	30
NM_012445	SPON2	0.608158	0.00207869	23
NM_016215	EGFL7	-0.565974	0.0020901	27
NM_001199021	SPON2	0.605192	0.00221566	23
NM_001128325	SPON2	0.605192	0.00221566	23
NM_198450	APOOL	0.533274	0.00240975	30
NM_032830	CIRH1A	0.531939	0.00248282	30

NM_017752	TBC1D8B	0.739274	0.00251628	14
NM_001193530	CCT6B	-0.928571	0.00251947	7
NR_026978	HAUS1	0.53795	0.00261305	29
NM_138443	HAUS1	0.53795	0.00261305	29
NM_031940	TM2D2	-0.528155	0.00270034	30
NM_001037533	GON4L	0.526152	0.00282202	30
NM_018019	MED9	0.617686	0.00284802	21
NM_017922	PRPF39	0.58094	0.00291257	24
NM_021241	WIZ	0.577459	0.00312891	24
NM_213654	ARMC8	-0.51992	0.00323129	30
NR_027992	NBEAP1	-0.748281	0.00326001	13
NR_033413	SLC29A3	0.554225	0.00330453	26
NM_014877	HELZ	0.516804	0.00345441	30
NM_018344	SLC29A3	0.550804	0.00354535	26
NM_001079691	N4BP2L1	-0.515023	0.00358775	30
NM_018079	SRBD1	0.522918	0.0036088	29
NM_001077474	NR1I3	0.85	0.00370478	9
NM_001142854	SPATC1L	0.880952	0.00385032	8
