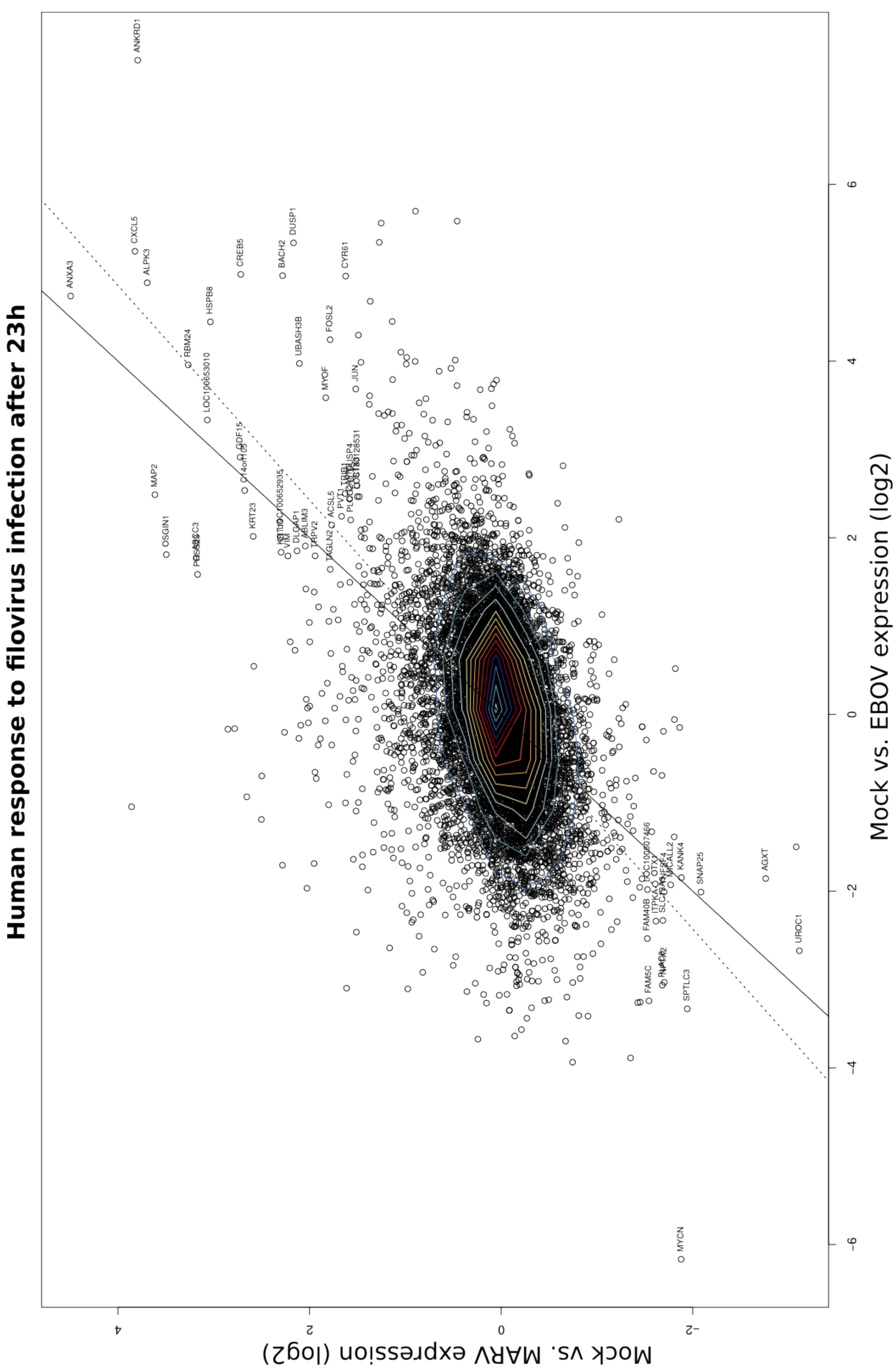
