TABLE S1. COMMON Pb CORRECTED U/Pb DETRITAL-ZIRCON GEOCHRONOLOGIC ANALYSES OF METASEDIMENTARY UNITS, GRAHAM LAND, ANTARCTICA.

		RATIOS									APPARENT AGES (Ma)								
GRAIN	U (ppm)	206Pb 204Pb	U Th	206Pb* 207Pb*	± (%)	207Pb* 235U*	± (%)	206Pb* 238U	± (%)	error corr.	206Pb* 238U*	± (Ma)	207Pb* 235U	± (Ma)	206Pb* 207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
SAMPLE KAYLEY1, Trinity Peninsula Group, Legoupil Formation(?), Wilhelmina Bay, 64˚ 17.002' S, 61˚ 4.067' W																			
KAYLEY1-61	57	17730	1.3	18.4132	29.9	0.3278	30.0	0.0438	2.7	0.09	276.2	7.4	287.9	75.4	383.9	686.1	28.0	276.2	7.4
KAYLEY1-48	221	11769	0.9	16.4512	15.2	0.3709	15.3	0.0443	0.9	0.06	279.2	2.4	320.4	41.9	631.6	329.7	*12.9*	279.2	2.4
KAYLEY1-38	221	17400	1.7	18.8600	8.0	0.3239	8.3	0.0443	2.1	0.25	279.5	5.7	284.9	20.6	329.7	182.0	15.2	279.5	5.7
KAYLEY1-10	250	29850	1.5	18.7907	3.2	0.3253	4.6	0.0443	3.3	0.72	279.6	9.1	286.0	11.5	338.1	72.2	17.3	279.6	9.1
KAYLEY1-56	101	13236	1.4	18.2518	25.0	0.3352	25.5	0.0444	4.7	0.18	279.9	12.9	293.6	65.0	403.6	568.6	*4.7*	279.9	12.9
KAYLEY1-75	326	15885	1.2	18.1893	8.2	0.3384	8.3	0.0446	1.7	0.20	281.6	4.5	296.0	21.4	411.3	182.8	*4.9*	281.6	4.5
KAYLEY1-71	232	29844	0.7	19.0619	3.6	0.3257	4.5	0.0450	2.7	0.60	283.9	7.4	286.2	11.1	305.5	81.5	7.1	283.9	7.4
KAYLEY1-70	213	36873	1.1	20.1532	7.1	0.3102	7.4	0.0453	1.9	0.26	285.9	5.4	274.4	17.7	177.2	165.7	*-4.2*	285.9	5.4
KAYLEY1-21	281	110457	1.1	19.8950	5.1	0.3151	5.5	0.0455	2.1	0.38	286.6	5.8	278.1	13.4	207.2	118.8	*-3.1*	286.6	5.8
KAYLEY1-69	87	7128	1.3	19.4476	14.3	0.3235	14.6	0.0456	2.5	0.17	287.6	7.1	284.6	36.1	259.7	330.7	*-1.1*	287.6	7.1
KAYLEY1-44	361	23541	1.0	18.7724	4.6	0.3357	4.8	0.0457	1.4	0.28	288.1	3.9	293.9	12.3	340.3	104.8	15.3	288.1	3.9
KAYLEY1-26	139	5406	1.0	18.2735	17.3	0.3449	17.3	0.0457	0.9	0.05	288.2	2.5	300.9	45.1	400.9	390.0	28.1	288.2	2.5
KAYLEY1-73	298	57891	1.3	19.1933	5.9	0.3285	6.0	0.0457	1.2	0.20	288.2	3.4	288.4	15.0	289.9	134.0	0.6	288.2	3.4
KAYLEY1-95	143	17115	1.4	19.1989	8.6	0.3285	9.3	0.0457	3.4	0.36	288.3	9.4	288.4	23.3	289.2	197.9	0.3	288.3	9.4
KAYLEY1-72	468	56097	1.6	18.7265	2.5	0.3369	2.9	0.0458	1.6	0.55	288.4	4.5	294.8	7.5	345.8	55.5	16.6	288.4	4.5
KAYLEY1-82	288	25776	0.8	19.3269	7.8	0.3275	8.2	0.0459	2.5	0.31	289.3	7.0	287.7	20.4	274.0	178.2	*-0.6*	289.3	7.0
KAYLEY1-09	332	45240	1.2	19.0891	4.9	0.3317	5.3	0.0459	1.9	0.36	289.4	5.4	290.9	13.4	302.3	112.4	4.2	289.4	5.4
KAYLEY1-23	109	915	1.5	11.0421	29.4	0.5737	29.6	0.0459	2.8	0.10	289.6	8.0	460.4	109.8	1437.4	573.6	*37.1*	289.6	8.0
KAYLEY1-78	176	17022	1.7	18.1624	11.9	0.3499	12.0	0.0461	1.6	0.13	290.5	4.5	304.7	31.5	414.6	266.2	29.9	290.5	4.5
KAYLEY1-31	333	29736	1.0	19.5630	3.9	0.3255	4.2	0.0462	1.4	0.33	291.1	4.0	286.2	10.4	246.1	90.7	*-1.7*	291.1	4.0
KAYLEY1-33	224	12630	1.4	19.0269	3.3	0.3356	3.6	0.0463	1.6	0.43	291.8	4.5	293.8	9.3	309.7	74.7	5.8	291.8	4.5
KAYLEY1-47	287	13068	1.0	17.4188	16.0	0.3670	16.3	0.0464	3.0	0.18	292.2	8.4	317.5	44.5	507.3	354.5	*8.0*	292.2	8.4
KAYLEY1-54	128	21000	1.4	20.5185	9.7	0.3124	9.9	0.0465	1.4	0.15	292.9	4.1	276.0	23.8	135.2	229.5	*-6.1*	292.9	4.1
KAYLEY1-02	519	48654	2.6	19.3973	2.9	0.3309	3.2	0.0465	1.2	0.38	293.3	3.5	290.2	8.0	265.6	67.1	*-1.1*	293.3	3.5
KAYLEY1-79	319	30930	1.7	18.8077	4.5	0.3414	4.5	0.0466	0.9	0.19	293.4	2.5	298.2	11.8	336.0	101.2	12.7	293.4	2.5
KAYLEY1-92	283	22464	1.9	19.3448	3.1	0.3323	3.4	0.0466	1.3	0.39	293.8	3.8	291.3	8.5	271.9	71.2	*-0.8*	293.8	3.8
KAYLEY1-37	98	9849	1.7	17.9482	9.1	0.3594	9.4	0.0468	2.4	0.26	294.7	7.0	311.7	25.3	441.0	203.3	*5.5*	294.7	7.0
KAYLEY1-05	685	68028	15.0	18.9594	2.4	0.3415	3.2	0.0470	2.2	0.67	295.8	6.2	298.3	8.3	317.8	54.2	6.9	295.8	6.2
KAYLEY1-36	186	32544	1.4	19.6845	8.4	0.3300	8.5	0.0471	1.4	0.16	296.8	4.0	289.6	21.3	231.8	193.3	*-2.5*	296.8	4.0
KAYLEY1-41	68	14238	1.1	19.2467	12.6	0.3378	12.8	0.0471	2.0	0.16	297.0	5.8	295.5	32.7	283.5	289.5	-4.8	297.0	5.8
KAYLEY1-07	157	11865	1.5	19.5765	6.2	0.3323	6.4	0.0472	1.4	0.22	297.2	4.0	291.3	16.2	244.5	143.9	*-2.0*	297.2	4.0
KAYLEY1-57	166	17844	1.3	18.4241	5.5	0.3542	5.5	0.0473	1.0	0.17	298.1	2.8	307.9	14.7	382.5	122.6	22.1	298.1	2.8
KAYLEY1-87	305	24309	1.0	17.4453	5.7	0.3747	6.0	0.0474	1.8	0.30	298.6	5.2	323.1	16.5	503.9	125.7	*7.6*	298.6	5.2
KAYLEY1-96	255	52992	1.3	18.5666	7.2	0.3532	7.3	0.0476	1.0	0.14	299.6	3.0	307.1	19.4	365.2	163.2	18.0	299.6	**3.0**
KAYLEY1-03	152	157176	1.5	18.1476	11.0	0.3621	11.0	0.0477	0.5	0.05	300.2	1.5	313.8	29.7	416.4	246.2	27.9	300.2	1.5
KAYLEY1-80	205	18804	1.2	19.7118	4.0	0.3343	4.9	0.0478	2.9	0.59	300.9	8.6	292.8	12.5	228.6	91.5	*-2.8*	300.9	8.6
KAYLEY1-28	96	5004	1.2	18.2512	9.3	0.3623	9.8	0.0480	3.0	0.30	301.9	8.7	313.9	26.4	403.7	209.3	25.2	301.9	8.7
KAYLEY1-16	269	57537	1.5	19.0899	3.2	0.3464	3.7	0.0480	2.0	0.53	302.0	5.9	302.0	9.7	302.2	71.9	0.1	302.0	5.9
KAYLEY1-52	273	21291	1.7	18.1532	4.9	0.3653	5.5	0.0481	2.6	0.47	302.9	7.7	316.2	15.0	415.7	108.7	27.2	302.9	7.7
KAYLEY1-22	131	19422	1.5	16.5748	14.2	0.4013	14.2	0.0482	0.8	0.06	303.7	2.4	342.6	41.4	615.5	308.3	*11.3*	303.7	2.4
KAYLEY1-12	100	13350	1.5	18.7287	12.3	0.3552	12.5	0.0482	1.9	0.15	303.7	5.6	308.6	33.2	345.5	279.5	12.1	303.7	5.6
KAYLEY1-01	178	13602	2.2	18.7636	5.5	0.3553	5.7	0.0483	1.5	0.27	304.4	4.5	308.7	15.1	341.3	123.5	10.8	304.4	4.5
KAYLEY1-59	97	12381	1.0	18.9025	7.8	0.3540	7.8	0.0485	0.9	0.11	305.5	2.5	307.8	20.8	324.6	177.2	5.9	305.5	2.5
KAYLEY1-97	199	585	0.8	12.9703	5.9	0.5160	6.2	0.0485	1.9	0.30	305.5	5.6	422.5	21.4	1123.7	117.6	*27.7*	305.5	5.6
KAYLEY1-88	294	45030	2.2	18.8189	4.1	0.3566	4.4	0.0487	1.6	0.35	306.3	4.7	309.7	11.8	334.7	94.1	8.5	306.3	4.7
KAYLEY1-63	507	33942	1.9	18.9116	3.6	0.3565	3.8	0.0489	1.3	0.34	307.8	4.0	309.6	10.3	323.5	82.0	4.9	307.8	4.0
KAYLEY1-08	104	8892	1.7	17.3619	6.6	0.3916	6.6	0.0493	0.9	0.14	310.3	2.8	335.5	19.0	514.5	144.7	*7.5*	310.3	2.8
KAYLEY1-15	127	18594	1.3	19.4574	5.8	0.3505	6.0	0.0495	1.5	0.25	311.2	4.6	305.1	15.8	258.5	133.2	*-2.0*	311.2	4.6
KAYLEY1-83	153	12054	1.1	18.0721	6.9	0.3775	7.0	0.0495	1.2	0.18	311.3	3.8	325.2	19.5	425.7	154.0	26.9	311.3	3.8
KAYLEY1-89	179	5232	2.3	16.2331	10.1	0.4207	10.3	0.0495	2.3	0.22	311.7	6.8	356.6	31.0	660.3	216.2	*12.6*	311.7	6.8
KAYLEY1-66	379	57933	1.6	19.0037	3.8	0.3599	3.9	0.0496	1.2	0.29	312.1	3.5	312.1	10.6	312.5	85.5	0.1	312.1	3.5
KAYLEY1-86	210	27903	1.0	18.9594	4.5	0.3617	4.5	0.0497	0.9	0.20	312.9	2.7	313.5	12.3	317.8	101.4	1.5	312.9	2.7
KAYLEY1-77	151	10041	1.1	17.8722	7.5	0.3865	8.0	0.0501	2.8	0.35	315.1	8.5	331.8	22.6	450.5	166.7	*5.0*	315.1	8.5
KAYLEY1-76	269	42249	2.7	18.8031	9.0	0.3686	9.2	0.0503	2.2	0.23	316.2	6.6	318.6	25.2	336.6	203.5	6.1	316.2	6.6
KAYLEY1-32	185	26589	2.8	19.6661	4.8	0.3540	5.0	0.0505	1.5	0.29	317.6	4.6	307.7	13.4	234.0	111.0	*-3.2*	317.6	4.6
KAYLEY1-81	94	12204	1.3	19.5159	10.1	0.3665	10.2	0.0519	1.0	0.10	326.1	3.3	317.1	27.7	251.6	233.3	*-2.8*	326.1	3.3
KAYLEY1-43	422	108498	2.6	18.4493	3.2	0.4040	3.3	0.0541	0.8	0.23	339.4	2.5	344.6	9.5	379.5	71.1	10.6	339.4	2.5
KAYLEY1-49	121	28080	1.8	18.1893	6.6	0.4717	6.7	0.0622	1.4	0.21	389.2	5.2	392.4	21.9	411.3	147.1	5.4	389.2	5.2
KAYLEY1-55	105	11538	1.4	16.4735	18.1	0.5240	18.2	0.0626	0.9	0.05	391.5	3.4	427.8	63.5	628.7	393.6	*8.5*	391.5	3.4
KAYLEY1-13	138	21861	1.7	18.6339	3.8	0.4646	4.2	0.0628	1.7	0.39	392.5	6.3	387.4	13.5	357.0	86.8	*-1.3*	392.5	6.3
KAYLEY1-46	104	4536	1.6	16.1701	9.2	0.5411	9.4	0.0635	1.6	0.17	396.6	6.1	439.1	33.4	668.7	198.0	*9.7*	396.6	6.1
KAYLEY1-25	243	51948	1.1	17.9549	6.8	0.4932	6.9	0.0642	1.0	0.15	401.2	3.9	407.1	23.0	440.2	151.3	8.9	401.2	3.9
KAYLEY1-50	163	27414	2.8	17.2113	4.5	0.5226	5.8	0.0652	3.6	0.62	407.4	14.3	426.9	20.2	533.6	99.2	23.6	407.4	14.3
KAYLEY1-17	867	78624	2.7	17.3046	2.3	0.5403	3.0	0.0678	1.8	0.62	422.9	7.5	438.6	10.6	521.7	51.1	18.9	422.9	7.5
KAYLEY1-90	264	47238	24.7	17.0043	1.5	0.5657	1.8	0.0698	0.9	0.52	434.7	4.0	455.2	6.6	560.0	33.6	22.4	434.7	4.0
KAYLEY1-74	342	56814	2.4	17.7252	2.1	0.5791	4.3	0.0745	3.8	0.88	462.9	16.8	463.9	15.9	468.8	45.7	1.3	462.9	16.8
KAYLEY1-30	247	37668	1.4	17.5368	3.2	0.5879	3.6	0.0748	1.7	0.47	464.8	7.5	469.5	13.5	492.4	70.3	5.6	464.8	7.5
KAYLEY1-14	311	31611	1.6	16.8841	6.5	0.6183	6.6	0.0757	1.5	0.23	470.5	6.9	488.8	25.8	575.4	140.7	18.2	470.5	6.9
KAYLEY1-40	145	21543	1.8	18.4690	4.9	0.5785	5.0	0.0775	0.9	0.18	481.1	4.1	463.5	18.6	377.1	110.5	*-3.8*	481.1	4.1
KAYLEY1-60	573	94434	2.1	17.3370	2.0	0.6182	3.3	0.0777	2.6	0.79	482.6	12.0	488.7	12.7	517.6	44.2	6.8	482.6	12.0
KAYLEY1-58	429	339363	14.2	16.3423	1.2	0.6590	2.8	0.0781	2.6	0.91	484.8	12.1	514.0	11.4	645.9	24.7	24.9	484.8	12.1
KAYLEY1-91	284	64155	2.1	17.7644	3.8	0.6068	5.3	0.0782	3.8	0.70	485.3	17.6	481.6	20.5	463.9	84.1	-4.6	485.3	17.6
