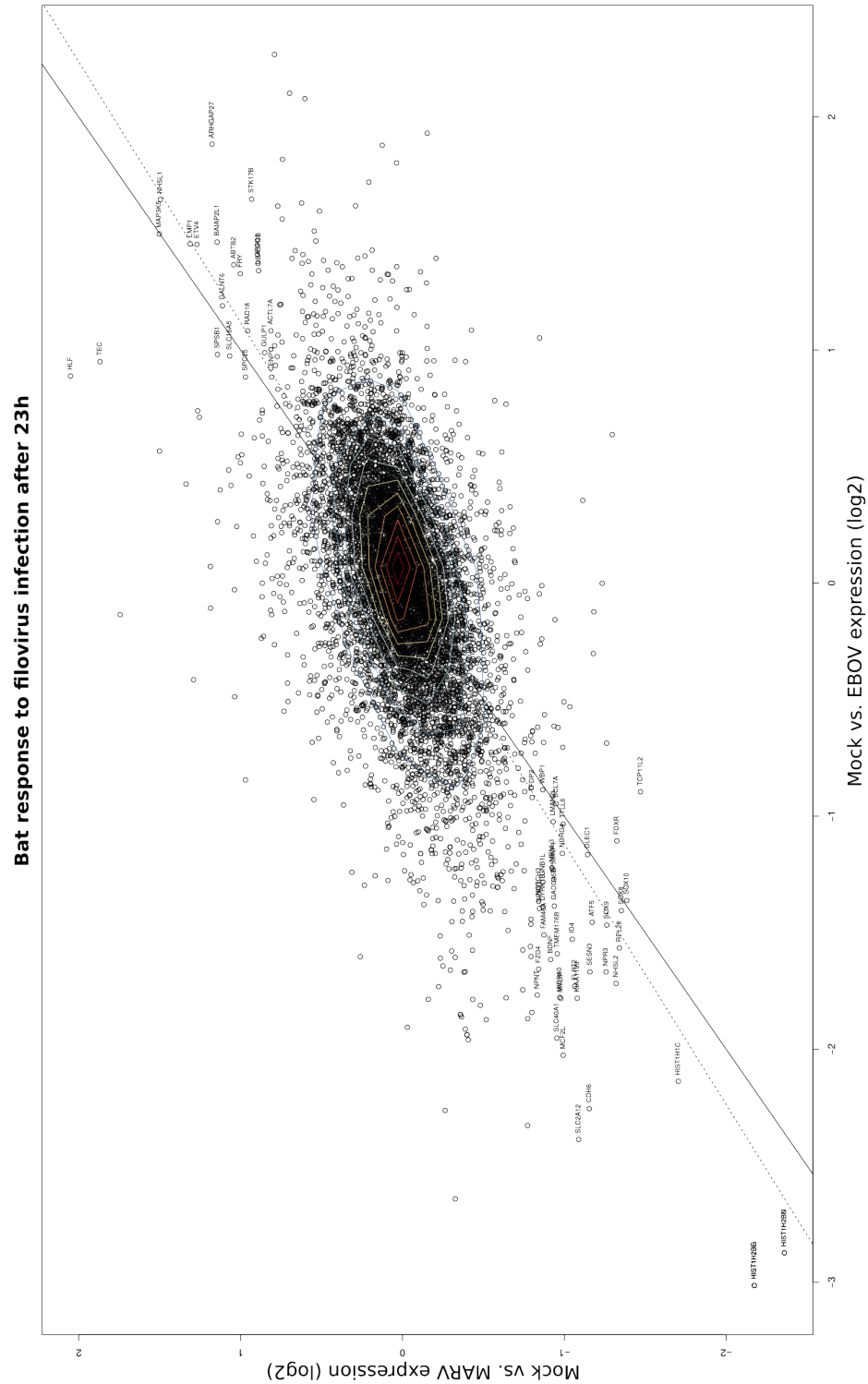
