

Appendix

Supplementary Figures and Tables

Parameter	Threshold
Map reads	5 million or higher.
Number of duplicates	Lower than 35 percent. Ideal lower than 20 percent. See samples between 20 and 35 and decide if they have higher duplicate counts since the beginning, then remove it.
Samples with high exonic reads.	If they have high intergenic + intronic reads remove it (more than 20 percent between both).
Proper pair	higher than 40 percent

Table S1: Quality control threshold for the different parameters

ID	logFC	adj.pvalue	ID	logFC	adj.pvalue
STAT1	-1.393	***	STAT1	-1.463	***
TBX21	1.266	***	TBX21	1.087	***
STAT4	0.6402	***	SOCS5	0.5578	***
SOCS5	0.6054	***	STAT4	0.448	***
TNF	-0.5945	***	TNF	-0.5926	***
SOCS1	0.598	**	SOCS1	0.5241	*
TLR4	0.2753	-	TLR4	0.1889	-
CD28	0.1084	-	CD28	0.1052	-

(a) START vs FINISH

(b) FINISH vs 24REST

ID	logFC	adj.pvalue
STAT4	0.1922	-
TBX21	0.1795	-
STAT1	0.07037	-
SOCS5	0.04766	-
TLR4	0.0864	-
SOCS1	0.07386	-
CD28	0.003178	-
TNF	-0.001909	-

(c) START vs 24REST

Table S2: Lymphocytes TH1 DE genes for each comparison (a), (b) and (c). (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 , respectively. (-) indicates no significant.

ID	logFC	adj.pvalue	ID	logFC	adj.pvalue
NFATC2	1.241	***	NFATC2	1.322	***
CEBPB	-1.235	***	CEBPB	-1.017	***
MAF	-0.9715	***	IL1R1	0.8245	***
IL1R1	0.6862	***	MAF	-1.004	***
STAT6	-1.399	***	GFI1	0.7767	***
ICOS	0.653	***	STAT6	-1.108	***
GFI1	0.8668	***	CCL5	0.744	***
CCL5	0.7068	***	ICOS	0.4613	***
CCR4	-0.7112	***	CCR4	-0.8518	***
CCR2	0.5805	***	IL1R2	-0.4633	***
IL1R2	-0.4037	**	CCR2	0.6099	***
GATA3	0.1996	-	GATA3	0.1239	-

(a) START vs FINISH

(b) FINISH vs 24REST

ID	logFC	adj.pvalue
STAT4	0.1922	-
TBX21	0.1795	-
STAT1	0.07037	-
SOCS5	0.04766	-
TLR4	0.0864	-
SOCS1	0.07386	-
CD28	0.003178	-
TNF	-0.001909	-

(c) START vs 24REST

Table S3: TH2 DE genes for each comparison (a), (b) and (c). (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 , respectively. (-) indicates no significant.

ID	logFC	adj.pvalue	ID	logFC	adj.pvalue
CXCL16	1.122	***	GPX4	-0.2182	-
IL1B	-1.077	***	MMP9	0.1419	-
IL4R	-1.225	***	IL4R	-0.1926	-
IL1R1	0.8245	***	IL1R1	-0.1383	-
IL6ST	1.033	***	TGFB3	0.1746	-
IL6R	1.501	***	IL1RN	0.1519	-
IL10RB	1.668	***	TGFBAP1	0.1397	-
TGFBAP1	-0.8836	***	IFNGR2	0.09865	-
CCL5	0.744	***	TLR2	0.05299	-
IL1RN	-0.752	***	HSPA6	-0.2022	-
CCR4	-0.8518	***	IL10RB	-0.191	-
TNF	-0.5926	***	GATA3	0.07573	-
CCR2	0.6099	***	IL6ST	0.1051	-
TGFB3	0.3561	-	GPX7	-0.07334	-
MMP9	-0.1601	-	CCR4	0.1406	-
HSPA6	-0.4656	-	TLR4	0.0864	-
GPX4	0.1606	-	SOD1	-0.03689	-
GATA3	0.1239	-	CCL5	-0.03727	-
GPX7	-0.1097	-	CCR2	-0.02936	-
SOD1	-0.1036	-	IL1B	-0.009502	-
TLR4	0.1889	-	CXCL16	-0.006543	-
TLR2	0.04009	-	IL6R	-0.002795	-
IFNGR2	0.06715	-	TNF	-0.001909	-

(a) FINISH vs 24REST

(b) START vs 24REST

Table S4: Inflammatory markers significance in two comparisons (a) and (b). (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 , respectively. (-) indicates no significant.