KAYLEY1-04	219	28755	2.0	17.5800	3.5	0.6247	3.7	0.0797	1.4	0.38	494.1	6.7	492.8	14.6	487.0	76.3	-1.5	494.1	6.7
KAYLEY1-29	179	43731	2.2	16.6817	5.2	0.6627	5.3	0.0802	1.1	0.20	497.2	5.1	516.2	21.4	601.6	112.3	17.4	497.2	5.1
KAYLEY1-98	505	206415	47.6	17.4166	2.5	0.6414	2.8	0.0810	1.3	0.46	502.2	6.1	503.2	10.9	507.5	53.9	1.0	502.2	6.1
KAYLEY1-65	264	86076	1.8	17.6021	1.3	0.6357	2.4	0.0812	2.0	0.84	503.0	9.9	499.6	9.6	484.2	29.3	-3.9	503.0	9.9
KAYLEY1-68	91	27522	1.2	17.9611	4.7	0.6410	6.6	0.0835	4.6	0.70	517.0	23.0	502.9	26.0	439.4	103.9	*-2.8*	517.0	23.0
KAYLEY1-62	143	44715	1.4	17.8967	4.1	0.6552	5.7	0.0850	4.0	0.70	526.1	20.3	511.7	23.0	447.4	90.3	*-2.8*	526.1	20.3
KAYLEY1-19	557	97146	1.9	17.0214	2.6	0.6940	2.8	0.0857	1.1	0.39	529.9	5.6	535.2	11.8	557.8	57.2	5.0	529.9	5.6
KAYLEY1-53	140	22239	4.5	17.3447	3.1	0.6878	3.5	0.0865	1.7	0.48	535.0	8.5	531.5	14.4	516.6	67.3	-3.5	535.0	8.5
KAYLEY1-18	275	97524	2.7	15.9103	3.1	0.8186	3.8	0.0945	2.2	0.58	581.9	12.2	607.3	17.3	703.2	65.6	17.3	581.9	12.2
KAYLEY1-45	922	165366	1.6	16.2738	1.8	0.9255	2.3	0.1092	1.5	0.63	668.3	9.3	665.3	11.3	655.0	38.4	-2.0	668.3	9.3
KAYLEY1-06	275	85008	10.8	14.7608	3.1	1.1561	5.6	0.1238	4.6	0.83	752.2	32.8	780.1	30.4	860.8	65.2	12.6	752.2	32.8
KAYLEY1-94	417	65745	1.0	15.2014	0.7	1.1699	2.1	0.1290	2.0	0.93	782.0	14.4	786.6	11.4	799.5	15.5	2.2	782.0	14.4
KAYLEY1-42	787	245022	2.7	14.9725	1.7	1.2618	1.9	0.1370	0.8	0.44	827.8	6.4	828.7	10.6	831.2	35.2	0.4	827.8	6.4
KAYLEY1-85	271	40158	6.2	15.1519	2.0	1.2550	2.1	0.1379	0.5	0.24	832.8	3.9	825.6	11.7	806.3	41.9	-3.3	832.8	3.9
KAYLEY1-27	332	223368	8.9	13.1063	2.9	1.5448	4.7	0.1468	3.7	0.79	883.3	30.5	948.4	28.8	1102.9	57.2	19.9	883.3	30.5
KAYLEY1-67	538	138840	3.6	13.7064	1.2	1.6282	1.5	0.1619	0.8	0.55	967.1	7.3	981.2	9.3	1012.8	25.1	4.5	967.1	7.3
KAYLEY1-39	791	191964	11.6	13.6006	1.8	1.7086	2.6	0.1685	1.9	0.72	1004.0	17.6	1011.8	16.9	1028.5	37.0	2.4	1028.5	37.0
KAYLEY1-24	306	127164	3.0	13.2709	1.8	1.9258	3.1	0.1854	2.4	0.80	1096.2	24.6	1090.1	20.4	1077.9	36.9	-1.7	1077.9	36.9
KAYLEY1-11	171	71484	1.6	12.6017	1.3	2.1807	1.7	0.1993	1.1	0.65	1171.6	11.8	1174.9	11.7	1181.0	25.2	0.8	1181.0	25.2
KAYLEY1-64	109	43215	2.8	11.1474	1.1	2.9817	1.5	0.2411	1.0	0.68	1392.2	12.4	1403.0	11.1	1419.3	20.5	1.9	1419.3	20.5

GRAIN	U (ppm)	RATIOS 206Pb/204Pb	U/Th	206Pb*/207Pb*	± (%)	207Pb*/235U*	± (%)	206Pb*/238U	± (%)	error corr.	APPARENT AGES (Ma) 206Pb*/238U*	± (Ma)	207Pb*/235U	± (Ma)	206Pb*/207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
KAYLEY1-20	168	95148	1.8	9.7195	1.6	4.0238	3.3	0.2836	2.9	0.87	1609.7	41.3	1639.0	27.0	1676.8	29.9	4.0	1676.8	29.9
KAYLEY1-35	168	89451	25.8	8.3515	1.8	5.8873	1.9	0.3566	0.6	0.29	1966.0	9.5	1959.4	16.5	1952.3	32.5	-0.7	1952.3	32.5
KAYLEY1-93	295	112752	0.9	8.2942	1.0	5.8882	1.7	0.3542	1.4	0.81	1954.7	22.9	1959.5	14.6	1964.6	17.7	0.5	1964.6	17.7
KAYLEY1-84	271	292503	1.7	5.4845	1.4	12.5577	1.5	0.4995	0.5	0.34	2611.7	10.7	2647.1	13.7	2674.2	22.7	2.3	2674.2	22.7
SAMPLE LAHILLE1, Trinity Peninsula Group, Legoupil Formation(?), Lahille Island, 65˚ 33.278' S, 64˚ 23.973'W																			
LAHILLE1-55	66	7965	2.4	17.6235	33.4	0.3041	33.4	0.0389	1.6	0.05	245.8	3.9	269.6	79.3	481.5	756.5	*8.8*	245.8	3.9
LAHILLE1-20	482	27456	1.1	19.7014	2.7	0.2760	2.9	0.0394	1.1	0.36	249.3	2.6	247.4	6.4	229.8	63.1	*-0.8*	249.3	2.6
LAHILLE1-79	415	11964	0.8	19.3126	3.2	0.2825	4.0	0.0396	2.5	0.62	250.1	6.1	252.6	9.0	275.7	72.4	9.3	250.1	6.1
LAHILLE1-59	474	108399	1.3	19.7673	3.7	0.2779	3.8	0.0398	1.1	0.28	251.9	2.7	249.0	8.5	222.1	85.0	*-1.2*	251.9	2.7
LAHILLE1-17	199	40890	1.3	17.4000	6.2	0.3169	6.2	0.0400	0.6	0.10	252.8	1.5	279.5	15.1	509.6	135.7	*9.6*	252.8	1.5
LAHILLE1-56	295	23340	1.2	19.0243	3.7	0.2921	5.7	0.0403	4.3	0.76	254.7	10.8	260.2	13.0	310.0	83.2	17.8	254.7	10.8
LAHILLE1-82	71	16098	1.0	19.2756	23.3	0.2898	23.4	0.0405	1.6	0.07	256.0	4.1	258.4	53.4	280.1	540.5	8.6	256.0	4.1
LAHILLE1-75	255	94443	1.3	18.9971	8.0	0.2942	8.1	0.0405	1.5	0.18	256.2	3.7	261.9	18.8	313.3	182.1	18.2	256.2	3.7
LAHILLE1-68	206	21498	0.9	20.7755	6.4	0.2698	6.5	0.0407	1.2	0.18	256.9	3.0	242.5	14.1	105.8	152.2	*-5.9*	256.9	3.0
LAHILLE1-24	197	10344	1.4	19.1272	15.0	0.2946	15.1	0.0409	1.5	0.10	258.2	3.7	262.2	34.9	297.7	344.7	13.3	258.2	3.7
LAHILLE1-49	123	29796	0.9	18.7391	9.4	0.3013	9.4	0.0410	0.8	0.09	258.7	2.1	267.4	22.2	344.3	212.9	24.8	258.7	2.1
LAHILLE1-91	115	8955	1.2	21.3901	10.4	0.2642	10.7	0.0410	2.7	0.25	258.9	6.8	238.0	22.8	36.5	249.0	*-8.8*	258.9	6.8
LAHILLE1-37	69	30543	1.5	23.6970	19.7	0.2388	19.7	0.0410	0.8	0.04	259.2	2.1	217.4	38.6	-214.6	499.3	*-19.2*	259.2	2.1
LAHILLE1-34	145	30630	1.5	21.4691	9.8	0.2635	9.9	0.0410	1.0	0.10	259.2	2.5	237.5	20.9	27.6	236.3	*-9.1*	259.2	2.5
LAHILLE1-61	256	28242	0.9	19.5233	3.7	0.2916	4.0	0.0413	1.5	0.39	260.8	3.9	259.8	9.1	250.8	84.0	-4.0	260.8	3.9
LAHILLE1-29	131	25566	1.4	21.1599	10.2	0.2694	10.3	0.0413	1.8	0.17	261.2	4.6	242.2	22.3	62.3	243.3	*-7.8*	261.2	4.6
LAHILLE1-76	242	45987	1.0	19.7045	3.5	0.2900	3.9	0.0415	1.7	0.43	261.8	4.3	258.6	8.8	229.5	80.5	*-1.2*	261.8	4.3
LAHILLE1-30	207	21351	1.3	19.8450	6.8	0.2886	7.4	0.0415	2.9	0.39	262.3	7.5	257.4	16.9	213.0	158.2	*-1.9*	262.3	7.5
LAHILLE1-90	228	37476	1.3	18.8241	10.3	0.3042	10.5	0.0415	2.0	0.19	262.4	5.1	269.7	24.9	334.0	234.1	21.5	262.4	5.1
LAHILLE1-89	199	38466	1.3	18.2071	6.6	0.3147	6.8	0.0416	1.4	0.21	262.5	3.6	277.8	16.4	409.1	148.1	*5.5*	262.5	3.6
LAHILLE1-43	103	27918	1.5	18.9057	16.8	0.3032	16.9	0.0416	0.8	0.05	262.6	2.1	268.9	39.8	324.2	384.7	19.0	262.6	2.1
LAHILLE1-46	648	195372	9.6	19.5324	2.4	0.2943	2.5	0.0417	0.6	0.26	263.3	1.7	262.0	5.7	249.7	55.0	*-0.5*	263.3	1.7
LAHILLE1-80	244	19311	1.0	18.9056	2.9	0.3054	3.2	0.0419	1.5	0.47	264.4	3.9	270.6	7.7	324.3	64.8	18.5	264.4	3.9
LAHILLE1-04	196	17898	2.0	18.3322	7.0	0.3150	7.3	0.0419	2.0	0.28	264.4	5.2	278.0	17.7	393.8	157.3	*4.9*	264.4	5.2
LAHILLE1-77	1343	20178	1.3	18.5450	3.0	0.3121	5.5	0.0420	4.6	0.84	265.1	11.9	275.8	13.2	367.8	66.5	27.9	265.1	11.9
LAHILLE1-94	155	35832	1.2	18.9840	8.0	0.3055	8.1	0.0421	0.5	0.06	265.6	1.3	270.7	19.2	314.8	183.3	15.6	265.6	1.3
LAHILLE1-08	370	39018	3.7	19.3626	4.0	0.2999	4.4	0.0421	1.8	0.42	265.9	4.8	266.3	10.3	269.7	91.7	1.4	265.9	4.8
LAHILLE1-39	80	12102	2.0	18.8545	24.3	0.3097	24.4	0.0424	1.9	0.08	267.4	5.0	274.0	58.7	330.4	559.2	19.1	267.4	5.0
LAHILLE1-63	289	40800	2.2	18.7098	5.8	0.3130	6.0	0.0425	1.4	0.23	268.2	3.5	276.5	14.5	347.8	132.1	22.9	268.2	3.5
LAHILLE1-31	248	27666	3.1	19.7221	4.1	0.2981	4.3	0.0426	1.4	0.33	269.2	3.8	264.9	10.0	227.4	93.8	*-1.6*	269.2	3.8
LAHILLE1-35	323	62655	1.9	18.9767	2.1	0.3103	2.4	0.0427	1.1	0.46	269.6	2.9	274.4	5.7	315.7	48.3	14.6	269.6	2.9
LAHILLE1-99	305	31449	1.4	18.8453	5.5	0.3128	5.8	0.0428	1.7	0.30	269.9	4.5	276.4	13.9	331.5	124.7	18.6	269.9	4.5
LAHILLE1-100	89	11520	1.9	17.6284	7.4	0.3363	7.5	0.0430	0.8	0.11	271.4	2.1	294.4	19.1	480.9	164.7	*7.8*	271.4	2.1
LAHILLE1-10	427	81084	2.3	19.6416	3.3	0.3029	3.4	0.0431	0.5	0.15	272.3	1.3	268.6	8.0	236.8	77.1	*-1.4*	272.3	1.3
LAHILLE1-66	329	27858	3.1	19.1468	3.6	0.3122	4.2	0.0434	2.1	0.51	273.6	5.7	275.9	10.1	295.4	81.8	7.4	273.6	5.7
LAHILLE1-57	74	19668	1.6	19.3492	16.4	0.3093	16.5	0.0434	1.2	0.07	273.9	3.2	273.7	39.6	271.3	379.1	-1.0	273.9	3.2
LAHILLE1-21	213	14040	2.4	19.8966	6.5	0.3026	6.9	0.0437	2.3	0.34	275.6	6.3	268.5	16.3	207.0	151.2	*-2.6*	275.6	6.3
LAHILLE1-64	365	18522	1.4	18.2075	3.2	0.3431	3.5	0.0453	1.4	0.41	285.7	3.9	299.5	9.0	409.0	70.6	*4.6*	285.7	3.9
LAHILLE1-69	108	20577	1.8	19.2647	15.3	0.3300	15.4	0.0461	1.3	0.09	290.6	3.8	289.6	38.8	281.4	352.7	-3.3	290.6	3.8
LAHILLE1-81	333	42825	1.7	19.5321	4.4	0.3310	4.7	0.0469	1.5	0.32	295.4	4.3	290.3	11.8	249.7	101.6	*-1.7*	295.4	4.3
LAHILLE1-97	124	27804	2.3	19.8875	17.6	0.3273	17.7	0.0472	1.1	0.06	297.4	3.1	287.5	44.3	208.1	411.9	*-3.4*	297.4	3.1
LAHILLE1-07	287	22677	2.5	19.6884	4.6	0.3329	4.7	0.0475	1.1	0.22	299.4	3.1	291.8	12.0	231.4	106.4	*-2.6*	299.4	3.1
LAHILLE1-38	556	87072	13.2	19.0176	2.3	0.3455	2.5	0.0477	0.9	0.37	300.1	2.7	301.3	6.4	310.8	52.2	3.5	300.1	2.7
LAHILLE1-06	297	40521	20.0	18.7518	3.9	0.3581	4.0	0.0487	1.2	0.29	306.5	3.6	310.8	10.8	342.8	87.5	10.6	306.5	3.6
LAHILLE1-53	389	15348	20.5	16.9913	11.5	0.4130	12.1	0.0509	3.8	0.32	320.0	11.9	351.0	35.9	561.7	251.0	*8.8*	320.0	11.9
LAHILLE1-98	350	33303	2.2	18.6014	5.1	0.4148	6.0	0.0560	3.0	0.50	351.0	10.2	352.3	17.7	361.0	116.2	2.8	351.0	10.2
LAHILLE1-18	1012	111717	2.1	18.6199	2.2	0.4413	3.2	0.0596	2.3	0.73	373.2	8.4	371.2	9.9	358.7	49.2	-4.0	373.2	8.4
LAHILLE1-84	600	348846	13.4	16.2218	2.8	0.5385	6.8	0.0634	6.2	0.91	396.0	23.7	437.4	24.0	661.8	58.9	*9.5*	396.0	23.7
LAHILLE1-05	493	67221	1.9	18.5165	3.0	0.4805	3.9	0.0645	2.5	0.65	403.1	9.9	398.4	12.9	371.3	67.1	*-1.2*	403.1	9.9
