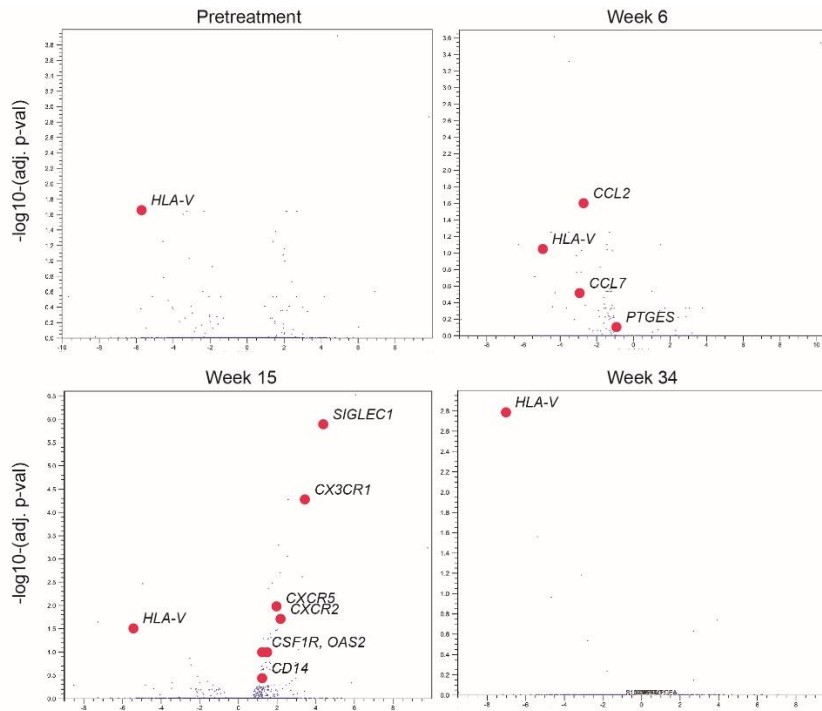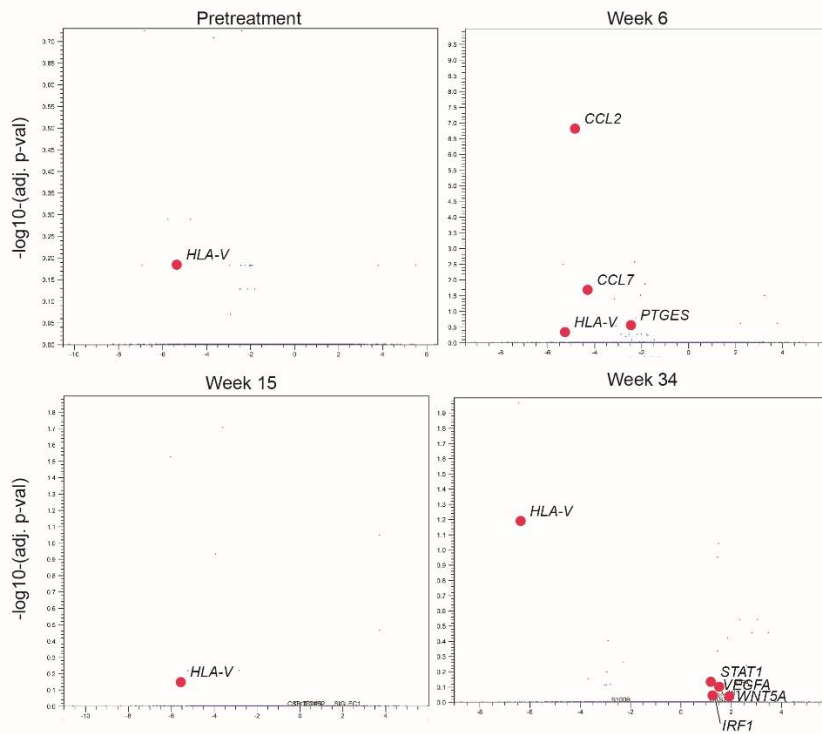Figure S1. Differential expression analysis reveals several immune related genes associated with response at various time points. Volcano plots comparing fold-change (x-axis) and <u>adjusted</u> p-value (y-axis, edgeR), for 36,410 expressed genes at weeks 0, 6, 15, and 34 between PR (n=3 patients) v.s. SD (n=7) and CR (n=2) vs. SD (n=7). Specific immune-related genes are highlighted in red.
