

- Table A1. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-bearing pelitic gneiss(504T01B).
- Table A2. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-bearing gabbroic amphibolite leucocratic portion (13002A).
- Table A3. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-bearing gabbroic amphibolite melanocratic portion (13002A).
- Table A4. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from clinopyroxene amphibolite(13002C).
- Table A5. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-free felsic gneiss (13002D).
- Table A6. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-bearing felsic gneiss (13004B).
- Table A7. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from quartz-bearing gneissose gabbro (40102A).
- Table A8. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from quartz-bearing gneissose diorite (50401).
- Table A9. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from quartz-bearing gneissose diorite (50301A).
- Table A10. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from quartz-bearing gneissose diorite (13001).
- Table A11. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-free gneissose tonalite(13007A1).
- Table A12. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from garnet-bearing gneissose tonalite (13006A).
- Table A13. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from quartz-free micro-diorite (13007E).
- Table A14. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from granitic mylonite (50305F).
- Table A15. LA-ICP-MS U–Pb isotope ratio and calculated age data of zircon from granitic mylonite (61202A).
- Table B. Chemical compositions and U–Th–Pb ages of monazites in pseudotachylite in garnet-bearing gneissose tonalite (504T02).

Table A1.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
04T01B-1-1*	0.2565	0.0071	4.0594	0.1281	1472	36	1646	26	0.05	12	core	discordant
04T01B-1-2*	0.2969	0.0083	4.7734	0.1535	1676	41	1780	27	0.13	6	rim	discordant
04T01B-3	0.2453	0.0072	3.7478	0.1334	1414	37	1582	29	0.25	12	core	discordant
04T01B-4	0.0838	0.0028	0.6617	0.0376	519	16	516	23	0.65	-1	core	
04T01B-5	0.2683	0.0087	4.3413	0.1751	1532	44	1701	33	0.49	11	core	discordant
04T01B-6	0.0416	0.0013	0.2973	0.0167	263	8	264	13	1.27	1	core	
04T01B-7	0.0415	0.0013	0.3105	0.0158	262	8	275	12	0.44	5	core	discordant
04T01B-8	0.0395	0.0012	0.2803	0.0135	250	8	251	11	0.31	0	core	
04T01B-9	0.0401	0.0014	0.2789	0.0205	254	9	250	16	0.30	-1	core	
04T01B-10	0.0390	0.0014	0.2681	0.0215	247	9	241	17	0.99	-2	core	
04T01B-11	0.0188	0.0008	0.1240	0.0151	120	5	119	14	0.06	-1	rim	
04T01B-13	0.3154	0.0092	5.3040	0.1876	1767	45	1870	30	0.43	6	core	discordant
04T01B-14	0.0381	0.0013	0.2814	0.0177	241	8	252	14	0.49	5	core	discordant
04T01B-15	0.0409	0.0013	0.3136	0.0166	258	8	277	13	1.16	7	core	discordant
04T01B-16-1*	0.0398	0.0012	0.2809	0.0113	252	7	251	9	0.38	0	core	
04T01B-16-2*	0.0187	0.0009	0.1210	0.0169	119	6	116	15	0.07	-3	rim	
04T01B-17	0.0401	0.0012	0.2798	0.0127	253	8	250	10	0.29	-1	core	
04T01B-18-1*	0.0392	0.0012	0.2743	0.0139	248	8	246	11	0.33	-1	core	
04T01B-18-2*	0.0186	0.0008	0.1316	0.0168	119	5	126	15	0.10	5	rim	discordant
04T01B-19	0.0388	0.0013	0.2775	0.0160	245	8	249	13	0.58	1	core	
04T01B-20	0.0952	0.0034	0.8444	0.0528	586	20	622	29	0.31	6	core	discordant
04T01B-21	0.3349	0.0101	5.4717	0.2133	1862	49	1896	33	0.55	2	core	
04T01B-24	0.0363	0.0011	0.2531	0.0111	230	7	229	9	0.63	0	core	
04T01B-25	0.0421	0.0014	0.3064	0.0167	266	9	271	13	0.37	2	core	
04T01B-26	0.0618	0.0021	0.4933	0.0297	387	13	407	20	0.65	5	core	discordant
04T01B-27	0.0317	0.0010	0.2237	0.0111	201	6	205	9	0.44	2	core	
04T01B-29	0.0455	0.0028	0.2911	0.0749	287	17	259	59	0.75	-9	core	reverse discordant
04T01B-30-1*	0.0850	0.0027	0.6634	0.0329	526	16	517	20	0.32	-2	core	
04T01B-30-2*	0.0319	0.0013	0.2870	0.0270	203	8	256	21	0.09	26	rim	discordant
04T01B-33	0.0653	0.0025	0.4883	0.0396	408	15	404	27	0.72	-1	core	
04T01B-34	0.0430	0.0015	0.3012	0.0180	272	9	267	14	0.56	-2	core	
04T01B-35	0.0449	0.0016	0.3269	0.0232	283	10	287	18	0.77	1	core	
04T01B-36	0.0243	0.0011	0.1639	0.0173	155	7	154	15	0.14	0	core	
04T01B-37	0.0613	0.0023	0.4613	0.0360	384	14	385	25	0.84	0	core	
04T01B-38	0.0427	0.0023	0.3078	0.0421	270	14	273	33	0.52	1	core	
04T01B-39	0.0407	0.0014	0.2876	0.0184	257	9	257	15	0.80	0	core	
04T01B-40	0.0437	0.0021	0.3040	0.0475	276	13	270	37	0.53	-2	core	
04T01B-41	0.2103	0.0068	3.1570	0.1532	1231	36	1447	37	0.05	18	core	discordant
04T01B-42	0.0426	0.0015	0.2972	0.0202	269	9	264	16	0.48	-2	core	
04T01B-43-1*	0.0682	0.0023	0.5210	0.0298	425	14	426	20	0.17	0	core	
04T01B-43-2*	0.0558	0.0021	0.5395	0.0402	350	13	438	26	0.23	25	rim	discordant
04T01B-44	0.0402	0.0014	0.2818	0.0155	254	8	252	12	0.34	-1	core	
04T01B-45	0.0969	0.0032	0.8416	0.0425	596	19	620	23	0.02	4	core	discordant
04T01B-46	0.0188	0.0008	0.1271	0.0122	120	5	121	11	0.06	1	rim	
04T01B-49	0.2162	0.0072	3.1862	0.1678	1262	38	1454	41	0.07	15	core	discordant
04T01B-50	0.0294	0.0011	0.2042	0.0160	186	7	189	14	0.25	1	core	
04T01B-51	0.0192	0.0008	0.1270	0.0116	122	5	121	10	0.09	-1	rim	
04T01B-53	0.0381	0.0015	0.2693	0.0237	241	10	242	19	0.73	1	core	
04T01B-54	0.0413	0.0015	0.2916	0.0193	261	9	260	15	0.34	0	core	
04T01B-55	0.0433	0.0015	0.3046	0.0185	273	10	270	14	0.58	-1	core	
04T01B-56	0.0436	0.0016	0.2974	0.0194	275	10	264	15	0.15	-4	core	
04T01B-57	0.0468	0.0019	0.3015	0.0265	295	12	268	21	0.26	-9	core	reverse discordant
04T01B-58-1*	0.0188	0.0008	0.1260	0.0117	120	5	121	11	0.09	0	rim	
04T01B-58-2*	0.0882	0.0031	0.6758	0.0402	545	19	524	24	0.34	-4	core	
04T01B-60	0.0397	0.0016	0.2794	0.0250	251	10	250	20	0.54	0	core	
04T01B-61-1*	0.0191	0.0008	0.1288	0.0127	122	5	123	11	0.11	1	rim	
04T01B-61-2*	0.0804	0.0030	0.6239	0.0396	499	18	492	25	0.27	-1	core	
04T01B-63	0.0410	0.0016	0.2938	0.0211	259	10	262	17	0.26	1	core	
04T01B-64-1*	0.2177	0.0080	3.3929	0.2103	1270	42	1503	49	0.10	18	rim	discordant
04T01B-64-2*	0.2843	0.0105	4.6585	0.2922	1613	53	1760	52	0.33	9	core	discordant
04T01B-66	0.0399	0.0016	0.2760	0.0198	252	10	247	16	0.42	-2	core	
04T01B-67	0.0453	0.0018	0.3217	0.0227	285	11	283	17	0.52	-1	core	
04T01B-68-1*	0.0195	0.0009	0.1285	0.0128	124	6	123	12	0.06	-1	rim	
04T01B-68-2*	0.0438	0.0018	0.3111	0.0244	276	11	275	19	0.68	0	core	
04T01B-70-1*	0.0364	0.0015	0.2382	0.0191	231	9	217	16	0.32	-6	rim	reverse discordant
04T01B-70-2*	0.0438	0.0017	0.2962	0.0205	276	10	263	16	0.44	-5	core	reverse discordant
T1B-3	0.0321	0.0011	0.2594	0.0165	204	7	234	13	0.33	15	rim	discordant
T1B-6	0.3292	0.0105	5.3457	0.2868	1834	51	1876	45	0.51	2	core	
T1B-8	0.0186	0.0007	0.1267	0.0118	119	5	121	11	0.13	2	rim	
T1B-9	0.0185	0.0009	0.1195	0.0169	118	6	115	15	0.10	-3	rim	
T1B-11-1*	0.0186	0.0009	0.1231	0.0151	119	5	118	14	0.01	-1	rim	
T1B-11-2*	0.0429	0.0025	0.3474	0.0628	270	15	303	47	0.68	12	core	discordant
T1B-13	0.0171	0.0007	0.1110	0.0145	109	5	107	13	0.14	-2	rim	
T1B-16	0.0449	0.0016	0.3170	0.0212	283	10	280	16	0.35	-1	core	
T1B-17	0.0647	0.0022	0.4990	0.0310	404	13	406	21	0.27	0	core	
T1B-19	0.0478	0.0020	0.3455	0.0360	301	13	301	27	0.41	0	core	
T1B-20	0.0188	0.0010	0.1954	0.0231	120	6	181	20	0.12	51	core	discordant
T1B-21	0.0176	0.0008	0.1220	0.0150	113	5	117	14	0.11	4	rim	
T1B-23	0.0181	0.0009	0.1197	0.0172	116	5	115	16	0.04	-1	rim	
T1B-24	0.0303	0.0012	0.4688	0.0347	192	8	390	24	0.08	103	rim	discordant
T1B-25	0.0164	0.0007	0.1106	0.0138	105	5	107	13	0.04	2	rim	
T1B-26	0.0172	0.0009	0.1139	0.0196	110	6	110	18	0.09	-1	rim	
T1B-27	0.0159	0.0007	0.1264	0.0126	101	4	121	11	0.10	19	rim	discordant
T1B-28	0.0266	0.0010	0.3350	0.0246	169	6	293	19	0.28	73	rim	discordant
T1B-29	0.0193	0.0010	0.1537	0.0208	123	6	145	18	0.07	18	core	discordant
T1B-30	0.0157	0.0008	0.1119	0.0182	100	5	108	17	0.08	7	core	discordant
T1B-31	0.0212	0.0010	0.1974	0.0236	135	6	183	20	0.09	35	core	discordant
T1B-32	0.0164	0.0007										

