Series GSE99254

Query DataSets for GSE99254

Status	Public on Jun 25, 2018
Title	T cell landscape of non-small cell lung cancer revealed by deep single-cell RNA sequencing
Organism	Homo sapiens
Experiment type	Expression profiling by high throughput sequencing
Summary	Cancer immunotherapies have shown sustained clinical responses in treating non-small cell lung cancer (NSCLC), but the clinical outcome is not uniform among patients, with complex tumour-immune interactions playing key roles. To depict and dissect the baseline landscape of the composition, lineage and functional states of tumor-infiltrating lymphocytes (TILs) in lung cancer, here we generated deep single-cell RNA sequencing data for 12346 T cells from the tumour, adjacent normal tissues and peripheral blood from 14 treatment-naïve NSCLC patients. Based on expression and TCR-based lineage tracking, we found a significant proportion of effector memory T cells with the same origin and similar functional states across peripheral blood and tumours, indicating the existence of systemic T cell immunity. We also observed tumour-infiltrating CD8+ T cells undergoing extensive clonal expansion and exhaustion in tumours, with two clusters of cells exhibiting states preceding exhaustion. Survival analysis on independent datasets suggested that high ratio of "pre-exhausted" to exhausted T cells was associated with better prognosis of lung adenocarcinoma. In addition, we observed a specific cluster of tumour-specific regulatory T cells (Tregs), characterized by a set of immunosuppressive genes, and high expression of their signature genes, including IL1R2, correlated with poor prognosis of lung adenocarcinoma. These findings and the accompanying compendium of single cell data will help the research community to gain further insight into the functional states and dynamics of T cell responses in lung cancer.
Overall design	T cells from NSCLC patients were sorted, profiled by Smart-seq2 and sequenced on Illumina HiSeq2500/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 lung 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 lung 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 lung 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 lung tissues), TTY(CD3+, CD4+ and CD25medate T cells from tumor). Raw data access provided at: European Genome-phenome Archive (EGA) under accession EGAS00001002430
Contributor(s)	Guo X, Zhang Y, Zheng L, Zheng C, Song J, Zhang Q, Kang B, Liu Z, Xing R, Gao R, Zhang L, Dong M, Hu X, Ren X, Gottfried Roider H, Yan T, Zhang Z
Citation(s)	Guo X, Zhang Y, Zheng L, Zheng C et al. Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. *Nat Med* 2018 Jul;24(7):978-985. PMID: 29942094
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Platforms (2) GPL16791 Illumina HiSeq 2500 (Homo sapiens)
GPL20301 Illumina HiSeq 4000 (Homo sapiens)

Samples (14) GSM2639575 P0617
More... GSM2639576 P0729
GSM2639577 P1118

Relations

BioProject PRJNA387726

Listing of Individual Cells header descriptions

UniqueCell_ID

Patient

majorCluster

sampleType

Data table

UniqueCell_ID	Patient	majorCluster	sampleType
NTH-86-0617	P0617	CD4_C1-CCR7	NTH
NTH69-0619	P0619	CD4_C1-CCR7	NTH
NTH19-0913	P0913	CD4_C1-CCR7	NTH
NTH21-0913	P0913	CD4_C1-CCR7	NTH
NTH25-0913	P0913	CD4_C1-CCR7	NTH
NTH37-0913	P0913	CD4_C1-CCR7	NTH
NTH51-0913	P0913	CD4_C1-CCR7	NTH
NTH69-0913	P0913	CD4_C1-CCR7	NTH
NTH77-0913	P0913	CD4_C1-CCR7	NTH
NTH87-0913	P0913	CD4_C1-CCR7	NTH
NTH95-0913	P0913	CD4_C1-CCR7	NTH
NTH14-1010	P1010	CD4_C1-CCR7	NTH
NTH85-1118	P1118	CD4_C1-CCR7	NTH
NTH3-20171219	P1219	CD4_C1-CCR7	NTH
NTR31-0619	P0619	CD4_C1-CCR7	NTR
NTR94-0619	P0619	CD4_C1-CCR7	NTR
NTS9-0729	P0729	CD4_C1-CCR7	NTR
NTY-A1-1202	P1202	CD4_C1-CCR7	NTY
NTY13-20171219	P1219	CD4_C1-CCR7	NTY

Total number of rows: **12346**

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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
GSE99254_NSCLC.TCell.S11769.norm.centered.txt.gz	342.4 Mb	(ftp)(http)	TXT
GSE99254_NSCLC.TCell.S12346.TPM.txt.gz	326.8 Mb	(ftp)(http)	TXT
GSE99254_NSCLC.TCell.S12346.count.txt.gz	67.8 Mb	(ftp)(http)	TXT

SRA Run Selector

Raw data not provided for this record

Processed data is available on Series record