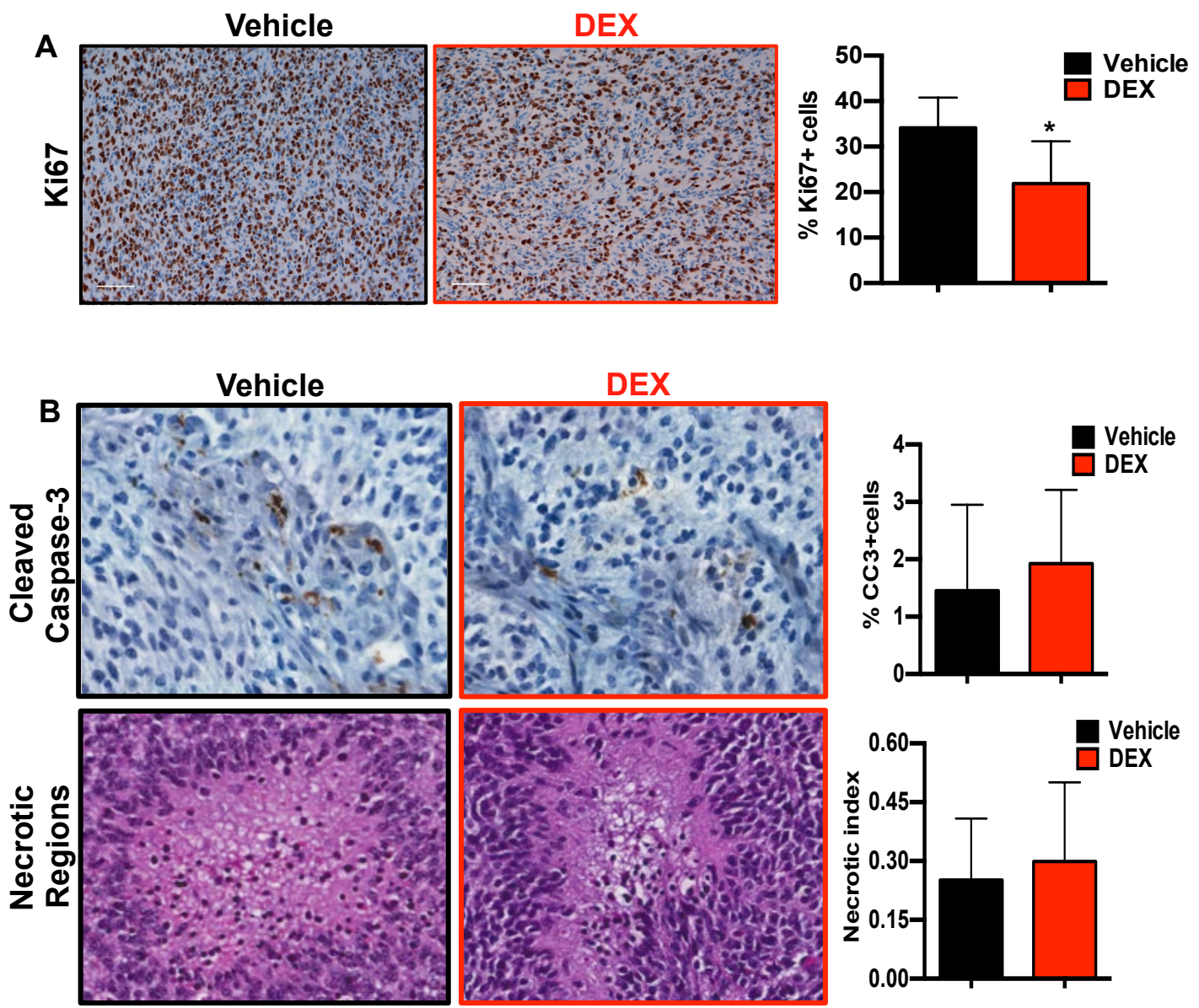
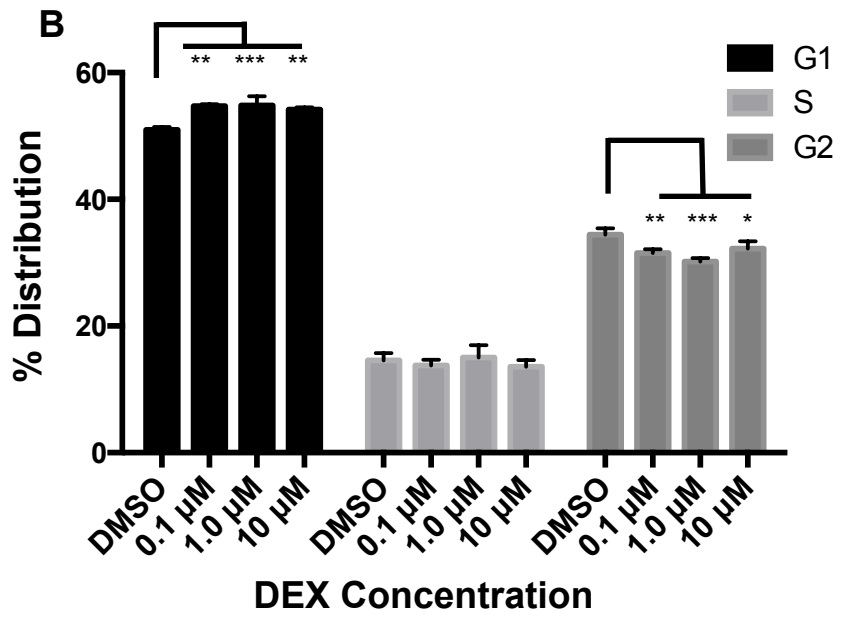
