

Supplemental Table 1: Source, Clinical, and Pathological Features of Sequenced HNSCC Cell Lines

Cell Line	Primary Site	Age	Sex	Primary/Recurrent/Metastatic	Tumor Grade	TMN Stage	Tumorigenic in Nude Mice	Primary Source
BB30-HNC	N/A	N/A	F	N/A	N/A	N/A	N/A	N/A
BB49-HNC	N/A	70	F	N/A	N/A	N/A	N/A	N/A
BHY	Oral Cavity	52	M	N/A	Well Differentiated	N/A	Yes	DSMZ
BICR 16	Oral Cavity	N/A	M	Recurrent	N/A	T2N0M0	Yes	ECACC
BICR 18	Larynx	N/A	M	Metastatic	N/A	N/A	Yes	ECACC
BICR 31	Oral Cavity	N/A	M	Primary	N/A	N/A	Yes	ECACC
BICR 56	Oral Cavity	N/A	F	Primary	N/A	T4N1M0	Yes	ECACC
BICR 6	Pharynx	N/A	M	Primary	N/A	T4N1M0	Yes	ECACC
Ca9-22	Oral Cavity	N/A	M	N/A	N/A	N/A	N/A	JCRB
CAL 27	Oral Cavity	56	M	N/A	N/A	N/A	N/A	ATCC
CAL-33	Oral Cavity	69	M	N/A	Moderately Differentiated	N/A	N/A	DSMZ
Detroit 562	Pharynx	Adult	F	Metastatic	N/A	N/A	N/A	ATCC
FaDu	Pharynx	56	M	Primary	N/A	N/A	Yes	ATCC
HN	Oral Cavity	60	M	Metastatic	Moderately Differentiated	N/A	Yes	DSMZ
HO-1-N-1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	JCRB
HSC-2	Oral Cavity	69	M	N/A	N/A	N/A	N/A	HSRRB
HSC-3	Oral Cavity	64	M	N/A	N/A	N/A	N/A	HSRRB
HSC-4	Oral Cavity	64	M	N/A	N/A	N/A	N/A	HSRRB
KOSC-2	N/A	51	M	N/A	Moderately Differentiated	N/A	N/A	JCRB
LB771-HNC	N/A	49	M	N/A	N/A	N/A	N/A	N/A
PE/CA-PJ15	Oral Cavity	45	M	N/A	N/A	N/A	N/A	ECACC
PE/CA-PJ34 (Clone C12)	Oral Cavity	60	M	N/A	N/A	N/A	N/A	ECACC
PE/CA-PJ41 (Clone D2)	Oral Cavity	67	F	N/A	N/A	N/A	N/A	ECACC
PE/CA-PJ49	Oral Cavity	57	M	N/A	N/A	N/A	N/A	ECACC
RPMI-2650	nasal septum	52	M	N/A	n/a	N/A	N/A	ATCC
SAS	Oral Cavity	N/A	N/A	N/A	Poorly Differentiated	N/A	N/A	JCRB
SCC-15	Oral Cavity	55	M	N/A	N/A	T4N1M0	N/A	ATCC
SCC-25	Oral Cavity	70	M	Primary	N/A	T1N1M0 (T2N1*)	Yes	ATCC
SCC-4	Oral Cavity	55	M	N/A	N/A	T3N0M0	Yes	ATCC
SCC-9	Oral Cavity	25	M	N/A	Well Differentiated	T2N1	Yes	ATCC
SNU-1041	Pharynx	N/A	N/A	N/A	N/A	N/A	N/A	KCLB
SNU-1066	Larynx	62	M	N/A	Moderately Differentiated	N/A	N/A	KCLB
SNU-1076	Larynx	60	M	N/A	Well Differentiated	N/A	N/A	KCLB
SNU-1214	Larynx	55	M	N/A	Moderately Differentiated	N/A	N/A	KCLB
SNU-46	Larynx	65	M	N/A	Moderately Differentiated	N/A	N/A	KCLB
SNU-899	Larynx	56	M	N/A	Moderately Differentiated	N/A	N/A	KCLB
YD-10B	Oral Cavity	67	M	Primary	Moderately Differentiated	N/A	N/A	KCLB
YD-38	Oral Cavity	67	M	N/A	Moderately Differentiated	N/A	No	KCLB
YD-8	Oral Cavity	46	F	Primary	Moderately Differentiated	N/A	No	KCLB

Supplemental Table 2: Genes Mutated in >50% in HNSCC Cell Lines

Gene Name	Number of Cell Lines with Mutation	Mutation Frequency (%)
TP53	33	84.62
NR1H2	31	79.49
VEGFC	31	79.49
CLTCL1	30	76.92
PRKDC	30	76.92
GRIA3	30	76.92
MAML3	27	69.23
ITPR2	24	61.54
MAP3K14	23	58.97
GPR112	23	58.97
NEK3	22	56.41
TTN	22	56.41
RECQL4	22	56.41