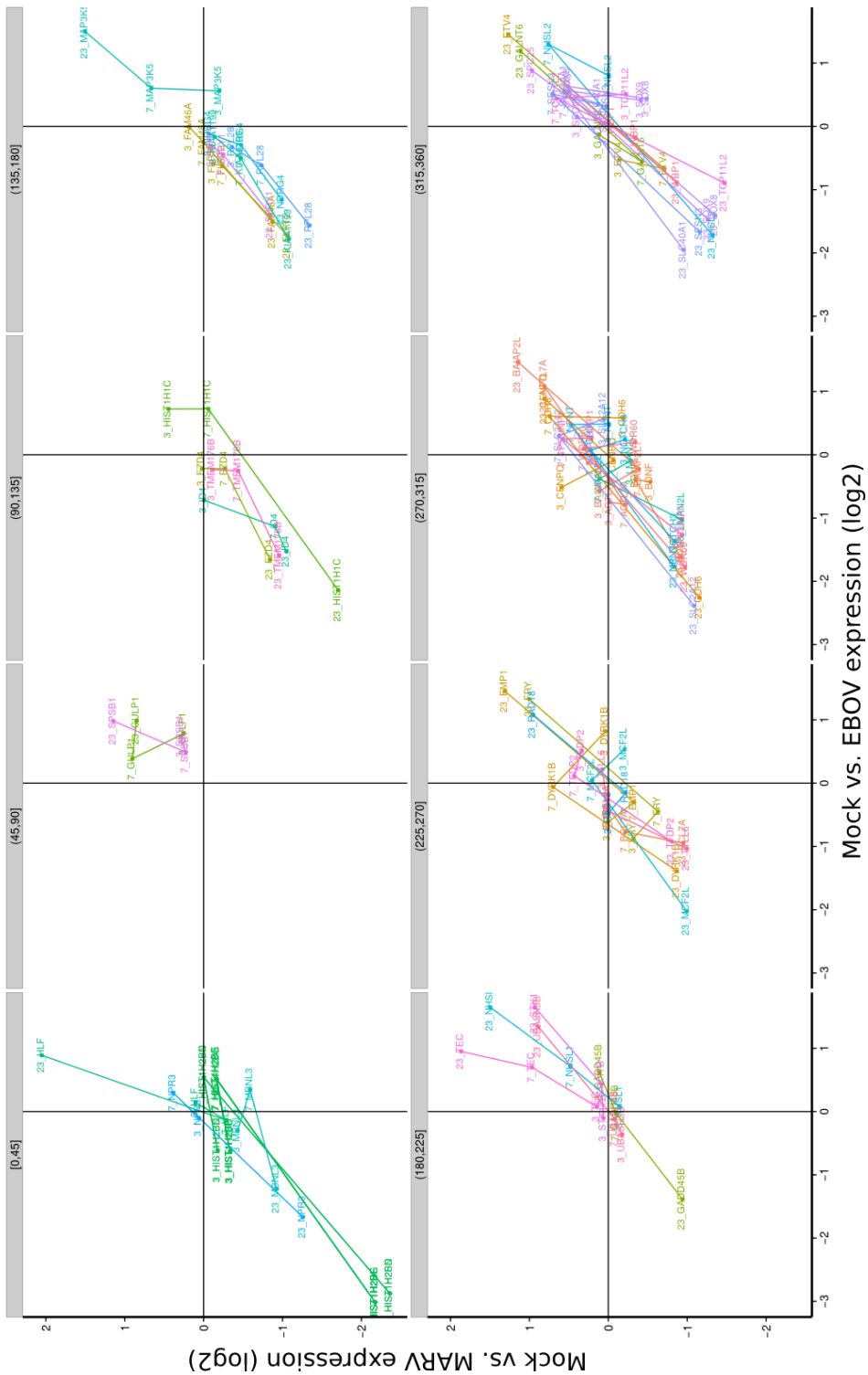
Scatterplot