LAHILLE1-95	858	69324	2.2	17.8054	2.2	0.5258	3.3	0.0679	2.5	0.74	423.5	10.1	429.0	11.6	458.8	49.3	7.7	423.5	10.1
LAHILLE1-47	1194	154212	9.2	18.1518	1.8	0.5340	3.8	0.0703	3.4	0.88	438.0	14.3	434.5	13.6	415.9	40.7	*-0.8*	438.0	14.3
LAHILLE1-58	127	16257	2.2	17.5895	5.1	0.5511	5.2	0.0703	0.8	0.15	438.0	3.4	445.7	18.7	485.8	113.3	9.8	438.0	3.4
LAHILLE1-03	294	108726	8.2	16.0029	1.9	0.6210	3.1	0.0721	2.5	0.79	448.7	10.7	490.5	12.1	690.9	40.5	*8.5*	448.7	10.7
LAHILLE1-73	627	131190	13.1	17.4616	1.0	0.5697	2.2	0.0721	1.9	0.89	449.1	8.4	457.8	8.0	501.9	21.8	10.5	449.1	8.4
LAHILLE1-15	163	11415	3.3	18.3888	4.3	0.5413	4.4	0.0722	0.9	0.21	449.3	3.9	439.3	15.7	386.8	96.8	*-2.3*	449.3	3.9
LAHILLE1-74	593	87309	28.3	16.9275	2.9	0.5911	3.0	0.0726	0.7	0.25	451.6	3.2	471.6	11.1	569.9	62.3	20.8	451.6	3.2
LAHILLE1-01	378	110208	9.5	18.0644	2.4	0.5602	4.1	0.0734	3.3	0.80	456.6	14.4	451.7	14.8	426.7	53.8	*-1.1*	456.6	14.4
LAHILLE1-44	210	69609	8.3	17.7471	3.1	0.5703	3.6	0.0734	1.8	0.50	456.6	7.9	458.2	13.2	466.1	68.8	2.0	456.6	7.9
LAHILLE1-78	166	22194	5.6	18.4583	4.4	0.5494	5.2	0.0736	2.7	0.53	457.5	12.1	444.6	18.6	378.4	98.7	*-2.9*	457.5	12.1
LAHILLE1-48	743	57951	2.4	17.8004	1.6	0.5723	1.7	0.0739	0.8	0.44	459.5	3.4	459.5	6.4	459.4	34.6	0.0	459.5	3.4
LAHILLE1-71	681	250665	6.7	17.8744	1.2	0.5709	1.7	0.0740	1.2	0.69	460.2	5.1	458.6	6.1	450.2	26.7	-2.2	460.2	5.1
LAHILLE1-51	551	91296	2.6	17.5792	2.6	0.5826	2.9	0.0743	1.3	0.44	461.9	5.7	466.1	11.0	487.1	58.3	5.2	461.9	5.7
LAHILLE1-26	186	26805	2.4	16.4219	12.3	0.6350	12.5	0.0756	2.3	0.18	470.0	10.2	499.2	49.3	635.5	265.6	26.0	470.0	10.2
LAHILLE1-14	336	92526	12.6	17.3633	4.4	0.6043	10.3	0.0761	9.3	0.90	472.8	42.5	479.9	39.5	514.3	97.6	8.1	472.8	42.5
LAHILLE1-85	272	74982	8.7	18.0283	3.1	0.5837	3.7	0.0763	2.1	0.57	474.1	9.7	466.9	13.9	431.1	68.2	*-1.6*	474.1	9.7
LAHILLE1-83	207	41910	2.6	17.4307	3.4	0.6081	3.5	0.0769	1.0	0.27	477.4	4.4	482.3	13.4	505.8	74.0	5.6	477.4	4.4
LAHILLE1-40	59	4830	4.2	15.6476	9.5	0.6800	9.5	0.0772	0.5	0.06	479.3	2.5	526.8	39.2	738.5	201.7	*9.0*	479.3	2.5
LAHILLE1-87	262	16050	4.5	17.4409	1.6	0.6112	1.9	0.0773	1.0	0.55	480.0	4.8	484.3	7.3	504.5	34.7	4.8	480.0	4.8
LAHILLE1-50	87	17802	3.7	17.5826	7.5	0.6528	7.6	0.0832	1.2	0.15	515.5	5.7	510.2	30.4	486.6	165.5	*-1.0*	515.5	5.7
LAHILLE1-13	495	115341	2.3	17.2735	1.9	0.6822	2.4	0.0855	1.6	0.64	528.6	8.0	528.1	10.0	525.7	40.8	-0.6	528.6	8.0
LAHILLE1-67	179	36669	0.9	17.4909	3.4	0.6782	3.5	0.0860	1.0	0.27	532.0	4.9	525.7	14.4	498.2	74.6	*-1.2*	532.0	4.9
LAHILLE1-11	289	34749	2.2	17.1096	3.1	0.7072	3.1	0.0878	0.5	0.17	542.3	2.8	543.1	13.2	546.5	67.3	0.8	542.3	2.8
LAHILLE1-27	342	190320	2.2	17.0792	2.4	0.7228	2.7	0.0895	1.3	0.47	552.8	6.7	552.3	11.5	550.4	52.0	-0.4	552.8	6.7
LAHILLE1-93	947	127359	6.9	16.5316	1.8	0.7610	2.0	0.0912	1.0	0.51	562.8	5.6	574.6	8.9	621.1	37.8	9.4	562.8	5.6
LAHILLE1-54	496	19620	1.8	15.6266	2.6	0.8172	3.6	0.0926	2.5	0.69	571.0	13.7	606.5	16.6	741.4	55.4	23.0	571.0	13.7
LAHILLE1-72	262	97959	6.9	16.5885	2.4	0.7831	2.5	0.0942	0.8	0.31	580.4	4.3	587.3	11.1	613.7	51.2	5.4	580.4	4.3
LAHILLE1-65	106	33138	2.5	15.8548	12.1	0.8245	12.2	0.0948	1.2	0.10	583.9	6.6	610.5	56.0	710.6	259.0	17.8	583.9	6.6
LAHILLE1-92	695	15555	4.2	15.4789	1.7	0.8736	2.1	0.0981	1.2	0.59	603.1	7.1	637.5	9.9	761.5	35.3	20.8	603.1	7.1
LAHILLE1-09	697	113496	4.1	14.8504	1.2	0.9662	8.3	0.1041	8.2	0.99	638.2	50.1	686.5	41.5	848.2	24.2	24.8	638.2	50.1
LAHILLE1-33	515	101427	3.6	16.1426	2.4	0.9068	3.0	0.1062	1.7	0.57	650.5	10.4	655.4	14.3	672.3	52.0	3.2	650.5	10.4
LAHILLE1-88	640	102378	3.9	15.8918	1.9	0.9576	2.4	0.1104	1.4	0.58	674.9	8.7	682.1	11.7	705.7	40.9	4.4	674.9	8.7
LAHILLE1-23	203	341007	7.7	15.0002	2.4	1.0473	3.6	0.1139	2.7	0.75	695.6	17.7	727.6	18.7	827.3	50.1	15.9	695.6	17.7
LAHILLE1-42	671	152265	5.2	16.0083	1.4	0.9950	2.4	0.1155	2.0	0.81	704.7	13.2	701.3	12.4	690.1	30.5	-2.1	704.7	13.2
LAHILLE1-28	1609	292884	13.6	14.8603	1.7	1.0749	2.1	0.1159	1.3	0.60	706.7	8.4	741.2	11.0	846.8	34.7	16.6	706.7	8.4
LAHILLE1-36	716	351216	35.6	15.4040	0.9	1.0527	1.3	0.1176	1.0	0.74	716.8	6.4	730.2	6.7	771.7	18.3	7.1	716.8	6.4
LAHILLE1-02	120	174780	2.8	14.1001	2.3	1.4206	2.8	0.1453	1.7	0.59	874.4	13.6	897.6	16.8	955.1	46.6	8.4	955.1	46.6
LAHILLE1-12	3272	345738	13.6	13.6073	2.4	1.6337	5.7	0.1612	5.2	0.91	963.6	46.1	983.3	35.8	1027.5	48.7	6.2	963.6	46.1
LAHILLE1-25	286	57918	1.5	13.9560	3.0	1.5375	3.4	0.1556	1.6	0.46	932.4	13.5	945.5	20.9	976.1	61.6	4.5	976.1	61.6
LAHILLE1-62	158	77490	3.2	13.9532	2.0	1.6294	2.6	0.1649	1.5	0.60	983.9	14.1	981.6	16.1	976.5	41.6	-0.8	976.5	41.6

		RATIOS									APPARENT AGES (Ma)								
GRAIN	U (ppm)	206Pb 204Pb	U Th	206Pb* 207Pb*	± (%)	207Pb* 235U*	± (%)	206Pb* 238U	± (%)	error corr.	206Pb* 238U*	± (Ma)	207Pb* 235U	± (Ma)	206Pb* 207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
LAHILLE1-32	279	387039	5.6	13.7951	1.1	1.6972	1.5	0.1698	1.0	0.67	1011.1	9.5	1007.5	9.6	999.7	22.6	-1.1	999.7	22.6
LAHILLE1-16	593	321720	2.3	13.5450	1.9	1.7534	3.1	0.1722	2.5	0.79	1024.5	23.3	1028.4	20.1	1036.7	38.4	1.2	1036.7	38.4
LAHILLE1-70	130	64392	3.1	13.3461	2.5	1.7689	4.0	0.1712	3.1	0.78	1018.8	29.2	1034.1	25.7	1066.6	49.7	4.5	1066.6	49.7
LAHILLE1-19	213	111282	1.8	10.8853	1.2	3.2609	1.7	0.2574	1.2	0.70	1476.7	15.7	1471.8	13.3	1464.6	23.2	-0.8	1464.6	23.2
LAHILLE1-45	294	233382	4.4	9.4816	1.3	4.1125	1.5	0.2828	0.8	0.50	1605.5	10.9	1656.8	12.5	1722.5	24.3	6.8	1722.5	24.3
LAHILLE1-22	228	244887	2.4	8.6822	2.3	4.4698	3.3	0.2815	2.3	0.70	1598.7	32.3	1725.4	27.1	1882.7	42.2	15.1	1882.7	42.2
LAHILLE1-86	159	191463	1.1	8.5582	1.8	5.1924	2.0	0.3223	0.9	0.44	1800.9	13.5	1851.4	16.8	1908.5	31.8	5.6	1908.5	31.8
SAMPLE MOLINA1, Trinity Peninsula Group, Legoupil Formation(?), Molina Rocks, 63˚ 22.356' S, 58˚ 26.868' W																			
MOLINA1-81	347	29598	1.8	18.7514	4.9	0.3097	5.8	0.0421	3.1	0.54	266.0	8.2	274.0	14.0	342.8	110.8	22.4	266.0	8.2
MOLINA1-83	226	30456	1.8	20.0878	7.3	0.2904	8.1	0.0423	3.6	0.44	267.1	9.3	258.9	18.6	184.8	170.0	*-3.2*	267.1	9.3
MOLINA1-16	248	24003	1.6	18.8548	3.9	0.3111	4.4	0.0425	2.0	0.45	268.6	5.2	275.1	10.5	330.3	88.3	18.7	268.6	5.2
MOLINA1-30	380	41736	14.8	19.0628	2.8	0.3083	3.4	0.0426	2.0	0.57	269.1	5.2	272.9	8.2	305.4	64.2	11.9	269.1	5.2
MOLINA1-66	218	26520	1.2	20.2665	4.8	0.2900	5.1	0.0426	1.6	0.32	269.1	4.3	258.6	11.6	164.1	112.4	*-4.1*	269.1	4.3
MOLINA1-62	220	24831	2.0	18.4069	11.1	0.3201	11.3	0.0427	1.9	0.17	269.7	4.9	282.0	27.8	384.6	250.6	29.9	269.7	4.9
MOLINA1-92	260	19347	2.2	19.1928	6.7	0.3079	6.9	0.0429	1.5	0.21	270.5	3.8	272.5	16.4	289.9	153.6	6.7	270.5	3.8
MOLINA1-21	223	36393	1.3	19.2025	5.0	0.3086	5.4	0.0430	2.1	0.38	271.3	5.5	273.1	13.0	288.8	114.8	6.0	271.3	5.5
MOLINA1-32	272	39957	1.8	18.8460	3.5	0.3156	4.0	0.0431	2.1	0.51	272.3	5.5	278.5	9.8	331.4	78.8	17.8	272.3	5.5
MOLINA1-71	450	183342	1.4	18.9722	7.8	0.3136	8.2	0.0432	2.6	0.31	272.4	6.8	277.0	19.8	316.3	176.7	13.9	272.4	6.8
MOLINA1-68	241	31506	1.1	19.0872	3.3	0.3125	4.4	0.0433	2.9	0.66	273.0	7.7	276.1	10.6	302.5	75.1	9.8	273.0	7.7
MOLINA1-17	151	12393	1.6	20.1382	4.6	0.2971	5.0	0.0434	1.8	0.36	273.8	4.7	264.1	11.5	178.9	108.2	*-3.7*	273.8	4.7
MOLINA1-69	385	72033	1.5	19.4681	3.7	0.3074	4.5	0.0434	2.6	0.58	273.9	7.0	272.2	10.8	257.3	84.7	*-0.6*	273.9	7.0
MOLINA1-12	371	83226	2.2	19.5479	4.1	0.3065	4.8	0.0435	2.6	0.53	274.2	6.8	271.4	11.5	247.9	94.7	*-1.0*	274.2	6.8
MOLINA1-26	236	24012	1.1	19.4023	5.2	0.3108	5.2	0.0437	0.8	0.16	275.9	2.2	274.8	12.6	265.0	118.9	-4.1	275.9	2.2
MOLINA1-97	280	22785	1.0	18.8639	6.8	0.3204	7.2	0.0438	2.4	0.34	276.5	6.5	282.2	17.7	329.3	153.4	16.0	276.5	6.5
MOLINA1-100	1020	102747	2.2	19.6561	2.7	0.3077	3.3	0.0439	1.9	0.57	276.8	5.2	272.4	7.9	235.1	62.8	*-1.6*	276.8	5.2
MOLINA1-07	139	13206	1.3	18.6305	10.8	0.3249	11.0	0.0439	2.2	0.20	276.9	5.9	285.6	27.4	357.4	244.2	22.5	276.9	5.9
MOLINA1-72	251	103947	1.5	18.4295	7.1	0.3284	8.1	0.0439	3.9	0.48	276.9	10.5	288.4	20.2	381.9	158.9	27.5	276.9	10.5
MOLINA1-94	160	39897	1.4	20.3201	6.6	0.2980	7.0	0.0439	2.4	0.34	277.1	6.5	264.9	16.3	157.9	154.0	*-4.6*	277.1	6.5
MOLINA1-78	723	37740	1.4	19.5605	2.4	0.3100	3.6	0.0440	2.7	0.75	277.5	7.3	274.2	8.6	246.4	54.5	*-1.2*	277.5	7.3
MOLINA1-34	157	36900	1.4	17.3359	11.1	0.3502	11.3	0.0440	2.4	0.21	277.8	6.6	304.9	29.8	517.8	243.4	*8.9*	277.8	6.6
MOLINA1-89	345	17565	0.8	19.7689	2.6	0.3074	2.9	0.0441	1.2	0.41	278.0	3.2	272.2	6.9	221.9	60.7	*-2.2*	278.0	3.2
MOLINA1-14	331	14340	1.2	19.4898	4.2	0.3132	4.4	0.0443	1.0	0.23	279.3	2.8	276.7	10.6	254.7	97.7	*-0.9*	279.3	2.8
MOLINA1-67	418	4830	1.8	16.1788	8.0	0.3774	8.1	0.0443	1.4	0.17	279.3	3.8	325.1	22.5	667.5	170.8	*14.1*	279.3	3.8
