Data S2. Distance-axis endpoints

Every distance-axis endpoint under both unit definitions, both capture-area sets and both matching rules where both exist. 144 cells.

item	kind	matching rule	units	n units	combined standardized statistic	null q97.5	null q84	detection limit per unit	direction	verdict	restriction
CDKN1A	gene	fixed	capture areas	6	2.8521	1.8308	1.1983	0.747	away from scar	exceeds null	all ten capture areas
CDKN1A	gene	fixed	capture areas	4	2.1084	1.8804	1.2135	0.94	away from scar	exceeds null	eight documented capture areas
CDKN1A	gene	fixed	components	10	3.2729	2.0253	1.3913	0.64	away from scar	exceeds null	all ten capture areas
CDKN1A	gene	fixed	components	7	2.4946	2.0959	1.3905	0.792	away from scar	exceeds null	eight documented capture areas
CDKN1A	gene	quantile	capture areas	6	2.7627	1.8336	1.1901	0.749	away from scar	exceeds null	all ten capture areas
CDKN1A	gene	quantile	capture areas	4	2.0724	1.9538	1.1775	0.977	away from scar	exceeds null	eight documented capture areas
CDKN1A	gene	quantile	components	10	3.2084	2.1607	1.4072	0.683	away from scar	exceeds null	all ten capture areas
CDKN1A	gene	quantile	components	7	2.4904	2.348	1.3943	0.887	away from scar	exceeds null	eight documented capture areas
CDKN2A	gene	fixed	capture areas							not analyzed	all ten capture areas
CDKN2A	gene	fixed	capture areas							not analyzed	eight documented capture areas
CDKN2A	gene	fixed	components	1						not analyzed	all ten capture areas
CDKN2A	gene	fixed	components	1						not analyzed	eight documented capture areas
CDKN2A	gene	quantile	capture areas							not analyzed	all ten capture areas
CDKN2A	gene	quantile	capture areas							not analyzed	eight documented capture areas
CDKN2A	gene	quantile	components	1						not analyzed	all ten capture areas
CDKN2A	gene	quantile	components	1						not analyzed	eight documented capture areas
COL1A1	gene	fixed	capture areas	4	-8.5477	2.3915	1.3061	1.196	toward scar	exceeds null	all ten capture areas
COL1A1	gene	fixed	capture areas	3	-6.9523	2.2276	1.3918	1.286	toward scar	exceeds null	eight documented capture areas
COL1A1	gene	fixed	components	4	-8.5477	2.3915	1.3061	1.196	toward scar	exceeds null	all ten capture areas
COL1A1	gene	fixed	components	3	-6.9523	2.2276	1.3918	1.286	toward scar	exceeds null	eight documented capture areas
COL1A1	gene	quantile	capture areas	5	-9.3675	1.4079	0.9972	0.63	toward scar	exceeds null	all ten capture areas
COL1A1	gene	quantile	capture areas	4	-7.7591	1.3801	1.0933	0.69	toward scar	exceeds null	eight documented capture areas
COL1A1	gene	quantile	components	8	-12.058	1.6853	1.1825	0.596	toward scar	exceeds null	all ten capture areas
COL1A1	gene	quantile	components	7	-10.8388	1.8558	1.1565	0.701	toward scar	exceeds null	eight documented capture areas
CYB5A	gene	fixed	capture areas	2	-0.007	2.3069	1.2036	1.631	toward scar	flat	all ten capture areas
CYB5A	gene	fixed	capture areas							not analyzed	eight documented capture areas
CYB5A	gene	fixed	components	2	-0.007	2.3069	1.2036	1.631	toward scar	flat	all ten capture areas
CYB5A	gene	fixed	components	1						not analyzed	eight documented capture areas
CYB5A	gene	quantile	capture areas	6	0.548	2.0302	1.361	0.829	away from scar	flat	all ten capture areas
CYB5A	gene	quantile	capture areas	4	0.914	1.8572	1.3154	0.929	away from scar	flat	eight documented capture areas
CYB5A	gene	quantile	components	10	0.7524	2.1823	1.9566	0.69	away from scar	flat	all ten capture areas
CYB5A	gene	quantile	components	7	0.932	2.3598	1.5867	0.892	away from scar	flat	eight documented capture areas
CYB5R3	gene	fixed	capture areas	6	-1.6622	1.7934	1.1153	0.732	toward scar	inconclusive	all ten capture areas
CYB5R3	gene	fixed	capture areas	4	-1.0457	1.8245	1.158	0.912	toward scar	flat	eight documented capture areas
CYB5R3	gene	fixed	components	10	-2.1568	2.3454	1.3051	0.742	toward scar	inconclusive	all ten capture areas

