**Title:** The proteomic response is linked to regional lung volumes in ventilator-induced lung injury

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**Supplementary Table 1A: Proteins identified from Acid/FB vs Saline/FB.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | T Test | | Two Way RM ANOVA\* | | |
| Protein ID | Gene name | Difference# | *p* | FDR, *q* | Treatment | Region | Interaction |
| P54823 | *Ddx6* | 0.368 | 0.000 | 0.000 | 0.010 | 0.487 | 0.345 |
| Q501J6 | *Ddx17* | 0.314 | 0.000 | 0.000 | 0.010 | 0.056 | 0.782 |
| P01869 | *Ighg1* | -0.687 | 0.000 | 0.000 | 0.012 | 0.325 | 0.519 |
| P21981 | *Tgm2* | -0.222 | 0.000 | 0.000 | 0.015 | 0.000 | 0.597 |
| Q3TJI8 | *Hsd11b1* | -0.338 | 0.000 | 0.000 | 0.018 | 0.000 | 0.615 |
| Q8CFQ9 | *Fus* | 0.519 | 0.000 | 0.000 | 0.018 | 0.051 | 0.154 |
| Q61792 | *Lasp1* | 0.228 | 0.000 | 0.000 | 0.025 | 0.156 | 0.079 |
| Q61990 | *Pcbp2* | 0.228 | 0.000 | 0.000 | 0.000 | 0.673 | 0.082 |
| Q9D1J3 | *Sarnp* | 0.459 | 0.000 | 0.000 | 0.000 | 0.839 | 0.293 |
| Q9ESB3 | *Hrg* | -0.406 | 0.000 | 0.000 | 0.000 | 0.541 | 0.643 |
| P62751 | *Rpl23a* | -0.293 | 0.000 | 0.001 | 0.064 | 0.000 | 0.180 |
| Q7TQD2 | *Tppp* | 0.487 | 0.000 | 0.003 | 0.007 | 0.272 | 0.226 |
| P97315 | *Csrp1* | 0.321 | 0.000 | 0.003 | 0.067 | 0.421 | 0.051 |
| Q9CQR2 | *Rps21* | 0.707 | 0.000 | 0.003 | 0.007 | 0.071 | 0.689 |
| Q9JM96 | *Cdc42ep4* | 0.287 | 0.000 | 0.004 | 0.038 | 0.069 | 0.945 |
| Q9QXS1 | *Plec* | -0.461 | 0.000 | 0.004 | 0.004 | 0.000 | 0.403 |
| P01872 | *Ighm* | -0.312 | 0.000 | 0.004 | 0.112 | 0.000 | 0.626 |
| Q9CX86 | *Hnrnpa0* | 0.374 | 0.000 | 0.005 | 0.002 | 0.367 | 0.354 |
| P97352 | *S100a13* | 0.357 | 0.000 | 0.005 | 0.026 | 0.702 | 0.540 |
| J3QP71 | *Bsg* | -0.372 | 0.000 | 0.005 | 0.003 | 0.000 | 0.286 |
| Q9EQI5 | *Ppbp* | 0.555 | 0.000 | 0.005 | 0.055 | 0.120 | 0.099 |
| Q08093 | *Cnn2* | 0.445 | 0.000 | 0.006 | 0.005 | 0.103 | 0.504 |
| P04224 | *H2-Ea-ps* | 0.395 | 0.000 | 0.006 | 0.077 | 0.010 | 0.300 |
| Q8BI29 | *AA986860* | 0.296 | 0.000 | 0.008 | 0.059 | 0.138 | 0.827 |
| P27005 | *S100a8* | 0.369 | 0.000 | 0.010 | 0.111 | 0.068 | 0.123 |
| P04441 | *Cd74* | 0.564 | 0.000 | 0.012 | 0.100 | 0.799 | 0.566 |
| Q8VCI5 | *Pex19* | 0.381 | 0.000 | 0.013 | 0.005 | 0.478 | 0.587 |
| Q9CQF3 | *Nudt21* | 0.302 | 0.000 | 0.013 | 0.019 | 0.219 | 0.337 |
| A0A075B5P5 | *Ighg3* | -0.624 | 0.001 | 0.016 | 0.225 | 0.233 | 0.213 |
| Q9Z1A1 | *Tfg* | 0.518 | 0.001 | 0.016 | 0.000 | 0.385 | 0.717 |
| O35593 | *Psmd14* | 0.487 | 0.001 | 0.018 | 0.015 | 0.621 | 0.781 |
| P04919 | *Slc4a1* | -0.399 | 0.001 | 0.018 | 0.072 | 0.000 | 0.469 |
| Q9Z1P7 | *Kank3* | 0.326 | 0.001 | 0.021 | 0.171 | 0.006 | 0.781 |
| P30681 | *Hmgb2* | 0.535 | 0.001 | 0.022 | 0.111 | 0.498 | 0.741 |
| Q6ZWV7 | *Rpl35* | -0.563 | 0.001 | 0.022 | 0.174 | 0.440 | 0.471 |
| G3UYV7 | *Rps28* | 0.614 | 0.002 | 0.026 | 0.033 | 0.526 | 0.599 |
| P08032 | *Spta1* | -0.867 | 0.002 | 0.026 | 0.054 | 0.000 | 0.063 |
| Q9CQB4 | *Uqcrb* | -0.351 | 0.002 | 0.033 | 0.053 | 0.000 | 0.160 |
| O89086 | *Rbm3* | 0.333 | 0.002 | 0.034 | 0.164 | 0.806 | 0.699 |
| E9QNT8 | *Ank1* | -0.632 | 0.002 | 0.034 | 0.064 | 0.000 | 0.006 |
| P84089 | *Erh* | 0.329 | 0.003 | 0.035 | 0.015 | 0.866 | 0.887 |
| P50543 | *S100a11* | 0.394 | 0.003 | 0.035 | 0.033 | 0.849 | 0.438 |
| E9PZ00 | *Psap* | 0.359 | 0.003 | 0.035 | 0.076 | 0.007 | 0.228 |
| Q99LC3 | *Ndufa10* | -0.349 | 0.003 | 0.036 | 0.016 | 0.000 | 0.854 |
| P01837 | *Igkc* | -0.377 | 0.003 | 0.036 | 0.169 | 0.019 | 0.809 |
| Q9DAS9 | *Gng12* | 0.570 | 0.004 | 0.042 | 0.031 | 0.429 | 0.993 |

FDR**:** false discovery rate; \**p* values are shown for treatment, region and interaction respectively; #difference between means.