NM_001174098	SLC29A3	0.546357	0.00388061	26
NR_002604	SNORD10	0.660123	0.00392858	17
NM_001080415	U2SURP	0.508569	0.00410886	30
NM_015542	UPF2	0.507456	0.00420497	30
NM_080599	UPF2	0.507456	0.00420497	30
NM_032292	GON4L	0.506566	0.00428324	30
NM_138798	MITD1	0.551087	0.00430187	25
NM_033016	PDGFB	-0.530463	0.00442179	27
NM_152549	CCDC112	0.607747	0.00447598	20
NR_036641	PDGFC	-0.503005	0.0046089	30
NM_016205	PDGFC	-0.501002	0.00480122	30
NM_003327	TNFRSF4	0.942857	0.00480466	6
NM_001163561	C2orf61	-0.942857	0.00480466	6
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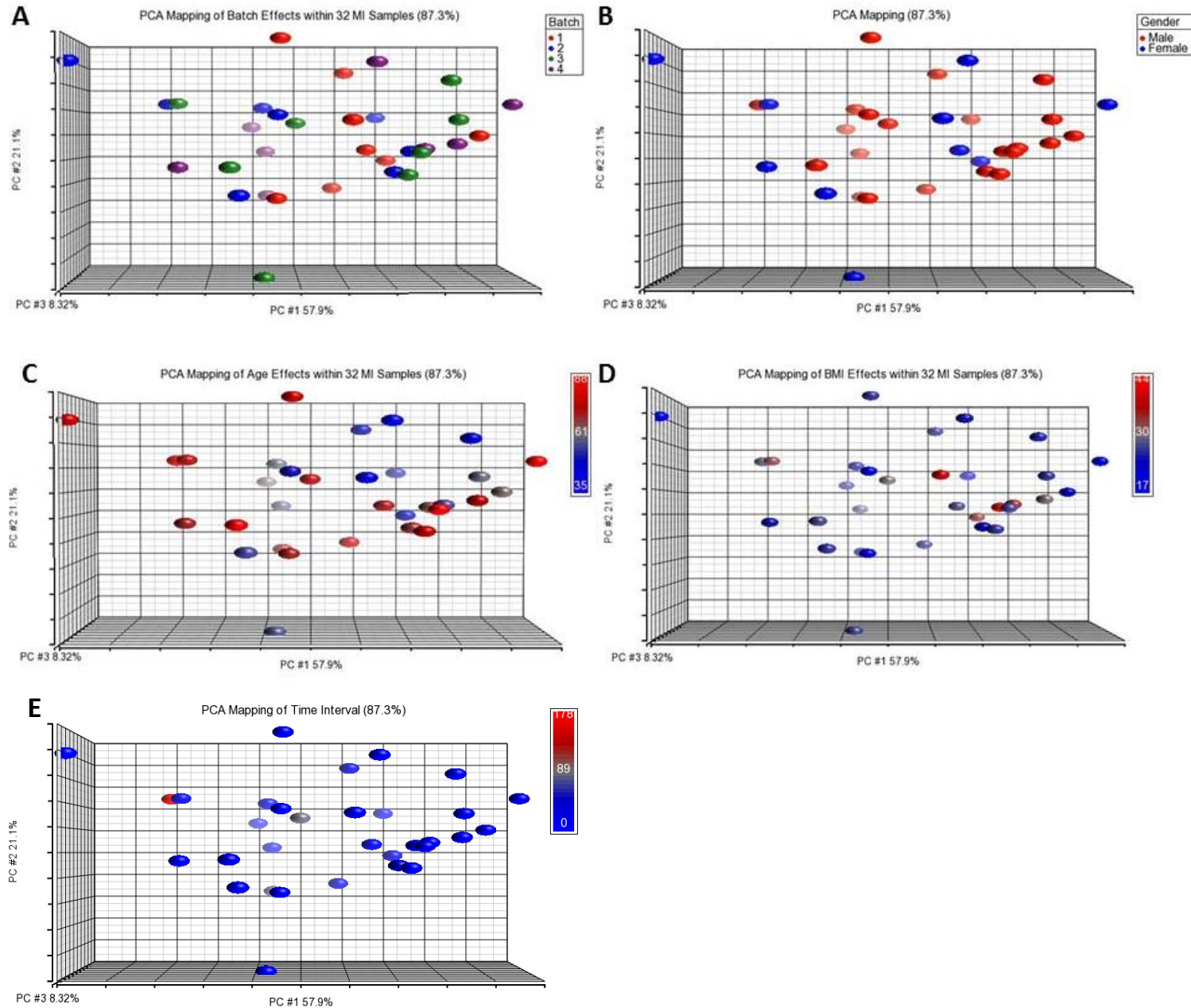
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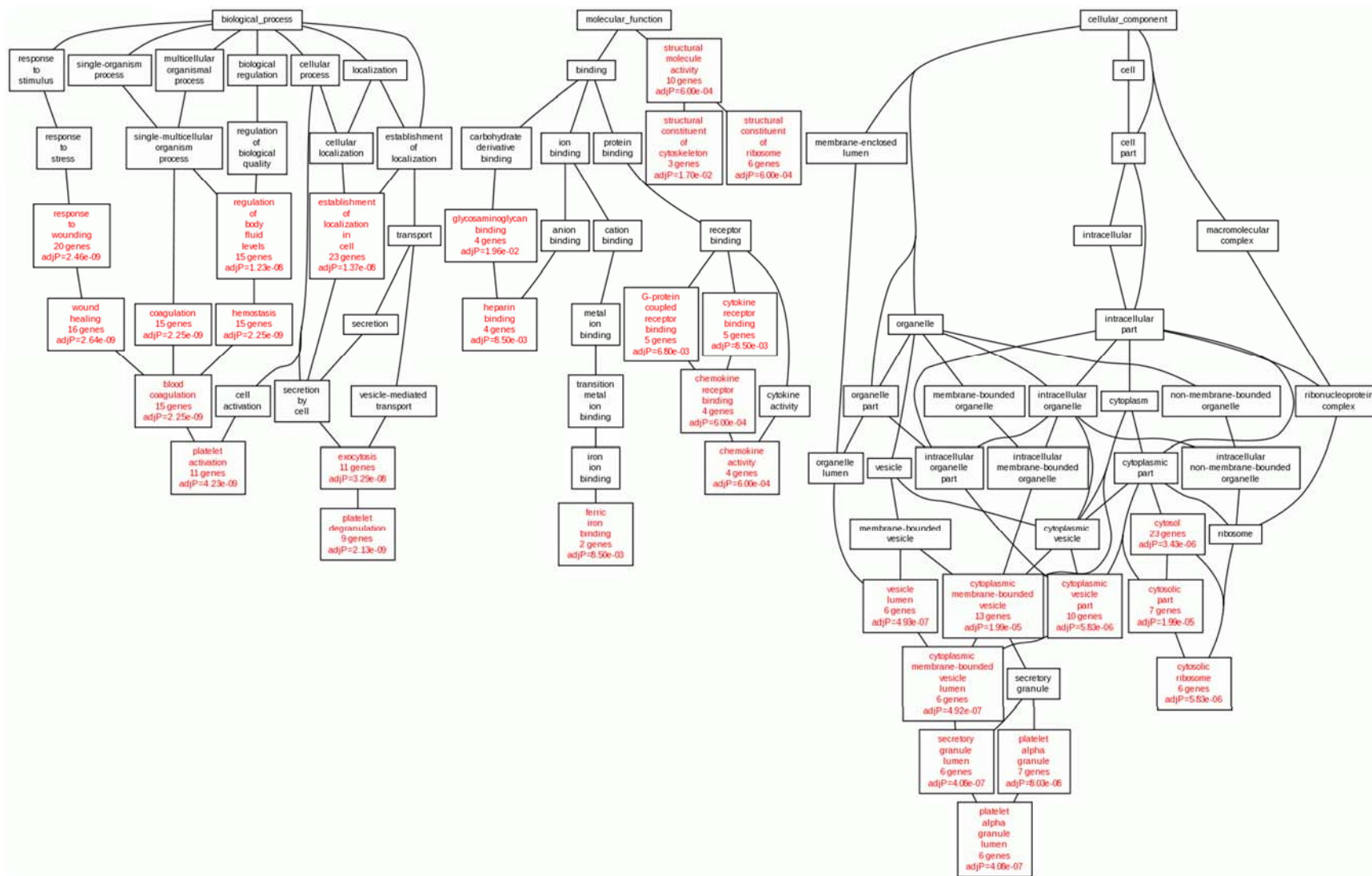
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Supplemental Figure 1: Principal component analysis (PCA) of transcripts from RNA-seq (with RPKM $\geq$ 0.3) of 32 MI platelets samples grouped by (A) batch, (B) Gender, (C) Age, (D) Body Mass Index (BMI), and (E) Time Interval from Event.