MOLINA1-39	133	83415	1.8	19.7068	10.1	0.3108	10.4	0.0444	2.4	0.23	280.2	6.5	274.8	25.0	229.2	234.1	*-2.0*	280.2	6.5
MOLINA1-25	526	32985	2.3	19.1578	2.9	0.3202	3.0	0.0445	0.8	0.28	280.6	2.3	282.0	7.5	294.1	66.7	4.6	280.6	2.3
MOLINA1-59	398	41283	1.6	19.1269	4.9	0.3209	4.9	0.0445	0.6	0.11	280.7	1.5	282.6	12.1	297.8	111.3	5.7	280.7	1.5
MOLINA1-35	227	43494	1.9	19.1565	5.4	0.3204	5.7	0.0445	1.9	0.33	280.8	5.1	282.2	14.1	294.2	123.4	4.6	280.8	5.1
MOLINA1-47	244	24132	2.0	20.2161	4.9	0.3041	5.0	0.0446	1.1	0.21	281.2	2.9	269.6	11.9	169.9	115.0	*-4.3*	281.2	2.9
MOLINA1-84	739	72294	15.5	18.8289	2.1	0.3269	2.8	0.0446	1.9	0.68	281.6	5.3	287.2	7.1	333.5	46.6	15.6	281.6	5.3
MOLINA1-90	327	32970	1.6	19.4300	4.5	0.3177	5.1	0.0448	2.4	0.46	282.3	6.6	280.1	12.6	261.8	104.4	*-0.8*	282.3	6.6
MOLINA1-19	516	29433	3.0	19.7050	10.7	0.3133	10.7	0.0448	0.7	0.06	282.4	1.8	276.7	25.9	229.4	246.6	*-2.0*	282.4	1.8
MOLINA1-05	225	42813	2.1	19.1332	6.8	0.3229	6.9	0.0448	1.3	0.18	282.6	3.5	284.1	17.2	297.0	156.1	4.9	282.6	3.5
MOLINA1-77	125	18336	1.3	20.5701	9.2	0.3012	9.3	0.0449	0.8	0.09	283.4	2.3	267.4	21.8	129.2	217.3	*-6.0*	283.4	2.3
MOLINA1-51	279	39534	1.7	19.5379	1.9	0.3173	3.1	0.0450	2.4	0.78	283.6	6.8	279.9	7.6	249.0	44.4	*-1.3*	283.6	6.8
MOLINA1-31	116	3348	0.9	9.9267	50.0	0.6290	50.3	0.0453	4.9	0.10	285.5	13.8	495.4	199.6	1637.7	998.3	*42.4*	285.5	13.8
MOLINA1-38	163	17628	1.9	16.4194	4.7	0.3809	6.0	0.0454	3.9	0.64	286.0	10.8	327.7	16.9	635.8	100.2	*12.7*	286.0	10.8
MOLINA1-06	230	40314	1.6	19.0203	6.6	0.3332	6.7	0.0460	1.1	0.16	289.7	3.0	292.0	16.9	310.5	149.8	6.7	289.7	3.0
MOLINA1-91	117	6423	1.5	21.3080	10.9	0.2989	10.9	0.0462	0.7	0.07	291.1	2.1	265.5	25.4	45.7	260.2	*-9.6*	291.1	2.1
MOLINA1-58	251	84498	2.4	18.0811	5.7	0.3546	5.8	0.0465	1.0	0.18	293.0	2.9	308.2	15.4	424.6	127.5	*4.9*	293.0	2.9
MOLINA1-48	201	58461	1.6	18.5471	4.8	0.3508	5.2	0.0472	2.0	0.39	297.2	5.8	305.3	13.6	367.6	107.6	19.1	297.2	5.8
MOLINA1-93	86	20886	1.2	18.7693	13.1	0.3471	13.2	0.0473	1.4	0.11	297.7	4.1	302.6	34.5	340.6	297.6	12.6	297.7	4.1
MOLINA1-56	371	101841	1.9	19.2499	4.2	0.3400	4.4	0.0475	1.3	0.30	299.0	3.9	297.2	11.4	283.1	96.6	*-0.6*	299.0	3.9
MOLINA1-43	375	25740	2.5	19.0816	1.7	0.3521	1.8	0.0487	0.6	0.31	306.7	1.7	306.3	4.8	303.2	39.6	-1.2	306.7	1.7
MOLINA1-22	67	21573	1.5	17.5765	16.5	0.3842	16.7	0.0490	2.0	0.12	308.2	6.1	330.1	47.0	487.4	367.5	*6.6*	308.2	6.1
MOLINA1-95	215	19371	1.8	18.0877	22.7	0.3759	22.7	0.0493	1.1	0.05	310.3	3.2	324.0	63.1	423.8	512.3	26.8	310.3	3.2
MOLINA1-74	58	33261	2.4	18.8874	18.7	0.3617	18.8	0.0495	1.7	0.09	311.7	5.1	313.5	50.7	326.4	427.7	4.5	311.7	5.1
MOLINA1-88	298	20958	1.6	19.1853	2.1	0.3608	2.2	0.0502	0.5	0.23	315.8	1.6	312.8	5.9	290.8	49.0	*-0.9*	315.8	1.6
MOLINA1-28	250	108714	6.1	19.3505	5.3	0.3654	5.3	0.0513	0.7	0.13	322.4	2.2	316.3	14.5	271.2	121.4	*-1.9*	322.4	2.2
MOLINA1-65	554	22182	1.6	17.1679	2.2	0.4908	3.1	0.0611	2.2	0.70	382.4	8.1	405.5	10.5	539.1	49.1	29.1	382.4	8.1
MOLINA1-99	367	59100	2.6	18.4400	2.9	0.4869	3.1	0.0651	1.3	0.42	406.6	5.2	402.8	10.5	380.6	64.1	*-1.0*	406.6	5.2
MOLINA1-54	229	83301	10.1	16.2101	3.2	0.5814	3.7	0.0684	1.9	0.51	426.2	7.7	465.3	13.7	663.4	68.0	*8.4*	426.2	7.7
MOLINA1-45	503	323943	14.7	16.7000	4.3	0.5693	7.2	0.0689	5.7	0.80	429.8	23.8	457.5	26.4	599.2	93.8	28.3	429.8	23.8
MOLINA1-50	166	29058	2.0	17.6932	3.6	0.5459	4.5	0.0701	2.7	0.60	436.5	11.3	442.3	16.0	472.8	79.2	7.7	436.5	11.3
MOLINA1-82	259	259974	2.4	17.5171	2.4	0.5591	4.0	0.0710	3.2	0.80	442.4	13.7	450.9	14.6	494.9	53.4	10.6	442.4	13.7
MOLINA1-15	495	85470	1.3	17.7511	1.9	0.5577	3.6	0.0718	3.1	0.85	447.0	13.3	450.0	13.1	465.6	41.5	4.0	447.0	13.3
MOLINA1-52	471	70947	2.1	17.7753	1.9	0.5628	2.9	0.0726	2.2	0.75	451.5	9.7	453.4	10.8	462.5	42.8	2.4	451.5	9.7
MOLINA1-73	315	61620	6.3	17.2274	4.2	0.5968	4.5	0.0746	1.6	0.36	463.6	7.2	475.2	16.9	531.5	91.2	12.8	463.6	7.2
MOLINA1-42	651	144105	19.7	17.7190	2.1	0.5827	2.9	0.0749	2.0	0.67	465.5	8.8	466.2	10.8	469.6	47.4	0.9	465.5	8.8
MOLINA1-98	275	60270	2.4	17.0133	8.4	0.6104	8.6	0.0753	2.1	0.25	468.1	9.6	483.8	33.3	558.8	183.0	16.2	468.1	9.6
MOLINA1-24	546	65070	5.3	16.4388	4.4	0.6332	5.9	0.0755	3.9	0.66	469.2	17.5	498.1	23.2	633.3	95.4	25.9	469.2	17.5
MOLINA1-70	463	96570	8.8	17.6825	1.6	0.5892	2.6	0.0756	2.1	0.79	469.6	9.4	470.3	9.9	474.1	35.9	1.0	469.6	9.4
MOLINA1-79	561	177012	15.0	17.7209	1.3	0.5882	2.1	0.0756	1.7	0.81	469.8	7.7	469.7	8.0	469.3	27.7	-0.1	469.8	7.7
MOLINA1-44	416	77652	2.0	17.6159	2.4	0.5949	2.6	0.0760	0.9	0.34	472.2	3.9	474.0	9.7	482.5	53.3	2.1	472.2	3.9
MOLINA1-01	38	10677	1.6	16.3488	12.7	0.6416	12.7	0.0761	0.7	0.05	472.7	3.0	503.3	50.5	645.1	273.8	26.7	472.7	3.0
MOLINA1-33	177	49581	1.4	17.6830	4.2	0.5951	4.5	0.0763	1.6	0.35	474.1	7.2	474.1	17.0	474.1	92.9	0.0	474.1	7.2
MOLINA1-49	438	79827	3.7	17.0021	3.5	0.6246	6.8	0.0770	5.8	0.86	478.3	26.7	492.7	26.4	560.3	75.9	14.6	478.3	26.7
MOLINA1-36	616	92541	14.5	17.0925	3.5	0.6226	3.9	0.0772	1.7	0.44	479.3	8.0	491.5	15.2	548.7	76.7	12.6	479.3	8.0
MOLINA1-75	241	92502	4.2	17.4874	2.6	0.6099	3.1	0.0774	1.7	0.55	480.3	7.9	483.5	12.0	498.6	57.3	3.7	480.3	7.9
MOLINA1-29	277	537309	9.4	16.9001	2.0	0.6353	2.5	0.0779	1.5	0.59	483.4	6.9	499.4	9.9	573.4	43.9	15.7	483.4	6.9
MOLINA1-09	80	4935	2.6	14.8599	12.3	0.7266	12.4	0.0783	1.1	0.09	486.0	5.2	554.6	52.9	846.9	257.3	*12.4*	486.0	5.2
MOLINA1-10	267	79452	1.7	17.7430	2.3	0.6300	3.4	0.0811	2.6	0.75	502.5	12.4	496.1	13.4	466.6	49.9	*-1.3*	502.5	12.4
MOLINA1-40	408	467343	4.1	17.6424	2.3	0.6451	2.8	0.0825	1.6	0.57	511.3	7.9	505.4	11.1	479.1	50.6	*-1.2*	511.3	7.9
MOLINA1-87	347	99993	3.8	17.0129	2.3	0.6813	3.3	0.0841	2.3	0.71	520.3	11.5	527.5	13.4	558.9	50.2	6.9	520.3	11.5
MOLINA1-03	555	110025	6.4	17.1876	2.5	0.6851	7.5	0.0854	7.0	0.94	528.3	35.7	529.9	30.9	536.6	55.2	1.5	528.3	35.7
MOLINA1-64	32	2043	1.9	13.9714	16.7	0.8570	16.8	0.0868	1.7	0.10	536.8	8.8	628.5	78.9	973.9	343.1	*14.6*	536.8	8.8
MOLINA1-18	1206	168402	1.6	16.9114	2.2	0.7459	2.5	0.0915	1.3	0.51	564.3	7.0	565.8	11.0	571.9	47.2	1.3	564.3	7.0
MOLINA1-55	255	173220	13.3	16.7710	3.4	0.7632	3.8	0.0928	1.7	0.44	572.3	9.1	575.9	16.8	590.0	74.4	3.0	572.3	9.1
MOLINA1-46	279	45627	1.4	16.6131	3.0	0.7804	3.4	0.0940	1.6	0.47	579.3	8.9	585.7	15.3	610.5	65.5	5.1	579.3	8.9
MOLINA1-60	306	177207	5.3	15.5423	4.2	0.8377	5.7	0.0944	3.9	0.68	581.7	21.9	617.9	26.6	752.8	88.5	22.7	581.7	21.9
MOLINA1-23	466	120150	25.5	16.3516	1.9	0.8383	4.1	0.0994	3.7	0.89	611.0	21.5	618.2	19.2	644.7	40.2	5.2	611.0	21.5
MOLINA1-04	325	286965	7.1	14.6601	3.7	1.0708	7.4	0.1138	6.4	0.87	695.1	42.0	739.1	38.7	875.0	76.2	20.6	695.1	42.0
MOLINA1-41	424	105402	3.8	15.6452	1.9	1.1070	2.7	0.1256	1.9	0.71	762.8	13.7	756.7	14.2	738.9	39.4	-3.2	762.8	13.7
MOLINA1-57	319	168519	4.5	15.2967	2.8	1.1702	2.9	0.1298	0.5	0.17	786.8	3.7	786.7	15.7	786.4	59.4	-0.1	786.8	3.7
MOLINA1-02	131	31944	1.5	12.3818	5.0	1.6525	7.6	0.1484	5.7	0.76	892.0	47.8	990.5	48.0	1215.7	97.7	26.6	892.0	47.8

GRAIN	U (ppm)	RATIOS 206Pb/204Pb	U/Th	206Pb*/207Pb*	± (%)	207Pb*/235U*	± (%)	206Pb*/238U	± (%)	error corr.	APPARENT AGES (Ma) 206Pb*/238U*	± (Ma)	207Pb*/235U	± (Ma)	206Pb*/207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
MOLINA1-76	326	356481	7.1	13.8532	3.7	1.5714	4.8	0.1579	3.1	0.64	945.0	27.3	959.0	30.0	991.2	75.5	4.7	945.0	27.3
MOLINA1-20	245	45051	2.8	13.5805	2.5	1.6397	3.0	0.1615	1.7	0.58	965.1	15.6	985.6	19.1	1031.5	50.0	6.4	965.1	15.6
MOLINA1-37	415	255861	3.2	13.5541	1.5	1.6685	4.3	0.1640	4.0	0.94	979.1	36.6	996.6	27.2	1035.4	29.3	5.4	979.1	36.6
MOLINA1-96	370	246261	4.1	13.3578	1.8	1.7112	2.6	0.1658	1.9	0.73	988.8	17.5	1012.7	16.9	1064.8	36.4	7.1	988.8	17.5
MOLINA1-86	417	83595	27.1	13.7418	1.4	1.6692	2.4	0.1664	2.0	0.82	992.0	18.2	996.9	15.3	1007.6	27.6	1.5	992.0	18.2
MOLINA1-13	239	145947	2.8	13.5385	2.2	1.8492	2.5	0.1816	1.2	0.47	1075.6	11.5	1063.1	16.3	1037.7	44.2	-3.6	1037.7	44.2
MOLINA1-53	156	48690	1.7	13.3784	2.1	1.8025	4.1	0.1749	3.5	0.86	1039.0	33.8	1046.4	26.7	1061.7	41.7	2.1	1061.7	41.7
MOLINA1-08	83	73431	3.2	13.2729	3.1	1.9353	3.2	0.1863	0.5	0.16	1101.3	5.2	1093.4	21.2	1077.6	62.9	-2.2	1077.6	62.9
MOLINA1-27	273	97194	4.7	12.4901	4.9	1.9349	6.9	0.1753	5.0	0.71	1041.1	47.6	1093.2	46.5	1198.5	95.9	13.1	1198.5	95.9
MOLINA1-61	80	30672	1.7	11.0579	2.6	2.9334	2.9	0.2353	1.3	0.44	1362.0	15.6	1390.6	22.0	1434.7	49.8	5.1	1434.7	49.8
MOLINA1-80	498	186066	1.8	5.5269	1.4	10.5479	3.8	0.4228	3.5	0.92	2273.2	66.9	2484.1	35.0	2661.4	23.9	14.6	2661.4	23.9
SAMPLE HOPE4, Trinity Peninsula Group, Hope Bay Formation(?), southeastern Hope Bay, 63˚ 24.569' S, 57˚2.345' W																			
HOPE4-61	62	13665	2.5	18.5345	41.4	0.3000	41.5	0.0403	1.6	0.04	254.9	4.1	266.4	97.4	369.1	972.1	*4.3*	254.9	4.1
HOPE4-34	71	10662	1.1	21.4390	26.5	0.2622	26.5	0.0408	1.3	0.05	257.6	3.3	236.5	55.9	31.0	643.7	*-9.0*	257.6	3.3
