

Project: Project_316_Eckstein_Deng_Li
Report generated: 04-06-2022 20:30:11
Flow cell ID: 220603_A00623_0585_BHF27WDRX2
Sequencer type: NovaSeq
BCL2Fastq pipeline version: 0.3.0
bcl2fastq version: v2.20.0.422
FastQC version: v0.11.9
151:151 base paired-end reads

Bioinformatics Platform

Sample ID	Sample Name	Barcode	Lane	# Reads	% Bases >= Q30 Read #1	Ave. Qual. Read #1	% Bases >= Q30 Read #2	Ave. Qual. Read #2
Sample_22L004999	22L004999	GAACTGAGCG+CGCTCCACGA	1	9207199	93.07	35.71	91.12	35.33
Sample_22L004999	22L004999	GAACTGAGCG+CGCTCCACGA	2	9218514	93.31	35.76	91.27	35.36
Sample_22L005000	22L005000	AGGTCAGATA+TATCTTGTAG	1	9024057	93.27	35.76	91.58	35.44
Sample_22L005000	22L005000	AGGTCAGATA+TATCTTGTAG	2	9032409	93.48	35.80	91.75	35.47
Sample_22L005001	22L005001	CGTCTCATAT+AGCTACTATA	1	11056553	92.11	35.53	91.43	35.39
Sample_22L005001	22L005001	CGTCTCATAT+AGCTACTATA	2	11107604	92.34	35.57	91.62	35.43
Sample_22L005002	22L005002	ATTCCATAAG+CCACCAGGCA	1	10581133	93.21	35.76	91.91	35.51
Sample_22L005002	22L005002	ATTCCATAAG+CCACCAGGCA	2	10618230	93.43	35.80	92.11	35.55
Sample_22L005003	22L005003	GACGAGATTAA+AGGATAATGT	1	9956172	92.04	35.56	91.40	35.44
Sample_22L005003	22L005003	GACGAGATTAA+AGGATAATGT	2	10067564	92.27	35.60	91.60	35.48
Sample_22L005004	22L005004	AACATCGCGC+ACAAGTGGAC	1	10819204	92.79	35.71	93.34	35.81
Sample_22L005004	22L005004	AACATCGCGC+ACAAGTGGAC	2	10816330	92.95	35.74	93.54	35.85
Sample_22L005005	22L005005	CTAGTGCTCT+TACTGTTCCA	1	13411570	93.61	35.84	92.97	35.72
Sample_22L005005	22L005005	CTAGTGCTCT+TACTGTTCCA	2	13454667	93.79	35.87	93.13	35.75
Sample_22L005006	22L005006	GATCAAGGCA+ATTAACAAGG	1	11547858	92.64	35.66	91.77	35.51

Sample ID	Sample Name	Barcode	Lane	# Reads	% Bases >= Q30 Read #1	Ave. Qual. Read #1	% Bases >= Q30 Read #2	Ave. Qual. Read #2
Sample_22L005006	22L005006	GATCAAGGCA+ATTAACAAGG	2	11619073	92.82	35.70	91.97	35.55
Sample_22L005007	22L005007	GACTGAGTAG+CACTATCAAC	1	11215701	92.69	35.69	91.84	35.53
Sample_22L005007	22L005007	GACTGAGTAG+CACTATCAAC	2	11250436	92.87	35.73	91.95	35.55
Sample_22L005008	22L005008	AGTCAGACGA+TGTCGCTGGT	1	11647475	93.51	35.83	92.15	35.57
Sample_22L005008	22L005008	AGTCAGACGA+TGTCGCTGGT	2	11704951	93.74	35.87	92.35	35.61
Sample_22L005009	22L005009	CCGTATGTTC+ACAGTGTATG	1	9851278	92.24	35.62	93.26	35.81
Sample_22L005009	22L005009	CCGTATGTTC+ACAGTGTATG	2	9868310	92.33	35.64	93.47	35.85
Sample_22L005010	22L005010	GAGTCATAGG+AGCGCCACAC	1	9965135	91.77	35.49	91.53	35.45
Sample_22L005010	22L005010	GAGTCATAGG+AGCGCCACAC	2	9992071	91.96	35.53	91.75	35.49
Sample_22L005011	22L005011	CTTGCCTTA+CCTTCGTGAT	1	11219482	88.20	34.67	87.57	34.49
Sample_22L005011	22L005011	CTTGCCTTA+CCTTCGTGAT	2	11221710	88.52	34.74	87.88	34.56
Sample_22L005012	22L005012	GAAGCGGCAC+AGTAGAGCCG	1	12610218	93.07	35.72	91.68	35.46
Sample_22L005012	22L005012	GAAGCGGCAC+AGTAGAGCCG	2	12601988	93.29	35.76	91.83	35.49
Sample_22L005013	22L005013	TCCATTGCCG+TCGTGCATT	1	11228433	92.80	35.71	92.65	35.69
Sample_22L005013	22L005013	TCCATTGCCG+TCGTGCATT	2	11242116	92.97	35.74	92.84	35.72
Sample_22L005014	22L005014	CGGTTACGGC+CTATAGTCTT	1	5425356	74.31	31.58	76.36	32.05
Sample_22L005014	22L005014	CGGTTACGGC+CTATAGTCTT	2	5503978	74.67	31.66	76.74	32.14
Sample_22L005015	22L005015	GAGAATGGTT+TTGCTGCCGA	1	3097233	89.75	35.03	87.76	34.65
Sample_22L005015	22L005015	GAGAATGGTT+TTGCTGCCGA	2	3131169	89.99	35.07	88.02	34.70
Sample_22L005016	22L005016	AGAGGCAACC+CCATCATTAG	1	3767812	83.96	33.73	83.95	33.73
Sample_22L005016	22L005016	AGAGGCAACC+CCATCATTAG	2	3768793	84.32	33.80	84.23	33.79
Sample_22L005017	22L005017	CCATCATTAG+AGAGGCAACC	1	3547168	92.78	35.75	91.78	35.54

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Sample_22L005017	22L005017	CCATCATTAG+AGAGGCAACC	2	3544413	92.94	35.79	92.01	35.58
Sample_22L005018	22L005018	GATAGGCCGA+GCCATGTGCG	1	2654564	81.87	33.40	86.09	34.26
Sample_22L005018	22L005018	GATAGGCCGA+GCCATGTGCG	2	2673097	81.92	33.42	86.35	34.31
Sample_22L005019	22L005019	ATGGTTGACT+AGGACAGGCC	1	1600393	94.12	36.01	92.61	35.73
Sample_22L005019	22L005019	ATGGTTGACT+AGGACAGGCC	2	1599990	94.21	36.03	92.86	35.78
Sample_22L005020	22L005020	TATTGCGCTC+CCTAACACAG	1	3443829	90.79	35.27	89.34	35.01
Sample_22L005020	22L005020	TATTGCGCTC+CCTAACACAG	2	3470363	90.98	35.30	89.59	35.06
Sample_22L005021	22L005021	ACGCCTTGT+ACGTTCCCTTA	1	5656518	91.86	35.50	90.43	35.24
Sample_22L005021	22L005021	ACGCCTTGT+ACGTTCCCTTA	2	5682795	92.04	35.53	90.69	35.29
Sample_22L005022	22L005022	TTCTACATAC+TTACAGTTAG	1	1934151	93.09	35.74	91.38	35.45
Sample_22L005022	22L005022	TTCTACATAC+TTACAGTTAG	2	1947307	93.29	35.78	91.60	35.50
Sample_22L005023	22L005023	AACCATAGAA+CCATCTGCC	1	4530028	94.79	36.11	92.82	35.73
Sample_22L005023	22L005023	AACCATAGAA+CCATCTGCC	2	4534010	94.98	36.15	93.03	35.77
Sample_22L005024	22L005024	GGTTGCGAGG+TTGCTCTATT	1	4934425	79.23	32.65	78.75	32.64
Sample_22L005024	22L005024	GGTTGCGAGG+TTGCTCTATT	2	4985000	79.48	32.70	78.94	32.69
Sample_22L005025	22L005025	TAAGCATCCA+AATGGATTGA	1	3641824	92.97	35.71	91.09	35.36
Sample_22L005025	22L005025	TAAGCATCCA+AATGGATTGA	2	3649192	93.17	35.74	91.29	35.40
Sample_22L005026	22L005026	ACCACGACAT+CCGCATACGA	1	5926835	90.59	35.23	89.51	35.04
Sample_22L005026	22L005026	ACCACGACAT+CCGCATACGA	2	5985549	90.68	35.25	89.70	35.07
Sample_22L005027	22L005027	GCCGCACTCT+CGAGGTCGGA	1	3725329	83.69	33.75	86.15	34.31
Sample_22L005027	22L005027	GCCGCACTCT+CGAGGTCGGA	2	3757637	83.91	33.80	86.43	34.37
Sample_22L005028	22L005028	CCACCAGGCA+ATTCCATAAG	1	556887	75.00	31.70	78.79	32.64

Sample ID	Sample Name	Barcode	Lane	# Reads	% Bases >= Q30 Read #1	Ave. Qual. Read #1	% Bases >= Q30 Read #2	Ave. Qual. Read #2
Sample_22L005028	22L005028	CCACCAGGCA+ATTCATAAG	2	564580	75.10	31.72	79.17	32.73
Sample_22L005029	22L005029	GTGACACGCA+GTCCGTAAGC	1	4560060	81.55	33.32	85.05	33.99
Sample_22L005029	22L005029	GTGACACGCA+GTCCGTAAGC	2	4573045	81.62	33.34	85.35	34.06
Sample_22L005030	22L005030	ACAGTGTATG+CCGTATGTTTC	1	6450191	92.61	35.66	90.48	35.28
Sample_22L005030	22L005030	ACAGTGTATG+CCGTATGTTTC	2	6447229	92.73	35.69	90.69	35.32
Sample_22L005031	22L005031	TGATTATACG+TGTAATCGAC	1	18510	80.91	33.04	84.44	33.89
Sample_22L005031	22L005031	TGATTATACG+TGTAATCGAC	2	18719	80.72	32.99	84.57	33.92
Sample_22L005032	22L005032	CAGCCGCGTA+CACGGCTAGT	1	7140122	83.30	33.70	83.18	33.66
Sample_22L005032	22L005032	CAGCCGCGTA+CACGGCTAGT	2	7221050	83.58	33.76	83.52	33.74
Sample_22L005033	22L005033	GGTAACTCGC+TCACCAACTT	1	3261897	80.76	33.10	82.90	33.56
Sample_22L005033	22L005033	GGTAACTCGC+TCACCAACTT	2	3322186	81.03	33.16	83.18	33.63
Sample_22L005034	22L005034	ACCGGCCGTA+AATATTGCCA	1	7990666	79.75	32.76	80.35	32.92
Sample_22L005034	22L005034	ACCGGCCGTA+AATATTGCCA	2	8097032	80.17	32.86	80.81	33.02
Sample_22L005035	22L005035	TGTAATCGAC+CGCGGTGATC	1	7941916	93.48	35.86	93.53	35.87
Sample_22L005035	22L005035	TGTAATCGAC+CGCGGTGATC	2	7932833	93.59	35.88	93.72	35.91
Sample_22L005036	22L005036	GTGCAGACAG+ACGGATGGTA	1	1499291	81.97	33.44	85.16	34.04
Sample_22L005036	22L005036	GTGCAGACAG+ACGGATGGTA	2	1509455	82.15	33.49	85.51	34.12
Sample_22L005037	22L005037	CAATCGGCTG+TTCCTACAGC	1	3118282	90.74	35.30	90.55	35.26
Sample_22L005037	22L005037	CAATCGGCTG+TTCCTACAGC	2	3133176	90.94	35.33	90.76	35.30
Sample_22L005038	22L005038	TATGTAGTCA+CATTAGTGC	1	6034715	86.20	34.33	85.80	34.26
Sample_22L005038	22L005038	TATGTAGTCA+CATTAGTGC	2	6089128	86.44	34.38	86.10	34.33
Sample_22L005039	22L005039	ACTCGGCAAT+TTCAGTTGTC	1	5986995	80.16	32.93	81.25	33.21

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Sample_22L005039	22L005039	ACTCGGCAAT+TTCAGTTGTC	2	6132620	80.35	32.97	81.56	33.28
Sample_22L005040	22L005040	GTCTAATGGC+CCTGACCACT	1	5844317	88.20	34.72	87.99	34.70
Sample_22L005040	22L005040	GTCTAATGGC+CCTGACCACT	2	5914497	88.42	34.76	88.20	34.75
Sample_22L005041	22L005041	CCATCTGCC+AACCATAGAA	1	9071981	90.04	35.18	92.55	35.64
Sample_22L005041	22L005041	CCATCTGCC+AACCATAGAA	2	9095442	90.15	35.21	92.78	35.68
Sample_22L005042	22L005042	CTGCGAGCCA+TGGCCGGATT	1	3297425	89.36	35.11	93.63	35.89
Sample_22L005042	22L005042	CTGCGAGCCA+TGGCCGGATT	2	3314998	89.34	35.12	93.85	35.94
Sample_22L005043	22L005043	CGTTATTCTA+AACCTTATGG	1	1779186	93.37	35.84	91.58	35.51
Sample_22L005043	22L005043	CGTTATTCTA+AACCTTATGG	2	1774191	93.53	35.87	91.68	35.53
Sample_22L005044	22L005044	AGATCCATTA+TGGTAGAGAT	1	8158319	92.39	35.60	91.18	35.37
Sample_22L005044	22L005044	AGATCCATTA+TGGTAGAGAT	2	8174589	92.62	35.64	91.37	35.41
Sample_22L005045	22L005045	GTCCTGGATA+TTCGCCACCG	1	4525397	84.42	33.88	85.25	34.04
Sample_22L005045	22L005045	GTCCTGGATA+TTCGCCACCG	2	4584121	84.64	33.93	85.50	34.09
Sample_22L005046	22L005046	CAGTGGCACT+CCTATTGTTA	1	12197858	90.43	35.16	89.36	34.93
Sample_22L005046	22L005046	CAGTGGCACT+CCTATTGTTA	2	12302748	90.75	35.22	89.62	34.98
Sample_22L005047	22L005047	AGTGTGCAC+CGTGTACCAG	1	1448550	93.27	35.80	92.78	35.72
Sample_22L005047	22L005047	AGTGTGCAC+CGTGTACCAG	2	1457357	93.50	35.85	92.98	35.76
Sample_22L005048	22L005048	GACACCATGT+TACACGTTGA	1	6706266	94.26	36.01	92.46	35.66
Sample_22L005048	22L005048	GACACCATGT+TACACGTTGA	2	6732841	94.49	36.06	92.64	35.70
Sample_22L005049	22L005049	CCTGTCTGTC+TCACAACAGT	1	1886889	94.06	35.97	92.54	35.68
Sample_22L005049	22L005049	CCTGTCTGTC+TCACAACAGT	2	1892702	94.25	36.01	92.71	35.71
Sample_22L005050	22L005050	TGATGTAAGA+AAGGACGCAC	1	5311296	76.15	31.99	78.78	32.61

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Sample_22L005050	22L005050	TGATGTAAGA+AAGGACGCAC	2	5378216	76.37	32.04	79.22	32.71
Sample_22L005051	22L005051	GGAATTGTAAGGATGTGCT	1	4609899	90.11	35.13	90.56	35.21
Sample_22L005051	22L005051	GGAATTGTAAGGATGTGCT	2	4610931	90.25	35.16	90.77	35.25
Sample_22L005052	22L005052	GCATAAGCTT+TGCGACGGAA	1	2892273	90.78	35.25	90.68	35.21
Sample_22L005052	22L005052	GCATAAGCTT+TGCGACGGAA	2	2897523	91.01	35.30	90.91	35.26
Sample_22L005053	22L005053	CTGAGGAATA+AGTGGTTAAC	1	3652758	84.46	33.91	85.41	34.11
Sample_22L005053	22L005053	CTGAGGAATA+AGTGGTTAAC	2	3688081	84.77	33.98	85.68	34.17
Sample_22L005054	22L005054	AACGCACGAG+TATCCGAGGC	1	2765206	92.38	35.61	91.30	35.40
Sample_22L005054	22L005054	AACGCACGAG+TATCCGAGGC	2	2775398	92.60	35.65	91.49	35.43
Sample_22L005055	22L005055	TCTATCCTAA+CCAGTCGACG	1	4478080	91.56	35.41	90.77	35.26
Sample_22L005055	22L005055	TCTATCCTAA+CCAGTCGACG	2	4494084	91.84	35.46	90.98	35.31
Sample_22L005056	22L005056	CTCGCTTCGG+TTGACTAGTA	1	1642979	87.88	34.62	88.74	34.79
Sample_22L005056	22L005056	CTCGCTTCGG+TTGACTAGTA	2	1652115	88.13	34.67	89.01	34.84
Sample_22L005057	22L005057	CTGTTGGTCC+AACGGTCTAT	1	4010671	83.39	33.66	84.57	33.89
Sample_22L005057	22L005057	CTGTTGGTCC+AACGGTCTAT	2	4056478	83.68	33.72	84.86	33.96
Sample_22L005058	22L005058	TTACCTGGAA+CTGGAACGT	1	3075096	79.87	32.87	80.80	33.09
Sample_22L005058	22L005058	TTACCTGGAA+CTGGAACGT	2	3130123	80.01	32.90	81.10	33.17
Sample_22L005059	22L005059	TGGCTAATCA+CTACATGCCT	1	1379081	89.38	34.94	88.98	34.88
Sample_22L005059	22L005059	TGGCTAATCA+CTACATGCCT	2	1390822	89.59	34.98	89.17	34.91
Sample_22L005060	22L005060	AACACTGTTA+TGAGACTTGC	1	5049315	89.88	35.08	88.70	34.83
Sample_22L005060	22L005060	AACACTGTTA+TGAGACTTGC	2	5063901	90.11	35.12	88.97	34.89
Sample_22L005061	22L005061	ATTGCGCGGT+GC GGAGCCAA	1	653667	89.10	35.01	92.14	35.58

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Sample_22L005061	22L005061	ATTGCGCGGT+GCGGAGCCAA	2	658015	89.12	35.01	92.38	35.63
Sample_22L005062	22L005062	TGGCGCGAAC+AGTATCAGTT	1	5076564	89.31	34.93	88.40	34.74
Sample_22L005062	22L005062	TGGCGCGAAC+AGTATCAGTT	2	5102412	89.65	35.00	88.69	34.80
Sample_22L005063	22L005063	TAATGTGTCT+TATGCCTTAC	1	4191380	90.12	35.11	89.30	34.96
Sample_22L005063	22L005063	TAATGTGTCT+TATGCCTTAC	2	4213181	90.34	35.15	89.59	35.02
Sample_22L005064	22L005064	ATACCAACGC+CGCAGCAATT	1	1520448	94.52	36.06	93.51	35.87
Sample_22L005064	22L005064	ATACCAACGC+CGCAGCAATT	2	1525209	94.69	36.09	93.64	35.89
Sample_22L005065	22L005065	AGGATGTGCT+GGAATTGTAA	1	5031036	88.38	34.85	91.02	35.35
Sample_22L005065	22L005065	AGGATGTGCT+GGAATTGTAA	2	5099396	88.60	34.89	91.32	35.41
Sample_22L005066	22L005066	CACGGAACAA+GTGCTAGGTT	1	3871726	78.06	32.58	86.68	34.35
Sample_22L005066	22L005066	CACGGAACAA+GTGCTAGGTT	2	3890127	77.86	32.54	86.99	34.42
Sample_22L005067	22L005067	TGGAGTACTT+TCCACACAGA	1	6702828	89.80	35.06	89.98	35.07
Sample_22L005067	22L005067	TGGAGTACTT+TCCACACAGA	2	6798092	90.06	35.11	90.19	35.11
Sample_22L005068	22L005068	GTATTGACGT+TTGGAATTCC	1	2489431	90.30	35.09	89.35	34.96
Sample_22L005068	22L005068	GTATTGACGT+TTGGAATTCC	2	2507885	90.41	35.10	89.50	34.99
Sample_22L005069	22L005069	CTTGTACACC+AAGCGCGCTT	1	6473021	92.56	35.61	91.85	35.46
Sample_22L005069	22L005069	CTTGTACACC+AAGCGCGCTT	2	6496829	92.84	35.67	92.04	35.50
Sample_22L005070	22L005070	ACACAGGTGG+ACAACGCTCA	1	4281383	86.35	34.29	88.82	34.83
Sample_22L005070	22L005070	ACACAGGTGG+ACAACGCTCA	2	4327410	86.51	34.33	89.08	34.89
Sample_22L005071	22L005071	CCTGCGGAAC+AGCCTATGAT	1	687541	93.63	35.90	94.24	36.01
Sample_22L005071	22L005071	CCTGCGGAAC+AGCCTATGAT	2	687045	93.74	35.93	94.43	36.05
Sample_22L005072	22L005072	TTCATAAGGT+CCTTCTAACAA	1	1675991	93.23	35.77	92.77	35.69

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Sample_22L005072	22L005072	TTCATAAGGT+CCTTCTAAC	2	1687635	93.39	35.80	92.93	35.72
Sample_22L005073	22L005073	CTCTGCAGCG+TACATCCATC	1	5211517	91.62	35.43	91.28	35.38
Sample_22L005073	22L005073	CTCTGCAGCG+TACATCCATC	2	5220991	91.79	35.46	91.46	35.41
Sample_22L005074	22L005074	CTGACTCTAC+TGACGGCCGT	1	3134849	82.69	33.58	87.36	34.51
Sample_22L005074	22L005074	CTGACTCTAC+TGACGGCCGT	2	3167561	82.74	33.59	87.68	34.58
Sample_22L005075	22L005075	TCTGGTATCC+GTAAGCAACG	1	2950568	86.60	34.43	89.78	34.96
Sample_22L005075	22L005075	TCTGGTATCC+GTAAGCAACG	2	2947617	86.71	34.46	90.04	35.01
Sample_22L005076	22L005076	CATTAGTGCAG+TATGTAGTCA	1	6204797	92.14	35.55	92.47	35.62
Sample_22L005076	22L005076	CATTAGTGCAG+TATGTAGTCA	2	6244594	92.32	35.58	92.63	35.65
Sample_22L005077	22L005077	ACGGTCAGGA+AACGAGGCCG	1	6350377	93.97	35.94	92.25	35.62
Sample_22L005077	22L005077	ACGGTCAGGA+AACGAGGCCG	2	6356826	94.16	35.97	92.45	35.66
Sample_22L005078	22L005078	GGCAAGCCAG+CGGATGCTTG	1	559122	88.29	34.72	89.84	35.08
Sample_22L005078	22L005078	GGCAAGCCAG+CGGATGCTTG	2	563703	88.39	34.74	89.95	35.11
Sample_22L005079	22L005079	TGTCGCTGGT+AGTCAGACGA	1	5040716	94.29	36.01	93.39	35.85
Sample_22L005079	22L005079	TGTCGCTGGT+AGTCAGACGA	2	5066389	94.47	36.04	93.53	35.87
Sample_22L005080	22L005080	ACCGTTACAA+TCGCTATGAG	1	3184302	86.63	34.36	87.00	34.49
Sample_22L005080	22L005080	ACCGTTACAA+TCGCTATGAG	2	3215751	86.85	34.41	87.28	34.55
Sample_22L005081	22L005081	TATGCCTTAC+TAATGTGTCT	1	3488326	84.59	33.90	84.76	33.92
Sample_22L005081	22L005081	TATGCCTTAC+TAATGTGTCT	2	3510683	84.83	33.96	85.02	33.98
Sample_22L005082	22L005082	ACAAGTGGAC+AACATCGCGC	1	1622056	94.07	35.97	92.02	35.58
Sample_22L005082	22L005082	ACAAGTGGAC+AACATCGCGC	2	1622067	94.25	36.01	92.22	35.62
Sample_22L005083	22L005083	TGGTACCTAA+AGTACTCATG	1	3792456	91.39	35.38	90.19	35.17

Sample ID	Sample Name	Barcode	Lane	# Reads	% Bases >= Q30 Read #1	Ave. Qual. Read #1	% Bases >= Q30 Read #2	Ave. Qual. Read #2
Sample_22L005083	22L005083	TGGTACCTAA+AGTACTCATG	2	3802467	91.59	35.42	90.46	35.22
Sample_22L005084	22L005084	TTGGAATTCC+GTATTGACGT	1	2330044	89.78	35.13	92.95	35.73
Sample_22L005084	22L005084	TTGGAATTCC+GTATTGACGT	2	2333934	89.79	35.14	93.12	35.77
Sample_22L005085	22L005085	CCTCTACATG+AGGAGGTATC	1	3050273	85.36	34.07	86.56	34.34
Sample_22L005085	22L005085	CCTCTACATG+AGGAGGTATC	2	3074714	85.55	34.10	86.84	34.40
Sample_22L005086	22L005086	GGAGCGTGTA+ACTTACGGAT	1	681495	91.35	35.44	92.69	35.71
Sample_22L005086	22L005086	GGAGCGTGTA+ACTTACGGAT	2	684977	91.45	35.46	92.84	35.74

Sample ID	The sample ID as provided to the sequencer in the sample sheet. This may not match the final file name, but will match the directory in which it's held.
Sample Name	The sample name as provided to the sequencer in the sample sheet. This should match the final file name.
Barcode	The sample barcode added by the sequencing facility (or you, if you created the libraries yourself). This will generally be 6 nucleotides long.
Lane	The lane number on the flow cell (there are 8 of them).
# Reads	The number of reads in a given file. For paired-end datasets, this is equivalent to the number of fragments sequenced, rather than summing the counts for read #1 and read #2. Note that this includes only reads passing the quality filter.
% Bases >= Q30 Read #1	The percentage of bases in read #1 of a pair having a Phred-scaled score of at least 30, meaning that the 0.1% or less chance that they're incorrect.
Ave. Qual. Read #1	The average Phred-scaled base quality of bases in read #1 of a pair. This number of $-10 \cdot \log_{10}(\text{Probability that the call is incorrect})$. In other words, if a call is 100% likely to be wrong, the score is 0 (or 10 for 10% likelihood, 20 for 1% likelihood, etc.).
% Bases >= Q30 Read #2	Identical to '% Bases >= Q30 Read #1', but for read #2 of a pair.

Ave. Qual.
Read #2 Identical to 'Ave. Qual. Read #1', but for read #1 of a pair.

Reads Identical to '% Bases >= Q30 Read #1', but for single-end datasets.

Ave. Qual. Identical to 'Ave. Qual. Read #1', but for single-end datasets.

Contaminant screen

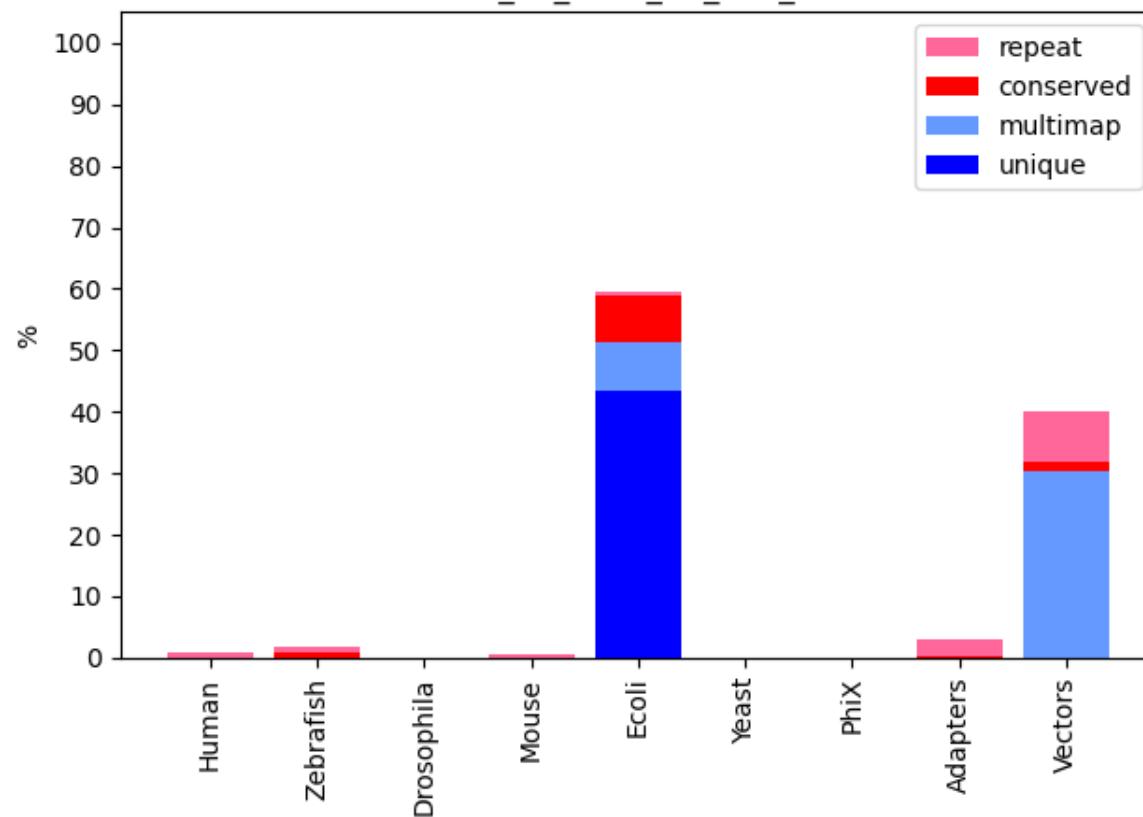
Below are images generated on the output of fastq_screen. In short, 1 million reads are randomly taken from each indicated sample. These reads are then aligned against a variety of organisms (mouse, human, etc.). The resulting alignments are then categorized as follows:

- unique: aligns only a single time within a single species.
- multimap: aligns multiple times, but only within a single species.
- conserved: aligns a single time to each of two or more species.
- repeat: aligns multiple times to each of two or more species.

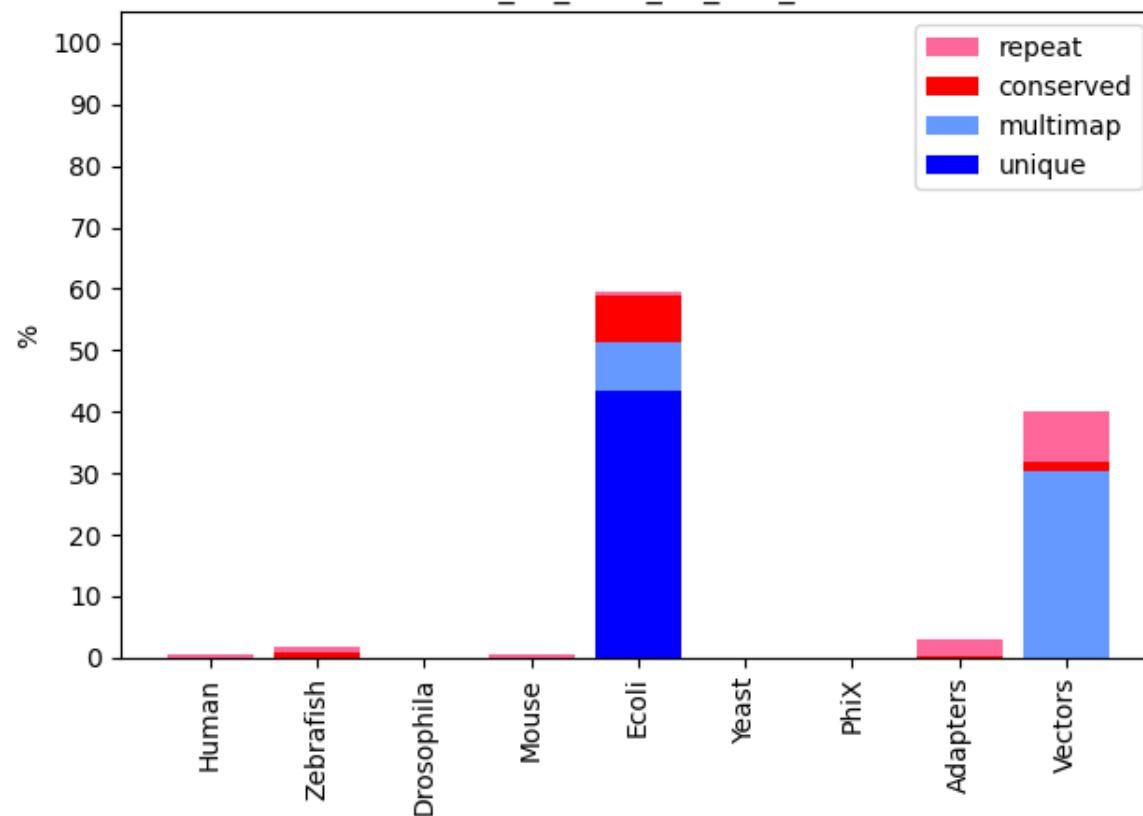
Ideally, the 'unique' and 'multimap' values will only be appreciably present in the species from which your sample should have arisen.

Note that as the mouse and human reference genomes are the best quality, many low complexity reads will align to them.

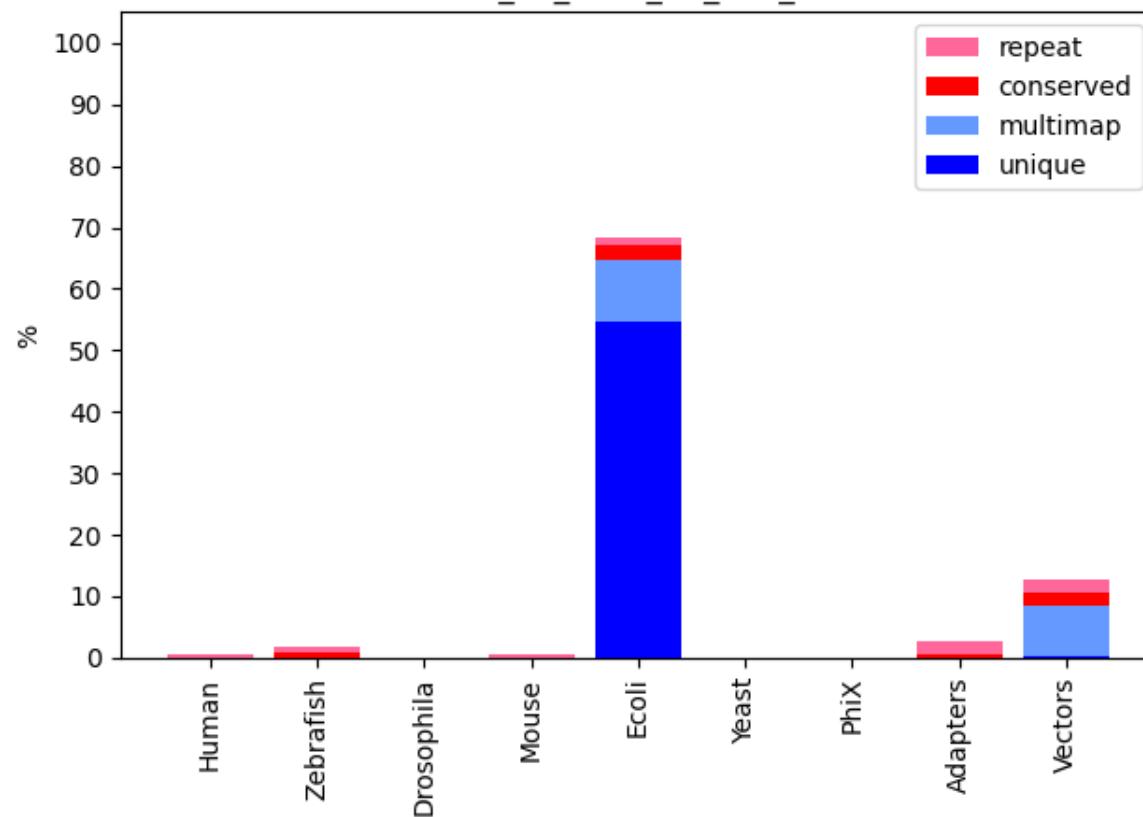
22L004999_S1_L001_R2_001_screen.txt



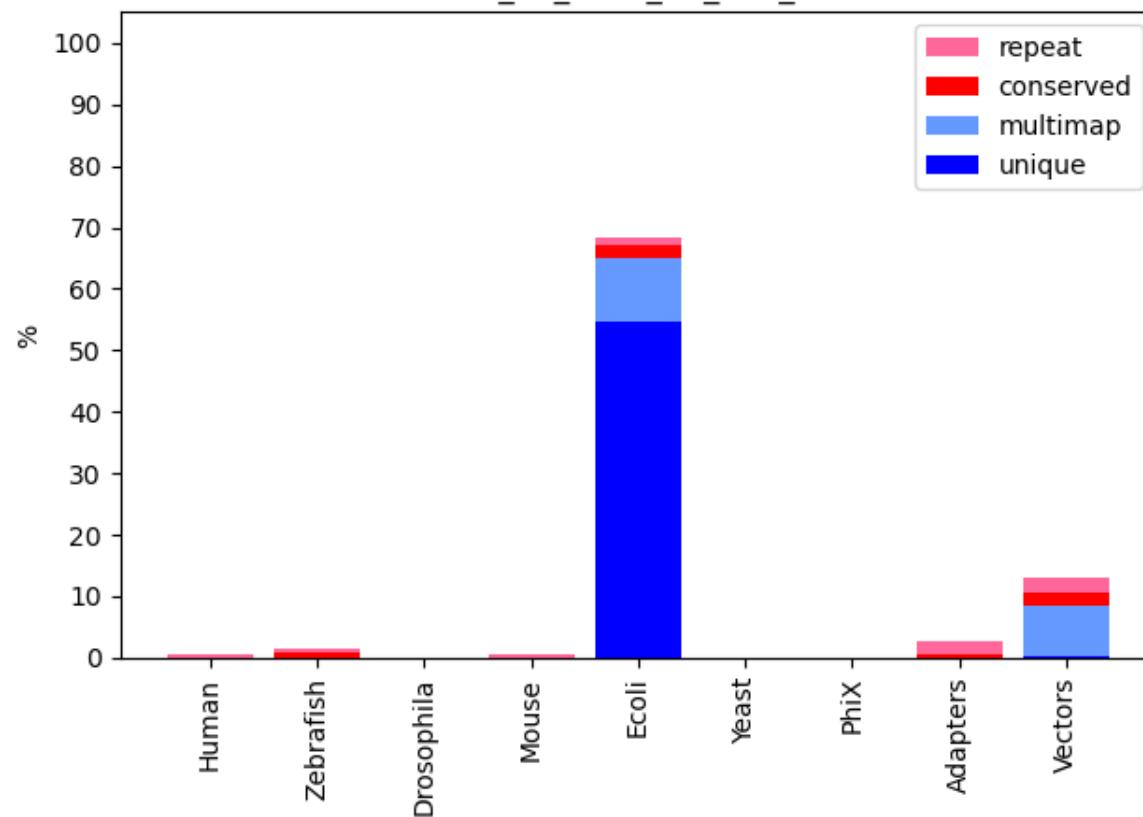
22L004999_S1_L002_R2_001_screen.txt



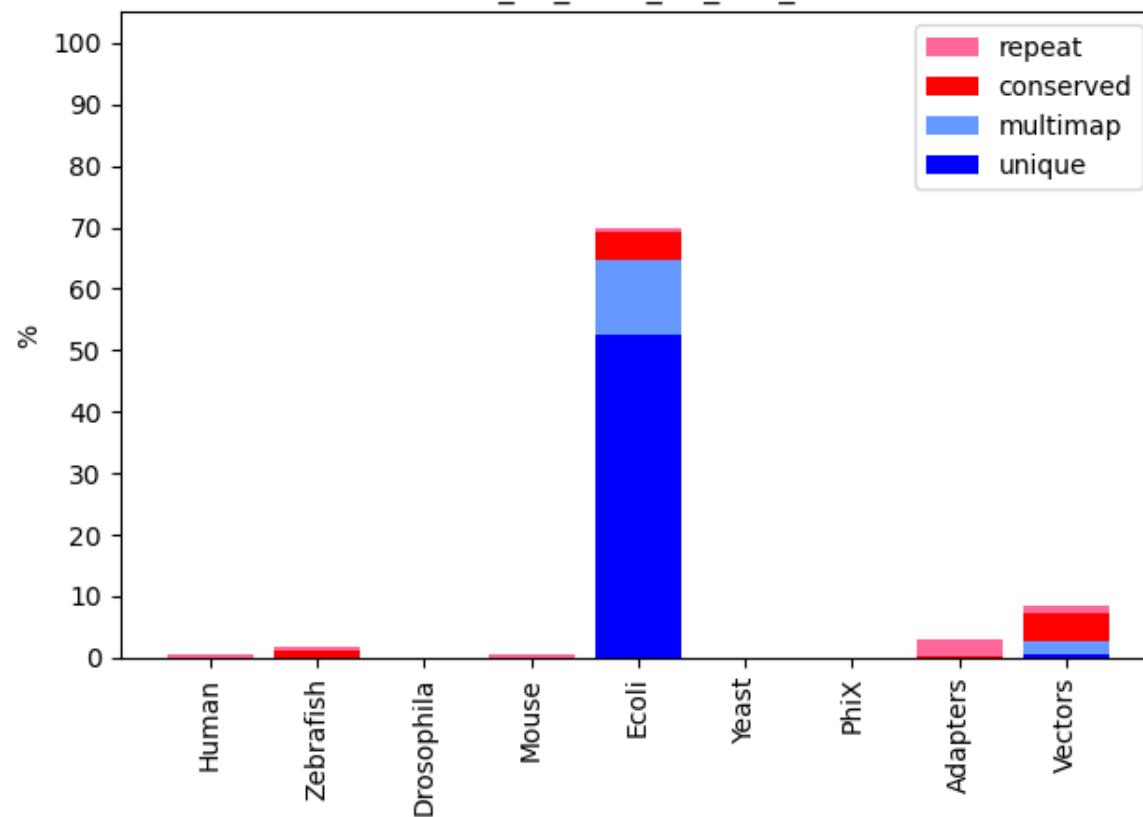
22L005000_S2_L001_R2_001_screen.txt



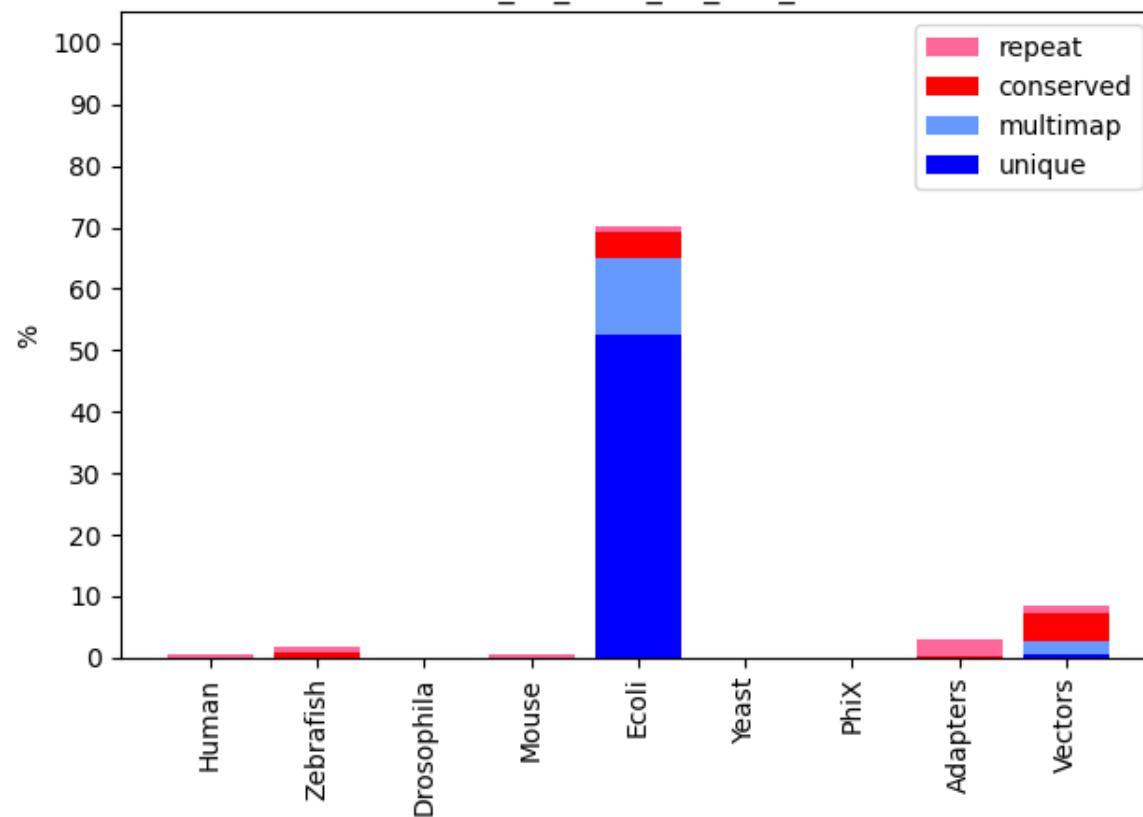
22L005000_S2_L002_R2_001_screen.txt



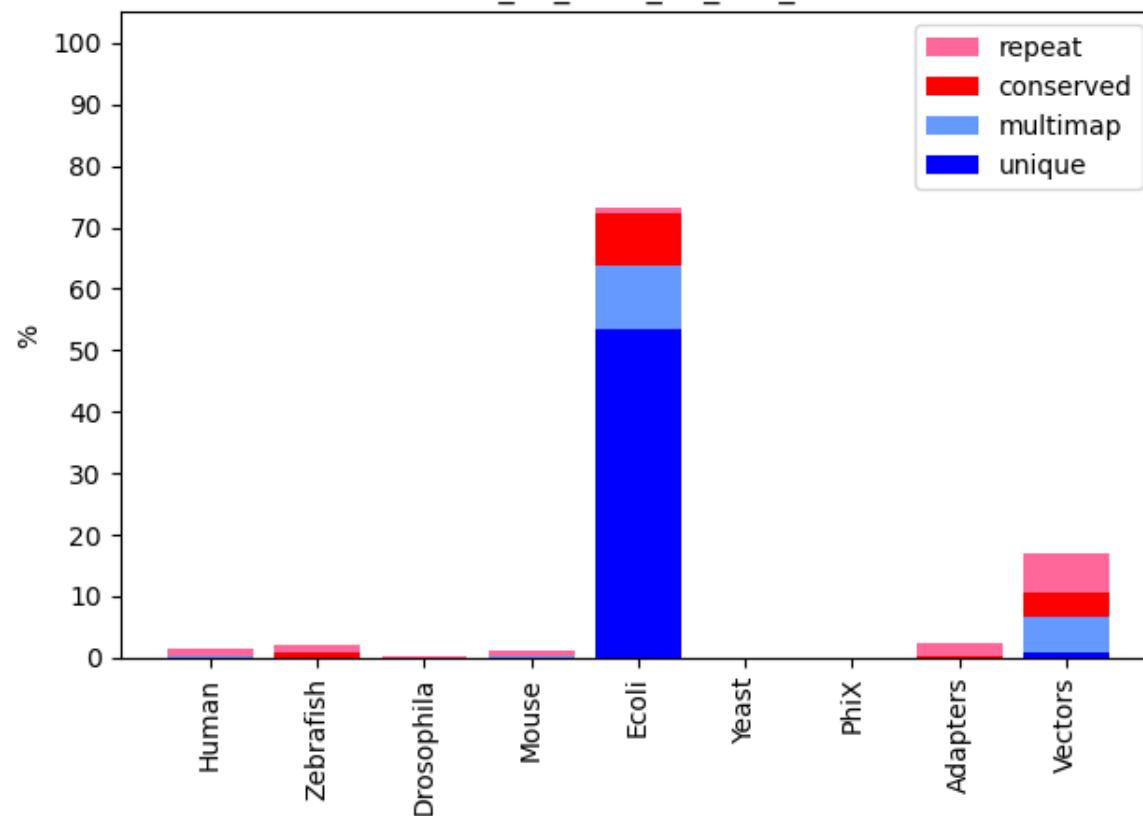
22L005001_S3_L001_R2_001_screen.txt



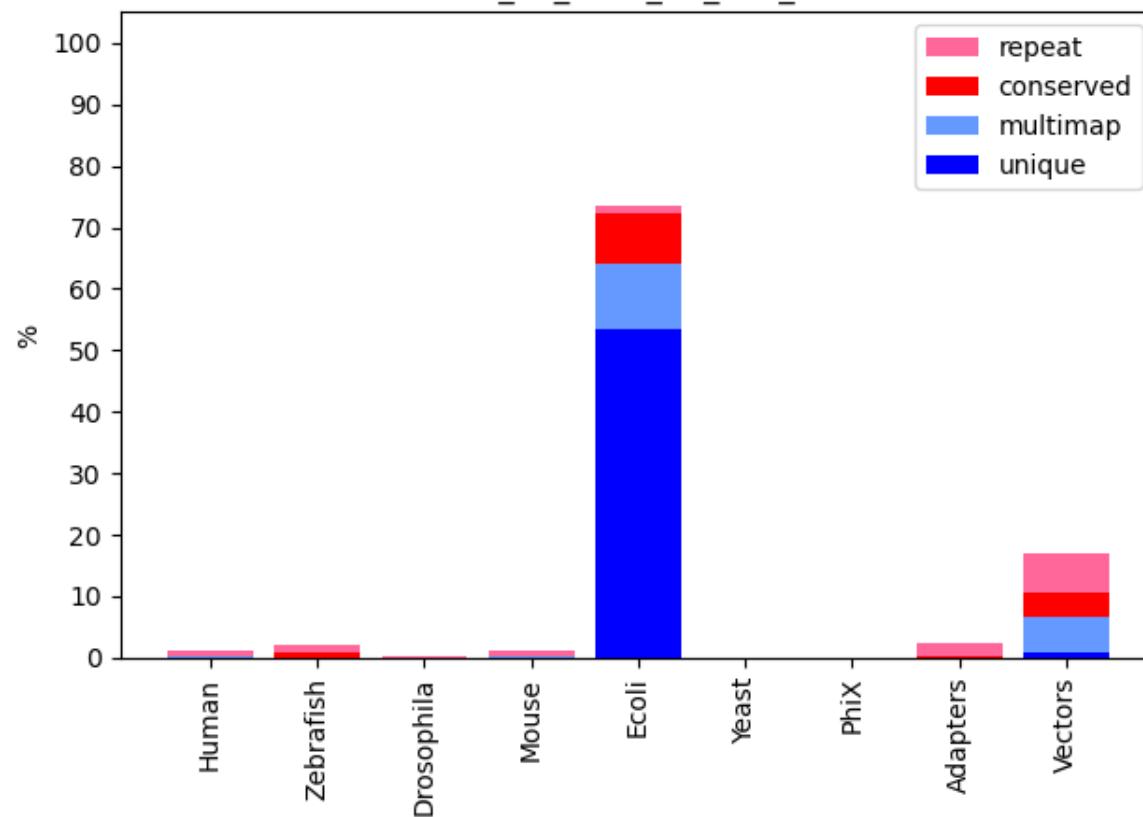
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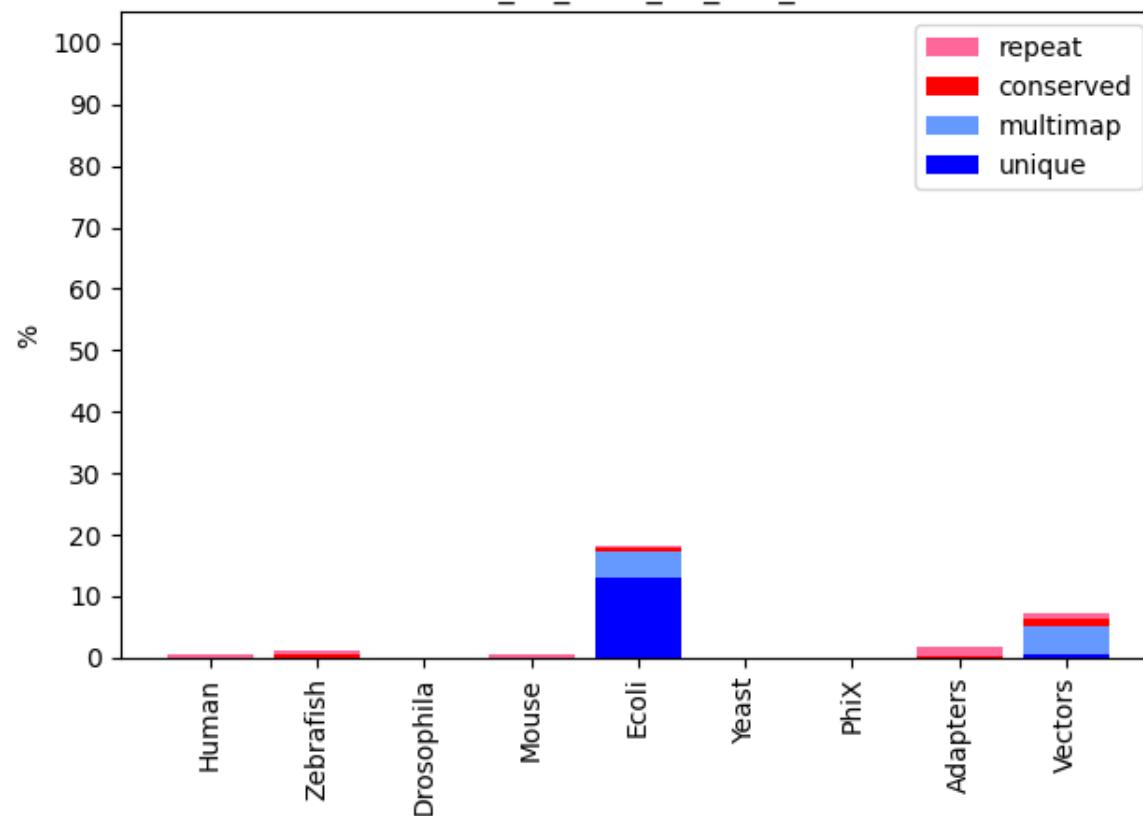
22L005002_S4_L001_R2_001_screen.txt



