



Supplementary Material

10.1302/2046-3758.1011.BJR-2021-0181.R1

Table i. The significant single-nucleotide polymorphisms interacted with *genus Dialister*_RNT for total bone mineral density.

SNP	Gene	ALT	A1	Beta	SE	P
rs201950816	LOC105378814	T	TA	0.653	0.106	7.05×10^{-10}
rs191380733	HSPA7	C	A	0.428	0.075	1.07×10^{-8}
rs6706665	/	A	G	0.085	0.016	4.49×10^{-8}
rs6710792	/	A	G	0.087	0.016	2.73×10^{-8}
rs6753388	/	C	T	0.087	0.016	2.65×10^{-8}
rs4663679	/	A	T	0.086	0.016	4.05×10^{-8}
rs79540008	PLD1	A	G	0.248	0.045	3.09×10^{-8}
rs78658424	EMCN	G	A	0.587	0.097	1.62×10^{-9}
rs72692714	/	G	A	0.607	0.108	1.98×10^{-8}
rs181259104	/	A	T	0.607	0.108	1.97×10^{-8}
rs147170032	/	G	A	0.567	0.103	3.40×10^{-8}
rs145159462	/	T	C	0.532	0.092	7.93×10^{-9}
rs117160188	RABGAP1	G	A	0.374	0.068	3.94×10^{-8}
rs150904119	STRBP	C	T	0.381	0.069	3.30×10^{-8}
rs78032159	/	C	G	0.485	0.086	2.06×10^{-8}
rs61870434	/	T	C	0.550	0.088	5.54×10^{-10}
rs118087764	GSG1L	G	C	0.268	0.047	1.31×10^{-8}
rs117755175	/	G	A	0.464	0.085	4.36×10^{-8}
rs117962699	LOC105372121	A	G	0.372	0.066	1.59×10^{-8}

ALT, alanine transaminase; SE, standard error; SNP, single-nucleotide polymorphism.

Table ii. The significant single-nucleotide polymorphisms interacted with *genus Lactococcus_HB* for femur total bone mineral density.

SNP	Gene	ALT	A1	Beta	SE	P
rs143918413	SLC44A5	C	T	-0.536	0.086	5.55×10 ⁻¹⁰
rs115253508	SLC44A5	T	G	-0.497	0.084	4.29×10 ⁻⁹
rs796992538	/	GACAC	GAC	-0.657	0.103	1.71×10 ⁻¹⁰
2:32747270_CTGTT_C	/	CTGTT	C	-0.695	0.102	1.06×10 ⁻¹¹
rs183477728	TTC27	C	T	-0.764	0.106	6.48×10 ⁻¹³
2:32913958_TC_T	/	TC	T	-0.738	0.109	1.60×10 ⁻¹¹
rs139994715	TTC27	G	T	-0.769	0.111	5.96×10 ⁻¹²
rs183142321	CNTNAP5	T	A	-0.666	0.101	5.15×10 ⁻¹¹
rs60403733	/	T	G	-0.551	0.098	2.06×10 ⁻⁸
rs148461179	/	G	A	-0.554	0.098	1.88×10 ⁻⁸
rs74852700	/	A	G	-0.579	0.100	6.69×10 ⁻⁹
rs116376069	CCDC141	G	T	-0.533	0.098	4.94×10 ⁻⁸
rs62241022	/	C	T	-0.319	0.055	7.13×10 ⁻⁹
rs77289770	LOC105374060	G	A	-0.356	0.064	3.40×10 ⁻⁸
rs59945500	LOC105374060	A	C	-0.353	0.064	4.38×10 ⁻⁸
rs114871025	LOC105374060	G	A	-0.353	0.064	4.37×10 ⁻⁸
rs75459588	LOC105374060	A	G	-0.353	0.064	4.38×10 ⁻⁸
rs143647278	LOC105374060	C	T	-0.358	0.065	3.39×10 ⁻⁸
rs148415407	LOC105374060	G	A	-0.353	0.064	4.37×10 ⁻⁸
rs77052599	LOC105374060	G	A	-0.354	0.064	4.18×10 ⁻⁸
rs74331876	LOC105374060	T	C	-0.361	0.066	4.97×10 ⁻⁸
rs138365559	CHCHD6	C	T	-0.660	0.118	2.57×10 ⁻⁸
rs190238591	/	C	T	-0.665	0.119	2.45×10 ⁻⁸
rs190606857	PLXNA1	C	T	-0.656	0.118	3.20×10 ⁻⁸
rs141065579	/	A	T	-0.427	0.076	1.77×10 ⁻⁸
3:166321059_CA_C	/	CA	C	-0.467	0.082	1.21×10 ⁻⁸
rs35190601	PPARGC1A	A	A	-0.833	0.147	1.45×10 ⁻⁸
rs75925548	/	T	C	-0.434	0.077	1.63×10 ⁻⁸
rs76052298	/	G	T	-0.433	0.077	1.74×10 ⁻⁸
rs114064439	/	G	A	-0.530	0.088	1.66×10 ⁻⁹
rs147658908	LOC101927421	T	G	-0.535	0.090	2.94×10 ⁻⁹