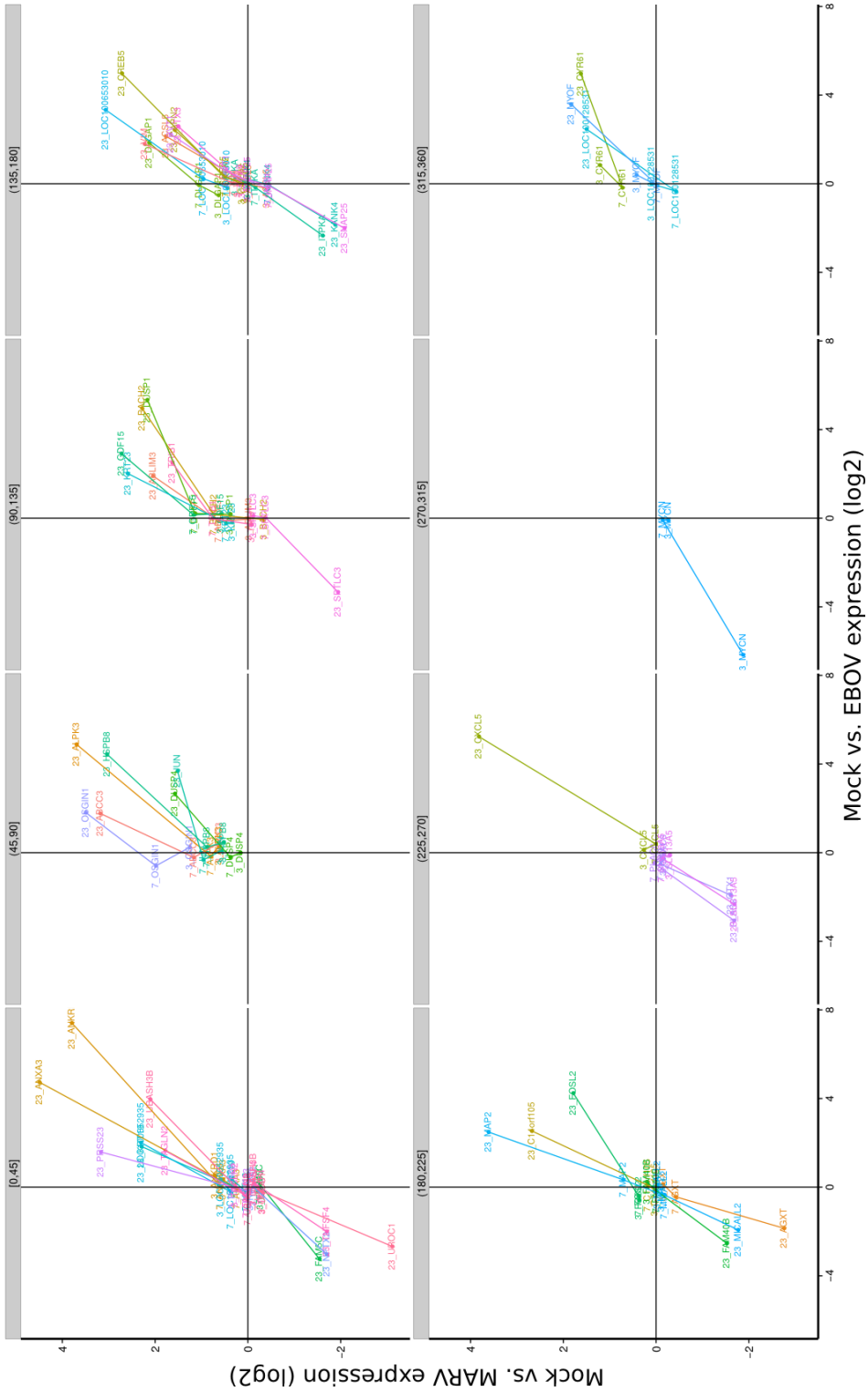
Scatterplot