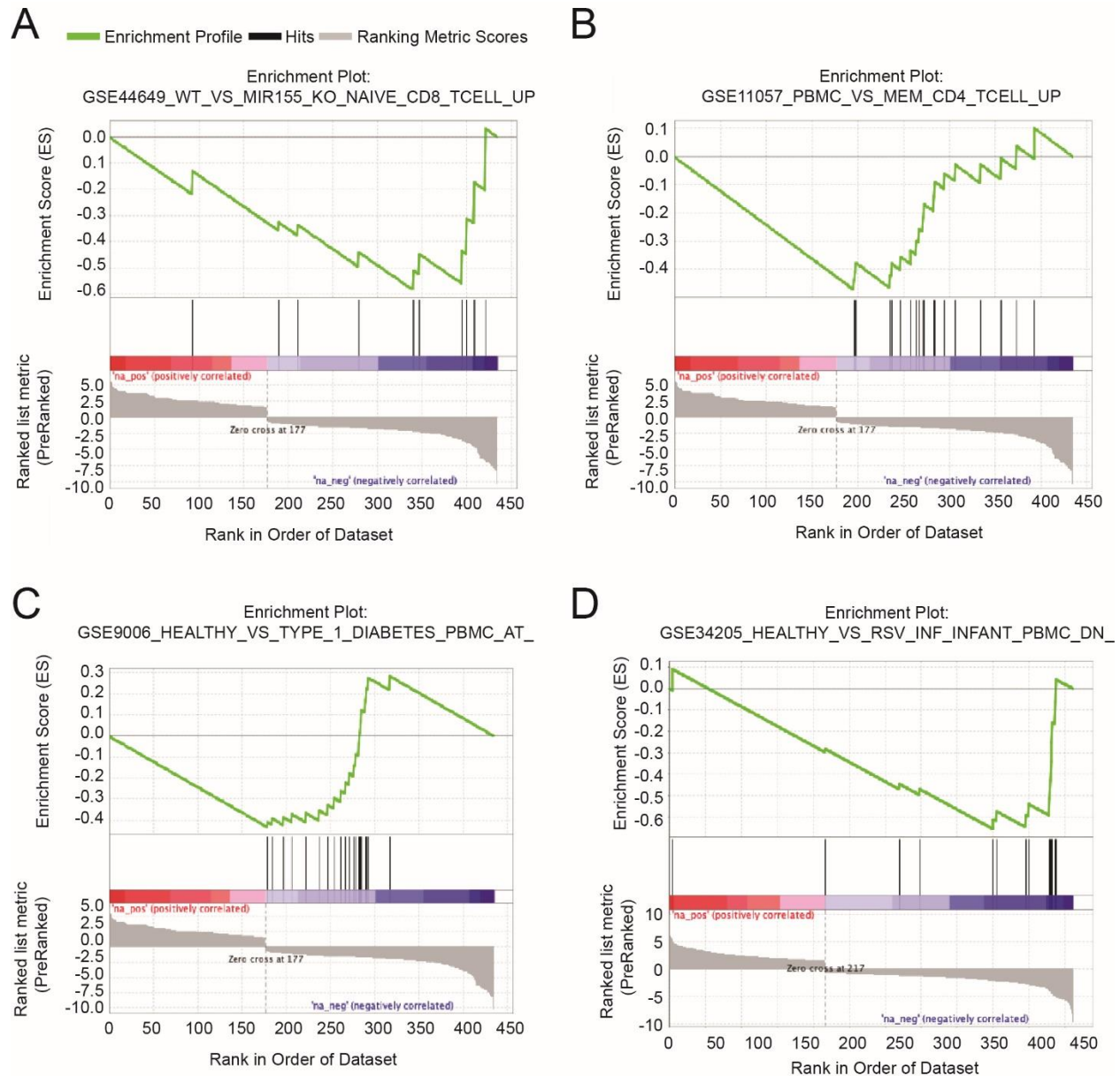
**Figure S2**. **Gene set enrichment analysis at week 0.** (A-C) In enrichment plots genes are ranked by signal/noise ratio according to their differential expression between SD and CR patients. Genes in the gene sets indicated on top of each figure are marked with vertical bars, and the enrichment score is shown in green. (D) Figure as in (A-C), with genes ranked according to differential expression between PR vs SD patients.