**Supplementary Table 1B: Proteins identified from Saline/MV vs Saline/FB.**

|  |  |  | T Test | | Two Way RM ANOVA\* | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein ID | Gene Name | Difference# | *p* | FDR, *q* | Treatment | Region | Interaction |
| A2AQ07 | *Tubb1* | 0.620 | 0.000 | 0.000 | 0.002 | 0.363 | 0.998 |
| D3Z5G7 | *Ces1b* | 0.247 | 0.000 | 0.000 | 0.002 | 0.002 | 0.913 |
| P08071 | *Ltf* | 0.785 | 0.000 | 0.000 | 0.002 | 0.000 | 0.075 |
| P32261 | *Serpinc1* | 0.282 | 0.000 | 0.000 | 0.002 | 0.037 | 0.169 |
| P49182 | *Serpind1* | 0.361 | 0.000 | 0.000 | 0.002 | 0.377 | 0.128 |
| Q9DBB9 | *Cpn2* | 0.448 | 0.000 | 0.000 | 0.005 | 0.071 | 0.770 |
| O08692 | *Ngp* | 0.754 | 0.000 | 0.000 | 0.006 | 0.000 | 0.765 |
| P07309 | *Ttr* | 0.367 | 0.000 | 0.000 | 0.006 | 0.000 | 0.935 |
| P34928 | *Apoc1* | 0.589 | 0.000 | 0.000 | 0.006 | 0.002 | 0.389 |
| O89053 | *Coro1a* | 0.277 | 0.000 | 0.000 | 0.007 | 0.000 | 0.315 |
| P51437 | *Camp* | 0.921 | 0.000 | 0.000 | 0.007 | 0.575 | 0.806 |
| Q542I8 | *Itgb2* | 0.360 | 0.000 | 0.000 | 0.007 | 0.482 | 0.427 |
| Q00623 | *Apoa1* | 0.331 | 0.000 | 0.000 | 0.008 | 0.000 | 0.227 |
| Q61599 | *Arhgdib* | 0.320 | 0.000 | 0.000 | 0.008 | 0.000 | 0.338 |
| Q64726 | *Azgp1* | 0.250 | 0.000 | 0.000 | 0.008 | 0.295 | 0.943 |
| Q06890 | *Clu* | 0.252 | 0.000 | 0.000 | 0.009 | 0.001 | 0.377 |
| Q8VDL4 | *Adpgk* | 0.233 | 0.000 | 0.000 | 0.012 | 0.011 | 0.104 |
| P08226 | *Apoe* | 0.277 | 0.000 | 0.000 | 0.013 | 0.000 | 0.456 |
| P11247 | *Mpo* | 0.544 | 0.000 | 0.000 | 0.013 | 0.050 | 0.211 |
| P11672 | *Lcn2* | 0.680 | 0.000 | 0.000 | 0.014 | 0.271 | 0.798 |
| P29351 | *Ptpn6* | 0.299 | 0.000 | 0.000 | 0.019 | 0.022 | 0.596 |
| Q61129 | *Cfi* | 0.301 | 0.000 | 0.000 | 0.019 | 0.007 | 0.089 |
| P21981 | *Tgm2* | -0.202 | 0.000 | 0.000 | 0.020 | 0.000 | 0.228 |
| O35744 | *Chil3* | 0.545 | 0.000 | 0.000 | 0.026 | 0.000 | 0.143 |
| P23953 | *Ces1c* | 0.269 | 0.000 | 0.000 | 0.027 | 0.000 | 0.394 |
| E9Q5L2 | *Itih4* | 0.317 | 0.000 | 0.000 | 0.030 | 0.002 | 0.168 |
| P28665 | *Mug1* | 0.343 | 0.000 | 0.000 | 0.032 | 0.000 | 0.132 |
| S4R1M0 | *Ptprc* | 0.224 | 0.000 | 0.000 | 0.033 | 0.001 | 0.209 |
| P07724 | *Alb* | 0.217 | 0.000 | 0.000 | 0.036 | 0.000 | 0.885 |
| E9Q035 | *Unknown* | 0.226 | 0.000 | 0.000 | 0.037 | 0.000 | 0.201 |
| O89020 | *Afm* | 0.295 | 0.000 | 0.000 | 0.037 | 0.000 | 0.220 |
| Q91X72 | *Hpx* | 0.246 | 0.000 | 0.000 | 0.039 | 0.001 | 0.677 |
| P06728 | *Apoa4* | 0.216 | 0.000 | 0.000 | 0.071 | 0.000 | 0.349 |
| D3Z6Q9 | *Bin2* | 0.345 | 0.000 | 0.000 | 0.000 | 0.000 | 0.944 |
| E9PV24 | *Fga* | 0.573 | 0.000 | 0.000 | 0.000 | 0.000 | 0.862 |
| O54890 | *Itgb3* | 0.415 | 0.000 | 0.000 | 0.000 | 0.000 | 0.028 |