HOPE4-37	290	18471	1.1	18.7536	6.1	0.3024	6.3	0.0411	1.4	0.22	259.8	3.5	268.3	14.8	342.5	138.5	24.2	259.8	3.5
HOPE4-05	410	29160	1.6	19.0372	3.1	0.2986	4.9	0.0412	3.8	0.78	260.4	9.8	265.3	11.5	308.5	70.8	15.6	260.4	9.8
HOPE4-70	469	18138	0.9	18.5491	4.4	0.3076	6.5	0.0414	4.9	0.75	261.4	12.5	272.3	15.6	367.3	98.2	28.8	261.4	12.5
HOPE4-97	316	28875	1.9	19.1570	3.7	0.2996	5.3	0.0416	3.7	0.71	262.9	9.6	266.1	12.3	294.2	84.6	10.6	262.9	9.6
HOPE4-95	314	16116	1.4	19.0331	6.8	0.3036	7.1	0.0419	1.9	0.27	264.7	4.9	269.2	16.8	309.0	155.7	14.3	264.7	4.9
HOPE4-62	221	70785	1.9	19.9973	4.4	0.2892	5.0	0.0419	2.3	0.47	264.9	6.0	257.9	11.4	195.3	102.6	-2.7	264.9	6.0
HOPE4-65	212	25527	1.6	19.6563	4.1	0.2943	4.6	0.0420	2.0	0.43	264.9	5.1	261.9	10.5	235.1	94.9	*-1.1*	264.9	5.1
HOPE4-30	114	6870	0.7	21.4816	14.3	0.2694	14.4	0.0420	1.7	0.12	265.0	4.5	242.2	31.1	26.3	345.1	*-9.4*	265.0	4.5
HOPE4-82	769	43485	1.3	19.3949	2.8	0.2992	3.0	0.0421	1.3	0.42	265.8	3.3	265.8	7.1	265.9	63.3	0.1	265.8	3.3
HOPE4-36	182	8415	0.5	19.2644	4.1	0.3014	4.7	0.0421	2.2	0.46	265.9	5.6	267.5	11.0	281.4	94.9	5.5	265.9	5.6
HOPE4-10	223	13119	1.7	19.0553	6.7	0.3048	6.8	0.0421	1.0	0.15	266.0	2.6	270.1	16.0	306.3	152.2	13.2	266.0	2.6
HOPE4-20	63	8613	1.8	15.7534	11.1	0.3689	11.3	0.0421	2.4	0.21	266.1	6.2	318.8	31.0	724.3	235.7	*16.5*	266.1	6.2
HOPE4-99	99	18207	2.1	20.2529	20.3	0.2884	20.5	0.0424	2.2	0.11	267.5	5.7	257.3	46.5	165.7	479.6	*-3.9*	267.5	5.7
HOPE4-63	372	32694	1.7	18.8867	3.4	0.3094	4.4	0.0424	2.8	0.64	267.6	7.4	273.7	10.6	326.5	77.0	18.0	267.6	7.4
HOPE4-08	137	24312	1.6	20.3163	6.6	0.2879	7.0	0.0424	2.4	0.34	267.8	6.2	256.9	15.9	158.4	154.5	*-4.3*	267.8	6.2
HOPE4-22	414	34431	2.2	20.2096	4.2	0.2896	4.6	0.0425	1.9	0.41	268.0	5.0	258.3	10.6	170.7	99.0	*-3.8*	268.0	5.0
HOPE4-66	813	10809	0.8	17.7751	2.8	0.3299	6.9	0.0425	6.3	0.91	268.5	16.5	289.5	17.3	462.6	63.1	*7.3*	268.5	16.5
HOPE4-50	479	38019	1.4	19.3502	3.7	0.3034	3.8	0.0426	1.0	0.25	268.8	2.5	269.0	9.0	271.2	84.4	0.9	268.8	2.5
HOPE4-35	206	16563	1.1	20.6986	6.7	0.2837	6.7	0.0426	1.1	0.16	268.8	2.8	253.6	15.1	114.6	157.0	*-6.0*	268.8	2.8
HOPE4-96	597	51981	1.4	19.4731	2.7	0.3030	3.6	0.0428	2.4	0.67	270.1	6.5	268.7	8.5	256.7	61.3	*-0.5*	270.1	6.5
HOPE4-86	457	41079	2.0	19.4540	3.2	0.3034	4.1	0.0428	2.7	0.64	270.2	7.0	269.0	9.8	258.9	73.3	-4.3	270.2	7.0
HOPE4-43	193	22614	2.2	19.8768	6.7	0.2972	7.0	0.0428	2.2	0.32	270.5	5.9	264.2	16.4	209.3	154.9	*-2.4*	270.5	5.9
HOPE4-98	764	17994	1.4	18.7291	3.0	0.3159	4.1	0.0429	2.8	0.68	270.8	7.4	278.7	10.0	345.5	68.7	21.6	270.8	7.4
HOPE4-13	247	44163	1.5	20.0839	4.8	0.2949	5.1	0.0429	1.6	0.32	271.1	4.4	262.4	11.8	185.2	112.1	*-3.3*	271.1	4.4
HOPE4-87	203	19113	1.6	18.8721	6.1	0.3152	6.7	0.0431	2.7	0.41	272.3	7.2	278.2	16.3	328.3	138.8	17.1	272.3	7.2
HOPE4-77	719	119451	2.4	19.1148	2.1	0.3116	2.7	0.0432	1.6	0.61	272.6	4.4	275.4	6.4	299.2	47.7	8.9	272.6	4.4
HOPE4-38	244	48456	1.8	19.0320	5.4	0.3130	5.7	0.0432	1.6	0.28	272.7	4.2	276.5	13.7	309.1	124.0	11.8	272.7	4.2
HOPE4-57	761	42021	1.1	18.5926	2.4	0.3205	5.4	0.0432	4.9	0.90	272.7	13.1	282.3	13.4	362.0	53.3	24.7	272.7	13.1
HOPE4-03	128	7692	1.7	20.4086	6.9	0.2922	7.0	0.0432	1.1	0.16	272.9	3.0	260.3	16.0	147.8	161.0	*-4.9*	272.9	3.0
HOPE4-12	352	18597	1.0	19.4789	3.6	0.3064	3.9	0.0433	1.5	0.38	273.1	3.9	271.3	9.2	256.0	82.7	*-0.7*	273.1	3.9
HOPE4-17	341	30960	1.1	18.4165	3.8	0.3243	4.4	0.0433	2.3	0.52	273.3	6.1	285.2	11.0	383.5	85.2	28.7	273.3	6.1
HOPE4-53	175	18585	1.2	20.1349	4.5	0.2968	4.9	0.0433	1.9	0.39	273.5	5.0	263.9	11.3	179.3	104.5	*-3.6*	273.5	5.0
HOPE4-69	145	12408	0.8	18.7727	6.3	0.3184	6.4	0.0434	1.2	0.18	273.6	3.1	280.7	15.6	340.2	142.0	19.6	273.6	3.1
HOPE4-94	402	38739	2.2	19.3979	3.7	0.3084	4.4	0.0434	2.4	0.55	273.8	6.5	272.9	10.5	265.6	84.1	-3.1	273.8	6.5
HOPE4-76	351	28485	1.4	19.7725	4.2	0.3027	5.1	0.0434	2.9	0.57	273.9	7.8	268.5	12.0	221.5	97.1	*-2.0*	273.9	7.8
HOPE4-01	520	22221	1.1	18.4925	2.5	0.3237	3.4	0.0434	2.3	0.67	274.0	6.2	284.8	8.5	374.2	56.6	26.8	274.0	6.2
HOPE4-51	538	54969	1.2	19.2089	2.4	0.3121	2.5	0.0435	0.5	0.21	274.4	1.4	275.8	6.0	288.0	55.5	4.7	274.4	1.4
HOPE4-75	43	4611	1.6	23.6780	26.6	0.2548	26.7	0.0438	2.3	0.08	276.1	6.1	230.5	55.1	-212.6	678.0	*-19.8*	276.1	6.1
HOPE4-04	126	8559	1.0	18.8477	8.3	0.3202	8.3	0.0438	0.6	0.07	276.2	1.6	282.1	20.5	331.2	188.7	16.6	276.2	1.6
HOPE4-78	83	16707	1.4	19.8038	14.3	0.3048	14.3	0.0438	1.6	0.11	276.2	4.2	270.1	34.0	217.8	331.5	*-2.2*	276.2	4.2
HOPE4-25	134	21840	2.2	17.7712	9.6	0.3402	9.8	0.0439	1.8	0.18	276.7	4.8	297.3	25.2	463.1	213.1	*7.0*	276.7	4.8
HOPE4-100	580	9345	0.8	16.6817	11.9	0.3626	12.3	0.0439	2.9	0.24	276.8	8.0	314.1	33.1	601.6	258.4	*11.9*	276.8	8.0
HOPE4-85	206	16887	0.9	20.2446	5.6	0.2988	5.9	0.0439	1.9	0.32	276.8	5.1	265.5	13.8	166.6	130.5	*-4.3*	276.8	5.1
HOPE4-92	80	5541	1.2	19.8971	18.6	0.3043	18.6	0.0439	1.0	0.05	277.1	2.6	269.8	44.2	206.9	435.2	*-2.7*	277.1	2.6
HOPE4-41	474	39963	1.3	19.2284	3.7	0.3150	4.0	0.0439	1.7	0.42	277.1	4.6	278.0	9.8	285.7	83.5	3.0	277.1	4.6
HOPE4-68	456	51210	1.0	18.1143	4.5	0.3350	4.7	0.0440	1.2	0.25	277.6	3.2	293.4	12.0	420.5	101.5	*5.4*	277.6	3.2
HOPE4-11	200	22848	1.4	19.9351	4.7	0.3056	4.8	0.0442	0.5	0.10	278.7	1.4	270.8	11.3	202.5	110.3	*-2.9*	278.7	1.4
HOPE4-93	120	16131	0.9	19.4280	8.8	0.3140	9.6	0.0442	3.7	0.38	279.1	10.1	277.3	23.3	262.0	203.5	*-0.7*	279.1	10.1
HOPE4-91	259	21810	2.2	16.9569	7.3	0.3599	7.9	0.0443	3.1	0.39	279.2	8.5	312.1	21.2	566.1	158.4	*10.6*	279.2	8.5
HOPE4-54	233	12807	1.8	18.7703	8.2	0.3260	8.3	0.0444	0.8	0.10	279.9	2.3	286.5	20.7	340.5	186.6	17.8	279.9	2.3
HOPE4-16	167	31404	2.5	19.7958	6.6	0.3109	6.6	0.0446	1.0	0.15	281.5	2.8	274.9	16.0	218.8	152.0	*-2.4*	281.5	2.8
HOPE4-06	241	16728	2.3	19.1542	4.1	0.3226	4.2	0.0448	0.7	0.16	282.6	1.8	283.9	10.4	294.5	94.6	4.0	282.6	1.8
HOPE4-56	199	10149	1.7	16.2982	13.6	0.3800	14.3	0.0449	4.4	0.31	283.3	12.2	327.1	39.9	651.7	292.5	*13.4*	283.3	12.2
HOPE4-40	533	94074	2.4	18.5594	1.4	0.3339	2.4	0.0450	1.9	0.81	283.4	5.4	292.6	6.1	366.1	32.2	22.6	283.4	5.4
HOPE4-59	775	53124	2.3	19.1973	0.8	0.3236	0.9	0.0451	0.5	0.53	284.1	1.4	284.7	2.3	289.4	18.1	1.8	284.1	1.4
HOPE4-71	268	48717	1.2	19.4755	6.9	0.3191	6.9	0.0451	0.5	0.07	284.2	1.4	281.2	17.0	256.4	158.4	*-1.1*	284.2	1.4
HOPE4-79	198	59814	2.5	19.1098	4.9	0.3258	5.3	0.0452	2.2	0.41	284.7	6.0	286.3	13.3	299.8	110.8	5.0	284.7	6.0
HOPE4-49	797	53817	1.1	19.1618	4.5	0.3251	5.0	0.0452	2.1	0.42	284.9	5.9	285.9	12.5	293.6	103.8	3.0	284.9	5.9
HOPE4-09	1106	55512	1.9	19.3959	1.9	0.3218	2.5	0.0453	1.6	0.64	285.4	4.5	283.3	6.1	265.8	43.6	*-0.7*	285.4	4.5
HOPE4-14	106	9873	1.2	19.6526	11.6	0.3177	11.7	0.0453	1.8	0.15	285.5	4.9	280.2	28.7	235.5	268.4	*-1.9*	285.5	4.9
HOPE4-27	387	6339	1.3	16.0954	13.7	0.3881	13.7	0.0453	0.7	0.05	285.6	2.0	333.0	39.0	678.6	294.6	*14.2*	285.6	2.0
HOPE4-15	180	27279	1.9	20.1506	10.3	0.3102	10.5	0.0453	2.2	0.21	285.8	6.0	274.3	25.3	177.5	240.3	*-4.2*	285.8	6.0
HOPE4-48	183	22665	1.4	20.8529	10.3	0.3013	10.4	0.0456	1.2	0.11	287.3	3.2	267.4	24.4	97.0	244.6	*-7.4*	287.3	3.2
HOPE4-29	333	8553	0.9	18.7046	5.3	0.3366	5.3	0.0457	0.5	0.09	287.8	1.4	294.6	13.6	348.5	119.4	17.4	287.8	1.4
HOPE4-55	665	38322	1.3	18.8584	2.8	0.3341	3.0	0.0457	0.9	0.30	288.0	2.5	292.7	7.5	329.9	63.8	12.7	288.0	2.5
HOPE4-33	75	10848	1.0	17.9121	13.6	0.3522	13.8	0.0458	2.0	0.14	288.4	5.6	306.4	36.4	445.5	304.0	*5.9*	288.4	5.6
HOPE4-74	163	8781	0.8	18.5759	9.1	0.3397	9.2	0.0458	0.8	0.08	288.5	2.1	297.0	23.6	364.1	206.1	20.8	288.5	2.1
HOPE4-31	83	5628	1.6	16.6826	14.1	0.3795	14.1	0.0459	0.7	0.05	289.4	2.1	326.7	39.5	601.5	307.2	*11.4*	289.4	2.1
HOPE4-52	444	48153	1.4	19.7446	3.6	0.3236	4.0	0.0463	1.7	0.43	292.0	4.9	284.7	9.9	224.8	83.6	*-2.6*	292.0	4.9
HOPE4-72	156	7197	0.8	19.1381	11.5	0.3372	11.5	0.0468	0.7	0.06	294.9	2.1	295.0	29.4	296.4	262.1	0.5	294.9	2.1
HOPE4-32	345	23529	2.5	18.5154	3.5	0.3497	3.7	0.0470	1.2	0.33	295.8	3.5	304.5	9.6	371.4	77.8	20.4	295.8	3.5
HOPE4-42	251	15513	1.4	18.9459	4.7	0.3437	4.9	0.0472	1.6	0.32	297.4	4.5	299.9	12.8	319.4	106.0	6.9	297.4	4.5
HOPE4-46	337	13599	1.3	18.5678	3.8	0.3515	4.3	0.0473	2.0	0.46	298.2	5.8	305.9	11.3	365.0	85.6	18.3	298.2	5.8
HOPE4-73	379	21744	0.7	18.5876	3.0	0.3573	3.0	0.0482	0.5	0.17	303.3	1.5	310.2	8.1	362.6	67.3	16.4	303.3	1.5
HOPE4-02	582	11655	1.2	18.5224	3.2	0.3613	3.5	0.0485	1.3	0.37	305.5	3.8	313.2	9.3	370.6	72.4	17.5	305.5	3.8
HOPE4-80	730	1731	0.7	12.8197	13.7	0.5291	13.9	0.0492	2.3	0.16	309.6	6.8	431.2	48.9	1147.0	273.7	*28.2*	309.6	6.8
HOPE4-39	263	19809	2.7	17.8966	8.2	0.4314	8.4	0.0560	1.8	0.22	351.2	6.3	364.2	25.7	447.4	182.4	21.5	351.2	6.3
HOPE4-67	294	5229	1.3	16.7807	20.9	0.4922	22.4	0.0599	8.2	0.36	375.1	29.7	406.4	75.3	588.8	458.1	7.7	375.1	29.7
