

Supplementary Figures.

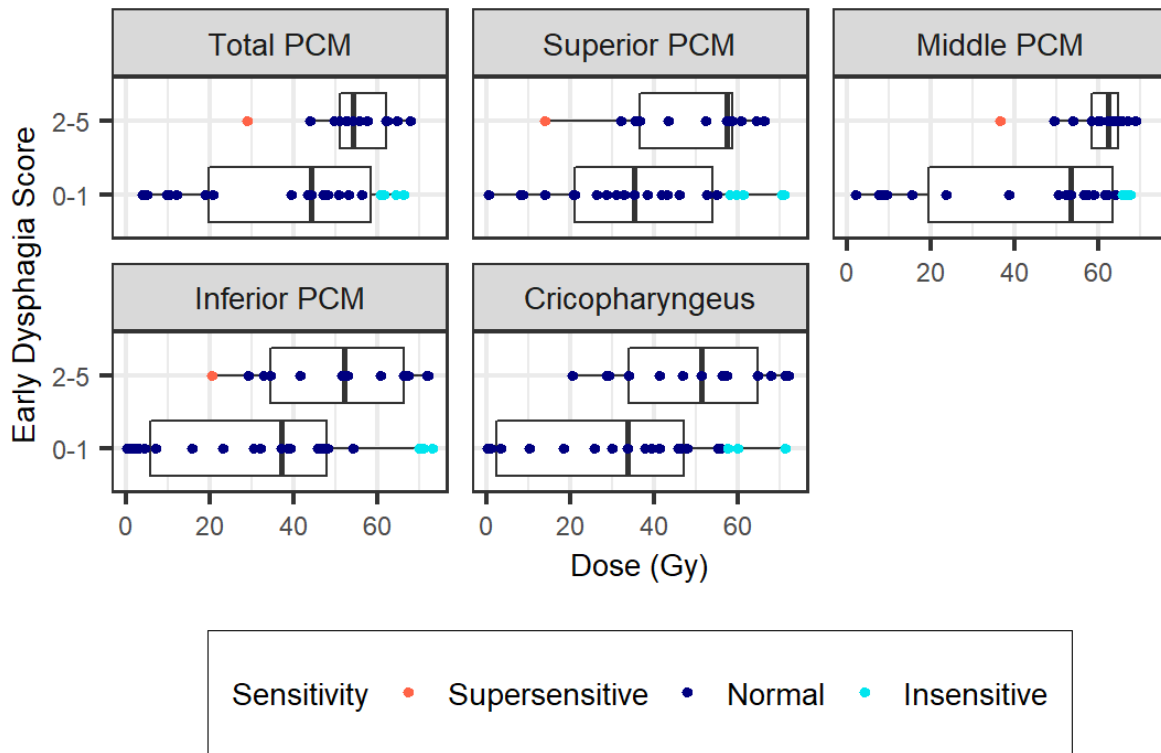


Figure S1. Early Dysphagia by RT Sensitivity. Mean doses to structures associated with early dysphagia versus early dysphagia outcomes for 36 patients are plotted. For a particular metric, patients were identified as sensitive if they received low dose (defined as a mean dose less than the 1st quartile dose value for the entire cohort) yet had poor outcomes (grade 2-5). Patients were identified as insensitive if they received high dose (defined as a mean dose greater than the 3rd quartile dose value for the entire cohort) yet had good outcomes (grade 0-1). Patients who were supersensitive or insensitive for more than two structures were selected as overall supersensitive or insensitive for further genetic analysis. Only 1 patient was identified as overall supersensitive and 8 patients were identified as overall insensitive. Thus a larger overall cohort is needed to investigate genetic differences between supersensitive and insensitive patients for this outcome.