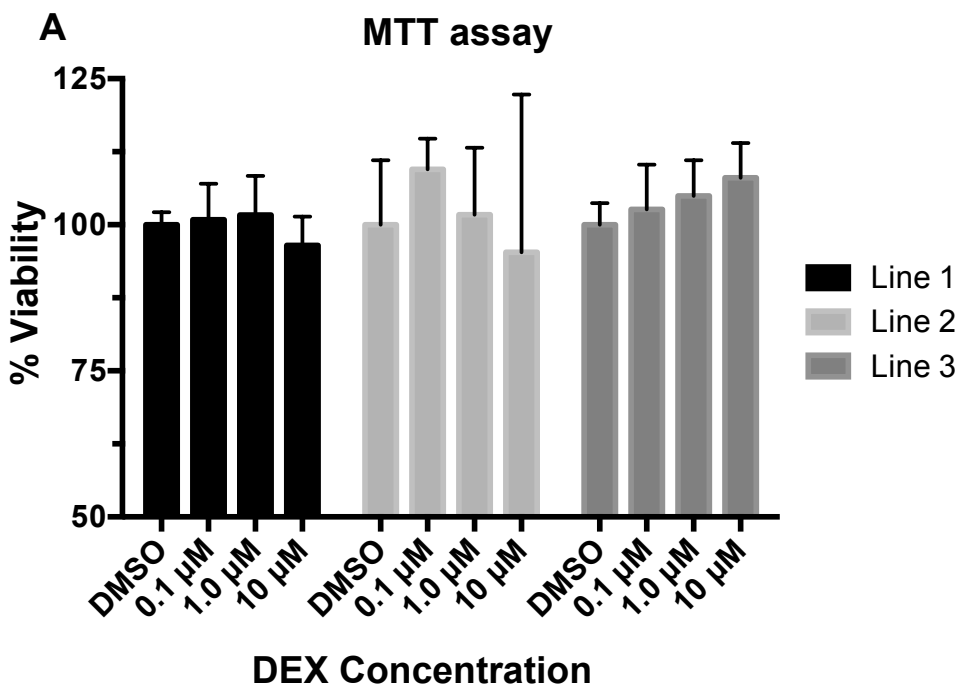