Table A2.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
2A-L-2	0.0166	0.0007	0.1101	0.0118	106	4	106	11	0.52	0	homo	
2A-L-3	0.0173	0.0006	0.1178	0.0115	111	4	113	10	0.27	2	core	
2A-L-4	0.0176	0.0007	0.1197	0.0136	113	5	115	12	0.02	2	core	
2A-L-5	0.0180	0.0007	0.1899	0.0189	115	5	177	16	0.06	54	core	discordant
2A-L-6-1*	0.0174	0.0007	0.1174	0.0160	111	5	113	15	0.25	1	core	
2A-L-6-2*	0.0167	0.0012	0.1174	0.0365	107	8	113	33	0.37	6	rim	large error
2A-L-8	0.0172	0.0006	0.1150	0.0090	110	4	110	8	0.25	1	core	
2A-L-9	0.0171	0.0010	0.1166	0.0281	109	7	112	26	0.31	3	homo	large error
2A-L-10	0.0185	0.0007	0.1263	0.0100	118	4	121	9	0.12	2	homo	
2A-L-11	0.0173	0.0006	0.1165	0.0083	110	4	112	8	0.29	1	core	
2A-L-12	0.0183	0.0006	0.1190	0.0082	117	4	114	7	0.13	-2	core	
2A-L-13	0.0167	0.0006	0.1174	0.0108	107	4	113	10	0.16	6	homo	discordant
2A-L-14	0.0164	0.0009	0.1139	0.0217	105	5	109	20	0.43	4	homo	
2A-L-15	0.0170	0.0008	0.1150	0.0219	109	5	111	20	0.23	2	homo	
2A-L-16	0.0170	0.0006	0.1143	0.0100	108	4	110	9	0.29	1	core	
2A-L-17	0.0169	0.0007	0.1155	0.0134	108	4	111	12	0.34	3	homo	
2A-L-18	0.0182	0.0007	0.1236	0.0113	116	5	118	10	0.14	2	homo	
2A-L-20	0.0169	0.0007	0.1146	0.0135	108	4	110	12	0.03	2	homo	
2A-L-21	0.0178	0.0008	0.1193	0.0143	114	5	114	13	0.06	1	homo	
2A-L-23	0.0176	0.0008	0.1185	0.0203	113	5	114	18	0.35	1	homo	
2A-L-24	0.0169	0.0007	0.1113	0.0130	108	4	107	12	0.32	-1	homo	
2A-L-25	0.0188	0.0007	0.1272	0.0111	120	4	122	10	0.27	2	homo	
2A-L-26	0.0181	0.0008	0.1447	0.0214	115	5	137	19	0.01	19	core	discordant
2A-L-27	0.0172	0.0007	0.1145	0.0114	110	4	110	10	0.36	0	homo	
2A-L-28	0.0185	0.0008	0.1213	0.0145	118	5	116	13	0.38	-2	homo	
2A-L-30	0.0170	0.0006	0.1147	0.0105	109	4	110	10	0.31	1	core	
2A-L-31	0.0162	0.0008	0.1070	0.0194	103	5	103	18	0.31	0	homo	
2A-L-32	0.0168	0.0006	0.1006	0.0083	107	4	97	8	0.05	-9	homo	reverse discordant
2A-L-33	0.0169	0.0007	0.1129	0.0137	108	4	109	13	0.42	0	homo	
2A-L-34	0.0146	0.0005	0.1137	0.0088	93	3	109	8	0.27	17	core	discordant
2A-L-35	0.0173	0.0007	0.1150	0.0146	110	5	111	13	0.40	0	core	
2A-L-37-1*	0.0172	0.0007	0.1190	0.0113	110	4	114	10	0.12	4	core	
2A-L-37-2*	0.0174	0.0007	0.1155	0.0135	111	5	111	12	0.28	0	rim	
2A-L-39	0.0183	0.0013	0.1377	0.0421	117	8	131	38	0.37	12	homo	large error
2A-L-40	0.0155	0.0012	0.1352	0.0460	99	8	129	41	0.03	30	core	large error
2A-L-41	0.0152	0.0006	0.1114	0.0103	97	4	107	9	0.27	10	homo	discordant
2A-L-42	0.0172	0.0010	0.1042	0.0275	110	7	101	25	0.44	-9	homo	large error
2A-L-44	0.0188	0.0013	0.1239	0.0625	120	8	119	56	0.15	-1	core	large error

*core-rim analyses from single grain

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U age} - ^{206}\text{Pb}/^{238}\text{U age}) / (^{206}\text{Pb}/^{238}\text{U age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$."large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U age}$ beyond 20 %

Table A3.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
2A-M-5	0.0188	0.0016	0.1225	0.0325	120	10	117	29	0.05	-2	homo	large error
2A-M-6	0.0188	0.0006	0.1297	0.0060	120	4	124	5	0.37	3	homo	
2A-M-8	0.0158	0.0017	0.1008	0.0455	101	11	98	42	0.04	-3	homo	large error
2A-M-11	0.0182	0.0026	0.1259	0.0818	116	17	120	74	0.06	3	core	large error
2A-M-13	0.0191	0.0028	0.1276	0.1228	122	18	122	111	0.04	0	core	large error
2A-M-14	0.0177	0.0007	0.1225	0.0886	113	4	117	8	0.24	4	homo	
2A-M-15	0.0180	0.0009	0.1136	0.0138	115	6	109	13	0.37	-5	homo	reverse discordant
2A-M-16	0.0185	0.0010	0.1298	0.0181	118	6	124	16	0.44	5	homo	discordant
2A-M-18	0.0195	0.0014	0.1371	0.0287	125	9	130	26	0.01	5	core	discordant
2A-M-19	0.0153	0.0014	0.1401	0.0330	98	9	133	29	0.14	36	core	discordant
2A-M-20	0.0176	0.0008	0.1229	0.0113	113	5	118	10	0.35	4	core	
2A-M-21	0.0160	0.0040	0.1948	0.1592	102	25	181	135	0.11	76	core	large error
2A-M-24	0.0183	0.0014	0.1226	0.0288	117	9	117	26	0.01	1	core	large error
2A-M-27	0.0170	0.0008	0.1126	0.0110	109	5	108	10	0.37	0	homo	
2A-M-28	0.0175	0.0010	0.1187	0.0205	112	6	114	19	0.34	2	core	
2A-M-29	0.0167	0.0007	0.1156	0.0113	107	5	111	10	0.23	4	homo	
2A-M-30	0.0162	0.0011	0.1086	0.0191	104	7	105	17	0.47	1	homo	
2A-M-31	0.0148	0.0010	0.1359	0.0195	95	6	129	17	0.04	37	homo	discordant
2A-M-32	0.0187	0.0009	0.1261	0.0121	119	5	121	11	0.41	1	homo	
2A-M-35	0.0186	0.0007	0.1198	0.0069	119	4	115	6	0.17	-3	homo	
2A-M-36	0.0171	0.0006	0.1153	0.0074	109	4	111	7	0.11	2	core	
2A-M-39	0.0154	0.0008	0.1134	0.0109	99	5	109	10	0.38	11	homo	discordant

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

"large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U}$ age beyond 20 %

Table A4.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
2C-1	0.0204	0.0009	0.1241	0.0135	130	6	119	12	0.47	-9	core	reverse discordant
2C-2	0.0170	0.0009	0.1087	0.0208	109	6	105	19	0.03	-4	core	
2C-3	0.0178	0.0007	0.1213	0.0116	114	4	116	11	0.45	2	core	
2C-4	0.0185	0.0007	0.1248	0.0098	118	4	119	9	0.81	1	homo	
2C-5-1*	0.0193	0.0008	0.1461	0.0170	123	5	138	15	0.07	12	core	discordant
2C-5-2*	0.0169	0.0006	0.1143	0.0075	108	4	110	7	0.88	2	rim	
2C-7	0.0188	0.0007	0.1292	0.0092	120	4	123	8	0.31	3	core	
2C-8	0.0185	0.0006	0.1220	0.0081	118	4	117	7	0.38	-1	core	
2C-9	0.0181	0.0006	0.1916	0.0105	116	4	178	9	0.30	54	core	discordant
2C-10	0.0155	0.0005	0.1030	0.0074	99	3	100	7	0.40	1	core	young
2C-11	0.0174	0.0007	0.1137	0.0121	111	4	109	11	0.57	-1	core	
2C-12	0.0181	0.0006	0.1244	0.0086	116	4	119	8	0.38	3	core	
2C-14	0.0190	0.0009	0.1247	0.0152	122	6	119	14	0.28	-2	rim	
2C-15	0.0184	0.0007	0.1243	0.0092	117	4	119	8	0.93	1	rim	
2C-16	0.0164	0.0006	0.1143	0.0072	105	4	110	7	0.28	5	rim	discordant
2C-17	0.0176	0.0006	0.1265	0.0083	112	4	121	7	1.26	8	core	discordant
2C-18	0.0188	0.0008	0.1254	0.0143	120	5	120	13	0.31	0	rim	
2C-20	0.0173	0.0009	0.1160	0.0186	111	6	111	17	0.70	1	homo	
2C-21	0.0182	0.0008	0.1226	0.0140	116	5	117	13	0.11	1	rim	
2C-22	0.0167	0.0009	0.1115	0.0181	107	5	107	17	0.32	0	homo	
2C-23	0.0172	0.0007	0.1147	0.0107	110	4	110	10	0.45	1	core	
2C-25-1*	0.0171	0.0007	0.1141	0.0127	109	5	110	12	0.02	1	core	
2C-25-2*	0.0158	0.0007	0.1059	0.0114	101	4	102	10	0.03	1	rim	young
2C-27	0.0183	0.0007	0.1244	0.0117	117	4	119	11	0.14	2	core	
2C-28	0.0173	0.0006	0.1151	0.0078	110	4	111	7	0.68	0	core	
2C-29	0.0184	0.0008	0.1278	0.0143	117	5	122	13	0.50	4	core	
2C-30	0.0185	0.0006	0.1248	0.0069	118	4	119	6	0.68	1	homo	