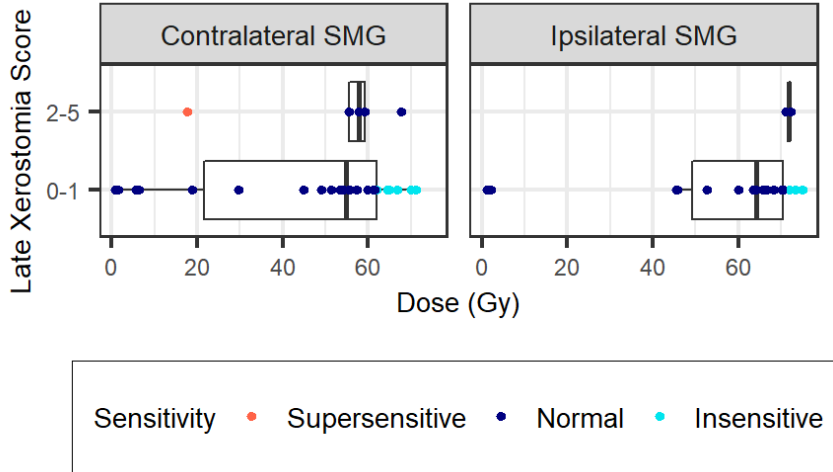


Figure S2. Late Xerostomia by RT Sensitivity. Mean doses to structures associated with late xerostomia versus late xerostomia outcomes for 36 patients are plotted. For a particular metric, patients were identified as sensitive if they received low dose (defined as a mean dose less than the 1st quartile dose value for the entire cohort) yet had poor outcomes (grade 2-5). Patients were identified as insensitive if they received high dose (defined as a mean dose greater than the 3rd quartile dose value for the entire cohort) yet had good outcomes (grade 0-1). Patients who were supersensitive or insensitive for more than two structures were selected as overall supersensitive or insensitive for further genetic analysis. Only 1 patient was identified as overall supersensitive while 2 patients were identified as overall insensitive. Thus a larger overall cohort is needed to investigate genetic differences between supersensitive and insensitive patients for this outcome.

Supplementary Tables.

Table S1. Differentially altered genes.

Gene	% Mutation in Group A	% Mutation in Group C	% Mutation in remaining
	(supersensitive, n=6)	(Insensitive, n=7)	Cohort (n=24)
BRCA2	0	28.6	25.81
ATR	16.7	28.6	12.5
ERBB3	0	0	20.8
TP53	50	42.9	75
NOTCH1	0	14.3	37.5
PIK3CA	0	28.6	25
CDKN2A	83.3	42.9	54.2
CASP8	33.3	0	16.7
NFE2L2	16.7	0	12.5
CCND1	16.7	14.3	33.3
ESR1	0	28.6	16.6
FAT1	66.7	28.6	37.5
Group	% HPV Positive		
A (supersensitive, n=6)	33.33		
C (insensitive, n=7)	71.43		

Table S2. Supersensitive group gene variants.

Gene	Group A (n=6) Supersensitive	Remaining Cohort (n=31)	Diff	Gene	Group A (n=6) Supersensitive	Remaining Cohort (n=31)	Diff
TNFAIP3	33.33333333	0	33.33333333	GNAS	0	16.12903226	16.12903226
MLL3	0	32.25806452	32.25806452	GPR124	0	16.12903226	16.12903226
NOTCH1	0	32.25806452	32.25806452	IKZF1	0	16.12903226	16.12903226
CDKN2A	83.33333333	51.61290323	31.72043011	MAP3K13	0	16.12903226	16.12903226
HNF1A	33.33333333	3.225806452	30.10752688	MYC	0	16.12903226	16.12903226
MAP3K1	33.33333333	3.225806452	30.10752688	PRKCI	0	16.12903226	16.12903226
FGF3	0	29.03225806	29.03225806	SPEN	0	16.12903226	16.12903226
MLL2	0	29.03225806	29.03225806	NOTCH2	33.33333333	19.35483871	13.97849462
FAT1	66.66666667	38.70967742	27.95698925	AKT2	16.66666667	3.225806452	13.44086022
BRCA2	0	25.80645161	25.80645161	BCOR	16.66666667	3.225806452	13.44086022
FGF19	0	25.80645161	25.80645161	BLM	16.66666667	3.225806452	13.44086022
FAT3	0	22.58064516	22.58064516	FAM46C	16.66666667	3.225806452	13.44086022
CASP8	33.33333333	12.90322581	20.43010753	MEN1	16.66666667	3.225806452	13.44086022
BCL6	0	19.35483871	19.35483871	MKNK1	16.66666667	3.225806452	13.44086022
ESR1	0	19.35483871	19.35483871	MST1R	16.66666667	3.225806452	13.44086022
FGF4	0	19.35483871	19.35483871	ALK	0	12.90322581	12.90322581
KLHL6	0	19.35483871	19.35483871	EPHA6	0	12.90322581	12.90322581
SOX2	0	19.35483871	19.35483871	EPHB4	0	12.90322581	12.90322581
TP53	50	67.74193548	17.74193548	FBXW7	0	12.90322581	12.90322581
SPTA1	33.33333333	16.12903226	17.20430108	FGFR1	0	12.90322581	12.90322581
DDR2	16.66666667	0	16.66666667	IRS2	0	12.90322581	12.90322581
FANCA	16.66666667	0	16.66666667	KDM5A	0	12.90322581	12.90322581
FANCI	16.66666667	0	16.66666667	MED12	0	12.90322581	12.90322581
FGF23	16.66666667	0	16.66666667	NF1	0	12.90322581	12.90322581
GEN1	16.66666667	0	16.66666667	PARP2	0	12.90322581	12.90322581
HRAS	16.66666667	0	16.66666667	RAC1	0	12.90322581	12.90322581
HSP90AA1	16.66666667	0	16.66666667	RPTOR	0	12.90322581	12.90322581
PARP1	16.66666667	0	16.66666667	SNCAIP	0	12.90322581	12.90322581
REL	16.66666667	0	16.66666667	TERC	0	12.90322581	12.90322581
SOCS1	16.66666667	0	16.66666667	TIPARP	0	12.90322581	12.90322581
TNKS2	16.66666667	0	16.66666667	ZNF703	0	12.90322581	12.90322581
BRD4	0	16.12903226	16.12903226	CCND1	16.66666667	29.03225806	12.3655914
ERBB3	0	16.12903226	16.12903226				

Table S3. Gene variants.

