Genetic polymorphisms of Wnt/β-catenin pathway genes are associated with the efficacy and toxicities of radiotherapy in patients with nasopharyngeal carcinoma

Supplementary Materials

Supplementary Table S1: Association between clinical factors and the efficacy of RT directly after treatment and 3 months after treatment in patients with NPC

Clinical Characteristics	After treatment						3 months after treatment					
	primary tumor (n = 188)			lymph node (n = 155)			primary tumor (n = 135)			lymph node (n = 114)		
	CR	Non-CR	*P*	CR	Non-CR	*P*	CR	Non-CR	*P*	CR	Non-CR	*P*
Age												
≤ 50	72	18	0.916	60	18	**0.001**	62	7	0.386	54	10	**0.045**
> 50	79	19		73	4		62	4		48	2	
Gender												
male	107	23	0.305	93	14	0.555	86	8	1.000	70	8	1.000
female	44	14		40	8		38	3		32	4	
Drinking												
Yes	42	5	**0.072**	34	4	0.456	31	3	1.000	26	0	0.104
No	109	32		99	18		93	8		76	12	
Smoking												
Yes	73	13	0.148	59	11	0.622	56	6	0.549	46	6	0.747
No	78	24		74	11		68	5		56	6	
Family history												
Yes	20	5	1.000	18	1	0.401	21	1	0.803	17	0	0.269
No	131	32		115	21		103	10		85	12	
BMI												
≤ 24.0	101	22	0.395	90	12	0.229	80	7	1.000	66	7	0.907
> 24.0	50	15		43	10		44	4		36	5	
Chemotherapy												
No	32	6	0.499	21	4	1.000	24	1	0.664	13	2	1.000
Yes	119	31		112	18		100	10		89	10	
Tumor classification												
T_1–T_2	45	6	**0.096**	32	7	0.437	35	1	0.308	23	3	1.000
T_3–T_4	106	31		101	15		89	10		79	9	
Lymph node metastasis												
N_0–N_1	73	20	0.534	57	3	**0.009**	61	2	**0.048**	39	3	0.560
N_2–N_3	78	17		76	19		63	9		63	9	
Distant metastasis												
M_0	147	35	0.739	130	19	**0.049**	120	10	0.351	98	11	0.433
M_1	4	2		3	3		4	1		4	1	
Clinical stage												
I–II	21	5	0.950	12	2	1.000	19	1	0.909	9	1	1.000
III–IV	130	32		121	20		105	10		93	11	
EBV-DNA												
Negative	46	15	0.241	35	4	0.415	43	1	0.162	26	3	1.000
Positive	105	22		98	18		81	10		76	9	

Abbreviations: RT, radiotherapy; BMI, body mass index. *P* value < 0.1 is shown in bold.

Supplementary Table S2: The association between clinical factors and the acute radiation-induced toxic reactions

Clinical characteristics	Dermatitis (n = 188)			Oral mucositis (n = 188)			Myelosuppression (n = 188)		
	Grade 0–2	Grade 3–4	*P*	Grade 0–2	Grade 3–4	*P*	Grade 0–2	Grade 3–4	*P*
Age									
≤ 50	81	9	0.483	49	41	0.639	67	23	0.504
> 50	91	7		50	48		77	21	
Gender									
male	119	11		66	64	0.437	102	28	0.366
female	53	5	0.971	33	25		42	16	
Drinking									
Yes	43	4	1.000	23	24	0.555	36	11	1.000
No	129	12		76	65		108	33	
Smoking			0.378						
Yes	77	9		44	42	0.706	69	17	0.280
No	95	7		55	47		75	27	
Family history									
Yes	23	2	0.922	14	11	0.719	19	6	0.940
No	149	14		85	78		125	38	
BMI									
≤ 24.0	115	8	0.175	59	64	**0.076**	91	32	0.245
> 24.0	57	8		40	25		53	12	
Chemotherapy									
No	35	3	0.879	21	17	0.719	37	1	**0.001**
Yes	137	13		78	72		107	43	
Tumor classification									
T_1–T_2	46	5	0.698	31	20	0.173	44	7	**0.056**
T_3–T_4	126	11		68	69		100	37	
Lymph node metastasis									
N_0–N_1	86	7	0.632	49	44	0.994	71	22	0.936
N_2–N_3	86	9		50	45		73	22	
Distant metastasis									
M_0	167	15	0.467	96	86	1.000	139	43	0.692
M_1	5	1		3	3		5	1	
Clinical stage									
I–II	23	3	0.551	14	12	0.896	22	4	0.298
III–IV	149	13		85	77		122	40	
EBV–DNA									
Negative	57	4	0.506	31	30	0.726	47	14	0.919
Positive	115	12		68	59		97	30	

Abbreviations: RT, radiotherapy; BMI, body mass index. *P* value < 0.1 is shown in bold.