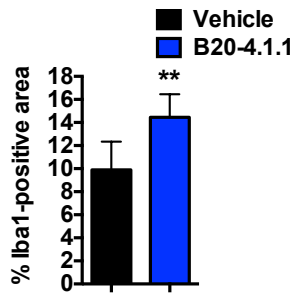
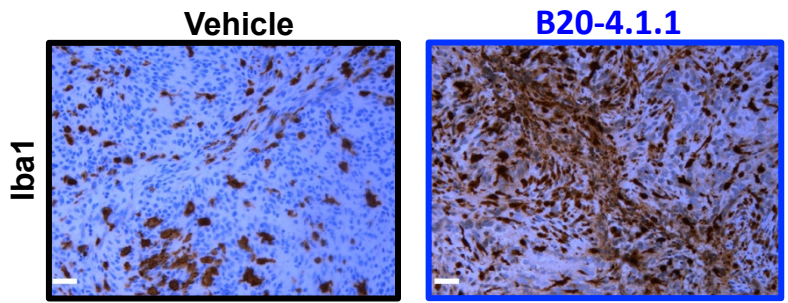
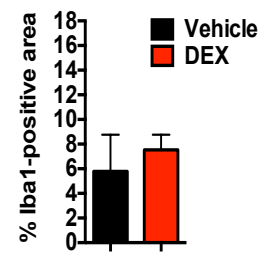
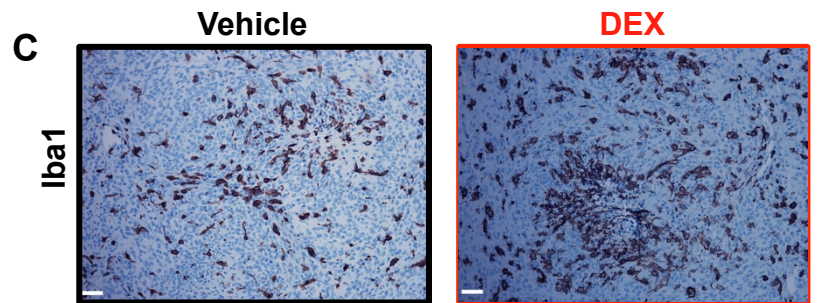
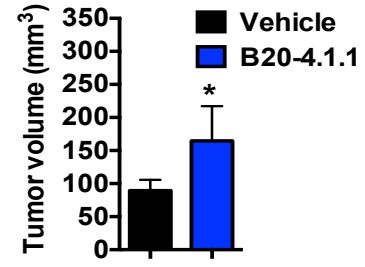
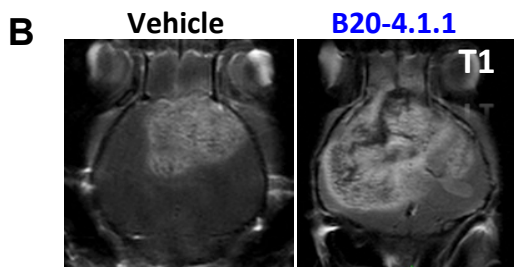
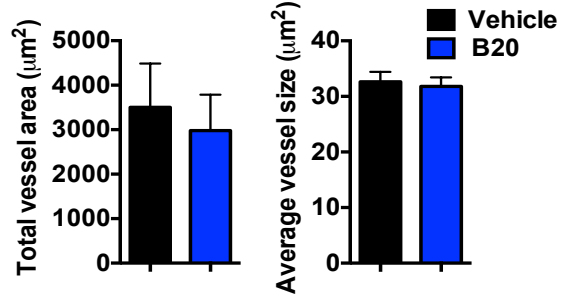
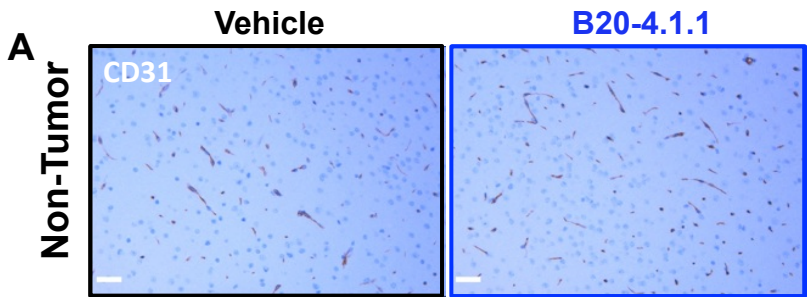
# Supplemental Figure 1