| P20918 | *Plg* | 0.256 | 0.000 | 0.000 | 0.000 | 0.001 | 0.293 |
| P27005 | *S100a8* | 0.993 | 0.000 | 0.000 | 0.000 | 0.250 | 0.125 |
| P31725 | *S100a9* | 0.876 | 0.000 | 0.000 | 0.000 | 0.000 | 0.020 |
| P35441 | *Thbs1* | 0.331 | 0.000 | 0.000 | 0.000 | 0.000 | 0.011 |
| Q8K0E8 | *Fgb* | 0.585 | 0.000 | 0.000 | 0.000 | 0.000 | 0.672 |
| Q8K1B8 | *Fermt3* | 0.284 | 0.000 | 0.000 | 0.000 | 0.000 | 0.748 |
| Q8VCM7 | *Fgg* | 0.565 | 0.000 | 0.000 | 0.000 | 0.000 | 0.928 |
| Q9QUM0 | *Itga2b* | 0.496 | 0.000 | 0.000 | 0.000 | 0.002 | 0.613 |
| Q60590 | *Orm1* | 0.423 | 0.000 | 0.000 | 0.015 | 0.852 | 0.548 |
| P33622 | *Apoc3* | 0.533 | 0.000 | 0.000 | 0.021 | 0.000 | 0.398 |
| P22907 | *Hmbs* | -0.275 | 0.000 | 0.000 | 0.006 | 0.024 | 0.000 |
| Q9DBD0 | *1300017J02Rik* | 0.384 | 0.000 | 0.000 | 0.035 | 0.131 | 0.077 |
| P07759 | *Serpina3k* | 0.334 | 0.000 | 0.000 | 0.141 | 0.000 | 0.385 |
| P62843 | *Rps15* | 0.723 | 0.000 | 0.001 | 0.035 | 0.102 | 0.593 |
| Q8K370 | *Acad10* | -0.269 | 0.000 | 0.001 | 0.002 | 0.009 | 0.515 |
| Q9EQI5 | *Ppbp* | 0.645 | 0.000 | 0.002 | 0.029 | 0.234 | 0.237 |
| Q61702 | *Itih1* | 0.479 | 0.000 | 0.002 | 0.034 | 0.534 | 0.974 |
| P04919 | *Slc4a1* | -0.487 | 0.000 | 0.003 | 0.032 | 0.000 | 0.545 |
| J3QP71 | *Bsg* | -0.303 | 0.000 | 0.003 | 0.002 | 0.000 | 0.093 |
| P03953 | *Cfd* | 0.617 | 0.000 | 0.004 | 0.039 | 0.625 | 0.840 |
| P61079 | *Ube2d3* | -0.789 | 0.000 | 0.004 | 0.002 | 0.703 | 0.243 |
| Q9JHK5 | *Plek* | 0.347 | 0.000 | 0.004 | 0.004 | 0.343 | 0.557 |
| Q99PV0 | *Prpf8* | 0.253 | 0.000 | 0.005 | 0.156 | 0.003 | 0.390 |
| P13634 | *Car1* | -0.269 | 0.000 | 0.005 | 0.202 | 0.000 | 0.160 |
| P08032 | *Spta1* | -0.983 | 0.000 | 0.008 | 0.039 | 0.000 | 0.174 |
| E9QAS4 | *Chd4* | 0.247 | 0.000 | 0.008 | 0.073 | 0.507 | 0.898 |
| P04224 | *H2-Ea-ps* | 0.289 | 0.000 | 0.012 | 0.006 | 0.012 | 0.199 |
| E9Q912 | *Rap1gds1* | 0.271 | 0.000 | 0.016 | 0.063 | 0.732 | 0.808 |
| Q9QXS1 | *Plec* | -0.353 | 0.001 | 0.020 | 0.032 | 0.000 | 0.963 |
| Q921I1 | *Trf* | 0.894 | 0.001 | 0.021 | 0.018 | 0.355 | 0.836 |
| Q9D6J6 | *Ndufv2* | -0.337 | 0.001 | 0.023 | 0.008 | 0.000 | 0.601 |
| Q01279 | *Egfr* | 0.331 | 0.001 | 0.024 | 0.184 | 0.470 | 0.721 |
| P42703 | *Lifr* | 0.285 | 0.001 | 0.024 | 0.054 | 0.254 | 0.598 |
| P97352 | *S100a13* | 0.285 | 0.001 | 0.027 | 0.130 | 0.748 | 0.230 |
| Q3UGX2 | *Sptb* | -0.996 | 0.001 | 0.027 | 0.072 | 0.000 | 0.517 |
| Q3UID0 | *Smarcc2* | 0.291 | 0.003 | 0.046 | 0.042 | 0.709 | 0.289 |
| E9QNT8 | *Ank1* | -0.606 | 0.003 | 0.046 | 0.080 | 0.000 | 0.600 |

FDR**:** false discovery rate; \**p* values are shown for treatment, region and interaction respectively; #difference between means.