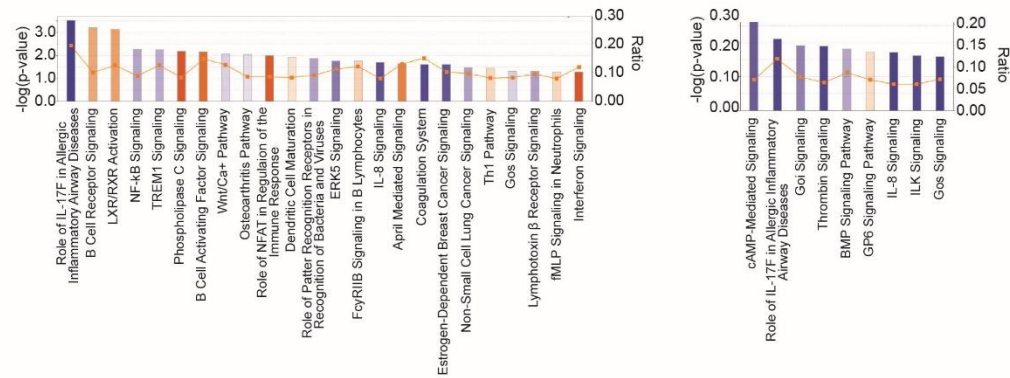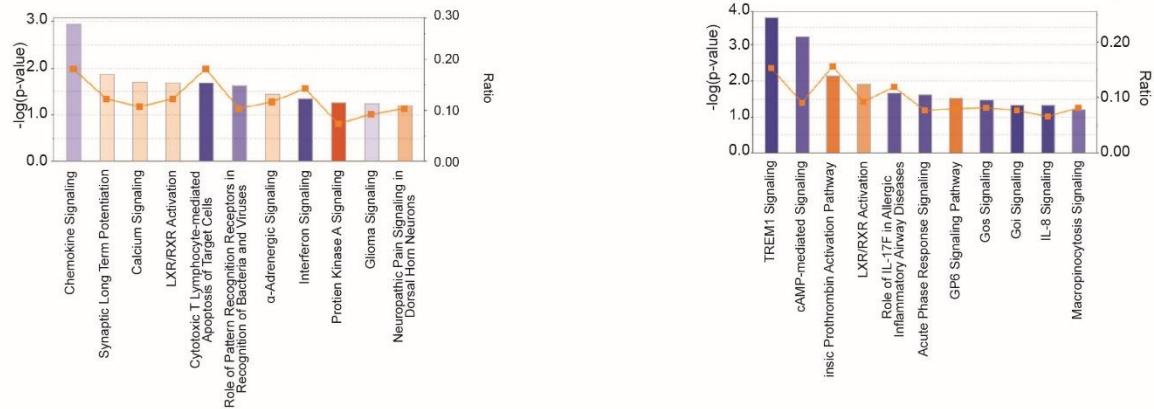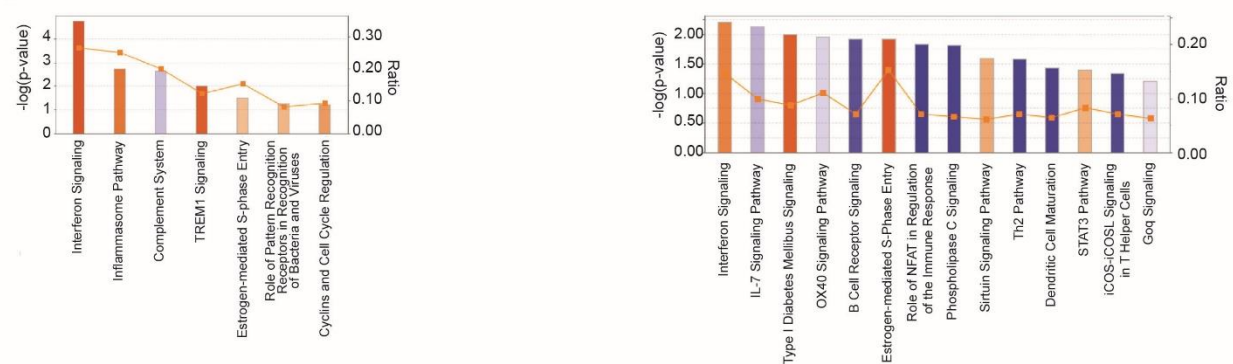
Figure S3. **Induced and repressed pathways associated with treatment response at different time points.** (A) Left: Significance (y-axis, Fisher's exact test) of pathway enrichment for genes differentially expressed between PR and SD patients at week 0. The ratio of differentially expressed genes to the total number of genes in the pathway is given by the orange line. The average expression of genes in each pathway is indicated by color (z-score). Right: Same as on the left for genes