# Supplemental Figure 2



# Supplemental Figure 3

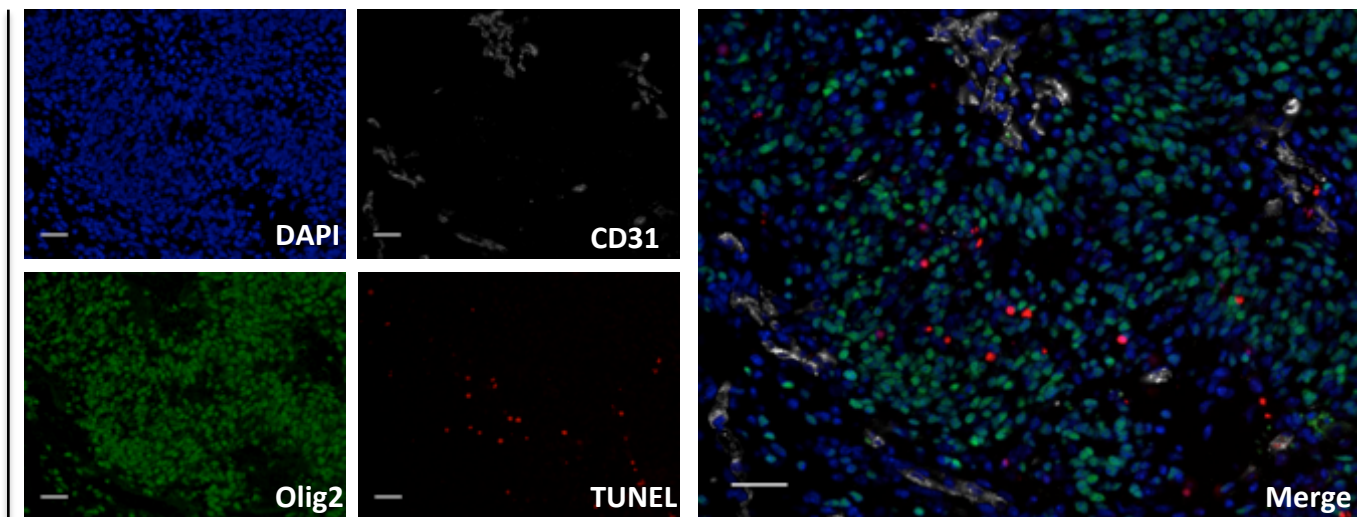




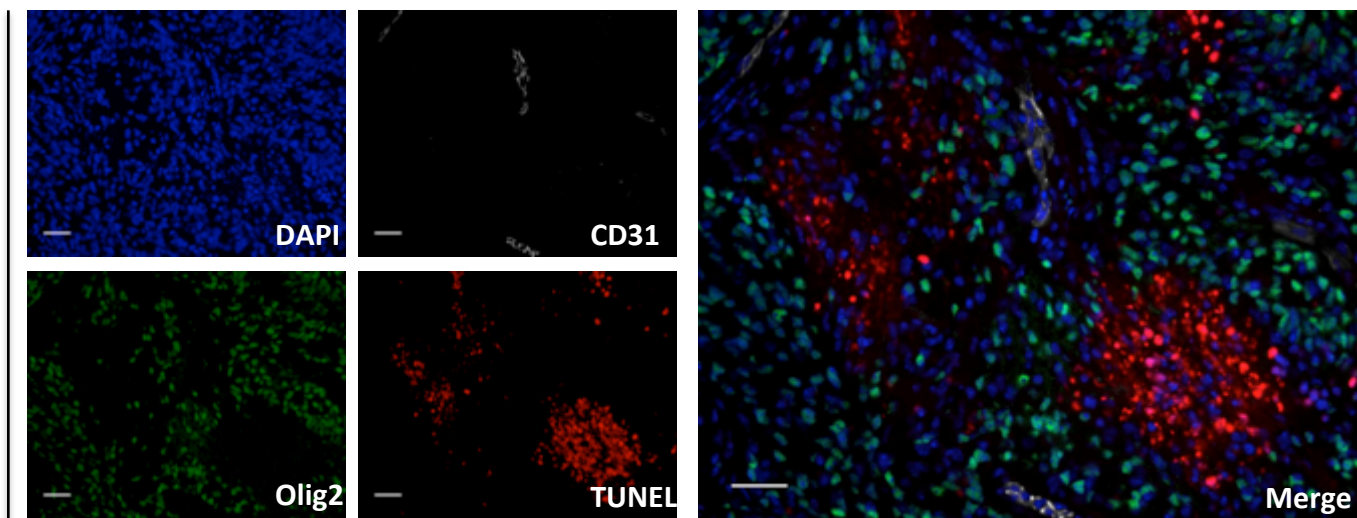
# Supplemental Figure 4

A

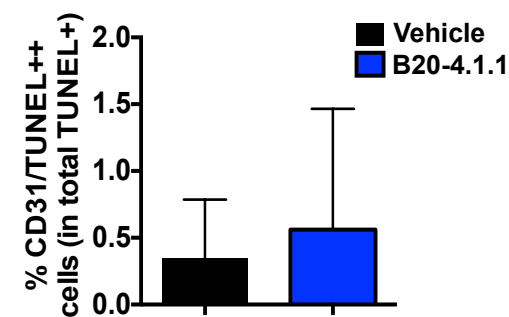
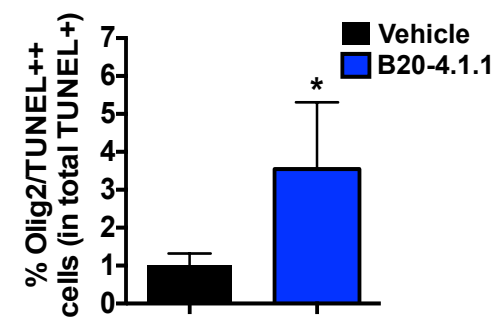
Vehicle



B20-4.1.1



B



# Table S1. Patient and treatment characteristics with or without DEX at the start of radiotherapy

A

Characteristic		N = 522 (84%) +Steroid	N= 100 (16%) -Steroid	p value <sup>^</sup>
<b>Sex n (%)</b>				
	M	326 (62.5%)	70 (70%)	0.1505
	F	196 (37.5%)	30 (30%)	
<b>Age, y</b>				
	Median	59	56	
<b>Age, n (%)</b>				
	<50	130 (24.9%)	27 (27%)	0.7063
	≥50	392 (75.1%)	73 (73%)	
<b>KPS, n (%)</b>				
	≥90	201 (38.5%)	68 (68%)	< 0.0001
	≥70 - <90	231 (44.3%)	28 (28%)	
	<70	90 (17.2%)	4 (4%)	
<b>Mental Satus, n (%)</b>				
	Normal	376 (72%)	85 (85%)	0.0207