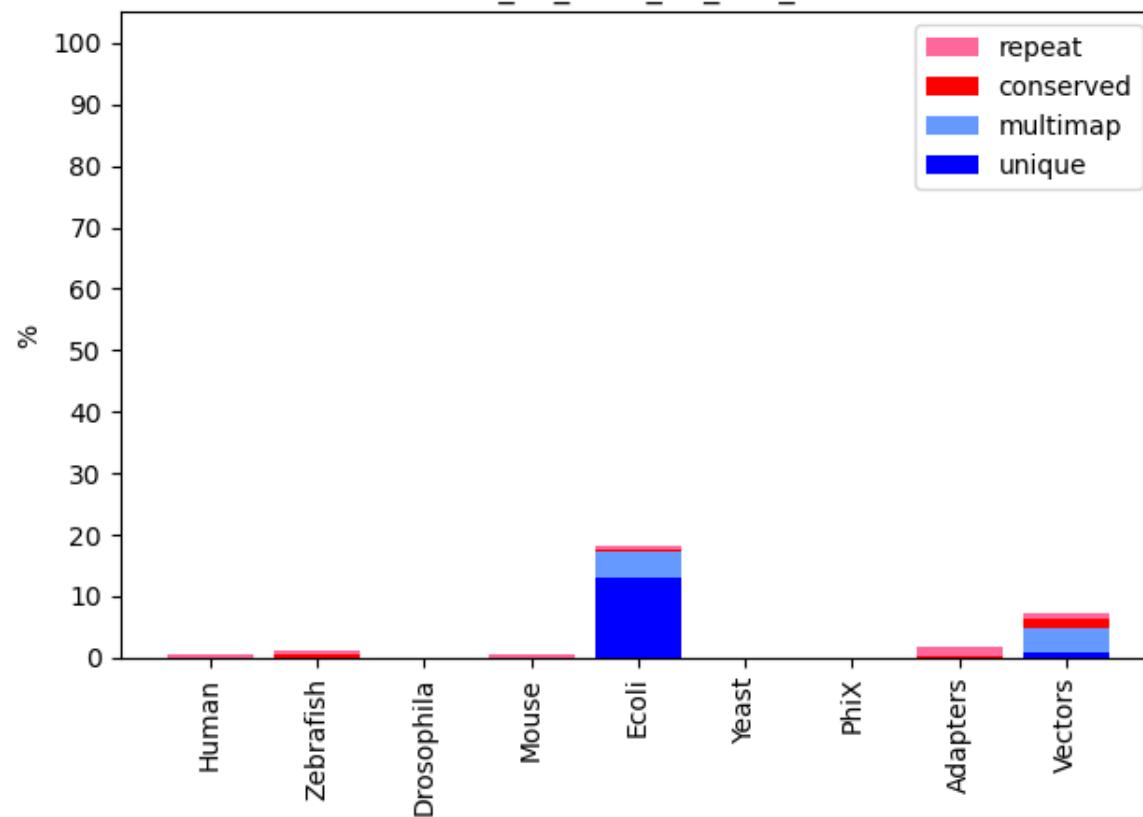
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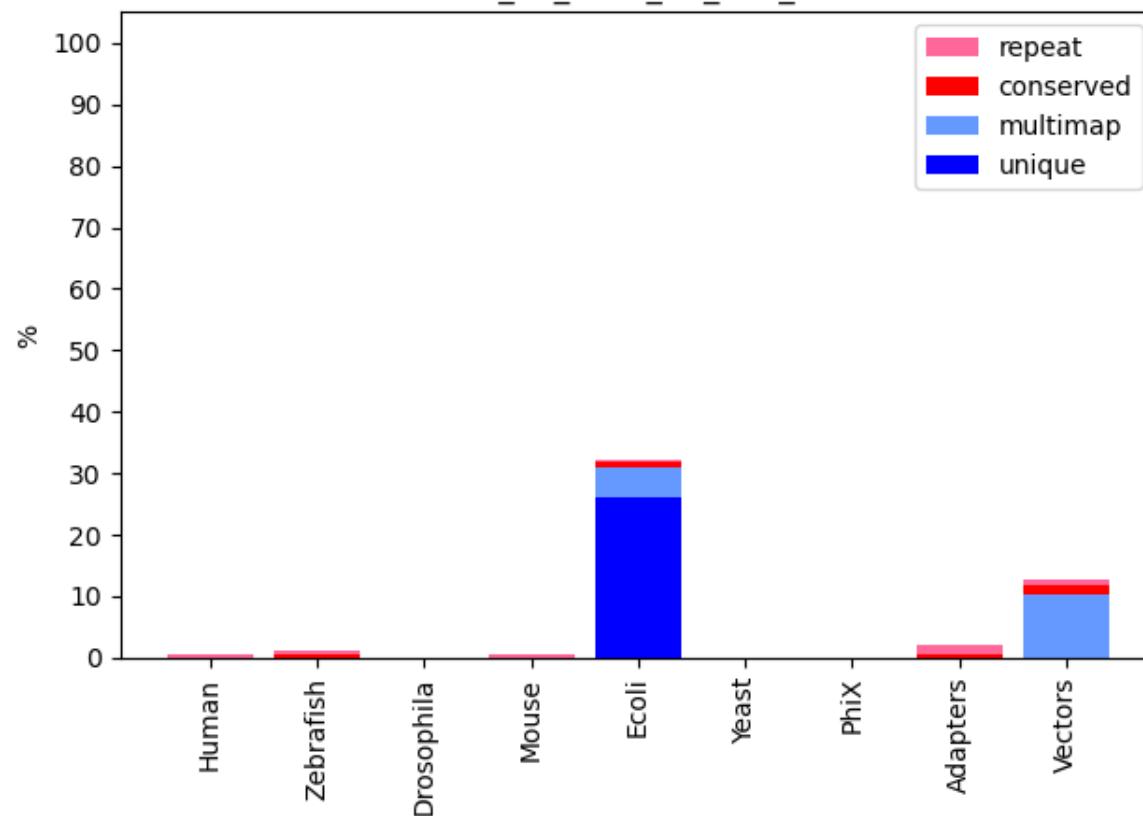
22L005003_S5_L001_R2_001_screen.txt



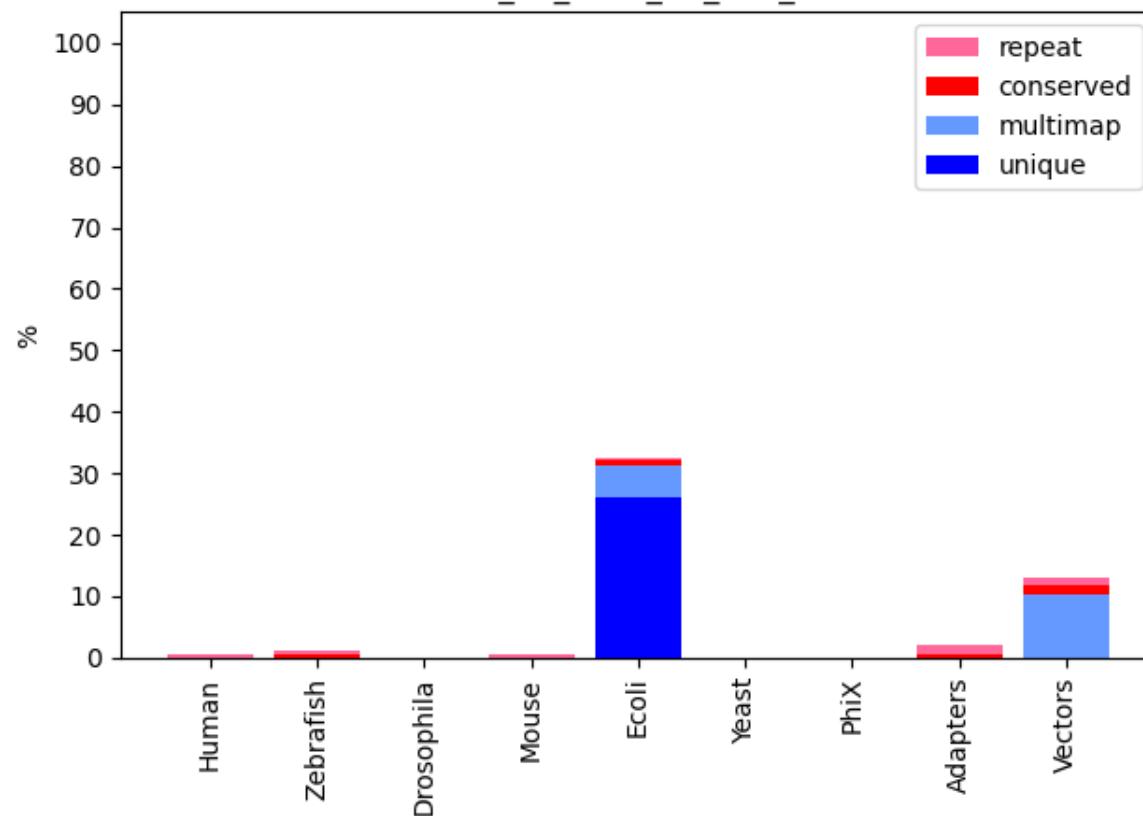
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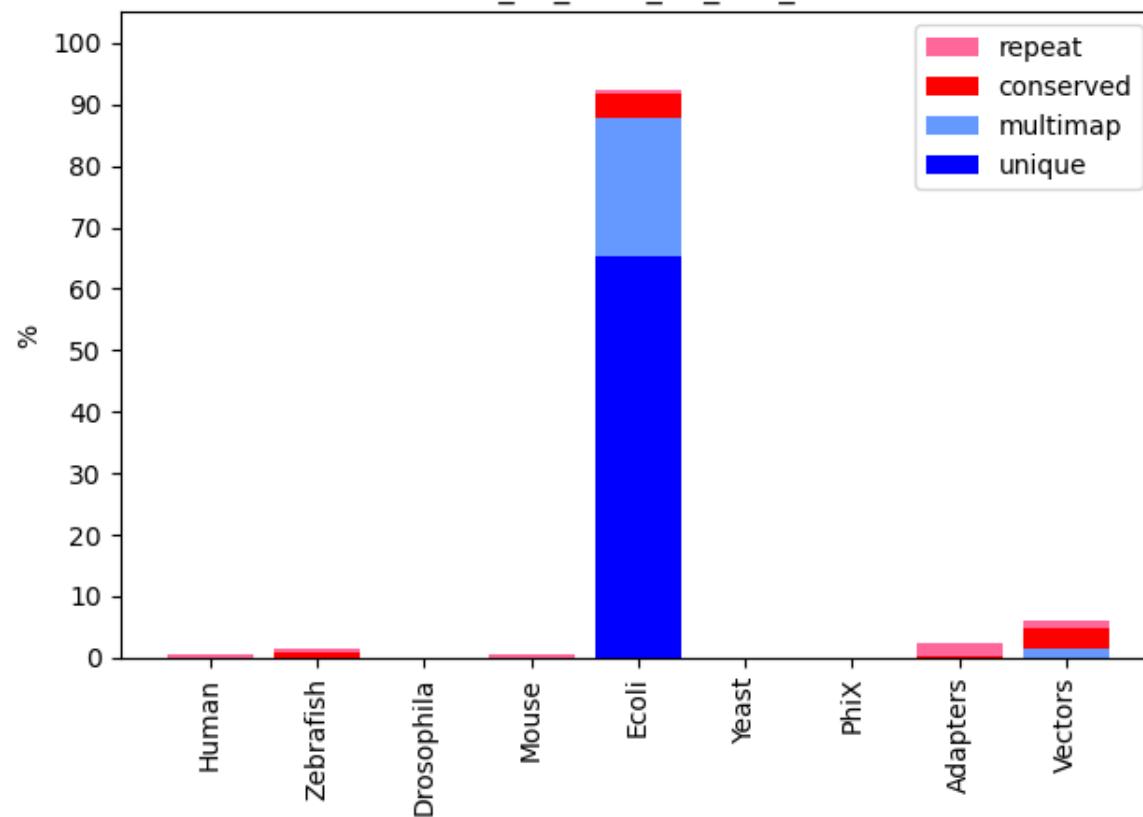
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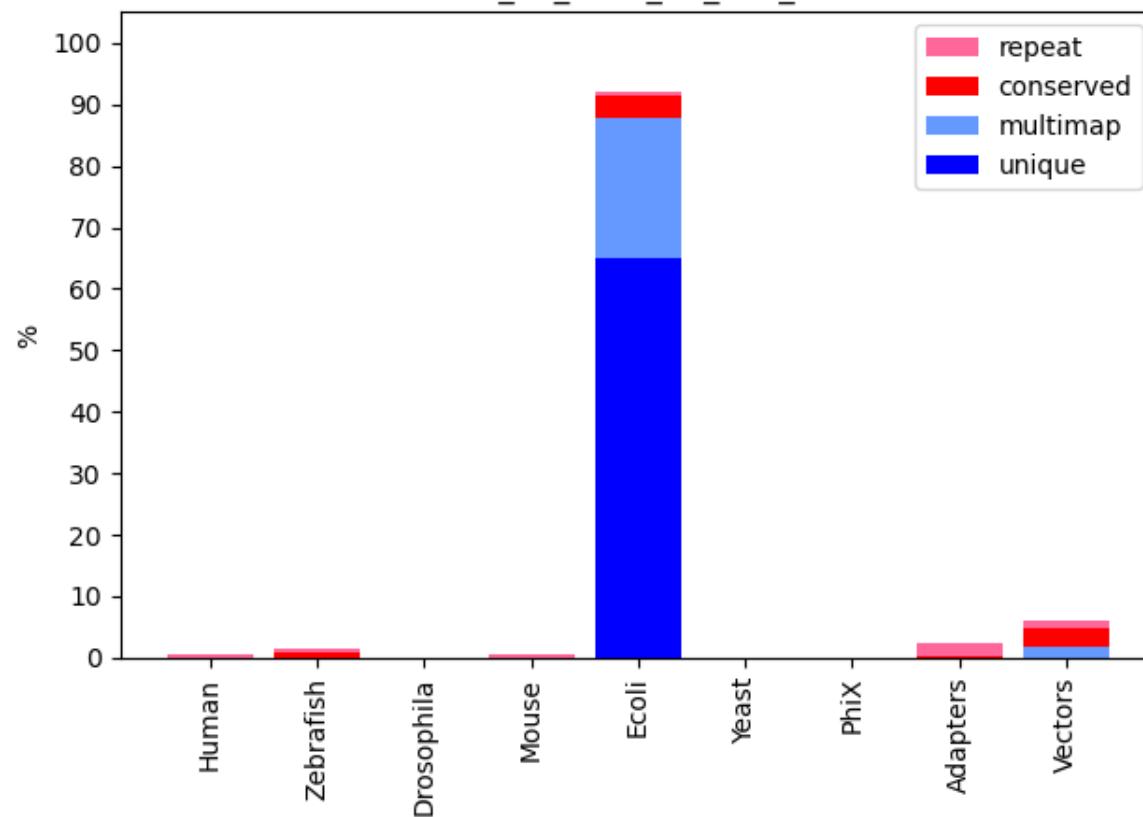
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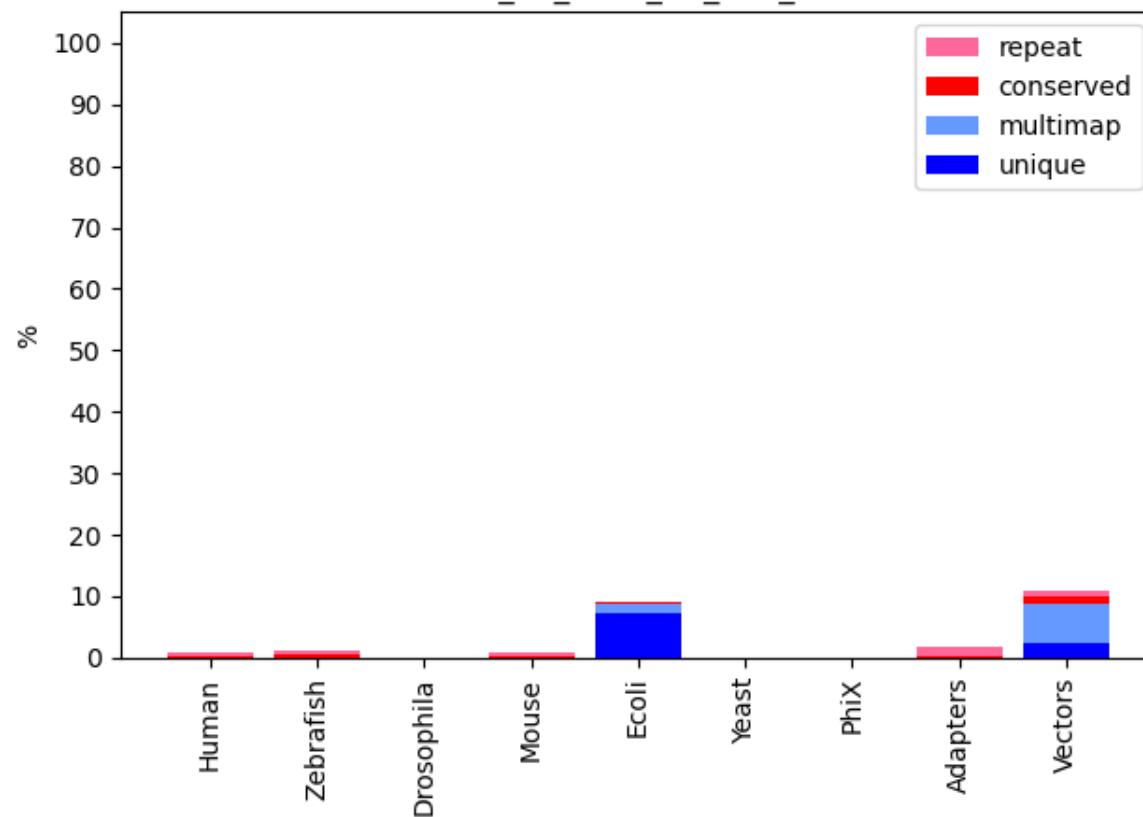
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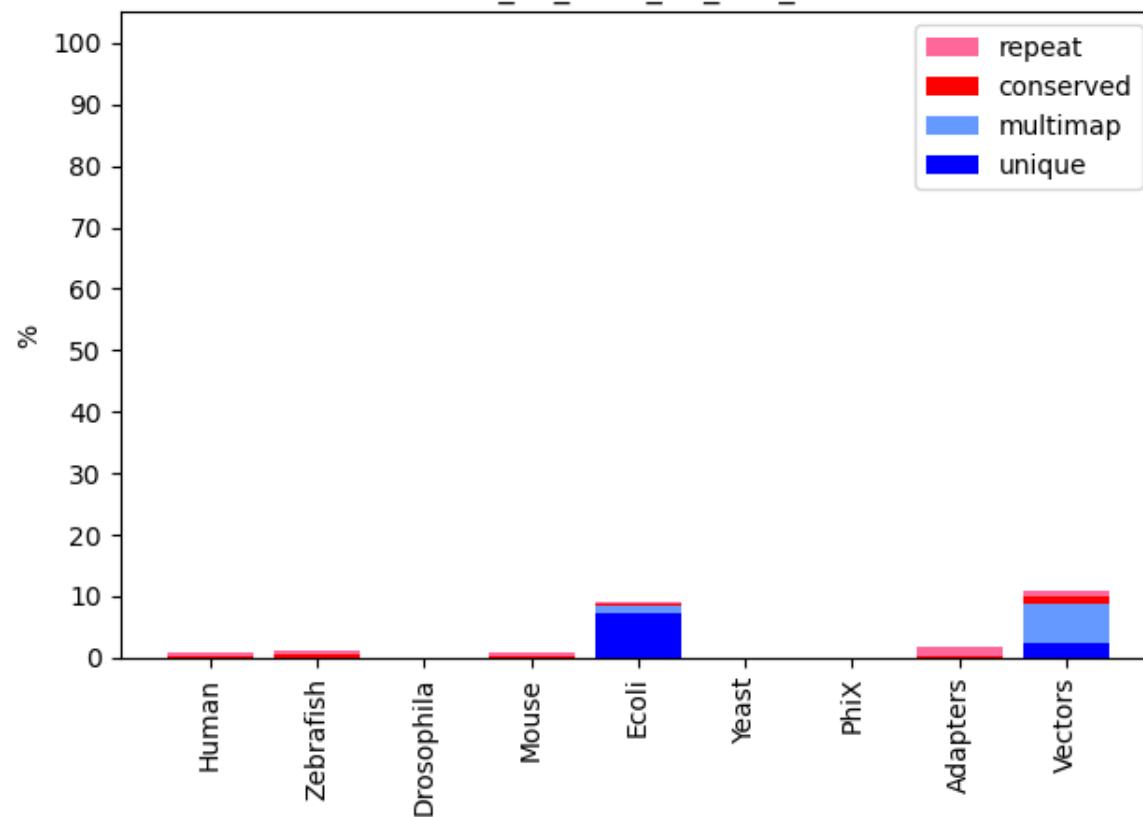
22L005005_S7_L002_R2_001_screen.txt



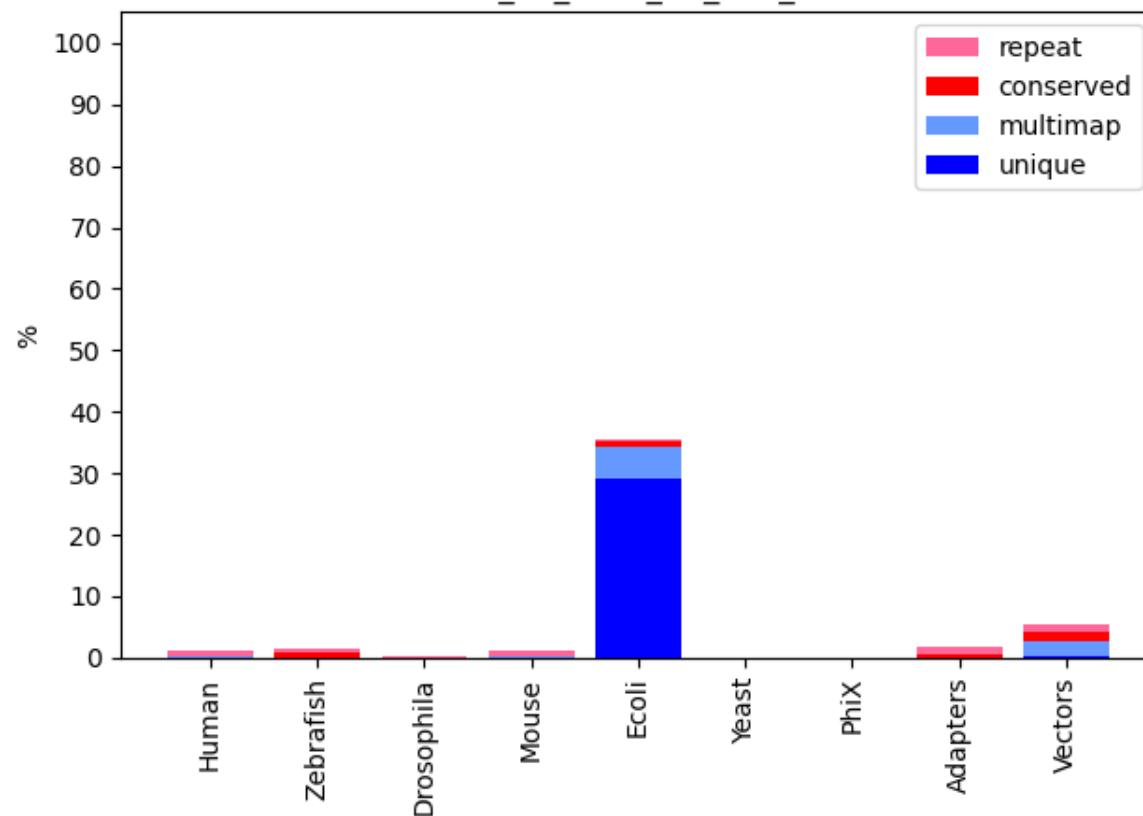
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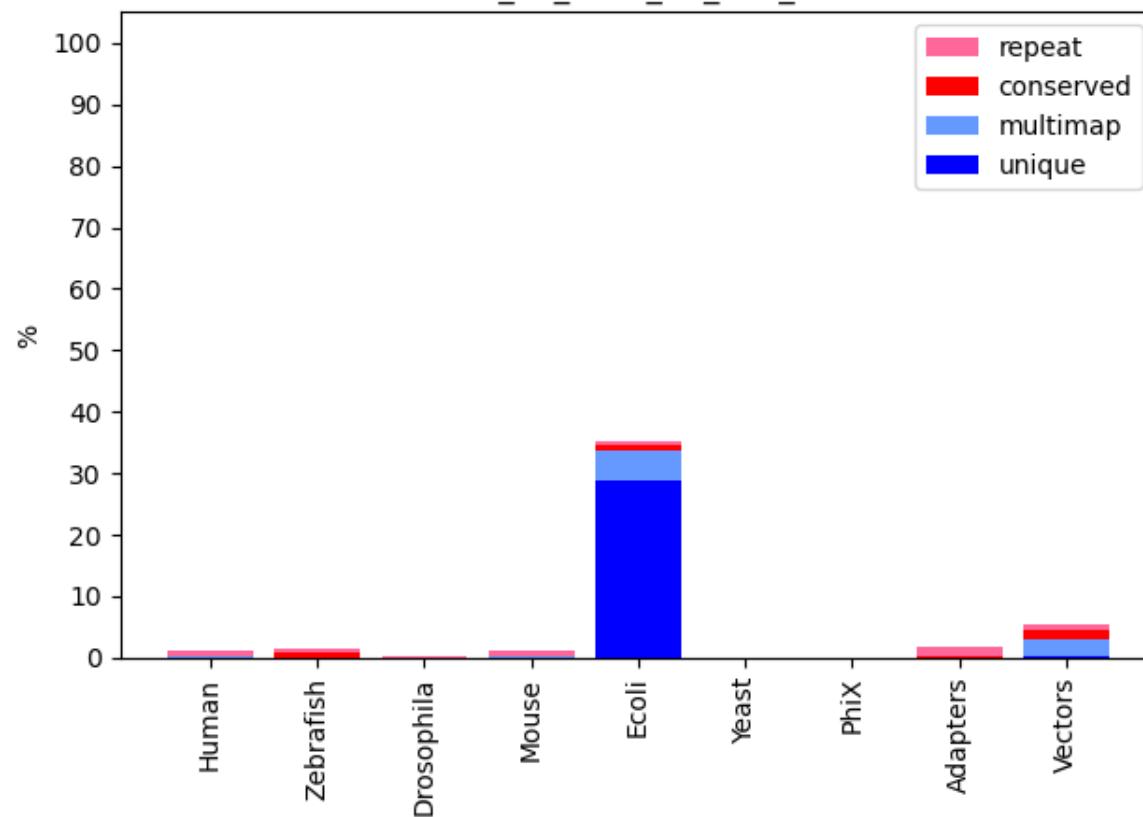
22L005006_S8_L002_R2_001_screen.txt



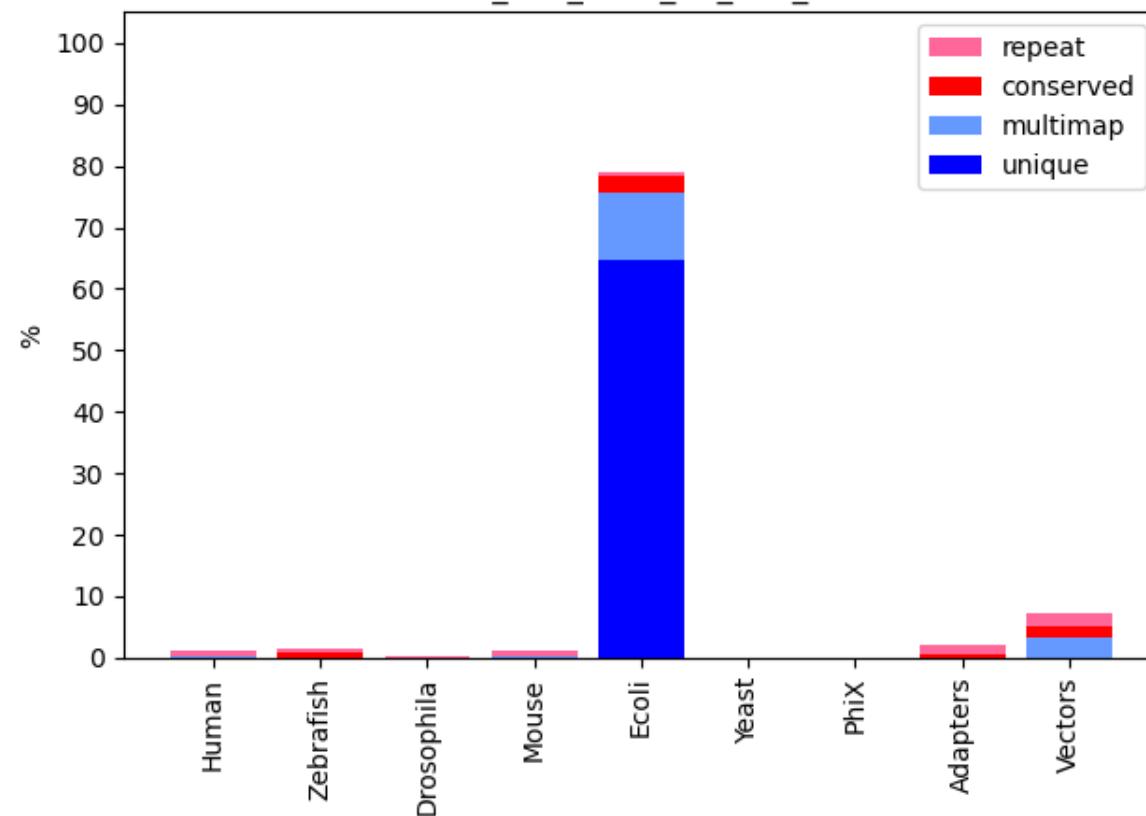
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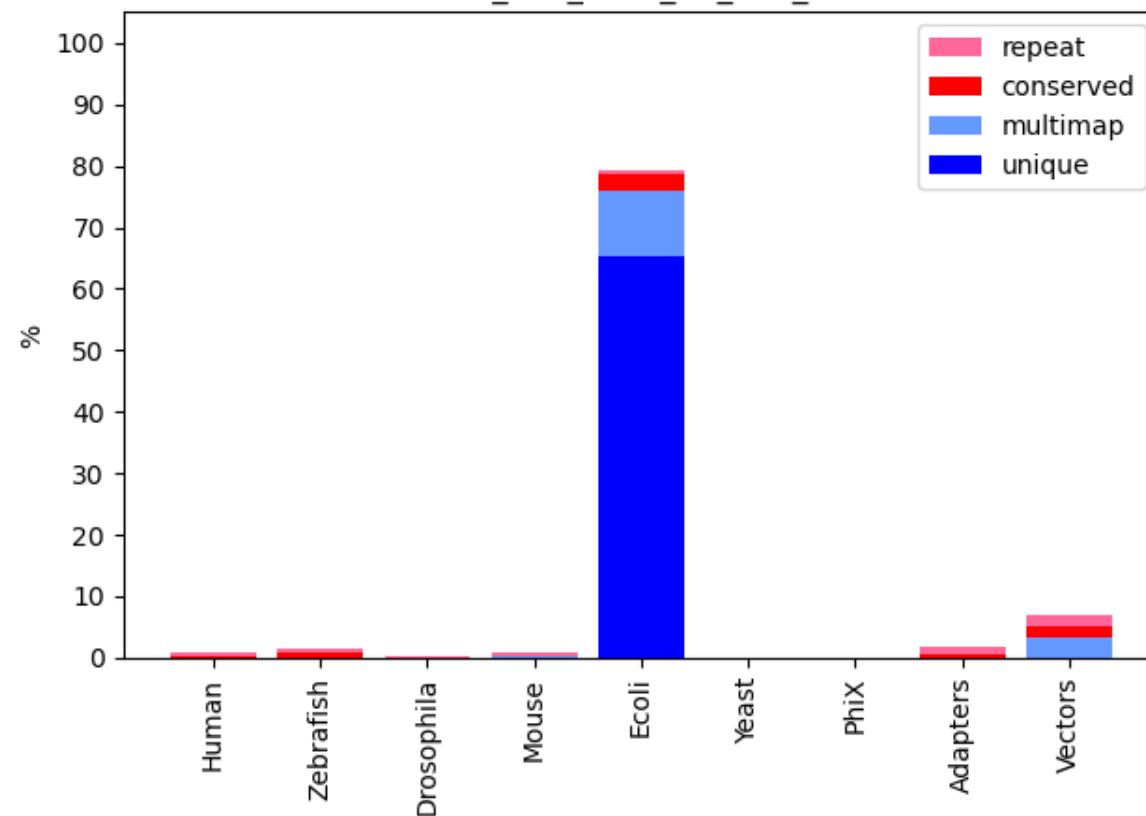
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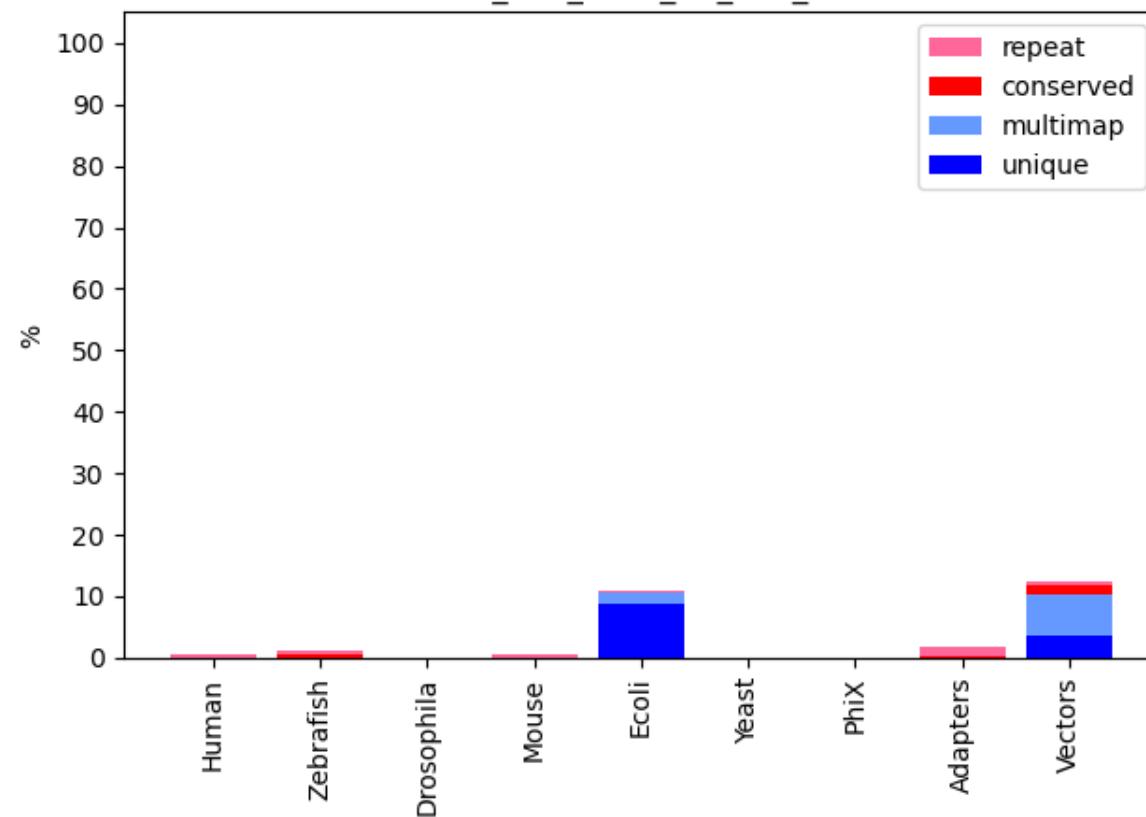
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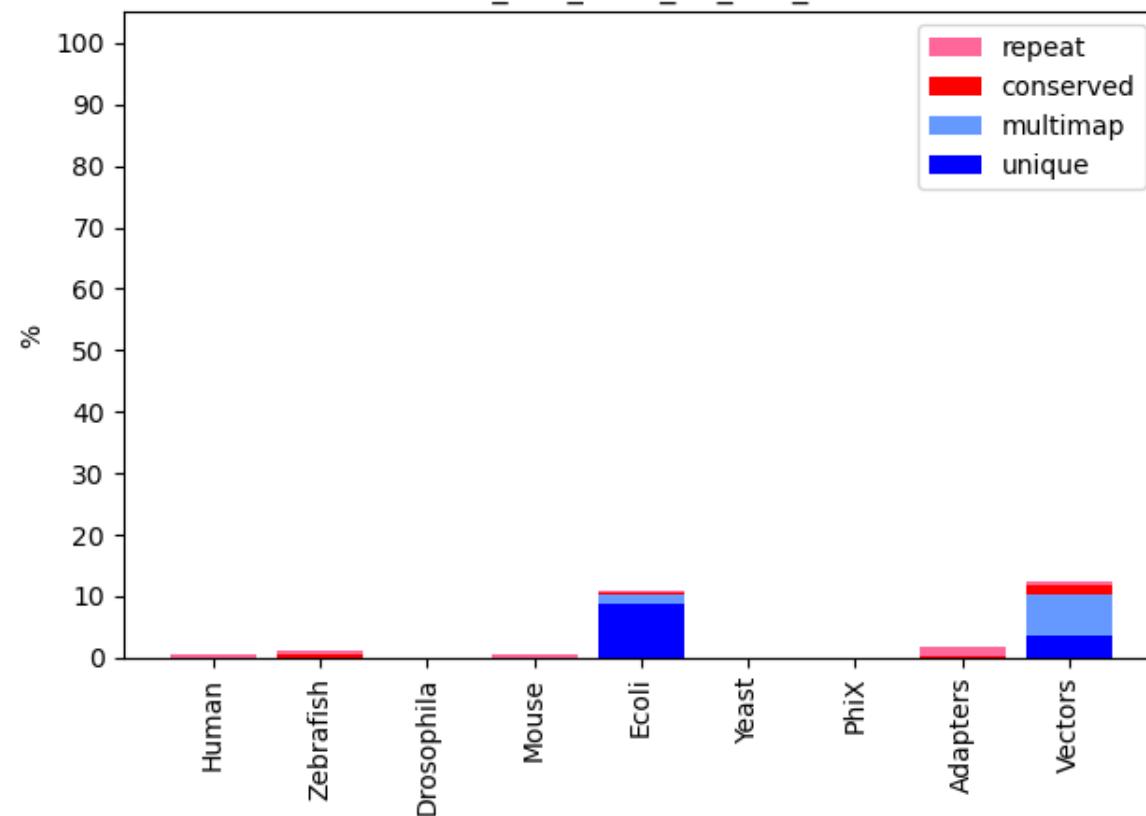
22L005008_S10_L002_R2_001_screen.txt