Gene	Group A (n=6)		Gene	Group A (n=6)		Gene	Group A (n=6)	
	Supersensitive	Insensitive		Supersensitive	Insensitive		Supersensitive	Insensitive
KLHL6	0	42.85714286	MEN1	16.66666667	0	HSD3B1	0	14.28571429
MAP3K13	0	42.85714286	MKNK1	16.66666667	0	IKBKE	0	14.28571429
SOX2	0	42.85714286	MLL	16.66666667	0	IKZF1	0	14.28571429
CDKN2A	83.33333333	42.85714286	MST1R	16.66666667	0	IRS2	0	14.28571429
HPV	33.33333333	71.42857143	NFE2L2	16.66666667	0	KDM5A	0	14.28571429
FAT1	66.66666666	28.57142857	NTRK3	16.66666667	0	KEAP1	0	14.28571429
CASP8	33.33333333	0	PARP1	16.66666667	0	LTK	0	14.28571429
HNF1A	33.33333333	0	REL	16.66666667	0	MEF2B	0	14.28571429
SPTA1	33.33333333	0	RICTOR	16.66666667	0	MITF	0	14.28571429
TERT	33.33333333	0	RNF43	16.66666667	0	MRE11A	0	14.28571429
TNFAIP3	33.33333333	0	SOCS1	16.66666667	0	MYCN	0	14.28571429
BCL6	0	28.57142857	TNKS2	16.66666667	0	NF1	0	14.28571429
BRCA2	0	28.57142857	TSC2	16.66666667	0	NKX2-1	0	14.28571429
BRD4	0	28.57142857	VEGFA	16.66666667	0	NOTCH1	0	14.28571429
ESR1	0	28.57142857	ABL2	0	14.28571429	NOTCH3	0	14.28571429
GPR124	0	28.57142857	ACVR1B	0	14.28571429	NSD1	0	14.28571429
GSK3B	0	28.57142857	AURKA	0	14.28571429	PAK7	0	14.28571429
MLL3	0	28.57142857	BCL2L2	0	14.28571429	PARP2	0	14.28571429
PIK3CB	0	28.57142857	CCNE1	0	14.28571429	PARP4	0	14.28571429
PRKCI	0	28.57142857	CD79A	0	14.28571429	PIK3C2B	0	14.28571429
SNCAIP	0	28.57142857	CDK12	0	14.28571429	PIK3R2	0	14.28571429
SUFU	0	28.57142857	CDK6	0	14.28571429	PLCG2	0	14.28571429
TERC	0	28.57142857	CDKN1A	0	14.28571429	PNRC1	0	14.28571429
TIPARP	0	28.57142857	CUL4A	0	14.28571429	POLE	0	14.28571429
ZNF703	0	28.57142857	EGFR	0	14.28571429	RAD50	0	14.28571429
MAP3K13	33.33333333	14.28571429	EPHA5	0	14.28571429	RAD51B	0	14.28571429
NOTCH2	33.33333333	14.28571429	EPHA6	0	14.28571429	RANBP2	0	14.28571429
AKT2	16.66666667	0	EPHB1	0	14.28571429	RBM10	0	14.28571429
AR	16.66666667	0	EPHB4	0	14.28571429	STAT3	0	14.28571429
ARID1B	16.66666667	0	ERRFI1	0	14.28571429	STK11	0	14.28571429
ARID2	16.66666667	0	FAM123B	0	14.28571429	TEK	0	14.28571429
ASXL1	16.66666667	0	FANCE	0	14.28571429	TOP2A	0	14.28571429
CSF1R	16.66666667	0	FANCL	0	14.28571429	TP53BP1	0	14.28571429
DDR2	16.66666667	0	FANCM	0	14.28571429	TRRAP	0	14.28571429
DIS3	16.66666667	0	FGF10	0	14.28571429	WHSC1L1	0	14.28571429
EP300	16.66666667	0	FGF12	0	14.28571429	XPO1	0	14.28571429
FAM46C	16.66666667	0	FGF14	0	14.28571429	ZNRF3	0	14.28571429
FANCA	16.66666667	0	FGF19	0	14.28571429	ATR	16.66666667	28.57142857
FANCI	16.66666667	0	FGF3	0	14.28571429	PIK3CA	16.66666667	28.57142857
FGF23	16.66666667	0	FGF4	0	14.28571429	PTCH1	16.66666667	28.57142857
GALNT12	16.66666667	0	FGFR1	0	14.28571429	PTPRD	16.66666667	28.57142857
GEN1	16.66666667	0	FH	0	14.28571429	RET	16.66666667	28.57142857
HRAS	16.66666667	0	GNA11	0	14.28571429	TP53BP1	50	42.85714286
HSP90AA1	16.66666667	0	GNA13	0	14.28571429	CDKN2B	33.33333333	28.57142857
KDR	16.66666667	0	GNAS	0	14.28571429			