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## Series GSE112996

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**Status** Public on Nov 04, 2018  
**Title** Transcript analysis of multi-locus sampled tumor tissue in patients with non-small cell lung cancer  
**Organism** [Homo sapiens](#)  
**Experiment type** Expression profiling by high throughput sequencing  
**Summary** we investigated the spatial features of surgically-removed biopsies from multiple loci in tumor masses of 15 patients with non-small cell lung cancer (NSCLC). We observed that the immune microenvironment is highly spatial heterogeneous such that intra-tumoral regional variation is as large as inter-personal variation. While the local mutational burden was associated with local T cell clonal expansion, observed local anti-tumor cytotoxicity is strongly associated with local tumoral circumstance rather than TMB alone  
**Overall design** We recruited 15 newly-diagnosed NSCLC patients who had surgery with curative intent, and multiple biopsy samples were collected from each individual tumor mass according to previously method. For each sample, we performed multiple genomic and immunogenomic assays including whole exome sequencing (WES), transcriptome profiling (RNA-Seq), and T cell repertoire sequencing (TCR-Seq).  
**Contributor(s)** [Jia Q](#), [Wu W](#), [Wang Y](#), [Alexander PB](#), [Sun C](#), [Gong Z](#), [Cheng J](#), [Sun H](#), [Guan Y](#), [Xia X](#), [Yang L](#), [Yi X](#), [Wan YY](#), [Wang H](#), [Futreal PA](#), [Li Q](#), [Zhu B](#)  
**Citation(s)** Jia Q, Wu W, Wang Y, Alexander PB et al. Local mutational diversity drives intratumoral immune heterogeneity in non-small cell lung cancer. *Nat Commun* 2018 Dec 18;9(1):5361. PMID: [30560866](#)  
**Submission date** Apr 11, 2018  
**Last update date** Mar 20, 2019  
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**Platforms (1)** [GPL20795](#) HiSeq X Ten (Homo sapiens)

**Samples (45)** [GSM3092983](#) 160003803T-1  
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