*core-rim analyses from single grain

$$\text{Concordancy (\%)} = (\frac{\text{age}_{^{207}\text{Pb}/^{235}\text{U}} - \text{age}_{^{206}\text{Pb}/^{238}\text{U}}}{\text{age}_{^{206}\text{Pb}/^{238}\text{U}}}) / (\text{age}_{^{206}\text{Pb}/^{238}\text{U}}) * 100$$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

Table A5.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
02D-1	0.0391	0.0019	0.2694	0.0154	248	12	242	12	0.87	-2	core	
02D-2	0.0411	0.0019	0.2810	0.0146	260	12	251	12	1.43	-3	core	reverse discordant
02D-5	0.0411	0.0019	0.5156	0.0250	259	12	422	17	1.25	63	core	discordant
02D-6	0.0161	0.0009	0.1135	0.0118	103	6	109	11	1.04	6	rim	discordant
02D-7	0.0372	0.0018	0.2712	0.0152	235	11	244	12	1.82	4	core	discordant
02D-8	0.0369	0.0017	0.3389	0.0177	234	11	296	13	0.69	27	core	discordant
02D-9	0.0172	0.0009	0.1069	0.0091	110	6	103	8	0.24	-6	rim	reverse discordant
02D-10	0.0192	0.0009	0.1322	0.0079	123	6	126	7	0.21	3	core	
02D-11	0.0291	0.0016	0.1992	0.0192	185	10	184	16	0.26	0	core	
02D-12	0.0359	0.0018	0.2473	0.0175	227	11	224	14	0.65	-1	core	
02D-13	0.0399	0.0019	0.2860	0.0176	252	12	255	14	0.71	1	core	
02D-14	0.0358	0.0018	0.2396	0.0184	227	11	218	15	0.53	-4	core	
02D-15	0.0402	0.0019	0.2803	0.0161	254	12	251	13	0.55	-1	core	
02D-16	0.0350	0.0016	0.2395	0.0127	221	10	218	10	0.56	-2	core	
02D-17	0.0393	0.0018	0.2638	0.0136	248	11	238	11	0.33	-4	core	reverse discordant
02D-18	0.0383	0.0018	0.2690	0.0154	242	11	242	12	0.64	0	core	
02D-19	0.0457	0.0022	0.3237	0.0180	288	13	285	14	0.57	-1	core	
02D-20	0.0343	0.0016	0.2374	0.0123	217	10	216	10	0.59	-1	core	
02D-21	0.0243	0.0012	0.1610	0.0100	155	7	152	9	0.27	-2	core	
02D-22	0.0358	0.0017	0.2404	0.0138	226	11	219	11	0.24	-3	core	
02D-23	0.0303	0.0014	0.2077	0.0104	193	9	192	9	0.63	-1	core	
02D-24	0.0355	0.0016	0.2638	0.0133	225	10	238	11	0.31	6	core	discordant
02D-25	0.0305	0.0014	0.2209	0.0125	194	9	203	10	0.30	5	core	discordant
02D-26-2	0.0308	0.0014	0.2120	0.0120	196	9	195	10	0.14	0	core	
02D-27	0.0513	0.0025	0.3777	0.0257	322	16	325	19	1.27	1	core	
02D-28	0.0386	0.0018	0.2675	0.0140	244	11	241	11	0.63	-2	core	
02D-30	0.4011	0.0198	8.7366	0.4644	2174	91	2311	48	1.08	6	core	discordant
02D-31	0.0165	0.0010	0.1094	0.0132	105	6	105	12	0.58	0	rim	
02D-32	0.0351	0.0017	0.2510	0.0172	222	11	227	14	0.51	2	core	
02D-33	0.0162	0.0008	0.1098	0.0081	103	5	106	7	1.00	2	homo	
02D-34	0.0167	0.0008	0.1129	0.0066	107	5	109	6	0.10	2	homo	
02D-35	0.0168	0.0008	0.1127	0.0070	108	5	108	6	0.09	1	homo	
02D-39	0.0709	0.0032	0.5318	0.0266	442	20	433	18	0.59	-2	core	
02D-40	0.0171	0.0008	0.1091	0.0072	109	5	105	7	0.51	-4	homo	
02D-43	0.3604	0.0164	9.2827	0.4510	1984	78	2366	45	0.13	19	core	discordant
02D-44	0.0182	0.0009	0.1180	0.0095	116	6	113	9	1.17	-2	homo	
02D-45	0.0399	0.0019	0.2676	0.0151	252	12	241	12	0.59	-5	core	reverse discordant
02D-46	0.0291	0.0015	0.1873	0.0143	185	9	174	12	0.33	-6	core	reverse discordant
02D-48	0.0170	0.0008	0.1098	0.0066	109	5	106	6	0.11	-3	core	
02D-49	0.0390	0.0018	0.2623	0.0154	247	11	237	12	0.55	-4	core	reverse discordant
02D-51	0.0315	0.0015	0.2178	0.0128	200	9	200	11	0.40	0	core	
02D-52	0.0171	0.0008	0.1093	0.0064	109	5	105	6	0.10	-4	core	reverse discordant
02D-54	0.0170	0.0012	0.1179	0.0203	109	8	113	18	0.83	4	rim	
02D-55	0.0344	0.0025	0.2402	0.0426	218	16	219	35	0.86	0	core	
02D-56	0.0399	0.0018	0.2778	0.0146	252	11	249	12	0.24	-1	core	
02D-57	0.0396	0.0018	0.2881	0.0156	251	11	257	12	2.22	3	core	
02D-58	0.0398	0.0019	0.2792	0.0162	252	12	250	13	0.87	-1	core	
02D-59	0.0292	0.0014	0.1989	0.0110	186	8	184	9	0.54	-1	core	
02D-60	0.0394	0.0020	0.2757	0.0199	249	12	247	16	0.48	-1	core	
02D-62	0.0433	0.0023	0.4072	0.0320	273	14	347	23	0.71	27	core	discordant
02D-64	0.0305	0.0014	0.2170	0.0122	193	9	199	10	0.53	3	core	
02D-65	0.0277	0.0013	0.1858	0.0107	176	8	173	9	0.28	-2	core	
02D-68	0.2421	0.0112	3.0033	0.1557	1398	58	1408	39	0.57	1	core	
02D-73	0.0317	0.0015	0.2194	0.0134	201	9	201	11	0.71	0	core	
02D-74	0.0391	0.0018	0.2814	0.0159	248	11	252	13	0.97	2	core	
02D-82	0.0150	0.0008	0.1097	0.0089	96	5	106	8	0.65	10	homo	discordant
02D-83	0.0228	0.0011	0.1623	0.0101	145	7	153	9	0.36	5	core	discordant
02D-84	0.0392	0.0018	0.2747	0.0163	248	11	246	13	0.62	-1	core	
02D-85	0.0360	0.0017	0.2455	0.0144	228	11	223	12	0.65	-2	core	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$ Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

Table A6.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
04B-2	0.0175	0.0009	0.1165	0.0081	112	6	112	7	0.21	0	core	
04B-3	0.0192	0.0010	0.1333	0.0087	123	6	127	8	0.19	4	core	
04B-5-1*	0.0170	0.0009	0.1141	0.0078	109	5	110	7	0.10	1	rim	
04B-5-2*	0.0398	0.0021	0.2890	0.0210	252	13	258	17	0.67	2	core	
04B-7	0.0212	0.0014	0.1910	0.0232	135	9	177	20	0.14	31	core	discordant
04B-8	0.0170	0.0009	0.1166	0.0075	109	5	112	7	0.32	3	core	
04B-10	0.0580	0.0028	0.4268	0.0221	364	17	361	16	0.50	-1	core	
04B-11	0.0192	0.0011	0.1517	0.0159	123	7	143	14	0.07	17	rim	discordant
04B-13	0.0132	0.0006	0.0884	0.0044	84	4	86	4	0.05	2	core	discordant
04B-14	0.0177	0.0009	0.1177	0.0075	113	6	113	7	0.15	0	rim	
04B-17	0.0180	0.0009	0.1213	0.0064	115	5	116	6	0.18	1	core	
04B-18	0.0171	0.0008	0.1150	0.0065	109	5	110	6	0.09	1	rim	
04B-19-1*	0.0388	0.0020	0.2829	0.0207	246	13	253	16	0.47	3	core	
04B-19-2*	0.0167	0.0010	0.1089	0.0117	107	6	105	11	0.36	-1	rim	
04B-20	0.0266	0.0013	0.1921	0.0097	169	8	178	8	0.25	5	core	discordant
04B-22	0.0187	0.0009	0.1348	0.0088	119	6	128	8	0.08	8	core	discordant
04B-33	0.0130	0.0006	0.0877	0.0045	83	4	85	4	0.06	3	core	discordant
04B-35	0.0197	0.0012	0.1286	0.0148	126	7	123	13	0.27	-2	homo	
04B-37	0.0465	0.0022	0.3481	0.0194	293	14	303	15	1.05	3	core	discordant
04B-38	0.0187	0.0011	0.1315	0.0132	119	7	125	12	0.06	5	homo	discordant
04B-39-1*	0.0185	0.0010	0.1307	0.0112	118	6	125	10	0.42	6	rim	discordant
04B-39-2*	0.0361	0.0018	0.2516	0.0155	229	11	228	13	0.45	0	core	
04B-40	0.0191	0.0010	0.1302	0.0115	122	7	124	10	0.05	2	homo	
04B-41	0.0165	0.0008	0.1125	0.0067	106	5	108	6	0.32	2	homo	
04B-43	0.0191	0.0010	0.1258	0.0086	122	6	120	8	0.06	-2	rim	
04B-44	0.0285	0.0015	0.1880	0.0141	181	9	175	12	0.38	-4	core	
04B-46	0.0395	0.0020	0.2837	0.0211	250	13	254	17	0.56	2	core	
04B-47	0.0177	0.0009	0.1126	0.0066	113	5	108	6	0.05	-4	core	reverse discordant
04B-48	0.0176	0.0009	0.1128	0.0083	112	6	109	8	0.15	-3	rim	
04B-49	0.0220	0.0012	0.1431	0.0116	140	7	136	10	0.41	-3	core	
04B-51	0.0133	0.0006	0.0898	0.0049	85	4	87	5	0.04	2	homo	discordant
04B-52	0.0224	0.0012	0.1561	0.0121	143	7	147	11	0.20	3	core	
04B-53	0.0214	0.0011	0.1496	0.0097	136	7	142	9	0.25	4	core	discordant
04B-54	0.0252	0.0018	0.2586	0.0342	160	11	234	28	0.14	46	core	discordant
04B-55	0.0143	0.0007	0.0903	0.0051	92	4	88	5	0.04	-4	core	reverse discordant
04B-56	0.0399	0.0020	0.2897	0.0183	252	12	258	14	0.82	3	core	
04B-57	0.0248	0.0014	0.1757	0.0171	158	9	164	15	0.29	4	core	
04B-59	0.0133	0.0006	0.0866	0.0048	85	4	84	5	0.03	-1	homo	young
04B-60	0.0234	0.0020	0.2159	0.0477	149	13	198	40	0.64	33	core	large error
04B-61	0.0238	0.0011	0.2184	0.0124	151	7	201	10	0.10	33	core	discordant
04B-62	0.0229	0.0012	0.1620	0.0118	146	7	152	10	0.23	5	core	discordant
04B-63	0.0191	0.0010	0.1293	0.0087	122	6	123	8	0.26	1	homo	