rs61228329	/	C	T	-0.283	0.051	2.56×10 ⁻⁸
rs58586550	/	T	G	-0.283	0.051	2.56×10 ⁻⁸
rs72825623	/	G	T	-0.283	0.051	2.56×10 ⁻⁸
rs72825635	/	A	C	-0.285	0.051	2.07×10 ⁻⁸
rs72825636	/	A	C	-0.285	0.051	2.07×10 ⁻⁸
rs191860862	COL12A1	G	A	-0.777	0.115	1.44×10 ⁻¹¹
rs116880189	SENP6	T	C	-0.666	0.106	3.01×10 ⁻¹⁰
rs199629641	IMPG1	C	CT	-0.393	0.071	3.70×10 ⁻⁸
rs142723847	IMPG1	C	T	-0.425	0.077	3.03×10 ⁻⁸
rs150815178	IMPG1	G	A	-0.412	0.069	2.41×10 ⁻⁹
rs144760455	IMPG1	G	A	-0.411	0.069	2.89×10 ⁻⁹
rs141513476	/	T	C	-0.453	0.080	1.84×10 ⁻⁸
6:76986122_GC_G	/	GC	G	-0.497	0.086	8.29×10 ⁻⁹
rs140678586	/	G	A	-0.483	0.087	2.70×10 ⁻⁸
rs117113548	/	G	A	-0.483	0.086	1.94×10 ⁻⁸
rs116891860	/	A	G	-0.483	0.086	1.72×10 ⁻⁸
rs117386887	/	C	T	-0.464	0.083	2.86×10 ⁻⁸
rs137905693	LINC02540	T	C	-0.474	0.085	3.13×10 ⁻⁸
rs142988447	/	C	T	-0.569	0.095	2.37×10 ⁻⁹
rs188350746	/	G	A	-0.505	0.088	8.64×10 ⁻⁹
rs141538029	/	G	C	-0.640	0.096	2.50×10 ⁻¹¹
rs146474675	/	G	C	-0.640	0.096	2.47×10 ⁻¹¹
rs143734051	TUSC3	T	A	-0.644	0.096	1.89×10 ⁻¹¹
rs140404020	TUSC3	G	A	-0.649	0.096	1.22×10 ⁻¹¹
rs147963206	TUSC3	C	A	-0.640	0.096	2.39×10 ⁻¹¹
rs144400955	TUSC3	A	G	-0.634	0.095	3.26×10 ⁻¹¹
rs148379500	TUSC3	G	C	-0.639	0.096	2.84×10 ⁻¹¹
rs78927039	/	T	C	-0.457	0.082	2.48×10 ⁻⁸
rs797016800	/	T	C	-0.500	0.088	1.25×10 ⁻⁸
rs145974327	/	C	A	-0.392	0.067	5.02×10 ⁻⁹
rs796131	/	T	C	-0.409	0.074	4.30×10 ⁻⁸
rs35192567	GRID1	A	G	-0.352	0.063	2.44×10 ⁻⁸
rs71503844	GRID1	C	T	-0.546	0.093	4.64×10 ⁻⁹

rs374678068	TCTN3	A	G	-0.702	0.122	8.68×10 ⁻⁹
rs10741150	DOCK1	C	T	0.108	0.019	1.95×10 ⁻⁸
rs10829439	DOCK1	G	A	0.109	0.019	1.60×10 ⁻⁸
rs74777764	DLG2	G	A	-0.285	0.051	2.90×10 ⁻⁸
rs117843475	CPSF2	G	C	-0.377	0.068	2.95×10 ⁻⁸
rs144971434	LOC101927079	C	CA	-0.975	0.177	3.73×10 ⁻⁸
rs141219442	CHST8	C	T	-0.458	0.078	3.99×10 ⁻⁹
rs117833372	SLC24A3	G	C	-0.397	0.072	4.37×10 ⁻⁸
rs117471436	SLC24A3	A	G	-0.396	0.072	4.44×10 ⁻⁸
rs117333800	SLC24A3	A	G	-0.396	0.072	4.55×10 ⁻⁸
rs111824870	NFATC2	G	C	-0.445	0.081	4.84×10 ⁻⁸
rs146664677	LOC107985558	C	T	-0.517	0.093	2.85×10 ⁻⁸

ALT, alanine transaminase; SE, standard error; SNP, single-nucleotide polymorphism.