

Human Radiotherapeutic Side Effect-Related Gene SNP Detection Kit

(Next Generation Sequencing)



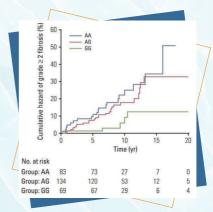
TUMOR AND RADIOTHERAPEUTIC

Radiotherapy is an effective means of comprehensive treatment for tumors. While inhibiting or killing tumor cells, it produces radiotherapy-induced toxic side effects that can cause great pain to patients and even affect the smooth progress of treatment. The differences in radiotherapy toxicity between individuals are significant. Detecting the expression of genes related to radiotherapy toxicity in tumor patients can predict the risk of adverse reactions in patients.

The variability of radiotherapy toxicity is related to single nucleotide polymorphisms (SNPs) in related genes. Evaluating the SNPs of patients' related genes can predict their sensitivity to radiotherapy, thus providing patients with effective and minimally toxic treatment options to minimize the adverse effects of radiotherapy on tumor patients and maximize the therapeutic effects to improve patient survival.

GENOTYPE AND RADIOTHERAPY

For example: In radiotherapy for breast cancer, individuals with different DNMT1 genotypes have different risks of developing fibrosis caused by radiotherapy. Compared to patients with AA/AG genotypes, patients with the GG genotype have a lower probability of developing radiation-induced skin fibrosis.



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Gene	Genotype	Types of Tumor Treatment	Types of Radiation Toxicity	
TGFB1	GG/GA/AA	Prostate cancer	The G genotype increases gastrointestinal and genitourinary toxicity.	
	AA/AG/GG	Head and neck cancer	Patients with the A genotype may have an increased risk of developing radiation dermatitis compared to patients with the GG genotype.	
GSTP1	AA/AG/GG	Breast cancer	Patients with the G genotype have an increased likelihood of developing radiation-induced skin fibrosis compared to patients with the the AA genotype.	
	CC/CG/GG	NSCLC	Patients with the CC genotype have a increased risk of radiation pneumonitis compared to patients with the GC/GG genotype.	
HSPB1		NSCLC	Patients with the GC/GG genotype have a decreased risk of radiation esophagitis compared to patients with the CC genotype.	
		Lung cancer	There is no direct correlation with radiation pneumonitis and lung injury.	

DETECTED GENES

Using high-throughput sequencing on peripheral blood samples from tumor patients, this method comprehensively tests 61 SNP loci in 41 radiation-induced toxicity-related genes including XRCC1, TNFa, TXNRD2, ERCC2, TGFBI, VEGF, DNMT1, TP53, XRCC3, LIN28B, MTHFR, PON1, GSTP1, ATM, NOS2, APEX1, MLH1, IL8, CD44, LIG4, IL1A, CYP2C8, IL4, NEIL1, NBN, APC, NFKBIA, DEAD, Tpa, RAD51, NFE2L2, GSTA1, MGMT, TDG, GSK3β, FSHR, MY03B, TGFBR2, KDM3B, HSPB1 and TXN. This method provides comprehensive information to aid clinicians in predicting the efficacy and toxicity of radiotherapy, and in developing rational and feasible radiotherapy plans.

PRODUCT INFORMATION

Product Name	Core Technology	Pack Size	Instruments Validated	Sample Type
Human Radiotherapeutic Side Effect-Related Gene SNP Detection Kit	RingCap®	16 Tests/Kit 32 Tests/Kit	Ion torrent Illumina MGI	Peripheral blood

DETECTION SIGNIFICANCE

Through the prediction of the probability of experiencing radiotherapy toxicity, adjustments can be made to therapeutic regimens to minimize the potential for adverse effects.

FEATURES & ADVANTAGES

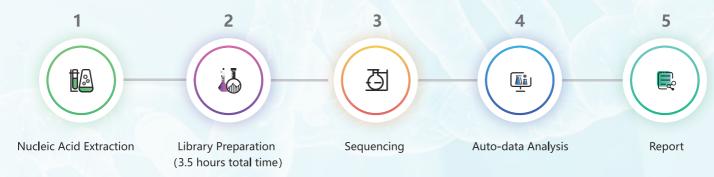
Ease of Use: Based on the independent patent technology RingCap®, Library preparation in 2 steps.

Fast Results: The library preparation takes only 3.5 hours.

Comprehensive Detection: Covers SNP loci related to the toxicity of radiotherapy-associated genes.

Accurate and Reliable: Specific primers are used to amplify and capture the target fragment, which is suitable for peripheral blood samples.

DETECTION PROCESS





Tel:+86-592-7578317

Email: spacegen@ispacegen.com

www.sspacegen.com

XIAMEN SPACEGEN CO.,LTD

XIAMEN SPACESEQ MEDLAB CO.,LTD

A d d : NO.2041,XizhouRoad,Xike Town, Tong'an District,Xiamen City, Fujian Province, China

SUZHOU SPACESEQ MEDLAB CO.,LTD

4th Floor, Building 1, No. 777 Kangyuan Road, Chengyang Street, Suzhou City 213000