item	kind	matching rule	units	n units	combined standardized statistic	null q97.5	null q84	detection limit per unit	direction	verdict	restriction
CYB5R3	gene	fixed	components	7	-1.1524	2.1921	1.4581	0.829	toward scar	flat	eight documented capture areas
CYB5R3	gene	quantile	capture areas	6	-1.6611	1.8371	1.1414	0.75	toward scar	inconclusive	all ten capture areas
CYB5R3	gene	quantile	capture areas	4	-0.9546	1.8259	1.1629	0.913	toward scar	flat	eight documented capture areas
CYB5R3	gene	quantile	components	10	-2.1885	2.2045	1.3074	0.697	toward scar	inconclusive	all ten capture areas
CYB5R3	gene	quantile	components	7	-1.1317	2.2071	1.3262	0.834	toward scar	flat	eight documented capture areas
GDF15	gene	fixed	capture areas	3	-0.8836	2.0472	1.2616	1.182	toward scar	flat	all ten capture areas
GDF15	gene	fixed	capture areas	2	-1.0941	2.4498	1.3822	1.732	toward scar	flat	eight documented capture areas
GDF15	gene	fixed	components	4	-0.7568	2.1276	1.4775	1.064	toward scar	flat	all ten capture areas
GDF15	gene	fixed	components	2	-1.0941	2.4498	1.3822	1.732	toward scar	flat	eight documented capture areas
GDF15	gene	quantile	capture areas	3	-0.8876	1.9224	1.2832	1.11	toward scar	flat	all ten capture areas
GDF15	gene	quantile	capture areas	2	-1.0123	2.3211	1.4712	1.641	toward scar	flat	eight documented capture areas
GDF15	gene	quantile	components	4	-0.8216	1.9881	1.3649	0.994	toward scar	flat	all ten capture areas
GDF15	gene	quantile	components	2	-1.0123	2.3211	1.4712	1.641	toward scar	flat	eight documented capture areas
GPAM	gene	fixed	capture areas	6	-0.2861	2.053	1.453	0.838	toward scar	flat	all ten capture areas
GPAM	gene	fixed	capture areas	4	-0.3372	1.6713	1.2162	0.836	toward scar	flat	eight documented capture areas
GPAM	gene	fixed	components	10	-0.9285	2.3147	1.4936	0.732	toward scar	flat	all ten capture areas
GPAM	gene	fixed	components	7	-1.1768	2.1306	1.5685	0.805	toward scar	flat	eight documented capture areas
GPAM	gene	quantile	capture areas	6	-0.1861	1.8491	1.2223	0.755	toward scar	flat	all ten capture areas
GPAM	gene	quantile	capture areas	4	-0.1797	1.7435	1.1865	0.872	toward scar	flat	eight documented capture areas
GPAM	gene	quantile	components	10	-0.7632	1.878	1.4054	0.594	toward scar	flat	all ten capture areas
GPAM	gene	quantile	components	7	-0.9474	2.0661	1.437	0.781	toward scar	flat	eight documented capture areas
MTARC1	gene	fixed	capture areas	6	1.9066	2.3125	1.1622	0.944	away from scar	inconclusive	all ten capture areas
MTARC1	gene	fixed	capture areas	4	1.9562	2.2727	1.2538	1.136	away from scar	inconclusive	eight documented capture areas
MTARC1	gene	fixed	components	10	3.2813	2.54	1.495	0.803	away from scar	exceeds null	all ten capture areas
MTARC1	gene	fixed	components	7	2.9405	2.6342	1.5486	0.996	away from scar	exceeds null	eight documented capture areas
MTARC1	gene	quantile	capture areas	6	1.7816	1.9181	1.2434	0.783	away from scar	inconclusive	all ten capture areas
MTARC1	gene	quantile	capture areas	4	1.9115	1.9208	1.2033	0.96	away from scar	inconclusive	eight documented capture areas
MTARC1	gene	quantile	components	10	3.1294	2.1406	1.4165	0.677	away from scar	exceeds null	all ten capture areas
MTARC1	gene	quantile	components	7	2.9026	2.2725	1.3756	0.859	away from scar	exceeds null	eight documented capture areas
MTARC2	gene	fixed	capture areas	6	1.5716	1.9694	1.287	0.804	away from scar	inconclusive	all ten capture areas
MTARC2	gene	fixed	capture areas	4	1.579	1.9137	1.3086	0.957	away from scar	inconclusive	eight documented capture areas
MTARC2	gene	fixed	components	10	2.4328	2.1357	1.2977	0.675	away from scar	exceeds null	all ten capture areas
MTARC2	gene	fixed	components	7	2.2861	2.2569	1.3239	0.853	away from scar	exceeds null	eight documented capture areas
MTARC2	gene	quantile	capture areas	6	1.3747	1.5364	0.9499	0.627	away from scar	inconclusive	all ten capture areas
MTARC2	gene	quantile	capture areas	4	1.2642	1.8552	1.1964	0.928	away from scar	inconclusive	eight documented capture areas
MTARC2	gene	quantile	components	10	2.2013	1.7762	1.3783	0.562	away from scar	exceeds null	all ten capture areas
MTARC2	gene	quantile	components	7	1.9556	2.3154	1.327	0.875	away from scar	inconclusive	eight documented capture areas