differentially expressed between CR and SD patients. (B) Figure as in (A) for week 6. (C) Figure as in (A) for week 15.
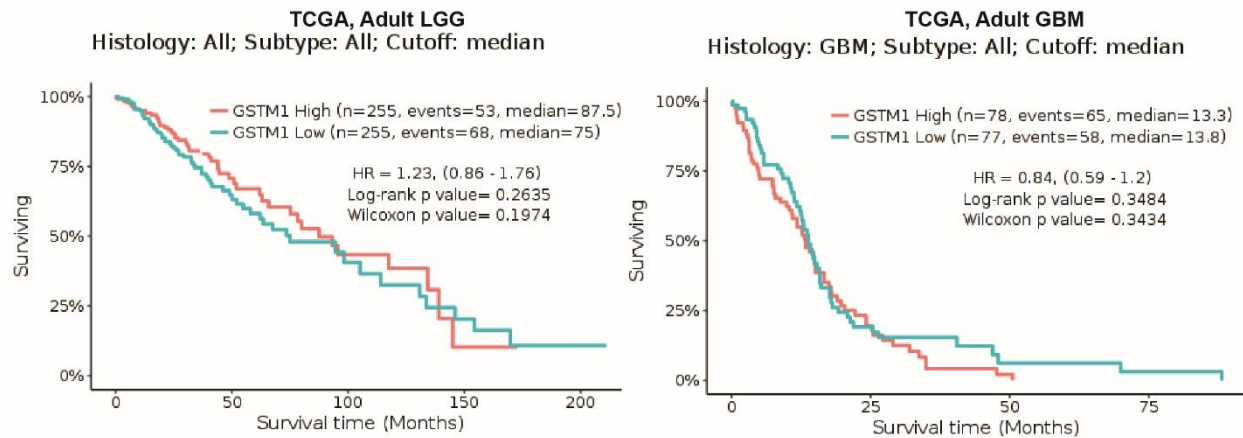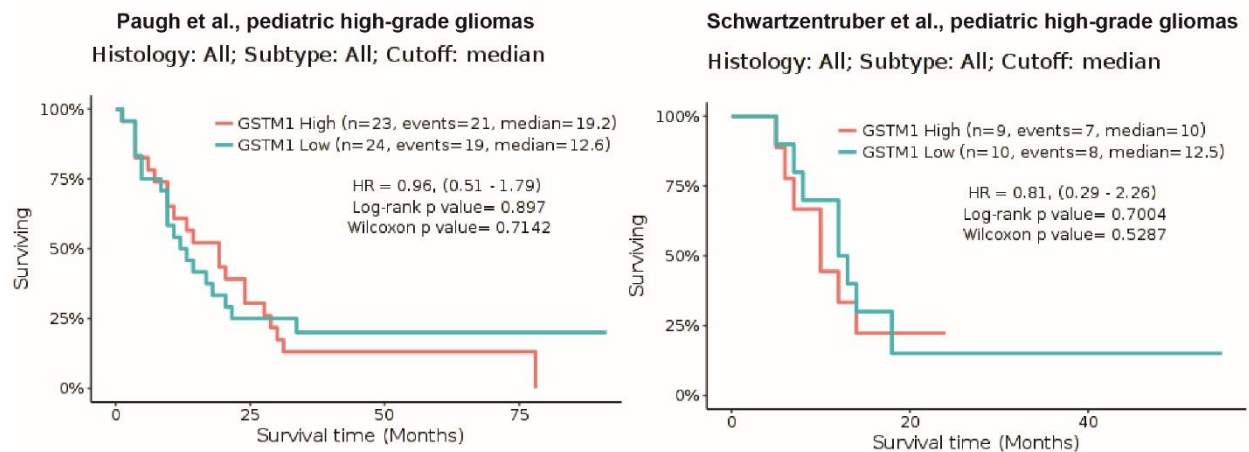
Figure S4. **Survival analysis for *GSTM1* expression in public pediatric and adult glioma datasets.** (A) Left: Survival analysis based on TCGA RNA-seq data of LGG tissues (n=510 adult patients). The two groups were determined based on median *GSTM1* expression. HR= Hazard Ratio. Right: Figure as in (A) for n=155 adult glioblastoma patients. (B) Left: Figure as in (A) for n=47 pediatric glioblastoma patients. Right: Figure as in (A) for n=19 pediatric glioblastoma patients.