ID	logFC	adj.pvalue	ID	logFC	adj.pvalue
LRRC8B	-1.687	***	LRRC8B	-0.3233	-
CCR9	-1.12	***	ICOS	0.1917	-
IL4R	-1.225	***	CLEC10A	0.2936	-
IL10RA	-1.091	***	IL4R	-0.1926	-
SOCS4	1.621	***	NADSYN1	0.111	-
NADSYN1	0.6154	***	SOCS6	0.149	-
CD48	-0.643	***	CCR10	-0.1467	-
IL32	-0.8615	***	CD19	-0.08198	-
CCR1	1.453	***	SOD2	0.1118	-
IL6ST	1.033	***	IL10RB	-0.191	-
IL6R	1.501	***	IL6ST	0.1051	-
IL10RB	1.668	***	LRRC8D	0.09817	-
IL15	-1.578	***	CCR1	0.1316	-
LRRC8D	-0.9206	***	IL32	0.0769	-
CCR5	-1.123	***	CCR4	0.1406	-
SOCS6	0.6181	***	SOCS2	0.04513	-
CCL5	0.744	***	SOCS4	0.09687	-
SOCS5	0.5578	***	SOCS5	0.04766	-
GPX1	-0.5111	***	DNMT3A	0.08595	-
CCR10	-0.5314	***	GPX1	0.03581	-
ICOS	0.4613	***	SOCS1	0.07386	-
CCR6	-0.7067	***	CCR9	0.03505	-
SOCS2	0.3546	***	GPX3	0.06348	-
GPX3	-0.9665	***	CCL5	-0.03727	-
SOD2	-0.4221	***	CCR5	0.04759	-
CCR4	-0.8518	***	IL10RA	0.02668	-
CD19	-0.246	***	IL15	0.0322	-
NADK	-0.4668	***	CCR2	-0.02936	-
LRRC8C	-0.4983	***	CD48	0.01062	-
CCR2	0.6099	***	NADK	0.0132	-
DNMT3A	0.6606	***	CCR6	-0.01051	-
SOCS1	0.5241	*	LRRC8C	-0.004385	-
CLEC10A	0.1289	-	IL6R	-0.002795	-

(a) FINISH vs 24REST

(b) START vs 24REST

Table S5: DEGs significance in (a) and (b). (***) , (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 , respectively. (-) indicates no significant.

Table S6: Table with differential express KEGG pathways in START vs FINISH comparison. (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001, < 0.01 and < 0.05 respectively.

Description	adj.pvalue
B cell receptor signaling pathway	***
Osteoclast differentiation	***
Epstein-Barr virus infection	***
Yersinia infection	***
Autophagy - animal	***
T cell receptor signaling pathway	***
Th17 cell differentiation	***
Shigellosis	***
NF-kappa B signaling pathway	***
Salmonella infection	***
Nucleocytoplasmic transport	***
Apoptosis	***
DNA replication	***
Th1 and Th2 cell differentiation	***
Lysosome	***
Endocytosis	***
PD-L1 expression and PD-1 checkpoint pathway in cancer	***
Hepatitis B	***
Human immunodeficiency virus 1 infection	***
NOD-like receptor signaling pathway	***
Ubiquitin mediated proteolysis	***
TNF signaling pathway	***
Toxoplasmosis	***
Human T-cell leukemia virus 1 infection	***
Leishmaniasis	***
Lipid and atherosclerosis	***
Kaposi sarcoma-associated herpesvirus infection	***
Antigen processing and presentation	***
Tuberculosis	***
Chagas disease	***
Chronic myeloid leukemia	***
Influenza A	***
Cellular senescence	**
Viral carcinogenesis	**
Acute myeloid leukemia	**
Necroptosis	**
Sphingolipid signaling pathway	**
Toll-like receptor signaling pathway	**
C-type lectin receptor signaling pathway	**
Renal cell carcinoma	**