item	kind	matching rule	units	n units	combined standardized statistic	null q97.5	null q84	detection limit per unit	direction	verdict	restriction
POR	gene	fixed	capture areas	6	1.1994	1.5074	1.1305	0.615	away from scar	inconclusive	all ten capture areas
POR	gene	fixed	capture areas	4	0.9034	1.8711	1.1347	0.936	away from scar	flat	eight documented capture areas
POR	gene	fixed	components	10	1.2638	1.9499	1.2664	0.617	away from scar	flat	all ten capture areas
POR	gene	fixed	components	7	0.8947	1.999	1.2949	0.756	away from scar	flat	eight documented capture areas
POR	gene	quantile	capture areas	6	1.2055	2.0917	1.1691	0.854	away from scar	inconclusive	all ten capture areas
POR	gene	quantile	capture areas	4	0.8869	1.888	1.227	0.944	away from scar	flat	eight documented capture areas
POR	gene	quantile	components	10	1.239	2.3312	1.4237	0.737	away from scar	flat	all ten capture areas
POR	gene	quantile	components	7	0.8724	2.356	1.2952	0.89	away from scar	flat	eight documented capture areas
SCD1	gene	fixed	capture areas	2	0.5548	1.691	1.5827	1.196	away from scar	flat	all ten capture areas
SCD1	gene	fixed	capture areas							not analyzed	eight documented capture areas
SCD1	gene	fixed	components	2	0.5548	1.691	1.5827	1.196	away from scar	flat	all ten capture areas
SCD1	gene	fixed	components	1						not analyzed	eight documented capture areas
SCD1	gene	quantile	capture areas	6	-0.5089	1.7246	1.1533	0.704	toward scar	flat	all ten capture areas
SCD1	gene	quantile	capture areas	4	-0.7008	1.8195	1.1695	0.91	toward scar	flat	eight documented capture areas
SCD1	gene	quantile	components	10	-1.7499	2.2571	1.5649	0.714	toward scar	inconclusive	all ten capture areas
SCD1	gene	quantile	components	7	-1.9752	2.2924	1.4895	0.866	toward scar	inconclusive	eight documented capture areas
SERPINE1	gene	fixed	capture areas	6	0.8602	1.7061	1.1789	0.697	away from scar	flat	all ten capture areas
SERPINE1	gene	fixed	capture areas	4	0.0429	1.9805	1.1182	0.99	away from scar	flat	eight documented capture areas
SERPINE1	gene	fixed	components	10	0.6002	1.9371	1.3285	0.613	away from scar	flat	all ten capture areas
SERPINE1	gene	fixed	components	7	-0.3502	2.1031	1.3843	0.795	toward scar	flat	eight documented capture areas
SERPINE1	gene	quantile	capture areas	6	0.7695	1.7851	1.1828	0.729	away from scar	flat	all ten capture areas
SERPINE1	gene	quantile	capture areas	4	-0.1116	1.9193	1.2472	0.96	toward scar	flat	eight documented capture areas
SERPINE1	gene	quantile	components	10	0.5065	2.3772	1.3624	0.752	away from scar	flat	all ten capture areas
SERPINE1	gene	quantile	components	7	-0.4821	2.2449	1.5579	0.848	toward scar	flat	eight documented capture areas
TBX3	gene	fixed	capture areas	6	0.3581	1.9348	1.2139	0.79	away from scar	flat	all ten capture areas
TBX3	gene	fixed	capture areas	4	0.5854	1.7459	1.1037	0.873	away from scar	flat	eight documented capture areas
TBX3	gene	fixed	components	10	0.5955	2.3644	1.4811	0.748	away from scar	flat	all ten capture areas
TBX3	gene	fixed	components	7	0.4807	1.989	1.3186	0.752	away from scar	flat	eight documented capture areas
TBX3	gene	quantile	capture areas	6	0.3239	1.9817	1.1301	0.809	away from scar	flat	all ten capture areas
TBX3	gene	quantile	capture areas	4	0.5487	1.8097	1.1984	0.905	away from scar	flat	eight documented capture areas
TBX3	gene	quantile	components	10	0.5249	2.172	1.3913	0.687	away from scar	flat	all ten capture areas
TBX3	gene	quantile	components	7	0.4222	2.0722	1.3685	0.783	away from scar	flat	eight documented capture areas
THBS2	gene	fixed	capture areas	6	-6.6571	1.6397	1.2335	0.669	toward scar	exceeds null	all ten capture areas
THBS2	gene	fixed	capture areas	4	-5.7241	1.862	1.212	0.931	toward scar	exceeds null	eight documented capture areas
THBS2	gene	fixed	components	10	-9.901	2.3179	1.3854	0.733	toward scar	exceeds null	all ten capture areas
THBS2	gene	fixed	components	7	-8.6417	2.2088	1.4723	0.835	toward scar	exceeds null	eight documented capture areas
THBS2	gene	quantile	capture areas	6	-6.3121	1.9815	1.1539	0.809	toward scar	exceeds null	all ten capture areas

