

	Identified Proteins (42)	Location			Function			Accession Number	QV infected*	QV control*	Infected/Control	Gene	Common Plasma EV-protein	Location in Vesiclepedia top 100 identified EV-proteins
		Plasma	Membrane	Other	Transport	Immunity	Hemostasis							
I N F E C T E D	fibronectin isoform X1							XP_005070574	170,62	-		FN1		58
	fibrinogen gamma chain isoform X1 ^D							XP_005076221	95,28	-		FGG		
	collagen alpha-3(VI) chain precursor							NP_001268084	68,69	-		COL6A3		
	spectrin alpha chain, erythrocytic 1							XP_005078300	24,37	-		SPTA1		
	inter-alpha-trypsin inhibitor heavy chain H3 precursor							NP_001268279	22,16	-		ITIH3		
	collagen alpha-2(VI) chain precursor							NP_001268478	19,94	-		COL6A2		
	haptoglobin precursor							NP_001268308	17,73	-		HP		
	ankyrin-1 isoform X3							XP_005066601	15,51	-		ANK1		
	band 3 anion transport protein isoform X1							XP_005070161	11,08	-		SLC4A1		
	fibroleukin precursor							NP_001274544	8,86	-		FGL2		
	collagen, type VI, alpha 1 precursor							NP_001268523	6,65	-		COL6A1		
	alpha-2-antiplasmin							XP_012967215	4,43	-		SERPINF2		
	thrombospondin-1 isoform X1							XP_005064576	4,43	-		THBS1		
	complement factor B							XP_005086893	4,43	-		CFB		
	vitamin D-binding protein							XP_012967480	4,43	3,52	1,26	GC		
	inter-alpha-trypsin inhibitor heavy chain H1-like							XP_021091699	6,65	5,62	1,18	ITIH1		
	von Willebrand factor							XP_021090951	6,65	2,81	2,37	VWF		
	inter-alpha-trypsin inhibitor heavy chain H2 precursor							NP_001268591	13,3	9,14	1,46	ITIH2		
	hemopexin							XP_005087494	15,51	11,25	1,38	HPX		
	C4b-binding protein alpha chain							XP_005079951	26,59	5,62	4,73	C4BPA		
	alpha-2-HS-glycoprotein (Fetuin A)							XP_012970060	39,88	11,95	3,34	AHSG		
	serotransferrin							XP_012970351	110,79	88,59	1,25	TF ^A		
	fibrinogen beta chain ^C							XP_005076224	135,17	92,1	1,47	FGB		
	apolipoprotein E							XP_005086377	168,4	158,89	1,06	APOE		
	apolipoprotein B-100							XP_005079141	210,51	130,07	1,62	APOB		
	alpha-2-macroglobulin-like							XP_012979079	589,4	453,48	1,30	A2ML1		
	serum albumin precursor							NP_001268578	483,05	483,01	1,00	ALB		22
	fibrinogen alpha chain ^B							XP_005076223	86,42	137,8	0,63	FGA		
	complement C3							XP_021089376	99,71	125,15	0,80	C3		54
	alpha-1-inhibitor 3-like							XP_012965811	11,08	80,15	0,14	MUG1 ^A		
	complement C4 isoform X1							XP_012981290	2,22	65,39	0,03	C4B ^A		
	apolipoprotein A-I precursor							NP_001268586	28,81	56,25	0,51	APOA1		
	inter-alpha-trypsin inhibitor heavy chain H4 isoform X1							XP_021091699	4,43	4,92	0,90	ITIH4		
	fetuin-B							XP_005071670	2,22	4,22	0,53	FETUB		
	complement factor H							XP_021084843	2,22	4,22	0,53	CFH		
C O N T R O L	plasminogen ^A							XP_021078698	-	9,14		PLG		
	alpha-1B-glycoprotein							XP_012974966	-	7,03		A1BG		
	inhibitor of carbonic anhydrase-like							XP_012970305	-	4,92		ICA ^A		
	actin, cytoplasmic 1							NP_001268524	-	2,81		ACTB		4
	phosphatidylinositol-glycan-specific phospholipase D							XP_021080705	-	2,11		GPLD1		
	gelsolin isoform X3							XP_005082184	-	2,11		GSN		70
	complement C1r subcomponent							XP_005065992	-	2,11		C1R		

* Quantative values for all identified proteins were correlated to the quantitative value of serum albumin

- Not detected in this sample

A Peptides detected indicate possible presence of both plasminogen and plasmine (Detection of (R)VVGCVANAHSWPWQVSLR(T) peptide indicates cleavage of Plasminogen in Plasmin A+B)

B Peptides detected indicate possible presence of both fibrin and fibrinogen in both samples (Detection of (S)DTGGEFVEQGGGVR(G) peptide indicates removal of signal peptide by thrombin)

C Peptides detected indicate possible presence of both fibrin and fibrinogen in both samples (Detection of (Q)AAEDDYDYSQDGLLVR(G) peptide indicates removal of signal peptide by thrombin and detection of (K)DNENVINEYSSILEDQR(L) Indicates possible cleavage by plasmin in both samples)

D Peptides detected indicate possible presence of fibrinogen and/or fibrin. Peptides do not exclude either option

^A Gene not yet annotated in *M. auratus* genome, allocated on basis of similarity identified via Smartblast*