

High-throughput sequencing metadata template (version 2.1).
All fields in this template must be completed.
Templates containing example data are found in the METADATA EXAMPLES spreadsheet tabs at the foot of this page.
Field names (in blue on this page) should not be edited. Hover over cells containing field names to view field content guidelines.
Human data. If there are patient privacy concerns regarding making data fully public through GEO, please submit to NCBI's dbGaP (<http://www.ncbi.nlm.nih.gov/gap>) database. dbGaP has controlled access mechanisms and is an appropriate resource for hosting sensitive patient data.

SERIES

This section describes the overall experiment.

title Gene expression profile of tumor-associated macrophages according to morphological features in human colorectal liver metastasis (CLM)

The immune landscape impacts outcome and therapeutic response in many tumor types, including colorectal liver metastases (CLM). It has long been known that in vitro polarized macrophages differ in morphology. Here we tested the hypothesis that morphology of tumor-associated macrophages (TAMs) in CLM represents a correlate of function with prognostic significance. Density and morphological metrics (area and perimeter) of TAMs were measured and correlated with clinic-pathological prognostic variables. While density of TAMs did not correlate with survival of CLM patients, cell area identified small and large macrophages that associated with 5-year disease-free survival rate of 27.8% and 0.2% respectively (P<0.001). RNA sequencing of morphologically distinct macrophages identified LXR/RXR as the most enriched pathway in large macrophages and upregulation of genes involved in cholesterol metabolism, phagocytosis and downregulation of the inflammatory program. These results support that accurate, morphometric characterization can serve as a simple readout of TAM diversity with prognostic significance.

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supplementary file
SRA_center_name_code [optional]

SAMPLES

This section lists and describes each of the biological Samples under investigation, as well as any protocols that are specific to individual Samples.

Sample name	title	source name	organism	characteristics: tumor	molecule	processed data file	processed data file	raw file	raw file
Sample 1	P8_large_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P8_large_Macrophages_Forward bw	P8_large_Macrophages_Reverse bw	P8_large_Macrophages_R1.fastq.gz	P8_large_Macrophages_R2.fastq.gz
Sample 2	P8_small_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P8_small_Macrophages_Forward bw	P8_small_Macrophages_Reverse bw	P8_small_Macrophages_R1.fastq.gz	P8_small_Macrophages_R2.fastq.gz
Sample 3	P9_large_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P9_large_Macrophages_Forward bw	P9_large_Macrophages_Reverse bw	P9_large_Macrophages_R1.fastq.gz	P9_large_Macrophages_R2.fastq.gz
Sample 4	P9_small_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P9_small_Macrophages_Forward bw	P9_small_Macrophages_Reverse bw	P9_small_Macrophages_R1.fastq.gz	P9_small_Macrophages_R2.fastq.gz
Sample 5	P10_large_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P10_large_Macrophages_Forward bw	P10_large_Macrophages_Reverse bw	P10_large_Macrophages_R1.fastq.gz	P10_large_Macrophages_R2.fastq.gz
Sample 6	P10_small_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P10_small_Macrophages_Forward bw	P10_small_Macrophages_Reverse bw	P10_small_Macrophages_R1.fastq.gz	P10_small_Macrophages_R2.fastq.gz
Sample 7	P11_large_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P11_large_Macrophages_Forward bw	P11_large_Macrophages_Reverse bw	P11_large_Macrophages_R1.fastq.gz	P11_large_Macrophages_R2.fastq.gz
Sample 8	P11_small_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P11_small_Macrophages_Forward bw	P11_small_Macrophages_Reverse bw	P11_small_Macrophages_R1.fastq.gz	P11_small_Macrophages_R2.fastq.gz
Sample 9	P12_large_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P12_large_Macrophages_Forward bw	P12_large_Macrophages_Reverse bw	P12_large_Macrophages_R1.fastq.gz	P12_large_Macrophages_R2.fastq.gz
Sample 10	P12_small_Macrophages	Human sapiens	Homo sapiens	Colorectal liver metastasis	mRNA	P12_small_Macrophages_Forward bw	P12_small_Macrophages_Reverse bw	P12_small_Macrophages_R1.fastq.gz	P12_small_Macrophages_R2.fastq.gz