**Supplementary Table 1C: Proteins identified from Acid /MV vs Saline/FB.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | T Test | | Two Way RM ANOVA\* | | |
| Protein ID | Gene Name | Difference# | *p* | FDR, *q* | Treatment | Region | Interaction |
| D3Z5G7 | *Ces1b* | 0.331 | 0.000 | 0.000 | 0.005 | 0.003 | 0.129 |
| E9PV24 | *Fga* | 0.655 | 0.000 | 0.000 | 0.000 | 0.000 | 0.454 |
| E9Q035 | *unknown* | 0.251 | 0.000 | 0.000 | 0.026 | 0.000 | 0.099 |
| E9Q5L2 | *Itih4* | 0.448 | 0.000 | 0.000 | 0.004 | 0.000 | 0.017 |
| O08677 | *Kng1* | 0.258 | 0.000 | 0.000 | 0.015 | 0.000 | 0.114 |
| O08692 | *Ngp* | 0.730 | 0.000 | 0.000 | 0.001 | 0.008 | 0.255 |
| O35744 | *Chil3* | 0.593 | 0.000 | 0.000 | 0.001 | 0.000 | 0.108 |
| O89020 | *Afm* | 0.362 | 0.000 | 0.000 | 0.024 | 0.000 | 0.505 |
| P04186 | *Cfb* | 0.239 | 0.000 | 0.000 | 0.020 | 0.000 | 0.188 |
| P08071 | *Ltf* | 0.822 | 0.000 | 0.000 | 0.000 | 0.000 | 0.224 |
| P08226 | *Apoe* | 0.293 | 0.000 | 0.000 | 0.003 | 0.000 | 0.284 |
| P10107 | *Anxa1* | 0.168 | 0.000 | 0.000 | 0.000 | 0.000 | 0.277 |
| P11247 | *Mpo* | 0.543 | 0.000 | 0.000 | 0.003 | 0.046 | 0.713 |
| P11672 | *Lcn2* | 0.843 | 0.000 | 0.000 | 0.000 | 0.366 | 0.923 |
| P20918 | *Plg* | 0.316 | 0.000 | 0.000 | 0.000 | 0.000 | 0.506 |
| P23953 | *Ces1c* | 0.324 | 0.000 | 0.000 | 0.008 | 0.000 | 0.005 |
| P25444 | *Rps2* | -0.182 | 0.000 | 0.000 | 0.005 | 0.000 | 0.840 |
| P27005 | *S100a8* | 0.868 | 0.000 | 0.000 | 0.006 | 0.012 | 0.170 |
| P31725 | *S100a9* | 0.972 | 0.000 | 0.000 | 0.000 | 0.000 | 0.418 |
| P32261 | *Serpinc1* | 0.383 | 0.000 | 0.000 | 0.000 | 0.004 | 0.157 |
| P49182 | *Serpind1* | 0.442 | 0.000 | 0.000 | 0.000 | 0.700 | 0.034 |
| Q06890 | *Clu* | 0.280 | 0.000 | 0.000 | 0.006 | 0.000 | 0.024 |
| Q542I8 | *Itgb2* | 0.335 | 0.000 | 0.000 | 0.001 | 0.351 | 0.454 |
| Q61129 | *Cfi* | 0.338 | 0.000 | 0.000 | 0.011 | 0.001 | 0.019 |
| Q61247 | *Serpinf2* | 0.287 | 0.000 | 0.000 | 0.002 | 0.000 | 0.000 |
| Q61599 | *GDI* | 0.303 | 0.000 | 0.000 | 0.006 | 0.000 | 0.355 |
| Q8K0E8 | *Fgb* | 0.618 | 0.000 | 0.000 | 0.000 | 0.000 | 0.628 |
| Q8VCM7 | *Fgg* | 0.615 | 0.000 | 0.000 | 0.000 | 0.000 | 0.660 |
| Q91X72 | *Hpx* | 0.328 | 0.000 | 0.000 | 0.008 | 0.000 | 0.250 |
| Q9Z0U1 | *Tjp2* | 0.228 | 0.000 | 0.000 | 0.026 | 0.000 | 0.054 |
| Q61702 | *Itih1* | 0.650 | 0.000 | 0.000 | 0.007 | 0.254 | 0.743 |
| D6RGQ0 | *Cfh* | 0.248 | 0.000 | 0.000 | 0.021 | 0.000 | 0.249 |
| Q8K1B8 | *Fermt3* | 0.220 | 0.000 | 0.000 | 0.006 | 0.000 | 0.666 |
| Q00623 | *Apoa1* | 0.295 | 0.000 | 0.000 | 0.017 | 0.000 | 0.006 |
| A2AVJ7 | *Rrbp1* | -0.200 | 0.000 | 0.000 | 0.002 | 0.006 | 0.717 |
| D3Z6Q9 | *Bin2* | 0.277 | 0.000 | 0.000 | 0.008 | 0.000 | 0.325 |
| Q9DBD0 | *1300017J02Rik* | 0.502 | 0.000 | 0.000 | 0.016 | 0.019 | 0.333 |