HOPE4-07	283	108822	2.0	18.3931	2.5	0.4686	2.9	0.0625	1.5	0.51	390.9	5.6	390.2	9.3	386.3	55.3	-1.2	390.9	5.6
HOPE4-45	397	37827	2.5	18.3334	2.6	0.4868	2.7	0.0647	0.5	0.19	404.3	2.0	402.7	8.9	393.6	58.8	-2.7	404.3	2.0

GRAIN	U (ppm)	RATIOS 206Pb/204Pb	U/Th	206Pb*/207Pb*	± (%)	207Pb*/235U*	± (%)	206Pb*/238U	± (%)	error corr.	APPARENT AGES (Ma) 206Pb*/238U*	± (Ma)	207Pb*/235U	± (Ma)	206Pb*/207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
HOPE4-83	348	184458	2.0	17.7833	1.4	0.5752	2.8	0.0742	2.4	0.87	461.3	10.6	461.3	10.2	461.5	30.4	0.1	461.3	10.6
HOPE4-23	314	31827	3.3	17.6072	3.6	0.5829	4.9	0.0744	3.4	0.69	462.8	15.2	466.3	18.5	483.6	79.2	4.3	462.8	15.2
HOPE4-26	916	139443	1.4	17.6885	1.2	0.5899	2.2	0.0757	1.9	0.84	470.2	8.4	470.8	8.3	473.4	26.1	0.7	470.2	8.4
HOPE4-58	145	28731	2.5	18.2012	4.2	0.5736	5.0	0.0757	2.7	0.54	470.5	12.2	460.3	18.4	409.8	93.7	*-2.2*	470.5	12.2
HOPE4-60	117	2130	1.8	13.2014	19.2	0.8015	19.6	0.0767	4.3	0.22	476.6	19.6	597.7	88.9	1088.4	387.5	*20.3*	476.6	19.6
HOPE4-28	134	16485	1.2	16.3916	8.0	0.7008	8.5	0.0833	2.8	0.33	515.9	13.8	539.3	35.5	639.5	172.4	19.3	515.9	13.8
HOPE4-81	701	85968	51.2	16.9184	1.0	0.7106	2.5	0.0872	2.3	0.91	538.9	11.8	545.1	10.6	571.0	22.6	5.6	538.9	11.8
HOPE4-18	377	171954	3.3	16.9751	2.1	0.7586	2.3	0.0934	0.9	0.42	575.6	5.2	573.2	9.9	563.7	44.9	-2.1	575.6	5.2
HOPE4-89	1048	206895	4.8	16.3894	2.0	0.8365	2.9	0.0994	2.1	0.72	611.1	12.3	617.2	13.5	639.7	43.7	4.5	611.1	12.3
HOPE4-88	559	64128	3.1	15.3255	2.8	0.9573	4.7	0.1064	3.8	0.80	651.9	23.3	681.9	23.4	782.4	59.7	16.7	651.9	23.3
HOPE4-19	478	85389	4.5	15.8887	1.5	1.0294	2.7	0.1186	2.3	0.83	722.7	15.6	718.6	14.1	706.1	32.4	-2.3	722.7	15.6
HOPE4-24	45	7953	3.1	12.8307	5.2	1.6197	5.9	0.1507	2.9	0.49	905.0	24.6	977.9	37.3	1145.3	103.1	21.0	905.0	24.6
HOPE4-21	111	41763	3.5	13.6168	2.8	1.5798	3.1	0.1560	1.3	0.42	934.6	11.5	962.3	19.4	1026.1	57.4	8.9	934.6	11.5
HOPE4-90	215	173085	4.1	12.3345	2.0	2.2632	2.9	0.2025	2.1	0.72	1188.5	22.5	1200.9	20.3	1223.2	39.5	2.8	1223.2	39.5
HOPE4-47	368	135333	2.9	10.2378	1.1	3.6448	1.7	0.2706	1.2	0.75	1544.0	16.9	1559.4	13.2	1580.2	20.6	2.3	1580.2	20.6
HOPE4-64	323	216582	2.1	8.2450	2.0	4.5245	3.6	0.2706	3.0	0.83	1543.6	41.5	1735.5	30.3	1975.2	36.3	21.8	1975.2	36.3
SAMPLE ANDVORD2, Trinity Peninsula Group, Legoupil Formation(?), Andvord Bay, 64˚ 53.114' S, 62˚ 28.56' W																			
ANDVORD2-95	675	19503	3.9	14.2286	3.8	0.2681	8.9	0.0277	8.0	0.90	176.0	13.9	241.2	19.0	936.5	77.6	*27.1*	176.0	13.9
ANDVORD2-90	552	31359	1.2	19.0736	3.4	0.2958	3.9	0.0409	2.0	0.50	258.5	5.0	263.1	9.0	304.1	76.6	15.0	258.5	5.0
ANDVORD2-10	158	13608	1.5	19.1076	10.5	0.2994	10.6	0.0415	1.4	0.13	262.1	3.6	265.9	24.7	300.1	239.2	12.7	262.1	3.6
ANDVORD2-100	221	3654	1.3	16.1623	9.4	0.3560	9.4	0.0417	0.6	0.07	263.6	1.6	309.2	25.1	669.7	201.0	*14.8*	263.6	1.6
ANDVORD2-97	300	28533	1.9	19.7081	4.9	0.2952	5.0	0.0422	1.4	0.27	266.4	3.5	262.6	11.7	229.0	112.3	*-1.4*	266.4	3.5
ANDVORD2-08	271	11691	1.3	19.1267	11.7	0.3049	12.0	0.0423	2.7	0.23	267.0	7.1	270.2	28.4	297.8	267.1	10.3	267.0	7.1
ANDVORD2-94	311	14823	1.6	18.7779	3.3	0.3111	3.4	0.0424	0.7	0.20	267.5	1.7	275.0	8.1	339.6	74.8	21.2	267.5	1.7
ANDVORD2-40	523	12759	0.7	18.7719	3.5	0.3123	3.7	0.0425	1.2	0.32	268.4	3.1	276.0	8.8	340.3	78.3	21.1	268.4	3.1
ANDVORD2-56	127	12561	1.5	20.4481	7.3	0.2877	7.4	0.0427	1.2	0.16	269.4	3.1	256.8	16.9	143.2	172.3	*-4.9*	269.4	3.1
ANDVORD2-44	604	48624	1.7	19.5384	3.1	0.3036	3.4	0.0430	1.6	0.46	271.6	4.2	269.2	8.2	249.0	70.4	*-0.9*	271.6	4.2
ANDVORD2-82	333	12066	1.5	19.6345	5.7	0.3026	5.8	0.0431	1.1	0.19	272.0	2.9	268.5	13.6	237.7	130.8	*-1.3*	272.0	2.9
ANDVORD2-15	307	18567	2.0	19.1613	2.8	0.3111	3.1	0.0432	1.3	0.41	272.9	3.4	275.1	7.4	293.7	63.7	7.1	272.9	3.4
ANDVORD2-22	535	52905	1.2	19.8695	4.1	0.3005	4.2	0.0433	1.1	0.25	273.3	2.8	266.8	9.8	210.2	94.2	*-2.4*	273.3	2.8
ANDVORD2-59	194	36369	1.5	18.9224	8.7	0.3164	8.8	0.0434	1.3	0.15	274.0	3.5	279.1	21.4	322.2	197.5	15.0	274.0	3.5
ANDVORD2-14	35	3408	1.3	21.9943	29.9	0.2725	30.0	0.0435	1.6	0.05	274.3	4.3	244.7	65.3	-30.6	740.3	*-12.1*	274.3	4.3
ANDVORD2-78	440	30441	1.1	19.6316	2.9	0.3061	3.1	0.0436	1.0	0.31	275.0	2.6	271.2	7.3	238.0	66.8	*-1.4*	275.0	2.6
ANDVORD2-84	839	65496	1.3	19.4644	2.2	0.3114	2.3	0.0440	0.8	0.36	277.4	2.3	275.3	5.6	257.7	49.4	*-0.8*	277.4	2.3
ANDVORD2-48	275	31251	1.8	20.6535	7.3	0.2937	7.3	0.0440	0.7	0.10	277.5	2.0	261.4	16.9	119.7	172.1	*-6.1*	277.5	2.0
ANDVORD2-01	196	17220	1.1	20.3173	6.0	0.2994	6.0	0.0441	0.5	0.08	278.3	1.4	265.9	14.1	158.3	140.5	*-4.7*	278.3	1.4
ANDVORD2-07	199	16587	1.5	20.2086	8.1	0.3014	8.3	0.0442	1.5	0.18	278.7	4.0	267.5	19.5	170.8	190.5	*-4.2*	278.7	4.0
ANDVORD2-42	335	30702	1.2	19.5592	4.0	0.3119	4.1	0.0443	1.2	0.28	279.1	3.2	275.7	9.9	246.5	91.1	*-1.2*	279.1	3.2
ANDVORD2-98	784	3465	1.3	15.2842	10.3	0.4031	10.4	0.0447	1.4	0.13	281.8	3.8	343.9	30.3	788.1	216.6	*18.1*	281.8	3.8
ANDVORD2-32	172	16815	1.2	19.3344	4.9	0.3188	5.1	0.0447	1.5	0.30	281.9	4.2	281.0	12.5	273.1	111.4	-3.2	281.9	4.2
ANDVORD2-68	520	41550	1.9	19.4107	3.5	0.3177	3.6	0.0447	0.9	0.24	282.0	2.4	280.1	8.9	264.1	81.3	*-0.7*	282.0	2.4
ANDVORD2-69	358	28917	1.5	19.7189	4.3	0.3140	4.4	0.0449	0.8	0.17	283.1	2.1	277.2	10.6	227.8	99.4	*-2.1*	283.1	2.1
ANDVORD2-83	490	38604	1.4	19.8635	3.4	0.3138	3.4	0.0452	0.7	0.19	285.1	1.9	277.2	8.3	210.9	78.2	*-2.9*	285.1	1.9
ANDVORD2-36	148	11115	1.2	20.0194	8.2	0.3126	8.4	0.0454	1.9	0.23	286.1	5.4	276.2	20.4	192.7	191.2	*-3.6*	286.1	5.4
ANDVORD2-31	464	22725	1.6	19.1979	4.2	0.3271	4.8	0.0455	2.3	0.48	287.1	6.5	287.4	11.9	289.3	95.2	0.7	287.1	6.5
ANDVORD2-51	94	7092	1.0	20.0044	10.6	0.3162	10.8	0.0459	2.3	0.21	289.2	6.5	279.0	26.4	194.5	246.8	*-3.6*	289.2	6.5
ANDVORD2-45	1278	48459	3.4	18.7014	2.9	0.3394	3.8	0.0460	2.4	0.65	290.1	6.9	296.7	9.7	348.9	65.4	16.8	290.1	6.9
ANDVORD2-17	245	24882	1.7	17.9734	7.9	0.3545	8.1	0.0462	2.0	0.25	291.2	5.7	308.1	21.6	437.9	175.3	*5.5*	291.2	5.7
ANDVORD2-33	205	15333	0.8	18.8575	9.0	0.3380	9.0	0.0462	1.2	0.13	291.3	3.3	295.7	23.2	330.0	203.7	11.7	291.3	3.3
ANDVORD2-60	558	35037	1.8	19.6288	3.7	0.3262	3.9	0.0464	1.4	0.36	292.6	4.0	286.7	9.8	238.4	84.3	*-2.1*	292.6	4.0
ANDVORD2-57	338	31134	2.2	19.2798	3.7	0.3333	3.8	0.0466	1.0	0.25	293.7	2.8	292.1	9.8	279.6	85.3	*-0.5*	293.7	2.8
ANDVORD2-21	70	4560	2.0	18.7725	20.6	0.3426	20.9	0.0466	3.4	0.16	293.9	9.9	299.1	54.1	340.3	470.4	13.6	293.9	9.9
ANDVORD2-35	316	47007	1.4	18.9990	5.7	0.3390	6.0	0.0467	1.8	0.30	294.3	5.2	296.4	15.4	313.0	129.7	6.0	294.3	5.2
ANDVORD2-53	129	31470	2.2	18.4968	11.7	0.3491	11.9	0.0468	2.4	0.20	295.1	7.0	304.1	31.3	373.7	263.5	21.0	295.1	7.0
ANDVORD2-18	190	10821	1.7	19.2038	2.3	0.3365	2.7	0.0469	1.4	0.52	295.3	4.0	294.6	6.8	288.6	52.0	-2.3	295.3	4.0
ANDVORD2-87	150	8367	2.2	19.9178	7.7	0.3255	8.4	0.0470	3.3	0.39	296.2	9.5	286.1	20.9	204.5	179.5	*-3.5*	296.2	9.5
ANDVORD2-13	1547	83010	1.1	18.8936	2.2	0.3439	2.3	0.0471	0.7	0.29	296.9	1.9	300.1	5.9	325.7	49.5	8.8	296.9	1.9
ANDVORD2-52	132	7137	1.6	15.7574	25.2	0.4141	25.5	0.0473	3.8	0.15	298.1	11.2	351.8	76.0	723.7	543.0	*15.3*	298.1	11.2
ANDVORD2-79	569	46635	2.4	18.5497	8.0	0.3539	8.6	0.0476	3.0	0.35	299.8	8.9	307.6	22.8	367.2	181.5	18.4	299.8	8.9
ANDVORD2-19	570	50583	1.3	19.5582	3.4	0.3359	3.5	0.0477	0.6	0.18	300.1	1.8	294.1	8.9	246.7	78.8	*-2.0*	300.1	1.8
ANDVORD2-64	288	19179	1.6	19.6705	4.1	0.3354	4.1	0.0479	0.5	0.12	301.3	1.5	293.7	10.5	233.4	94.7	*-2.6*	301.3	1.5
ANDVORD2-61	602	53346	86.3	18.7799	1.5	0.3534	2.7	0.0481	2.3	0.84	303.1	6.8	307.3	7.2	339.4	33.2	10.7	303.1	6.8
ANDVORD2-26	249	18351	1.0	19.7476	5.2	0.3377	5.3	0.0484	0.9	0.17	304.5	2.7	295.4	13.5	224.4	119.7	*-3.1*	304.5	2.7
ANDVORD2-76	659	3945	3.5	15.7786	7.7	0.4261	7.9	0.0488	1.7	0.22	306.9	5.2	360.4	24.0	720.9	164.0	*14.8*	306.9	5.2
ANDVORD2-29	130	18642	1.5	20.7865	10.7	0.3590	10.9	0.0541	1.8	0.17	339.8	6.1	311.5	29.2	104.6	254.1	*-9.1*	339.8	6.1
ANDVORD2-80	969	60156	4.0	18.2359	2.0	0.4110	2.6	0.0544	1.6	0.62	341.2	5.4	349.6	7.7	405.6	45.7	15.9	341.2	5.4
ANDVORD2-47	1351	95829	4.0	18.3223	1.3	0.4199	2.6	0.0558	2.3	0.88	350.0	7.9	356.0	7.9	395.0	28.1	11.4	350.0	7.9
ANDVORD2-43	227	8670	0.9	17.9892	4.4	0.4389	5.0	0.0573	2.4	0.48	359.0	8.4	369.5	15.4	436.0	97.0	17.7	359.0	8.4
ANDVORD2-65	731	58713	7.3	18.6605	1.5	0.4279	1.9	0.0579	1.1	0.59	362.9	4.0	361.7	5.8	353.8	34.6	-2.6	362.9	4.0
ANDVORD2-16	376	32733	1.4	18.0981	2.9	0.4834	2.9	0.0635	0.5	0.18	396.6	2.0	400.4	9.7	422.5	64.3	6.1	396.6	2.0
ANDVORD2-46	618	53421	2.6	18.3671	1.3	0.4894	1.6	0.0652	0.9	0.54	407.2	3.4	404.5	5.3	389.5	29.9	-4.5	407.2	3.4
ANDVORD2-73	1701	86349	1.7	17.8050	1.3	0.5407	1.9	0.0698	1.4	0.75	435.1	6.0	438.9	6.8	458.8	28.2	5.2	435.1	6.0