Supplementary Table S3: Association between SNPs in WNT/β-catenin pathway genes and the efficacy of RT at the primary tumor after treatment

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	non-CR (MAF)	CR (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	6/23/8 (0.47)	37/68/46 (0.47)	allelic	1.01 (0.61–1.68)	0.966	—	—
			additive	1.01 (0.61–1.67)	0.966	0.99 (0.59–1.67)	0.968
			dominant	1.59 (0.67–3.74)	0.290	1.43 (0.60–3.43)	0.417
			recessive	0.60 (0.23–1.54)	0.286	0.63 (0.24–1.66)	0.350
rs2896218	2/19/16 (0.31)	8/68/75 (0.28)	allelic	1.17 (0.67–2.03)	0.577	—	—
			additive	1.20 (0.66–2.19)	0.549	1.22 (0.66–2.26)	0.530
			dominant	1.30 (0.63–2.67)	0.484	1.28 (0.61–2.68)	0.509
			recessive	1.02 (0.21–5.02)	0.979	1.16 (0.22–5.98)	0.861
rs6947329	9/16/11 (0.47)	38/69/44 (0.48)	allelic	0.97 (0.58–1.62)	0.904	—	—
			additive	0.97 (0.59–1.59)	0.908	0.99 (0.59–1.64)	0.961
			dominant	0.93 (0.42–2.06)	0.867	0.91 (0.41–2.03)	0.814
			recessive	0.99 (0.43–2.29)	0.984	1.08 (0.46–2.53)	0.867
rs454886	4/21/12 (0.39)	31/3/117 (0.38)	allelic	1.05 (0.62–1.77)	0.860	—	—
			additive	1.05 (0.62–1.79)	0.858	1.01 (0.59–1.73)	0.976
			dominant	1.30 (0.61–2.79)	0.501	1.26 (0.58–2.73)	0.562
			recessive	0.71 (0.23–2.20)	0.554	0.65 (0.21–2.05)	0.463
rs1880481	3/18/16 (0.32)	9/51/91 (0.23)	allelic	1.62 (0.93–2.83)	0.087	—	—
			additive	1.62 (0.92–2.83)	0.092	1.61 (0.91–2.87)	0.104
			dominant	1.99 (0.96–4.12)	0.064	2.05 (0.97–4.32)	0.060
			recessive	1.39 (0.36–5.42)	0.633	1.25 (0.31–5.04)	0.753
rs3864004	3/15/19 (0.28)	4/63/83 (0.24)	allelic	1.28 (0.72–2.26)	0.399	—	—
			additive	1.33 (0.72–2.46)	0.369	1.3 (0.7–2.42)	0.414
			dominant	1.17 (0.57–2.41)	0.663	1.18 (0.56–2.45)	0.665
			recessive	3.22 (0.69–15.06)	0.137	2.74 (0.56–13.4)	0.214
rs3755557	1/9/27 (0.15)	8/39/104 (0.18)	allelic	0.78 (0.39–1.59)	0.498	—	—
			additive	0.80 (0.41–1.57)	0.522	0.84 (0.43–1.67)	0.627
			dominant	0.82 (0.37–1.83)	0.627	0.87 (0.38–1.97)	0.732
			recessive	0.50 (0.06–4.10)	0.516	0.55 (0.06–4.62)	0.578

[a]In the order of homozygote / heterozygote / wild type.

[b]Adjusted for T stage and drinking status.

Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. *P* value < 0.05 is shown in bold.