| O89053 | *Coro1a* | 0.197 | 0.000 | 0.000 | 0.010 | 0.000 | 0.702 |
| P01869 | *Ighg1* | 0.806 | 0.000 | 0.000 | 0.018 | 0.304 | 0.539 |
| P54823 | *Ddx6* | 0.392 | 0.000 | 0.000 | 0.004 | 0.727 | 0.153 |
| O54890 | *Itgb3* | 0.297 | 0.000 | 0.000 | 0.023 | 0.000 | 0.517 |
| P21981 | *Tgm2* | -0.243 | 0.000 | 0.000 | 0.015 | 0.000 | 0.437 |
| Q60590 | *Orm1* | 0.475 | 0.000 | 0.000 | 0.003 | 0.676 | 0.500 |
| P01027 | *C3* | 0.312 | 0.000 | 0.000 | 0.045 | 0.000 | 0.071 |
| P07724 | *Alb* | 0.280 | 0.000 | 0.000 | 0.010 | 0.000 | 0.285 |
| P21614 | *Gc* | 0.246 | 0.000 | 0.000 | 0.056 | 0.000 | 0.102 |
| P26231 | *Ctnna1* | 0.191 | 0.000 | 0.000 | 0.027 | 0.000 | 0.148 |
| Q02257 | *Jup* | 0.195 | 0.000 | 0.000 | 0.009 | 0.000 | 0.006 |
| Q9DBB9 | *Cpn2* | 0.507 | 0.000 | 0.000 | 0.000 | 0.009 | 0.954 |
| Q8BP92 | *Rcn2* | -0.214 | 0.000 | 0.000 | 0.007 | 0.448 | 0.682 |
| P51437 | *Camp* | 0.856 | 0.000 | 0.000 | 0.002 | 0.561 | 0.817 |
| P06728 | *Apoa4* | 0.213 | 0.000 | 0.000 | 0.040 | 0.000 | 0.009 |
| P29351 | *Ptpn6* | 0.276 | 0.000 | 0.000 | 0.008 | 0.009 | 0.843 |
| Q501J6 | *Ddx17* | 0.257 | 0.000 | 0.000 | 0.025 | 0.163 | 0.330 |
| A2ACG7 | *Rpn2* | -0.193 | 0.000 | 0.000 | 0.018 | 0.049 | 0.719 |
| P35441 | *Thbs1* | 0.229 | 0.000 | 0.001 | 0.083 | 0.000 | 0.570 |
| Q64726 | *Azgp1* | 0.246 | 0.000 | 0.001 | 0.017 | 0.089 | 0.438 |
| P22907 | *Hmbs* | -0.223 | 0.000 | 0.001 | 0.026 | 0.118 | 0.222 |
| P29699 | *Ahsg* | 0.224 | 0.000 | 0.001 | 0.061 | 0.000 | 0.310 |
| Q06318 | *Scgb1a1* | -0.509 | 0.000 | 0.001 | 0.016 | 0.457 | 0.056 |
| G5E924 | *Hnrnpl* | 0.214 | 0.000 | 0.001 | 0.037 | 0.503 | 0.442 |
| Q02013 | *Aqp1* | -0.285 | 0.000 | 0.001 | 0.007 | 0.000 | 0.786 |
| P07759 | *Serpina3k* | 0.344 | 0.000 | 0.001 | 0.120 | 0.000 | 0.596 |
| P55284 | *Cdh5* | 0.211 | 0.000 | 0.001 | 0.027 | 0.009 | 0.311 |
| Q9D1J3 | *Sarnp* | 0.465 | 0.000 | 0.001 | 0.001 | 0.994 | 0.238 |
| P28665 | *Mug1* | 0.296 | 0.000 | 0.001 | 0.092 | 0.000 | 0.226 |
| P97290 | *Serping1* | 0.225 | 0.000 | 0.001 | 0.052 | 0.003 | 0.044 |
| Q9QUM0 | *Itga2b* | 0.308 | 0.000 | 0.001 | 0.064 | 0.000 | 0.845 |
| Q61656 | *Ddx5* | 0.215 | 0.000 | 0.001 | 0.063 | 0.490 | 0.087 |
| P97315 | *Csrp1* | 0.347 | 0.000 | 0.002 | 0.063 | 0.389 | 0.030 |
| O35129 | *Phb2* | -0.305 | 0.000 | 0.003 | 0.033 | 0.000 | 0.737 |
| Q9CX86 | *Hnrnpa0* | 0.421 | 0.000 | 0.003 | 0.001 | 0.456 | 0.803 |
| P62751 | *Rpl23a* | -0.275 | 0.000 | 0.003 | 0.030 | 0.052 | 0.243 |
| Q7TQD2 | *Tppp* | 0.481 | 0.000 | 0.003 | 0.003 | 0.812 | 0.287 |
| P01837 | *Igkc* | 0.494 | 0.000 | 0.003 | 0.044 | 0.142 | 0.391 |
| Q60932 | *Vdac1* | -0.295 | 0.000 | 0.003 | 0.017 | 0.000 | 0.778 |
| Q60930 | *Vdac2* | -0.319 | 0.000 | 0.003 | 0.035 | 0.000 | 0.593 |