Table S6: Table with differential express KEGG pathways in START vs FINISH comparison. (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001, < 0.01 and < 0.05 respectively.

Description	adj.pvalue
Human cytomegalovirus infection	**
MAPK signaling pathway	**
Fc gamma R-mediated phagocytosis	*
Ribosome	*
Chemical carcinogenesis - reactive oxygen species	*
Peroxisome	*
Non-small cell lung cancer	*
Protein processing in endoplasmic reticulum	*
Notch signaling pathway	*
Carbon metabolism	*
Pathogenic Escherichia coli infection	*
Natural killer cell mediated cytotoxicity	*
Pancreatic cancer	*
Neurotrophin signaling pathway	*
Lysine degradation	*
Fc epsilon RI signaling pathway	*
Measles	*
Epithelial cell signaling in Helicobacter pylori infection	*
Fatty acid metabolism	*
Propanoate metabolism	*

Table S7: Table with differential express KEGG pathways in FINISH vs 24REST comparison. (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001, < 0.01 and < 0.05 respectively.

Description	adj.pvalue (%)
Salmonella infection	***
B cell receptor signaling pathway	***
T cell receptor signaling pathway	***
Osteoclast differentiation	***
Autophagy - animal	***
Yersinia infection	***
Lysosome	***
Epstein-Barr virus infection	***
Shigellosis	***
Th17 cell differentiation	***
PD-L1 expression and PD-1 checkpoint pathway in cancer	***
Apoptosis	***

Table S7: Table with differential express KEGG pathways in FINISH vs 24REST comparison. (***) , (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 respectively.

Description	adj.pvalue (%)
Endocytosis	***
Human immunodeficiency virus 1 infection	***
NF-kappa B signaling pathway	***
Th1 and Th2 cell differentiation	***
Kaposi sarcoma-associated herpesvirus infection	***
Hepatitis B	***
Ubiquitin mediated proteolysis	***
Human T-cell leukemia virus 1 infection	***
Non-small cell lung cancer	***
Tuberculosis	***
DNA replication	***
Toxoplasmosis	***
Chronic myeloid leukemia	***
Nucleocytoplasmic transport	***
NOD-like receptor signaling pathway	***
Lipid and atherosclerosis	***
Neurotrophin signaling pathway	***
Antigen processing and presentation	***
Viral carcinogenesis	***
Protein processing in endoplasmic reticulum	***
Sphingolipid signaling pathway	***
Renal cell carcinoma	***
Influenza A	***
TNF signaling pathway	***
Fc gamma R-mediated phagocytosis	***
Cellular senescence	***
Leishmaniasis	***
Measles	***
Pancreatic cancer	***
Chagas disease	***
Epithelial cell signaling in Helicobacter pylori infection	***
Legionellosis	***
C-type lectin receptor signaling pathway	***
Acute myeloid leukemia	***
Mitophagy - animal	***
Notch signaling pathway	***
Human cytomegalovirus infection	***
Fc epsilon RI signaling pathway	***
Carbon metabolism	***
Insulin resistance	***

Table S7: Table with differential express KEGG pathways in FINISH vs 24REST comparison. (***), (**) and (*) indicate an adjusted p-value (Bonferroni) < 0.001 , < 0.01 and < 0.05 respectively.

Description	adj.pvalue (%)
Fatty acid metabolism	***
RNA degradation	***
VEGF signaling pathway	***
Pathogenic Escherichia coli infection	***
Phagosome	***
Endometrial cancer	***
Natural killer cell mediated cytotoxicity	***