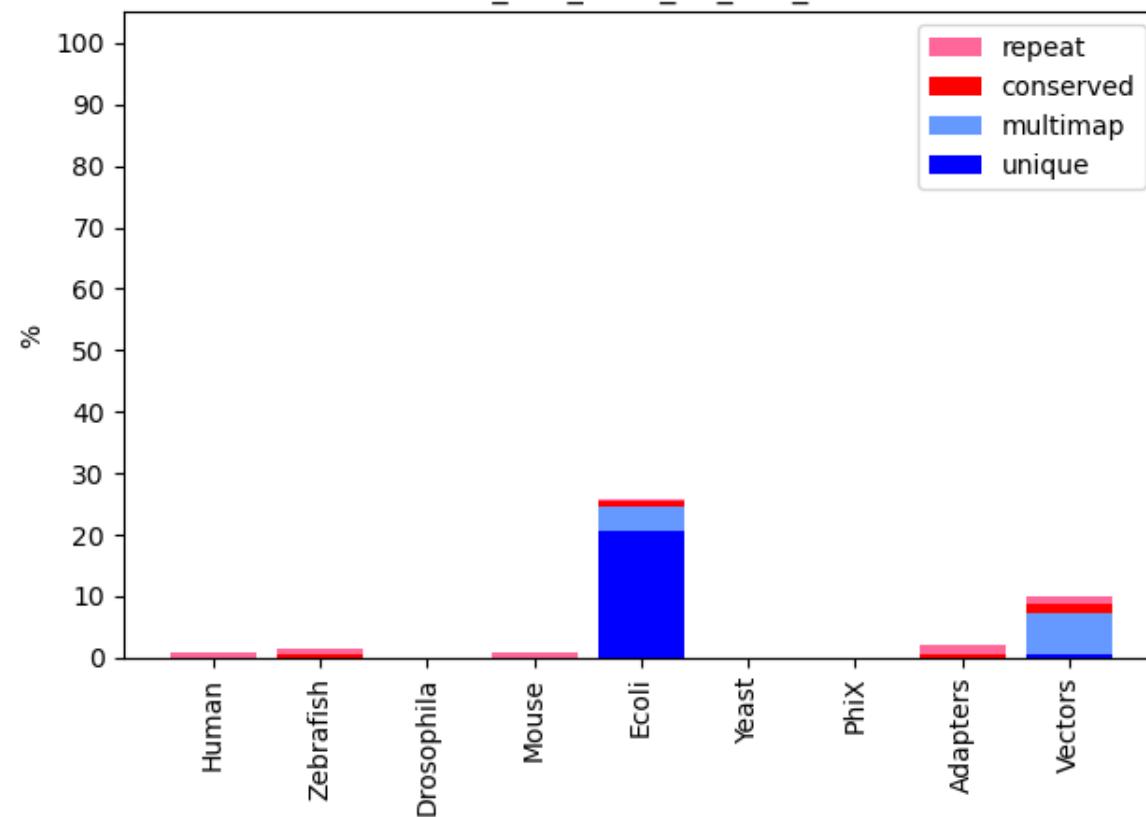
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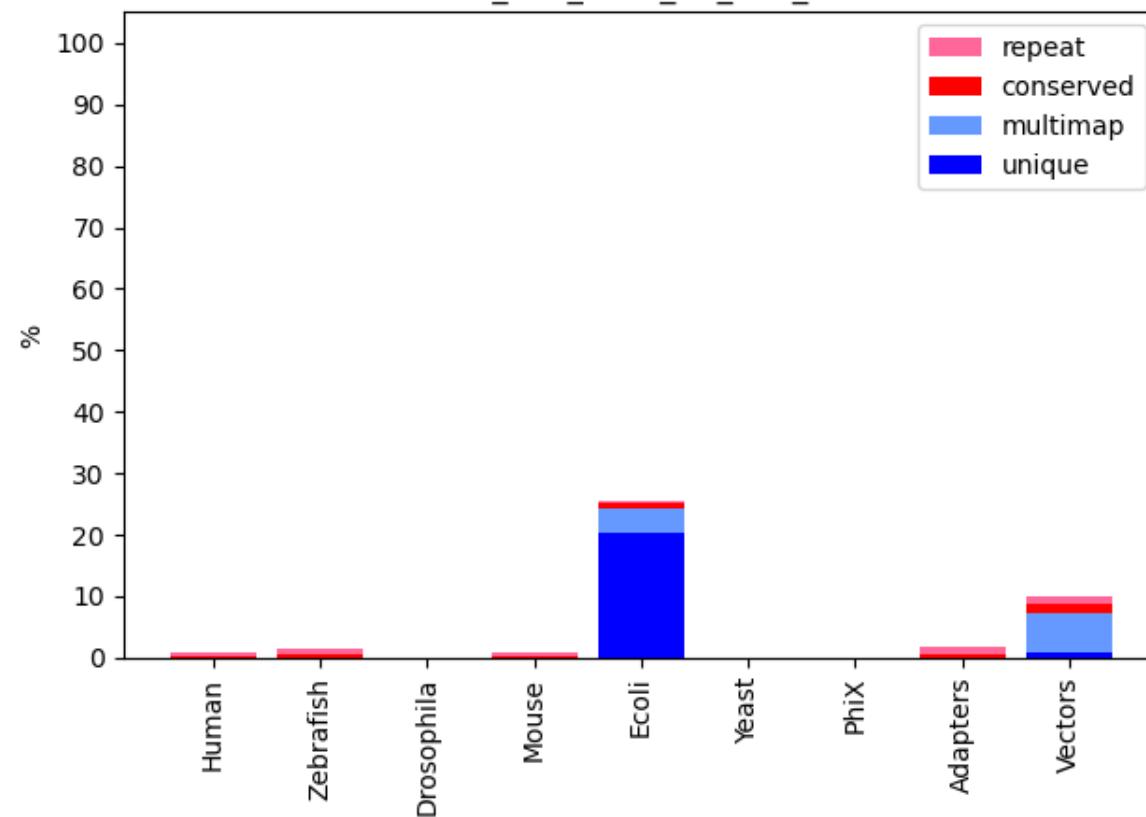
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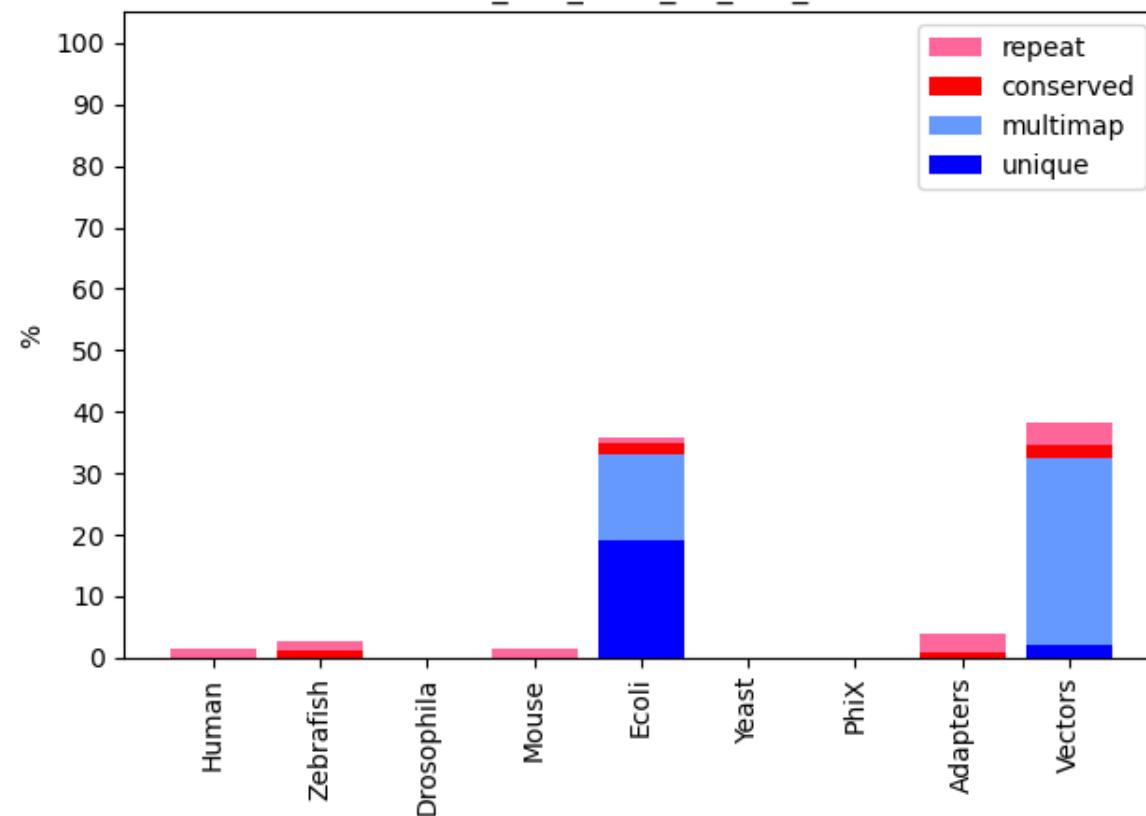
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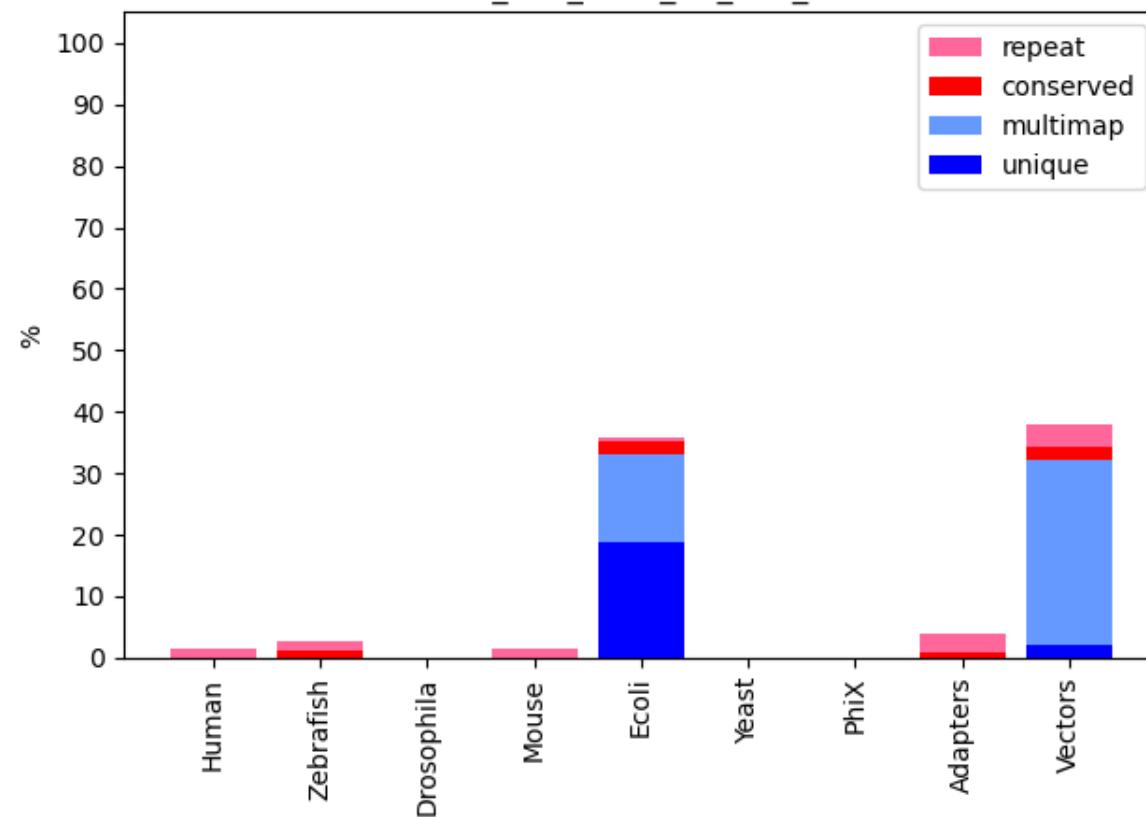
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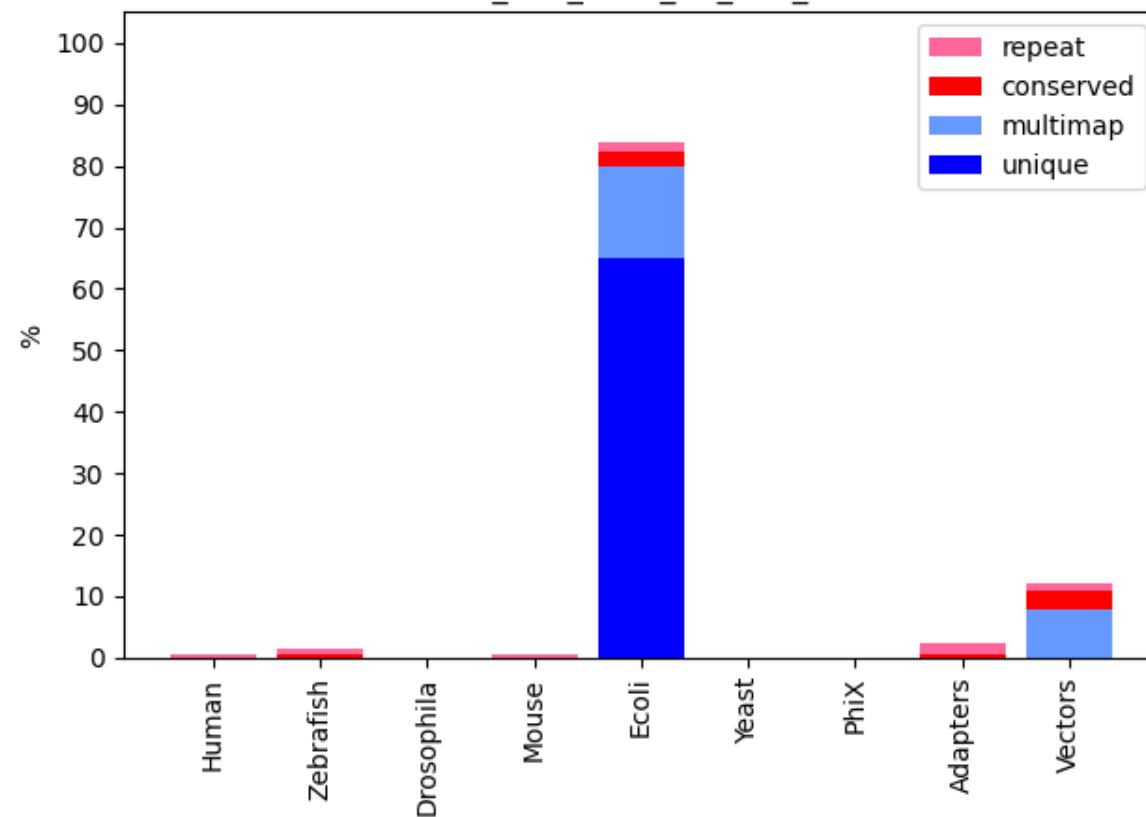
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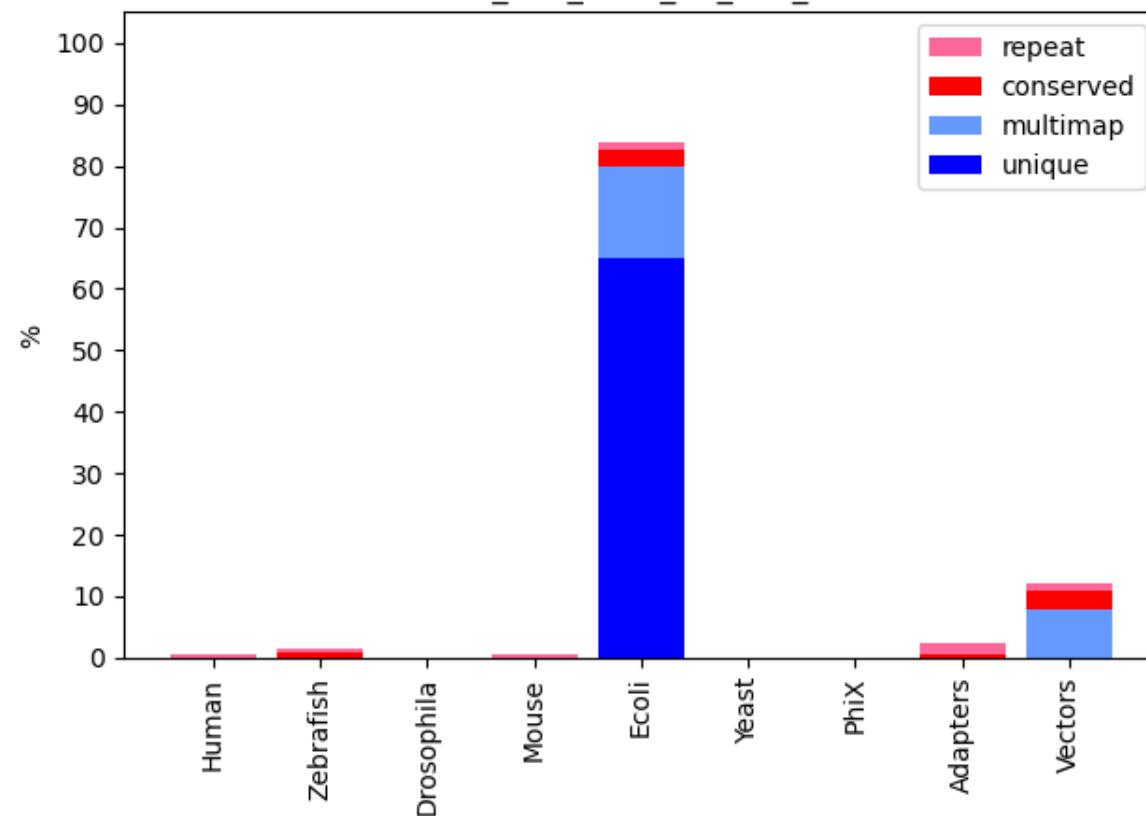
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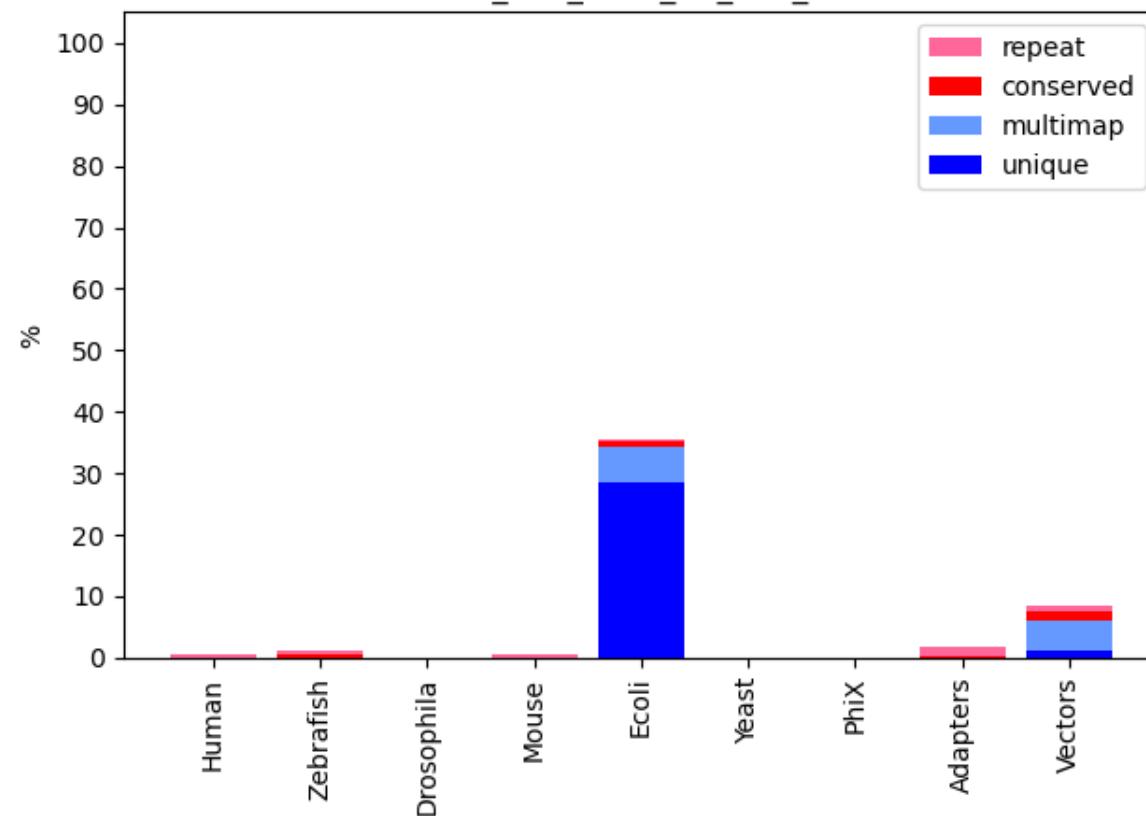
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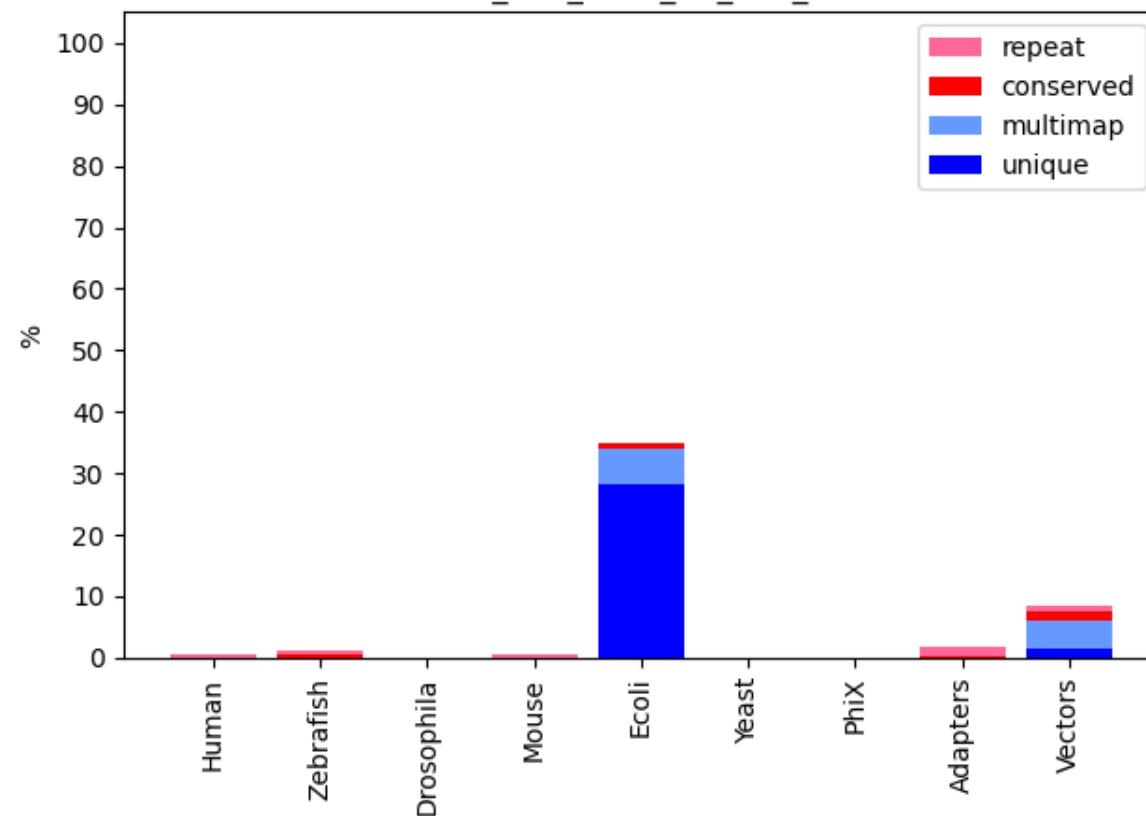
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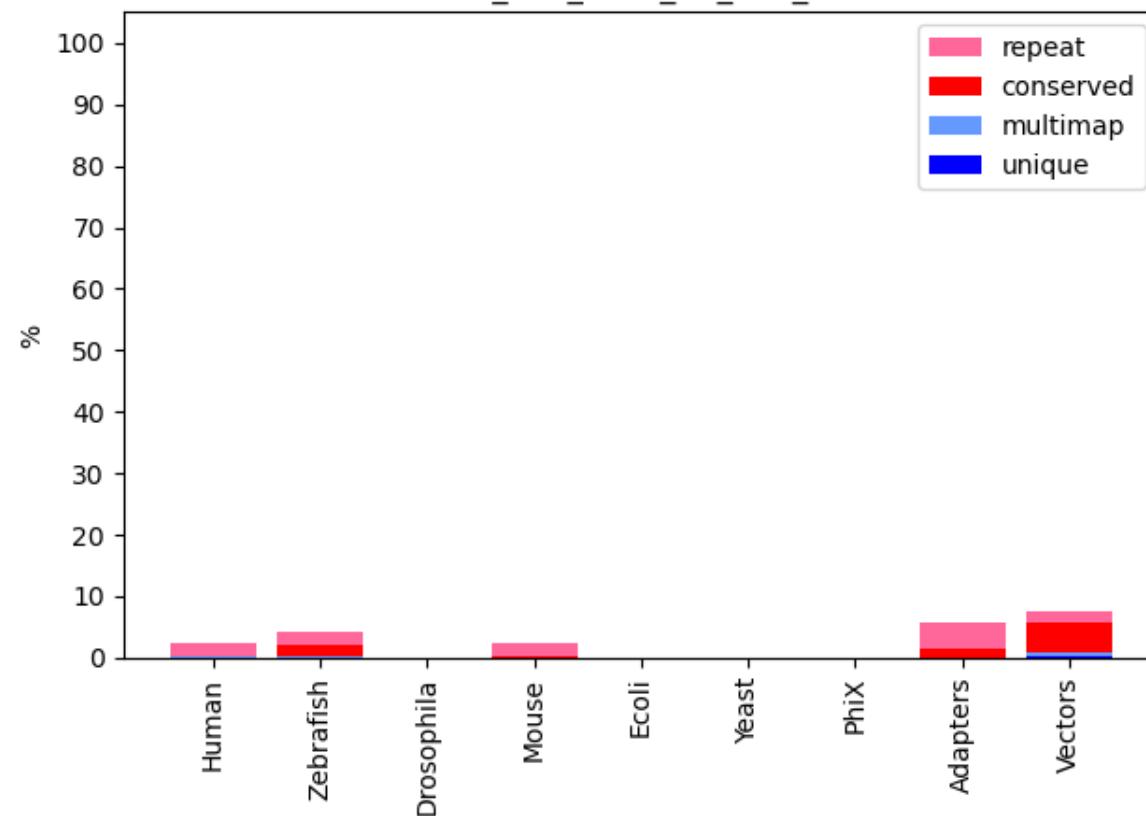
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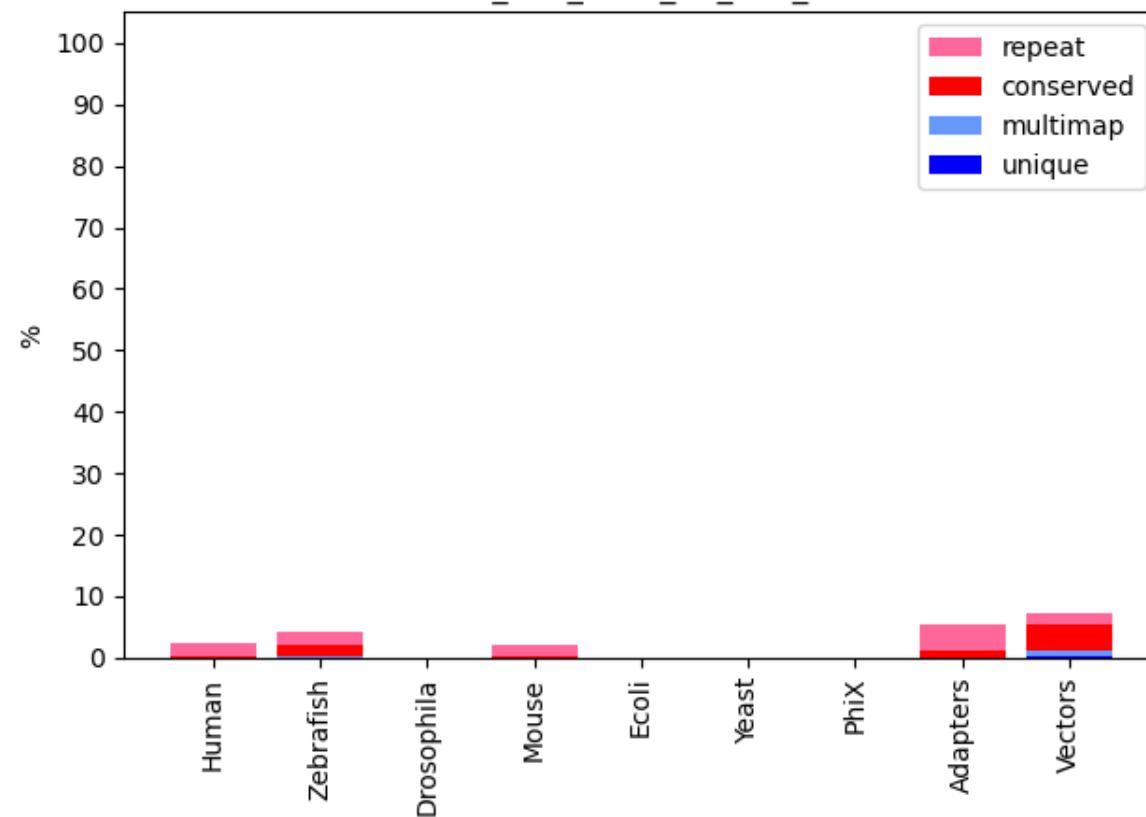
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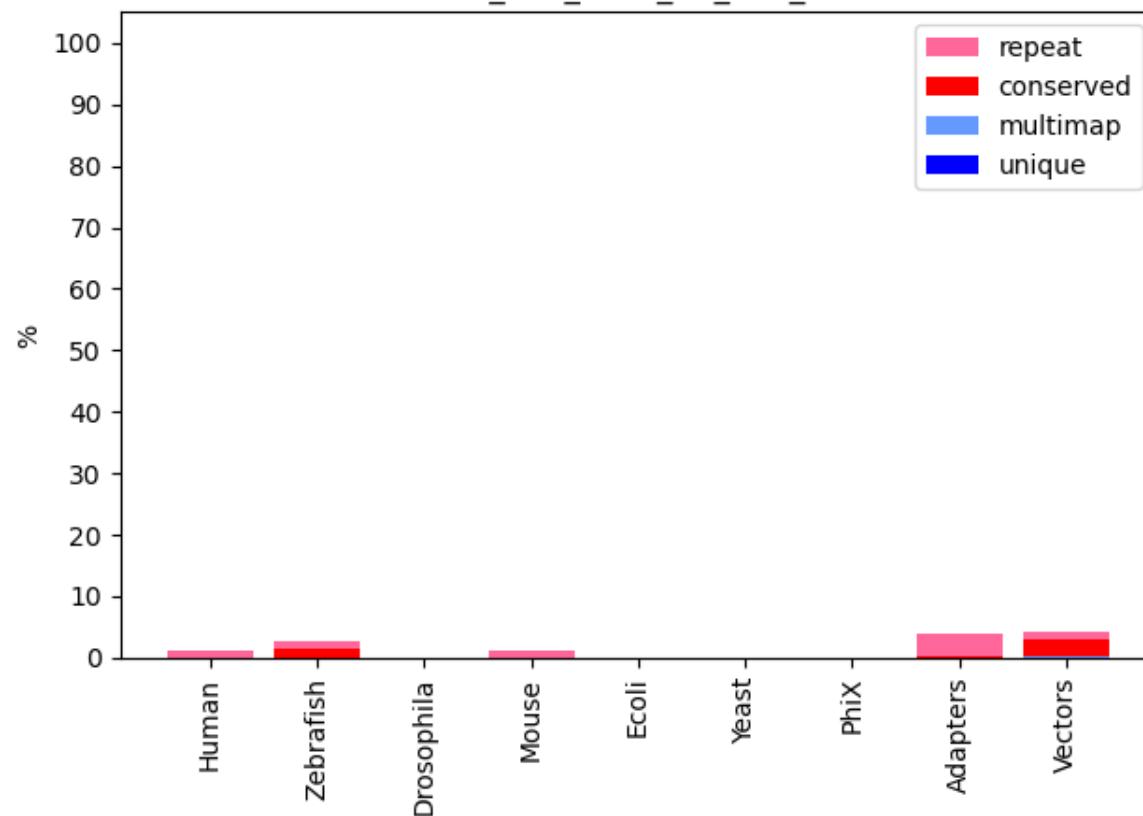
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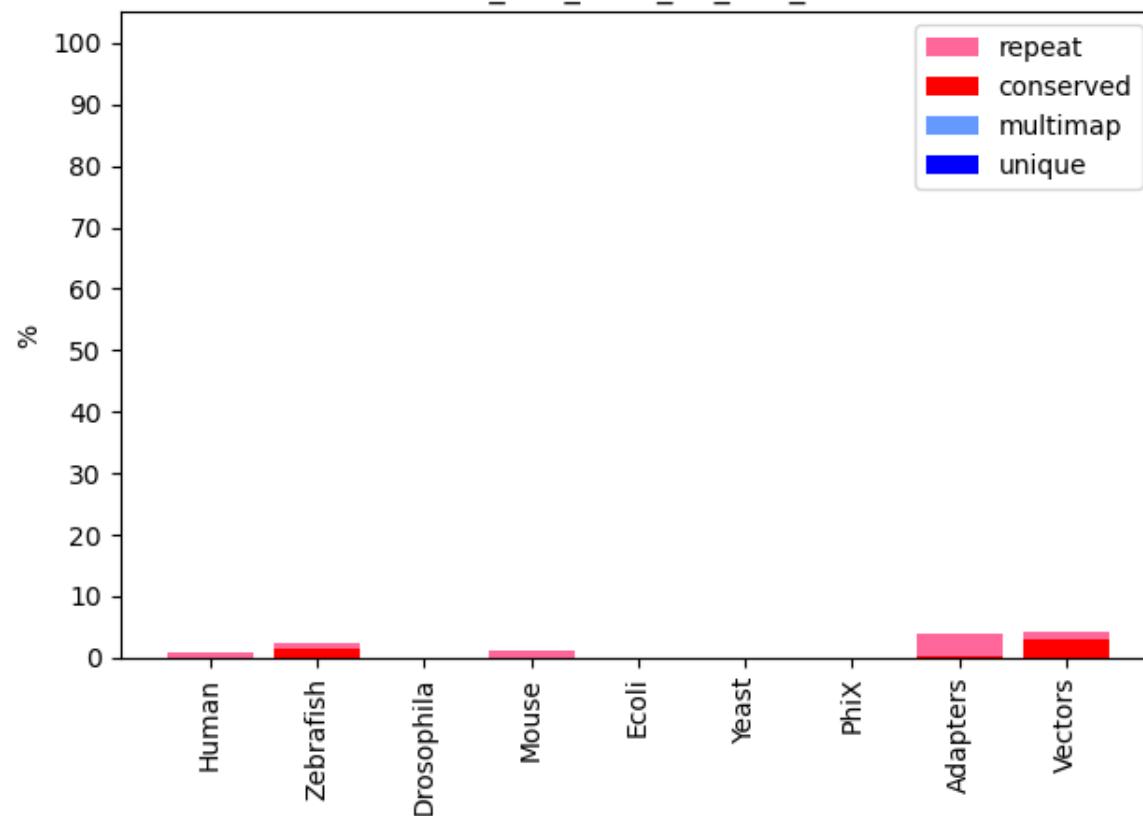
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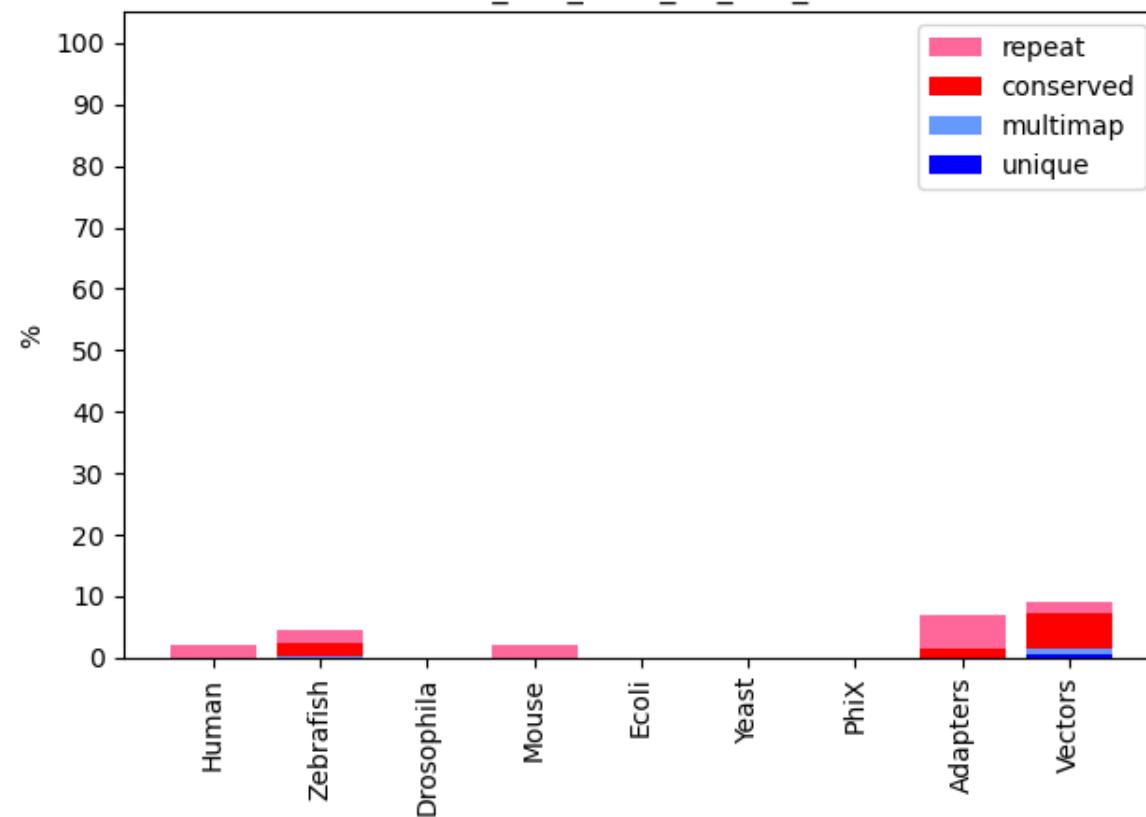
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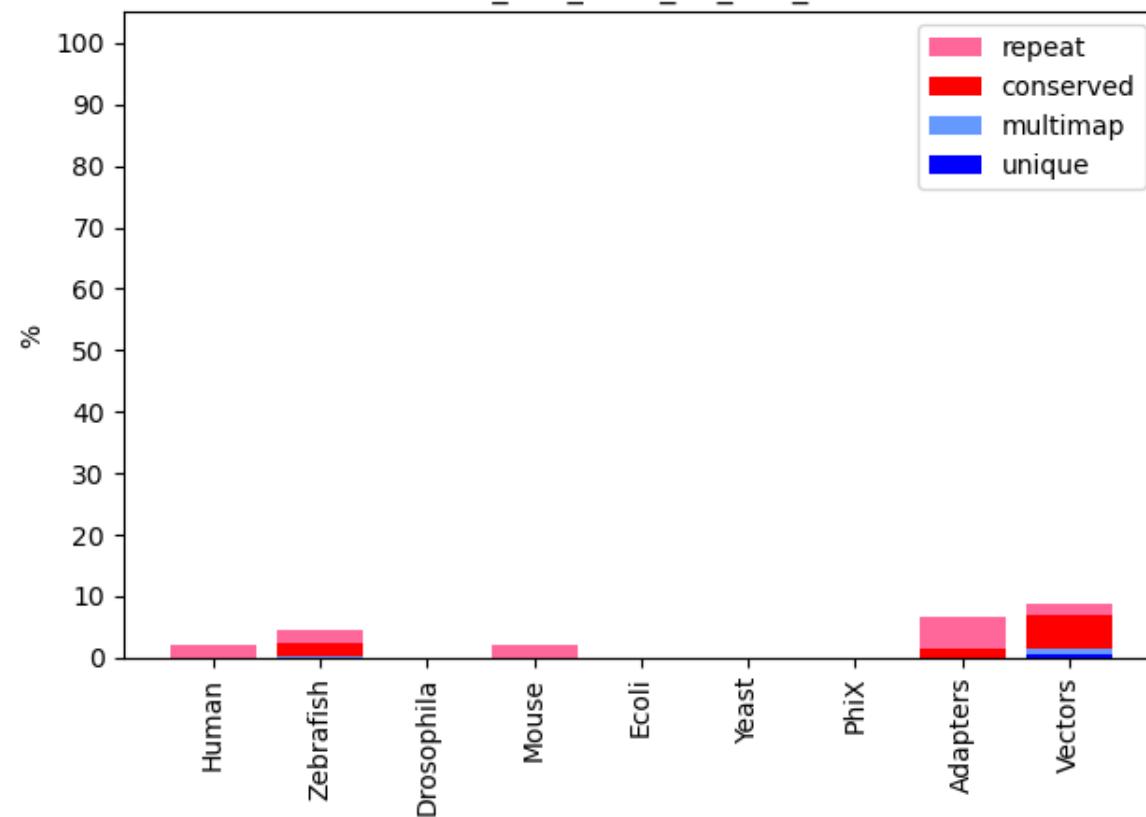
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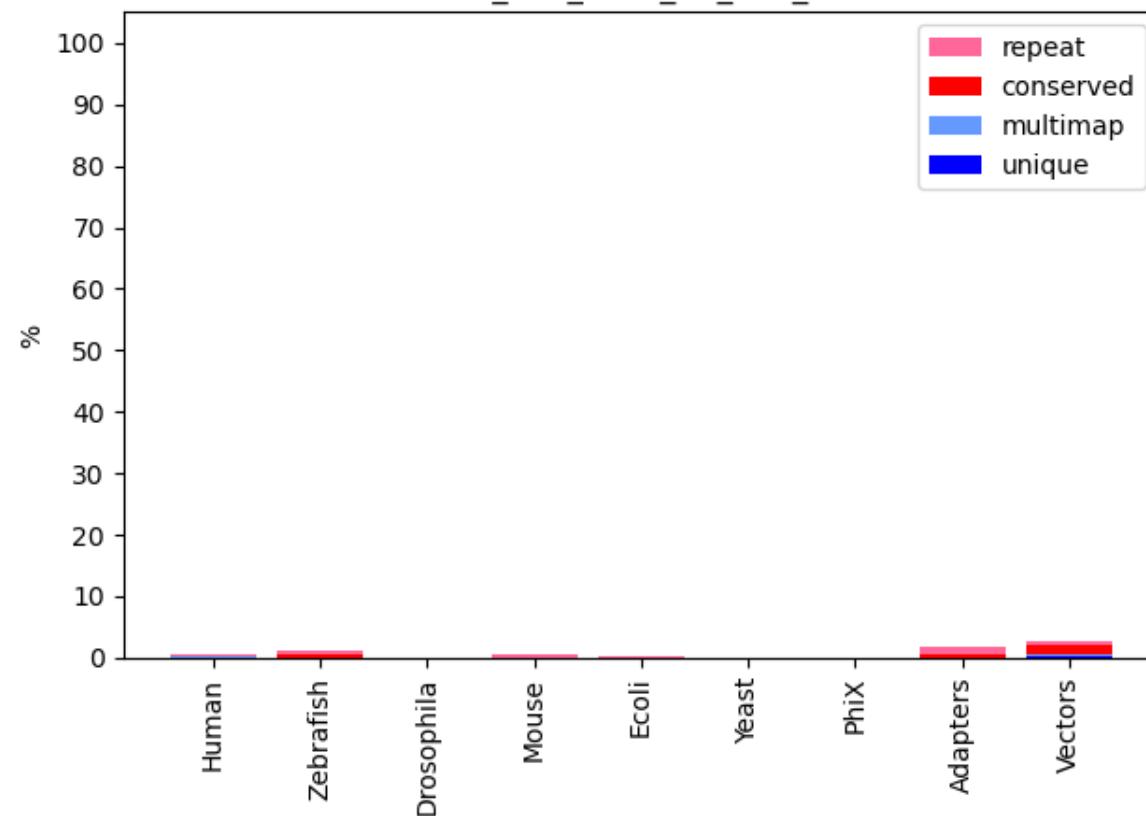
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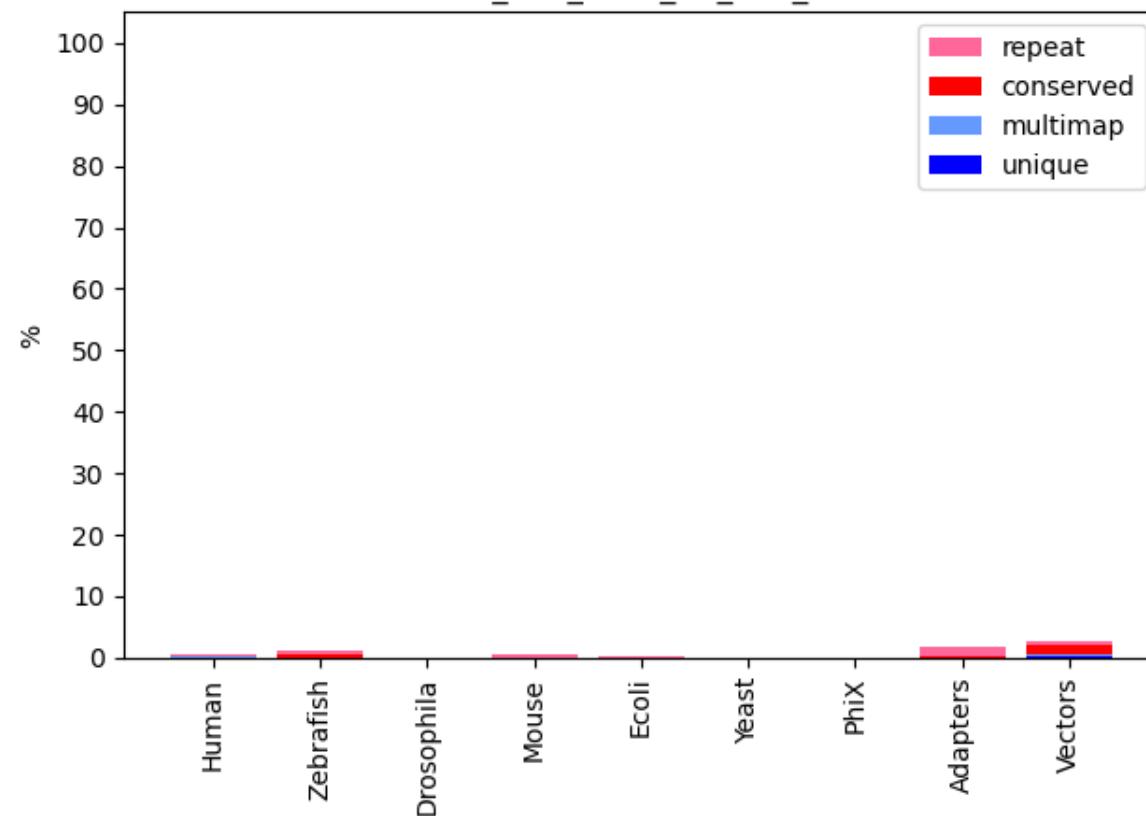
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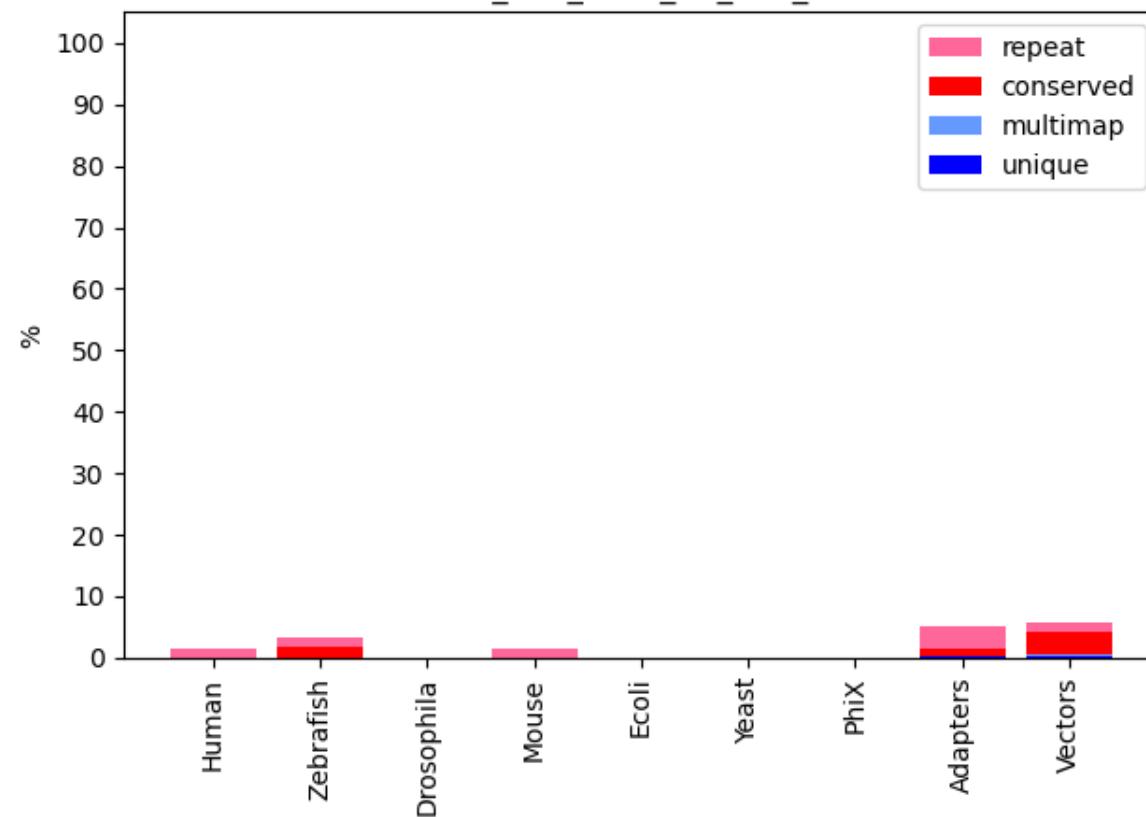
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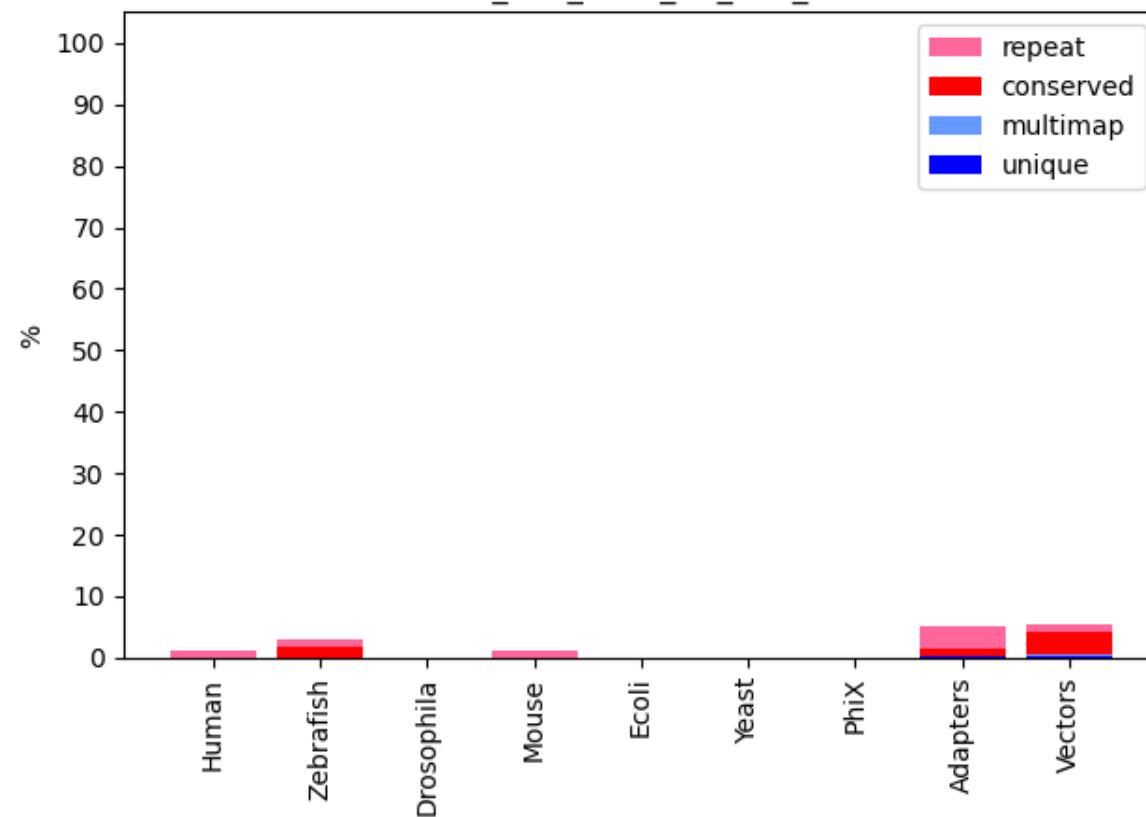