| P01029 | *LOC102643089* | 0.266 | 0.000 | 0.004 | 0.035 | 0.006 | 0.674 |
| Q8C2Q8 | *Atp5c1* | -0.234 | 0.000 | 0.004 | 0.053 | 0.027 | 0.725 |
| Q9CZ13 | *Uqcrc1* | -0.303 | 0.000 | 0.005 | 0.011 | 0.000 | 0.676 |
| Q99LC3 | *Ndufa10* | -0.483 | 0.000 | 0.005 | 0.006 | 0.000 | 0.733 |
| P61079 | *Ube2d3* | -0.824 | 0.000 | 0.005 | 0.001 | 0.332 | 0.992 |
| Q9D0M3 | *Cyc1* | -0.330 | 0.000 | 0.005 | 0.015 | 0.000 | 0.842 |
| Q9JM96 | *Cdc42ep4* | 0.289 | 0.000 | 0.005 | 0.051 | 0.249 | 0.906 |
| Q9DB77 | *Uqcrc2* | -0.315 | 0.000 | 0.006 | 0.009 | 0.000 | 0.693 |
| P97447 | *Fhl1* | 0.296 | 0.000 | 0.006 | 0.089 | 0.250 | 0.240 |
| F6TFN2 | *Lmo7* | -0.302 | 0.000 | 0.007 | 0.090 | 0.000 | 0.546 |
| P12787 | *Cox5a* | -0.422 | 0.000 | 0.007 | 0.009 | 0.000 | 0.833 |
| Q9D6J6 | *Ndufv2* | -0.398 | 0.000 | 0.007 | 0.003 | 0.000 | 0.563 |
| P30681 | *Hmgb2* | 0.687 | 0.000 | 0.008 | 0.058 | 0.700 | 0.746 |
| P46978 | *Stt3a* | -0.265 | 0.000 | 0.008 | 0.040 | 0.832 | 0.163 |
| Q9DC69 | *Ndufa9* | -0.415 | 0.000 | 0.010 | 0.016 | 0.000 | 0.057 |
| Q9Z1P7 | *Kank3* | 0.391 | 0.000 | 0.012 | 0.074 | 0.069 | 0.491 |
| G3X9L6 | *Gm10250* | -0.232 | 0.000 | 0.012 | 0.049 | 0.000 | 0.459 |
| Q99JY8 | *Plpp3* | -0.227 | 0.000 | 0.013 | 0.005 | 0.000 | 0.064 |
| G3X977 | *Itih2* | 0.358 | 0.000 | 0.013 | 0.144 | 0.048 | 0.205 |
| Q8R1G6 | *Pdlim2* | 0.250 | 0.000 | 0.016 | 0.079 | 0.012 | 0.112 |
| Q61704 | *Itih3* | 0.553 | 0.000 | 0.017 | 0.062 | 0.933 | 0.582 |
| Q8C181 | *Mbnl2* | 0.348 | 0.000 | 0.019 | 0.048 | 0.581 | 0.338 |
| P21995 | *Emb* | -0.249 | 0.000 | 0.020 | 0.000 | 0.233 | 0.247 |
| Q8K310 | *Matr3* | 0.354 | 0.000 | 0.021 | 0.123 | 0.173 | 0.346 |
| P08228 | *Sod1* | -0.232 | 0.000 | 0.021 | 0.196 | 0.391 | 0.655 |
| P63280 | *LOC102641751* | 0.237 | 0.000 | 0.021 | 0.105 | 0.687 | 0.831 |
| Q9EPT5 | *Slco2a1* | -0.241 | 0.001 | 0.029 | 0.056 | 0.000 | 0.903 |
| P62320 | *Snrpd3* | 0.268 | 0.001 | 0.030 | 0.009 | 0.994 | 0.550 |
| Q9CQF3 | *Nudt21* | 0.294 | 0.001 | 0.032 | 0.032 | 0.453 | 0.369 |
| Q9QXS1 | *Plec* | -0.340 | 0.001 | 0.034 | 0.032 | 0.000 | 0.626 |
| Q9CQL1 | *Magohb* | 0.252 | 0.001 | 0.035 | 0.010 | 0.904 | 0.739 |
| P19783 | *Cox4i1* | -0.336 | 0.001 | 0.035 | 0.058 | 0.000 | 0.477 |
| Q8BX02 | *Kank2* | 0.272 | 0.001 | 0.036 | 0.147 | 0.027 | 0.806 |
| P33622 | *Apoc3* | 0.397 | 0.001 | 0.036 | 0.046 | 0.002 | 0.425 |
| P04919 | *Slc4a1* | -0.384 | 0.001 | 0.038 | 0.091 | 0.000 | 0.912 |
| Q80ZP8 | *Manf* | 0.398 | 0.002 | 0.045 | 0.014 | 0.562 | 0.528 |
| Q921I1 | *Trf* | 0.885 | 0.002 | 0.048 | 0.045 | 0.617 | 0.514 |

FDR**:** false discovery rate; \**p* values are shown for treatment, region and interaction respectively; #difference between means.