	Abnormal	140 (26.8%)	15 (15%)	
	Data Missing	6 (1.1%)	0 (0%)	
<b>Symptom Length</b>				
	<12 wk	405 (77.6%)	76 (76%)	0.7285
	≥12 wk	117 (22.4%)	24 (24%)	
<b>Neurologic functional status, n (%)</b>				
	Working	162 (31%)	57 (57%)	< 0.0001
	Not Working	357 (68.4%)	43 (43%)	
	Data Missing	3 (0.6%)	0 (0%)	
<b>Surgical Extent</b>				
	Biopsy	97 (18.6%)	9 (9%)	0.0032
	Resection			
	STR	231 (44.3%)	37 (37%)	
	GTR	194 (37.2%)	54 (54%)	
<b>Radiation Dose</b>				
	>54.4 Gy	407 (78%)	90 (90%)	0.0019
	≤54.4	105 (20.1%)	6 (6%)	
	Data Missing	10 (1.9%)	4 (4%)	
<b>RPA Class</b>				
	Class 3	72 (13.8%)	23 (23%)	0.0004
	Class 4	145 (27.8%)	40 (40%)	
	Class 5	243 (46.6%)	34 (34%)	
	Class 6	62 (11.9%)	3 (3%)	
<b>Concurrent Chemotherapy</b>				
	TMZ	166 (31.8%)	46 (46%)	0.1381
	No TMZ	359 (67.5%)	51 (56.7%)	