*core-rim analyses from single grain

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U age} - ^{206}\text{Pb}/^{238}\text{U age}) / (^{206}\text{Pb}/^{238}\text{U age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$."large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U age}$ beyond 20 %

Table A7.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
02A-2	0.0162	0.0011	0.1098	0.0213	103	7	106	19	0.58	2	homo	
02A-3	0.0178	0.0013	0.1167	0.0334	114	8	112	30	0.63	-2	homo	large error
02A-4	0.0163	0.0014	0.1472	0.0553	104	9	139	49	0.53	34	homo	large error
02A-5	0.0170	0.0013	0.1130	0.0366	109	8	109	33	0.52	0	homo	large error
02A-6	0.0165	0.0012	0.1141	0.0281	105	8	110	26	0.72	4	homo	large error
02A-7	0.0167	0.0010	0.0949	0.0168	107	7	92	16	0.55	-14	homo	reverse discordant
02A-8	0.0161	0.0012	0.1059	0.0294	103	7	102	27	0.64	0	homo	large error
02A-10	0.0172	0.0010	0.1202	0.0155	110	6	115	14	0.68	5	homo	discordant
02A-12	0.0179	0.0012	0.1199	0.0267	114	8	115	24	0.68	1	homo	large error
02A-13	0.0171	0.0013	0.1157	0.0385	109	9	111	35	0.44	2	homo	large error
02A-16	0.0183	0.0012	0.1222	0.0268	117	8	117	24	0.57	0	homo	large error
02A-17	0.0170	0.0017	0.3420	0.0758	109	11	299	57	0.56	175	homo	discordant
02A-20	0.0156	0.0010	0.1313	0.0202	100	6	125	18	0.89	25	homo	discordant
02A-21	0.0149	0.0014	0.1309	0.0599	95	9	125	54	0.46	31	homo	large error
02A-23	0.0191	0.0018	0.3010	0.0645	122	11	267	50	0.42	120	homo	discordant
02A-24	0.0163	0.0009	0.1395	0.0098	104	6	133	9	1.48	27	homo	discordant
02A-25	0.0170	0.0011	0.1105	0.0187	109	7	106	17	0.56	-2	homo	
02A-27	0.0177	0.0013	0.1155	0.0384	113	8	111	35	0.77	-2	homo	large error
02A-29	0.0183	0.0010	0.2172	0.0165	117	7	200	14	0.36	71	homo	discordant
02A-30	0.0180	0.0012	0.1229	0.0294	115	8	118	27	0.55	3	homo	large error
02A-32	0.0158	0.0018	0.1875	0.0794	101	11	174	68	0.77	73	homo	large error
02A-33	0.0180	0.0012	0.1195	0.0258	115	8	115	23	0.57	0	homo	
02A-34	0.0179	0.0010	0.1189	0.0115	114	6	114	10	0.69	0	homo	
02A-43	0.0181	0.0015	0.1183	0.0588	116	9	114	53	0.64	-2	homo	large error
02A-44	0.0187	0.0013	0.2017	0.0338	120	8	187	29	0.75	56	homo	discordant
02A-47	0.0208	0.0020	0.2251	0.0897	133	13	206	74	0.49	56	homo	large error
02A-48	0.0182	0.0012	0.2234	0.0322	116	8	205	27	0.83	76	homo	discordant
02A-49	0.0180	0.0017	0.1762	0.0652	115	11	165	56	0.72	43	homo	large error
02A-52	0.0198	0.0019	0.2353	0.0779	127	12	215	64	0.49	69	homo	large error
02A-53	0.0176	0.0014	0.1144	0.0394	112	9	110	36	0.93	-2	homo	large error
02A-54	0.0212	0.0018	0.5971	0.0864	135	11	475	55	0.57	251	homo	discordant
02A-56	0.0154	0.0010	0.1275	0.0237	98	7	122	21	0.57	24	homo	discordant
02A-57	0.0180	0.0011	0.1431	0.0279	115	7	136	25	0.66	18	homo	discordant
02A-60	0.0147	0.0010	0.1206	0.0207	94	6	116	19	0.37	23	homo	discordant
02A-61	0.0174	0.0013	0.1162	0.0365	111	8	112	33	0.53	0	homo	large error
02A-62	0.0201	0.0014	0.3620	0.0384	128	9	314	29	0.85	145	homo	discordant
02A-63	0.0189	0.0018	0.1884	0.0559	121	11	175	48	0.58	45	homo	large error
02A-65	0.0148	0.0017	0.1756	0.0690	95	11	164	60	0.51	73	homo	large error
02A-66	0.0159	0.0012	0.1128	0.0303	102	8	109	28	0.63	7	homo	large error
02A-67	0.0164	0.0011	0.1096	0.0175	105	7	106	16	0.55	1	homo	
02A-68	0.0158	0.0011	0.1150	0.0241	101	7	111	22	1.04	9	homo	discordant
02A-69	0.0177	0.0016	0.1098	0.0462	113	10	106	42	0.54	-6	homo	large error
02A-70	0.0173	0.0013	0.1135	0.0236	110	8	109	21	1.06	-1	homo	
02A-71	0.0175	0.0023	0.2025	0.0918	112	14	187	77	0.49	67	homo	large error
02A-72	0.0188	0.0017	0.2812	0.0616	120	11	252	49	0.63	110	homo	discordant
02A-73	0.0189	0.0015	0.1767	0.0400	120	9	165	35	0.72	37	homo	large error
02A-74	0.0200	0.0013	0.1560	0.0220	128	8	147	19	0.14	15	homo	discordant
02A-75	0.0166	0.0012	0.1084	0.0300	106	8	105	27	0.49	-1	homo	large error
02A-76	0.0159	0.0021	0.1924	0.0826	102	13	179	70	0.62	76	homo	large error
02A-77	0.0175	0.0012	0.1169	0.0220	112	8	112	20	1.04	0	homo	
02A-78	0.0177	0.0015	0.1261	0.0453	113	10	121	41	0.52	7	homo	large error
02A-80	0.0181	0.0012	0.1172	0.0229	116	8	113	21	0.81	-3	homo	
02A-81	0.0197	0.0013	0.3389	0.0360	125	8	296	27	0.37	136	homo	discordant
02A-82	0.0175	0.0013	0.2027	0.0411	112	8	187	35	0.66	68	homo	discordant
02A-83	0.0199	0.0013	0.4419	0.0402	127	8	372	28	0.71	193	homo	discordant
02A-86	0.0163	0.0013	0.1357	0.0347	104	8	129	31	0.70	24	homo	large error
02A-87	0.0167	0.0011	0.1164	0.0243	107	7	112	22	0.64	5	homo	discordant
02A-88	0.0178	0.0012	0.2020	0.0296	113	8	187	25	0.52	65	homo	discordant
02A-90	0.0180	0.0014	0.1816	0.0452	115	9	169	39	0.36	47	homo	discordant
02A-91	0.0175	0.0015	0.1328	0.0497	112	10	127	45	0.52	13	homo	large error
02A-92	0.0169	0.0012	0.1106	0.0227	108	7	106	21	1.00	-1	homo	
02A-93	0.0184	0.0014	0.1381	0.0382	118	9	131	34	0.42	12	homo	large error
02A-94	0.0168	0.0011	0.1137	0.0218	107	7	109	20	0.99	2	homo	
02A-96	0.0148	0.0012	0.0755	0.0306	95	7	74	29	0.86	-22	homo	large error
02A-101	0.0179	0.0014	0.2214	0.0460	114	9	203	38	0.47	78	homo	discordant
02A-102	0.0172	0.0012	0.1929	0.0311	110	7	179	26	0.49	63	homo	discordant
02A-103	0.0240	0.0018	0.8105	0.0871	153	11	603	49	0.39	295	homo	discordant
02A-104	0.0158	0.0010	0.1062	0.0192	101	7	102	18	0.62	1	homo	
02A-105	0.0180	0.0016	0.1185	0.0504	115	10	114	46	0.67	-1	homo	large error
02A-106	0.0162	0.0012	0.1401	0.0290	103	7	133	26	0.67	29	homo	discordant
02A-108	0.0172	0.0017	0.1235	0.0589	110	11	118	53	0.65	8	homo	large error
02A-109	0.0183	0.0012	0.1217	0.0215	117	7	117	19	0.59	0	homo	
02A-110	0.0167	0.0013	0.1128	0.0331	107	8	109	30	0.58	2	homo	large error
02A-111	0.0168	0.0010	0.1105	0.0177	107	7	106	16	0.69	-1	homo	
02A-112	0.0166	0.0010	0.1100	0.0160	106	6	106	15	0.43	0	homo	
02A-113	0.0164	0.0011	0.1040	0.0221	105	7	100	20	0.48	-4	homo	
02A-114	0.0145	0.0010	1.0003	0.0227	93	6	97	21	0.52	5	homo	large error
02A-115	0.0166	0.0010	0.1096	0.0181	106	7	106	17	0.51	0	homo	
02A-116	0.0191	0.0013	0.3395	0.0458	122	8	297	35	0.76	144	homo	discordant
02A-118	0.0175	0.0013	0.1337	0.0405	112	8	127	36	0.57	14	homo	large error