PROTOCOLS

Any of the protocols below which are applicable to only a subset of Samples should be included as additional columns of the SAMPLES section instead.

growth protocol
treatment protocol
extract protocol Total RNA was extracted using the Single Cell RNA Purification Kit (Norgen Biotek), following the manufacturer's recommendations for extraction from low cell numbers.
library construction protocol Libraries were constructed by SMARTer Stranded Total RNA Kit (Clontech) according to manufacturer's instructions.
library strategy Paired-end sequence reads (75-tp in length) were generated on an Illumina NextSeq 500.

DATA PROCESSING PIPELINE

Data processing steps include base-calling, alignment, filtering, peak-calling, generation of normalized abundance measurements etc...
 # For each step provide a description, as well as software name, version, parameters, if applicable.
 # Include additional steps, as necessary.
data processing step RNA-seq reads were aligned to the Ensembl GRCh38 genome assembly using STAR (02021) with the following parameters: --outFilterIntronMotifs RemoveNoncanonical --quantMode TranscriptomeSAM GeneCounts.
data processing step Differential expression analysis was performed using the GLM approach implemented in the R/Bioconductor package EdgeR.
Ensembl/ Homo Sapiens release GRCh38
processed data files format and content bigWig were generated using bam2wig.py module in RSeQC v2.5

For each file listed in the "processed data file" columns of the SAMPLES section, provide additional information below.

PROCESSED DATA FILES	file type	file checksum
P8_large_Macrophages_Forward bw	bigWig	84713503ee1446a60eefa5027138585
P8_large_Macrophages_Reverse bw	bigWig	23454c2420204d1f1ce0f8603336
P8_small_Macrophages_Forward bw	bigWig	5727002c3e20a2c272327a7686c4
P8_small_Macrophages_Reverse bw	bigWig	657204024b02f0c229a94ac09b2e26b
P9_large_Macrophages_Forward bw	bigWig	60e67001c724c624044c0a0701a9
P9_large_Macrophages_Reverse bw	bigWig	42ee483203c4c48f9f5c447327ba0f
P9_small_Macrophages_Forward bw	bigWig	347acba00097ee6d9a03a05095
P9_small_Macrophages_Reverse bw	bigWig	008c0aa7488a970d979e053eb47552
P10_large_Macrophages_Forward bw	bigWig	3263586f142a26071c731815d67796
P10_large_Macrophages_Reverse bw	bigWig	28c2716264b61150e0c4ef926271
P10_small_Macrophages_Forward bw	bigWig	9e0a55916ea89f16251ce1ee0882550
P10_small_Macrophages_Reverse bw	bigWig	4e02695918111802a09486e64e2
P11_large_Macrophages_Forward bw	bigWig	856af05c414b2b7ad429f938f9b2e
P11_large_Macrophages_Reverse bw	bigWig	16856d869952232903b6fca8738
P11_small_Macrophages_Forward bw	bigWig	c2b0468ad8e0e201003a033c0ad7
P11_small_Macrophages_Reverse bw	bigWig	13a68516521b1611048c92079f6c96
P12_large_Macrophages_Forward bw	bigWig	384544717234268c0330b6e4c19
P12_large_Macrophages_Reverse bw	bigWig	c09842232a20124449604c0e35e38
P12_small_Macrophages_Forward bw	bigWig	5a0c2591656978a2cc2c34603a0e87
P12_small_Macrophages_Reverse bw	bigWig	bb8a2a73cc09f044498571a0af91

For each file listed in the "raw file" columns of the SAMPLES section, provide additional information below.