item	kind	matching rule	units	n units	combined standardized statistic	null q97.5	null q84	detection limit per unit	direction	verdict	restriction
THBS2	gene	quantile	capture areas	4	-5.4905	1.7708	1.1922	0.885	toward scar	exceeds null	eight documented capture areas
THBS2	gene	quantile	components	10	-9.2484	2.1474	1.3712	0.679	toward scar	exceeds null	all ten capture areas
THBS2	gene	quantile	components	7	-8.1788	2.1431	1.4956	0.81	toward scar	exceeds null	eight documented capture areas
TIMP1	gene	fixed	capture areas	6	-7.9905	2.0531	1.1213	0.838	toward scar	exceeds null	all ten capture areas
TIMP1	gene	fixed	capture areas	4	-5.9166	1.5661	0.9702	0.783	toward scar	exceeds null	eight documented capture areas
TIMP1	gene	fixed	components	7	-8.4376	2.1451	1.1788	0.811	toward scar	exceeds null	all ten capture areas
TIMP1	gene	fixed	components	5	-6.5223	1.9289	1.1212	0.863	toward scar	exceeds null	eight documented capture areas
TIMP1	gene	quantile	capture areas	6	-8.3529	2.0978	1.343	0.856	toward scar	exceeds null	all ten capture areas
TIMP1	gene	quantile	capture areas	4	-6.6388	2.0155	1.2771	1.008	toward scar	exceeds null	eight documented capture areas
TIMP1	gene	quantile	components	10	-10.722	2.4788	1.4879	0.784	toward scar	exceeds null	all ten capture areas
TIMP1	gene	quantile	components	7	-9.0752	2.4187	1.471	0.914	toward scar	exceeds null	eight documented capture areas
fibrosis_set	module	quantile	capture areas	6	-12.2866	1.9573	1.1406	0.799	toward scar	exceeds null	all ten capture areas
fibrosis_set	module	quantile	capture areas	4	-9.9189	1.8232	1.1646	0.912	toward scar	exceeds null	eight documented capture areas
fibrosis_set	module	quantile	components	10	-15.7321	2.2681	1.4706	0.717	toward scar	exceeds null	all ten capture areas
fibrosis_set	module	quantile	components	7	-13.2968	2.0343	1.4177	0.769	toward scar	exceeds null	eight documented capture areas
hepatocyte_set	module	quantile	capture areas	6	3.2377	1.9114	1.1664	0.78	away from scar	exceeds null	all ten capture areas
hepatocyte_set	module	quantile	capture areas	4	2.265	2.1224	1.1377	1.061	away from scar	exceeds null	eight documented capture areas
hepatocyte_set	module	quantile	components	10	3.8874	1.9679	1.3192	0.622	away from scar	exceeds null	all ten capture areas
hepatocyte_set	module	quantile	components	7	3.3651	2.2076	1.2005	0.834	away from scar	exceeds null	eight documented capture areas
pls_contrast	module	quantile	capture areas	6	-2.4599	1.8859	1.1167	0.77	toward scar	exceeds null	all ten capture areas
pls_contrast	module	quantile	capture areas	4	-2.8548	1.7384	1.143	0.869	toward scar	exceeds null	eight documented capture areas
pls_contrast	module	quantile	components	10	-3.5354	2.2382	1.4105	0.708	toward scar	exceeds null	all ten capture areas
pls_contrast	module	quantile	components	7	-3.7697	2.1933	1.3876	0.829	toward scar	exceeds null	eight documented capture areas
pls_high	module	quantile	capture areas	6	-3.916	1.8784	1.1558	0.767	toward scar	exceeds null	all ten capture areas
pls_high	module	quantile	capture areas	4	-4.1075	1.857	1.1503	0.929	toward scar	exceeds null	eight documented capture areas
pls_high	module	quantile	components	10	-5.3313	2.2316	1.4088	0.706	toward scar	exceeds null	all ten capture areas
pls_high	module	quantile	components	7	-5.3077	2.1081	1.3389	0.797	toward scar	exceeds null	eight documented capture areas
pls_low	module	quantile	capture areas	6	0.0944	1.969	1.1307	0.804	away from scar	flat	all ten capture areas
pls_low	module	quantile	capture areas	4	0.4741	1.6463	1.1234	0.823	away from scar	flat	eight documented capture areas
pls_low	module	quantile	components	10	0.4581	2.3262	1.4347	0.736	away from scar	flat	all ten capture areas
pls_low	module	quantile	components	7	0.7795	2.1017	1.3594	0.794	away from scar	flat	eight documented capture areas
senescence	module	quantile	capture areas	3	0.6701	1.7389	1.0684	1.004	away from scar	flat	all ten capture areas
senescence	module	quantile	capture areas	2	0.0666	1.6341	1.1643	1.155	away from scar	flat	eight documented capture areas
senescence	module	quantile	components	5	1.7325	1.9405	1.3542	0.868	away from scar	inconclusive	all ten capture areas
senescence	module	quantile	components	3	1.0052	1.9354	1.3566	1.117	away from scar	flat	eight documented capture areas