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{age} - ^{206}\text{Pb}/^{238}\text{U} \text{age}) / (^{206}\text{Pb}/^{238}\text{U} \text{age}) * 100$ Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$."large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U}$ age beyond 20 %

Table A8.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
401-1	0.0180	0.0009	0.1731	0.0131	115	6	162	11	0.77	41	homo	discordant
401-2	0.0183	0.0010	0.1351	0.0131	117	6	129	12	0.68	10	homo	discordant
401-3	0.0183	0.0010	0.1243	0.0131	117	6	119	12	0.61	2	homo	
401-4	0.0188	0.0012	0.1224	0.0264	120	8	117	24	0.70	-2	homo	large error
401-5	0.0199	0.0013	0.1514	0.0275	127	8	143	24	0.67	13	homo	discordant
401-7	0.0189	0.0011	0.1673	0.0176	121	7	157	15	1.00	30	homo	discordant
401-8	0.0189	0.0014	0.1559	0.0363	121	9	147	32	0.62	22	homo	large error
401-9	0.0179	0.0012	0.1182	0.0217	114	7	113	20	0.71	-1	homo	
401-12	0.0180	0.0011	0.1208	0.0254	115	7	116	23	0.47	1	homo	
401-13	0.0181	0.0011	0.1199	0.0220	115	7	115	20	0.79	0	homo	
401-14	0.0167	0.0011	0.1096	0.0261	106	7	106	24	0.73	-1	homo	large error
401-15	0.0194	0.0023	0.1800	0.0925	124	15	168	80	0.68	36	homo	large error
401-16	0.0160	0.0015	0.1055	0.0478	102	9	102	44	0.64	0	homo	large error
401-19	0.0177	0.0011	0.1174	0.0203	113	7	113	18	0.62	0	homo	
401-20	0.0169	0.0011	0.1125	0.0217	108	7	108	20	0.75	0	homo	
401-21	0.0212	0.0014	0.1956	0.0337	135	9	181	29	0.63	34	homo	discordant
401-22	0.0168	0.0011	0.1125	0.0217	107	7	108	20	0.67	1	homo	
401-25	0.0211	0.0014	0.1544	0.0307	134	9	146	27	0.86	8	homo	discordant
401-26	0.0191	0.0013	0.1274	0.0243	122	8	122	22	0.61	0	homo	
401-27	0.0165	0.0010	0.1102	0.0151	105	7	106	14	0.70	1	homo	
401-28	0.0173	0.0013	0.1155	0.0282	110	8	111	26	0.68	1	homo	large error
401-29	0.0167	0.0012	0.0995	0.0218	107	7	96	20	0.81	-10	homo	large error
401-30	0.0189	0.0012	0.1001	0.0172	121	7	97	16	0.85	-20	homo	reverse discordant
401-31	0.0168	0.0011	0.1136	0.0210	107	7	109	19	0.61	2	homo	
401-32	0.0173	0.0010	0.1153	0.0153	110	6	111	14	0.53	0	homo	
401-33	0.0169	0.0010	0.1194	0.0157	108	6	115	14	0.53	6	homo	discordant
401-34	0.0171	0.0009	0.1128	0.0117	109	6	109	11	1.24	-1	homo	
401-35	0.0167	0.0011	0.1118	0.0218	107	7	108	20	0.55	1	homo	
401-36	0.0173	0.0010	0.1149	0.0172	110	6	110	16	0.72	0	homo	
401-37	0.0174	0.0010	0.1156	0.0160	111	6	111	15	0.82	0	homo	
401-38	0.0172	0.0009	0.1140	0.0137	110	6	110	13	0.81	0	homo	
401-39	0.0169	0.0009	0.1155	0.0133	108	6	111	12	0.77	3	homo	
401-40	0.0165	0.0010	0.1075	0.0162	105	6	104	15	0.60	-2	homo	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$ Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$."large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U}$ age beyond 20 %

Table A9.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
0301A-1	0.0176	0.0006	0.1182	0.0098	112	4	113	9	0.66	1	core	
0301A-2	0.0178	0.0006	0.1214	0.0083	114	4	116	7	0.78	2	core	
0301A-3-1	0.0171	0.0006	0.1238	0.0102	109	4	118	9	0.56	8	core	discordant
0301A-5	0.0175	0.0007	0.1168	0.0133	112	4	112	12	0.80	0	core	
0301A-6	0.0178	0.0006	0.1233	0.0115	114	4	118	10	0.85	4	core	
0301A-7	0.0172	0.0007	0.1158	0.0120	110	5	111	11	0.56	1	core	
0301A-8-2	0.0179	0.0007	0.1190	0.0144	114	5	114	13	0.64	0	rim	
0301A-9	0.0177	0.0006	0.1203	0.0091	113	4	115	8	0.73	2	rim	
0301A-10	0.0180	0.0006	0.1203	0.0104	115	4	115	9	0.85	1	core	
0301A-12	0.0181	0.0011	0.1215	0.0314	116	7	116	28	0.64	1	rim	large error
0301A-16	0.0180	0.0006	0.1196	0.0096	115	4	115	9	0.70	0	core	
0301A-19	0.0176	0.0006	0.1197	0.0108	113	4	115	10	0.68	2	core	
0301A-22	0.0181	0.0006	0.1210	0.0077	115	4	116	7	0.43	1	rim	
0301A-23	0.0170	0.0006	0.1180	0.0086	109	4	113	8	0.82	4	core	
0301A-24	0.0177	0.0006	0.1195	0.0096	113	4	115	9	0.55	1	core	
0301A-25	0.0179	0.0006	0.1206	0.0089	114	4	116	8	0.79	1	rim	
0301A-26	0.0172	0.0007	0.1189	0.0111	110	4	114	10	0.78	4	core	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

"large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U}$ age beyond 20 %

Table A10.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
01-1	0.0173	0.0010	0.1127	0.0126	111	6	108	11	0.67	-2	homo	
01-2	0.0174	0.0010	0.1187	0.0133	111	6	114	12	0.77	3	homo	
01-3	0.0168	0.0009	0.1132	0.0112	107	6	109	10	0.47	2	homo	
01-4	0.0158	0.0009	0.1094	0.0126	101	6	105	12	0.81	4	homo	
01-5	0.0168	0.0009	0.1120	0.0113	107	6	108	10	0.67	1	homo	
01-6	0.0168	0.0010	0.1096	0.0130	108	6	106	12	0.63	-2	homo	
01-7	0.0170	0.0008	0.1204	0.0085	109	5	115	8	0.65	6	homo	discordant
01-9	0.0171	0.0010	0.1093	0.0125	109	6	105	11	0.55	-4	homo	
01-10	0.0165	0.0009	0.1113	0.0095	106	5	107	9	0.64	1	homo	
01-11	0.0170	0.0010	0.1164	0.0128	108	6	112	12	0.58	3	homo	
01-12-2	0.0173	0.0010	0.1165	0.0128	111	6	112	12	0.57	1	homo	
01-13	0.0194	0.0014	0.1267	0.0262	124	9	121	24	0.74	-2	homo	large error
01-14	0.0164	0.0009	0.1147	0.0109	105	6	110	10	0.53	5	homo	discordant
01-15	0.0170	0.0010	0.1155	0.0130	108	6	111	12	0.71	2	homo	
01-16	0.0161	0.0009	0.1142	0.0124	103	6	110	11	0.63	7	homo	discordant
01-18	0.0190	0.0010	0.1340	0.0120	121	6	128	11	0.75	5	homo	discordant
01-19	0.0331	0.0016	0.2181	0.0135	210	10	200	11	0.33	-5	homo	reverse discordant
01-21	0.0171	0.0009	0.1215	0.0127	110	6	116	11	0.52	6	homo	discordant
01-22	0.0168	0.0009	0.1053	0.0122	107	6	102	11	0.66	-5	homo	reverse discordant
01-24	0.0163	0.0008	0.1126	0.0071	104	5	108	6	0.55	4	homo	discordant
01-26	0.0176	0.0009	0.1195	0.0110	113	6	115	10	0.65	2	homo	
01-27	0.0171	0.0009	0.1199	0.0104	109	6	115	9	0.83	5	homo	discordant
01-28	0.0170	0.0010	0.1161	0.0136	108	6	112	12	0.80	3	homo	
01-29	0.0167	0.0008	0.1156	0.0091	107	5	111	8	0.60	4	homo	
01-31	0.0167	0.0009	0.1146	0.0099	107	5	110	9	0.52	3	homo	
01-32	0.0175	0.0010	0.1183	0.0149	112	7	114	14	0.68	2	homo	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U age} - ^{206}\text{Pb}/^{238}\text{U age}) / (^{206}\text{Pb}/^{238}\text{U age}) * 100$ Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$."large error" is indicative of omitted data due to the error of $^{207}\text{Pb}/^{235}\text{U age}$ beyond 20 %