Supplementary Table S4: Association between SNPs in WNT/β-catenin pathway genes and the efficacy of RT at the primary tumor 3 months after treatment

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	non-CR(MAF)	CR (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	3/4/4 (0.45)	30/63/31 (0.50)	allelic	0.85 (0.35–2.03)	0.710	—	—
			additive	0.85 (0.35–2.03)	0.711	0.85 (0.35–2.03)	0.711
			dominant	0.58 (0.16–2.13)	0.414	0.58 (0.16–2.13)	0.414
			recessive	1.18 (0.29–4.71)	0.820	1.18 (0.29–4.71)	0.820
rs2896218	1/3/7 (0.23)	4/60/60 (0.27)	allelic	0.78 (0.28–2.19)	0.635	—	—
			additive	0.74 (0.24–2.29)	0.600	0.74 (0.24–2.29)	0.600
			dominant	0.54 (0.15–1.92)	0.338	0.54 (0.15–1.92)	0.338
			recessive	3.00 (0.31–29.46)	0.346	3.00 (0.31–29.46)	0.346
rs6947329	3/2/6 (0.36)	33/57/33 (0.50)	allelic	0.57 (0.23–1.41)	0.220	—	—
			additive	0.60 (0.26–1.43)	0.253	0.6 (0.26–1.43)	0.253
			dominant	0.31 (0.09–1.07)	0.063	0.31 (0.09–1.07)	0.063
			recessive	1.02 (0.26–4.09)	0.975	1.02 (0.26–4.09)	0.975
rs454886	0/6/5 (0.27)	20/61/43 (0.41)	allelic	0.55 (0.21–1.44)	0.216	—	—
			additive	0.53 (0.20–1.44)	0.214	0.53 (0.20–1.44)	0.214
			dominant	0.64 (0.18–2.21)	0.477	0.64 (0.18–2.21)	0.477
			recessive	—	0.997	—	0.997
rs1880481	2/4/5 (0.36)	7/43/74 (0.23)	allelic	1.92 (0.76–4.79)	0.160	—	—
			additive	1.86 (0.75–4.59)	0.177	1.86 (0.75–4.59)	0.177
			dominant	1.78 (0.51–6.14)	0.364	1.78 (0.51–6.14)	0.364
			recessive	3.71 (0.67–20.57)	0.133	3.71 (0.67–20.57)	0.133
rs3864004	1/4/6 (0.27)	4/49/70 (0.23)	allelic	1.24 (0.46–3.33)	0.664	—	—
			additive	1.28 (0.45–3.63)	0.648	1.28 (0.45–3.63)	0.648
			dominant	1.10 (0.32–3.80)	0.880	1.10 (0.32–3.80)	0.880
			recessive	2.98 (0.30–29.21)	0.350	2.98 (0.3–29.21)	0.350
rs3755557	1/2/8 (0.18)	7/34/83 (0.19)	allelic	0.93 (0.30–2.86)	0.894	—	—
			additive	0.93 (0.32–2.69)	0.901	0.93 (0.32–2.69)	0.901
			dominant	0.76 (0.19–3.01)	0.695	0.76 (0.19–3.01)	0.695
			recessive	1.67 (0.19–14.97)	0.646	1.67 (0.19–14.97)	0.646

[a]In the order of homozygote / heterozygote / wild type; [b] Adjusted for N stage.
Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. *P* value < 0.05 is shown in bold.

Supplementary Table S5: Association between SNPs in WNT/β-catenin pathway genes with the efficacy of RT at the lymph node after treatment