Data S3. Register of registered endpoints

Every endpoint registered in this program, across all families, with its registered status and the deposited file it comes from.

family	endpoint	registered status	units	statistic	null q97.5	detection limit per unit	verdict	source file
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	MTARC1	registered; F-4 and the PLS modules exploratory	10	3.1294	2.1406	0.677	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	MTARC2	registered; F-4 and the PLS modules exploratory	10	2.2013	1.7762	0.562	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	CYB5R3	registered; F-4 and the PLS modules exploratory	10	-2.1885	2.2045	0.697	inconclusive	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	CYB5A	registered; F-4 and the PLS modules exploratory	10	0.7524	2.1823	0.69	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	POR	registered; F-4 and the PLS modules exploratory	10	1.239	2.3312	0.737	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	COL1A1	registered; F-4 and the PLS modules exploratory	8	-12.058	1.6853	0.596	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	THBS2	registered; F-4 and the PLS modules exploratory	10	-9.2484	2.1474	0.679	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	TIMP1	registered; F-4 and the PLS modules exploratory	10	-10.722	2.4788	0.784	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	SCD1	registered; F-4 and the PLS modules exploratory	10	-1.7499	2.2571	0.714	inconclusive	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	GPAM	registered; F-4 and the PLS modules exploratory	10	-0.7632	1.878	0.594	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	TBX3	registered; F-4 and the PLS modules exploratory	10	0.5249	2.172	0.687	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	CDKN1A	registered; F-4 and the PLS modules exploratory	10	3.2084	2.1607	0.683	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	CDKN2A	registered; F-4 and the PLS modules exploratory	1				not analyzed	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	GDF15	registered; F-4 and the PLS modules exploratory	4	-0.8216	1.9881	0.994	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	SERPINE1	registered; F-4 and the PLS modules exploratory	10	0.5065	2.3772	0.752	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	pls_high	registered; F-4 and the PLS modules exploratory	10	-5.3313	2.2316	0.706	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	pls_low	registered; F-4 and the PLS modules exploratory	10	0.4581	2.3262	0.736	flat	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	pls_contrast	registered; F-4 and the PLS modules exploratory	10	-3.5354	2.2382	0.708	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	senescence	registered; F-4 and the PLS modules exploratory	5	1.7325	1.9405	0.868	inconclusive	outputs/pf_clustered_20261028/PF_verdict.tsv
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	fibrosis_set	registered; F-4 and the PLS modules exploratory	10	-15.7321	2.2681	0.717	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv

family	endpoint	registered status	units	statistic	null q97.5	detection limit per unit	verdict	source file
F-2 redox node, F-3 orientation, F-4 senescence, PLS modules	hepatocyte_set	registered; F-4 and the PLS modules exploratory	10	3.8874	1.9679	0.622	exceeds null	outputs/pf_clustered_20261028/PF_verdict.tsv
Z-D lipotoxicity-avoidance genes	CIDEB	exploratory at registration	22	-1.1974	2.8994	0.618	flatness replicated	outputs/ZD_D3_verdict.tsv
Z-D lipotoxicity-avoidance genes	GPAM	exploratory at registration	22	17.5927	2.4765	0.528	DISCREPANCY: exceeds null, not registered as confirmatory	outputs/ZD_D3_verdict.tsv
Z-D lipotoxicity-avoidance genes	FOXO1	exploratory at registration	22	-1.0499	2.129	0.454	flatness replicated	outputs/ZD_D3_verdict.tsv
Z-D lipotoxicity-avoidance genes	TBX3	exploratory at registration	22	20.0365	1.8241	0.389	DISCREPANCY: exceeds null, not registered as confirmatory	outputs/ZD_D3_verdict.tsv
Z-D lipotoxicity-avoidance genes	SCD1	exploratory at registration	22	11.0059	2.5726	0.548	DISCREPANCY: exceeds null, not registered as confirmatory	outputs/ZD_D3_verdict.tsv
Z-A flatness replication	MTARC1	registered confirmatory	22	-0.8276	2.2506	0.48	flatness replicated	outputs/ZA_D3_verdict.tsv
Z-A flatness replication	MTARC2	registered confirmatory	22	-0.3528	2.2251	0.474	flatness replicated	outputs/ZA_D3_verdict.tsv
Z-A flatness replication	CYB5R3	registered confirmatory	22	-0.7473	2.2495	0.48	flatness replicated	outputs/ZA_D3_verdict.tsv
Z-A flatness replication	CYB5A	registered confirmatory	22	1.0871	2.6164	0.558	flatness replicated	outputs/ZA_D3_verdict.tsv
Z-A flatness replication	POR	registered confirmatory	22	3.4151	2.0861	0.445	DISCREPANCY: exceeds null, not registered as confirmatory	outputs/ZA_D3_verdict.tsv
Z-A flatness replication	SCD1	registered confirmatory	22	11.021	2.4251	0.517	DISCREPANCY: exceeds null, not registered as confirmatory	outputs/ZA_D3_verdict.tsv
Z3-1 zone 3 scar	Z3-1 relocation null (amended, primary)	registered primary and variants	10	-1.6599	1.8512	0.585	inconclusive	outputs/z3_scar/Z3_1_verdict.tsv
Z3-1 zone 3 scar	Z3-1 permutation null (originally registered, anticonservative)	registered primary and variants	10	-5.5646	2.3482	0.743	exceeds null	outputs/z3_scar/Z3_1_verdict.tsv
Z3-1 zone 3 scar	Z3-1 reduced zonation index (P-Z2)	registered primary and variants	10	-2.7703	1.7511	0.554	exceeds null	outputs/z3_scar/Z3_1_verdict.tsv
Z-E PLS spatial position	high_risk	exploratory at registration	22	1.0886	2.3282	0.496	flat	outputs/ZE_PLS_verdict.tsv
Z-E PLS spatial position	low_risk	exploratory at registration	22	-0.5177	1.9993	0.426	flat	outputs/ZE_PLS_verdict.tsv
Z-E PLS spatial position	contrast_high_minus_low	exploratory at registration	22	1.1779	2.006	0.428	flat	outputs/ZE_PLS_verdict.tsv
D1 independent replication	pls_high	registered; stopped at the premise check	2	-1.9964	2.0397	1.442	inconclusive	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	pls_low	registered; stopped at the premise check	2	1.849	2.4683	1.745	inconclusive	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	pls_contrast	registered; stopped at the premise check	2	-2.5723	2.287	1.617	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	fibrosis_set	registered; stopped at the premise check	2	-7.7079	2.2342	1.58	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	hepatocyte_set	registered; stopped at the premise check	2	2.5394	2.1364	1.511	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	senescence	registered; stopped at the premise check	2	0.1137	2.7354	1.934	flat	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	MTARC1	registered; stopped at the premise check	2	0.8754	2.2413	1.585	flat	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	MTARC2	registered; stopped at the premise check	2	0.359	2.0856	1.475	flat	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	CYB5R3	registered; stopped at the premise check	2	-1.5211	2.5317	1.79	inconclusive	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	CYB5A	registered; stopped at the premise check	2	1.8042	2.3386	1.654	inconclusive	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	POR	registered; stopped at the premise check	2	0.4924	2.3293	1.647	flat	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	COL1A1	registered; stopped at the premise check	2	-4.1996	2.1865	1.546	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	THBS2	registered; stopped at the premise check	2	-3.5841	2.3038	1.629	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	TIMP1	registered; stopped at the premise check	2	-4.0311	2.4239	1.714	exceeds null	outputs/d1_replication/D1_verdict.tsv

