Series GSE108989

Query DataSets for GSE108989

Status	Public on Oct 29, 2018
Title	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer
Organism	Homo sapiens
Experiment type	Expression profiling by high throughput sequencing
Summary	T cells are central players in cancer immunotherapy1, yet some of their fundamental properties such as development and migration within tumours remain elusive. The enormous T cell receptor (TCR) repertoire, required for recognising foreign and self-antigens2,3, could serve as lineage tags to track these T cells in tumours4. Here, we obtained transcriptomes of 11,138 single T cells from 12 colorectal cancer (CRC) patients and developed STARTRAC (Single T-cell Analysis by Rna-seq and Tcr TRACking) indices to quantitatively analyse dynamic relationships among 20 identified T cell subsets with distinct functions and clonalities. While both CD8+ effector and ?exhausted? T cells exhibited high clonal expansion, they were independently connected with tumour-resident CD8+ effector memory cells, implicating a TCR-based fate decision. Of the CD4+ T cells, the majority of tumour-infiltrating Tregs showed clonal exclusivity, whereas certain Treg clones were developmentally linked to multiple TH clones. Notably, we identified two IFNG+ TH1-like clusters in tumours, the GZMK+ TEM and CXCL13+ TH1-like clusters, which were associated with distinct IFN-?-regulating transcription factors, EOMES/RUNX3 and BHLHE40, respectively. Only BHLHE40+ CXCL13+ TH1-like cells were preferentially enriched in tumours of microsatellite-instable (MSI) patients, which might explain their favourable response rates to immune-checkpoint blockade. Furthermore, we found IGFLR1 to be highly expressed in both BHLHE40+CXCL13+ TH1-like and CD8+ exhausted T cells and possessed co-stimulatory functions. Our integrated STARTRAC analyses provided a powerful avenue to comprehensively dissect the T cell properties in CRC, which could shed new insights into the dynamic relationships of T cells in other cancers.
Overall design	T cells from CRC patients were sorted, profiled by Smart-seq2 and sequenced on HiSeq4000. Based on FACS analysis, single cells of different subtypes, including CD8+ T cells (CD3+ and CD8+), T helper cells (CD3+, CD4+ and CD25-), and regulatory T cells (CD3+, CD4+ and CD25high) were sorted to perform RNA sequencing. The categories ?""sampleType"" column in the SAMPLES section? contain PTC(CD8+ T cells from peripheral blood), NTC(CD8+ T cells from adjacent normal colonrectal tissues) ,TTC (CD8+ T cells from tumor), PTH(CD3+, CD4+ and CD25- T cells from peripheral blood), NTH(CD3+, CD4+ and CD25- T cells from adjacent normal colonrectal tissues), TTH(CD3+, CD4+ and CD25- T cells from tumor), PTR(CD3+, CD4+ and CD25high T cells from peripheral blood), NTR(CD3+, CD4+ and CD25high T cells from adjacent normal colonrectal tissues), TTR(CD3+, CD4+ and CD25high T cells from tumor), PTY(CD3+, CD4+ and CD25mediate T cells from peripheral blood), NTY(CD3+, CD4+ and CD25mediate T cells from adjacent normal colonrectal tissues), TTY(CD3+, CD4+ and CD25medate T cells from tumor), PP7(CD3+, CD4+ T cells from peripheral blood), NP7(CD3+, CD4+ T cells from adjacent normal colonrectal tissues), TP7(CD3+, CD4+ T cells from tumor). Raw data access provided at: European Genome-phenome Archive (EGA) under accession EGAS00001002791
Contributor(s)	Zhang L, Yu X, Zheng L, Zhang Y, Li Y, Fang Q, Gao R, Kang B, Zhang Q, Huang JY, Konno H, Guo X, Ye Y, Gao S, Wang S, Hu X, Ren X, Shen Z, Ouyang W, Zhang Z
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Platforms (1) GPL20301 Illumina HiSeq 4000 (Homo sapiens)

Samples (12) GSM3356219 P0123
More... GSM3356220 P0215
GSM3356221 P0309

Relations

BioProject PRJNA429424

Listing of Individual Cells header descriptions

UniqueCell_ID

Patient_ID

majorCluster

sampleType

Data table

UniqueCell_ID	Patient_ID	majorCluster	sampleType
NTH5-20180123	P0123	CD4_C01-CCR7	NTH
NTH64-20180123	P0123	CD4_C01-CCR7	NTH
NTR57-20180123	P0123	CD4_C01-CCR7	NTR
PP7-100-20180123	P0123	CD4_C01-CCR7	PP7
PP7-106-20180123	P0123	CD4_C01-CCR7	PP7
PP7-109-20180123	P0123	CD4_C01-CCR7	PP7
PP7-114-20180123	P0123	CD4_C01-CCR7	PP7
PP7-118-20180123	P0123	CD4_C01-CCR7	PP7
PP7-129-20180123	P0123	CD4_C01-CCR7	PP7
PP7-134-20180123	P0123	CD4_C01-CCR7	PP7
PP7-137-20180123	P0123	CD4_C01-CCR7	PP7
PP7-145-20180123	P0123	CD4_C01-CCR7	PP7
PP7-152-20180123	P0123	CD4_C01-CCR7	PP7
PP7-160-20180123	P0123	CD4_C01-CCR7	PP7
PP7-162-20180123	P0123	CD4_C01-CCR7	PP7
PP7-171-20180123	P0123	CD4_C01-CCR7	PP7
PP7-178-20180123	P0123	CD4_C01-CCR7	PP7
PP7-182-20180123	P0123	CD4_C01-CCR7	PP7
PP7-185-20180123	P0123	CD4_C01-CCR7	PP7

Total number of rows: **11138**

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Download family	Format
SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

Supplementary file	Size	Download	File type/resource
GSE108989_CRC.TCell.S10805.norm.centered.txt.gz	368.5 Mb	(ftp)(http)	TXT
GSE108989_CRC.TCell.S11138.TPM.txt.gz	351.6 Mb	(ftp)(http)	TXT
GSE108989_CRC.TCell.S11138.count.txt.gz	69.7 Mb	(ftp)(http)	TXT

SRA Run Selector

Processed data are available on Series record

Raw data not provided for this record