**Supplementary Table 2A: Functional analysis of the identified proteins for Acid/FB vs Saline/FB.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Functional Category** | Count | % | *p* | Benjamini *p* |
| Phosphoprotein | 21 | 77.8 | 0.000 | 0.001 |
| Methylation | 9 | 33.3 | 0.000 | 0.000 |
| RNA-binding | 7 | 25.9 | 0.000 | 0.001 |
| Acetylation | 13 | 48.1 | 0.000 | 0.002 |
| **Gene Ontology** |  |  |  |  |
| Cell-cell adhesion | 5 | 18.5 | 0.000 | 0.024 |

**Supplementary Table 2B: Functional analysis of the identified proteins from Saline/MV vs Saline/FB.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Functional Category** | Count | % | *p* | Benjamini *p* |
| Secreted | 33 | 53.2 | 0.000 | 0.000 |
| Signal | 42 | 67.7 | 0.000 | 0.000 |
| Glycoprotein | 34 | 54.8 | 0.000 | 0.000 |
| Disulfide bond | 31 | 50.0 | 0.000 | 0.000 |
| Hemostasis | 6 | 9.7 | 0.000 | 0.000 |
| Blood coagulation | 6 | 9.7 | 0.000 | 0.000 |
| Immunity | 10 | 16.1 | 0.000 | 0.000 |
| Innate immunity | 8 | 12.9 | 0.000 | 0.000 |
| Oxidation | 4 | 6.5 | 0.000 | 0.000 |
| Protease inhibitor | 6 | 9.7 | 0.000 | 0.000 |
| Calcium | 11 | 17.7 | 0.000 | 0.001 |
| Serine protease inhibitor | 5 | 8.1 | 0.000 | 0.001 |
| VLDL | 3 | 4.8 | 0.000 | 0.005 |
| Heparin-binding | 4 | 6.5 | 0.001 | 0.010 |
| Lipid transport | 4 | 6.5 | 0.002 | 0.016 |
| Iron transport | 3 | 4.8 | 0.002 | 0.017 |
| Iron | 6 | 9.7 | 0.003 | 0.029 |
| Transport | 13 | 21.0 | 0.004 | 0.032 |
| **Gene ontology** |  |  |  |  |
| Platelet aggregation | 8 | 12.9 | 0.000 | 0.000 |
| Hemostasis | 6 | 9.7 | 0.000 | 0.000 |
| Cell-matrix adhesion | 6 | 9.7 | 0.000 | 0.001 |
| Blood coagulation | 6 | 9.7 | 0.000 | 0.001 |
| Leukocyte migration involved in inflammatory response | 4 | 6.5 | 0.000 | 0.001 |
| Integrin-mediated signaling pathway | 6 | 9.7 | 0.000 | 0.001 |
| Fibrinolysis | 4 | 6.5 | 0.000 | 0.001 |
| Phospholipid efflux | 4 | 6.5 | 0.000 | 0.001 |
| Immune system process | 9 | 14.5 | 0.000 | 0.002 |
| Negative regulation of peptidase activity | 6 | 9.7 | 0.000 | 0.002 |
| Innate immune response | 9 | 14.5 | 0.000 | 0.002 |
| Cholesterol efflux | 4 | 6.5 | 0.000 | 0.005 |
| Regulation of Cdc42 protein signal transduction | 3 | 4.8 | 0.000 | 0.005 |
| Blood coagulation, fibrin clot formation | 3 | 4.8 | 0.000 | 0.005 |
| Lipoprotein metabolic process | 4 | 6.5 | 0.000 | 0.006 |
| Chylomicron remnant clearance | 3 | 4.8 | 0.000 | 0.009 |
| Positive regulation of peptide hormone secretion | 3 | 4.8 | 0.000 | 0.009 |
| Platelet activation | 4 | 6.5 | 0.000 | 0.010 |
| Plasminogen activation | 3 | 4.8 | 0.000 | 0.016 |
| Positive regulation of heterotypic cell-cell adhesion | 3 | 4.8 | 0.000 | 0.016 |
| High-density lipoprotein particle remodeling | 3 | 4.8 | 0.001 | 0.022 |
| Protein polymerization | 3 | 4.8 | 0.001 | 0.024 |
| Regulation | 3 | 4.8 | 0.001 | 0.027 |
| Positive regulation of T cell proliferation | 4 | 6.5 | 0.001 | 0.032 |
| Response to calcium ion | 4 | 6.5 | 0.001 | 0.036 |
| Neutrophil chemotaxis | 4 | 6.5 | 0.001 | 0.036 |
| Cellular protein complex assembly | 3 | 4.8 | 0.001 | 0.037 |
| Heterotypic cell-cell adhesion | 3 | 4.8 | 0.002 | 0.040 |
| Retinoid metabolic process | 3 | 4.8 | 0.002 | 0.040 |
| Triglyceride catabolic process | 3 | 4.8 | 0.002 | 0.043 |

**Supplementary Table 2C: Functional analysis of the shared set of proteins (42) from Saline/MV vs Saline/FB and Acid/MV vs Saline/FB.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Functional Category** | Count | % | *p* | Benjamini *p* |
| Secreted | 27 | 64.3 | 0.000 | 0.000 |
| Signal | 31 | 73.8 | 0.000 | 0.000 |
| Disulfide bond | 25 | 59.5 | 0.000 | 0.000 |
| Glycoprotein | 25 | 59.5 | 0.000 | 0.000 |
| Hemostasis | 6 | 14.3 | 0.000 | 0.000 |