family	endpoint	registered status	units	statistic	null q97.5	detection limit per unit	verdict	source file
D1 independent replication	SCD1	registered; stopped at the premise check	2	0.7762	2.3466	1.659	flat	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	GPAM	registered; stopped at the premise check	2	2.2848	2.1512	1.521	exceeds null	outputs/d1_replication/D1_verdict.tsv
D1 independent replication	TBX3	registered; stopped at the premise check	2	-0.2187	2.3986	1.696	flat	outputs/d1_replication/D1_verdict.tsv
H-S1 SCD1 lobular positive control	primary: component unit	registered positive control	6	4.7579	2.3629		confirmed	outputs/HS1_verdict.tsv
H-S1 SCD1 lobular positive control	sensitivity: capture-area unit	registered positive control	5	4.7295	2.0626		confirmed	outputs/HS1_verdict.tsv

Data S4. Component-level gates and verdicts

The 22 analyzed tissue components of cohort D3, drawn from 69 enumerated, and every section of cohort D1, with each registered gate value.

unit	cohort	capture area	spots	fibrotic fraction	F2a	n at distance 0	n beyond distance 3	size ok (original)	n first bin	n last bin	size ok (amended)	F2b fibrosis vs distance	F2c hepatocyte vs distance	F2c matched control	F2c	Moran's I	quintile ratio	passed as registered	passed as amended
VLP115_A_c1	D3	VLP115_A	670	0.2	True	134	22	False	134	22	False	-14.758	9.49	3.657	True			False	False
VLP115_A_c2	D3	VLP115_A	423	0.2009	True	85	79	False	85	79	True	-12.709	8.27	-0.63	True			False	True
VLP115_D_c2	D3	VLP115_D	515	0.2	True	103	30	False	103	30	True	-13.271	12.598	3.314	True			False	True
VLP115_D_c4	D3	VLP115_D	332	0.2018	True	67	9	False	67	9	False	-10.948	5.384	4.747	True			False	False
VLP116_A_c1	D3	VLP116_A	684	0.2003	True	137	70	False	137	70	True	-16.79	4.493	3.068	True			False	True
VLP116_A_c4	D3	VLP116_A	333	0.2012	True	67	58	False	67	58	True	-14.768	9.453	7.242	True			False	True
VLP116_D_c2	D3	VLP116_D	622	0.201	True	125	36	False	125	36	True	-13.97	3.522	4.139	False			False	False
VLP119_A_c1	D3	VLP119_A	631	0.2013	True	127	6	False	127	6	False	-15.373	-3.299	-0.474	False			False	False
VLP119_A_c3	D3	VLP119_A	232	0.2026	True	47	18	False	47	18	False	-7.825	0.162	1.218	False			False	False
VLP119_A_c4	D3	VLP119_A	203	0.202	True	41	52	False	41	52	True	-12.201	6.267	8.893	False			False	False
VLP119_D_c1	D3	VLP119_D	390	0.2	True	78	18	False	78	18	False	-12.609	2.885	1.249	True			False	False
VLP119_D_c2	D3	VLP119_D	289	0.2007	True	58	15	False	58	15	False	-11.922	3.212	5.237	False			False	False
VLP120_A_c2	D3	VLP120_A	575	0.2	True	115	106	True	115	106	True	-19.024	4.475	12.105	False			False	False
VLP120_A_c3	D3	VLP120_A	421	0.2019	True	85	41	False	85	41	True	-12.285	-1.32	-0.963	False			False	False