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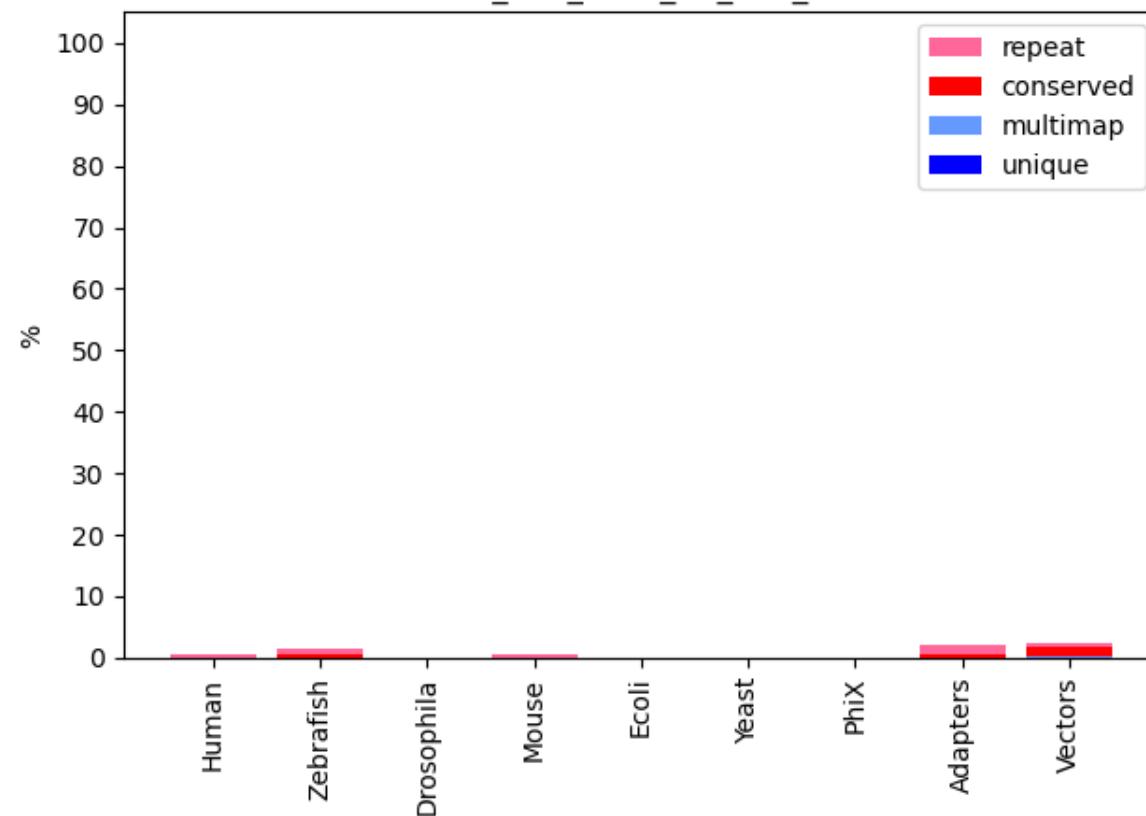
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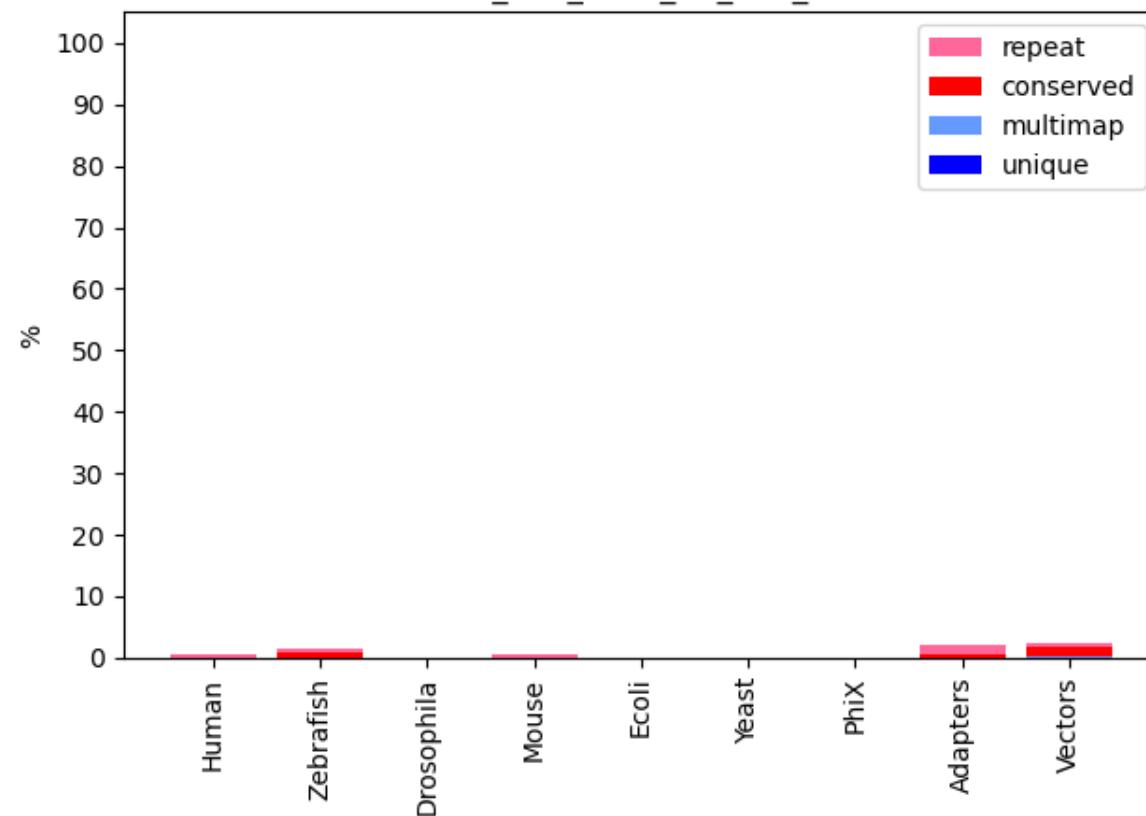
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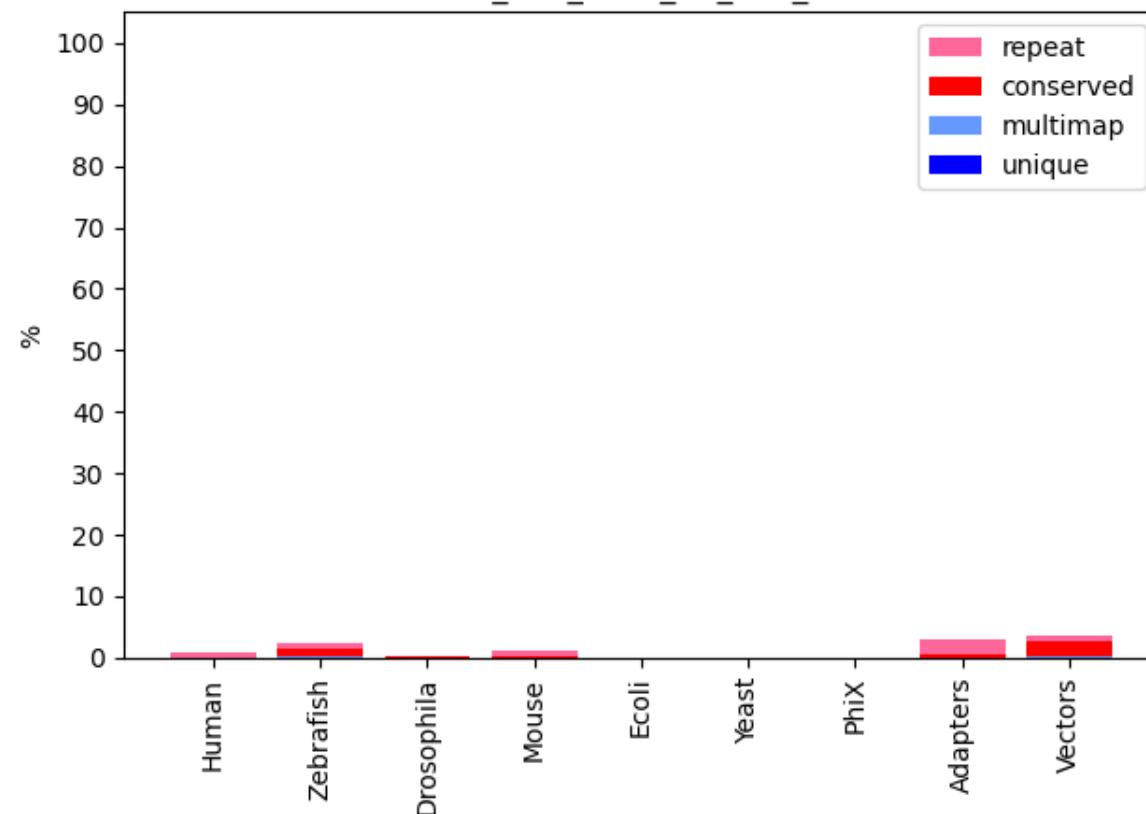
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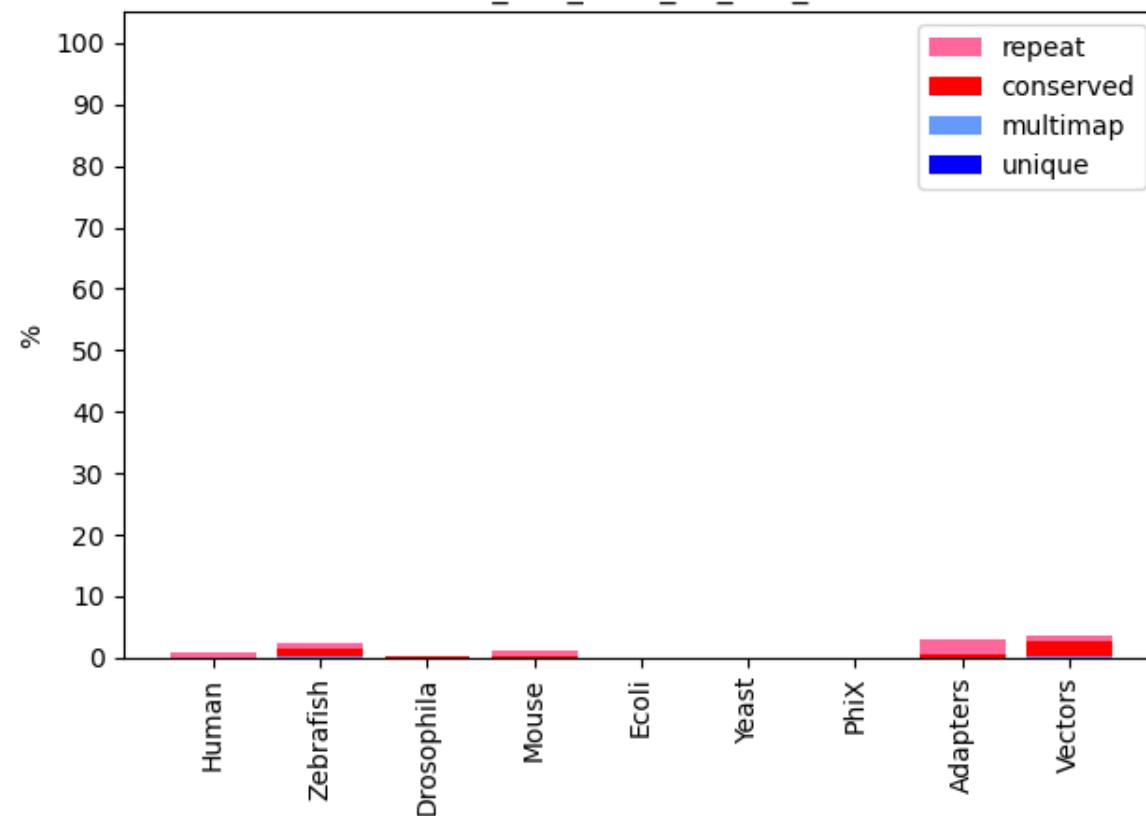
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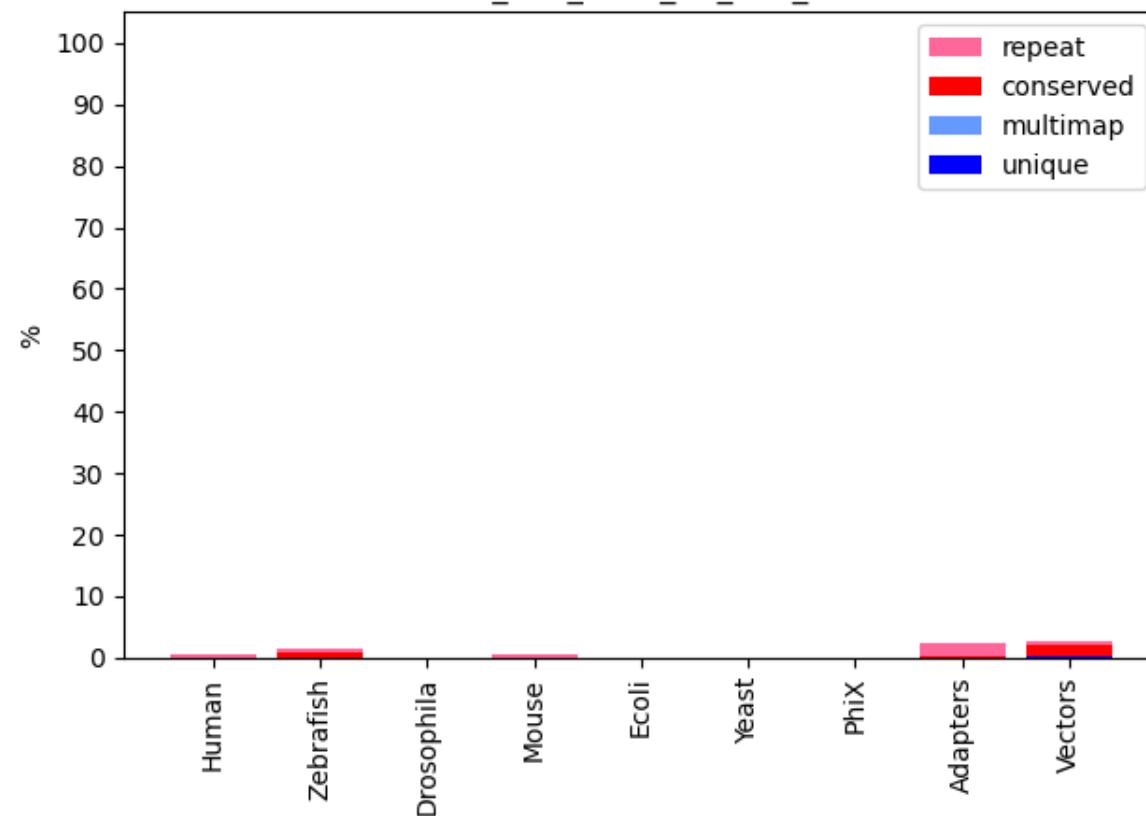
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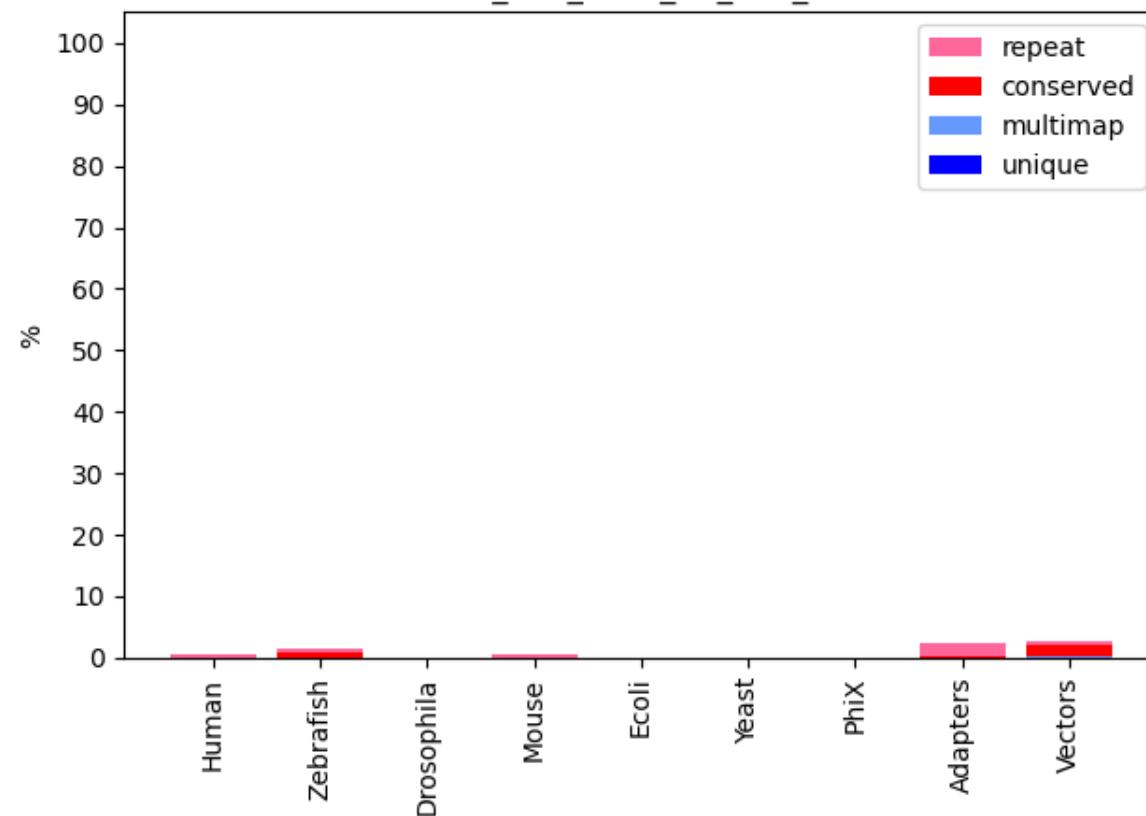
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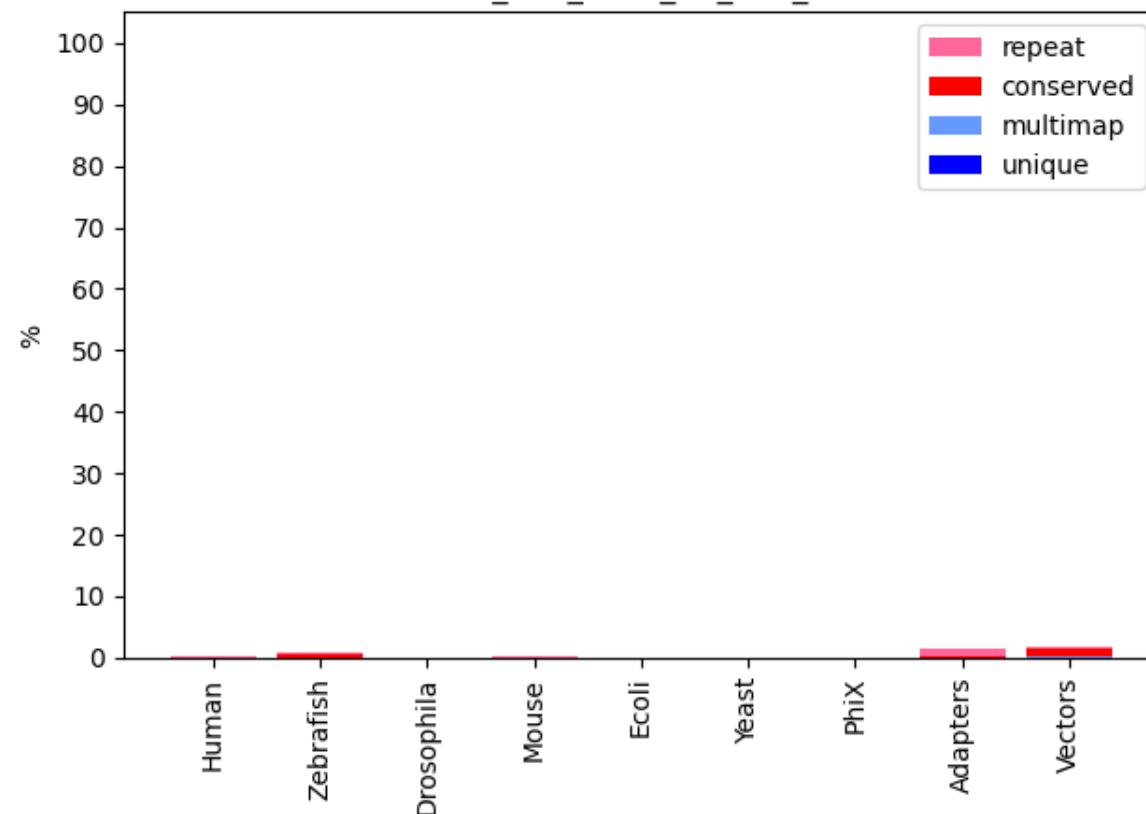
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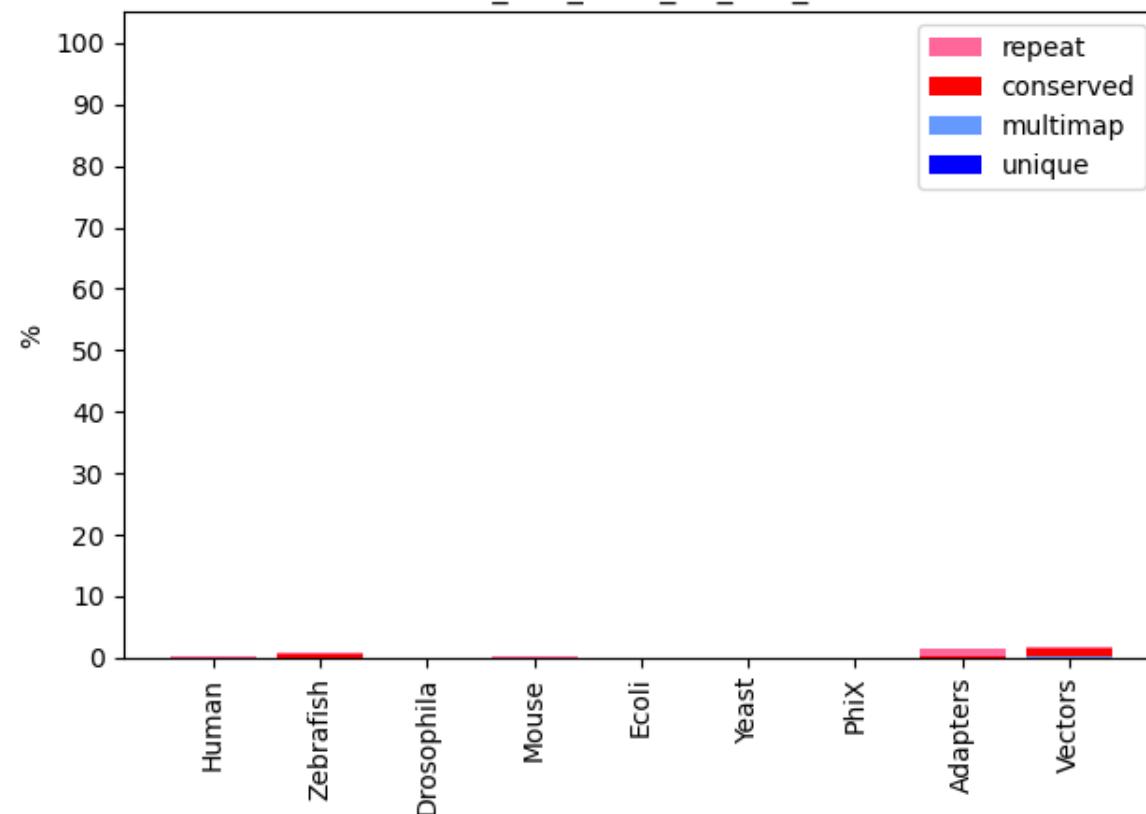
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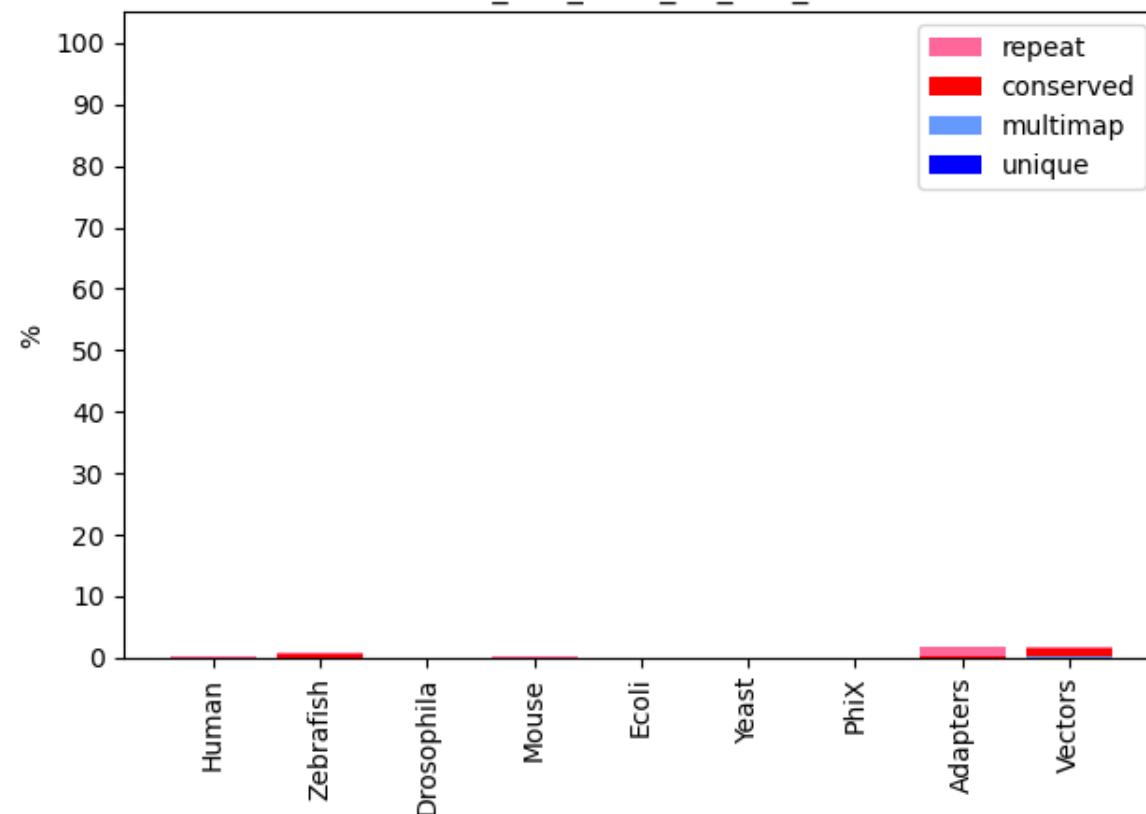
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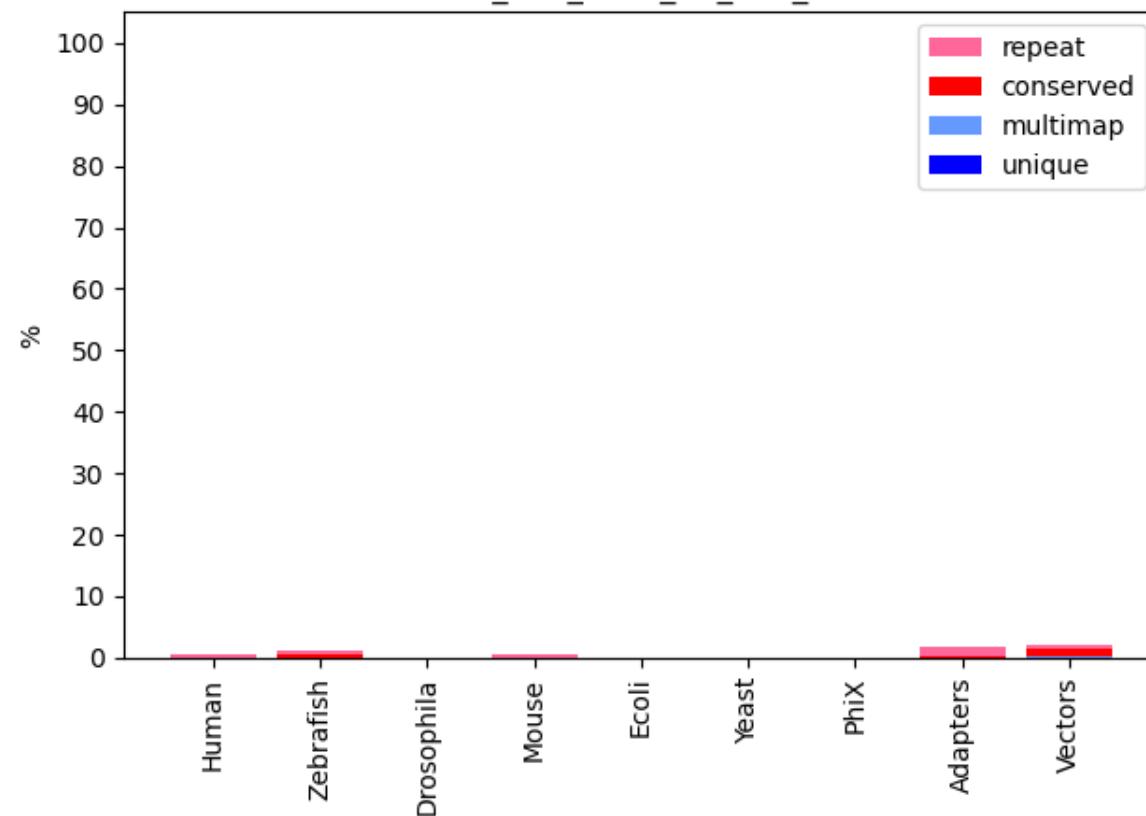
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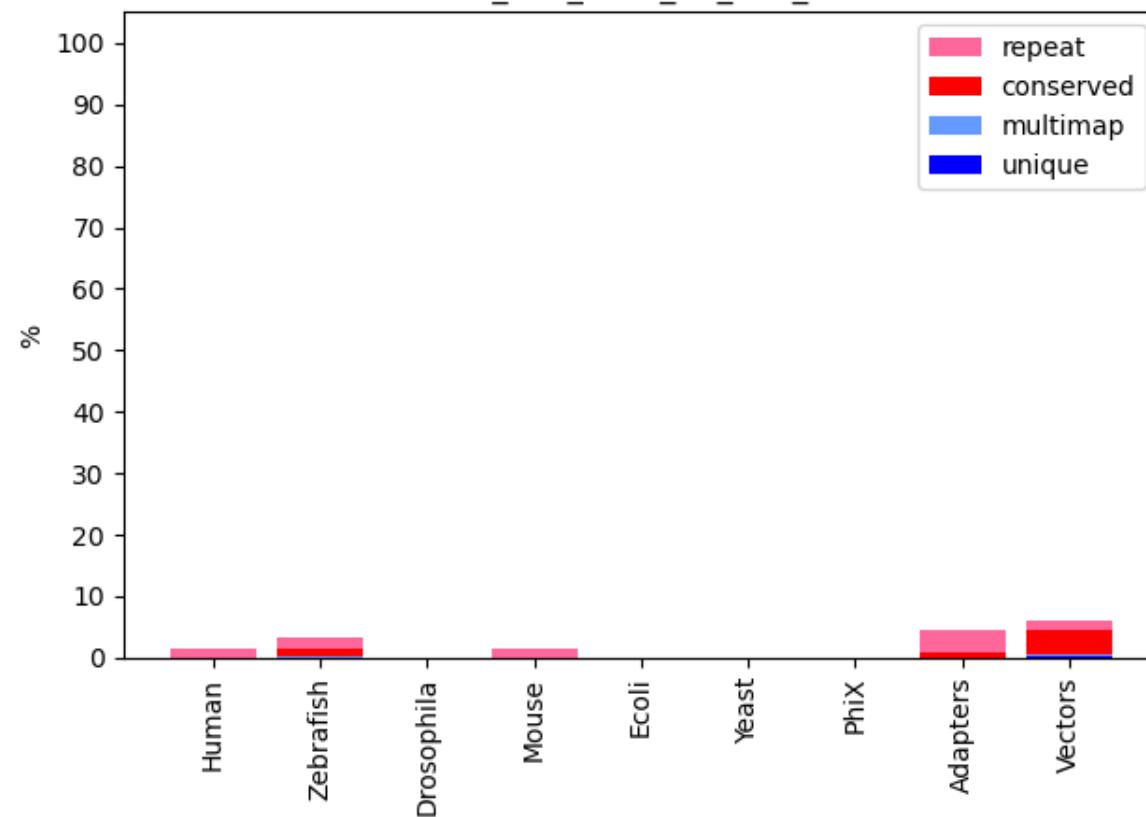
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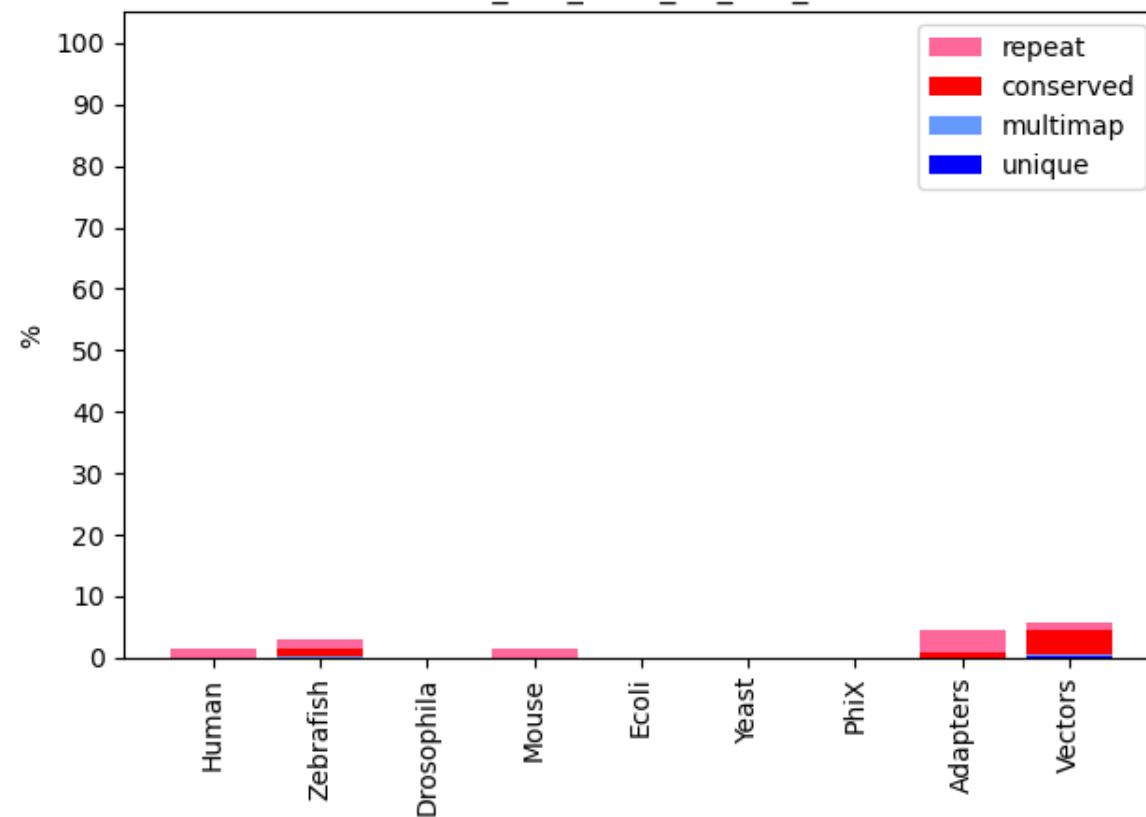
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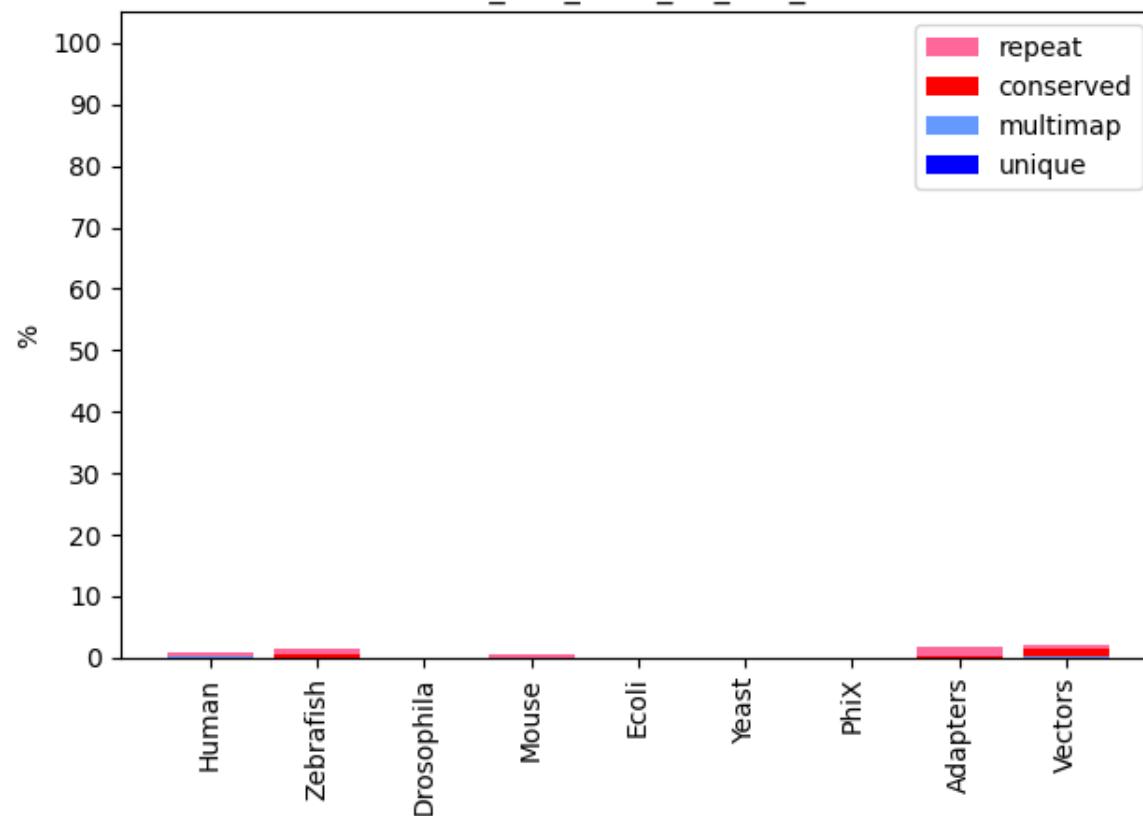
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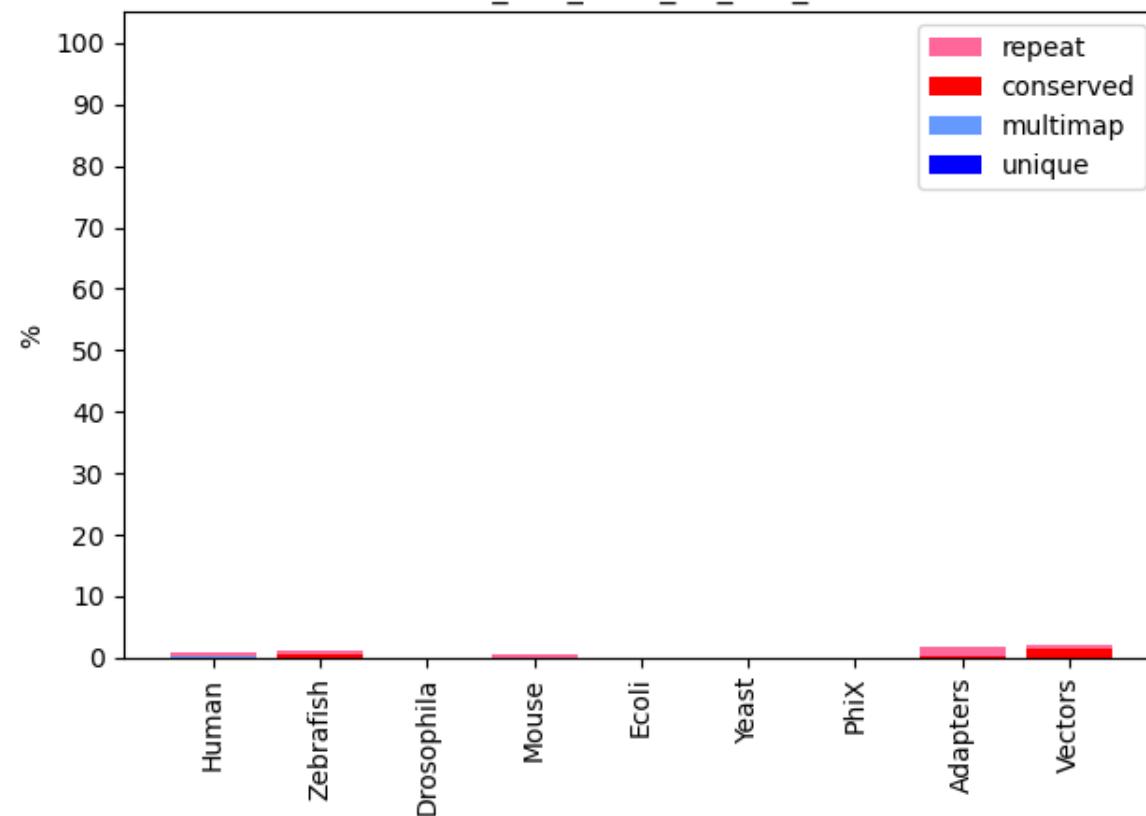
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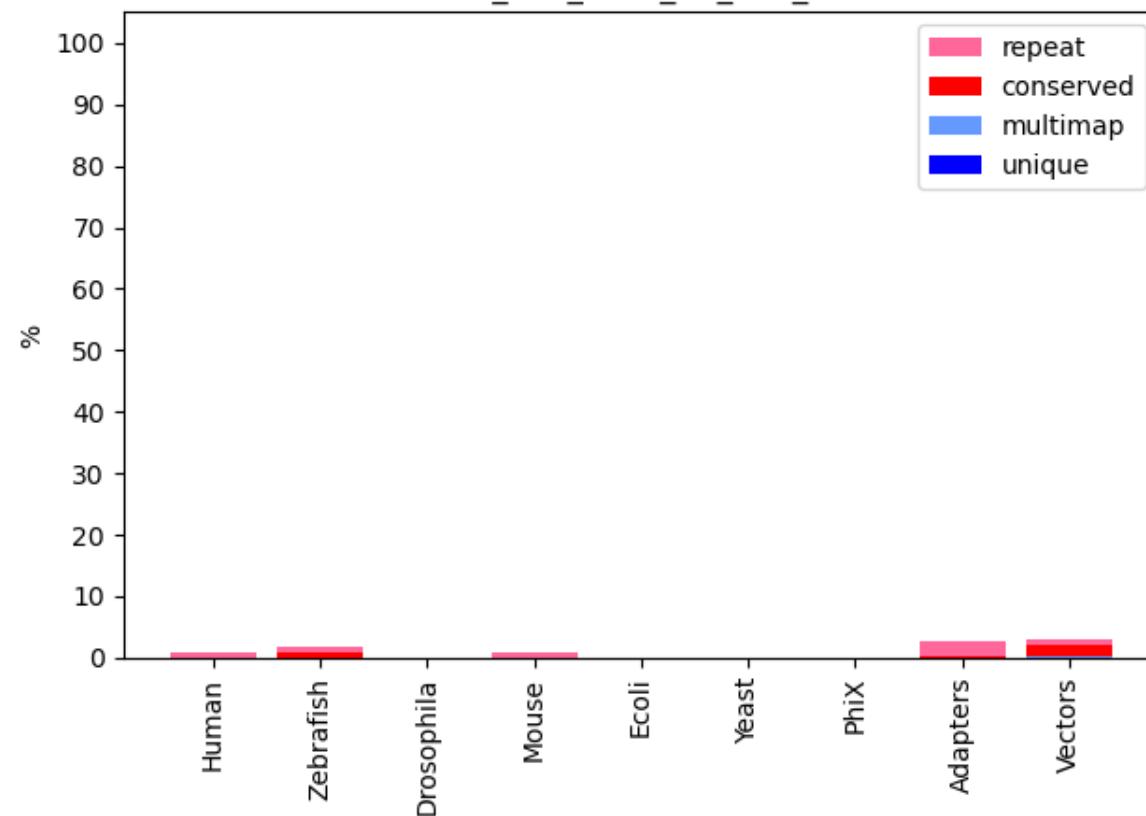
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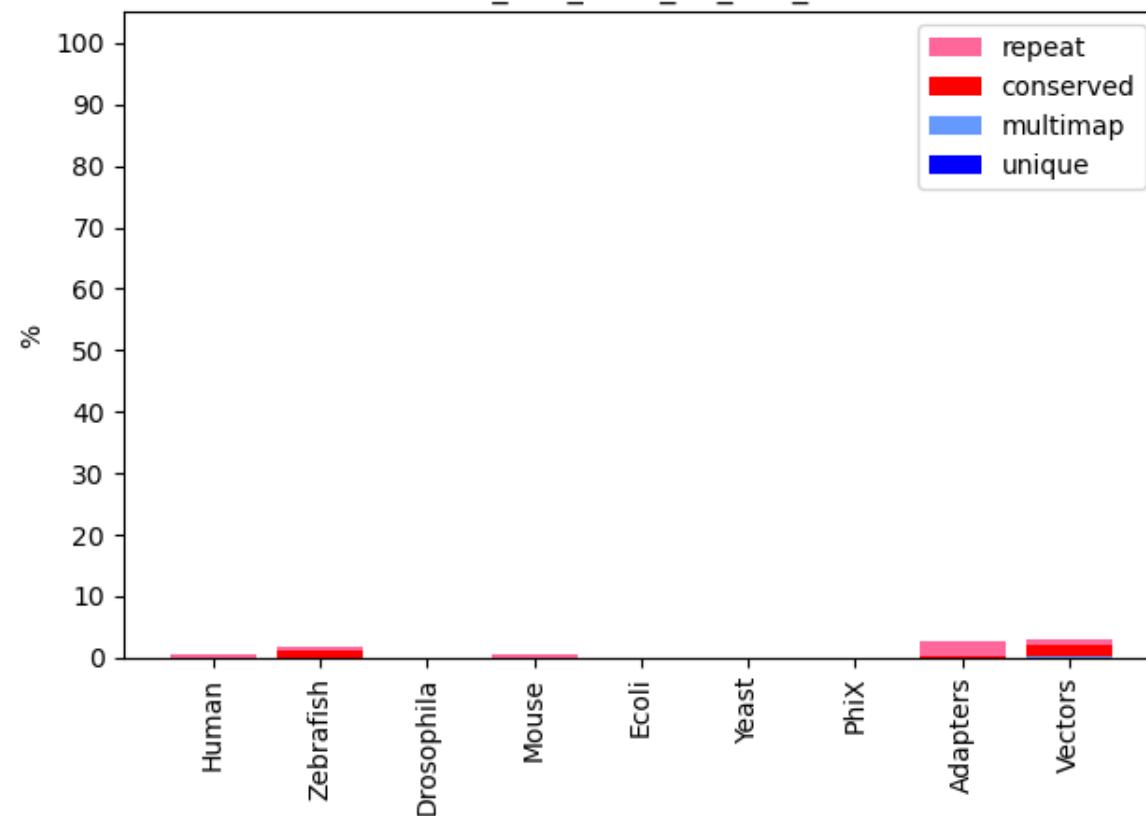
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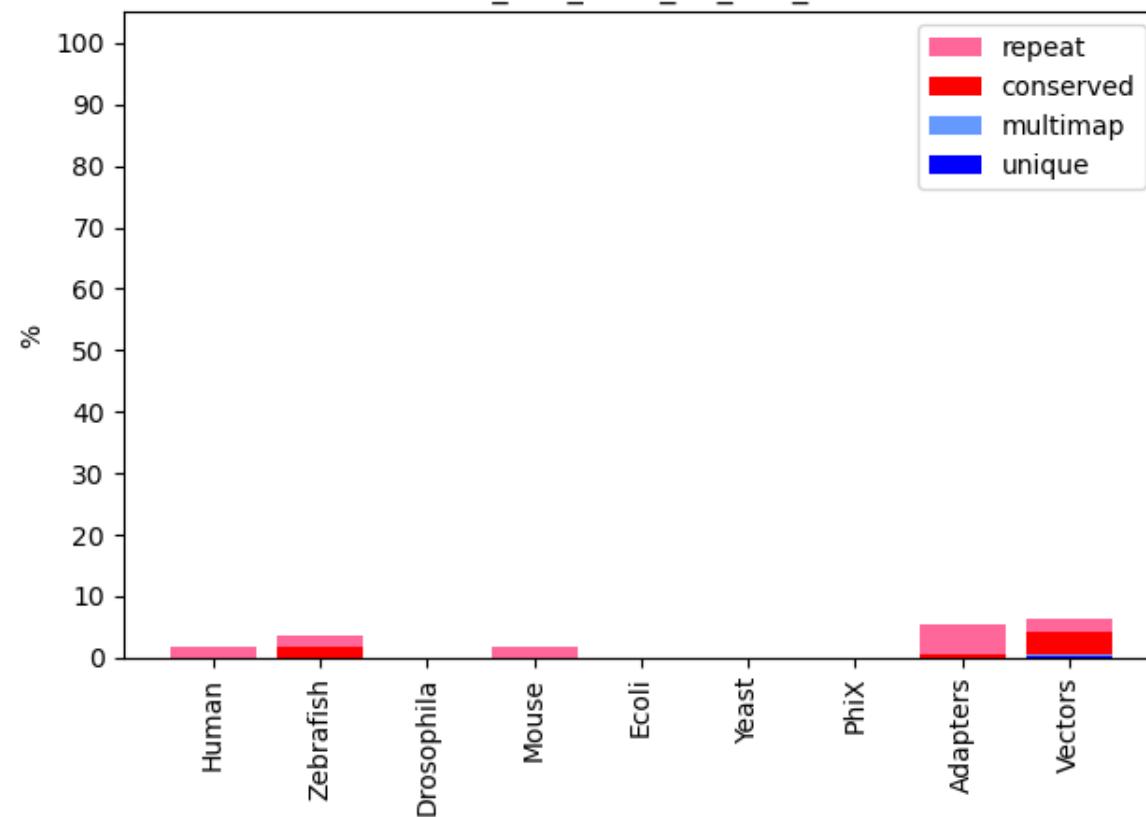
22L005026_S28_L001_R2_001_screen.txt



