

Supplemental data

Supplemental Table S1. Multivariate Cox Regression for Overall Survival based on clinical and pathological features. SE - standard error. Significant P values highlighted in bold.

Variable	Coefficients	SE (Coefficient)	P-value
Lymph node Stage: N2	1.566168	0.330852	2.20E-06
Lymph node Stage: N1b	-20.8274	43635.87	0.999619
Lymph node Stage: N1	-0.12928	0.451136	0.774446
Lymph node Stage: N2a	-16.4087	45044.82	0.999709
Rectum	-0.73874	0.420725	0.07911
Cecum	-0.70427	0.383579	0.06635
Ascending Colon	-0.37758	0.457874	0.409577
Descending Colon	-0.09332	0.731384	0.89847
Transverse Colon	0.413982	0.604313	0.493315
Sigmoid Colon	-1.20682	0.445007	0.00669
Hepatic Flexure	0.527133	0.733024	0.472066
Splenic Flexure	-0.41201	1.023062	0.687154
Rectosigmoid Junction	1.778123	0.74561	0.017089
AJCC Tumour Stage Code: T3	0.226892	0.381172	0.551678
AJCC Tumour Stage Code: T2	-0.61901	0.728314	0.395372
AJCC Tumour Stage Code: T4	1.606711	0.447427	0.000329
Age	0.046981	0.013578	0.00054
Gender: Female	0.368668	0.323521	0.254474
No. Mutations	-0.00183	0.000274	2.32E-11
KRAS	-0.71053	0.337987	0.035533
TP53	-0.94261	0.324816	0.003708
TTN	0.6454	0.331183	0.051323
ZIC1	8.316058	1.025217	5.00E-16
KDM5C	-1.63656	0.741345	0.027276
SMAD4	0.645602	0.45269	0.153826
THBS1	1.468005	0.530649	0.005667
PLXNB1	-15.0342	4917.707	0.997561
CDH13	3.190195	0.75598	2.44E-05
DMBT1	-4.73145	1.02518	3.93E-06
NDRG4	4.488365	1.143605	8.68E-05
PTPN1	-14.6279	2955.821	0.996051

Supplemental Table S2. Personalised Cancer Genome Reporter' (PCGR) chromosomal instability analysis results for the tumour. Chromosomal segment – chromosome number followed by start and end position; Segment length megabase (MB) value; Log Ratio – positive and negative value, for segment gain and loss, respectively; event type – broad or focal.

Chromosomal segment	Segment length (MB)	Log R	Event type
chr4:153276999-189549276	36.272	-0.802	broad
chr8:12613531-37145961	24.532	-1.446	broad
chr8:51307370-75313553	24.006	0.84	focal
chr18:51208501-69150727	17.942	-0.807	broad
chr18:384153-15042098	14.658	-0.804	broad
chr18:69294340-78016309	8.722	-0.805	focal
chr8:164860-71548	6.967	-1.456	focal
chr18:38180664-44471541	6.291	-0.864	focal
chr8:139420362-145027855	5.607	0.822	focal
chr8:42601586-46850220	4.249	0.9	broad
chr8:8232443-12148644	3.916	-1.415	focal
chr18:27137107-30241431	3.104	-0.847	focal
chr8:46850531-48980850	2.130	0.864	focal
chr21:14339867-15896600	1.557	-1.438	focal
chr16:21392689-22699303	1.307	0.971	focal
chr21:15996236-17085531	1.089	-1.469	focal
chr8:7138465-8204572	1.066	-1.224	focal
chr8:41884175-42599971	0.716	1.49	focal
chr16:18099913-18796468	0.697	0.845	focal
chr8:38606727-39284877	0.678	-1.448	focal
chr8:12148928-12608523	0.460	-1.007	focal
chr15:101753918-101980585	0.227	0.875	focal
chr8:41735999-41883748	0.148	1.874	focal
chr18:69152402-69294129	0.142	-1.245	focal
chr6:76182448-76322000	0.140	0.989	focal
chr8:8208060-8229113	0.021	-2.356	focal
chr6:58449983-58453090	0.003	0.963	focal

Supplemental Table S3: sCNA (somatic Copy Number Variation) analysis results for cancer associated genes on chromosome 8. Gene symbol; Gene Name; Chromosomal segment – chromosome number, start and end position.

SYMBOL	GENE NAME	SEGMENT
WRN	WRN RecQ like helicase	chr8:12613531-37145961
UNC5D	unc-5 netrin receptor D	chr8:12613531-37145961
TUSC3	tumour suppressor candidate 3	chr8:12613531-37145961
SOX7	SRY-box transcription factor 7	chr8:8232443-12148644
RHOBTB2	Rho related BTB domain containing 2	chr8:12613531-37145961
ARHGEF10	Rho guanine nucleotide exchange factor 10	chr8:164860-7131548
NKX3-1	NK3 homeobox 1	chr8:12613531-37145961
MTUS1	microtubule associated scaffold protein 1	chr8:12613531-37145961
MCPH1	microcephalin 1	chr8:164860-7131548
LZTS1	leucine zipper tumour suppressor 1	chr8:12613531-37145961
DUSP4	dual specificity phosphatase 4	chr8:12613531-37145961
DLC1	DLC1 Rho GTPase activating protein	chr8:12613531-37145961
CLU	clusterin	chr8:12613531-37145961