Table A11.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
07A1-1	0.0174	0.0008	0.1254	0.0069	111	5	120	6	0.27	8	homo	discordant
07A1-2	0.0169	0.0009	0.1158	0.0103	108	6	111	9	0.58	3	homo	
07A1-3	0.0396	0.0020	0.2789	0.0188	250	12	250	15	0.20	0	core	
07A1-5	0.0169	0.0009	0.1107	0.0087	108	5	107	8	0.43	-1	homo	
07A1-6	0.0234	0.0011	0.1484	0.0085	149	7	140	8	0.40	-6	homo	reverse discordant
07A1-8	0.0178	0.0008	0.1107	0.0061	114	5	107	6	0.23	-6	homo	reverse discordant
07A1-9	0.0173	0.0008	0.1143	0.0064	110	5	110	6	0.23	0	rim	
07A1-10	0.0178	0.0008	0.1181	0.0067	114	5	113	6	0.19	0	core	
07A1-11	0.0199	0.0010	0.1135	0.0097	127	7	109	9	0.74	-14	homo	reverse discordant
07A1-12	0.0176	0.0009	0.1464	0.0122	112	6	139	11	0.37	23	core	discordant
07A1-16	0.0432	0.0027	0.3141	0.0377	273	16	277	29	0.41	2	core	
07A1-18	0.0444	0.0030	0.3117	0.0562	280	19	275	44	0.67	-2	core	
07A1-19	0.0206	0.0011	0.1513	0.0115	132	7	143	10	0.44	9	core	discordant
07A1-21	0.0171	0.0008	0.1184	0.0069	109	5	114	6	0.16	4	homo	discordant
07A1-22	0.0173	0.0008	0.1153	0.0066	110	5	111	6	0.25	0	rim	
07A1-23	0.0189	0.0010	0.1289	0.0107	120	6	123	10	0.79	2	homo	
07A1-26	0.0171	0.0009	0.1181	0.0087	109	5	113	8	0.38	4	core	
07A1-27	0.0173	0.0010	0.1408	0.0141	110	6	134	13	0.64	21	core	discordant
07A1-28	0.0169	0.0008	0.1113	0.0064	108	5	107	6	0.39	-1	homo	
07A1-29	0.0180	0.0009	0.1171	0.0074	115	6	112	7	0.25	-2	homo	
07A1-30	0.0196	0.0009	0.1265	0.0069	125	6	121	6	0.29	-3	core	reverse discordant
07A1-33	0.0396	0.0019	0.2734	0.0173	251	12	245	14	0.43	-2	core	
07A1-34	0.0178	0.0011	0.1215	0.0162	114	7	116	15	0.71	2	core	
07A1-35	0.0166	0.0009	0.1152	0.0105	106	6	111	10	0.71	4	core	
07A1-37	0.0178	0.0009	0.1244	0.0078	114	6	119	7	0.52	4	core	discordant
07A1-38	0.0236	0.0011	0.1586	0.0088	150	7	150	8	0.21	-1	homo	
07A1-39	0.0165	0.0009	0.1147	0.0095	105	5	110	9	0.83	5	core	discordant
07A1-40	0.0164	0.0009	0.1119	0.0100	105	6	108	9	0.73	3	core	
07A1-41	0.0185	0.0010	0.1259	0.0111	118	6	120	10	0.95	2	homo	
07A1-42	0.0166	0.0008	0.1122	0.0065	106	5	108	6	0.26	2	homo	
07A1-44	0.0175	0.0010	0.1109	0.0105	112	6	107	10	0.76	-5	homo	reverse discordant
07A1-45	0.0180	0.0009	0.1207	0.0072	115	6	116	7	0.19	1	core	
07A1-49	0.0184	0.0009	0.1142	0.0068	117	6	110	6	0.21	-7	core	reverse discordant
07A1-52	0.0163	0.0009	0.1158	0.0102	104	6	111	9	0.61	6	core	discordant
07A1-54	0.0389	0.0026	0.2696	0.0403	246	16	242	32	0.52	-1	core	
07A1-56	0.0170	0.0009	0.1231	0.0092	108	6	118	8	0.21	9	core	discordant
07A1-57	0.0191	0.0010	0.1344	0.0116	122	6	128	10	0.50	5	core	discordant
07A1-58	0.0681	0.0032	0.5151	0.0282	425	20	422	19	0.07	-1	core	
07A1-59	0.0171	0.0009	0.1143	0.0114	109	6	110	10	0.26	1	rim	
07A1-60	0.0161	0.0008	0.1150	0.0086	103	5	111	8	0.30	8	rim	discordant
07A1-62	0.0191	0.0011	0.1214	0.0136	122	7	116	12	0.75	-5	homo	reverse discordant
07A1-63	0.0242	0.0012	0.1574	0.0105	154	8	148	9	0.21	-4	core	
07A1-65	0.0245	0.0012	0.1637	0.0115	156	8	154	10	0.18	-1	rim	
07A1-67	0.0170	0.0010	0.1088	0.0112	109	6	105	10	0.63	-3	homo	
07A1-68	0.0387	0.0019	0.2750	0.0169	244	12	247	13	0.49	1	core	
07A1-69	0.0278	0.0014	0.1867	0.0118	177	9	174	10	0.20	-2	core	
07A1-70	0.0176	0.0010	0.1132	0.0115	112	6	109	10	0.59	-3	rim	
07A1-72	0.0381	0.0024	0.3427	0.0389	241	15	299	29	0.58	24	core	discordant
07A1-77	0.0385	0.0021	0.2642	0.0222	243	13	238	18	0.58	-2	core	
07A1-78	0.0174	0.0009	0.1230	0.0089	111	6	118	8	0.76	6	homo	discordant
07A1-79	0.0166	0.0009	0.1104	0.0108	106	6	106	10	0.51	0	homo	
07A1-80	0.0547	0.0032	0.4083	0.0418	343	20	348	30	0.57	1	core	
07A1-82	0.0197	0.0010	0.1313	0.0094	126	6	125	8	1.20	-1	homo	
07A1-83	0.0193	0.0010	0.1339	0.0089	123	6	128	8	0.24	3	homo	
07A1-84	0.0327	0.0017	0.2192	0.0158	207	10	201	13	0.29	-3	core	
07A1-85	0.0480	0.0031	0.3524	0.0446	302	19	307	34	0.55	1	core	
07A1-86	0.0275	0.0014	0.1891	0.0150	175	9	176	13	0.26	0	core	
07A1-87	0.0170	0.0010	0.1147	0.0124	108	6	110	11	0.36	2	homo	
07A1-88	0.0224	0.0013	0.1588	0.0165	143	8	150	14	0.72	5	homo	discordant
07A1-89	0.0177	0.0010	0.1163	0.0110	113	6	112	10	0.11	-1	rim	
07A1-90	0.0168	0.0009	0.1130	0.0111	107	6	109	10	0.11	2	rim	

$$\text{Concordancy (\%)} = \frac{(\text{}^{207}\text{Pb}/\text{}^{235}\text{U age} - \text{}^{206}\text{Pb}/\text{}^{238}\text{U age}) / (\text{}^{206}\text{Pb}/\text{}^{238}\text{U age})}{(\text{}^{206}\text{Pb}/\text{}^{238}\text{U age})} * 100$$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

Table A12.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
06A-1	0.0182	0.0009	0.1271	0.0082	117	6	121	7	0.29	4	homo	
06A-3	0.0179	0.0009	0.1215	0.0085	115	6	116	8	0.34	2	homo	
06A-4	0.0171	0.0009	0.1166	0.0085	109	6	112	8	0.48	2	homo	
06A-5	0.0183	0.0009	0.1221	0.0091	117	6	117	8	0.31	0	homo	
06A-6	0.0170	0.0009	0.1196	0.0086	108	6	115	8	0.65	6	homo	discordant
06A-8	0.0176	0.0009	0.1239	0.0081	112	6	119	7	0.29	5	homo	discordant
06A-11	0.0179	0.0009	0.1230	0.0074	114	6	118	7	0.10	3	homo	
06A-12	0.0183	0.0009	0.1201	0.0084	117	6	115	8	0.13	-1	homo	
06A-13	0.0173	0.0008	0.1139	0.0070	110	5	110	6	0.13	-1	homo	
06A-14	0.0172	0.0008	0.1111	0.0068	110	5	107	6	0.10	-3	homo	
06A-15	0.0182	0.0009	0.1219	0.0093	117	6	117	8	0.73	0	homo	
06A-17	0.0186	0.0010	0.1245	0.0118	119	7	119	11	0.54	0	homo	
06A-18	0.0185	0.0010	0.1178	0.0112	118	6	113	10	0.80	-4	homo	
06A-19	0.0168	0.0009	0.1136	0.0088	107	6	109	8	0.39	2	homo	
06A-20	0.0180	0.0009	0.1181	0.0078	115	6	113	7	0.24	-2	homo	
06A-22	0.0178	0.0009	0.1144	0.0090	114	6	110	8	0.52	-3	homo	
06A-23	0.0178	0.0009	0.1191	0.0081	114	6	114	7	0.26	1	homo	
06A-24	0.0175	0.0009	0.1154	0.0075	112	6	111	7	0.12	-1	homo	
06A-26	0.0182	0.0009	0.1294	0.0077	116	6	124	7	0.11	6	homo	discordant
06A-28	0.0177	0.0009	0.1212	0.0080	113	6	116	7	0.19	3	homo	
06A-29	0.0181	0.0009	0.1193	0.0089	116	6	114	8	0.78	-1	homo	
06A-37	0.0178	0.0009	0.1192	0.0084	113	6	114	8	0.49	1	homo	
06A-42	0.0177	0.0009	0.1197	0.0095	113	6	115	9	0.24	1	homo	
06A-46	0.0172	0.0009	0.1122	0.0068	110	5	108	6	0.10	-2	homo	
06A-50	0.0180	0.0009	0.1166	0.0080	115	6	112	7	0.33	-3	homo	
06A-52	0.0178	0.0010	0.1146	0.0101	114	6	110	9	0.47	-3	homo	
06A-55	0.0180	0.0009	0.1162	0.0084	115	6	112	8	0.25	-3	homo	
06A-62	0.0172	0.0009	0.1171	0.0087	110	6	112	8	0.50	2	homo	
06A-64	0.0173	0.0010	0.1138	0.0112	111	6	109	10	0.76	-1	homo	

Concordancy (%) = ($^{207}\text{Pb}/^{235}\text{U}$ age - $^{206}\text{Pb}/^{238}\text{U}$ age) / ($^{206}\text{Pb}/^{238}\text{U}$ age) * 100

Concordant data was defined as the data plotted on the concordia curve with -5 % < concordancy < 5 %.