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	non-CR (MAF)	CR (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	7/9/6 (0.52)	27/64/42 (0.44)	allelic	1.37 (0.73–2.60)	0.329	—	—
			additive	1.35 (0.72–2.53)	0.343	1.51 (0.76–2.99)	0.235
			dominant	1.23 (0.45–3.37)	0.686	1.44 (0.48–4.35)	0.518
			recessive	1.83 (0.68–4.94)	0.231	2.14 (0.71–6.44)	0.175
rs2896218	2/8/12 (0.27)	7/63/63 (0.29)	allelic	0.92 (0.45–1.88)	0.820	—	—
			additive	0.91 (0.43–1.95)	0.809	0.88 (0.38–2.02)	0.760
			dominant	0.75 (0.30–1.86)	0.534	0.68 (0.25–1.83)	0.441
			recessive	1.80 (0.35–9.29)	0.483	2.22 (0.36–13.82)	0.391
rs6947329	6/10/6 (0.50)	33/60/39 (0.48)	allelic	1.1 (0.58–2.07)	0.780	—	—
			additive	1.09 (0.59–2.00)	0.789	1.15 (0.60–2.21)	0.681
			dominant	1.12 (0.41–3.07)	0.828	1.34 (0.44–4.11)	0.606
			recessive	1.13 (0.41–3.11)	0.821	1.10 (0.37–3.30)	0.868
rs454886	3/11/8 (0.39)	17/63/53 (0.36)	allelic	1.10 (0.57–2.11)	0.782	—	—
			additive	1.10 (0.57–2.14)	0.779	1.42 (0.67–3.00)	0.365
			dominant	1.16 (0.45–2.96)	0.757	1.62 (0.56–4.66)	0.372
			recessive	1.08 (0.29–4.03)	0.912	1.45 (0.34–6.18)	0.619
rs1880481	4/7/11 (0.34)	6/51/76 (0.24)	allelic	1.67 (0.84–3.30)	0.141	—	—
			additive	1.67 (0.84–3.33)	0.147	1.71 (0.81–3.6)	0.156
			dominant	1.33 (0.54–3.29)	0.533	1.54 (0.57–4.22)	0.397
			recessive	4.70 (1.21–18.29)	0.025	3.79 (0.84–17.17)	0.084
rs3864004	1/9/12 (0.25)	5/55/72 (0.25)	allelic	1.02 (0.49–2.13)	0.957	—	—
			additive	1.02 (0.47–2.25)	0.954	1.16 (0.49–2.76)	0.735
			dominant	1.00 (0.40–2.48)	1.000	1.16 (0.42–3.17)	0.775
			recessive	1.21 (0.13–10.87)	0.865	1.38 (0.13–14.84)	0.792
rs3755557	1/6/15 (0.18)	6/31/96 (0.16)	allelic	1.15 (0.50–2.65)	0.738	—	—
			additive	1.13 (0.52–2.47)	0.754	1.11 (0.47–2.63)	0.815
			dominant	1.21 (0.46–3.21)	0.700	1.13 (0.39–3.28)	0.824
			recessive	1.01 (0.12–8.80)	0.994	1.18 (0.12–11.97)	0.889

[a]In the order of homozygote / heterozygote / wild type.

[b]Adjusted for N stage, M stage and age.

Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. P value < 0.05 is shown in bold.

Supplementary Table S6: Association between SNPs in WNT/β-catenin pathway genes and the efficacy of RT at the lymph node 3 months after treatment

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	non-CR (MAF)	CR (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	4/5/3 (0.54)	24/50/28 (0.48)	allelic	1.28 (0.55–2.99)	0.570	—	—
			additive	1.27 (0.55–2.93)	0.577	1.38 (0.59–3.26)	0.462
			dominant	1.14 (0.29–4.50)	0.857	1.25 (0.31–5.06)	0.758
			recessive	1.63 (0.45–5.87)	0.459	1.86 (0.49–6.97)	0.360
rs2896218	0/5/7 (0.21)	4/48/50 (0.27)	allelic	0.70 (0.25–1.95)	0.489	—	—
			additive	0.65 (0.21–1.98)	0.445	0.65 (0.21–2.00)	0.456
			dominant	0.69 (0.2–2.31)	0.543	0.71 (0.21–2.43)	0.584
			recessive	—	0.999	NA	0.999
rs6947329	4/4/4 (0.50)	28/45/28 (0.50)	allelic	1.00 (0.43–2.33)	1.000	—	—
			additive	1.00 (0.45–2.22)	1.000	0.98 (0.44–2.19)	0.962
			dominant	0.77 (0.21–2.75)	0.684	0.75 (0.21–2.77)	0.671
			recessive	1.30 (0.36–4.67)	0.684	1.26 (0.34–4.61)	0.732
rs454886	2/5/5 (0.38)	15/50/37 (0.39)	allelic	0.93 (0.39–2.23)	0.871	—	—
			additive	0.93 (0.39–2.24)	0.870	1.02 (0.42–2.51)	0.966
			dominant	0.80 (0.24–2.69)	0.715	0.89 (0.26–3.07)	0.849
			recessive	1.16 (0.23–5.83)	0.857	1.35 (0.26–7.09)	0.723
rs1880481	3/3/6 (0.38)	6/36/60 (0.24)	allelic	1.95 (0.80–4.74)	0.135	—	—
			additive	1.85 (0.78–4.36)	0.160	1.82 (0.76–4.31)	0.177
			dominant	1.43 (0.43–4.74)	0.560	1.44 (0.43–4.90)	0.555
			recessive	5.33 (1.14–25.01)	**0.034**	5.05 (1.02–25.03)	**0.048**
rs3864004	2/4/6 (0.33)	3/40/58 (0.23)	allelic	1.70 (0.68–4.21)	0.251	—	—
			additive	1.78 (0.68–4.68)	0.240	1.78 (0.64–4.94)	0.270
			dominant	1.35 (0.41–4.47)	0.625	1.21 (0.35–4.10)	0.765
			recessive	6.53 (0.97–43.85)	0.053	10.94 (1.24–96.68)	0.031
rs3755557	1/2/9 (0.17)	5/27/70 (0.18)	allelic	0.90 (0.29–2.80)	0.859	—	—
			additive	0.91 (0.32–2.65)	0.868	0.94 (0.32–2.79)	0.914
			dominant	0.73 (0.18–2.88)	0.652	0.75 (0.19–3.01)	0.681
			recessive	1.76 (0.19–16.5)	0.619	1.98 (0.20–20.00)	0.562