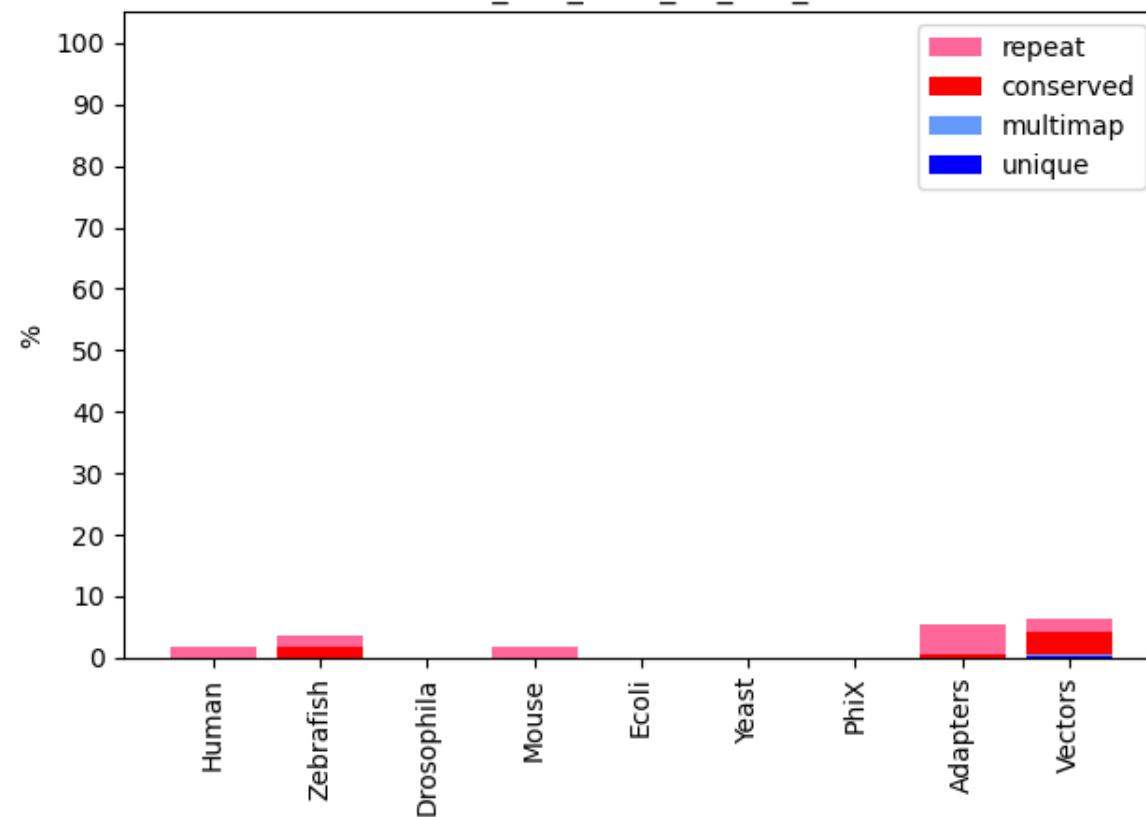
22L005026_S28_L002_R2_001_screen.txt



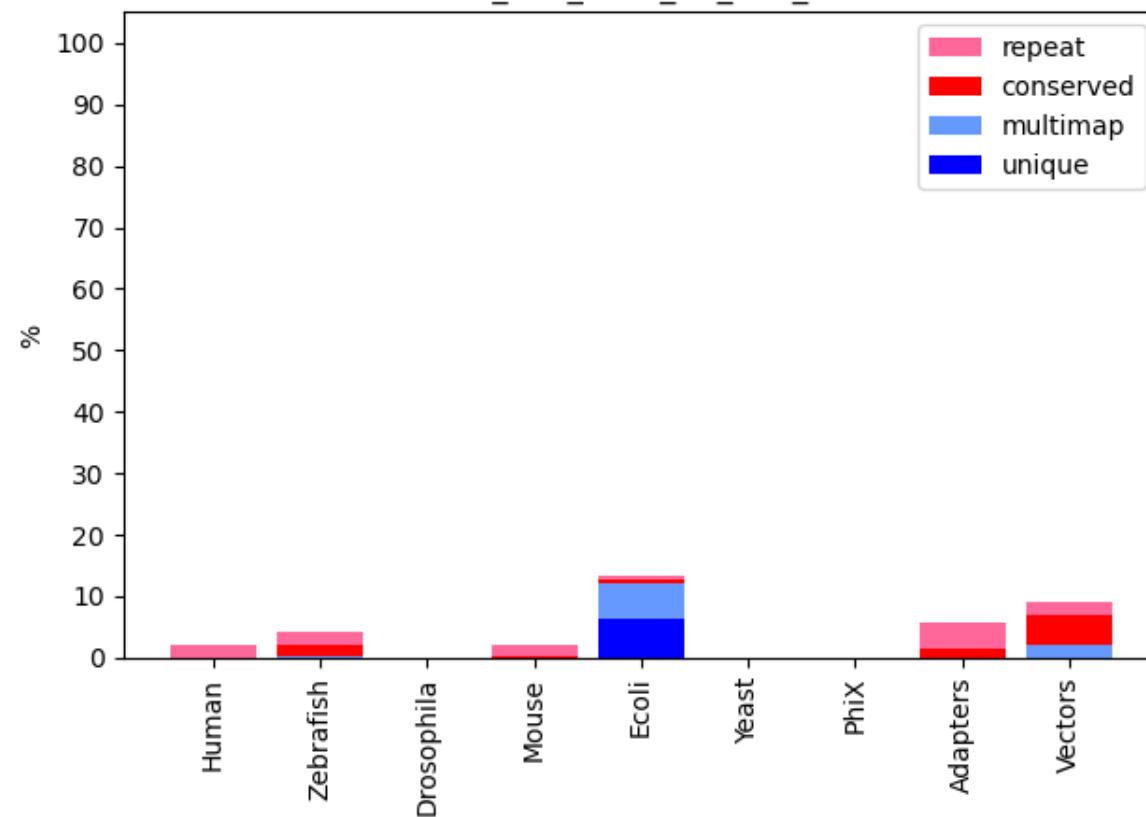
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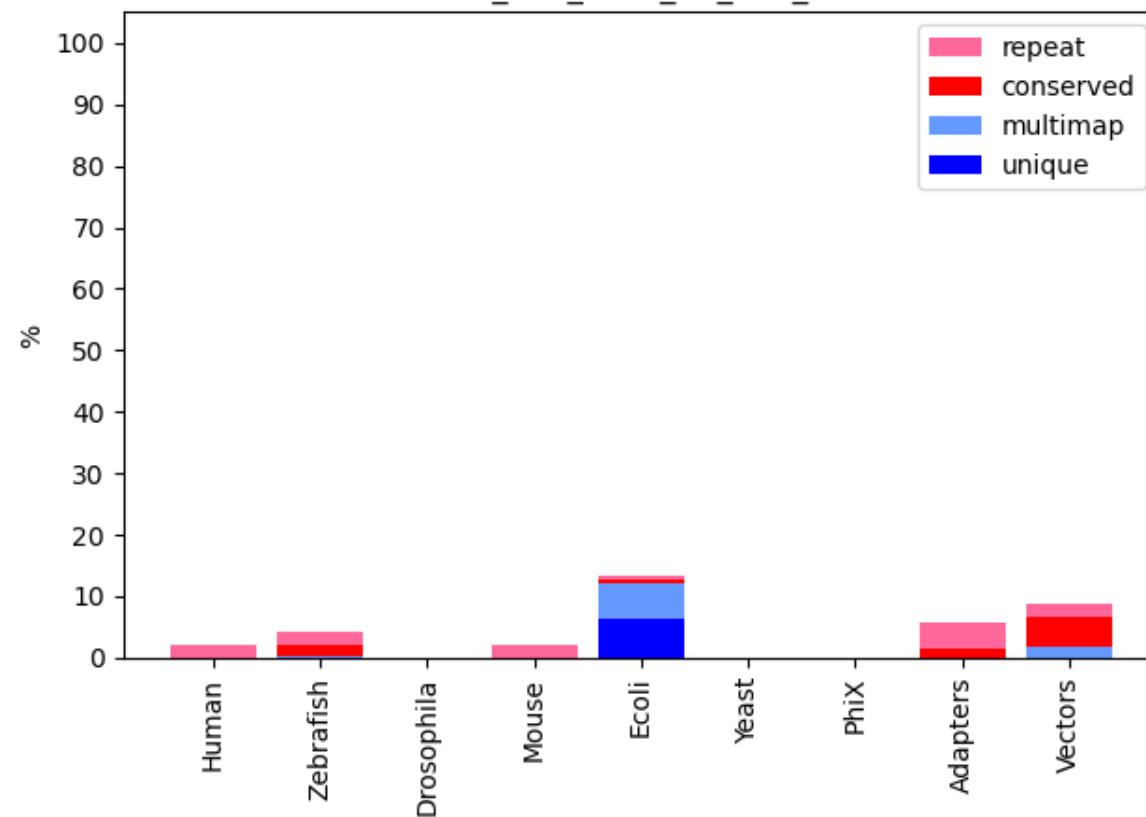
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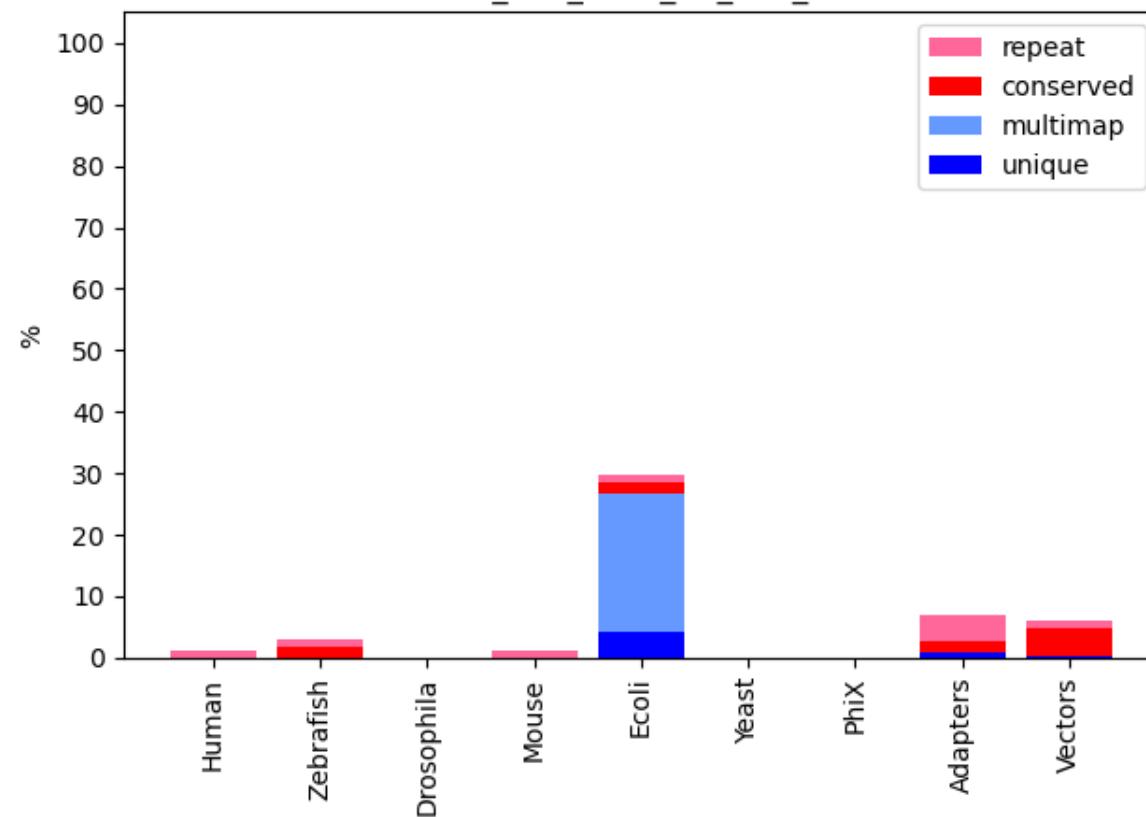
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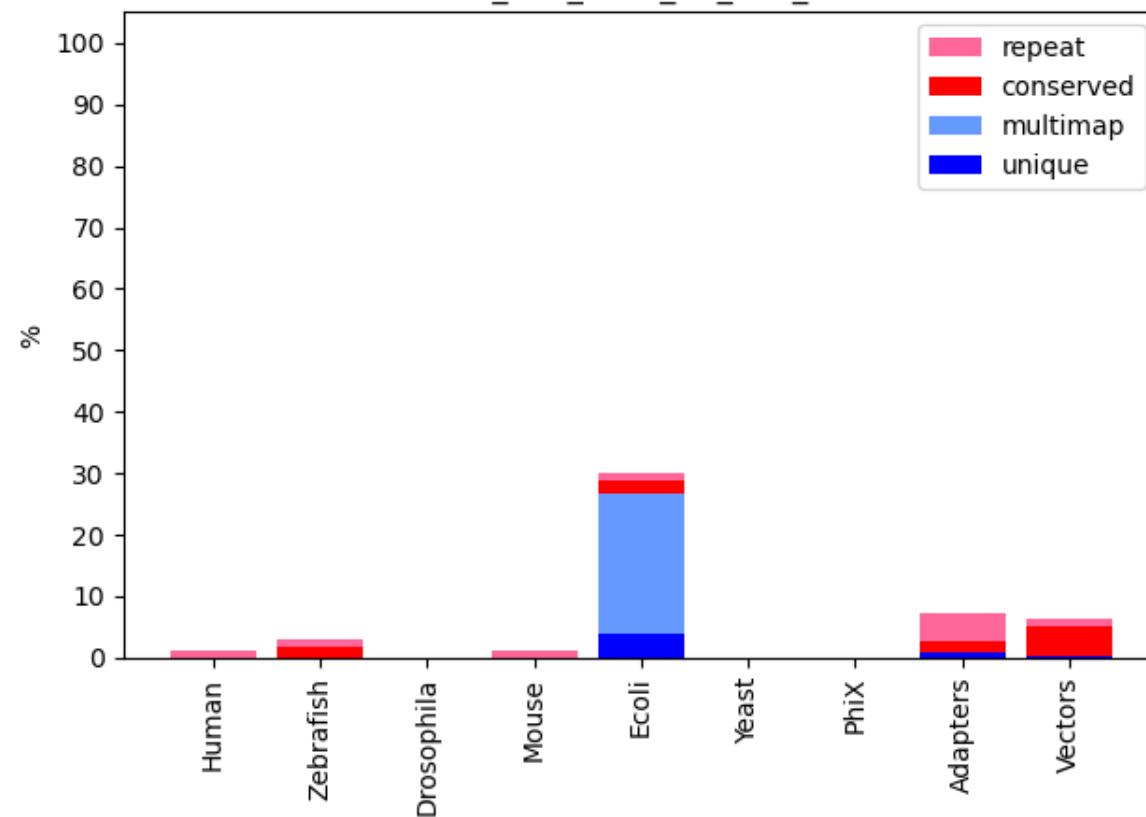
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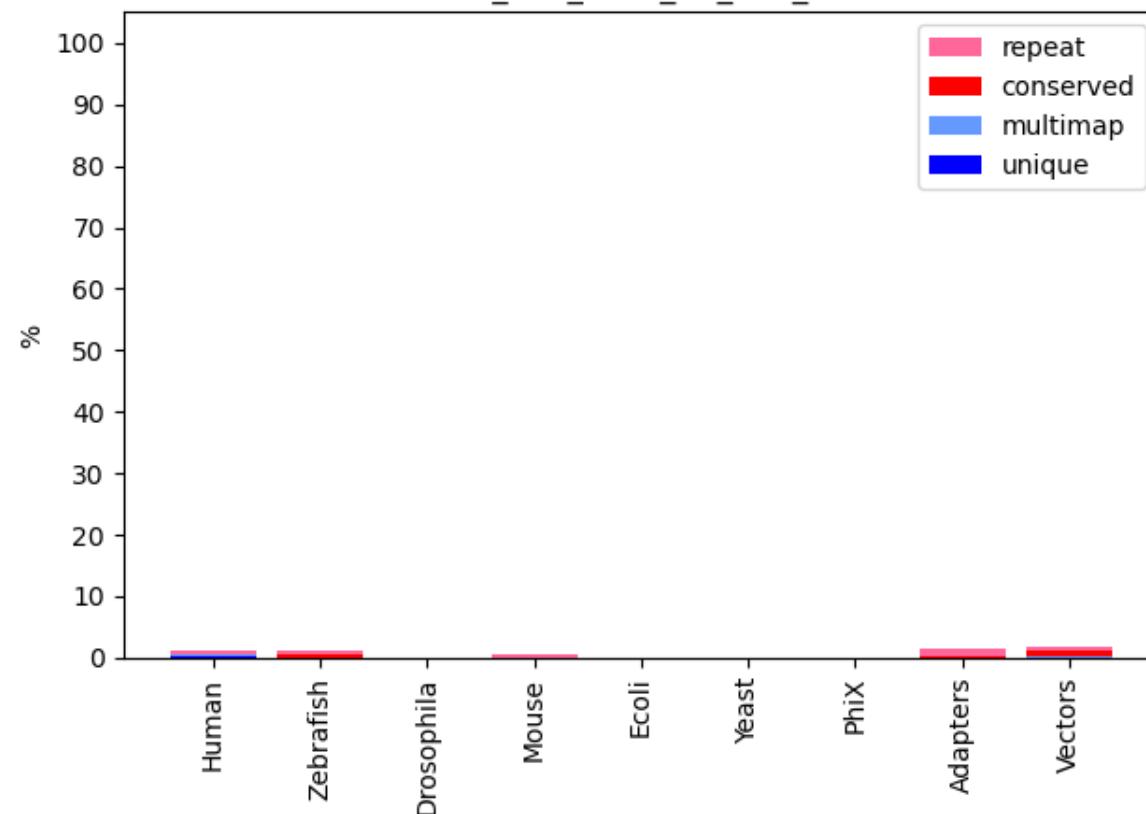
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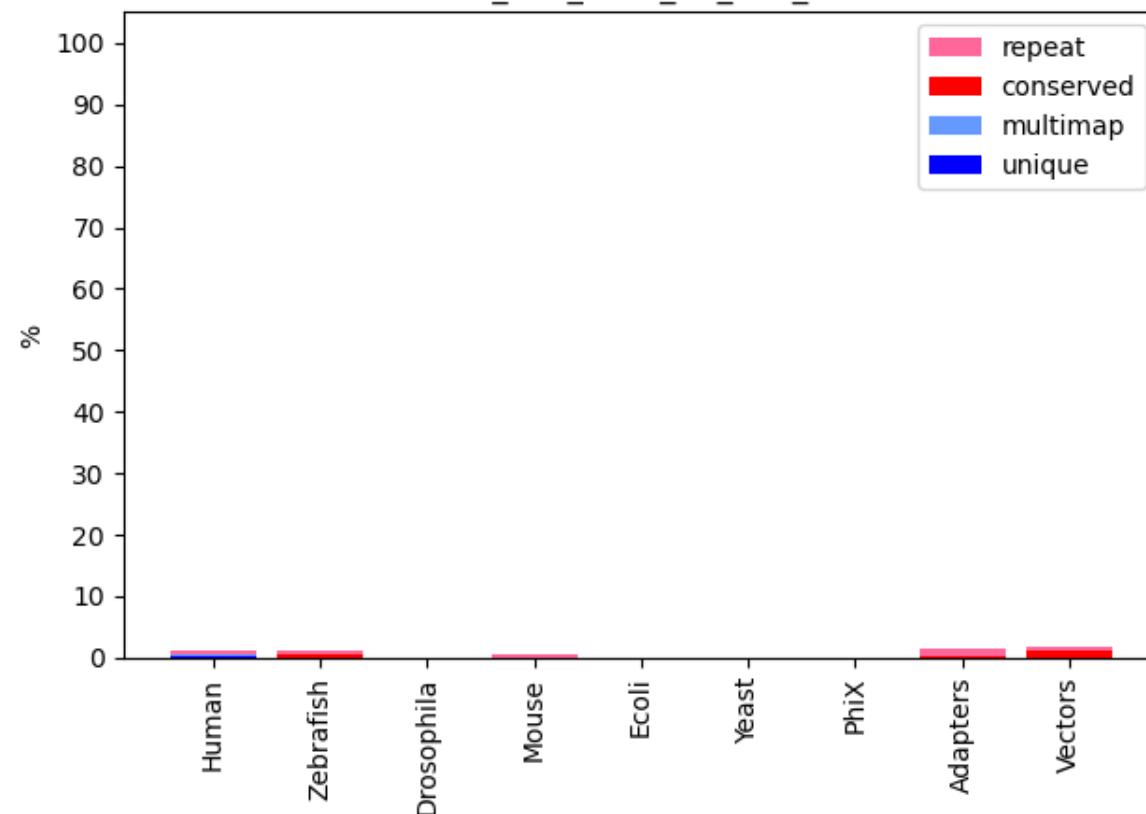
22L005029_S31_L002_R2_001_screen.txt



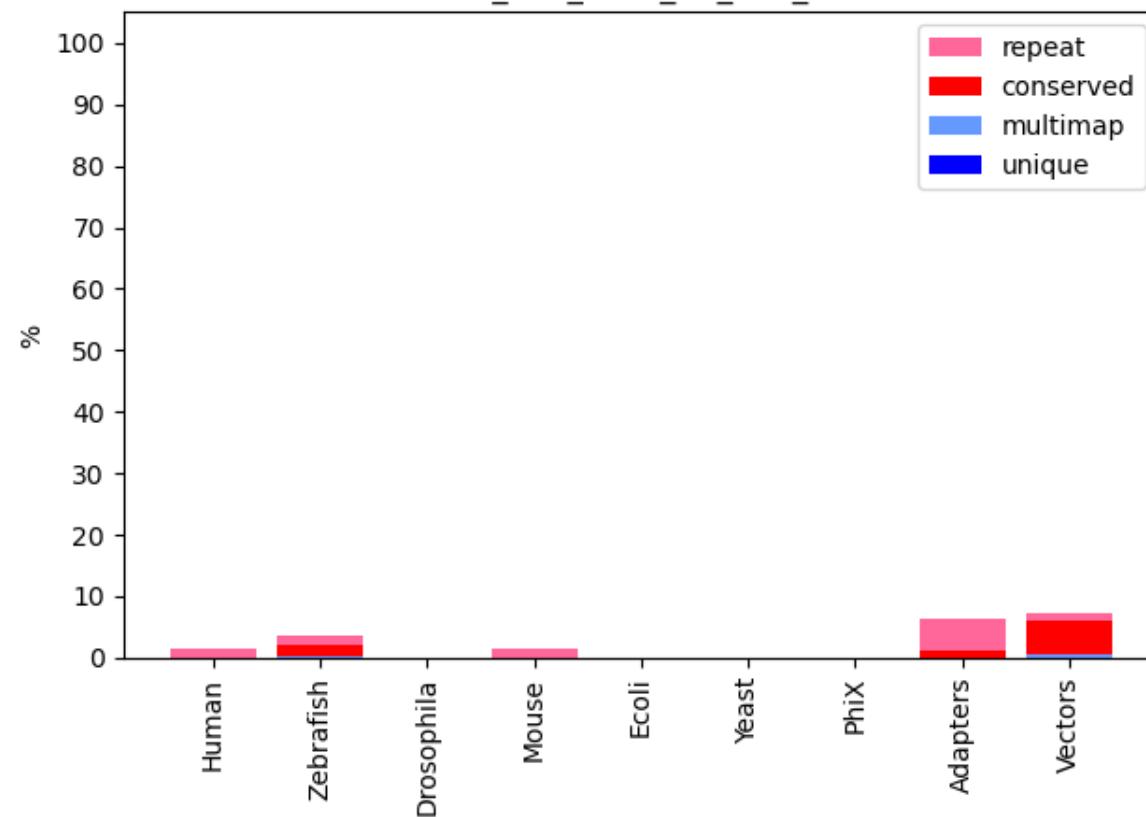
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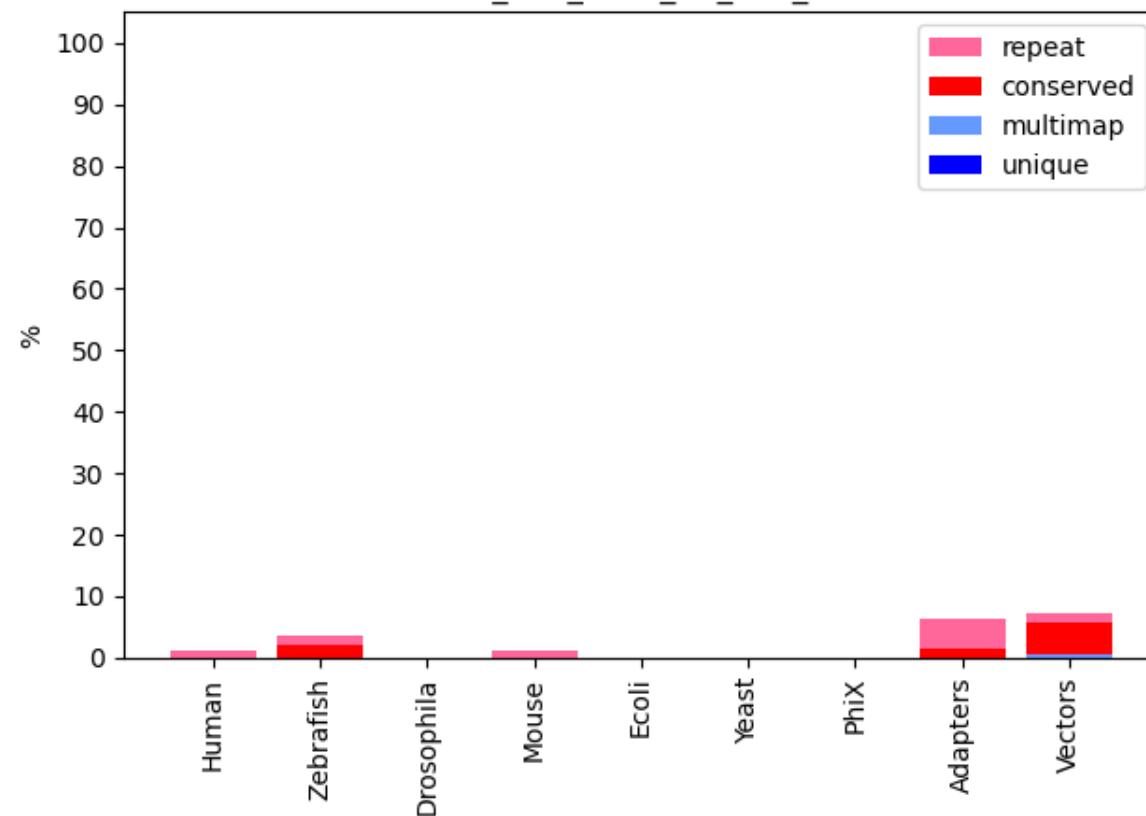
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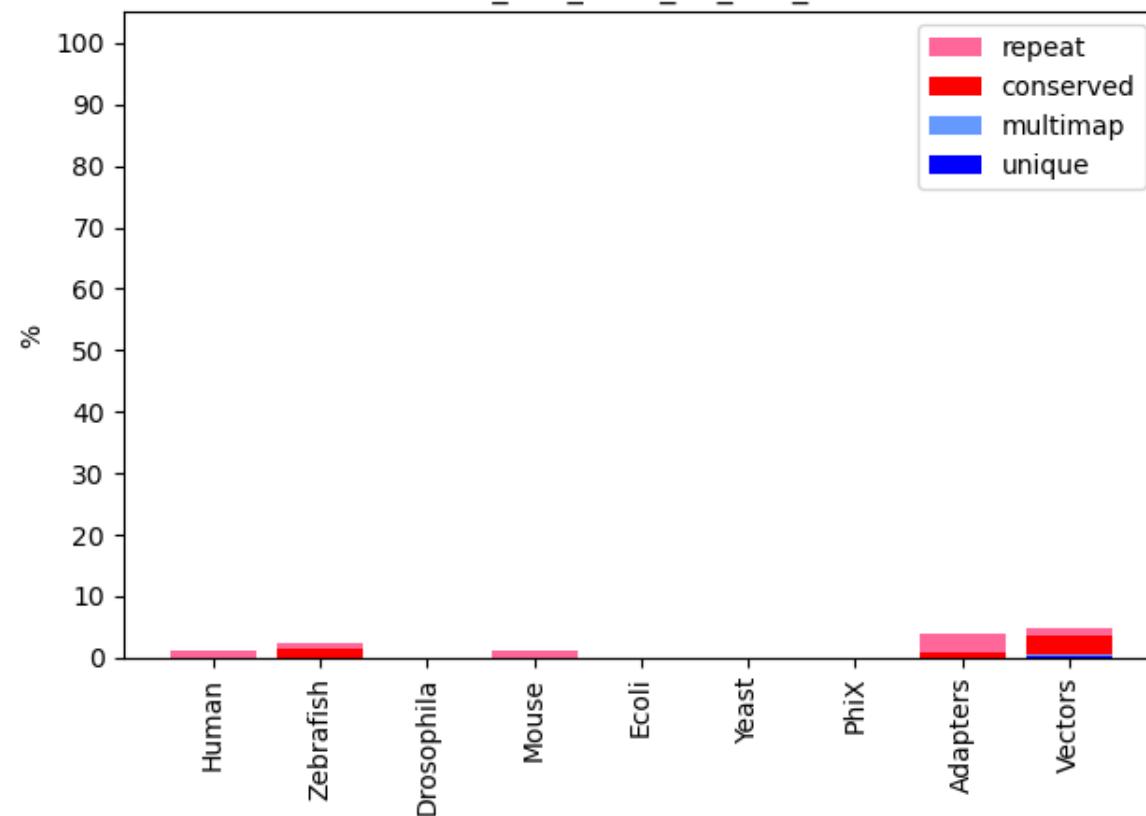
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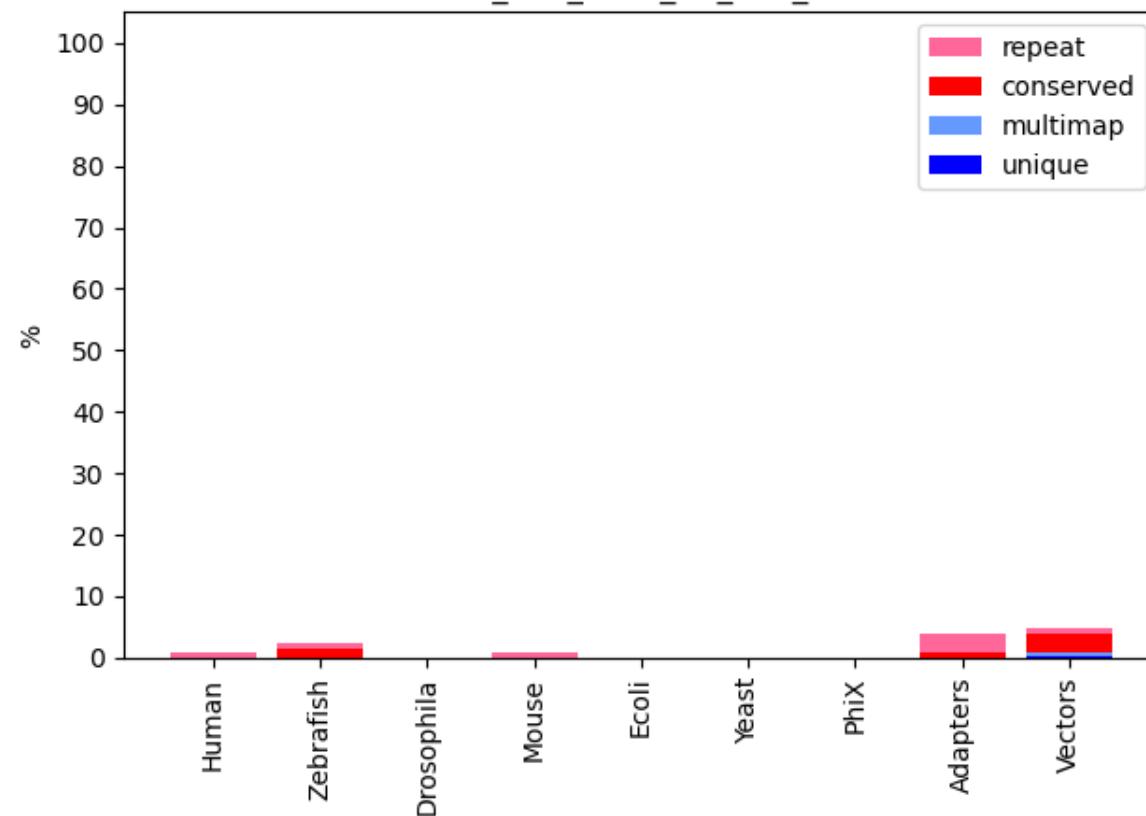
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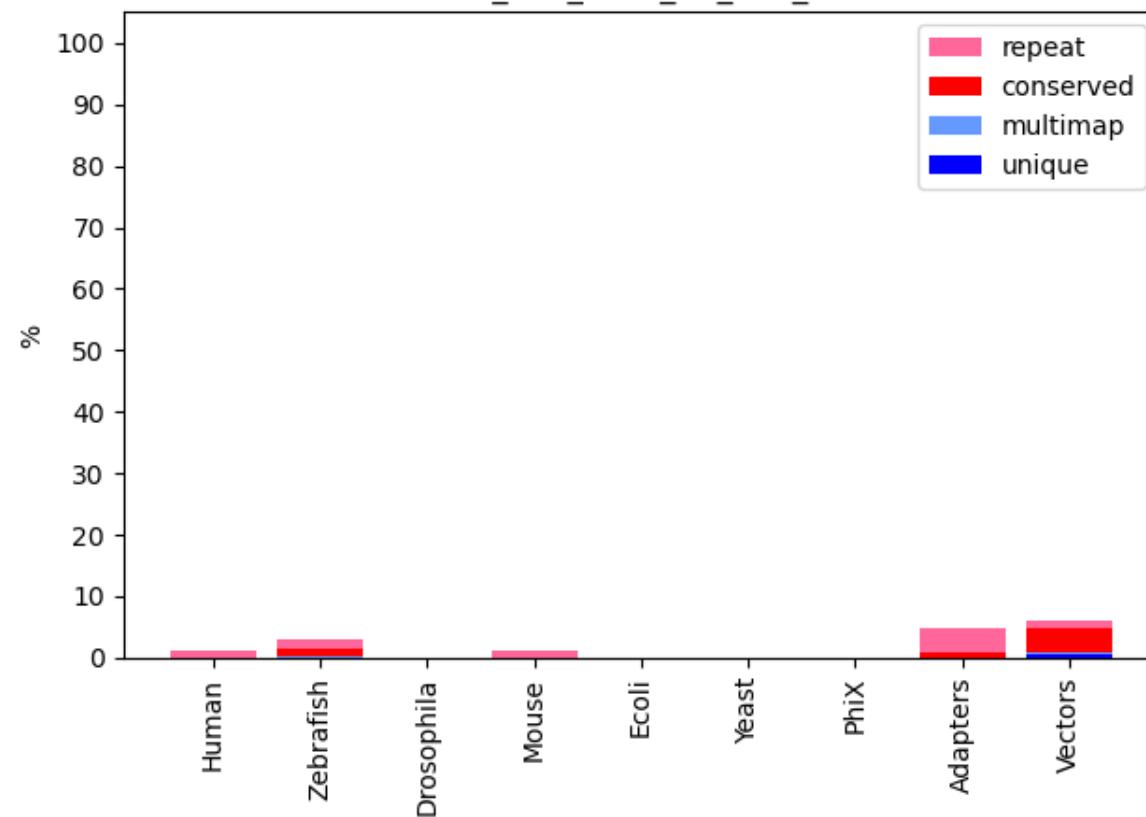
22L005032_S34_L001_R2_001_screen.txt



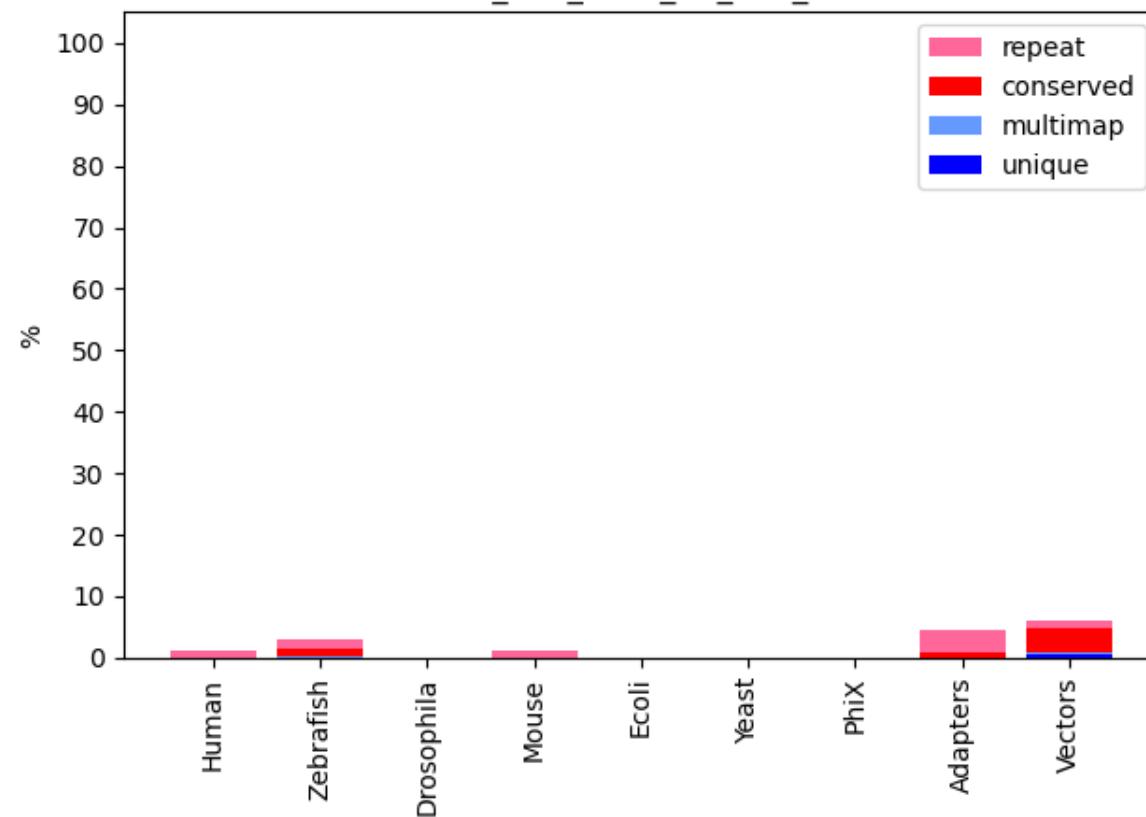
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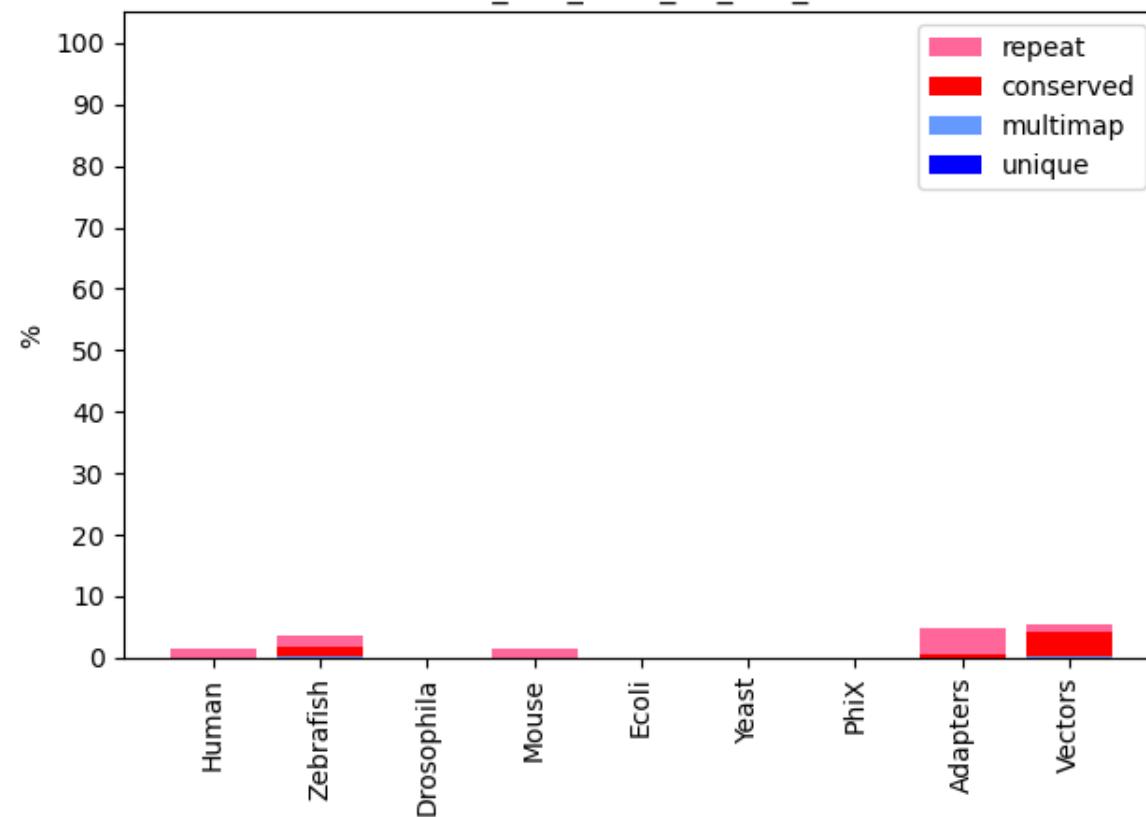
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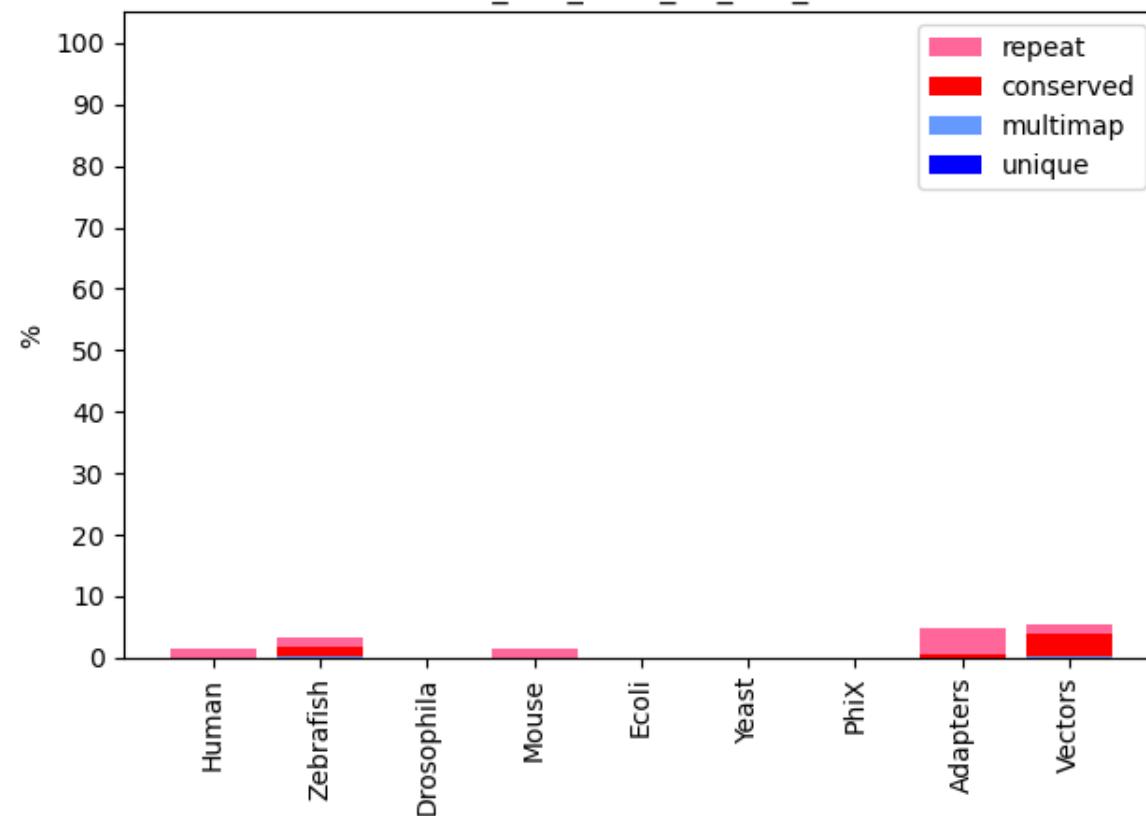
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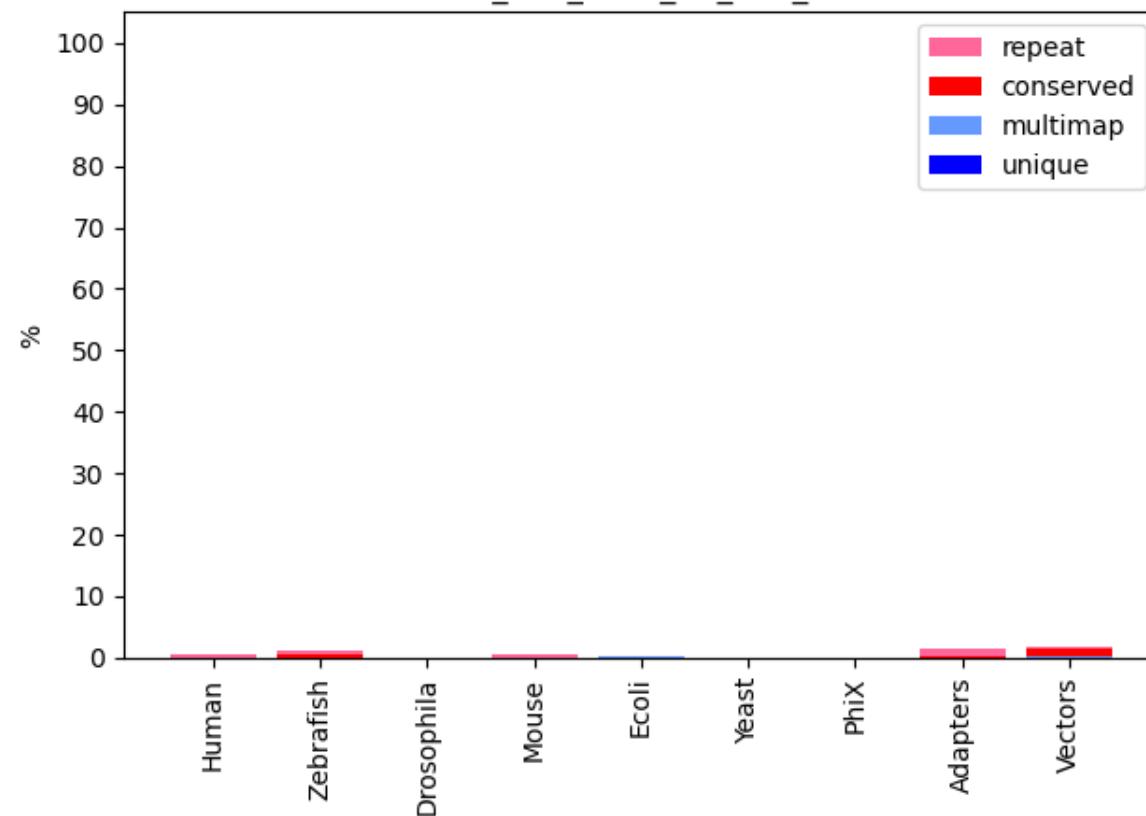
22L005034_S36_L001_R2_001_screen.txt



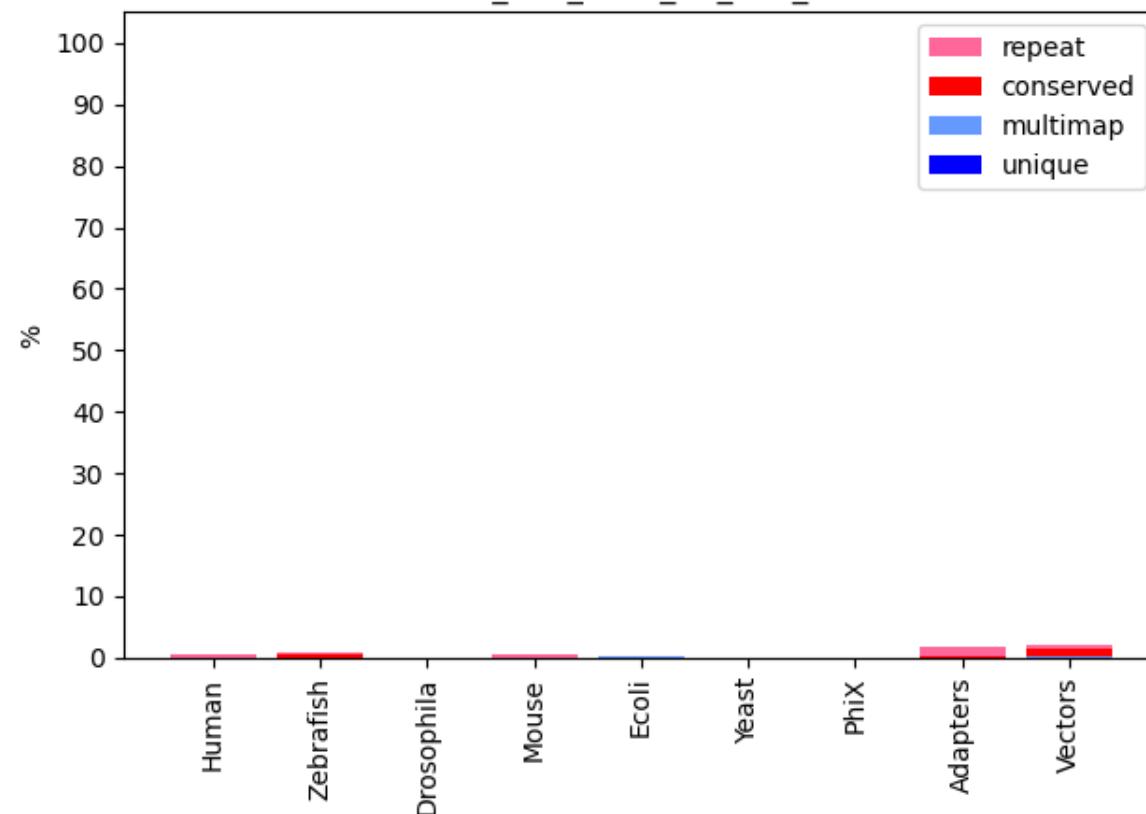
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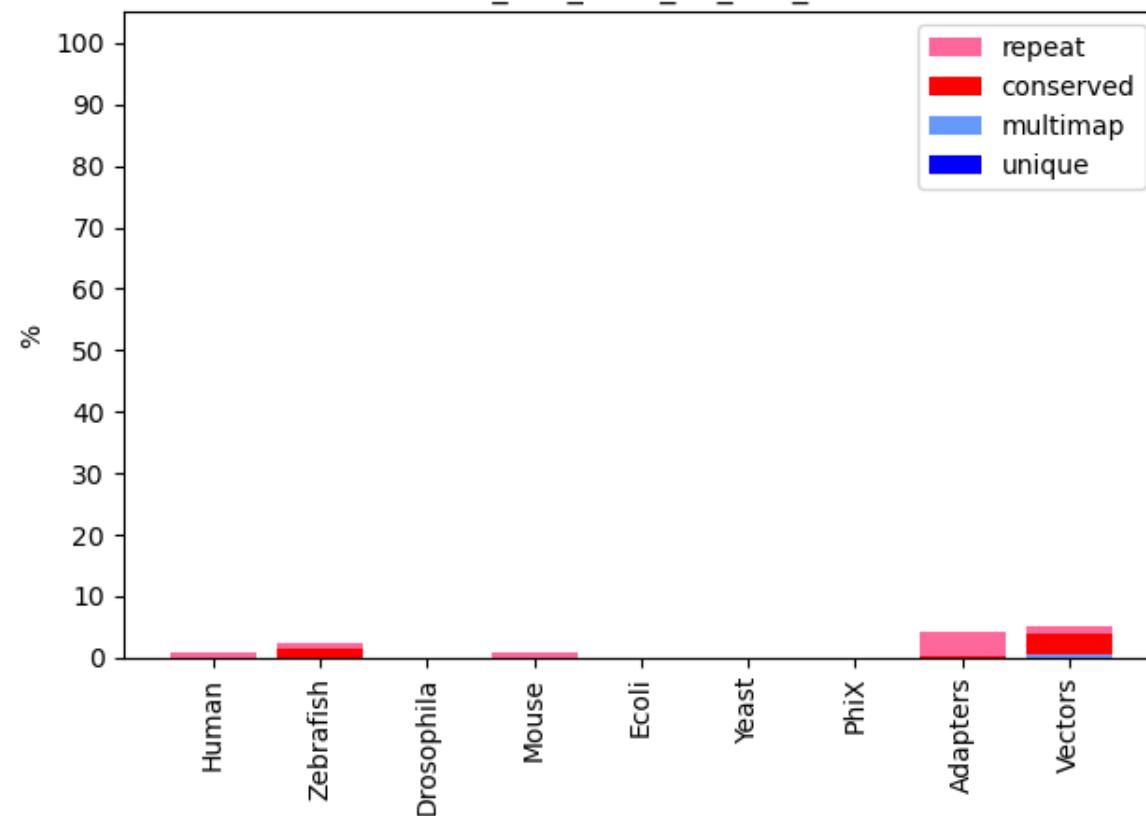
22L005035_S37_L001_R2_001_screen.txt



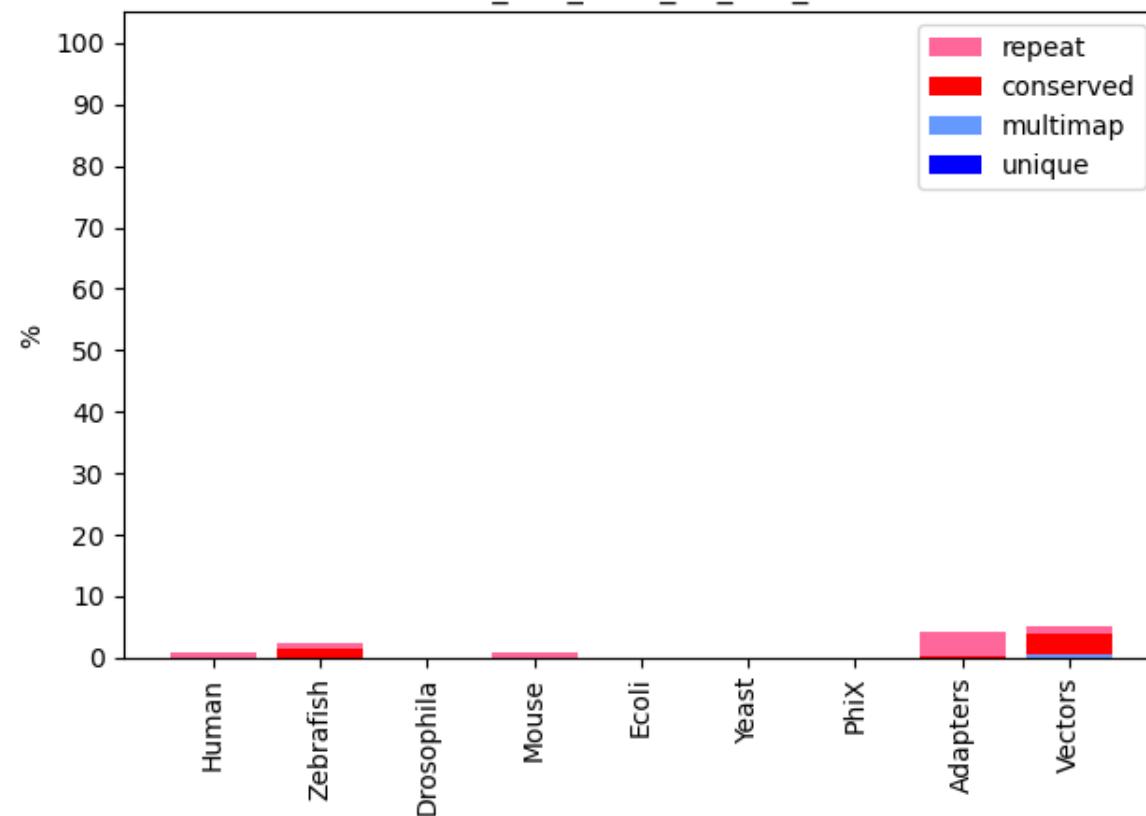
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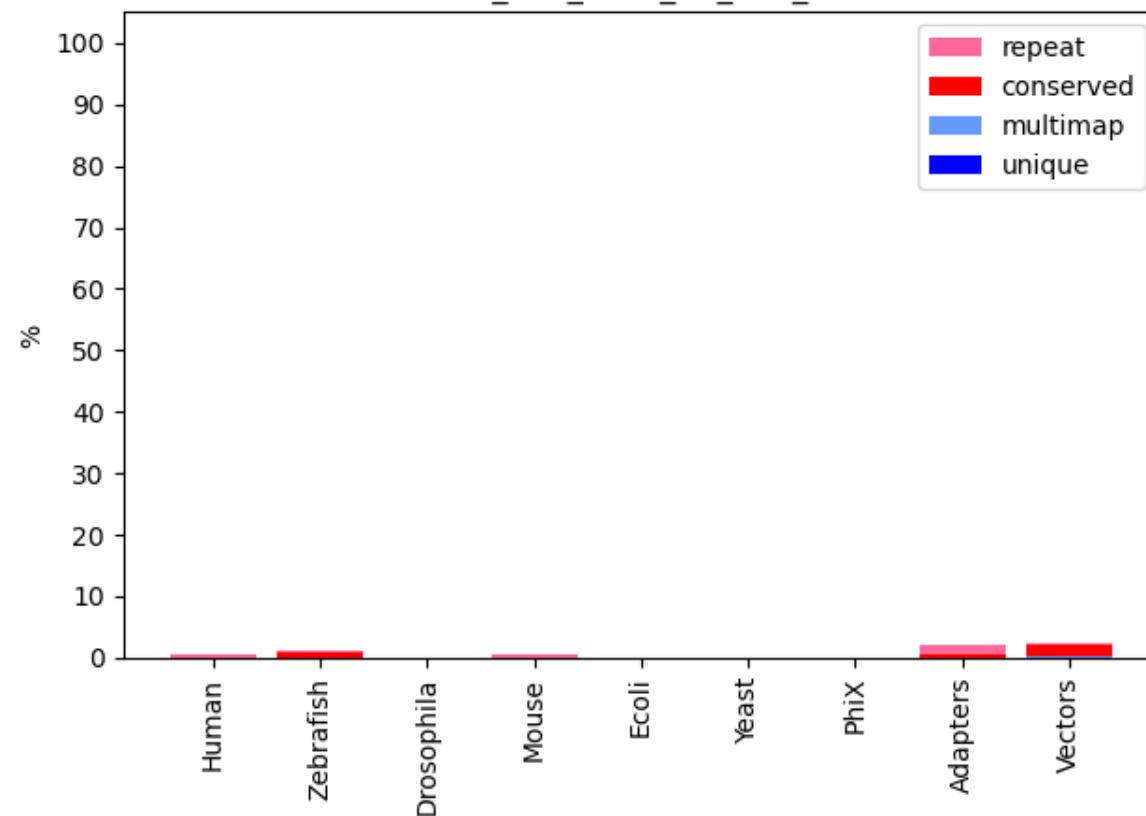
22L005036_S38_L001_R2_001_screen.txt