Table A13.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
07E-1	0.0169	0.0009	0.1122	0.0107	108	6	108	10	0.31	0	homo	
07E-3	0.0178	0.0009	0.1186	0.0082	113	5	114	7	0.28	0	homo	
07E-6	0.0166	0.0008	0.1161	0.0074	106	5	112	7	0.46	5	homo	discordant
07E-7	0.0164	0.0008	0.1094	0.0069	105	5	105	6	0.53	1	homo	
07E-9	0.0174	0.0008	0.1317	0.0084	111	5	126	8	0.34	13	homo	discordant
07E-11	0.0210	0.0010	0.1507	0.0081	134	6	143	7	0.21	6	homo	discordant
07E-12	0.0169	0.0008	0.1138	0.0084	108	5	109	8	0.53	1	homo	
07E-16	0.0175	0.0009	0.1228	0.0092	112	6	118	8	0.49	5	homo	discordant
07E-19	0.0161	0.0008	0.1145	0.0065	103	5	110	6	0.37	7	homo	discordant
07E-20	0.0167	0.0009	0.1107	0.0099	107	6	107	9	0.45	0	homo	
07E-21	0.0162	0.0009	0.1468	0.0126	104	6	139	11	0.49	34	homo	discordant
07E-22	0.0183	0.0009	0.1197	0.0091	117	6	115	8	0.12	-2	homo	
07E-23	0.0198	0.0009	0.1366	0.0074	126	6	130	7	0.10	3	homo	discordant
07E-24	0.0166	0.0008	0.1099	0.0069	106	5	106	6	0.51	0	homo	
07E-27	0.0171	0.0009	0.1150	0.0097	109	6	111	9	0.23	1	homo	
07E-28	0.0171	0.0008	0.1155	0.0078	109	5	111	7	0.34	2	homo	
07E-31	0.0174	0.0010	0.1174	0.0137	111	6	113	12	0.52	1	homo	
07E-32	0.0163	0.0009	0.1158	0.0114	104	6	111	10	0.61	7	homo	discordant
07E-33	0.0168	0.0008	0.1138	0.0079	107	5	109	7	0.42	2	homo	
07E-34	0.0163	0.0010	0.1934	0.0183	104	6	180	16	0.57	72	homo	discordant
07E-38	0.0180	0.0010	0.1195	0.0134	115	6	115	12	0.23	0	homo	
07E-41	0.0167	0.0009	0.1196	0.0109	106	6	115	10	0.29	8	homo	discordant
07E-42	0.0166	0.0008	0.1111	0.0067	106	5	107	6	0.57	1	homo	
07E-48	0.0178	0.0009	0.1253	0.0103	114	6	120	9	0.46	5	homo	discordant
07E-51	0.0173	0.0008	0.1147	0.0071	110	5	110	6	0.29	0	homo	
07E-52	0.0167	0.0008	0.1067	0.0084	107	5	103	8	0.39	-4	homo	
07E-54	0.0172	0.0008	0.1186	0.0081	110	5	114	7	0.92	3	homo	
07E-63	0.0164	0.0008	0.1152	0.0092	105	5	111	8	0.38	5	homo	discordant
07E-65	0.0166	0.0008	0.1152	0.0085	106	5	111	8	0.39	4	homo	
07E-68	0.0169	0.0009	0.1175	0.0096	108	6	113	9	0.42	4	homo	
07E-69	0.0173	0.0008	0.1152	0.0065	111	5	111	6	0.61	0	homo	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

Table A14.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
0305F-2	0.0230	0.0010	0.1614	0.0172	146	6	152	15	0.40	4	homo	
0305F-3	0.0256	0.0008	0.1753	0.0097	163	5	164	8	0.80	1	homo	
0305F-4	0.0279	0.0010	0.2129	0.0128	177	6	196	11	0.47	11	homo	discordant
0305F-5	0.0265	0.0009	0.1756	0.0103	169	6	164	9	0.37	-3	homo	
0305F-7	0.0261	0.0011	0.1760	0.0181	166	7	165	16	0.37	-1	homo	
0305F-8	0.0267	0.0011	0.1836	0.0167	170	7	171	14	0.34	1	homo	
0305F-9	0.0255	0.0009	0.1708	0.0103	162	5	160	9	0.35	-1	homo	
0305F-10	0.0262	0.0009	0.1757	0.0125	167	6	164	11	0.40	-1	homo	
0305F-11	0.0270	0.0011	0.1866	0.0182	171	7	174	16	0.43	1	homo	
0305F-12	0.0274	0.0009	0.1841	0.0105	174	6	172	9	0.38	-2	homo	
0305F-13	0.0265	0.0011	0.1821	0.0160	168	7	170	14	0.49	1	homo	
0305F-14	0.0263	0.0011	0.1807	0.0176	167	7	169	15	0.55	1	homo	
0305F-15	0.0273	0.0011	0.1730	0.0146	174	7	162	13	0.42	-7	homo	reverse discordant
0305F-16	0.0270	0.0011	0.1770	0.0164	172	7	165	14	0.39	-4	homo	
0305F-17	0.0293	0.0012	0.2004	0.0184	186	8	186	16	0.39	0	homo	
0305F-18	0.0262	0.0011	0.1759	0.0162	167	7	165	14	0.45	-1	homo	
0305F-19	0.0260	0.0012	0.1766	0.0191	165	7	165	16	0.48	0	homo	
0305F-20	0.0240	0.0011	0.1611	0.0183	153	7	152	16	0.28	-1	homo	
0305F-21	0.0273	0.0011	0.1901	0.0154	173	7	177	13	0.64	2	homo	
0305F-22	0.0257	0.0011	0.1748	0.0190	163	7	164	16	0.46	0	homo	
0305F-23	0.0271	0.0012	0.1889	0.0186	172	8	176	16	0.44	2	homo	
0305F-24	0.0266	0.0012	0.1832	0.0214	169	8	171	18	0.33	1	homo	
0305F-25	0.0282	0.0016	0.1961	0.0312	179	10	182	26	0.31	2	homo	
0305F-27	0.0259	0.0011	0.1748	0.0151	165	7	164	13	0.82	-1	homo	
0305F-28	0.0229	0.0011	0.1586	0.0168	146	7	149	15	0.50	3	homo	
0305F-29	0.0269	0.0012	0.2207	0.0187	171	7	202	16	0.53	18	homo	discordant
0305F-31	0.0263	0.0013	0.1775	0.0199	167	8	166	17	0.57	-1	homo	
0305F-32	0.0264	0.0013	0.1832	0.0179	168	8	171	15	0.87	2	homo	
0305F-33	0.0277	0.0014	0.1891	0.0216	176	9	176	18	0.47	0	homo	
0305F-34	0.0277	0.0015	0.1885	0.0243	176	9	175	21	0.29	-1	homo	
0305F-35	0.0248	0.0014	0.1750	0.0232	158	9	164	20	0.32	4	homo	
0305F-36	0.0280	0.0014	0.1909	0.0200	178	9	177	17	0.38	0	homo	
0305F-37	0.0267	0.0014	0.1832	0.0209	170	9	171	18	0.38	1	homo	
0305F-38	0.0266	0.0014	0.1833	0.0234	169	9	171	20	0.39	1	homo	
0305F-39	0.0261	0.0016	0.1800	0.0281	166	10	168	24	0.26	1	homo	
0305F-40	0.0272	0.0014	0.1834	0.0212	173	9	171	18	0.63	-1	homo	

Concordancy (%) = ($^{207}\text{Pb}/^{235}\text{U}$ age - $^{206}\text{Pb}/^{238}\text{U}$ age) / ($^{206}\text{Pb}/^{238}\text{U}$ age) * 100

Concordant data was defined as the data plotted on the concordia curve with -5 % < concordancy < 5 %.

Table A15.

Analysis No.	Isotopic ratios and errors (2σ)				Calculated ages and errors (Ma, 2σ)				Th/U	Concordancy (%)	Analyzed portion	Remarks
	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error	$^{206}\text{Pb}/^{238}\text{U}$	error	$^{207}\text{Pb}/^{235}\text{U}$	error				
1202A-1	0.0260	0.0010	0.2027	0.0157	165	7	187	13	0.40	13	homo	discordant
1202A-3	0.0276	0.0014	0.1886	0.0284	175	9	175	24	0.52	0	homo	
1202A-4	0.0257	0.0013	0.1736	0.0222	163	8	163	19	0.43	-1	homo	
1202A-5	0.0267	0.0010	0.2415	0.0132	170	6	220	11	0.86	29	homo	discordant
1202A-6	0.0300	0.0015	0.2079	0.0267	190	10	192	22	0.69	1	homo	
1202A-7	0.0261	0.0013	0.1716	0.0224	166	8	161	19	0.38	-3	homo	
1202A-9	0.0275	0.0011	0.1816	0.0131	175	7	169	11	1.03	-3	homo	
1202A-10	0.0247	0.0011	0.1679	0.0159	157	7	158	14	0.66	0	homo	
1202A-12	0.0255	0.0014	0.1748	0.0235	162	9	164	20	0.59	1	homo	
1202A-14	0.0262	0.0015	0.1774	0.0258	167	9	166	22	0.66	-1	homo	
1202A-15	0.0265	0.0011	0.1822	0.0152	169	7	170	13	0.27	1	homo	
1202A-16	0.0269	0.0011	0.1834	0.0146	171	7	171	13	0.89	0	homo	
1202A-17	0.0253	0.0010	0.1668	0.0111	161	6	157	10	0.41	-3	homo	
1202A-18	0.0289	0.0011	0.2559	0.0161	184	7	231	13	0.71	26	homo	discordant
1202A-19	0.0279	0.0013	0.1951	0.0196	177	8	181	17	0.31	2	homo	
1202A-20	0.0257	0.0010	0.1724	0.0128	163	6	162	11	0.37	-1	homo	
1202A-21	0.0261	0.0010	0.1819	0.0102	166	6	170	9	0.87	2	homo	
1202A-22	0.0246	0.0009	0.1645	0.0097	157	6	155	8	0.94	-1	homo	
1202A-23	0.0260	0.0012	0.1673	0.0162	165	8	157	14	0.65	-5	homo	reverse discordant
1202A-24	0.0248	0.0010	0.1710	0.0131	158	7	160	11	0.47	1	homo	
1202A-26	0.0287	0.0013	0.1968	0.0166	182	8	182	14	0.42	0	homo	
1202A-27	0.0298	0.0013	0.1789	0.0157	189	8	167	14	0.50	-12	homo	reverse discordant
1202A-28	0.0274	0.0013	0.1886	0.0172	174	8	175	15	0.46	1	homo	
1202A-29	0.0267	0.0010	0.1770	0.0105	170	6	166	9	0.26	-3	homo	
1202A-30	0.0260	0.0012	0.1772	0.0169	166	7	166	15	0.50	0	homo	

Concordancy (%) = $(^{207}\text{Pb}/^{235}\text{U} \text{ age} - ^{206}\text{Pb}/^{238}\text{U} \text{ age}) / (^{206}\text{Pb}/^{238}\text{U} \text{ age}) * 100$

Concordant data was defined as the data plotted on the concordia curve with $-5\% < \text{concordancy} < 5\%$.