[a]In the order of homozygote / heterozygote / wild type.

[b]Adjusted for age.

Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval; NA, not applicable. *P* value < 0.05 is shown in bold.

Supplementary Table S7: Association between SNPs in WNT/β-catenin pathway genes and acute grade 3–4 radiation-induced oral mucositis

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	Grade 3–4 (MAF)	Grade 0–2 (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	21/45/23 (0.49)	22/46/31 (0.45)	allelic	1.15 (0.76–1.72)	0.507	—	—
			additive	1.14 (0.77–1.71)	0.513	1.17 (0.78–1.76)	0.443
			dominant	1.31 (0.69–2.47)	0.408	1.35 (0.71–2.56)	0.364
			recessive	1.08 (0.55–2.14)	0.823	1.12 (0.56–2.23)	0.743
rs2896218	6/45/38 (0.32)	4/42/53 (0.25)	allelic	1.39 (0.89–2.19)	0.146	—	—
			additive	1.47 (0.90–2.40)	0.120	1.5 (0.91–2.46)	0.110
			dominant	1.55 (0.87–2.75)	0.138	1.63 (0.91–2.93)	0.102
			recessive	1.72 (0.47–6.29)	0.415	1.50 (0.40–5.58)	0.542
rs6947329	23/38/27 (0.48)	24/47/28 (0.48)	allelic	0.99 (0.66–1.49)	0.961	—	—
			additive	0.99 (0.67–1.46)	0.963	1.01 (0.68–1.49)	0.979
			dominant	0.89 (0.47–1.67)	0.719	0.89 (0.47–1.68)	0.721
			recessive	1.11 (0.57–2.14)	0.766	1.16 (0.59–2.25)	0.674
rs454886	17/43/29 (0.43)	9/49/41 (0.34)	allelic	1.49 (0.98–2.26)	0.061	—	—
			additive	1.52 (0.99–2.34)	0.058	1.57 (1.01–2.43)	**0.045**
			dominant	1.46 (0.81–2.66)	0.212	1.50 (0.82–2.73)	0.191
			recessive	2.36 (0.99–5.61)	0.052	2.54 (1.06–6.13)	**0.038**
rs1880481	7/32/50 (0.26)	5/37/57 (0.24)	allelic	1.12 (0.70–1.79)	0.637	—	—
			additive	1.12 (0.70–1.78)	0.639	1.16 (0.72–1.85)	0.549
			dominant	1.06 (0.59–1.89)	0.847	1.1 (0.61–1.97)	0.752
			recessive	1.61 (0.49–5.25)	0.434	1.69 (0.51–5.61)	0.390
rs3864004	4/38/47 (0.26)	3/40/55 (0.23)	allelic	1.14 (0.71–1.82)	0.595	—	—
			additive	1.16 (0.70–1.92)	0.570	1.22 (0.73–2.04)	0.447
			dominant	1.14 (0.64–2.03)	0.650	1.2 (0.67–2.15)	0.546
			recessive	1.49 (0.32–6.85)	0.608	1.73 (0.37–8.14)	0.490
rs3755557	7/24/58 (0.21)	2/24/73 (0.14)	allelic	1.65 (0.96–2.82)	0.067	—	—
			additive	1.57 (0.94–2.63)	0.086	1.62 (0.96–2.73)	0.071
			dominant	1.50 (0.80–2.80)	0.203	1.57 (0.83–2.95)	0.166
			recessive	4.14 (0.84–20.48)	0.082	4.21 (0.84–21.04)	0.080

[a]In the order of homozygote / heterozygote / wild type.