VLP120_D_c1	D3	VLP120_D	620	0.2	True	124	77	False	124	77	True	-19.199	14.509	3.655	True			False	True
VLP120_D_c2	D3	VLP120_D	607	0.201	True	122	35	False	122	35	True	-15.81	9.629	0.804	True			False	True
VLP120_D_c3	D3	VLP120_D	339	0.2006	True	68	18	False	68	18	False	-14.233	9.447	8.636	True			False	False
VLP121_A_c3	D3	VLP121_A	334	0.2006	True	67	89	False	67	89	True	-13.367	4.713	3.878	True			False	True
VLP121_D_c1	D3	VLP121_D	444	0.2005	True	89	82	False	89	82	True	-19.8	14.791	0.184	True			False	True
VLP121_D_c2	D3	VLP121_D	405	0.2	True	81	4	False	81	4	False	-10.81	3.551	1.103	True			False	False
VLP121_D_c3	D3	VLP121_D	361	0.2022	True	73	105	False	73	105	True	-14.754	12.732	6.097	True			False	True
VLP121_D_c4	D3	VLP121_D	284	0.2007	True	57	59	False	57	59	True	-15.177	10.655	7.189	True			False	True
JBO014	D1		1248	0.2003	True	250	93	False	250	93	True	-21.123	9.234	-3.468	True	0.3746	2.843	False	True
JBO015	D1		532	0.2011	True	107	10	False	107	10	False	-15.486	3.17	3.376	False	0.2276	2.343	False	False
JBO018	D1		2501	0.2003	True	501	83	False	501	83	True	-30.085	-4.945	4.178	False	0.4294	1.94	False	False
JBO019	D1		1185	0.2	True	237	17	False	237	17	False	-20.104	8.782	-2.537	True	0.2552	2.426	False	False
JBO022	D1		1423	0.2003	True	285	134	True	285	134	True	-22.856	16.723	-1.799	True	0.4942	3.426	True	True

Data S5. Reference quality control and premise-threshold sensitivity

Cells and transcript counts per class for the single-nucleus subset, and the pooled median hepatocyte fraction against premise thresholds from 0.25 to 0.55.

ck	col1	col2	col3	col4	col5	col6	col7	col8	col9	
erence QC, gle-nucleus subset	klass	cells	total_counts	albumin_cpm	albumin_counts	clears_min_cells				
	Hepatocytes	2000	76254848	5381.3	410349.0	True				
	Endothelial cells	1187	4577188	2510.7	11492.0	True				
	Fibroblasts	823	2618939	3402.9	8912.0	True				
	Cholangiocytes	297	1158280	2869.8	3324.0	True				
	Macrophages	317	978216	2554.7	2499.0	True				
	T cells	11	29212	10783.2	315.0	False				
	pDCs	2	5587	8591.4	48.0	False				
	Plasma cells	2	2792	7879.7	22.0	False				
	Neutrophils	2	1864	0.0	0.0	False				
	Resident NK	1	1693	11813.3	20.0	False				
mise-threshold sitivity	cell	pooled_median_hepatocyte	hepatocytes_most_abundant	passes_at_0.25	passes_at_0.30	passes_at_0.35	passes_at_0.40	passes_at_0.45	passes_at_0.50	passes_at_0.55
	CARD / dissociated	0.3137	False	False	False	False	False	False	False	False
	CARD / single-nucleus	0.095	False	False	False	False	False	False	False	False
	NNLS / dissociated	0.5639	True	True	True	True	True	True	True	True
	NNLS / single-nucleus	0.0	False	False	False	False	False	False	False	False
	NNLS / single-nucleus, min 25 cells	0.2357	False	False	False	False	False	False	False	False