| Blood coagulation | 6 | 14.3 | 0.000 | 0.000 |
| Oxidation | 4 | 9.5 | 0.000 | 0.000 |
| Innate immunity | 7 | 16.7 | 0.000 | 0.000 |
| Immunity | 8 | 19.0 | 0.000 | 0.000 |
| Protease inhibitor | 5 | 11.9 | 0.000 | 0.001 |
| Serine protease inhibitor | 4 | 9.5 | 0.001 | 0.006 |
| Iron | 6 | 14.3 | 0.001 | 0.007 |
| Calcium | 8 | 19.0 | 0.001 | 0.007 |
| Iron transport | 3 | 7.1 | 0.001 | 0.008 |
| Pyrrolidone carboxylic acid | 3 | 7.1 | 0.005 | 0.045 |
| **Gene Ontology** |  |  |  |  |
| Platelet aggregation | 6 | 14.3 | 0.000 | 0.000 |
| Hemostasis | 6 | 14.3 | 0.000 | 0.000 |
| Blood coagulation | 6 | 14.3 | 0.000 | 0.000 |
| Fibrinolysis | 4 | 9.5 | 0.000 | 0.001 |
| Immune system process | 8 | 19.0 | 0.000 | 0.002 |
| Innate immune response | 8 | 19.0 | 0.000 | 0.002 |
| Cell-matrix adhesion | 5 | 11.9 | 0.000 | 0.002 |
| Blood coagulation, fibrin clot formation | 3 | 7.1 | 0.000 | 0.003 |
| Regulation of Cdc42 protein signal transduction | 3 | 7.1 | 0.000 | 0.003 |
| Platelet activation | 4 | 9.5 | 0.000 | 0.004 |
| Positive regulation of peptide hormone secretion | 3 | 7.1 | 0.000 | 0.005 |
| Negative regulation of peptidase activity | 5 | 11.9 | 0.000 | 0.005 |
| Plasminogen activation | 3 | 7.1 | 0.000 | 0.008 |
| Positive regulation of heterotypic cell-cell adhesion | 3 | 7.1 | 0.000 | 0.008 |
| High-density lipoprotein particle remodeling | 3 | 7.1 | 0.000 | 0.011 |
| Protein polymerization | 3 | 7.1 | 0.000 | 0.012 |
| Leukocyte migration involved in inflammatory response | 3 | 7.1 | 0.000 | 0.012 |
| Regulation of release of sequestered calcium ion | 3 | 7.1 | 0.000 | 0.013 |
| Phospholipid efflux | 3 | 7.1 | 0.001 | 0.016 |
| Cellular protein complex assembly | 3 | 7.1 | 0.001 | 0.019 |
| Retinoid metabolic process | 3 | 7.1 | 0.001 | 0.020 |
| Triglyceride catabolic process | 3 | 7.1 | 0.001 | 0.021 |
| integrin-mediated signaling pathway | 4 | 9.5 | 0.001 | 0.025 |
| Negative regulation of extrinsic apoptotic signaling | 3 | 7.1 | 0.001 | 0.030 |
| Retina homeostasis | 3 | 7.1 | 0.001 | 0.030 |
| Triglyceride homeostasis | 3 | 7.1 | 0.002 | 0.033 |
| Positive regulation of exocytosis | 3 | 7.1 | 0.002 | 0.034 |
| Cholesterol efflux | 3 | 7.1 | 0.002 | 0.034 |
| Negative regulation of endothelial cell apoptotic process | 3 | 7.1 | 0.002 | 0.034 |
| Positive regulation of intrinsic apoptotic signaling | 3 | 7.1 | 0.002 | 0.037 |
| Lipoprotein metabolic process | 3 | 7.1 | 0.002 | 0.041 |

**Supplementary Table 2D: Functional analysis of the unique set of proteins (37) identified from Acid/MV vs Saline/FB.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Functional Category** | Count | % | *p* | Benjamini *p* |
| Complement alternate pathway | 3 | 8.1 | 0.000 | 0.011 |
| Respiratory chain | 4 | 10.8 | 0.000 | 0.007 |
| Innate immunity | 5 | 13.5 | 0.001 | 0.019 |
| Electron transport | 4 | 10.8 | 0.001 | 0.017 |
| Acetylation | 14 | 37.8 | 0.001 | 0.014 |
| Mitochondrion inner membrane | 5 | 13.5 | 0.001 | 0.012 |
| Secreted | 10 | 27.0 | 0.001 | 0.015 |
| Mitochondrion | 8 | 21.6 | 0.001 | 0.016 |
| Phosphoprotein | 22 | 59.5 | 0.002 | 0.023 |
| Inflammatory response | 4 | 10.8 | 0.002 | 0.022 |
| Transport | 10 | 27.0 | 0.002 | 0.022 |
| Isopeptide bond | 7 | 18.9 | 0.004 | 0.031 |
| Immunity | 5 | 13.5 | 0.004 | 0.029 |
| Cell junction | 6 | 16.2 | 0.004 | 0.027 |
| Phospholipase A2 inhibitor | 2 | 5.4 | 0.005 | 0.033 |
| Cleavage on pair of basic residues | 4 | 10.8 | 0.007 | 0.045 |
| **Gene Ontology** |  |  |  |  |
| Complement activation, alternative pathway | 3 | 8.1 | 0.000 | 0.053 |
| Mitochondrial electron transport,  ubiquinol to cytochrome c | 3 | 8.1 | 0.000 | 0.046 |
| Complement activation | 3 | 8.1 | 0.000 | 0.042 |