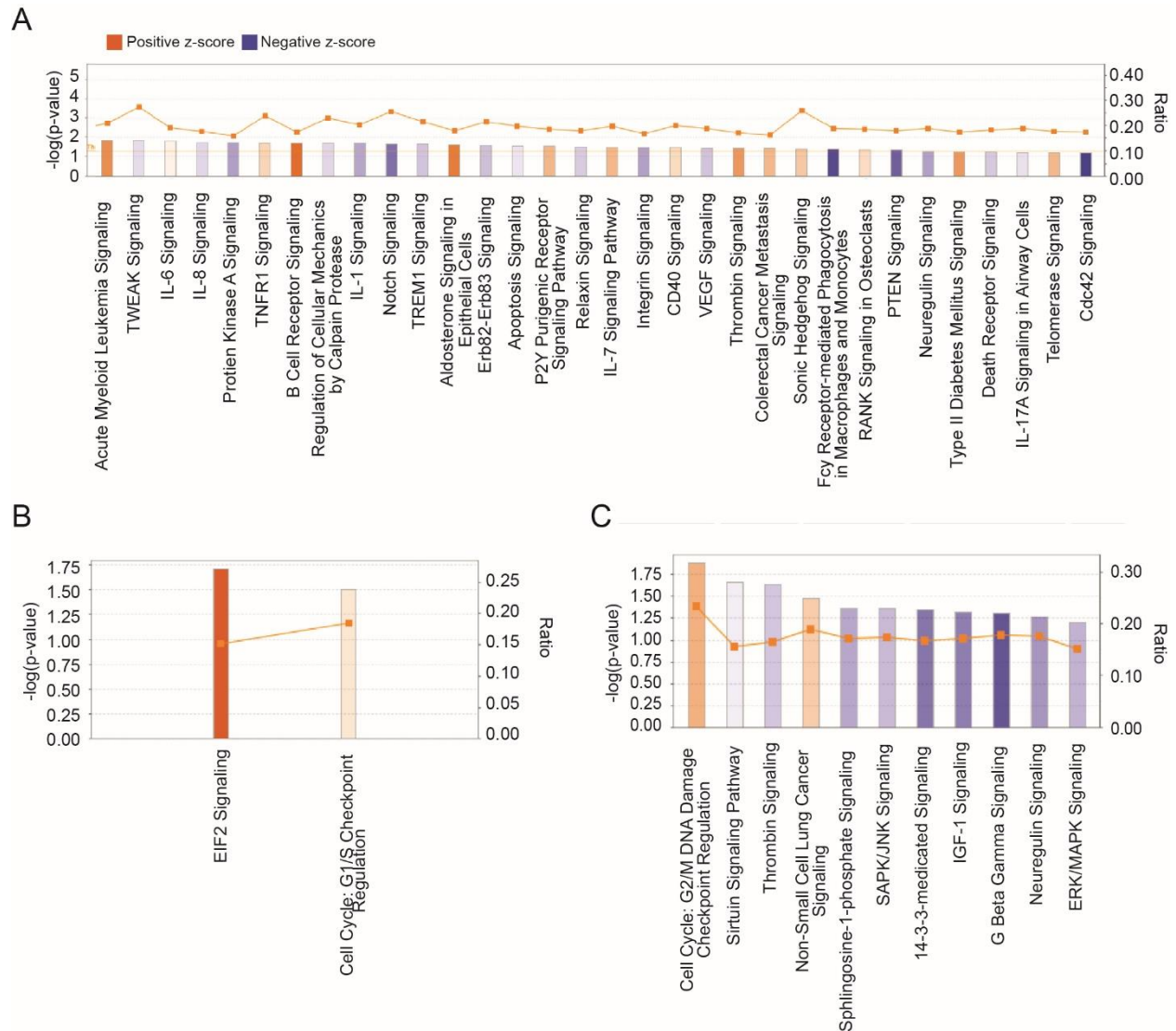
Figure S5. **Pathway analysis of genes correlating with ELISPOT counts.** (A) Significance (y-axis, Fisher's exact test) of pathway enrichment for genes correlating with Survivin ELISPOT counts. The ratio of differentially correlated genes to the total number of genes in the pathway is given by the orange line. The average correlation z-score of genes in each pathway is indicated by color. (A) Additional pathways (in addition to Figure 5A) correlating with Survivin ELISPOT counts (B) Pathways correlating with IL-13Ra2 ELISPOT counts. (C) Pathways correlating with EphA2 ELSPOT counts.

	HLA-V	GSTM1	Week 6 Monocyte	Week 15 Monocyte	Week 34 STAT1/IFN	Week 34 Poly-ICLC
CR	↓	↓	↓	↓	↑	↑
PR	↓	↑	↓	↑	↓	↑
SD	↑	↑	↑	—	—	—

Figure S6. **Summary of potential biomarkers of vaccination response at different time points.** Arrows pointing up indicate an induction of the indicated gene, pathway/cell type (columns) in each of the three groups (rows). Time points are indicated below the markers. If no time point is mentioned, the markers are predictive at every given time point including week 0 (pre-treatment).