[b]Adjusted for BMI.

Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. P value < 0.05 is shown in bold.

Supplementary Table S8: Association between SNPs in WNT/β-catenin pathway genes and acute grade 3–4 radiation-induced dermatitis

SNP	Genotype distribution[a]		Model	OR (95% CI)	*P*
	Grade 3–4 (MAF)	Grade 0–2 (MAF)			
rs10487362	3/6/7 (0.38)	40/85/47 (0.48)	allelic	0.65 (0.31–1.37)	0.257
			additive	0.66 (0.31–1.38)	0.267
			dominant	0.48 (0.17–1.37)	0.172
			recessive	0.46 (0.18–1.17)	0.102
rs2896218	0/7/9 (0.22)	10/80/82 (0.29)	allelic	0.68 (0.29–1.63)	0.388
			additive	0.65 (0.26–1.63)	0.356
			dominant	0.71 (0.25–1.99)	0.513
			recessive	2.30 (0.62–8.55)	0.214
rs6947329	4/6/5 (0.47)	43/79/50 (0.48)	allelic	0.95 (0.45–2.01)	0.891
			additive	0.95 (0.47–1.95)	0.896
			dominant	0.82 (0.27–2.52)	0.729
			recessive	0.88 (0.39–1.95)	0.746
rs454886	1/7/8 (0.28)	25/85/62 (0.39)	allelic	0.61 (0.27–1.35)	0.216
			additive	0.59 (0.26–1.35)	0.212
			dominant	0.56 (0.20–1.58)	0.274
			recessive	1.25 (0.49–3.19)	0.649
rs1880481	1/6/9 (0.25)	11/63/98 (0.25)	allelic	1.02 (0.44–2.35)	0.971
			additive	1.02 (0.44–2.33)	0.971
			dominant	1.03 (0.37–2.89)	0.955
			recessive	1.10 (0.28–4.25)	0.893
rs3864004	0/8/8 (0.25)	7/70/94 (0.25)	allelic	1.02 (0.44–2.37)	0.956
			additive	1.03 (0.42–2.52)	0.953
			dominant	1.22 (0.44–3.40)	0.703
			recessive	0.55 (0.06–4.68)	0.582
rs3755557	2/6/8 (0.31)	7/42/123 (0.31)	allelic	2.34 (1.05–5.21)	**0.033**
			additive	2.13 (1.00–4.55)	0.051
			dominant	2.51 (0.89–7.06)	0.081
			recessive	0.40 (0.05–3.25)	0.388

[a]In the order of homozygote / heterozygote / wild type.
Abbreviations: MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. *P* value < 0.05 is shown in bold.

Supplementary Table S9: Association between SNPs in WNT/β-catenin pathway genes and acute grade 3–4 radiation-induced dermatitis myelosuppression