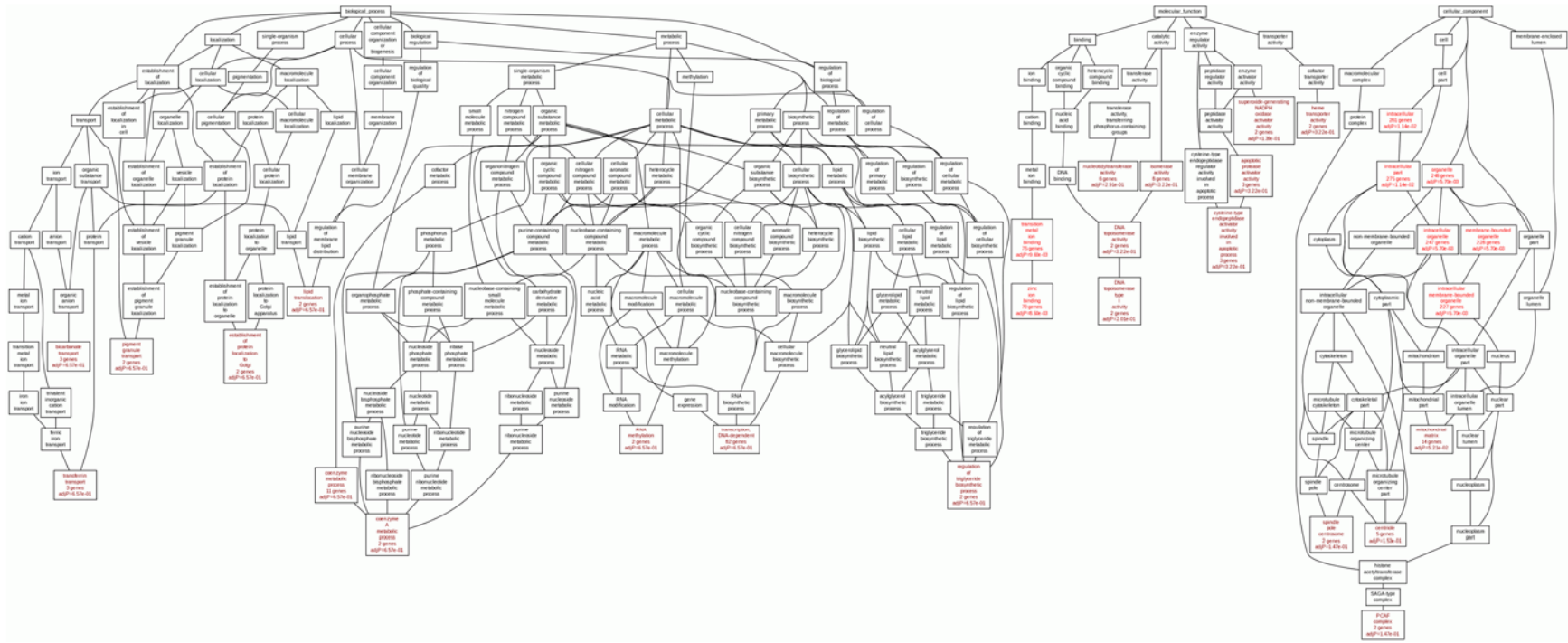
Supplemental Figure 2: Top Gene Ontology (GO) pathways for all MI Cases (n=32) with logRPKM  $\geq$  3.0.







Supplemental Figure 4: Top Gene Ontology (GO) pathways for differentially expressed transcripts ( $p \leq 0.05$ ) between STEMI and NSTEMI cases (ANOVA).





Supplemental Figure 6: Principal component analysis (PCA) grouped by STEMI (n=16) and NSTEMI (n=16) case status