Supplementary Figure 1: Scatterplot showing the $\log_2$ expression fold changes of coding and non-coding RNAs in human cells 23 h after EBOV and MARV infection, respectively. Outliers are labeld.

Groupplot



Supplementary Figure 2: **Timeseries human 23h p.i. with EBOV or MARV.** Human genes that have a similar or approximately time-course with respect to their differential expression are grouped. The angle defined by the differential expression 23 h p.i. was used for the grouping.

Supplementary Table 1: : **Common features of filovirus infection.** To compare the differential expression of Mock/EBOV and Mock/MARV in human and bat cells, log2 fold changes as computed by `DEseq` were visualized using scatter plots. Outliers (highly up-/down-regulated genes during both, EBOV and MARV infection in human and bat cells) were collected and further investigated based on the different scatter plots (see electronical Supplement) and listed here with their function. If publications concerning the immune response and/or viruses could be found for a gene, the corresponding `Pubmed` identifiers (PMID) were additionally listed. bold – interesting outliers with known relation to the immune response and/or viruses.

	Human up-regulated 23 h p.i.	
ANXA3	Annexin A3; inhibitor of phospholipase A2; also possesses anti-coagulant properties	25344230
CXCL5	**involved in neutrophil activation**	10095777
ANKRD1	may also be involved in the myofibrillar stretch-sensor system	22808421
ALPK3	kinase; plays a role in cardiomyocyte differentiation (similarity)	11418590
RBM24	plays a role in myogenic differentiation	
HSPB8	belongs to the superfamily of small heat-shock proteins; appears to be involved in regulation of cell proliferation, apoptosis, and carcinogenesis, and mutations in this gene have been associated with different neuromuscular diseases	23056924
CREB5	CAMP reponsive element binding; transcription factor	
BACH2	BTB And CNC Homology 1; transcriptional regulator that acts as repressor or activator	25355872 24968937
DUSP1	Dual specifity phosphatase	
CYR61	**matricellular protein; *CYR61* is highly expressed at sites of inflammation and wound repair, and is associated with diseases involving chronic inflammation and tissue injury; wound healing and fibrosis**	15890942 22129992
FOSL2	part of transcription factor complex AP-1	
UBASH3B	supress T-cell-driven inflammatory response	25047644
MYOF	calcium/phospholipid-binding protein that plays a role in the plasmalemma repair mechanism of endothelial cells that permits rapid resealing of membranes disrupted by mechanical stress	
JUN	part of transcription factor complex AP-1	
LOC100653010	reported as an uncaracterized ncRNA, WITHDRAWN	
MAP2	Microtubule-Associated Protein 2; the exact function of *MAP2* is unknown but MAPs may stabilize the microtubules against depolymerization	
OSGIN1	Oxidative Stress Induced Growth Inhibitor; regulates the differentiation and proliferation of normal cells through the regulation of cell death	
GDF5	member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily; regulators of cell growth and differentiation in both embryonic and adult tissues	
KRT23	histone deacetylase inducible keratin 23; related to cellular proliferation, cell cycle, DNA replication, recombination and repair	24039993
ABCC3	may act as an inducible transporter in the biliary and intestinal excretion of organic anions	
PRSS23	member of the trypsin family of serine proteases; may be an important ovarian protease	
	Human down-regulated 23 h p.i.	
MYCN	described in Sec. **??**	
UROC1	involved in histidine catabolism, metabolizing urocanic acid to formiminoglutamic acid; known to protect the skin from ultra violet rays and is contained in human sweat	
AGXT	Alanine-glyoxylate aminotransferase; this gene is expressed only in the liver and the encoded protein is localized mostly in the peroxisomes, where it is involved in glyoxylate detoxification	24012869

SNAP25	Synaptosomal-associated protein 25; component of the trans-SNARE complex, which is proposed to account for the specificity of membrane fusion	
SPTLC3	Serine C-palmitoyltransferase; acyltransferase transferring groups other than aminoacyl groups	
FAM5C	accepted name: *BRINP3*; bone morphogenetic Protein/Retinoic Acid Inducible Neural-Specific; inhibits neuronal cell proliferation by negative regulation of the cell cycle transition	
PLAC8	placenta-specific 8	
NPTX2	member of the family of neuronal petraxins; is involved in excitatory synapse formation; plays a role in clustering of alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA)-type glutamate receptors at established synapses, resulting in non-apoptotic cell death of dopaminergic nerve cells	
FAM40B	accepted name: *STRIP2*, plays a role in the regulation of cell morphology and cytoskeletal organization; required in the control of cell shape	
SNAP25	Synaptosomal-Associated Protein, 25kDa; t-SNARE involved in the molecular regulation of neurotransmitter release; proposed to account for the specificity of membrane fusion and to directly execute fusion by forming a tight complex that brings the synaptic vesicle and plasma membranes together	19546860 12154365
KANK4	may be involved in the control of cytoskeleton formation by regulating actin polymerization	