ANDVORD2-34	264	28263	3.4	16.5737	3.4	0.5809	4.0	0.0698	2.1	0.52	435.1	8.9	465.0	15.1	615.6	74.4	29.3	435.1	8.9
ANDVORD2-62	828	3933	1.2	15.6113	2.6	0.6293	2.9	0.0713	1.1	0.40	443.7	4.9	495.7	11.2	743.5	55.4	*10.5*	443.7	4.9
ANDVORD2-23	471	62385	2.0	17.7069	3.7	0.5580	4.0	0.0717	1.5	0.38	446.2	6.6	450.2	14.6	471.1	82.2	5.3	446.2	6.6
ANDVORD2-37	304	39453	6.6	17.4605	4.1	0.5770	4.4	0.0731	1.6	0.36	454.6	6.9	462.5	16.3	502.0	90.1	9.4	454.6	6.9
ANDVORD2-25	223	38118	4.3	17.6101	14.9	0.5770	15.0	0.0737	1.9	0.12	458.3	8.2	462.5	55.8	483.2	330.3	5.1	458.3	8.2
ANDVORD2-39	138	12237	1.7	18.7523	5.9	0.5425	6.0	0.0738	0.6	0.10	458.9	2.7	440.1	21.4	342.7	134.7	*-4.3*	458.9	2.7
ANDVORD2-11	356	38808	1.8	17.1965	2.8	0.5921	5.5	0.0739	4.7	0.86	459.3	20.8	472.2	20.7	535.4	62.2	14.2	459.3	20.8
ANDVORD2-54	496	43752	8.4	17.7818	1.7	0.5870	1.8	0.0757	0.7	0.39	470.4	3.3	468.9	6.9	461.7	37.3	-1.9	470.4	3.3
ANDVORD2-88	1450	102666	1.1	17.8583	4.4	0.5866	4.7	0.0760	1.6	0.35	472.0	7.4	468.7	17.5	452.2	96.8	-4.4	472.0	7.4
ANDVORD2-81	456	32445	2.0	17.8292	1.9	0.5883	2.2	0.0761	1.2	0.56	472.7	5.7	469.8	8.4	455.8	41.1	-3.7	472.7	5.7
ANDVORD2-12	359	40971	1.1	17.7168	2.1	0.5933	3.0	0.0762	2.1	0.70	473.6	9.6	473.0	11.3	469.8	47.4	-0.8	473.6	9.6
ANDVORD2-06	533	48855	3.1	17.8681	1.5	0.5911	2.2	0.0766	1.7	0.75	475.8	7.7	471.6	8.4	451.0	32.9	*-0.9*	475.8	7.7
ANDVORD2-96	369	96603	3.8	17.9242	2.6	0.5917	3.7	0.0769	2.6	0.70	477.7	12.0	471.9	14.0	444.0	58.8	*-1.2*	477.7	12.0
ANDVORD2-89	1031	121104	4.2	17.6147	1.7	0.6023	2.6	0.0769	2.1	0.78	477.9	9.4	478.7	10.0	482.6	36.5	1.0	477.9	9.4
ANDVORD2-27	270	28740	1.9	18.1539	3.6	0.5923	3.7	0.0780	0.5	0.14	484.1	2.3	472.3	13.9	415.6	81.2	*-2.5*	484.1	2.3
ANDVORD2-75	389	33255	3.8	16.9806	2.2	0.6479	3.0	0.0798	2.0	0.66	494.9	9.3	507.2	11.9	563.0	48.6	12.1	494.9	9.3
ANDVORD2-66	403	80967	2.1	17.5691	2.6	0.6281	3.1	0.0800	1.6	0.54	496.3	7.8	494.9	12.0	488.3	56.9	-1.6	496.3	7.8
ANDVORD2-67	374	23193	1.8	17.4774	2.6	0.6394	3.2	0.0810	1.9	0.58	502.3	9.0	501.9	12.6	499.9	57.2	-0.5	502.3	9.0
ANDVORD2-91	396	48441	7.2	15.9824	2.5	0.7498	3.1	0.0869	1.8	0.58	537.2	9.2	568.1	13.4	693.6	53.5	22.5	537.2	9.2
ANDVORD2-58	134	7248	1.6	15.0380	9.1	0.8191	9.3	0.0893	1.7	0.18	551.6	8.7	607.6	42.3	822.1	190.5	*9.2*	551.6	8.7
ANDVORD2-86	184	61584	2.6	14.8186	2.9	0.8432	5.1	0.0906	4.2	0.82	559.2	22.6	620.9	23.8	852.7	60.1	*9.9*	559.2	22.6
ANDVORD2-49	996	87951	7.0	16.1904	2.2	0.8134	3.1	0.0955	2.2	0.70	588.0	12.2	604.4	14.0	666.0	46.9	11.7	588.0	12.2

GRAIN	U (ppm)	RATIOS 206Pb/204Pb	U/Th	206Pb*/207Pb*	± (%)	207Pb*/235U*	± (%)	206Pb*/238U	± (%)	error corr.	APPARENT AGES (Ma) 206Pb*/238U*	± (Ma)	207Pb*/235U	± (Ma)	206Pb*/207Pb*	± (Ma)	disc (%)	Preferred Age (Ma)	± (Ma)
ANDVORD2-70	265	46968	3.2	15.8039	2.4	1.0296	3.0	0.1180	1.9	0.61	719.1	12.6	718.7	15.5	717.5	50.6	-0.2	719.1	12.6
ANDVORD2-30	165	30717	2.1	15.1347	3.6	1.0899	4.5	0.1196	2.7	0.60	728.5	18.9	748.5	24.0	808.7	75.6	9.9	728.5	18.9
ANDVORD2-24	455	110940	2.2	15.8621	2.0	1.0443	2.1	0.1201	0.8	0.38	731.4	5.7	726.1	11.1	709.7	42.1	-3.1	731.4	5.7
ANDVORD2-38	279	38115	2.6	13.9544	1.8	1.3761	2.9	0.1393	2.2	0.78	840.6	17.6	878.8	16.8	976.3	36.5	13.9	840.6	17.6
ANDVORD2-85	349	186453	4.2	14.1512	0.8	1.4169	1.3	0.1454	1.0	0.78	875.3	8.3	896.1	7.7	947.7	16.8	7.6	875.3	8.3
ANDVORD2-50	706	168909	2.8	13.9880	2.5	1.5283	2.7	0.1550	1.1	0.42	929.2	9.9	941.8	16.6	971.4	50.0	4.3	929.2	9.9
ANDVORD2-72	1341	34242	3.3	13.4163	3.7	1.6509	3.9	0.1606	1.1	0.28	960.3	9.9	989.9	24.6	1056.0	75.2	9.1	960.3	9.9
ANDVORD2-55	308	35313	3.7	13.1187	3.9	1.7280	4.3	0.1644	1.9	0.45	981.2	17.7	1019.0	27.9	1101.0	77.6	10.9	981.2	17.7
ANDVORD2-28	506	145068	1.6	12.6251	3.4	1.8092	4.1	0.1657	2.3	0.56	988.2	20.8	1048.8	26.5	1177.3	66.5	16.1	988.2	20.8
ANDVORD2-03	735	138666	6.8	13.5875	2.7	1.7393	3.4	0.1714	2.0	0.60	1019.8	19.1	1023.2	21.8	1030.4	55.0	1.0	1030.4	55.0
ANDVORD2-99	111	38565	1.3	13.5595	3.3	1.7372	3.6	0.1708	1.3	0.38	1016.8	12.6	1022.4	23.0	1034.6	66.8	1.7	1034.6	66.8
ANDVORD2-41	763	145227	4.9	13.2364	1.7	1.9237	1.9	0.1847	0.8	0.43	1092.4	8.1	1089.3	12.5	1083.1	33.7	-0.9	1083.1	33.7
ANDVORD2-09	204	71451	1.9	12.1884	2.7	2.4065	2.8	0.2127	1.0	0.34	1243.4	10.7	1244.5	20.3	1246.6	52.1	0.3	1246.6	52.1
ANDVORD2-04	397	79674	2.8	11.9423	0.9	2.5274	1.4	0.2189	1.1	0.79	1276.1	12.5	1279.9	10.0	1286.4	16.6	0.8	1286.4	16.6
ANDVORD2-92	276	24606	3.1	11.0435	1.7	3.0288	2.0	0.2426	1.0	0.49	1400.1	12.1	1414.9	15.0	1437.2	32.7	2.6	1437.2	32.7
ANDVORD2-77	696	260100	4.8	8.2539	1.8	5.8021	2.2	0.3473	1.2	0.54	1921.8	19.4	1946.7	18.7	1973.3	32.4	2.6	1973.3	32.4
SAMPLE FLORA2, Botany Bay Group, Mount Flora Formation, 63˚ 24.815' S, 57˚ 1.293' W																			
FLORA2-60	756	29187	1.6	20.2207	2.1	0.1733	2.6	0.0254	1.5	0.59	161.8	2.4	162.3	3.9	169.4	48.3	4.5	161.8	2.4
FLORA2-52	501	25920	3.6	20.6261	2.7	0.1759	3.0	0.0263	1.3	0.44	167.5	2.2	164.5	4.6	122.8	63.4	*-1.8*	167.5	2.2
FLORA2-14	434	31152	1.7	19.3465	1.6	0.3050	5.6	0.0428	5.3	0.96	270.1	14.1	270.3	13.2	271.6	37.2	0.6	270.1	14.1
FLORA2-27	95	21585	1.4	20.1268	9.3	0.2981	10.4	0.0435	4.5	0.43	274.5	12.1	264.9	24.1	180.3	217.7	*-3.6*	*274.5*	*12.1*
FLORA2-24	91	21060	2.0	18.8507	15.7	0.3207	16.4	0.0438	4.8	0.29	276.6	13.0	282.4	40.6	330.8	358.5	16.4	276.6	13.0
FLORA2-97	406	31581	1.5	19.0036	3.6	0.3189	3.8	0.0440	1.2	0.32	277.3	3.3	281.0	9.4	312.5	82.6	11.3	277.3	3.3
FLORA2-66	167	16746	1.0	18.8597	6.8	0.3220	7.0	0.0440	1.7	0.24	277.9	4.7	283.5	17.4	329.8	155.0	15.7	277.9	4.7
FLORA2-41	333	31839	1.1	18.8533	4.0	0.3222	4.2	0.0441	1.2	0.28	277.9	3.2	283.6	10.3	330.5	91.1	15.9	277.9	3.2
FLORA2-29	426	177297	1.4	19.3960	3.5	0.3137	3.6	0.0441	0.7	0.20	278.4	2.0	277.0	8.8	265.8	81.3	-4.7	278.4	2.0
FLORA2-49	260	46227	1.2	18.8288	4.3	0.3233	4.9	0.0442	2.3	0.48	278.5	6.3	284.5	12.1	333.5	96.8	16.5	278.5	6.3
FLORA2-31	311	98973	0.7	19.8145	3.6	0.3077	4.0	0.0442	1.6	0.40	278.9	4.4	272.4	9.5	216.6	84.3	*-2.4*	*278.9*	*4.4*
FLORA2-25	92	7827	1.4	20.0571	13.0	0.3053	13.3	0.0444	3.1	0.23	280.1	8.4	270.5	31.7	188.3	303.0	*-3.5*	*280.1*	*8.4*
FLORA2-69	481	80361	1.6	19.5420	2.6	0.3135	3.4	0.0444	2.2	0.64	280.3	6.1	276.9	8.3	248.6	60.8	*-1.2*	*280.3*	*6.1*
FLORA2-04	214	44958	1.6	19.1996	9.6	0.3195	9.8	0.0445	1.7	0.18	280.6	4.7	281.5	24.0	289.1	220.3	2.9	280.6	4.7
FLORA2-19	138	14745	1.0	18.7489	5.7	0.3273	6.1	0.0445	2.4	0.39	280.7	6.6	287.5	15.4	343.1	128.1	18.2	280.7	6.6
FLORA2-94	186	54819	1.4	19.8418	9.8	0.3104	9.9	0.0447	1.0	0.10	281.7	2.7	274.5	23.7	213.4	227.7	*-2.6*	*281.7*	*2.7*
FLORA2-68	99	8730	1.4	17.5323	7.9	0.3515	8.3	0.0447	2.5	0.30	281.9	7.0	305.8	22.0	493.0	175.2	*7.8*	281.9	7.0
FLORA2-50	208	142950	1.4	19.2112	5.1	0.3208	5.5	0.0447	2.0	0.37	281.9	5.6	282.5	13.5	287.7	116.4	2.0	281.9	5.6
FLORA2-73	311	38520	1.3	19.6346	3.4	0.3140	3.5	0.0447	0.9	0.25	282.0	2.5	277.3	8.5	237.7	78.6	*-1.7*	*282.0*	*2.5*
FLORA2-30	219	79557	1.8	18.7598	13.9	0.3286	13.9	0.0447	1.0	0.07	282.0	2.8	288.5	34.9	341.8	315.1	17.5	282.0	2.8
FLORA2-71	279	23457	1.0	18.4775	11.2	0.3337	11.2	0.0447	1.4	0.12	282.0	3.8	292.4	28.6	376.0	251.9	25.0	282.0	3.8
FLORA2-15	983	18531	1.1	17.8151	9.1	0.3463	9.5	0.0447	3.0	0.31	282.2	8.2	302.0	24.9	457.6	201.4	*6.5*	282.2	8.2
FLORA2-34	419	18498	1.1	18.9496	8.4	0.3256	8.5	0.0448	1.4	0.16	282.2	3.8	286.2	21.2	319.0	190.5	11.5	282.2	3.8
FLORA2-67	706	45519	1.2	19.3572	2.7	0.3193	2.9	0.0448	1.0	0.35	282.7	2.8	281.4	7.1	270.4	62.2	-4.6	282.7	2.8
FLORA2-05	180	24702	1.8	20.2808	6.0	0.3048	6.1	0.0448	0.9	0.14	282.7	2.4	270.1	14.4	162.5	140.3	*-4.7*	*282.7*	*2.4*
FLORA2-100	300	21618	0.8	18.8427	3.8	0.3281	4.1	0.0448	1.4	0.35	282.8	3.9	288.1	10.3	331.8	87.0	14.8	282.8	3.9
FLORA2-48	198	44382	0.8	19.5092	3.3	0.3176	3.6	0.0449	1.3	0.37	283.4	3.7	280.1	8.7	252.4	76.1	*-1.2*	*283.4*	*3.7*
FLORA2-40	38	5577	0.6	17.0817	33.4	0.3632	34.1	0.0450	6.5	0.19	283.7	18.0	314.6	92.4	550.1	749.7	*9.8*	283.7	18.0
FLORA2-89	421	33669	1.7	18.9245	3.2	0.3282	3.8	0.0450	2.0	0.52	284.0	5.4	288.2	9.4	322.0	73.2	11.8	284.0	5.4
FLORA2-53	90	15411	1.3	18.2899	16.0	0.3399	16.0	0.0451	1.3	0.08	284.3	3.7	297.1	41.3	398.9	359.7	28.7	284.3	3.7
FLORA2-26	270	26973	1.4	18.8732	5.0	0.3296	5.1	0.0451	1.0	0.20	284.5	2.9	289.3	12.8	328.1	112.7	13.3	284.5	2.9
FLORA2-01	388	30669	1.5	19.1943	4.0	0.3242	4.7	0.0451	2.4	0.51	284.6	6.7	285.2	11.6	289.7	91.7	1.8	284.6	6.7
FLORA2-91	129	9507	2.2	20.2965	9.3	0.3067	9.8	0.0452	2.9	0.30	284.7	8.2	271.6	23.3	160.7	218.5	*-4.8*	*284.7*	*8.2*
FLORA2-23	129	13839	1.4	20.3072	10.2	0.3070	10.3	0.0452	1.3	0.13	285.0	3.7	271.8	24.5	159.4	238.4	*-4.9*	*285.0*	*3.7*
FLORA2-70	561	49485	0.9	19.2569	1.8	0.3237	2.1	0.0452	1.1	0.51	285.1	3.0	284.8	5.2	282.3	40.8	-1.0	285.1	3.0