<sup>^</sup>p value calculated using Chi squared test

KPS - Karnofsky Performance Status; STR - Subtotal Resection

GTR - Gross Total Resection, RTOG – Radiation Therapy Oncology Group

RPA - Recursive Partitioning Analysis; TMZ - Temozolomide

B

Cox proportional multivariate hazards analysis of patient prognostic survival factors			
Variables	p value	HR	95% CI
Dexamethasone	p = 0.00034	1.512	1.2058 - 1.8960
RTOG RPA Class	p < 0.0001	1.5461	1.3989 - 1.7088
Temozolomide	p = 0.00096	0.749	0.6312 - 0.8892

HR = hazard ratio CI = confidence interval

RTOG - Radiation Therapy Oncology Group

RPA - Recursive Partitioning Analysis

**Table S2. Patient and treatment characteristics with or without DEX at the start of radiotherapy in EORTC (A) and GGN (B)**

**A**

Characteristics	Steroids at baseline			Total (N=573)
	Missing N=1 (0.17%)	No N=164 (28.6%)	Yes N=408 (71.2%)	
<b>Treatment</b>				
RT	1 (100.0)	70 (42.7)	215 (52.7)	286 (49.9)
TMZ/RT	0 (0.0)	94 (57.3)	193 (47.3)	287 (50.1)
<b>WHO Performance Status</b>				
0	0 (0.0)	80 (48.8)	143 (35.0)	223 (38.9)
>0	1 (100.0)	84 (51.2)	265 (65.0)	350 (61.1)
<b>Extent of surgery</b>				
Biopsy	0 (0.0)	8 (4.9)	85 (20.8)	93 (16.2)
Partial Resection	0 (0.0)	65 (39.6)	189 (46.3)	254 (44.3)
Complete Resection	1 (100.0)	91 (55.5)	134 (32.8)	226 (39.4)
<b>Age (continuous)</b>				
Median	62.4	54.0	56.7	55.8
Range	62.4 - 62.4	19.0 - 70.8	18.6 - 70.5	18.6 - 70.8
N obs	1	164	408	573
<b>Age (class)</b>				
<=50	0 (0.0)	23 (14.0)	41 (10.0)	64 (11.2)
51-60	0 (0.0)	99 (60.4)	240 (58.8)	339 (59.2)
>60	1 (100.0)	42 (25.6)	127 (31.1)	170 (29.7)
<b>last daily dose administered (mg)</b>				
Median			8.0	8.0
Range			1.0 - 160.0	1.0 - 160.0
N obs	0	0	397	397
<b>Tercile1</b>				1-4
Median			4	4
Range			1-4	1-4
<b>Tercile2</b>				
Median			8	8
Range			5-10	5-10
<b>Tercile3</b>				
Median			16	16
<b>Range</b>			<b>12-160</b>	<b>12-160</b>