Table B

Analysis No.	P ₂ O ₅	SiO ₂	CaO	Y ₂ O ₃	La ₂ O ₃	Ce ₂ O ₃	Pr ₂ O ₃	Nd ₂ O ₃	Sm ₂ O ₃	Gd ₂ O ₃	Dy ₂ O ₃	Er ₂ O ₃	Yb ₂ O ₃	UO ₂	ThO ₂	PbO	Total	Age (Ma)	2σ error
Mnz-1	30.86	0.51	1.26	0.20	12.07	29.54	2.80	11.65	1.96	1.30	0.39	0.00	0.00	0.48	5.02	0.03	98.09	127	48
Mnz-2	31.28	0.39	1.02	0.55	13.10	29.73	2.82	11.07	1.37	1.29	0.33	0.00	0.38	0.23	4.40	0.02	97.97	91	61
Mnz-3	30.90	0.39	1.10	0.55	13.74	29.86	2.80	11.57	1.86	1.42	0.06	0.00	0.33	0.23	4.33	0.01	99.12	59	62
Mnz-4	30.60	0.76	1.07	0.58	13.43	29.67	2.95	12.12	1.64	1.33	0.33	0.00	0.00	0.19	4.57	0.01	99.24	40	60
Mnz-5	31.83	0.40	1.26	0.42	14.16	29.84	2.85	11.40	1.69	1.25	0.08	0.00	0.15	0.21	4.62	0.03	100.17	119	59
Mnz-6	31.45	0.37	1.30	0.69	13.37	29.30	2.51	12.13	2.31	1.43	0.00	0.00	0.00	0.24	5.17	0.02	100.27	90	52
Mnz-7	31.31	0.28	1.31	0.57	13.18	28.58	2.59	12.18	2.19	1.44	0.06	0.02	0.00	0.26	5.58	0.03	99.57	121	49
Mnz-8	31.22	0.41	1.28	0.52	13.53	29.14	2.71	12.29	2.07	1.24	0.38	0.00	0.00	0.27	5.48	0.03	100.56	111	49
Mnz-9	31.14	0.31	1.27	0.61	13.00	29.11	2.52	11.58	1.91	1.17	0.21	0.16	0.31	0.24	5.67	0.03	99.23	102	48
Mnz-10	31.43	0.35	1.14	0.55	13.93	29.54	2.72	11.65	1.87	1.33	0.30	0.00	0.21	0.23	5.23	0.04	100.52	146	52
Mnz-11	31.20	0.53	1.14	0.64	12.94	29.36	3.11	12.19	1.85	1.60	0.22	0.00	0.18	0.22	5.08	0.02	100.26	85	54
Mnz-12	31.32	0.71	1.02	0.56	13.26	29.39	2.45	11.65	1.66	1.25	0.10	0.00	0.19	0.47	4.87	0.02	98.45	94	57
Mnz-13	30.83	0.51	1.21	0.54	12.84	28.97	2.53	11.96	2.18	1.46	0.05	0.00	0.31	0.23	5.77	0.03	99.41	101	48
Mnz-14	30.88	0.78	1.15	0.64	13.95	28.92	2.96	11.95	1.78	1.37	0.00	0.00	0.01	0.21	5.21	0.02	99.83	95	53
Mnz-15	30.79	0.76	1.14	0.56	14.08	28.99	3.01	12.32	2.01	1.40	0.03	0.00	0.04	0.20	5.32	0.02	100.67	94	52
Mnz-16	30.70	0.50	1.25	0.57	13.94	30.11	2.63	12.35	2.01	1.60	0.21	0.00	0.00	0.19	4.75	0.02	100.80	100	58
Mnz-17	30.94	0.76	1.11	0.64	13.62	28.89	2.82	12.12	1.73	1.38	0.22	0.00	0.00	0.18	5.44	0.02	99.87	70	51
Mnz-18	30.42	0.95	2.11	0.39	13.15	28.55	2.78	11.65	1.60	1.15	0.40	0.00	0.00	0.21	5.58	0.01	98.94	33	50
Mnz-19	31.07	0.48	1.09	0.49	13.48	29.73	2.67	11.73	2.09	1.43	0.36	0.00	0.00	0.22	4.94	0.03	99.80	125	55
Mnz-20	30.92	0.54	1.14	0.42	13.03	29.05	2.99	11.66	1.56	1.28	0.11	0.00	0.00	0.23	5.59	0.02	98.54	66	49
Mnz-21	30.71	0.78	1.32	0.45	13.69	28.98	3.02	11.97	1.43	1.29	0.12	0.00	0.07	0.20	5.36	0.02	99.39	90	52
Mnz-22	31.28	0.35	1.14	0.39	13.40	30.02	2.88	12.05	2.08	1.33	0.11	0.00	0.00	0.22	5.00	0.02	100.25	90	55
Mnz-23	30.76	0.82	1.14	0.35	13.83	29.53	2.90	11.81	1.69	1.13	0.21	0.03	0.24	0.17	4.54	0.02	99.15	78	61
Mnz-24	30.40	0.94	0.91	0.40	13.82	30.57	2.94	11.47	1.27	1.26	0.09	0.00	0.04	0.19	4.42	0.02	98.72	103	62
Mnz-25	30.70	0.55	1.53	0.45	12.79	29.00	2.85	11.89	1.27	1.42	0.17	0.00	0.08	0.19	4.55	0.01	97.46	58	60
Mnz-26	30.47	0.83	1.18	0.42	12.89	28.98	3.13	11.82	1.50	1.37	0.24	0.00	0.18	0.20	4.96	0.01	98.14	41	55
Mnz-27	30.31	0.93	0.85	0.05	15.57	30.86	2.45	10.36	0.98	0.69	0.00	0.00	0.16	0.07	5.71	0.02	98.99	68	52
Mnz-28	31.76	0.48	1.29	0.16	13.68	30.06	2.63	11.34	1.42	1.03	0.01	0.00	0.00	0.43	5.54	0.02	99.82	62	45
Mnz-29	30.02	1.66	1.05	0.02	15.49	30.32	2.68	10.48	0.49	0.46	0.00	0.00	0.18	0.07	5.77	0.03	98.72	103	51
Mnz-30	31.04	0.68	1.55	0.07	14.47	30.10	2.72	11.16	0.88	0.62	0.00	0.00	0.00	0.20	5.78	0.02	99.29	84	48
Mnz-31	29.97	1.08	1.44	0.16	14.57	29.20	2.74	11.69	0.27	0.84	0.05	0.00	0.00	0.21	6.18	0.03	98.43	92	45
Mnz-32	30.68	0.84	2.65	0.87	12.41	27.37	2.56	11.51	1.31	1.47	0.38	0.20	0.17	1.09	7.15	0.05	100.69	114	30
Mnz-33	29.38	1.57	1.79	0.56	13.35	26.83	2.62	11.26	1.58	1.24	0.23	0.05	0.03	0.61	8.16	0.04	99.30	96	31
Mnz-34	29.47	2.24	2.64	0.78	12.45	27.10	2.69	11.38	1.22	1.14	0.06	0.00	0.00	1.22	7.21	0.04	99.63	82	29
Mnz-35	28.55	2.48	2.39	0.82	12.82	25.88	2.58	10.68	1.04	1.39	0.35	0.09	0.07	1.24	7.87	0.06	98.30	125	27
Mnz-36	28.32	3.71	3.36	0.88	12.08	24.61	2.55	10.86	0.00	1.58	0.24	0.00	0.10	1.40	7.30	0.05	97.03	101	27
Mnz-37	29.20	2.28	2.83	0.89	11.60	26.13	2.59	10.78	0.74	1.34	0.30	0.01	0.01	1.36	7.54	0.05	97.64	108	27
Mnz-38	30.20	1.22	2.34	0.81	12.64	27.65	2.73	11.11	1.62	1.48	0.25	0.00	0.00	1.17	7.85	0.05	101.12	97	27
Mnz-39	29.39	2.13	2.37	0.86	12.60	26.00	2.30	11.04	0.92	1.34	0.17	0.12	0.00	1.13	8.31	0.07	98.73	133	27
Mnz-40	28.93	2.48	3.39	0.83	12.08	25.19	2.37	11.01	1.10	1.54	0.11	0.00	0.15	1.25	8.02	0.05	98.50	104	27
Mnz-41	32.99	1.60	16.61	0.03	10.72	21.51	2.18	8.78	0.49	0.61	0.00	0.04	0.00	0.37	4.86	0.02	100.79	60	52
Mnz-42	33.93	1.86	19.80	0.07	10.05	19.73	1.95	8.30	0.47	0.77	0.10	0.00	0.07	0.25	4.13	0.01	101.46	60	63
Mnz-43	31.00	1.16	1.10	0.21	14.99	30.62	2.71	12.73	0.85	0.94	0.17	0.00	0.09	0.22	2.75	0.01	99.54	66	91