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

Groupplot



Supplementary Figure 2: **Timeseries bat 23h p.i. with EBOV or MARV.** Bat 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.

	Bat up-regulated 23 h p.i.	
HLF	Hepatic Leukemia Factor; promoted resistanceto cell death	23415677
TEC	Non-receptor tyrosine kinase that contributes to signaling from many receptors and participates as a signal transducer in multiple downstream pathways, including regulation of the actin cytoskeleton	24722985
MAP3K5	Apoptosis signal-regulating kinase 1 (*ASK1*) also known as mitogen-activated protein kinase kinase kinase 5 (*MAP3K5*); MAP kinase kinase kinase, activates *JNK* and *p38*	12878192
NHSL1	Nance-Horan syndrome (NHS); the NHS gene forms a new gene family with a closely related novel gene NHS-Like1	
ARHGAP27	may pay a role in clathrin-mediated endocytosis	
EMP1	Epithelial Membrane protein1; tomor-associated glycoprotein	8996089
ETV4	ETS translocation variant 4	
BAIAP2L1	involved in signal transduction pathways that link deformation of the plasma membrane and remodeling of the actin cytoskeleton	
STK17B	serine/threonine kinase 17b	
FRY	plays a crucial role in the structural integrity of mitotic centrosomes and in the maintenance of spindle bipolarity	25740997
GALNT6	Polypeptide N-acetylgalactosaminyltransferase 6	
GFOD1	Glucose-Fructose Oxidoreductase Domain-Containing Protein 1; related to attention deficit hyperactivity disorder	18821565
UBASH3B	Promotes accumulation of activated target receptors, such as T-cell receptors and *EGFR*, on the cell surface	
SPSB1	Probable substrate recognition component of a SCF-like ECS (Elongin BC-CUL2/5-SOCS-box protein) E3 ubiquitin-protein ligase complex which mediates the ubiquitination and subsequent proteasomal degradation of target proteins	
	Bat down-regulated 23 h p.i.	
HIST1H2B6	histone	
HIST1H2B	histone	
HIST1H1C	histone	
CDH6	Cadherins are calcium-dependent cell adhesion proteins; they preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types	
SLC2A12	Solute carrier family 2; facilitated glucose transporter member 1	
NHSL2	see above	
SOX8/9/10	family of transcription factors; cell development	
RPL28	Ribosomal Protein L28; component of the 60S ribosomal subunit	
NPR3	**Natriuretic peptide receptor3; regulate blood volume and pressure, pulmonary hypertension, and cardiac function as well as some metabolic and growth processes**	23493048
FDXR	see above	
TCP11L2	t-complex 11; testis-specific-like 2	
MCF2L	Guanine nucleotide exchange factor that potentially links pathways that signal through *RAC1*, *RHOA* and *CDC42*	

SLC40A1	may be involved in iron export from duodenal epithelial cell and also in transfer of iron between maternal and fetal circulation	22249207
SESN3	member of the sestrin family of stress-induced proteins; the protein is required for normal regulation of blood glucose, insulin resistance and plays a role in lipid storage in obesity	
ATF5	transcription factor	
WDR60	this gene encodes a member of the WD repeat protein family; WD repeats are minimally conserved regions of approximately 40 amino acids typically bracketed by gly-his and trp-asp (GH-WD) and may facilitate the formation of heterotrimeric or multiprotein complexes	
MYLIP	Myosin Regulatory Light Chain Interacting Protein; E3 ubiquitin-protein ligase that mediates ubiquitination and subsequent proteasomal degradation of myosin regulatory light chain (*MRLC*), *LDLR*, *VLDLR* and *LRP8*	
FLRT2	may function in cell adhesion and/or receptor signalling	
ID4	inhibitor of DNA binding 4; dominant negative helix-loop-helix; transcription factor, which can act as tumor supressor but lack DNA binding activity	
DLEC1	unkown function; aberrant transcription of this gene may be involved in carcinogenesis of the lung, esophagus, and kidney	