**B**

Characteristics	Steroids N=370 (44.5%)	No Steroids N=462 (55.5%)	p-value
<b>Gender</b>			
Male	213 (57.6%)	284 (61.5%)	0.254
Female	157 (42.4%)	178 (38.5%)	
<b>Age, y</b>			
Median (range)	63 (19 - 83)	60 (22 - 86)	0.194
≤60 y	158 (42.7%)	233 (50.4%)	
>60 y	212 (57.3%)	229 (49.6%)	
<b>KPS</b>			
<70	28 (7.6%)	22 (4.8%)	0.238
70-80	180 (48.6%)	233 (50.4%)	
≥90	162 (43.8%)	207 (44.8%)	
<b>Surgical Extent</b>			
biopsy	92 (24.9%)	72 (15.6%)	0.001
partial	48 (13.0%)	43 (9.3%)	
subtotal	113 (30.5%)	163 (35.3%)	
total	117 (31.6%)	184 (39.8%)	
<b>Radiation Dose</b>			
≤54 Gy	43 (13.2%)	37 (9.8%)	0.152
>54 Gy	282 (86.8%)	341 (90.2%)	
Data Missing	45	84	
<b>Therapy</b>			
RT	77 (20.8%)	104 (22.5%)	0.555
RT+CT	293 (79.2%)	358 (77.5%)	

**Table S3. A) PFS and OS in the GGN cohort by steroid use. B) Multivariate analysis of the association of steroid administration and outcome in the GGN cohort.**

**A**

	N (events)	PFS Median in months (95% CI) Events	PFS Median in months (95% CI) Events	HR, p value	OS Median in months (95% CI) Events	OS Median in months (95% CI) Events	HR, p value
Steroids		-	+		-	+	
Events							
All patients & events	832	7.0 (6.5-7.6) 441/462	6.1 (5.5-6.8) 358/370	1.21 0.008	15.7 (14.0-17.4) 408/462	12.1 (10.9-13.2) 337/370	1.32 <0.001
RT only	181	5.6 (4.8-6.5) 102/104	4.9 (4.2-5.6) 75/77	1.21 0.215	8.8 (7.1-10.5) 99/104	6.8 (5.7-8.0) 74/77	1.23 0.178
RT/CT	651	7.5 (6.6-8.5) 339/358	6.7 (5.9-7.5) 283/293	1.23 0.010	18.8 (16.8-20.7) 309/358	13.3 (11.7-14.9) 263/293	1.37 <0.001
GTR	301	9.5 (7.7-11.4) 171/184	6.7 (5.6-7.7) 114/117	1.51 0.001	22.1 (18.7-25.5) 158/184	15.0 (13.2-16.8) 105/117	1.40 0.008
No GTR	531	6.1 (5.3-6.9) 270/278	5.6 (4.8-6.4) 244/253	1.00 0.992	12.8 (11.1-14.4) 250/278	10.4 (8.7-12.0) 232/253	1.12 0.048
GTR							
RT only	51	5.8 (3.8-7.7) 33/34	5.4 (3.7-7.2) 17/17	1.05 0.863	9.9 (8.0-11.8) 32/34	10.9 (6.0-15.7) 17/17	1.20 0.539
RT/CT only	250	11.1 (9.3-13.0) 138/150	6.7 (5.1-8.3) 97/100	1.60 <0.001	24.5 (20.3-28.7) 126/150	15.3 (13.4-17.2) 88/100	1.47 0.006
No GTR							
RT only	130	5.3 (4.2-6.4) 69/70	4.5 (3.3-5.6) 58/60	1.24 0.239	8.0 (6.2-9.8) 67/70	6.4 (4.8-8.0) 57/60	1.20 0.320
RT/CT only	401	6.4 (5.5-7.3) 201/208	6.5 (5.3-7.6) 186/193	0.98 0.844	15.2 (13.1-17.3) 183/208	12.1 (10.7-13.4) 175/193	1.23 0.048