SNP	Genotype distribution[a]		Model	Unadjusted		Adjusted[b]	
	Grade 3–4 (MAF)	Grade 0–2 (MAF)		OR (95% CI)	*P*	OR (95% CI)	*P*
rs10487362	6/29/9 (0.47)	37/62/45 (0.47)	allelic	0.98 (0.60–1.57)	0.917	—	—
			additive	0.98 (0.61–1.56)	0.919	0.95 (0.58–1.56)	0.849
			dominant	1.77 (0.78–3.99)	0.170	1.79 (0.77–4.14)	0.175
			recessive	0.46 (0.18–1.17)	0.102	0.42 (0.16–1.11)	0.081
rs2896218	4/23/17 (0.35)	6/64/74 (0.26)	allelic	1.52 (0.91–2.53)	0.108	—	—
			additive	1.64 (0.93–2.87)	0.086	1.54 (0.86–2.75)	0.143
			dominant	1.68 (0.84–3.35)	0.141	1.63 (0.8–3.33)	0.182
			recessive	2.30 (0.62–8.55)	0.214	1.88 (0.48–7.34)	0.362
rs6947329	10/22/11 (0.49)	37/63/44 (0.48)	allelic	1.05 (0.65–1.70)	0.836	—	—
			additive	1.05 (0.66–1.66)	0.843	1.06 (0.66–1.70)	0.808
			dominant	1.28 (0.59–2.77)	0.531	1.45 (0.65–3.21)	0.363
			recessive	0.88 (0.39–1.95)	0.746	0.80 (0.35–1.82)	0.588
rs454886	7/18/19 (0.36)	19/74/51 (0.39)	allelic	0.90 (0.55–1.47)	0.670	—	—
			additive	0.89 (0.54–1.48)	0.664	0.81 (0.48–1.37)	0.441
			dominant	0.72 (0.36–1.44)	0.352	0.64 (0.31–1.32)	0.230
			recessive	1.25 (0.49–3.19)	0.649	1.08 (0.41–2.86)	0.881
rs1880481	3/13/28 (0.22)	9/56/79 (0.26)	allelic	0.80 (0.45–1.41)	0.435	—	—
			additive	0.80 (0.45–1.41)	0.439	0.65 (0.36–1.17)	0.152
			dominant	0.69 (0.35–1.39)	0.305	0.54 (0.26–1.13)	0.103
			recessive	1.10 (0.28–4.25)	0.893	0.78 (0.19–3.10)	0.720
rs3864004	1/15/27 (0.20)	6/63/75 (0.26)	allelic	0.70 (0.39–1.27)	0.236	—	—
			additive	0.67 (0.35–1.25)	0.207	0.53 (0.27–1.03)	0.059
			dominant	0.64 (0.32–1.30)	0.218	0.5 (0.24–1.05)	0.067
			recessive	0.55 (0.06–4.68)	0.582	0.38 (0.04–3.27)	0.376
rs3755557	1/12/31 (0.16)	8/36/100 (0.18)	allelic	0.86 (0.45–1.64)	0.643	—	—
			additive	0.87 (0.47–1.61)	0.662	0.83 (0.44–1.56)	0.560
			dominant	0.95 (0.46–1.99)	0.899	0.90 (0.42–1.95)	0.793
			recessive	0.40 (0.05–3.25)	0.388	0.36 (0.04–3.05)	0.350

[a]In the order of / heterozygote / wild type.

[b]Adjusted for T stage and chemotherapy.

Abbreviations: MAF, minor alle homozygote le frequency; OR, odds ratio; CI, confidence interval. *P* value < 0.05 is shown in bold.

Supplementary Table S10: Primer sequences for 9 SNPs in genotyping

SNP-ID	Forward primer	Reverse primer	Extension primer
rs10487362	ACGTTGGATGTGCCCCTCCAAGAGTAAAAG	ACGTTGGATGGTGAACTAATGCATCAGCAG	ATTCATCAGCAGACTATATCTATCG
rs2896218	ACGTTGGATGCTAGGAATGTCTTCCTTTTG	ACGTTGGATGAATTCCAACACAGAGCGGAC	ACAGTCACGAGGCAT
rs6947329	ACGTTGGATGATCATTTCCAGCCTCTCCCC	ACGTTGGATGACCACAAGTACCTTCAAGGC	CCTCCCACCCTAGGTTCTAATTT
rs3777860	ACGTTGGATGACCAGGAAAGTGGTGTATGC	ACGTTGGATGACTGCAAGCACTCATGCTGG	GGGGAAGGTCACTGGCACATTTCAA
rs454886	ACGTTGGATGTATGCAGTAAGAGAAGAAG	ACGTTGGATGGTCAGCTCTCCTTTCTTTGG	CTAGGCCTCATTTTGTATCATATAAAAC
rs4135385	ACGTTGGATGGGAGTTACTTGTTCCTTTTG	ACGTTGGATGAGCAAGGAAGAATAGAAAGC	CATGAAAATTCTCAAAAGTACACTAA
rs1880481	ACGTTGGATGCCCGTGCTTAATTCTTAGTC	ACGTTGGATGGCTGTCATTTCTCCCATAAC	CTCCCATAACACTCATTCTAATTTA
rs3864004	ACGTTGGATGAGGACTTGTTGAATTGCGGG	ACGTTGGATGTTCTGTCCCCACTCACGAAG	GTGAACTCTCCGTAGAA
rs3755557	ACGTTGGATGCCTGCAGAGTCATCTCTTTC	ACGTTGGATGGTTTCAAAGCAAGAGCCAGG	CTACTCTGATCAAATATAGGTCCTTT