Best Response: PR vs SD					
Week 0		Week 6		Week 15	
Activated	Inhibited	Activated	Inhibited	Activated	Inhibited
2-aminopurine	leukotriene D4	2-aminopurine	leukotriene D4	Lipopolysaccharide	Etanercept
prednisolone	Inosine	Prednisolone	Inosine	IFNA2	Ptprd
anakinra	Bromodeoxyuridine	Anakinra	Bromodeoxyuridine	IRF7	PDCD1
alefacept	Uric acid	Alefacept	Uric acid	IFNG	GPS2
infliximab	Isobutyl-methylxanthine	Infliximab	Isobutyl-methylxanthine	Interferon alpha	Garcinol
asoprisnil	E. coli lipopolysaccharide	Asoprisnil	E. coli lipopolysaccharide	CSF2	Immunoglobulin
CDK4/6	E. coli B4 lipopolysaccharide	CDK4/6	E. coli B4 lipopolysaccharide	IFNL1	miR-34a-5p (and othermiRNAs w/seed GGCAGUG)
CD3	Peptidoglycan	CD3	Peptidoglycan	PRL	
NPM1	17α-ethinylestradiol	NPM1	17α-ethinylestradiol	IRF3	FSH
Ptprd	Linoleic acid	Ptprd	Linoleic acid	TGM2	DNASE2
MKL2	Oblimersen	MKL2	Oblimersen	STAT1	Let-7
EGLN	Salmonella minnesota R595 lipopolysaccharides	EGLN	Salmonella minnesota R595 lipopolysaccharides	Poly rI:rC-RNA	Baicalein
26s Proteasome		26s Proteasome		IL21	PTX3
Immunoglobulin	PI3K (complex)	Immunoglobulin	PI3K (complex)	IRF1	DYRK1A
ACKR2	ERK1/2	ACKR2	ERK1/2	SMARCA4	Fontolizumab
	P38 MAPK		P38 MAPK	IFN Beta*	SB203580
	TCR*		TCR*		

Best Response: CR vs SD					
Week 0		Week 6		Week 15	
Activated	Inhibited	Activated	Inhibited	Activated	Inhibited
PD98059	Pka	PD98059	Pka	CCND1	Rb
SB203580	LCN2	SB203580	LCN2	PD98059	RBM5
SFTPA1	CHADL	SFTPA1	CHADL	CD3	SCAP
Salicylic acid	SELPLG	salicylic acid	SELPLG	CD28	Aldesleukin
miR-199a-5p (and other miRNAs w/seed CCAGUGU)	RNASE1	miR-199a-5p (and other miRNAs w/seed CCAGUGU)	RNASE1	RICTOR	Nitroarginine
	SELP		SELP	KDM5A	Butyric acid
NCSTN	TYROBP	NCSTN	TYROBP	Dihydrotestosterone	FGF2
COL18A1	BET	COL18A1	BET	RABL6	Tnf (family)
APOE	HRG	APOE	HRG	INSIG1	TLR7
let-7a-5p (and other miRNAs w/seed GAGGUAG)	Fenamic acid	let-7a-5p (and other miRNAs w/seed GAGGUAG)	fenamic acid	Methotrexate	ADORA2A
	Carboplatin		carboplatin	Alefacept	Ca2+
U0126	Triamterene	U0126	triamterene	TSC2	Tretinoin
CA4	lomustine	CA4	lomustine	CD 437	PDGF BB
Diphenyleneiodonium	Bezafibrate	Diphenyleneiodonium	bezafibrate	Igm	SAMSN1
Bisindolylmaleimide I	Tnf (family)	Bisindolylmaleimide I	Tnf (family)	AREG	IL18
miR-1-3p (and other miRNAs w/seed GGAAUGU)		miR-1-3p (and other miRNAs w/seed GGAAUGU)	Tnf (family)	mir-1	NFKB1
			ABCB4	EP400	Dimethyl sulfoxide
			ABCB4	TBX2	RNASE2
				Aspirin	Poly rI:rC-RNA

Table ST1. **Predicted upstream regulators of our gene pathways at time points 0, 6, 15 using IPA software.** Analysis was performed based on up-/downregulated genes between groups.