**B**

Factor	HR	95% CI	P value
Steroids Yes vs. no (ref.)	1.18	1.02 - 1.37	0.024
Therapy RT vs. RT/CT (ref.)	1.75	1.47 - 2.09	<0.001
Resection No gross total vs. gross total (ref.)	1.59	1.36 - 1.85	<0.001
Age >60 vs. ≤ 60 (ref.)	2.07	1.78 - 2.41	<0.001
KPS ≤ 80 vs. >80 (ref.)	1.17	1.00 - 1.36	0.041

**Table S4. Genes and top predicted cellular functions and canonical pathways of DEX regulated gene set.**

**A** The 25 most significantly changed probes on illumina mouse-ref-8 array. Gene list based on a greater than 1.5 fold change, with an ANOVA p value > 0.0005.

Illumina Probeset ID	SYMBOL	ANOVA p-value	Fold-Change (Dex vs. Untreated)
1340056	6720463M24Rik	0.00031	-1.75208
4780193	Aspm	0.00036	-1.59169
380520	Aurka	0.00017	-2.39294
7400215	Birc5	0.00019	-2.15796
2810612	Birc5	0.0003	-2.01431
1240446	Birc5	0.00047	-2.25534
5910528	Bub1b	0.00019	-2.06295
2190164	Ccnb1	6.56E-05	-3.06757
7550156	Ccnb1	0.00047	-3.03562
4610722	Cdc20	0.00012	-3.2905
4390228	Cdc20	0.00019	-2.93043
2320678	Cdc25c	3.38E-05	-1.81601
3830328	Cdc25c	5.71E-05	-2.0114
1050170	Cdca3	7.99E-05	-2.96694
4920148	Cdca3	0.00032	-1.91606
1500446	Cdca8	0.00038	-2.00116
7200519	Cenpa	2.32E-05	-3.48198
2710703	E130306D19Rik	3.77E-05	-1.94952
630634	Incenp	0.00016	-1.9118
4210246	Kif22	8.05E-05	-2.67197
1780543	Kif2c	0.00011	-2.61431
6940411	Pif1	8.06E-05	-2.43358
520427	Plk1	0.00012	-2.58357
780475	Prc1	0.00049	-2.65046
6620184	Spc25	0.00029	-1.94168

**B** The top 5-enriched predicted cellular function and canonical pathways, based on the 19 DEX-regulated genes.

Predicted Cellular Functions	p-value	Molecules
Cell Cycle	1.97E-17 - 3.87E-02	CDC25C, CDCA8, CDC20, PRC1, PLK1, AURKA, BUB1B, BIRC5, CCNB1, KIF22, ASPM, CENPA, KIF2C, INCENP
Cellular Assembly and Organization	1.94E-11 - 3.87E-02	CDC25C, CDCA8, CDC20, PRC1, PLK1, AURKA, BUB1B, BIRC5, PIF1, CCNB1, KIF22, CENPA, KIF2C, INCENP
DNA Replication, Recombination, and Repair	1.94E-11-3.78E-02	CDC25C, CDCA8, CDC20, PRC1, PLK1, AURKA, BUB1B, BIRC5, CCNB1 KIF22, CENPA, KIF2C, INCENP
Cellular Movement	2.49E-11-3.36E-02	CDC20, PRC1, PLK1, AURKA, BIRC5, CCNB1, INCENP
Cancer	1.22E-09-3.91E-02	CDC25C, CDCA8, CDC20, PRC1, PLK1, AURKA, BUB1B, BIRC5, CCNB1, KIF22, ASPM, CENPA, KIF2C, INCENP

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Ingenuity Canonical Pathways	-log(p-value)	Molecules
Mitotic Roles of Polo-Like Kinase	8.64E+00	CDC25C, CDC20, PRC1, PLK1, CCNB1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	5.15E+00	CDC25C, PLK1, CCNB1
Role of CHK Proteins in Cell Cycle Checkpoint Control	2.99E+00	CDC25C, PLK1
ATM Signaling	2.91E+00	CDC25C, CCNB1
Hereditary Breast Cancer Signaling	2.35E+00	CDC25C, CCNB1

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