RAW FILES	file type	file checksum	instrument model	read length
P8_large_Macrophages_R1.fastq.gz	fastq	50e97a096f7186c21316a4944d0d4	NextSeq500	78bp
P8_large_Macrophages_R2.fastq.gz	fastq	6aa03030e1149f7ed3c5302403a3b	NextSeq500	78bp
P8_small_Macrophages_R1.fastq.gz	fastq	780c8009f9da374b14292a89151c2	NextSeq500	78bp
P8_small_Macrophages_R2.fastq.gz	fastq	6c34c7cf24240880e858150a87e6	NextSeq500	78bp
P9_large_Macrophages_R1.fastq.gz	fastq	89502303b9e09e844229f6a3a98f	NextSeq500	78bp
P9_large_Macrophages_R2.fastq.gz	fastq	797320c0e44830e3264e0f816995d	NextSeq500	78bp
P9_small_Macrophages_R1.fastq.gz	fastq	36e530a8836932c2a1988b9841	NextSeq500	78bp
P9_small_Macrophages_R2.fastq.gz	fastq	51901e15c071101489f1d95188f	NextSeq500	78bp
P10_large_Macrophages_R1.fastq.gz	fastq	43c6147171bc01c747050e375	NextSeq500	78bp
P10_large_Macrophages_R2.fastq.gz	fastq	13735185c5c22f8a21544110468184	NextSeq500	78bp
P10_small_Macrophages_R1.fastq.gz	fastq	1e6d4c258f89203704569058f	NextSeq500	78bp
P10_small_Macrophages_R2.fastq.gz	fastq	7230b0895eacc24b16671c6819107d0c	NextSeq500	78bp
P11_large_Macrophages_R1.fastq.gz	fastq	2624a72a4830c190080760f6a30c	NextSeq500	78bp
P11_large_Macrophages_R2.fastq.gz	fastq	49f4aa6893a3417a1064e29f4c2	NextSeq500	78bp
P11_small_Macrophages_R1.fastq.gz	fastq	86a07350c0d41b3070d51864470974	NextSeq500	78bp
P11_small_Macrophages_R2.fastq.gz	fastq	3881100c09c301018689a054c2b	NextSeq500	78bp
P12_large_Macrophages_R1.fastq.gz	fastq	7c7d831d8907e75d08a38922c06b	NextSeq500	78bp
P12_large_Macrophages_R2.fastq.gz	fastq	6a7b003a4c8d895385302c2298035	NextSeq500	78bp
P12_small_Macrophages_R1.fastq.gz	fastq	64ee2a26a745e98844200514618cf	NextSeq500	78bp
P12_small_Macrophages_R2.fastq.gz	fastq	2d47e20e3a7647d95aea7a2328a148f1	NextSeq500	78bp

For paired-end experiments, list the 2 associated raw files, and provide average insert size and standard deviation, if known. For SOLID experiments, list the 4 file names (include "file name 3" and "file name 4" columns).

PAIRED-END EXPERIMENTS	file name 1	file name 2	average insert size	standard deviation
	P8_large_Macrophages_R1.fastq.gz	P8_large_Macrophages_R2.fastq.gz	44.78	57.69
	P8_small_Macrophages_R1.fastq.gz	P8_small_Macrophages_R2.fastq.gz	37.97	54.16
	P9_large_Macrophages_R1.fastq.gz	P9_large_Macrophages_R2.fastq.gz	41.64	57.82
	P9_small_Macrophages_R1.fastq.gz	P9_small_Macrophages_R2.fastq.gz	44.82	57.34
	P10_large_Macrophages_R1.fastq.gz	P10_large_Macrophages_R2.fastq.gz	45.14	56.32
	P10_small_Macrophages_R1.fastq.gz	P10_small_Macrophages_R2.fastq.gz	43.44	55.4
	P11_large_Macrophages_R1.fastq.gz	P11_large_Macrophages_R2.fastq.gz	39.12	55.39
	P11_small_Macrophages_R1.fastq.gz	P11_small_Macrophages_R2.fastq.gz	42.25	56.94
	P12_large_Macrophages_R1.fastq.gz	P12_large_Macrophages_R2.fastq.gz	47.45	57.45
	P12_small_Macrophages_R1.fastq.gz	P12_small_Macrophages_R2.fastq.gz	20.07	51.09