Supplemental Table 3: *TP53* Mutations in HNSCC Cell Lines

Cell Line ID	Location (AA Change)	Location (DNA Change)
BB30-HNC	p.S183*	c.548C>A
BICR 16	p.W146*	c.438G>A
BICR 56	p.Y126_splice	c.376_splice
BICR 6	p.Q192*	c.574C>T
Ca9-22	p.R248W	c.742C>T
CAL 27	p.H193L	c.578A>T
CAL-33	p.R175H	c.524G>A
Detroit 562	p.R175H	c.524G>A
FaDu	p.R248L	c.743G>T
	p.V225_splice	c.673_splice
HN	p.H193L	c.578A>T
HO-1-N-1, (Salivary Gland)	p.G266R	c.796G>C
HSC-2	p.E224_splice	c.672_splice
HSC-3	p.K305fs	c.915_916insTAAG
HSC-4	p.R248Q	c.743G>A
KOSC-2	p.Q52>P*	c.154_155insCAT
LB771-HNC	p.H179R	c.536A>G
PE/CA-PJ15	p.R248Q	c.743G>A
PE/CA-PJ34 (Clone C12)	p.A159V	c.476C>T
PE/CA-PJ41 (Clone D2)	p.A307_splice	c.920_splice
SAS	p.E336*	c.1006G>T
SCC-15	p.E224_splice	c.672_splice
SCC-25	p.R209fs	c.626_627delGA
SCC-4	p.P151S	c.451C>T
SNU-1066	p.G187_splice	c.559_splice
SNU-1214	p.A159P	c.475G>C
SNU-46	p.G245C	c.733G>T
YD-10B	p.Y236*	c.708C>A
YD-38	p.G199*	c.595G>T

**Supplemental Table 4: The Numbers of HNSCC Cell Lines and Tumors
Derived from Larynx, Oral Cavity and Pharynx**

		Tumor Site			
		Larynx	Oral Cavity	Pharynx	Total
Source	Cell Lines	6	23	4	33
	Tumors	17	62	24	103
	Total	23	85	28	136

Supplemental Table 5: Mutation Frequency Comparison by Gene

rank	Gene	Percent Mutation		raw p	adjusted p
		Cell Line (N = 33)	Tumor (N = 103)		
1	CDKN2A	42.4	10.7	.0002	.0046
2	MLL3	30.3	5.8	.0004	.0046
3	TTN	60.6	28.1	.0008	.0061
4	FMN2	30.3	5.8	.0010	.0061
5	DST	15.2	7.8	.1366	.6284
6	LRP1B	24.2	13.6	.1429	.6284
7	TP53	81.8	65.0	.1458	.6284
8	ATRX	12.1	4.9	.1843	.6284
9	HERC2	12.1	5.8	.1954	.6284
10	NSD1	12.1	6.8	.3625	.8338
11	EPHA7	6.1	10.8	.3684	.8338
12	NOTCH1	9.1	14.6	.3899	.8338
13	HRAS	3.0	6.8	.4007	.8338
14	CASP8	12.1	6.8	.4029	.8338
15	PIK3CA	12.1	7.8	.4120	.8338
16	CUBN	6.1	9.7	.4877	.8338
17	NAV3	6.1	8.7	.5504	.8338
18	CSMD3	24.2	18.4	.5897	.8338
19	PCDH15	12.1	8.7	.6615	.8338
20	RIMS2	6.1	7.8	.6730	.8338
21	LAMA1	6.1	6.8	.8184	.8963
22	DNAH8	6.1	5.8	.8226	.8963
23	PKHD1	6.1	5.8	.9917	.9917

**Supplemental Table 6: Genes Mutated in >10% of HNSCC Tumors
But Not Mutated in Human HNSCC Cell Lines**

Gene Name	Number of Tumors with Mutation	Mutation Frequency (%)
SYNE1	20	18.87
MUC16	17	16.04
USH2A	14	13.21
SI	13	12.26
RYR2	12	11.32
PRDM9	11	10.38
THSD7A	11	10.38
COL22A1	11	10.38
FAT4	11	10.38
FAT2	11	10.38
PCLO	11	10.38

Supplemental Table 7: EGFR Pathway Mutations in HNSCC Cell Lines and Tumors

Gene Name	Cell Line Name	Tumor ID
RAF1	BICR 18	478*
MAPK1 (ERK 1)	BICR 6	325*
GAB1	BICR 18	HN_62863
MTOR	BICR 18	HN_62421 HN_62469
RAC1	HSC-2	HN_63058
MAP3K3	SNU 1066	HN11PT*
MAP3K4	SCC-4	HN_00190
MAP3K6	SCC-15	HN_62995
MAP2K4 (MEK 4)	BICR 56	HN_62421
STAT1	SNU 1066	388* HN_63080
MAP2K1 (MEK 1)	HSC-3	
MAP2K1 (MEK 1)	BICR 6	
MAPK8 (JNK 1)	BICR 18	
MAPK8 (JNK 1)	BICR 18	
MAPK8 (JNK 1)	HSC-3	
AKT1S1		HN_62854
MAPK8IP2		HN_62426
MAPK9 (JNK 2)		HN_62376
STAT3		HN 01000

Note: HNSCC tumor samples marked with * are from the Agrawal *et al* database. All of the other tumor samples are from the Stransky *et al* database.