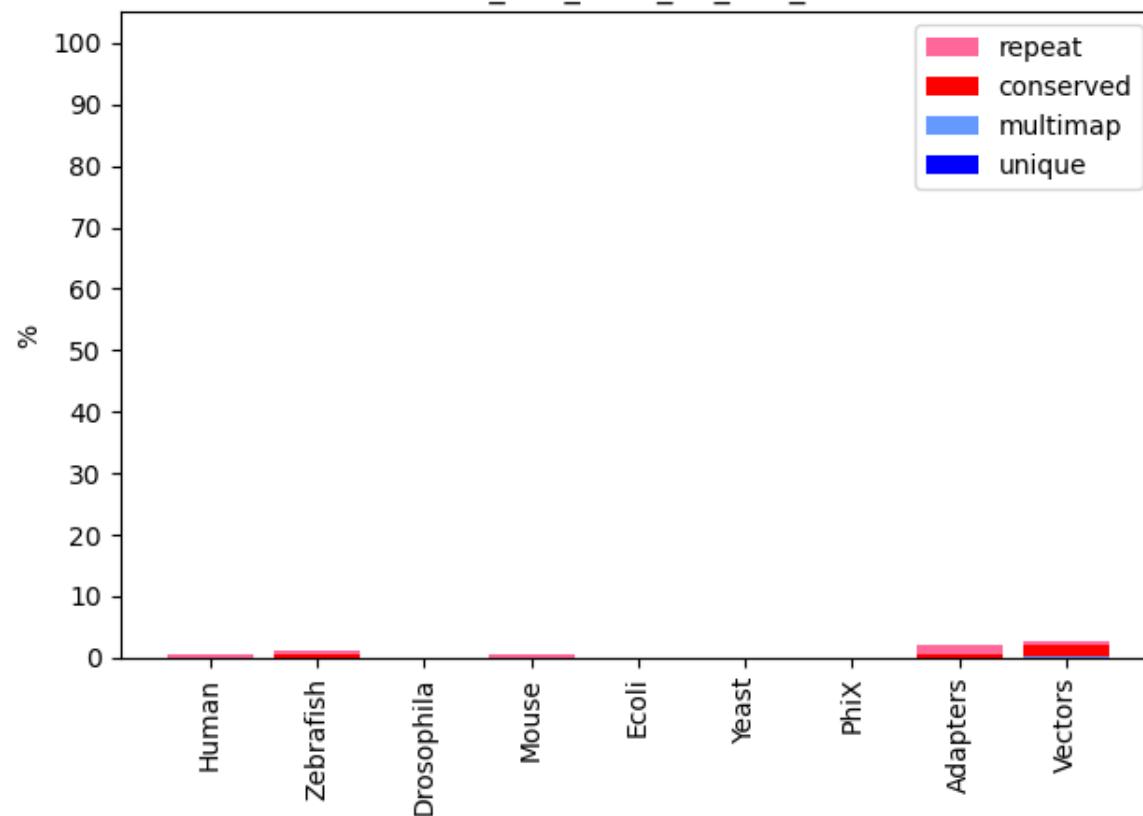
22L005036_S38_L002_R2_001_screen.txt



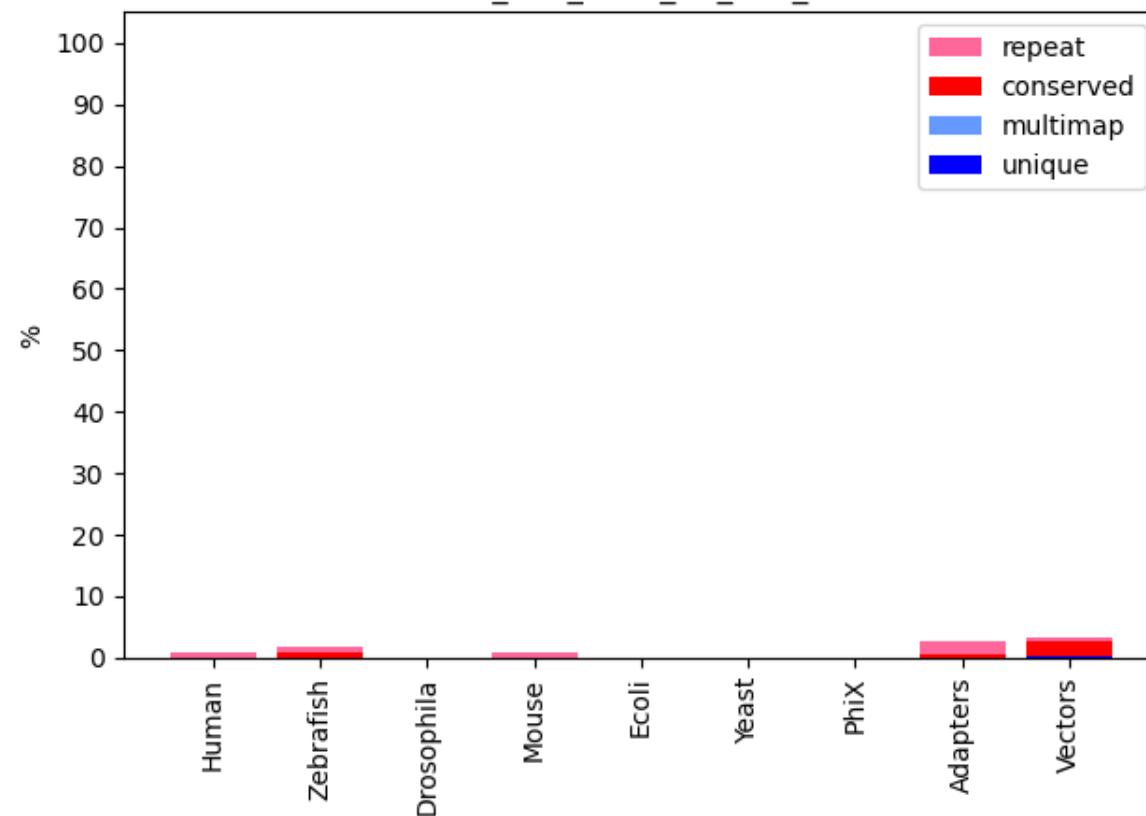
22L005037_S39_L001_R2_001_screen.txt



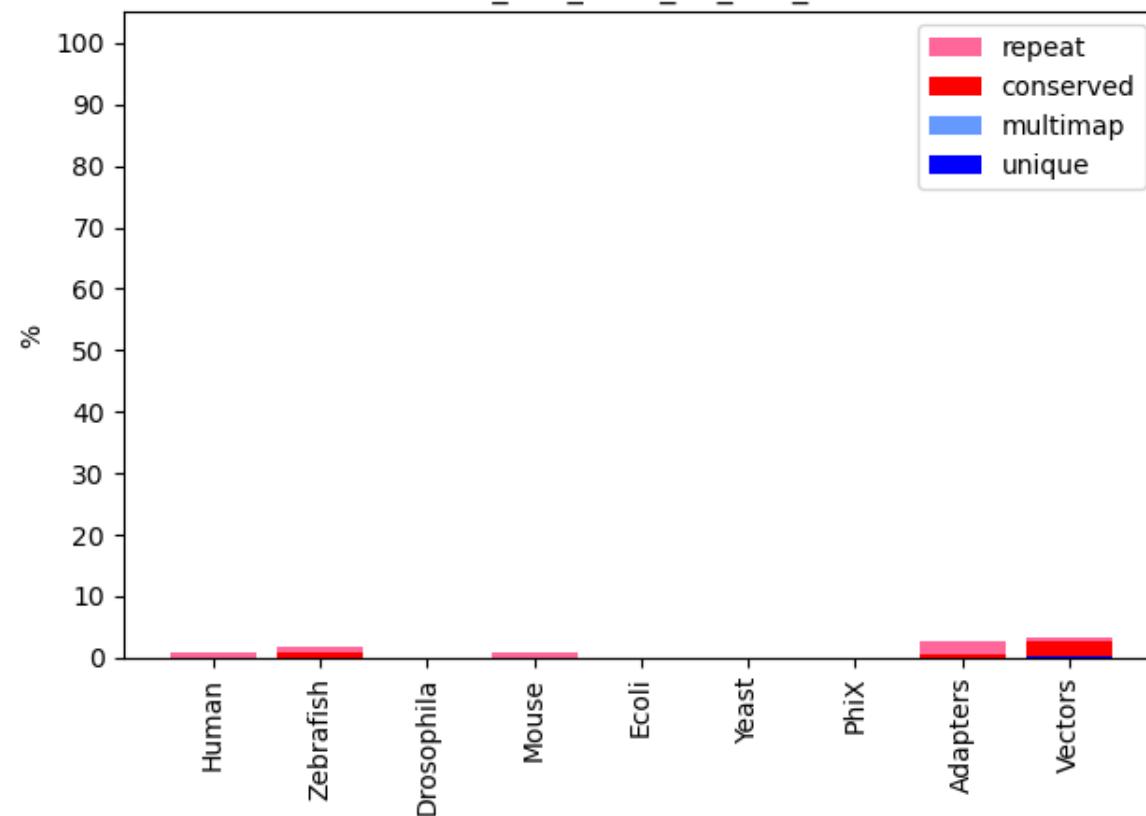
22L005037_S39_L002_R2_001_screen.txt



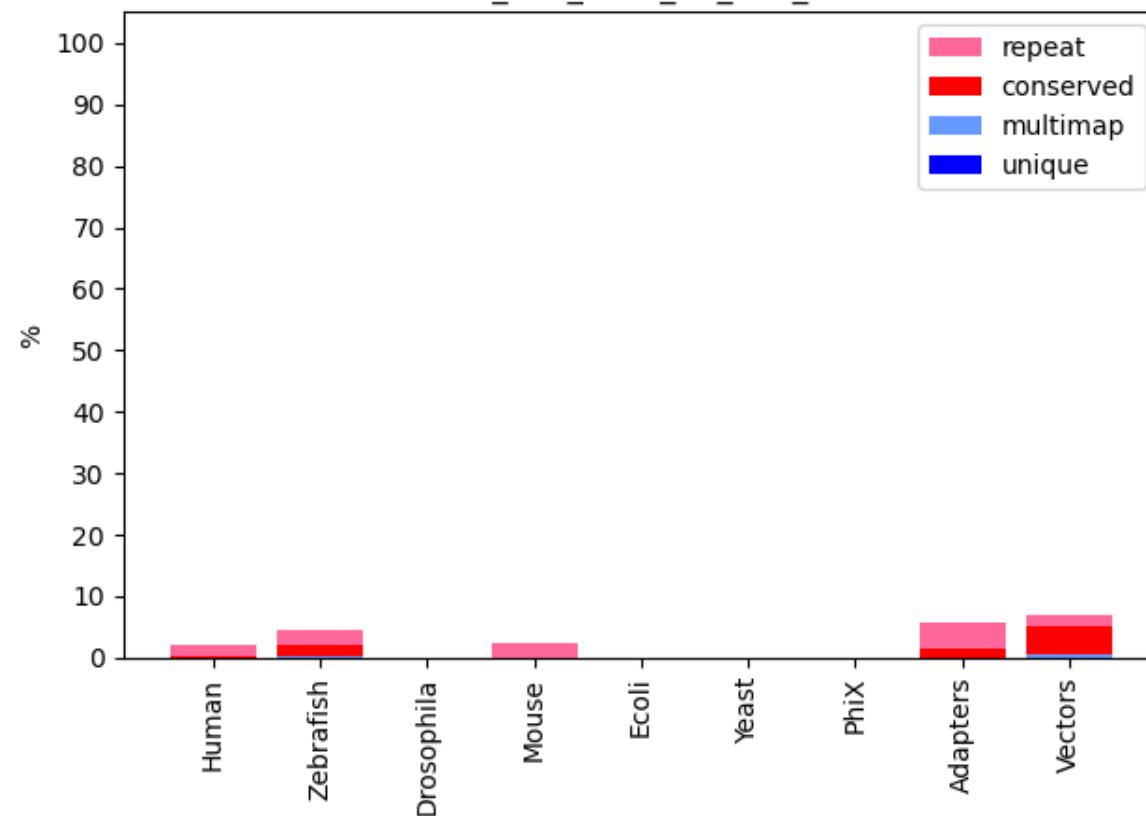
22L005038_S40_L001_R2_001_screen.txt



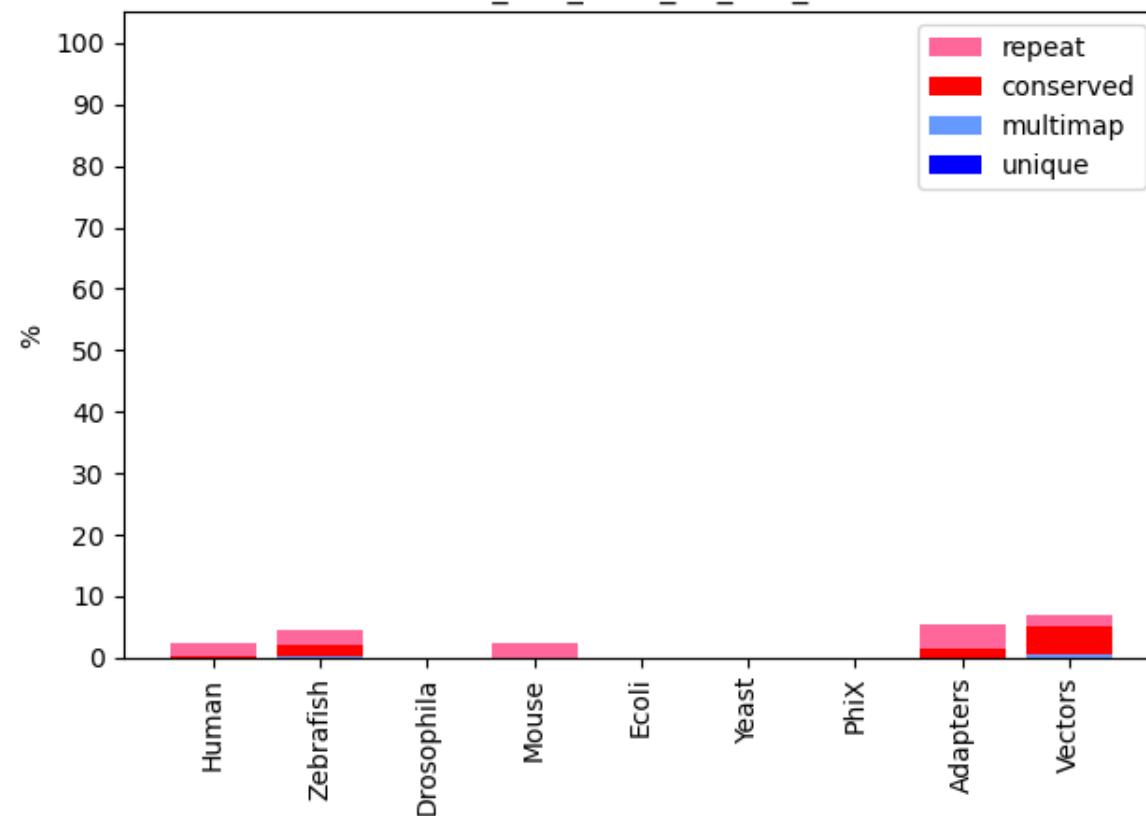
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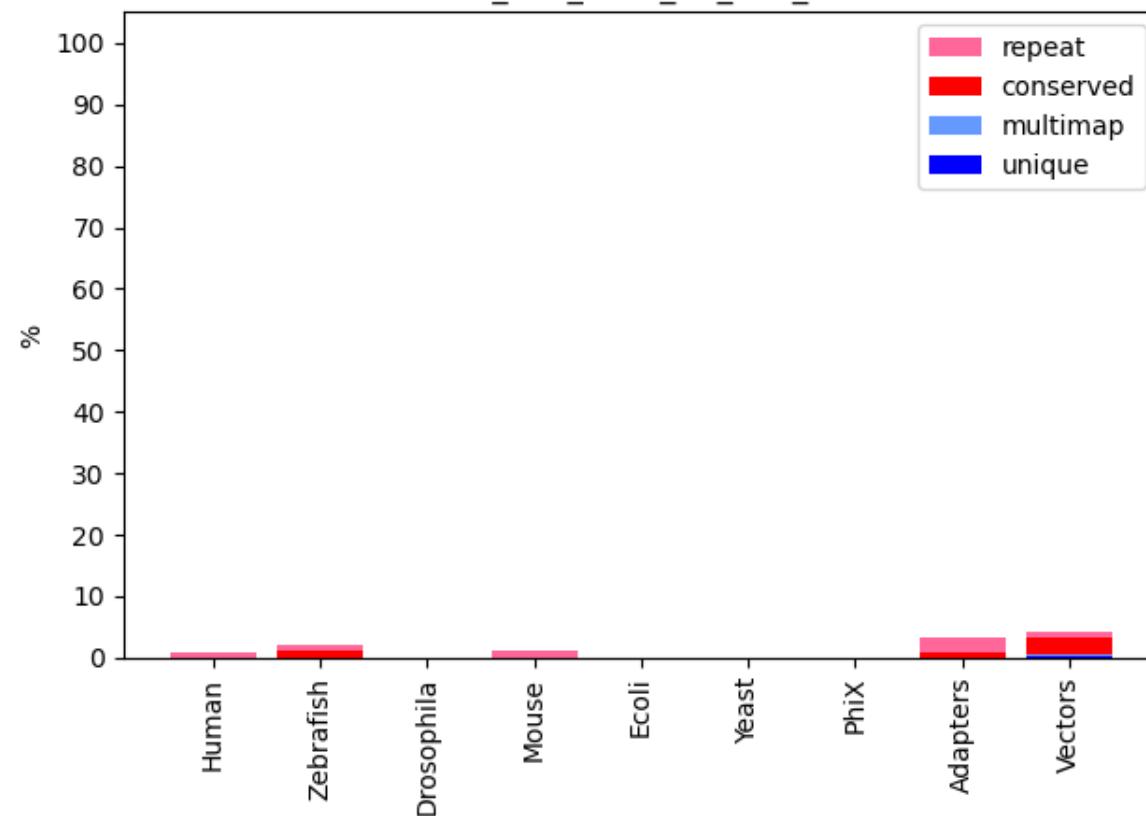
22L005039_S41_L001_R2_001_screen.txt



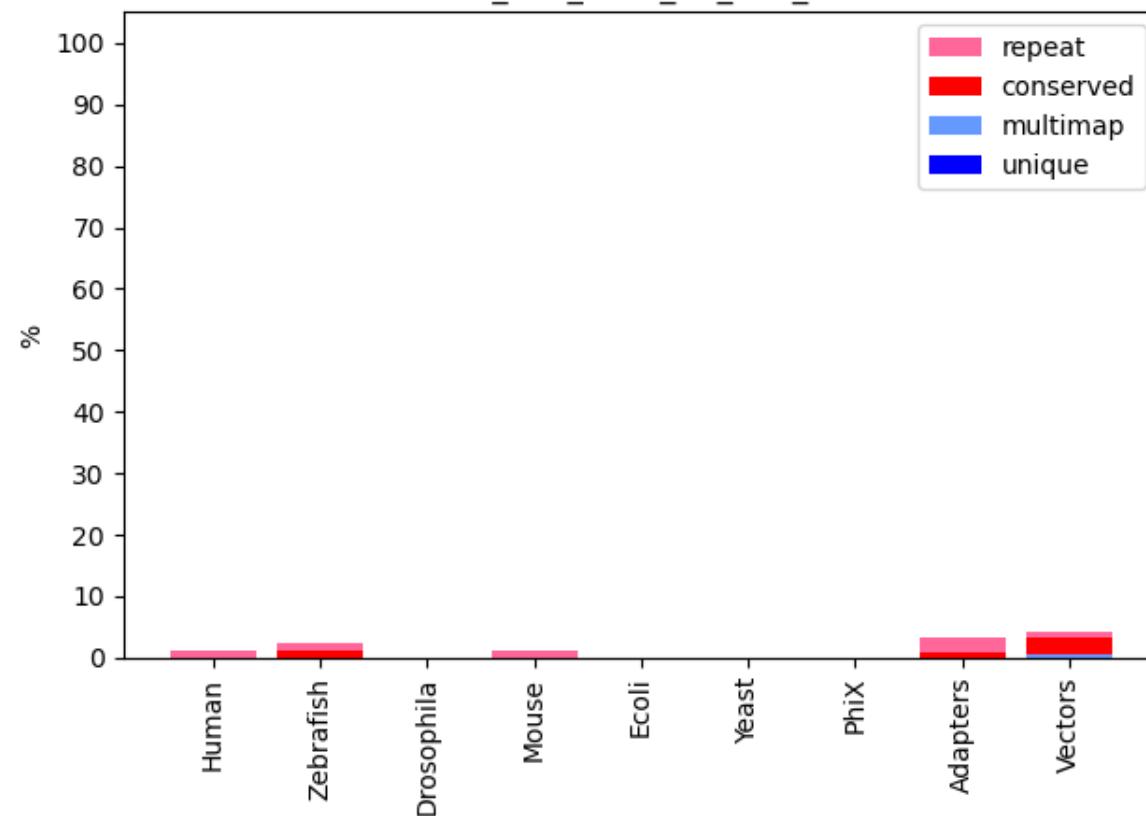
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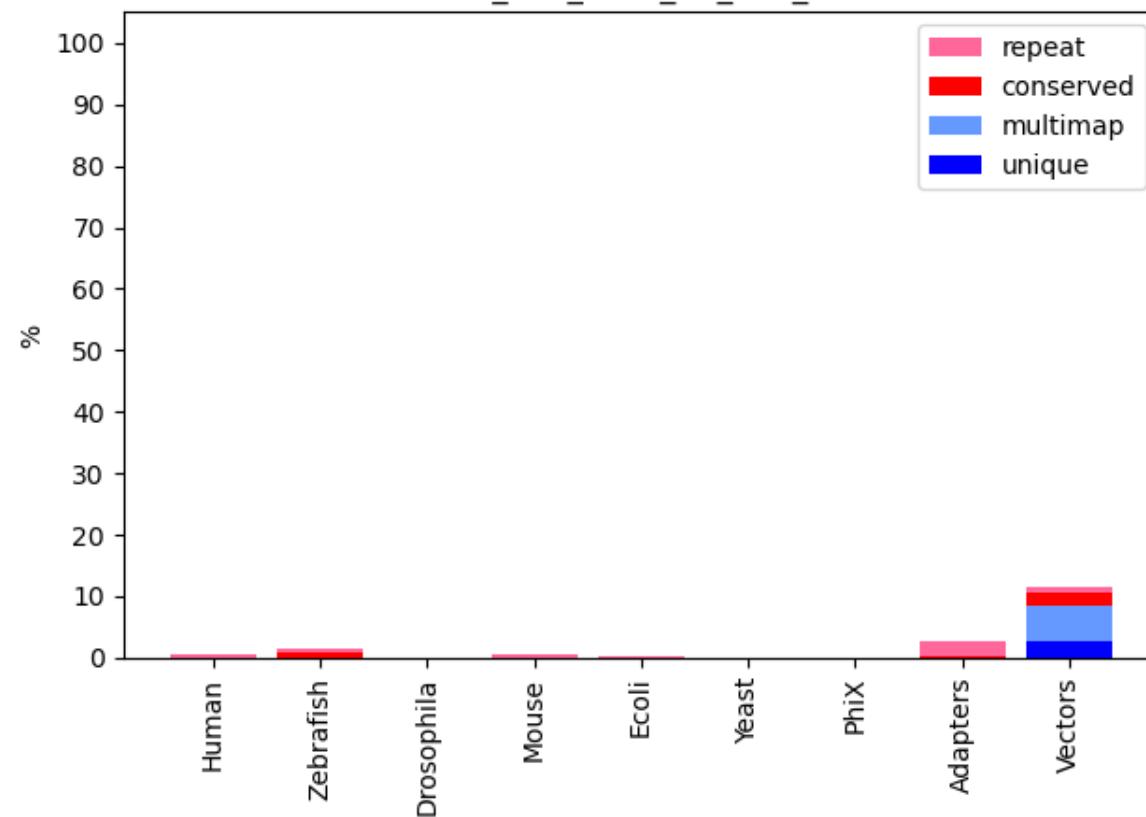
22L005040_S42_L001_R2_001_screen.txt



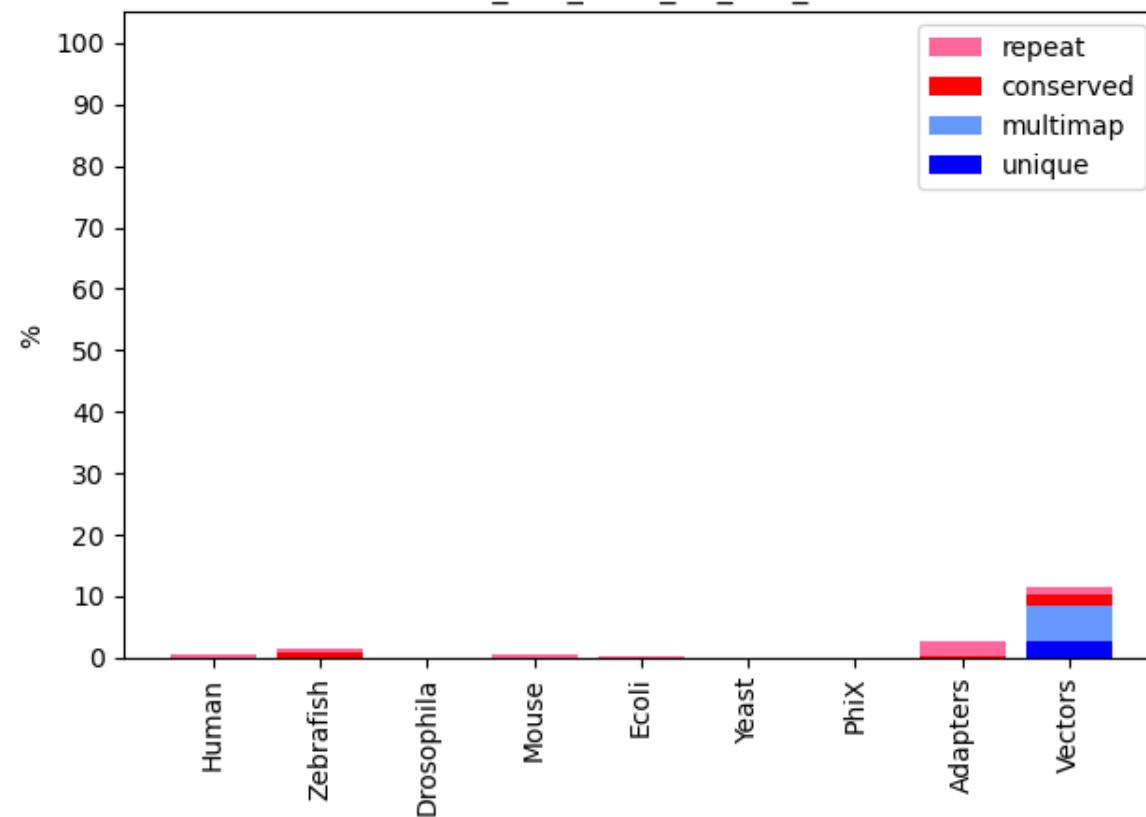
22L005040_S42_L002_R2_001_screen.txt



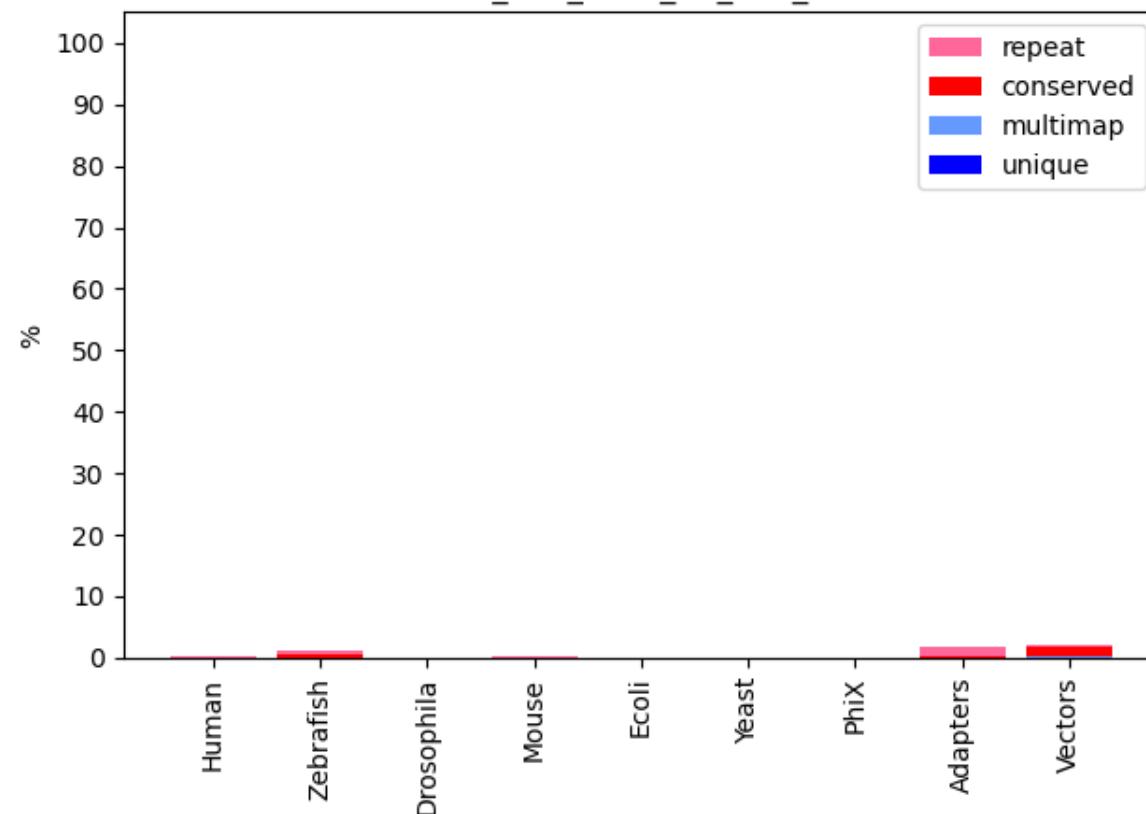
22L005041_S43_L001_R2_001_screen.txt



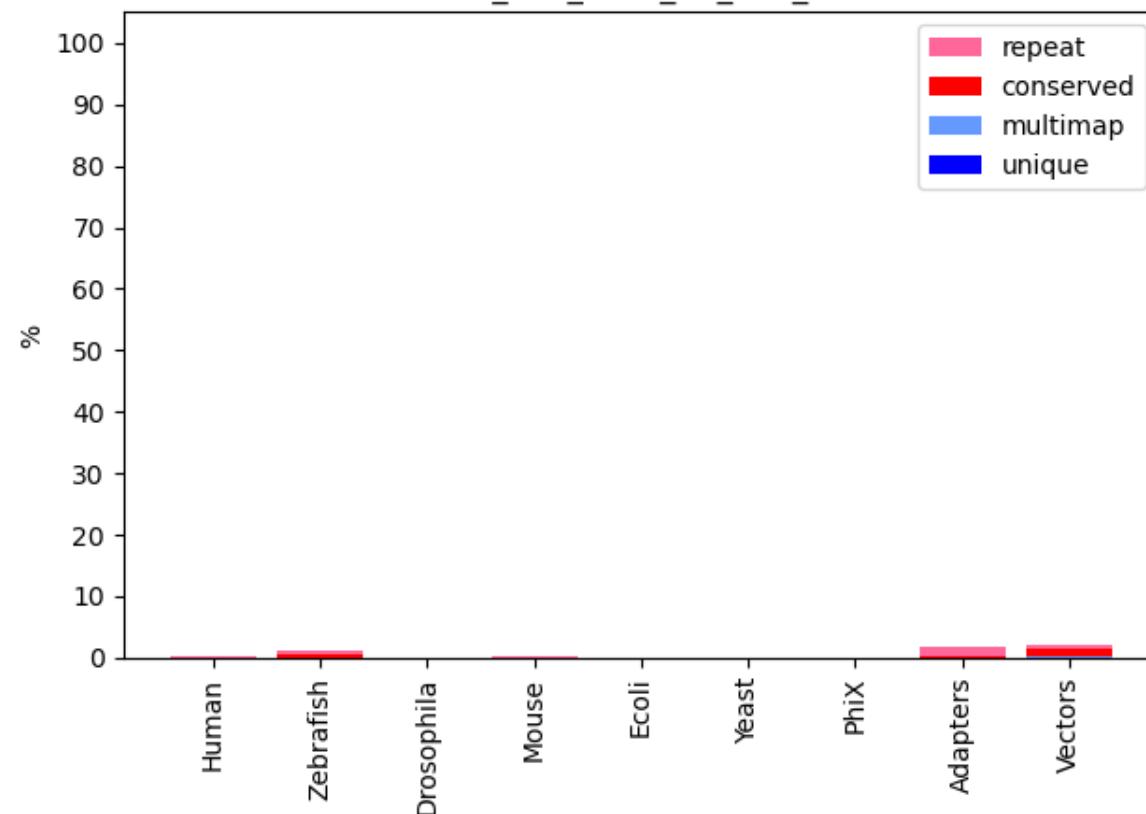
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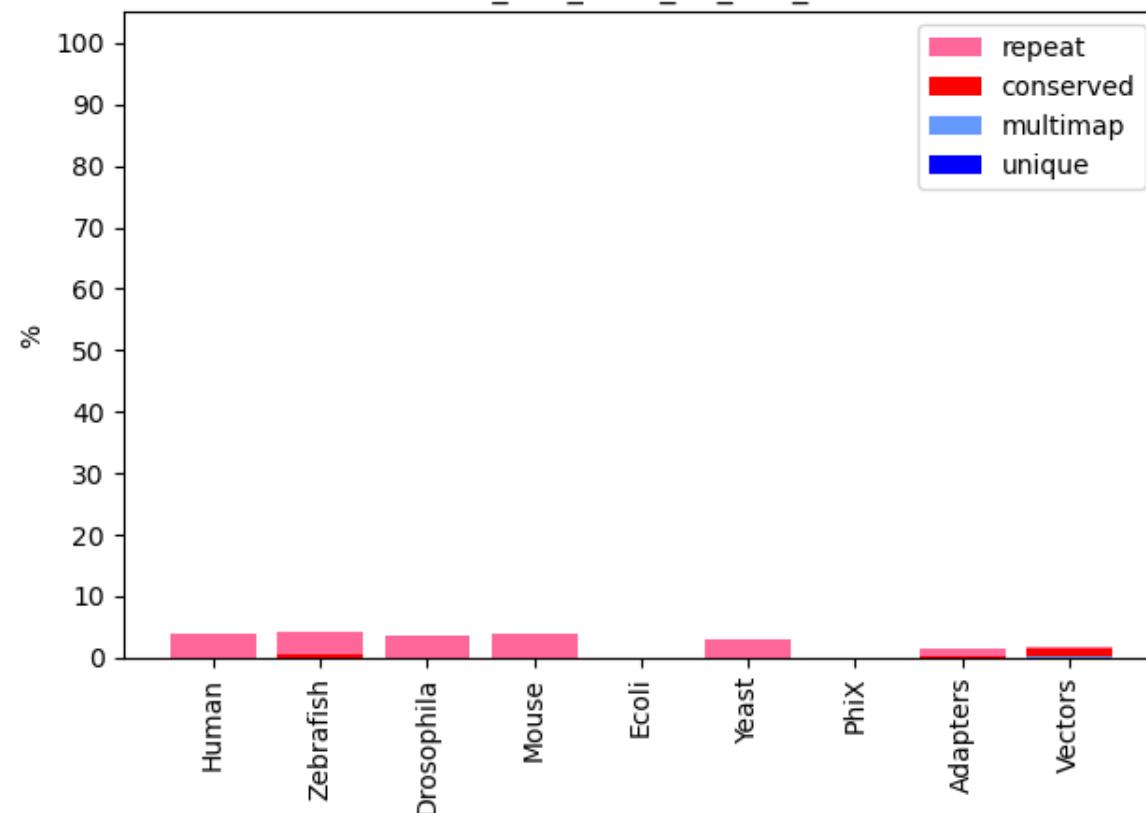
22L005042_S44_L001_R2_001_screen.txt



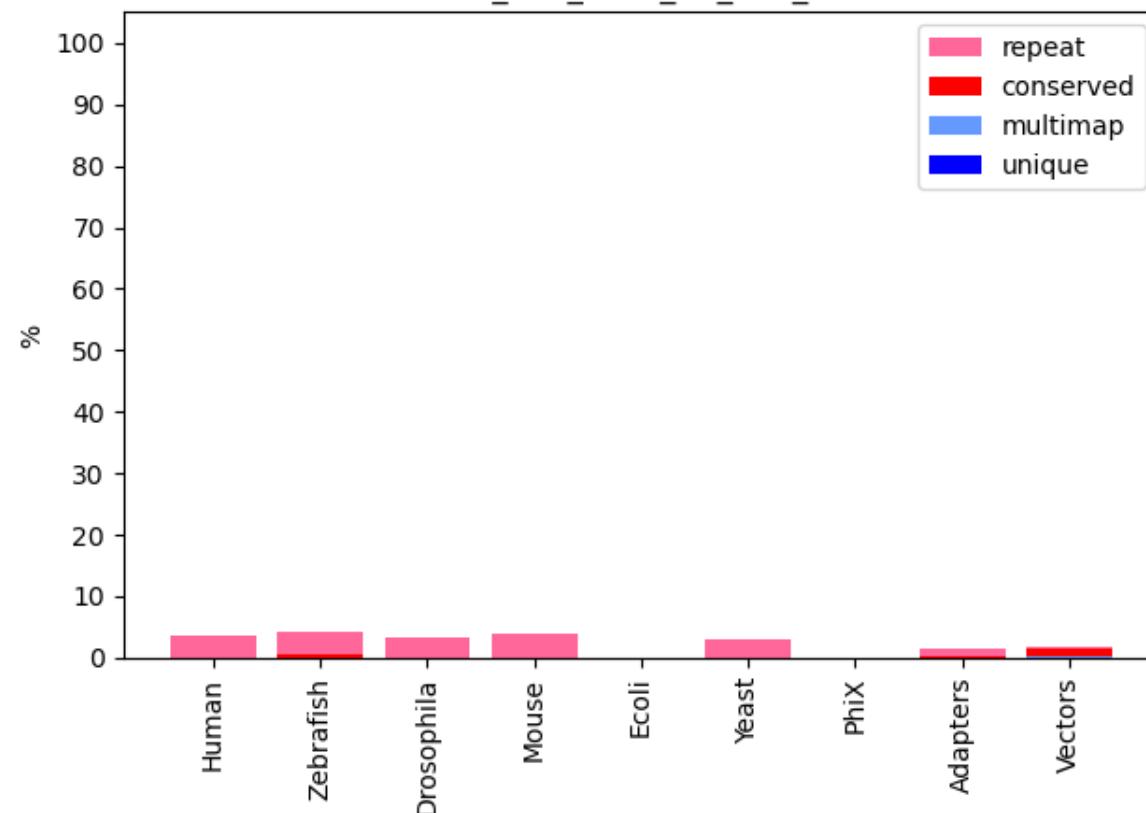
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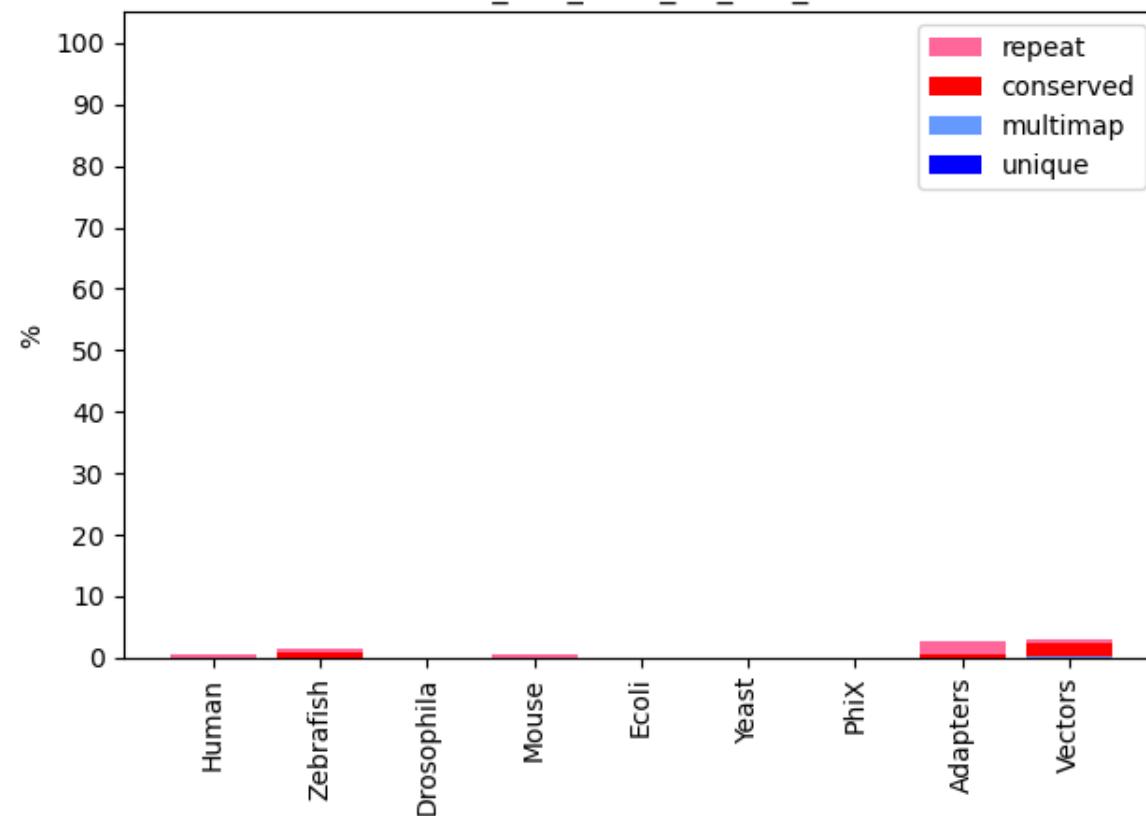
22L005043_S45_L001_R2_001_screen.txt



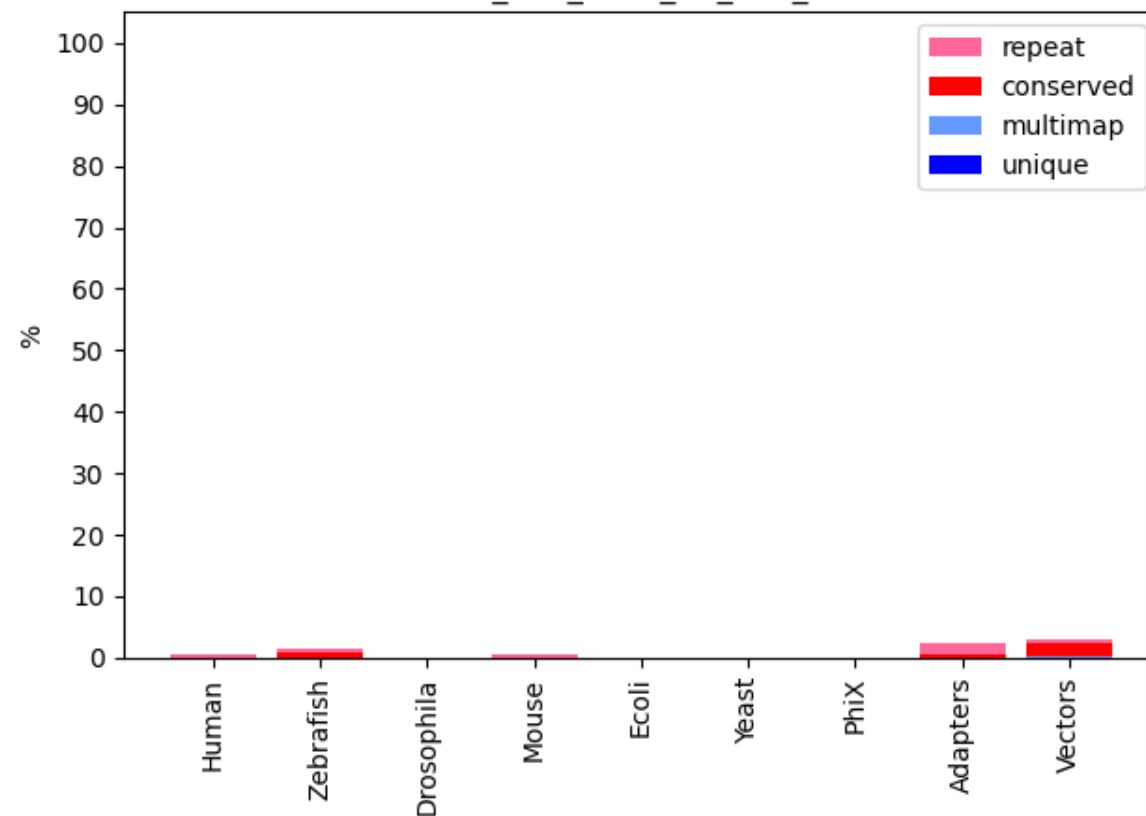
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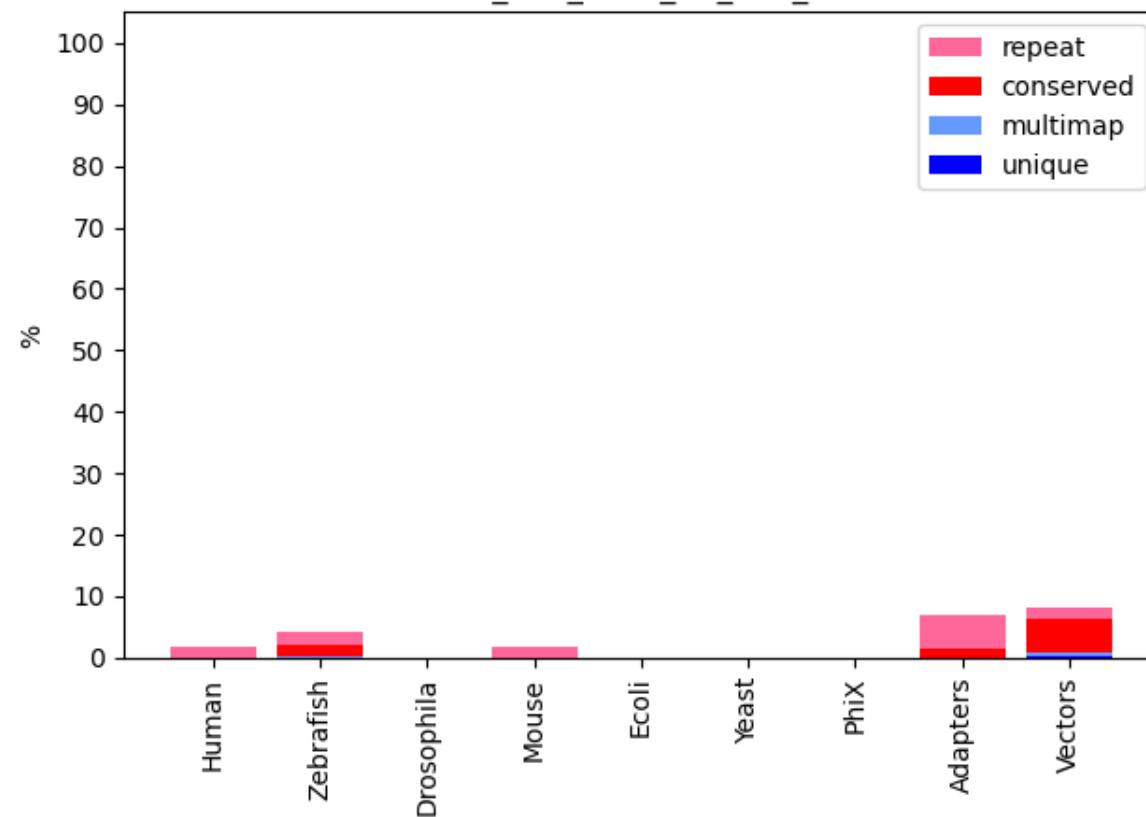
22L005044_S46_L001_R2_001_screen.txt