FLORA2-42	715	61254	1.0	19.4162	2.6	0.3214	3.4	0.0453	2.1	0.62	285.4	5.8	283.0	8.3	263.4	60.5	*-0.8*	*285.4*	*5.8*
FLORA2-92	177	21147	1.2	19.3862	12.0	0.3223	12.1	0.0453	1.7	0.14	285.7	4.6	283.7	30.0	267.0	276.4	*-0.7*	*285.7*	*4.6*
FLORA2-77	114	28704	1.6	19.9868	5.6	0.3129	5.8	0.0454	1.5	0.26	286.0	4.3	276.4	14.1	196.5	131.1	*-3.4*	*286.0*	*4.3*
FLORA2-44	223	16083	1.4	18.6545	5.3	0.3356	6.4	0.0454	3.6	0.56	286.2	10.2	293.8	16.5	354.5	120.5	19.3	286.2	10.2
FLORA2-07	153	5727	1.8	16.0864	9.0	0.3892	10.3	0.0454	4.9	0.48	286.3	13.8	333.8	29.2	679.8	192.3	*14.2*	286.3	13.8
FLORA2-21	236	89334	2.0	19.9499	4.8	0.3141	5.1	0.0454	1.8	0.36	286.5	5.1	277.3	12.3	200.8	110.4	*-3.3*	*286.5*	*5.1*
FLORA2-93	844	37959	1.2	18.8488	1.9	0.3327	2.4	0.0455	1.5	0.63	286.7	4.3	291.6	6.1	331.1	42.2	13.4	286.7	4.3
FLORA2-86	230	49848	0.8	19.9506	6.1	0.3151	6.4	0.0456	2.0	0.32	287.4	5.7	278.1	15.7	200.7	142.0	*-3.3*	*287.4*	*5.7*
FLORA2-56	111	22398	1.1	17.3473	10.9	0.3645	11.0	0.0459	1.2	0.10	289.0	3.3	315.6	29.7	516.3	240.0	*8.4*	289.0	3.3
FLORA2-47	219	158928	1.2	18.7444	8.6	0.3374	8.7	0.0459	1.5	0.17	289.1	4.2	295.2	22.2	343.7	193.8	15.9	289.1	4.2
FLORA2-08	507	65958	1.4	18.9940	2.2	0.3330	3.6	0.0459	2.8	0.78	289.2	7.9	291.9	9.1	313.6	50.9	7.8	289.2	7.9
FLORA2-90	168	211560	1.2	17.9838	7.6	0.3521	7.6	0.0459	0.6	0.08	289.4	1.8	306.3	20.1	436.6	169.0	*5.5*	289.4	1.8
FLORA2-75	795	43053	1.3	18.8591	3.4	0.3358	3.8	0.0459	1.7	0.44	289.5	4.8	294.0	9.8	329.8	77.9	12.2	289.5	4.8
FLORA2-35	131	10347	1.7	18.4452	7.1	0.3435	7.4	0.0460	2.1	0.28	289.6	5.9	299.8	19.2	380.0	159.4	23.8	289.6	5.9
FLORA2-85	107	21306	1.1	19.5534	8.6	0.3241	8.7	0.0460	1.4	0.16	289.7	3.8	285.0	21.5	247.2	197.2	*-1.6*	*289.7*	*3.8*
FLORA2-55	150	40899	1.9	18.2721	6.9	0.3476	7.0	0.0461	1.3	0.19	290.3	3.8	302.9	18.3	401.1	154.2	27.6	290.3	3.8
FLORA2-43	128	59256	1.8	19.9478	10.1	0.3189	10.1	0.0461	0.9	0.08	290.8	2.4	281.1	24.9	201.0	235.0	*-3.5*	*290.8*	*2.4*
FLORA2-88	17	2865	0.8	19.0754	40.9	0.3336	41.1	0.0462	4.2	0.10	290.8	11.9	292.3	104.9	303.9	970.3	4.3	290.8	11.9
FLORA2-45	132	17022	1.4	18.7031	9.5	0.3406	9.7	0.0462	2.0	0.21	291.2	5.8	297.7	25.1	348.6	215.2	16.5	291.2	5.8
FLORA2-87	117	17256	1.7	19.5380	6.9	0.3273	7.7	0.0464	3.5	0.46	292.3	10.1	287.5	19.3	249.0	158.2	*-1.7*	*292.3*	*10.1*
FLORA2-82	119	9189	1.0	19.1943	9.2	0.3332	9.2	0.0464	1.0	0.11	292.3	3.0	292.0	23.4	289.7	209.8	-0.9	292.3	3.0
FLORA2-62	170	19152	1.4	19.5329	4.3	0.3277	4.5	0.0464	1.5	0.33	292.5	4.3	287.8	11.3	249.6	97.9	*-1.6*	*292.5*	*4.3*
FLORA2-51	144	13986	2.0	20.2768	6.2	0.3159	6.4	0.0465	1.7	0.27	292.7	5.0	278.7	15.7	162.9	145.2	*-5.0*	292.7	5.0
FLORA2-54	642	87627	4.0	19.0144	2.3	0.3369	2.6	0.0465	1.3	0.49	292.8	3.6	294.8	6.7	311.2	51.9	5.9	292.8	3.6
FLORA2-09	113	24771	1.5	19.8983	12.5	0.3240	12.5	0.0468	0.8	0.06	294.6	2.2	285.0	31.2	206.8	291.4	*-3.4*	*294.6*	*2.2*
FLORA2-13	107	23763	1.2	21.1709	11.9	0.3048	12.4	0.0468	3.7	0.30	294.9	10.8	270.2	29.5	61.1	283.8	*-9.1*	294.9	10.8
FLORA2-95	398	58248	2.2	19.0604	3.0	0.3400	3.3	0.0470	1.4	0.41	296.1	3.9	297.2	8.4	305.7	68.0	3.1	296.1	3.9
FLORA2-59	176	43926	1.8	18.4470	7.5	0.3544	7.5	0.0474	0.8	0.11	298.6	2.4	308.0	20.0	379.7	168.7	21.4	298.6	2.4
FLORA2-99	204	5154	1.6	17.1320	5.4	0.3834	5.6	0.0476	1.4	0.25	300.0	4.0	329.6	15.7	543.7	118.1	*9.0*	300.0	4.0
FLORA2-12	503	65142	2.2	17.3335	8.8	0.3808	9.4	0.0479	3.3	0.35	301.4	9.8	327.6	26.5	518.0	194.5	*8.0*	301.4	9.8
FLORA2-79	206	23775	1.7	19.6498	4.9	0.3362	6.2	0.0479	3.7	0.60	301.7	10.9	294.3	15.8	235.9	114.0	*-2.5*	*301.7*	*10.9*
FLORA2-63	588	44163	2.3	19.2597	2.4	0.3459	2.6	0.0483	1.2	0.45	304.2	3.5	301.7	6.9	281.9	54.1	*-0.8*	*304.2*	*3.5*
FLORA2-98	117	24639	2.0	17.9202	7.1	0.3719	7.4	0.0483	1.9	0.26	304.3	5.6	321.1	20.2	444.5	158.2	*5.2*	304.3	5.6
FLORA2-83	1618	48720	8.2	18.5776	2.4	0.3898	2.7	0.0525	1.1	0.40	330.0	3.4	334.2	7.6	363.9	55.1	9.3	330.0	3.4
FLORA2-6	87	11343	2.3	18.5987	10.1	0.4509	10.4	0.0608	2.7	0.26	380.6	10.1	377.9	33.0	361.3	227.9	*-0.7*	*380.6*	*10.1*
FLORA2-61	958	202485	2.0	18.2840	2.0	0.4616	2.4	0.0612	1.4	0.58	383.0	5.3	385.3	7.8	399.7	44.6	4.2	383.0	5.3
FLORA2-11	104	20322	2.8	14.8883	25.6	0.5686	25.7	0.0614	2.2	0.09	384.1	8.4	457.1	94.8	842.9	541.1	*16.0*	384.1	8.4
FLORA2-17	237	29442	2.0	18.5729	4.5	0.4598	4.6	0.0619	1.2	0.25	387.4	4.3	384.1	14.8	364.4	100.9	*-0.9*	*387.4*	*4.3*
FLORA2-39	157	19065	1.8	18.5148	7.8	0.4679	8.0	0.0628	1.8	0.23	392.8	6.9	389.7	25.9	371.5	175.8	*-0.8*	*392.8*	*6.9*
FLORA2-84	364	31242	1.8	17.9490	4.6	0.4833	6.0	0.0629	3.9	0.64	393.3	14.8	400.3	19.9	440.9	102.7	10.8	393.3	14.8
FLORA2-72	358	17790	1.2	18.2126	3.1	0.4776	3.2	0.0631	0.9	0.27	394.4	3.3	396.5	10.4	408.4	68.4	3.4	394.4	3.3
FLORA2-74	456	48714	1.9	18.2080	2.6	0.4804	3.0	0.0634	1.4	0.47	396.5	5.3	398.4	9.7	409.0	58.5	3.0	396.5	5.3

GRAIN	U (ppm)	RATIOS									APPARENT AGES (Ma)						disc (%)	Preferred Age (Ma)	± (Ma)
		206Pb / 204Pb	U / Th	206Pb* / 207Pb*	± (%)	207Pb* / 235U*	± (%)	206Pb* / 238U	± (%)	error corr.	206Pb* / 238U*	± (Ma)	207Pb* / 235U	± (Ma)	206Pb* / 207Pb*	± (Ma)			
FLORA2-32	1002	57732	1.8	17.9606	3.0	0.5045	3.8	0.0657	2.4	0.62	410.3	9.3	414.8	12.9	439.5	65.7	6.6	410.3	9.3
FLORA2-76	71	9846	1.4	17.7452	9.7	0.5152	9.9	0.0663	2.2	0.22	413.8	8.7	421.9	34.3	466.3	214.9	11.3	413.8	8.7
FLORA2-65	980	81738	2.3	17.9358	2.4	0.5116	2.7	0.0666	1.1	0.42	415.4	4.5	419.6	9.2	442.6	54.3	6.1	415.4	4.5
FLORA2-28	1610	27342	2.3	17.5767	2.8	0.5315	3.8	0.0678	2.5	0.65	422.6	10.0	432.8	13.2	487.4	62.8	13.3	422.6	10.0
FLORA2-80	283	37758	2.4	17.6256	4.6	0.5813	4.6	0.0743	0.8	0.18	462.0	3.6	465.3	17.3	481.3	100.7	4.0	462.0	3.6
FLORA2-20	105	18552	1.8	17.7488	4.8	0.5949	5.1	0.0766	1.6	0.32	475.7	7.5	474.0	19.3	465.9	106.9	-2.1	475.7	7.5
FLORA2-16	328	59214	3.0	17.2135	2.1	0.6138	3.2	0.0766	2.4	0.76	476.0	11.2	485.9	12.3	533.3	45.2	10.8	476.0	11.2
FLORA2-96	361	64908	2.4	17.6769	1.8	0.6030	2.0	0.0773	0.7	0.36	480.0	3.3	479.1	7.5	474.8	40.5	-1.1	480.0	3.3
FLORA2-03	244	21876	1.6	17.4182	3.1	0.6208	3.3	0.0784	1.2	0.36	486.7	5.6	490.3	12.9	507.3	67.9	4.1	486.7	5.6
FLORA2-18	375	219606	2.0	17.5790	1.2	0.6188	1.6	0.0789	1.1	0.68	489.5	5.2	489.1	6.4	487.1	26.7	-0.5	489.5	5.2
FLORA2-02	47	8628	1.2	18.8041	12.8	0.6337	13.1	0.0864	3.1	0.24	534.3	16.0	498.4	51.7	336.5	290.0	*-7.2*	*534.3*	*16.0*
FLORA2-36	274	243003	26.0	17.1615	2.0	0.7248	2.4	0.0902	1.3	0.55	556.8	7.1	553.5	10.3	539.9	44.0	-3.1	556.8	7.1
FLORA2-46	217	164742	4.5	14.2224	2.3	1.3768	3.8	0.1420	3.0	0.80	856.1	24.4	879.1	22.3	937.4	46.2	8.7	856.1	24.4
FLORA2-33	92	22017	2.6	13.7692	3.3	1.5769	3.4	0.1575	0.9	0.25	942.7	7.5	961.1	21.3	1003.5	67.2	6.1	942.7	7.5
FLORA2-57	263	77100	2.6	13.5898	3.7	1.6468	4.0	0.1623	1.5	0.37	969.6	13.4	988.3	25.3	1030.1	75.0	5.9	969.6	13.4
FLORA2-78	689	192834	3.7	13.4256	2.0	1.8433	2.3	0.1795	1.0	0.44	1064.1	9.7	1061.0	14.9	1054.6	40.9	-0.9	1054.6	40.9
FLORA2-37	232	213360	3.2	13.4170	1.1	1.8379	2.0	0.1788	1.7	0.82	1060.6	16.1	1059.1	13.2	1055.9	23.0	-0.4	1055.9	23.0
FLORA2-10	193	61473	1.6	13.0758	3.0	1.9915	3.7	0.1889	2.2	0.58	1115.2	22.0	1112.6	25.1	1107.6	60.6	-0.7	1107.6	60.6
FLORA2-38	559	108210	7.7	12.7200	3.1	2.1419	3.6	0.1976	1.9	0.53	1162.4	20.5	1162.4	25.2	1162.5	61.3	0.0	1162.5	61.3
FLORA2-58	90	53067	3.5	9.5963	1.6	4.0969	2.5	0.2851	1.9	0.77	1617.2	27.5	1653.7	20.4	1700.3	29.3	4.9	1700.3	29.3
FLORA2-81	126	118200	1.6	6.9266	3.3	7.2492	5.9	0.3642	4.9	0.83	2001.9	83.8	2142.6	52.4	2280.3	56.5	12.2	2280.3	56.5

All uncertainties are reported at the 1-sigma level, and include only measurement errors. Systematic errors would increase age uncertainties by 1-2%.

U concentration and U/Th are calibrated relative to a Sri Lanka standard zircon, and are accurate to ~20%.

Data is corrected for common Pb using measured ^{204}Pb, with composition interpreted from [Stacey, J.S., & Kramers, J.D., Approximation of terrestrial lead isotope evolution by a two−stage model, *Earth and Planetary Science Letters* **26,** 207−221 (1975)] and uncertainties of 1.0 for ^{206}Pb/ ^{204}Pb, 0.3 for ^{207}Pb/ ^{204}Pb, and 2.0 for ^{208}Pb/ ^{204}Pb.

U/Pb and ^{206}Pb/ ^{207}Pb fractionation is calibrated relative to fragments of a large Sri Lanka zircon of 564 ± 4 Ma (2-sigma).

U decay constants and compositions as follows: ^{238}U = 9.8485 x 10^{-10}, ^{235}U = 1.55125 x 10^{-10}, ^{238}U/ ^{235}U = 137.88

Discordance is calculated between ^{206}Pb*/^{238}U and ^{206}Pb*/^{207}Pb* except for young grains with large ^{206}Pb*/^{207}Pb* errors, in which case discordance is measured between ^{206}Pb*/^{238}U and ^{207}Pb*/^{235}U, and are indicated by italics.

Due to high errors or discordance, data in red are not used in probability plots, K-S tests or interpretations.