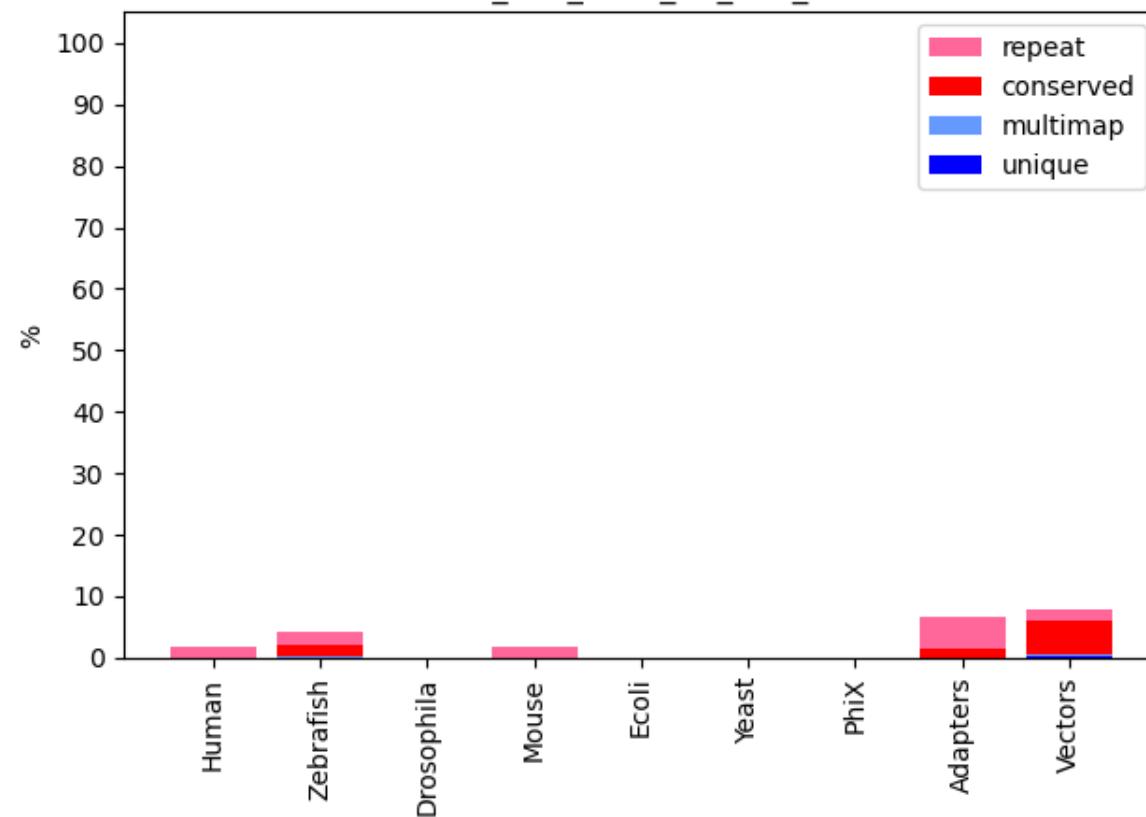
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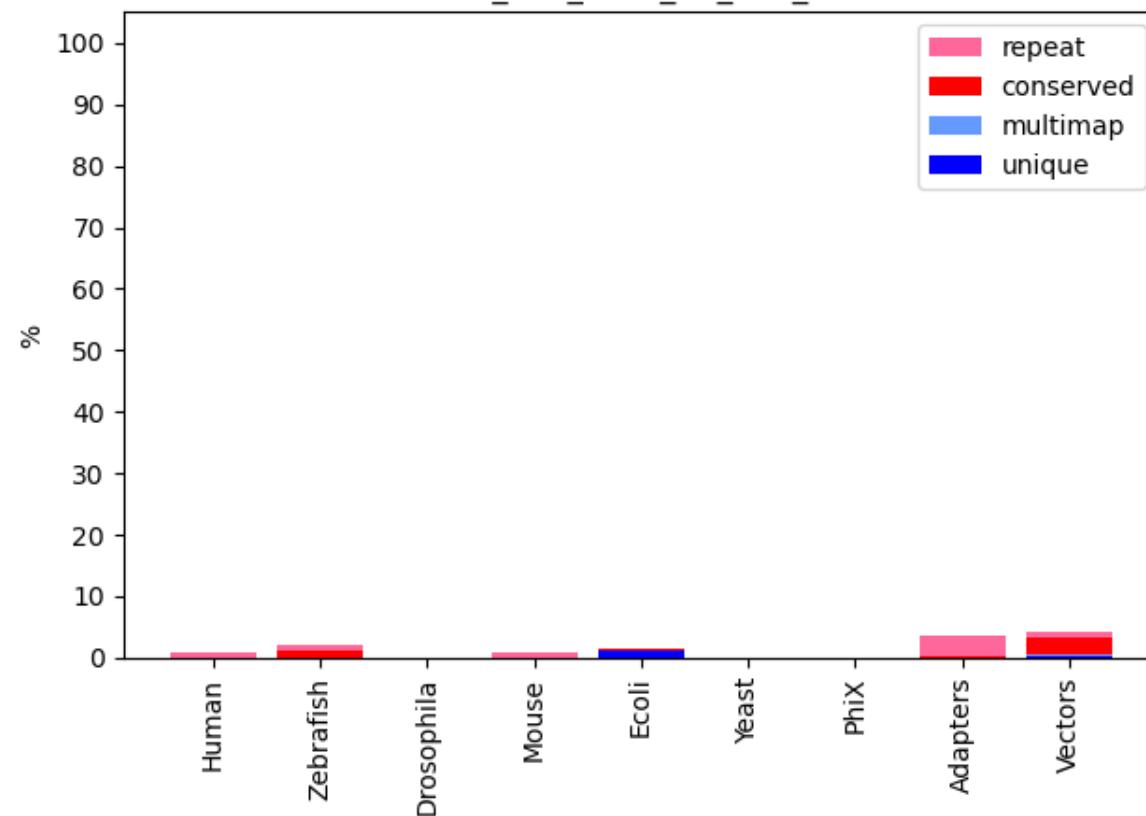
22L005045_S47_L001_R2_001_screen.txt



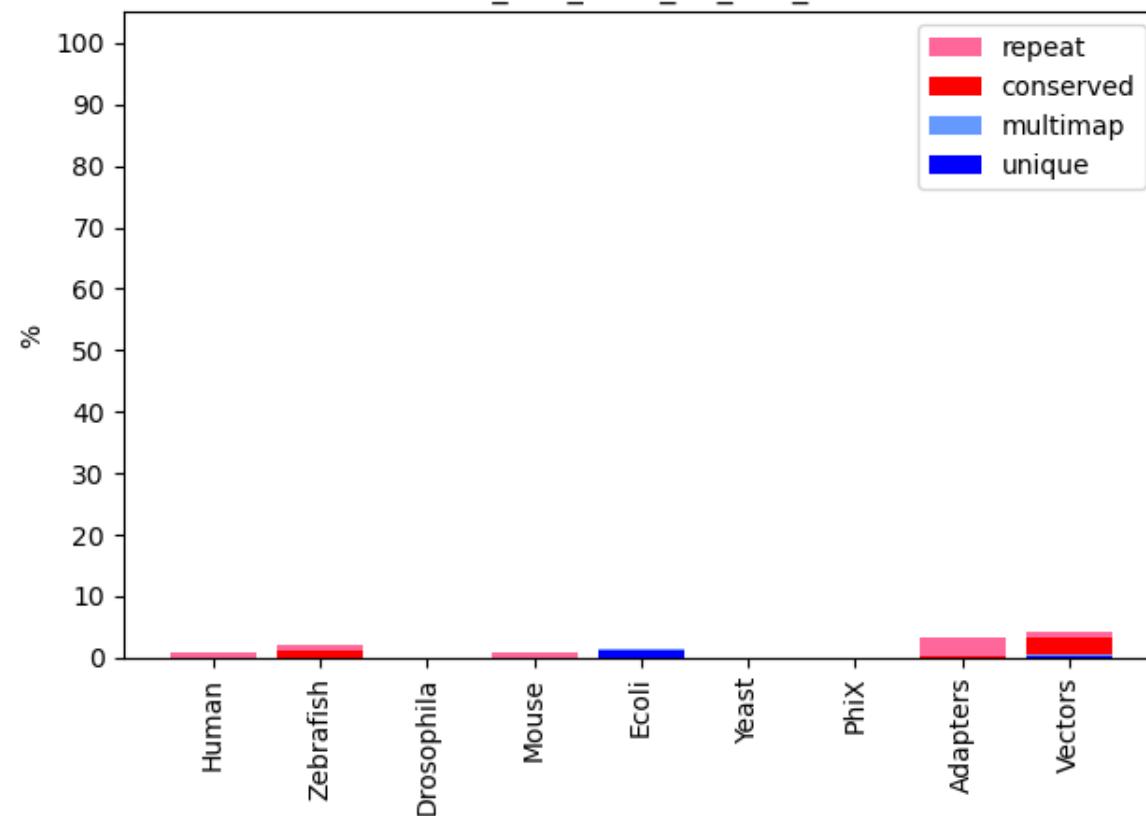
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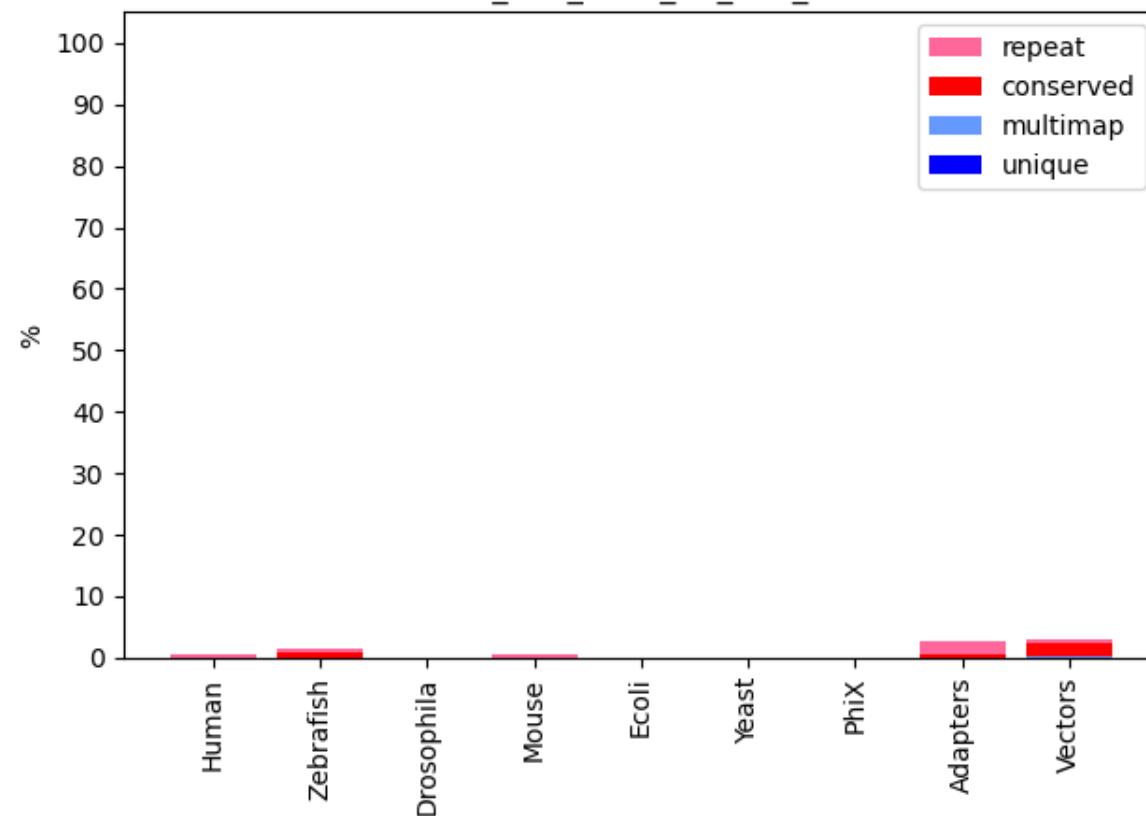
22L005046_S48_L001_R2_001_screen.txt



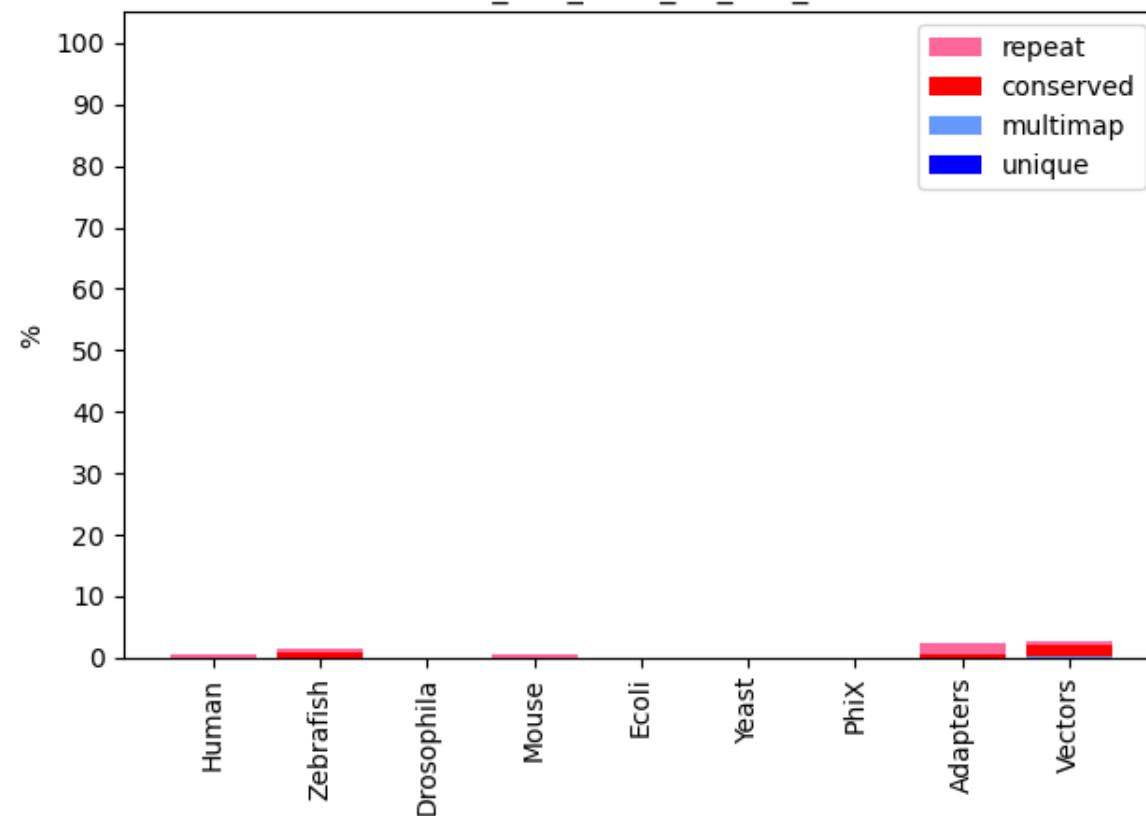
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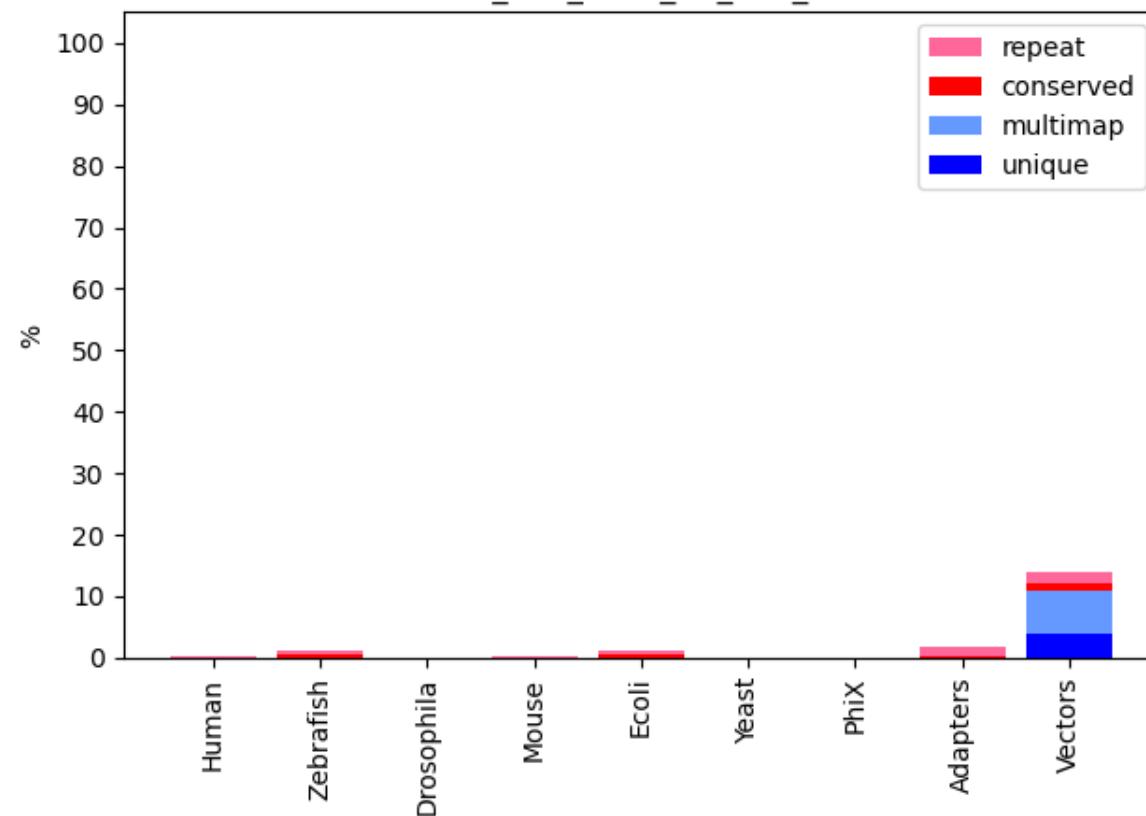
22L005047_S49_L001_R2_001_screen.txt



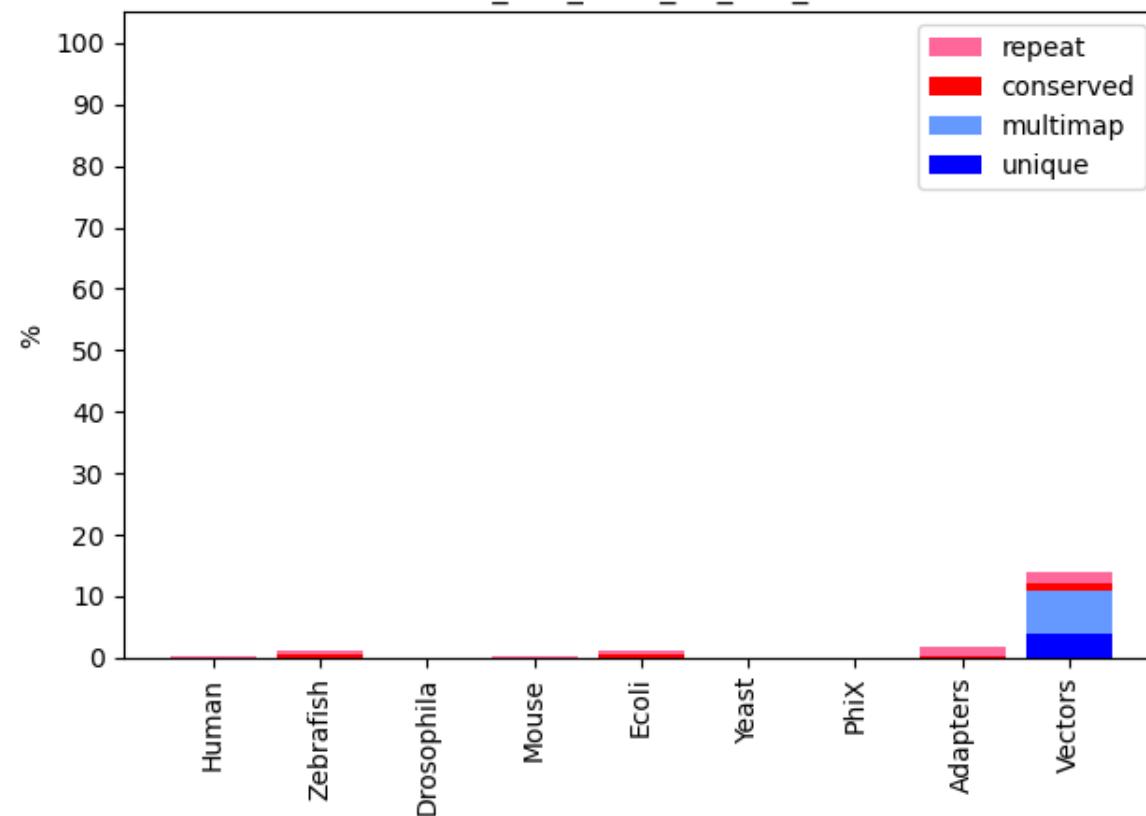
22L005047_S49_L002_R2_001_screen.txt



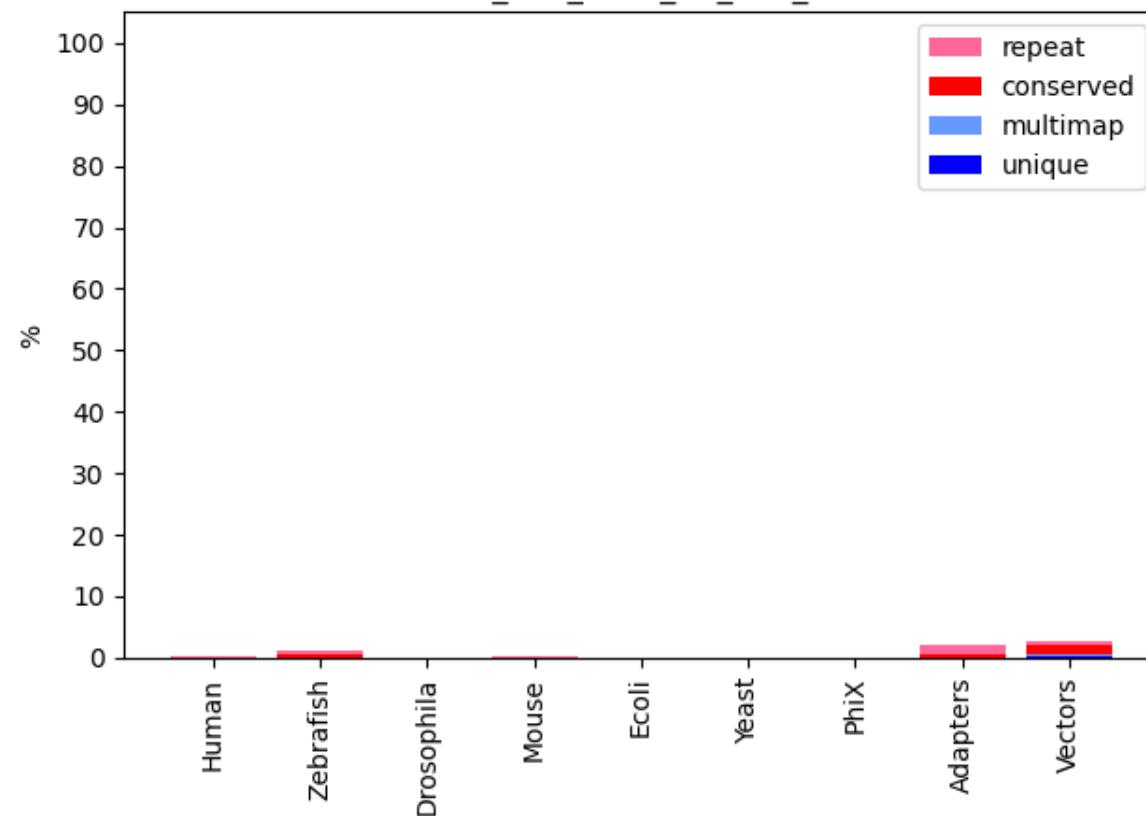
22L005048_S50_L001_R2_001_screen.txt



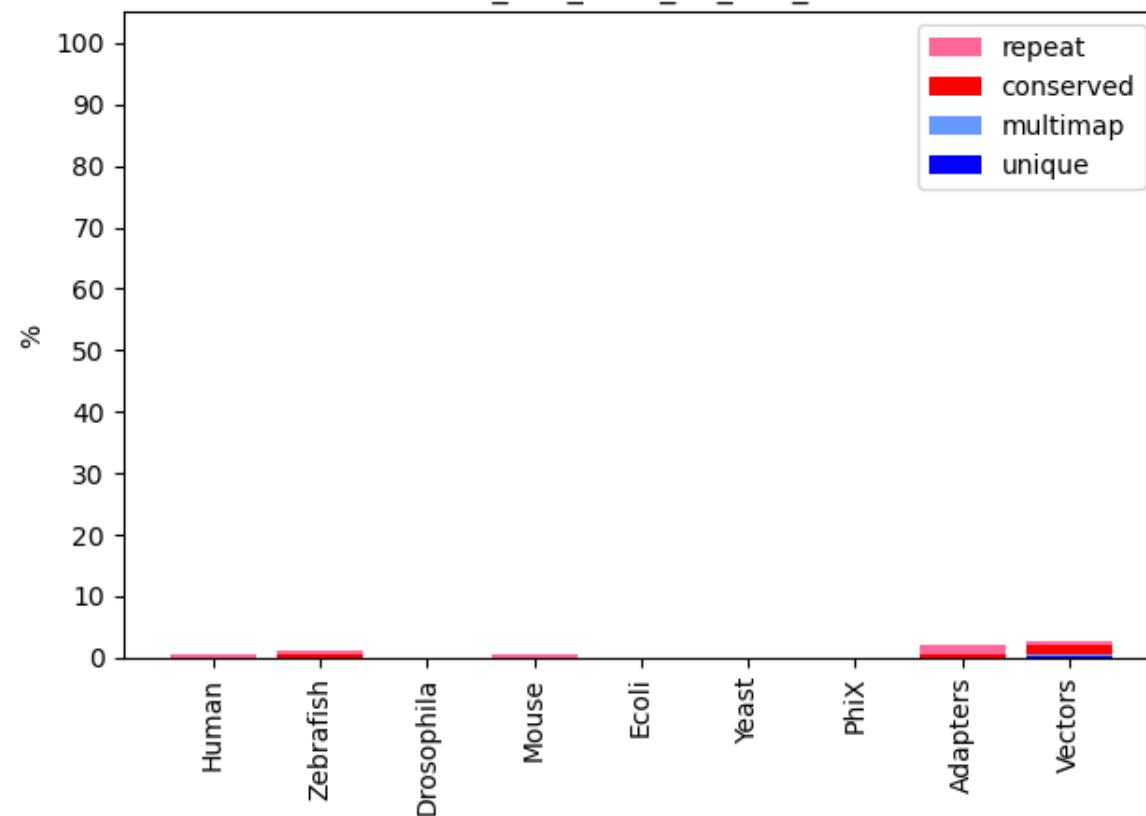
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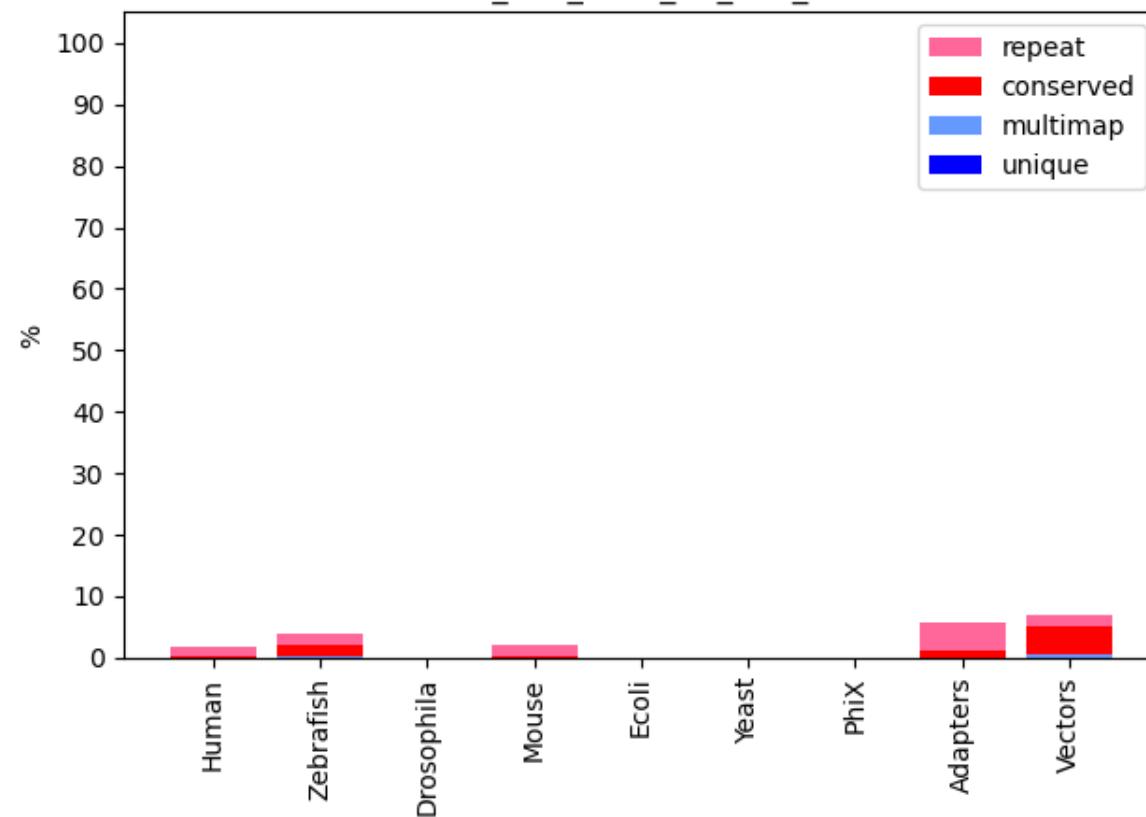
22L005049_S51_L001_R2_001_screen.txt



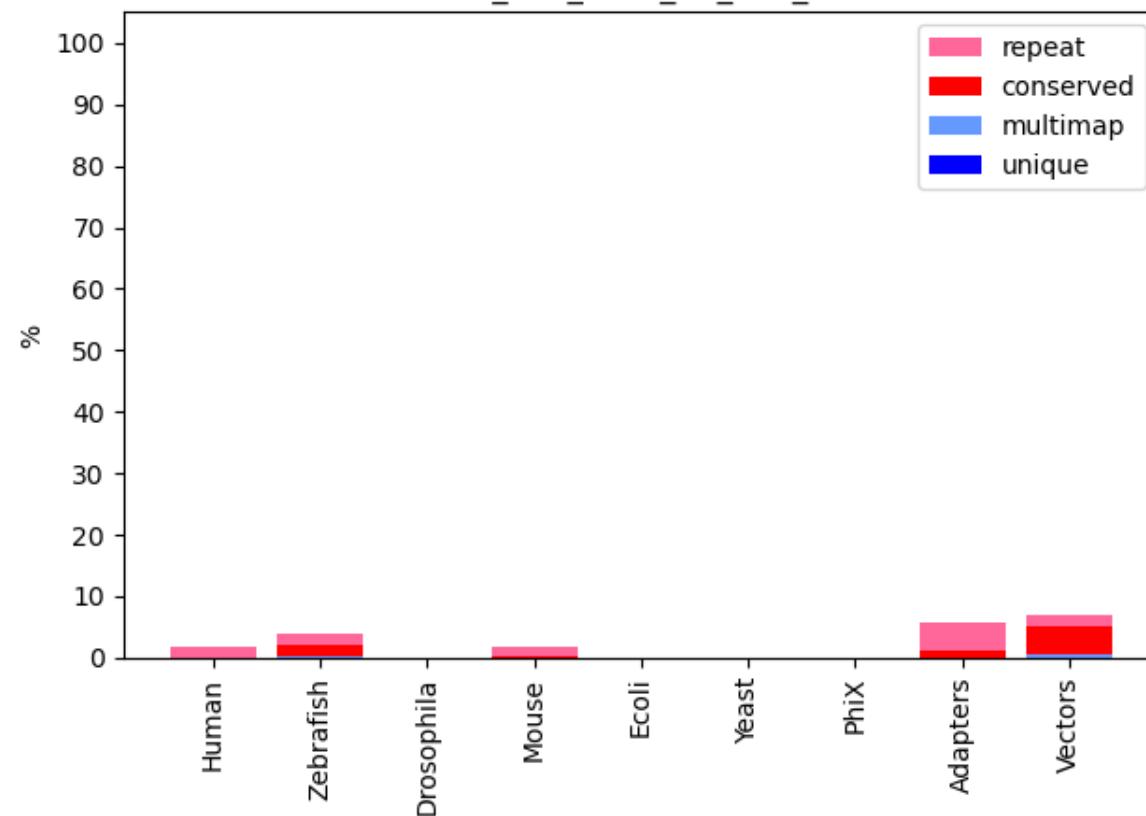
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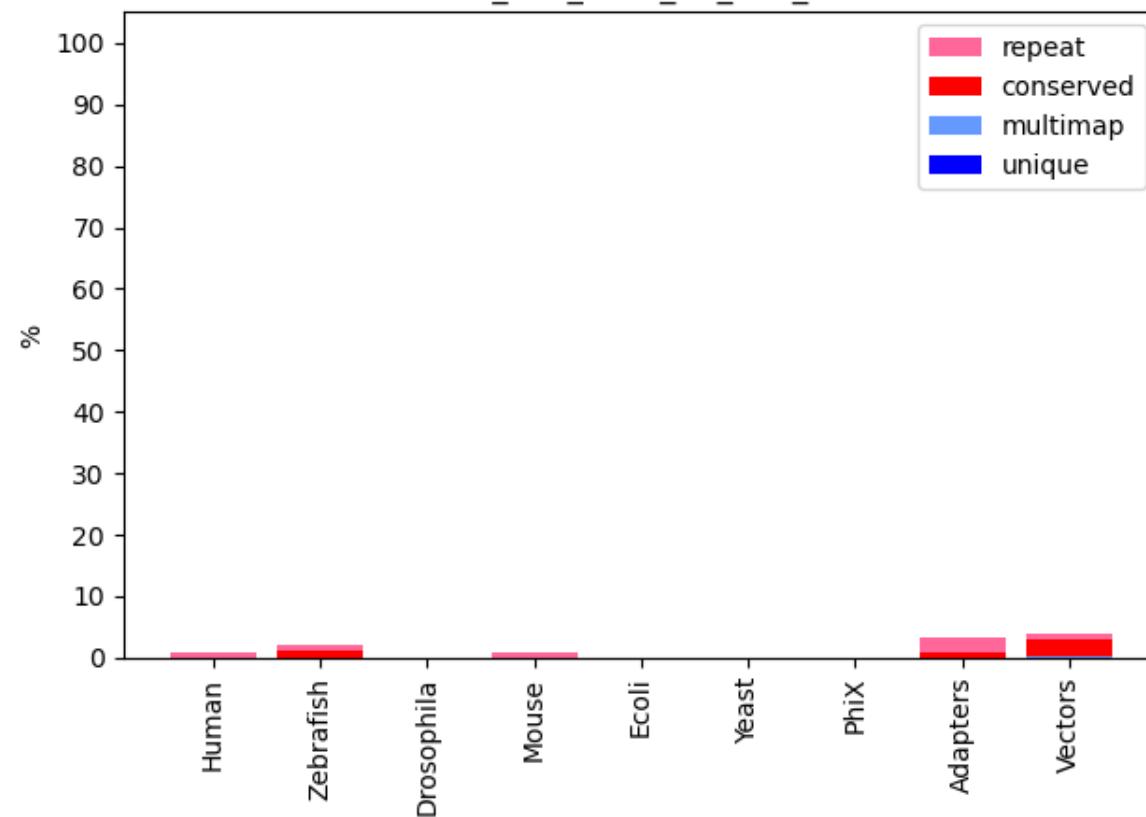
22L005050_S52_L001_R2_001_screen.txt



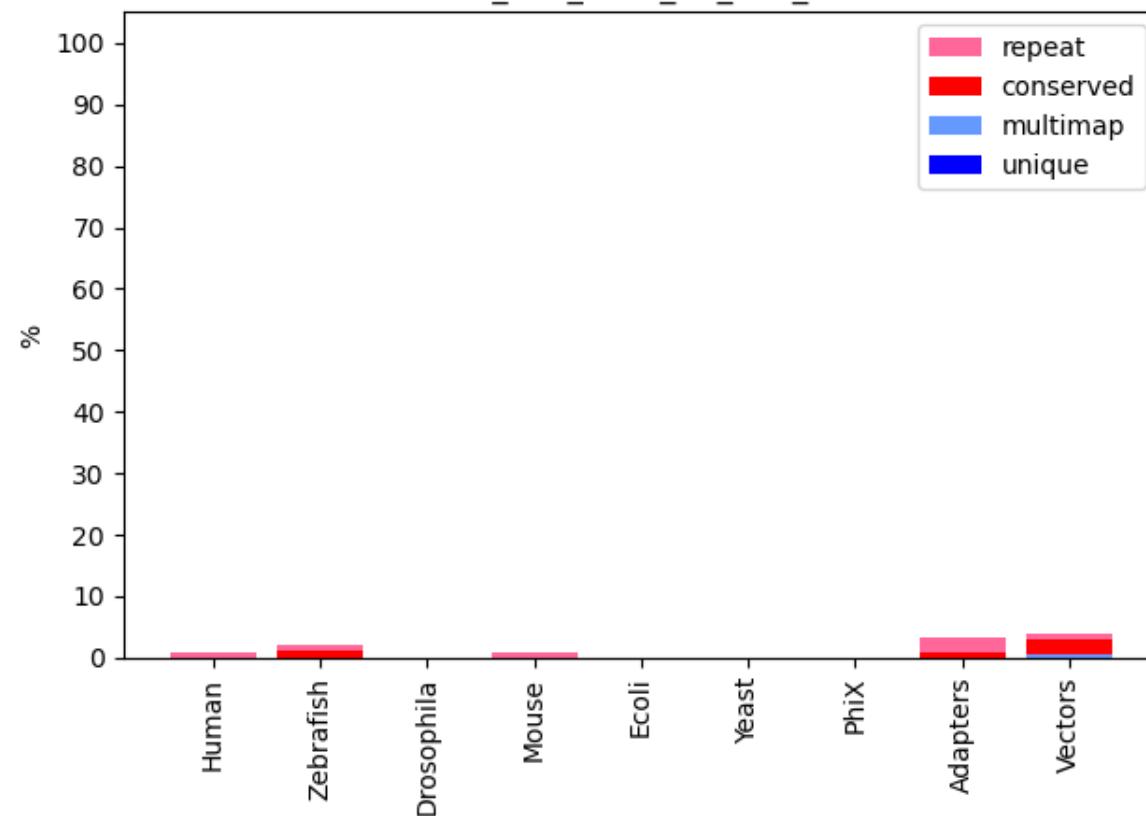
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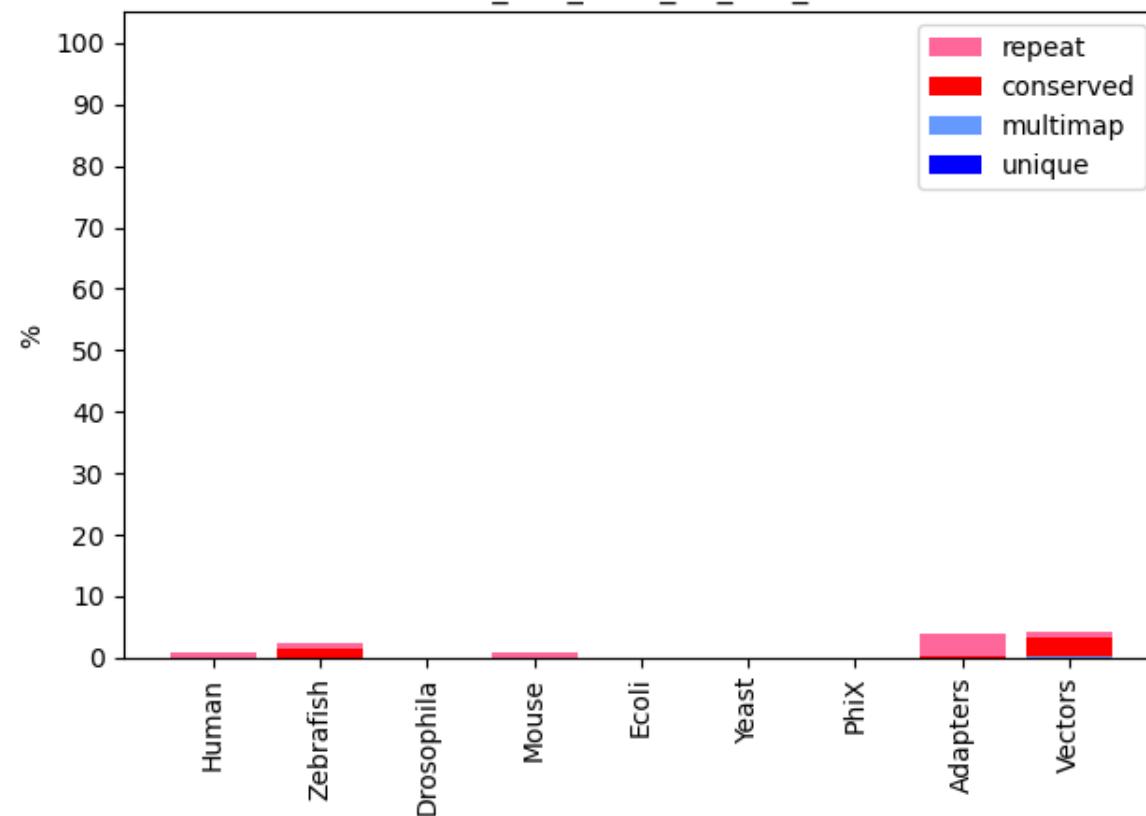
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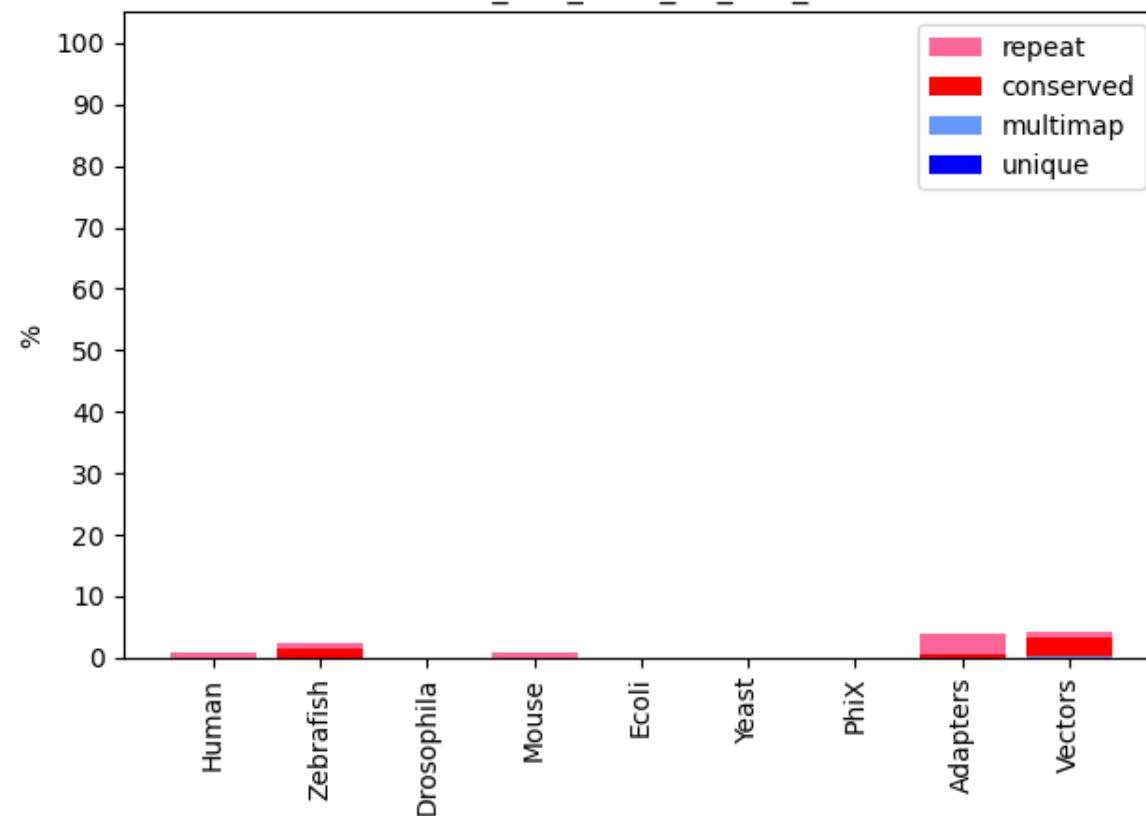
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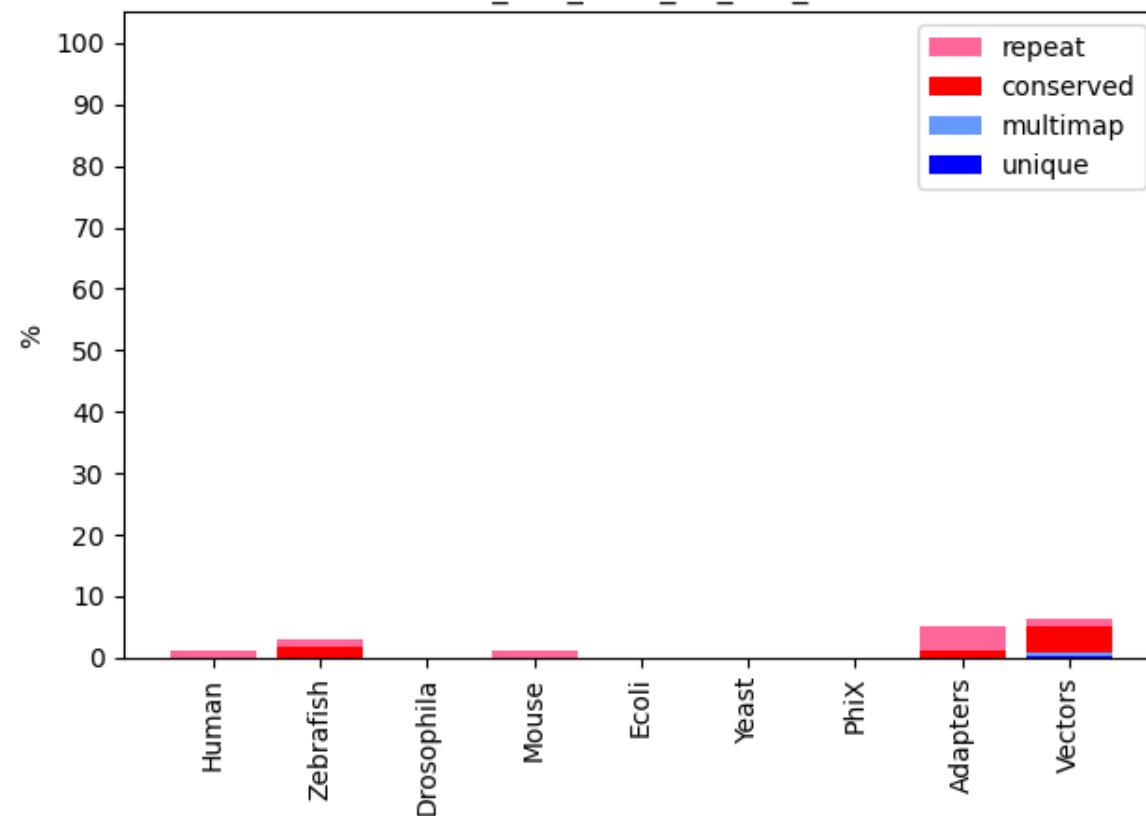
22L005052_S54_L001_R2_001_screen.txt



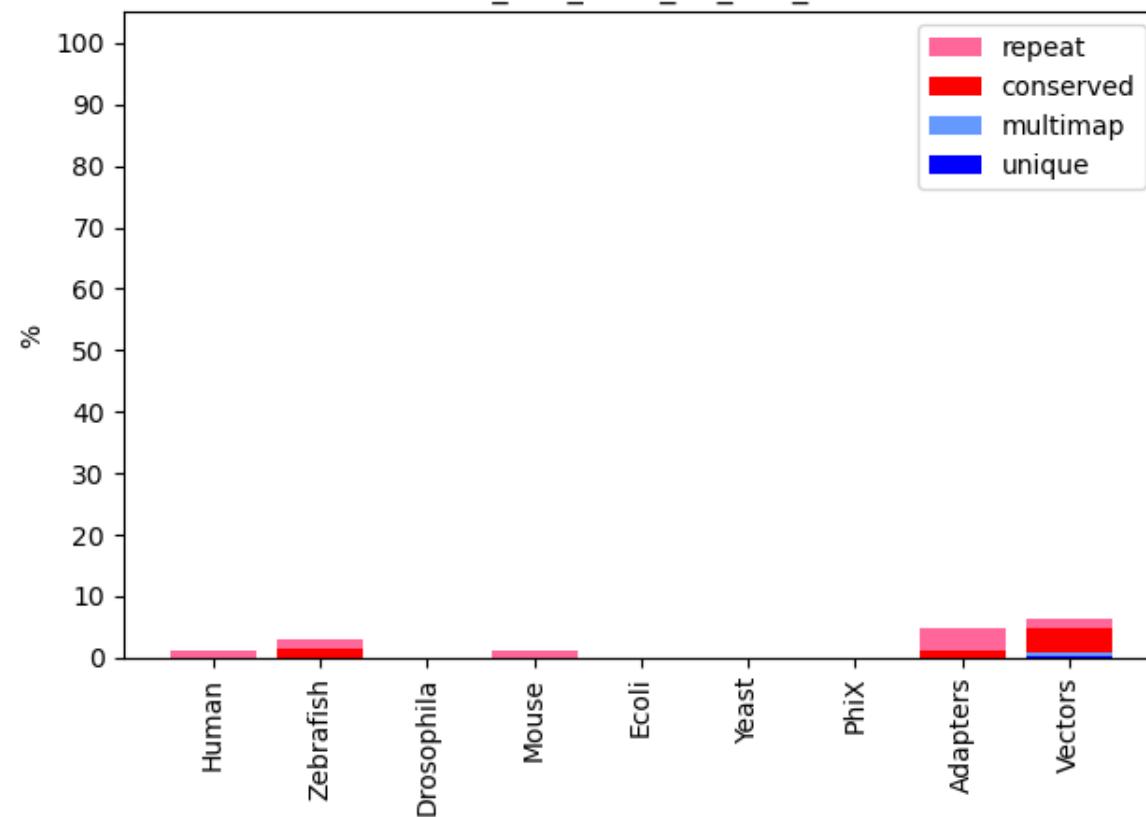
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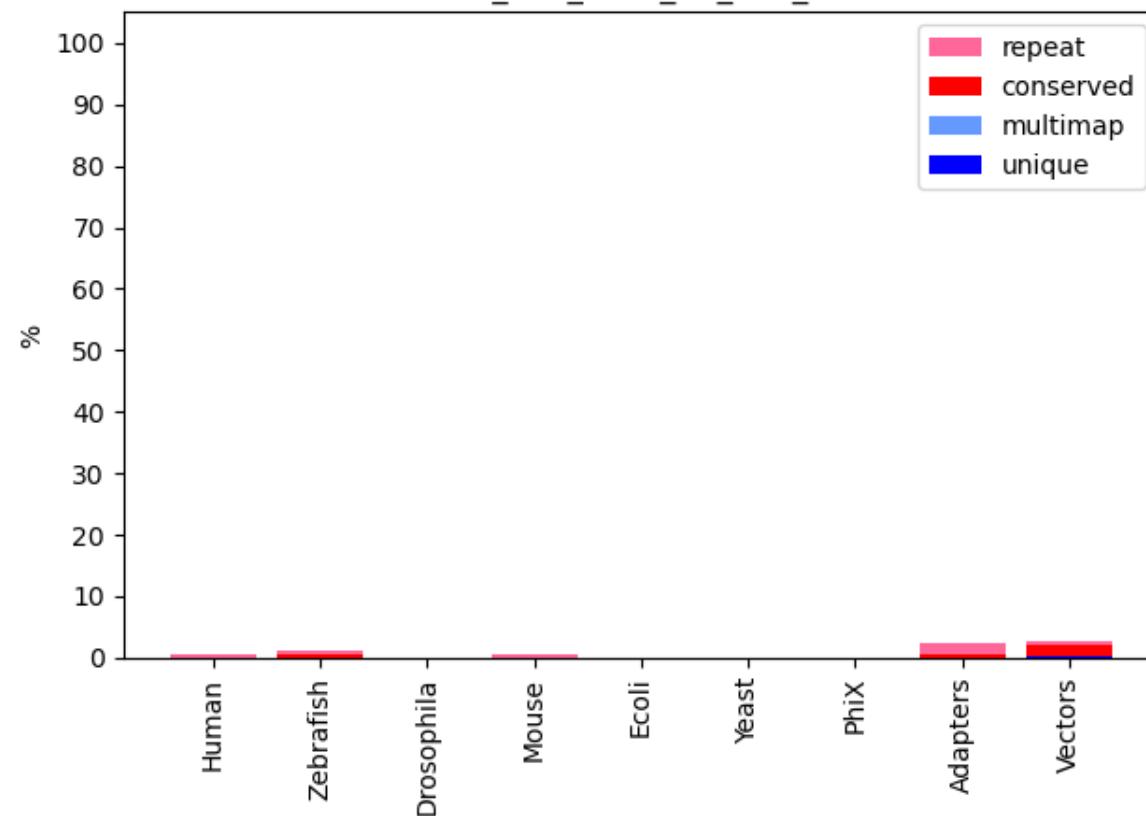
22L005053_S55_L001_R2_001_screen.txt



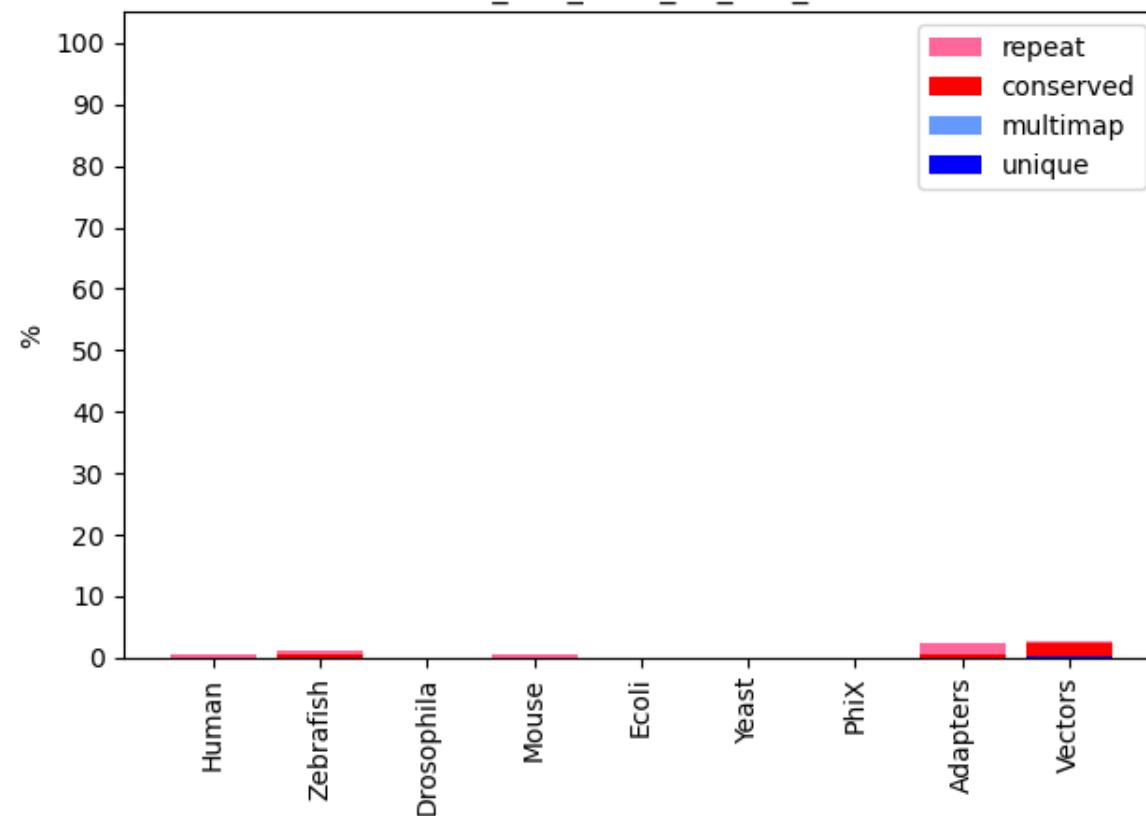
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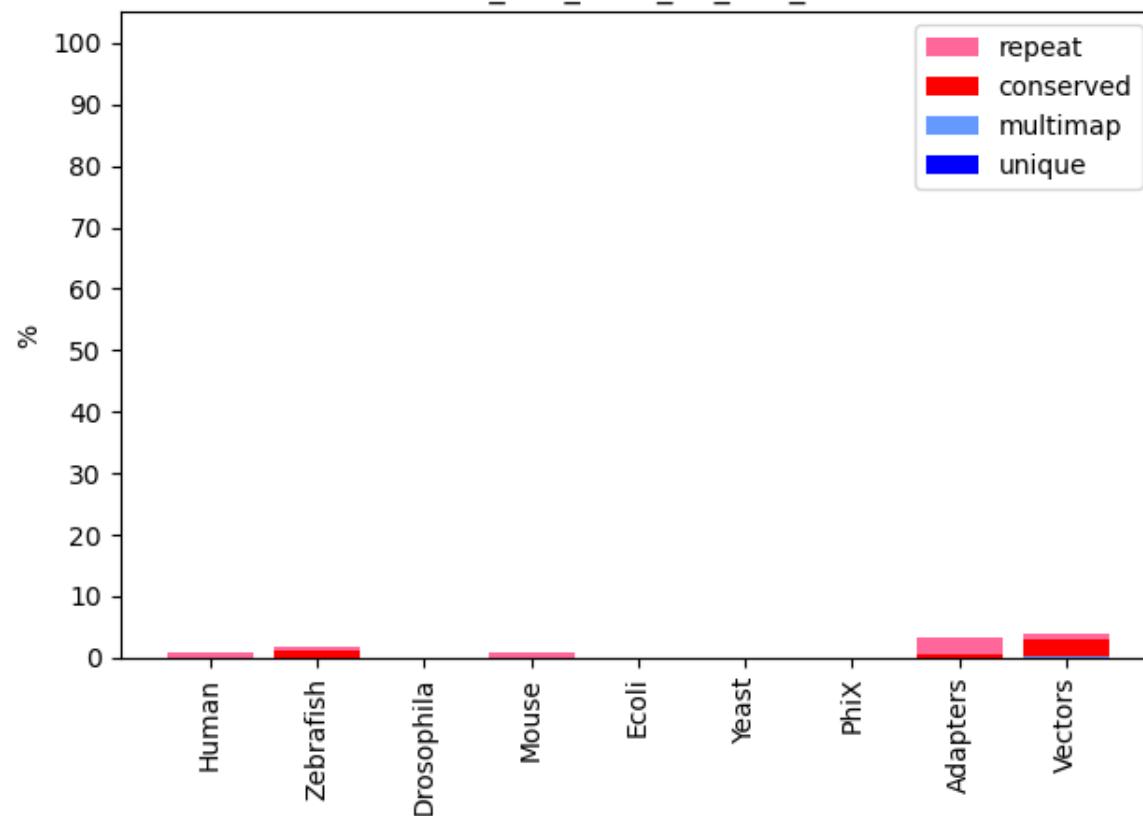
22L005054_S56_L001_R2_001_screen.txt



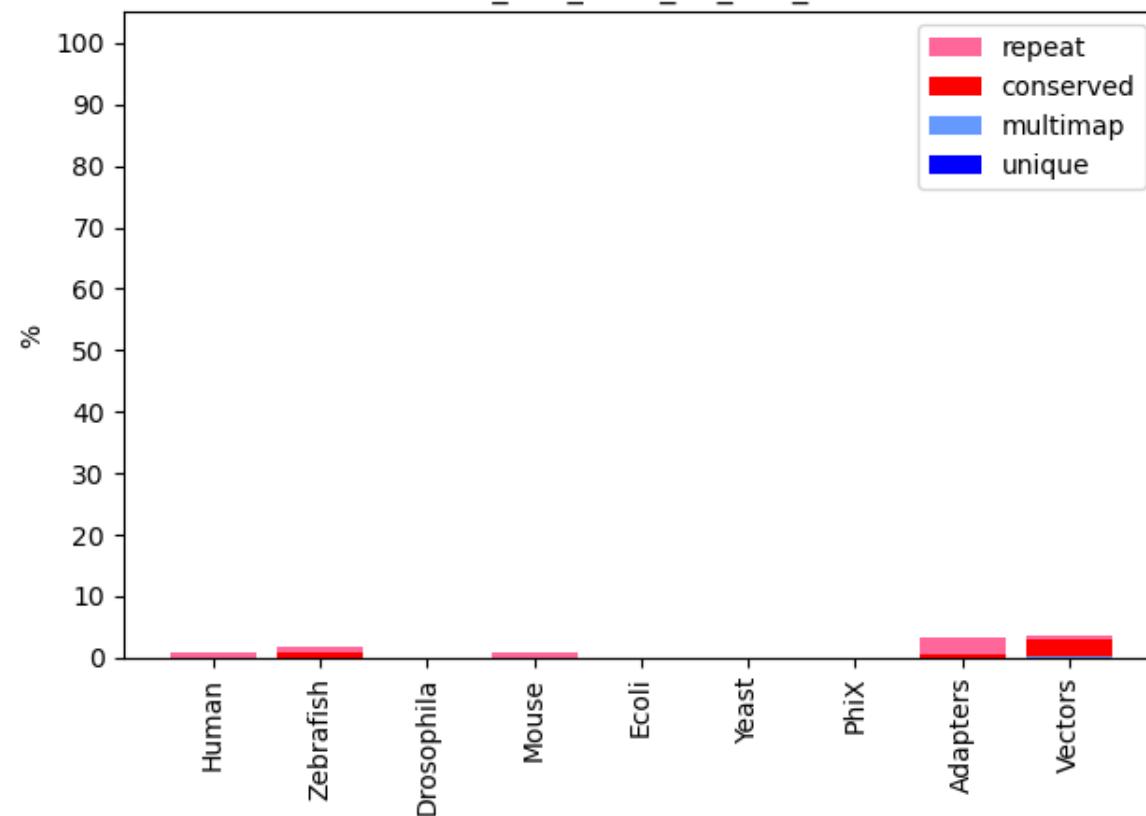
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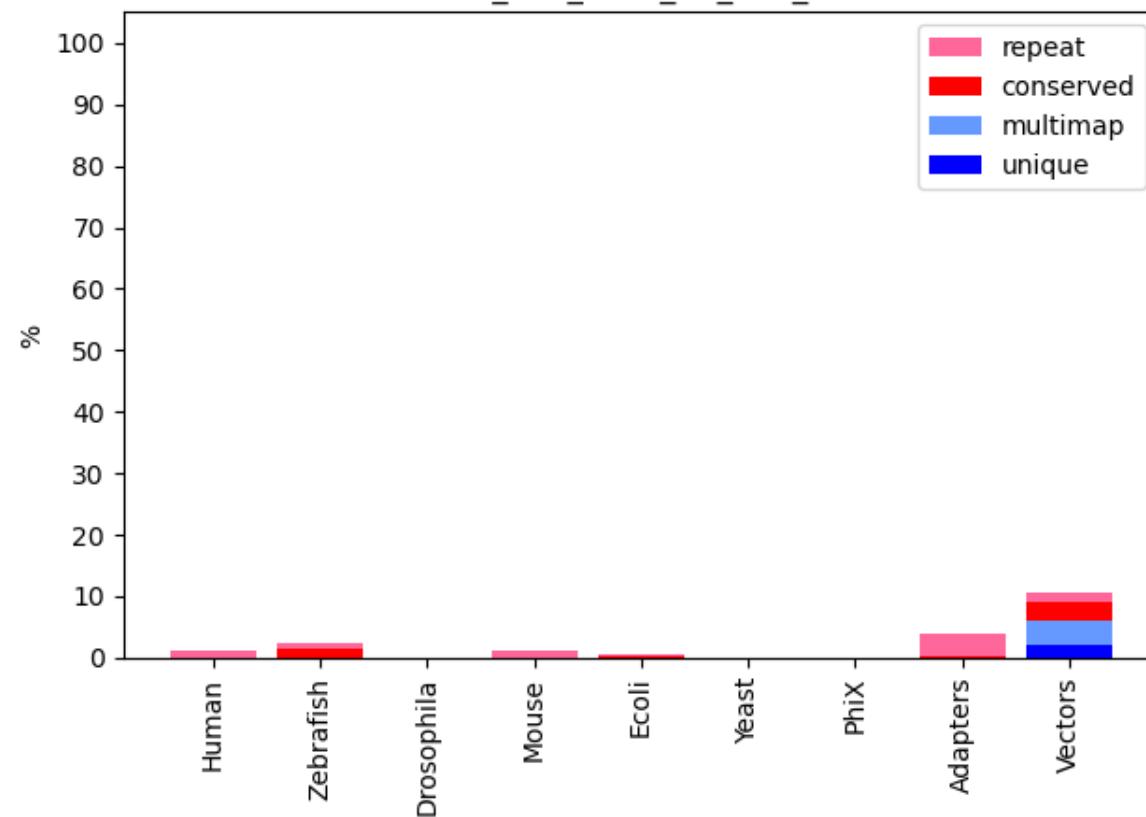
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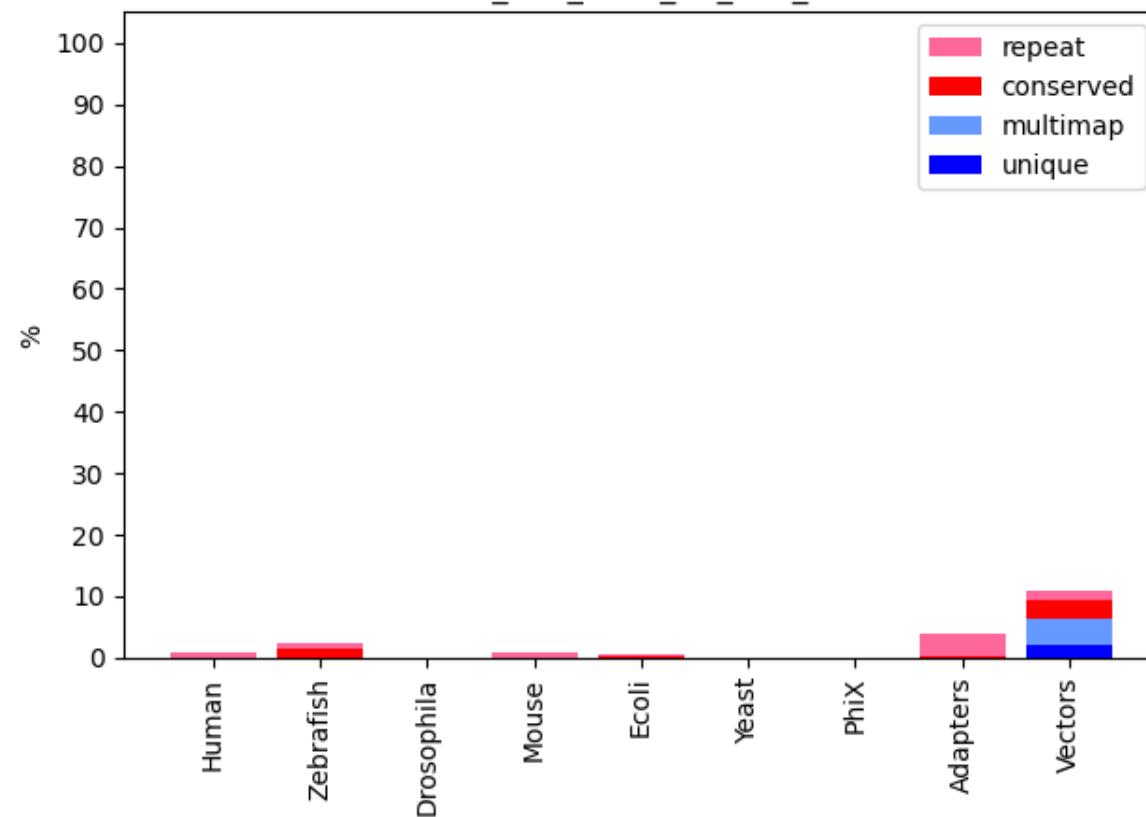
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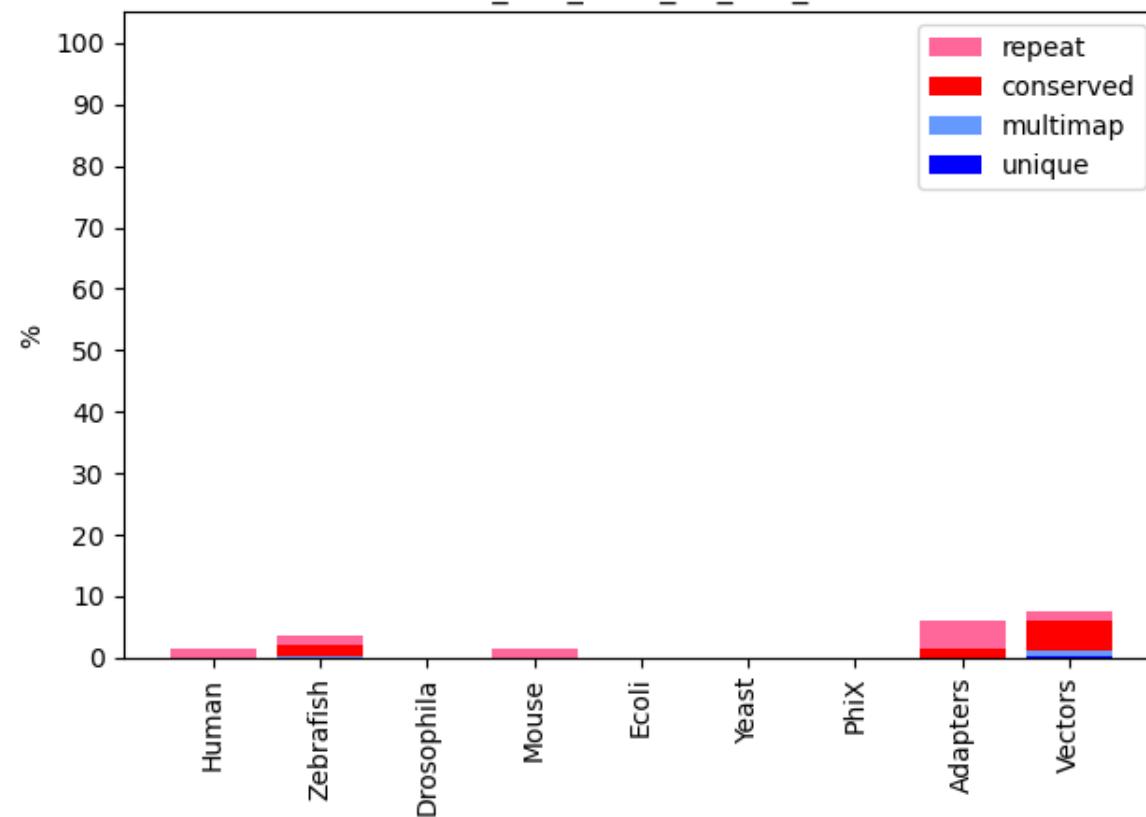
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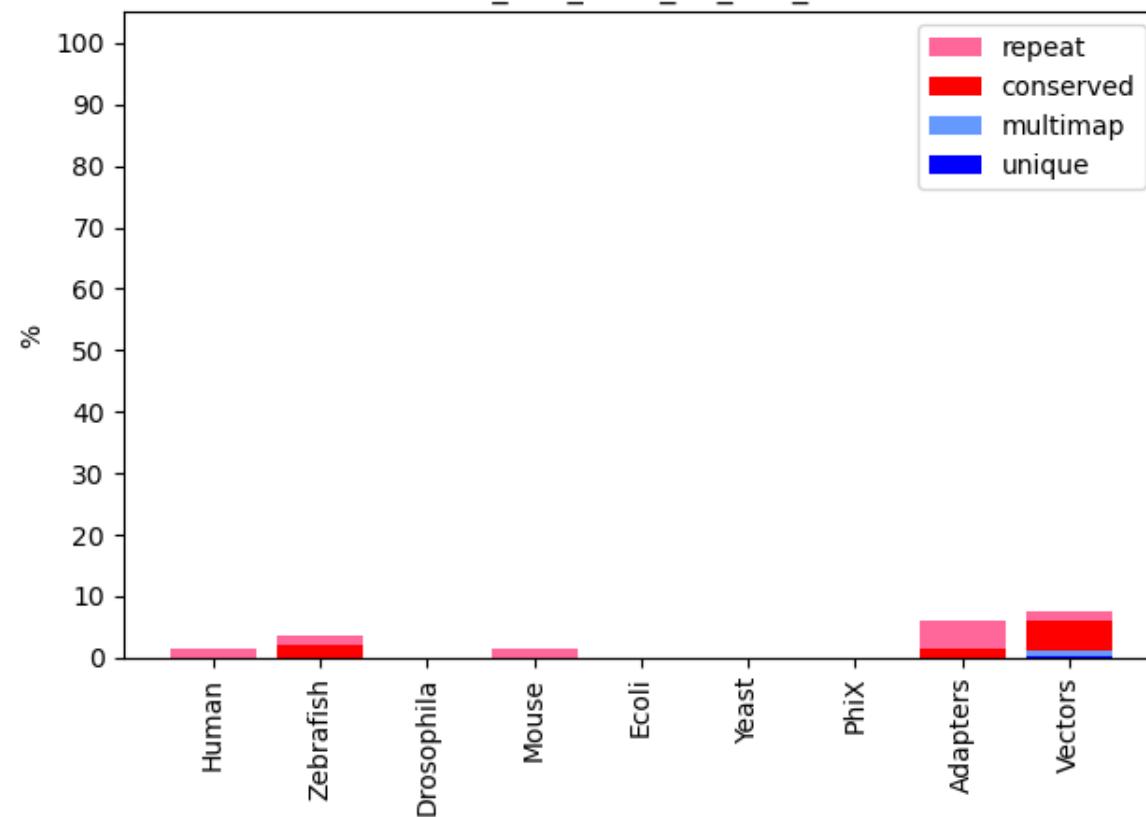
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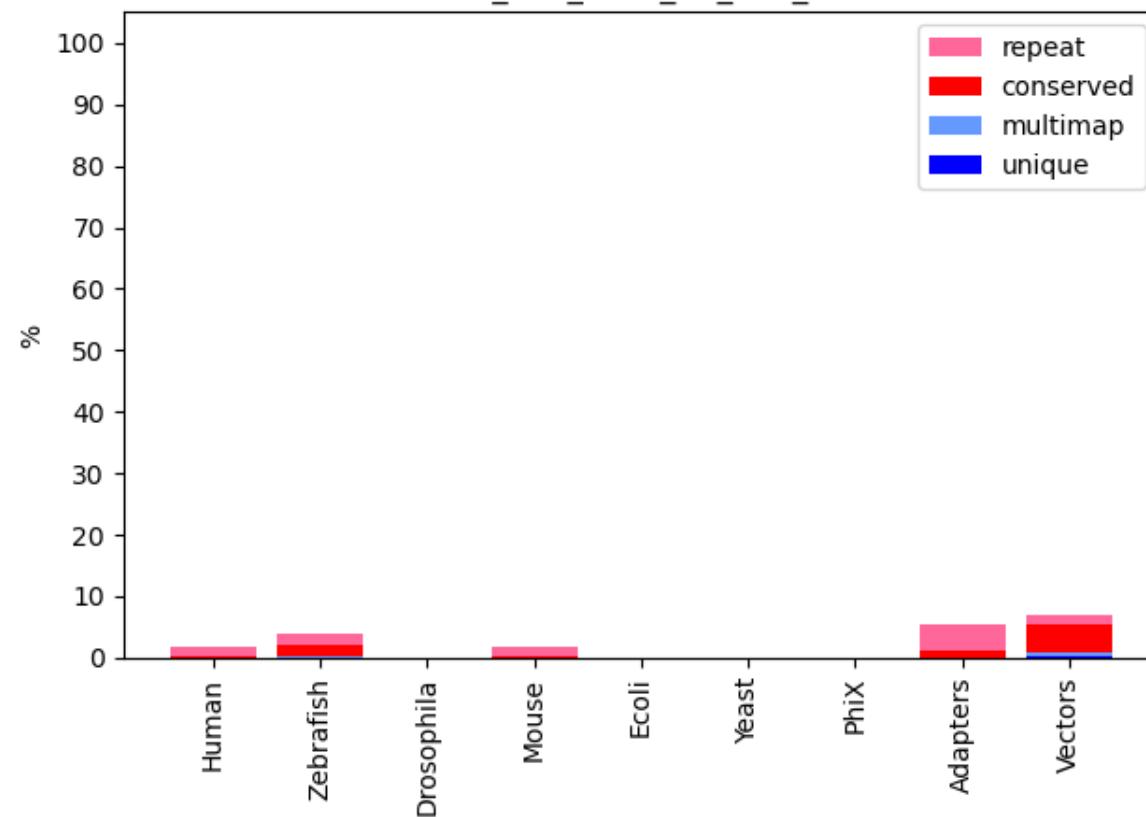
22L005057_S59_L001_R2_001_screen.txt



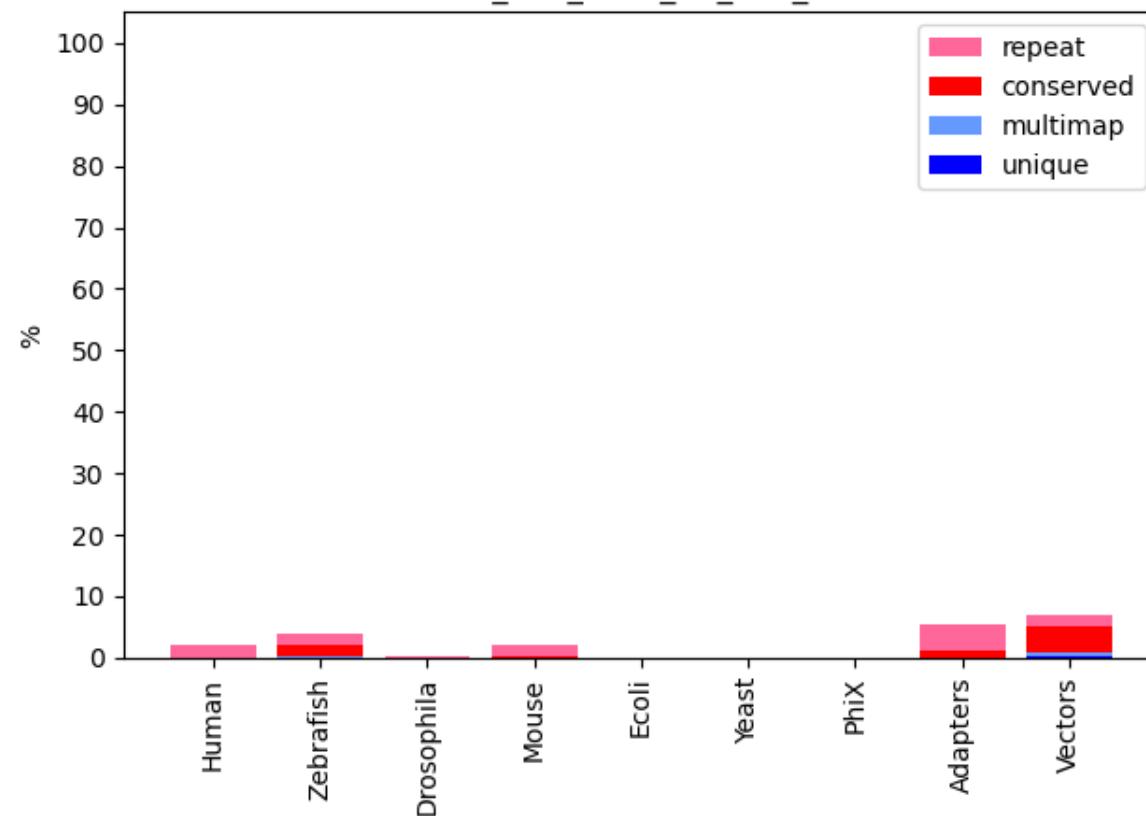
22L005057_S59_L002_R2_001_screen.txt



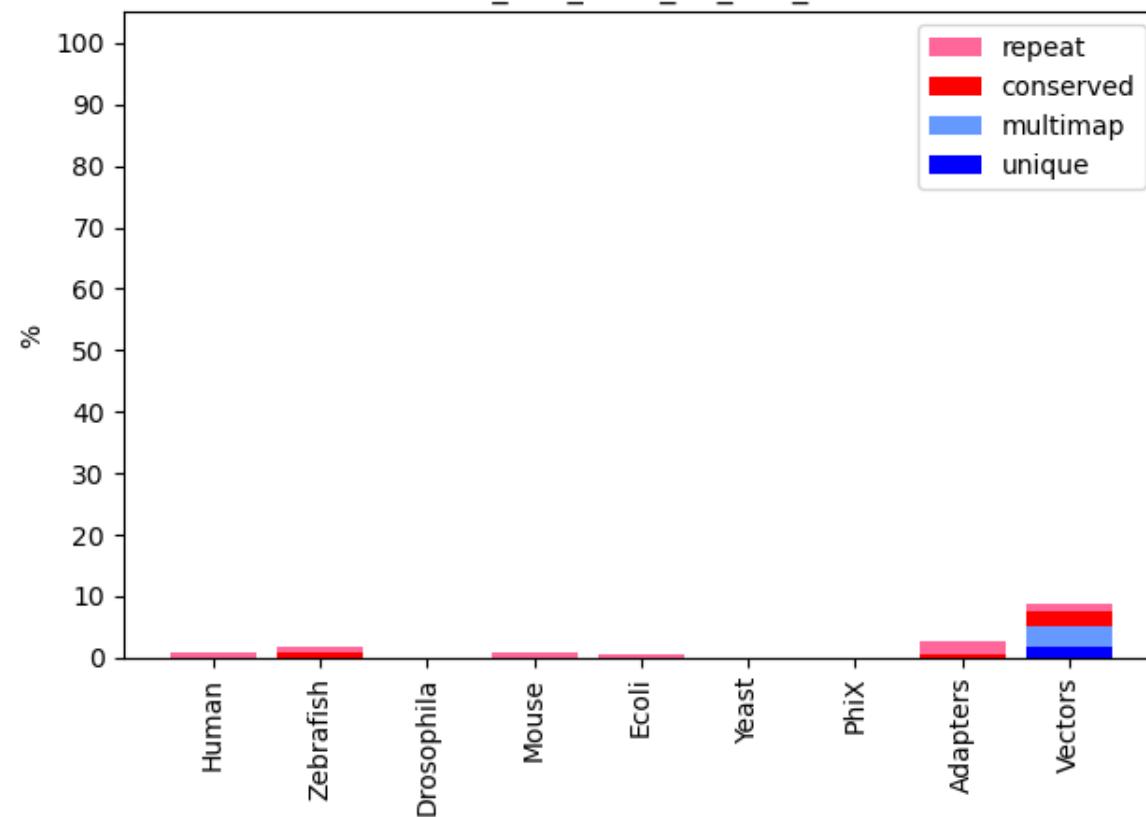
22L005058_S60_L001_R2_001_screen.txt



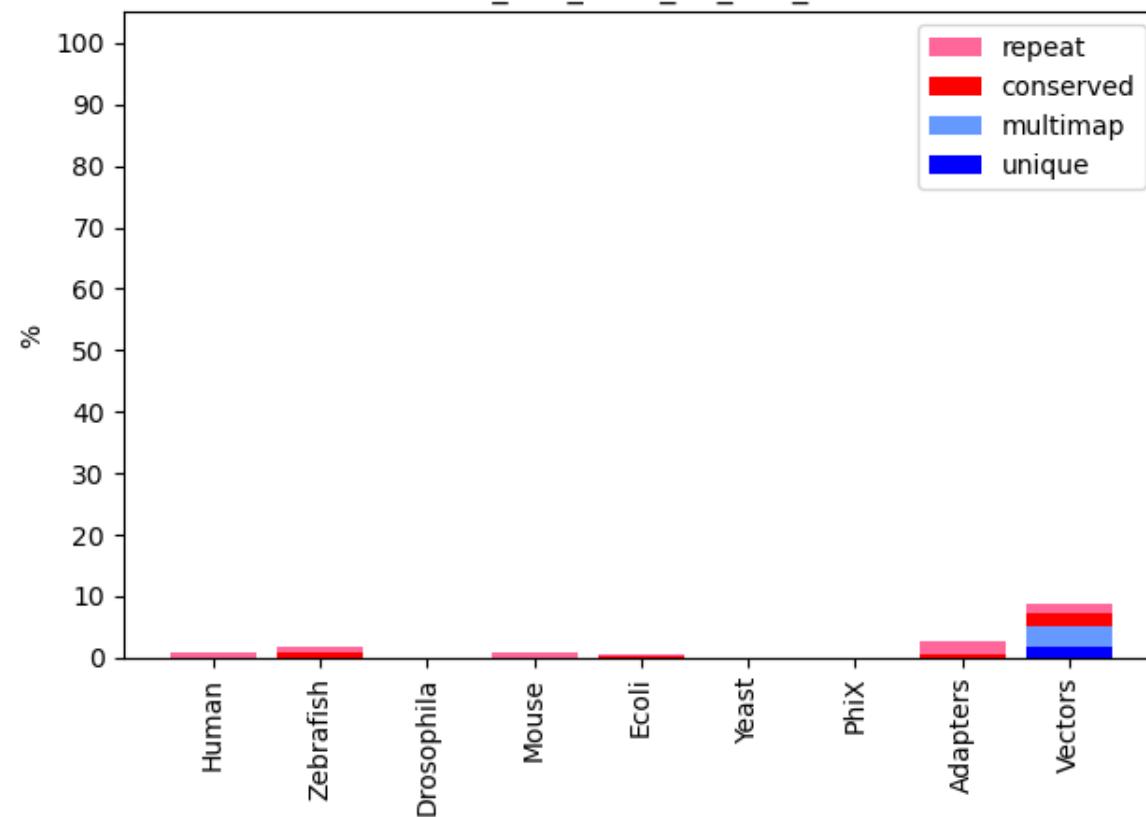
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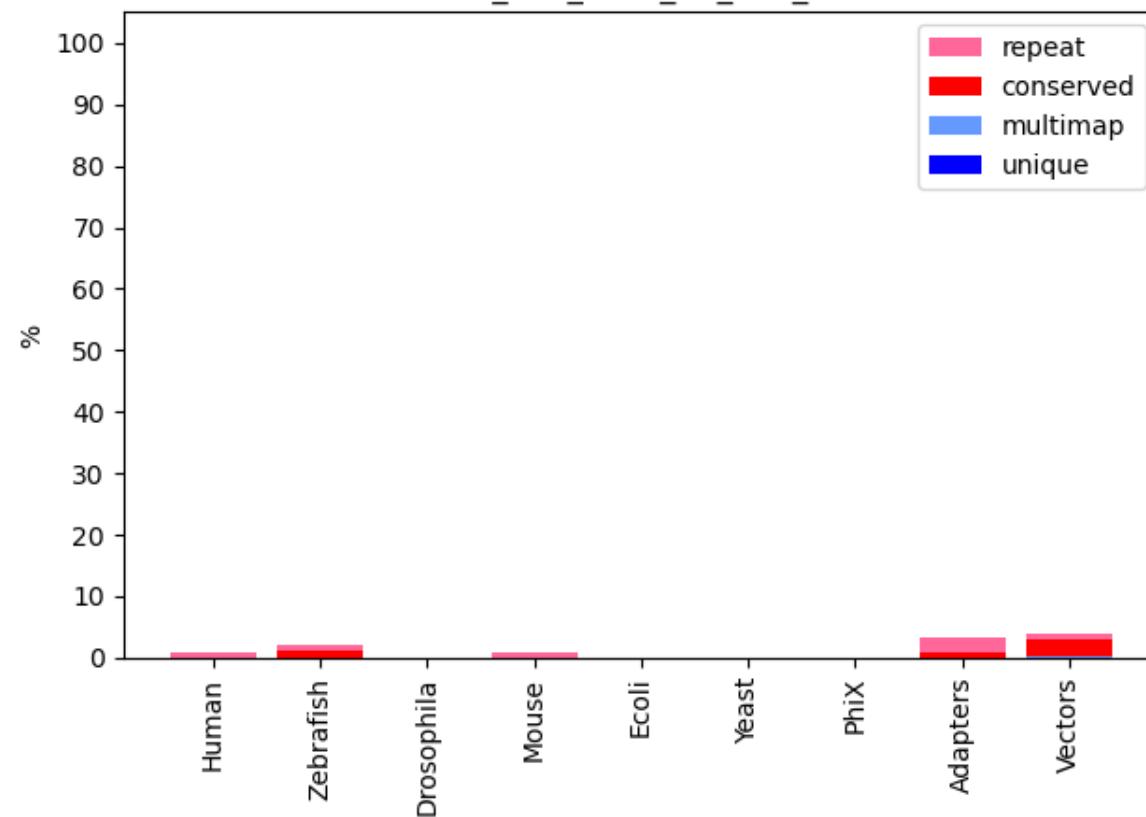
22L005059_S61_L001_R2_001_screen.txt



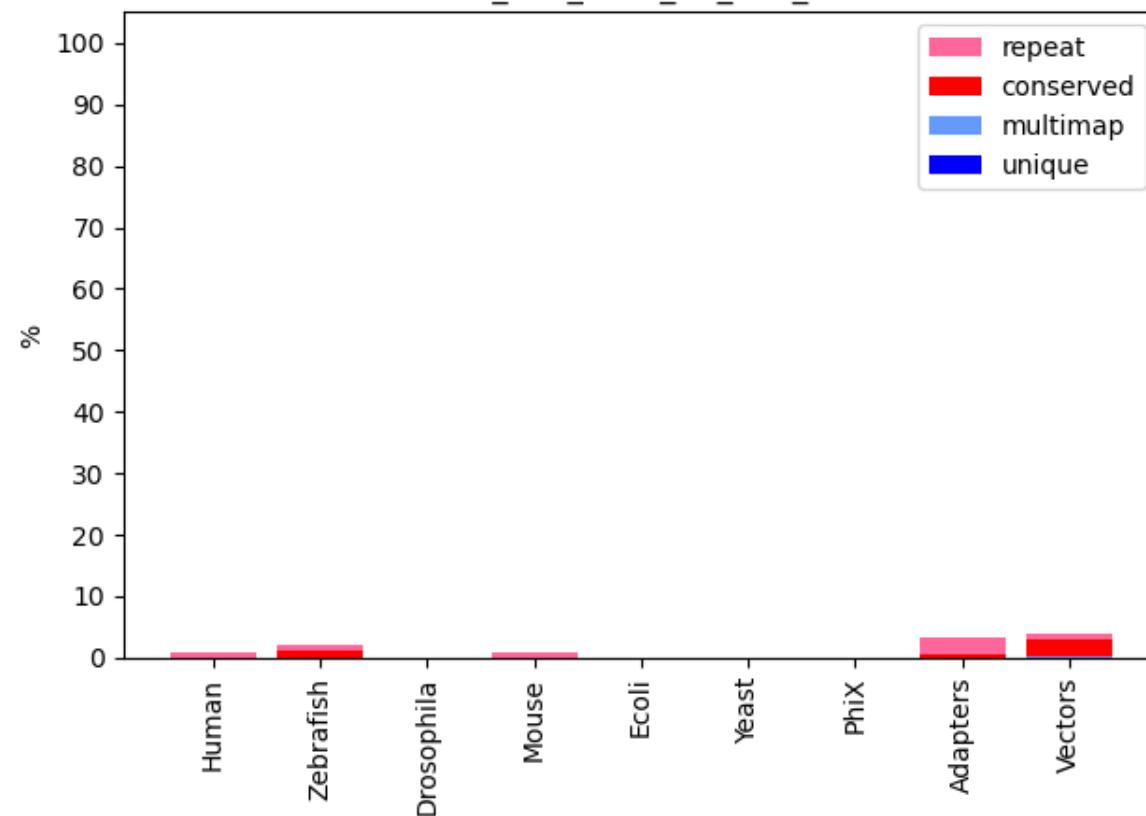
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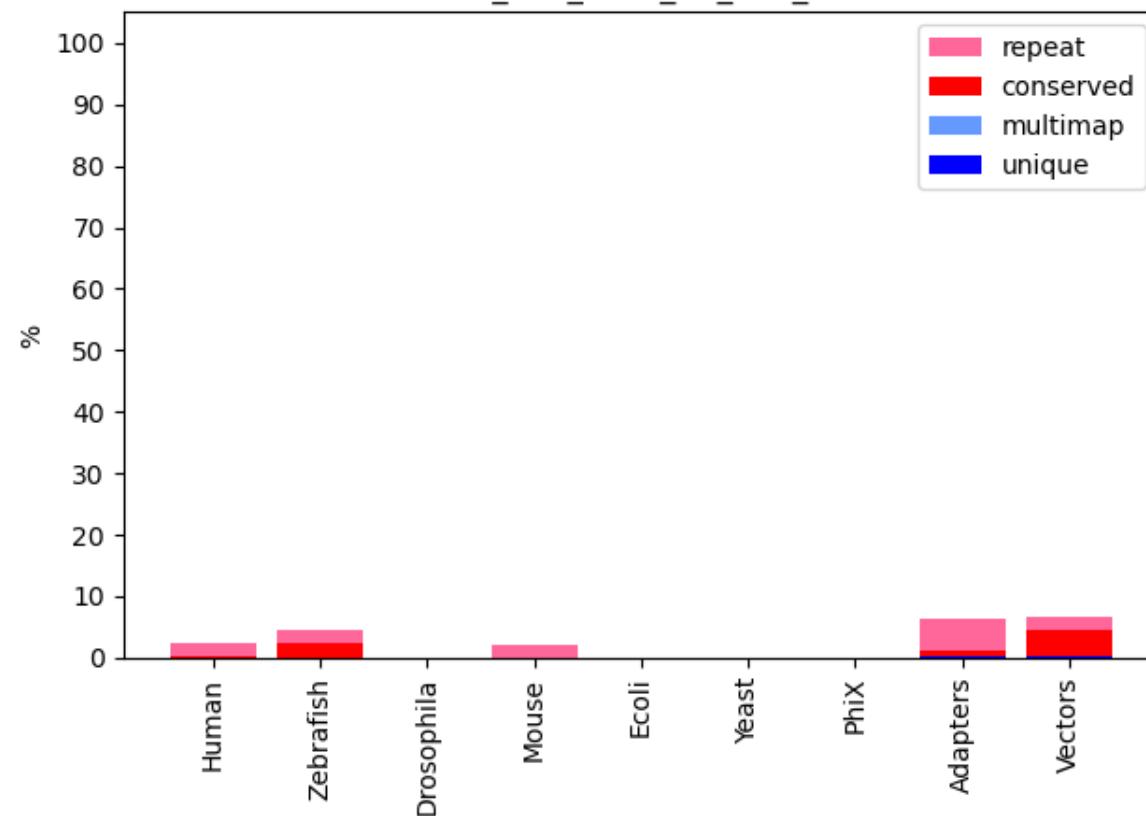
22L005060_S62_L001_R2_001_screen.txt



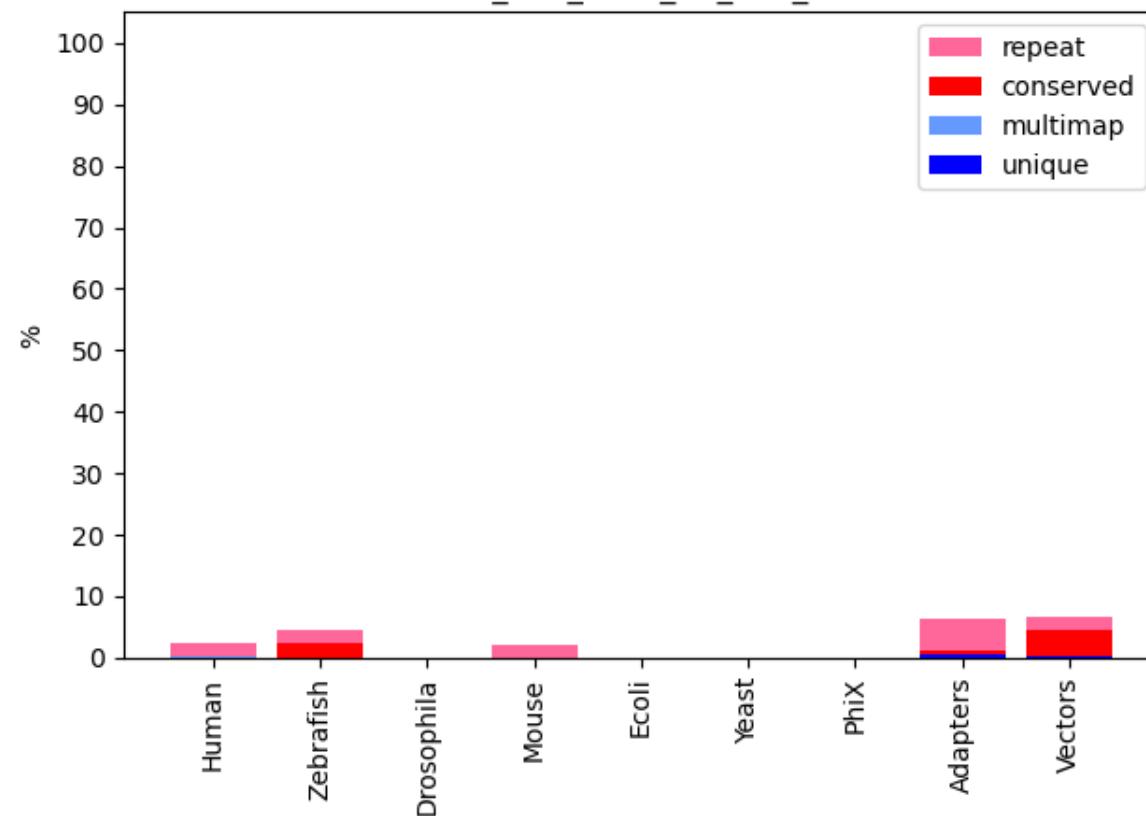
22L005060_S62_L002_R2_001_screen.txt



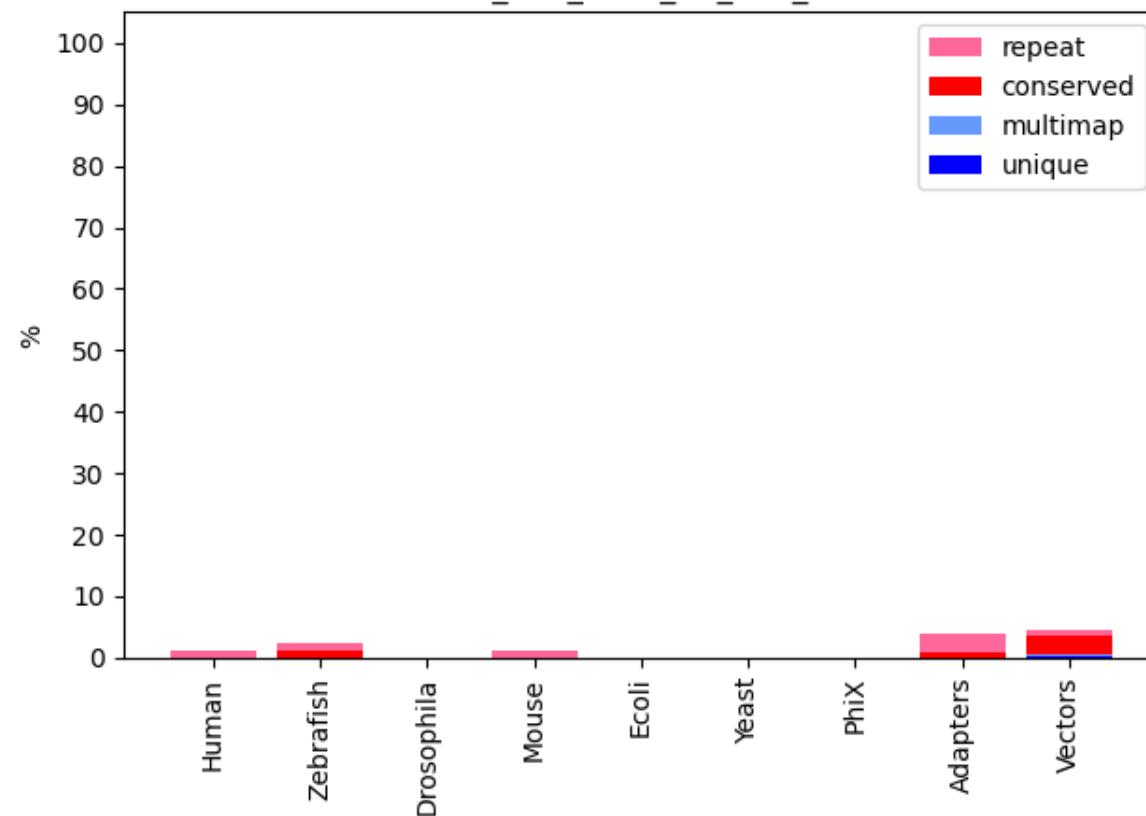
22L005061_S63_L001_R2_001_screen.txt



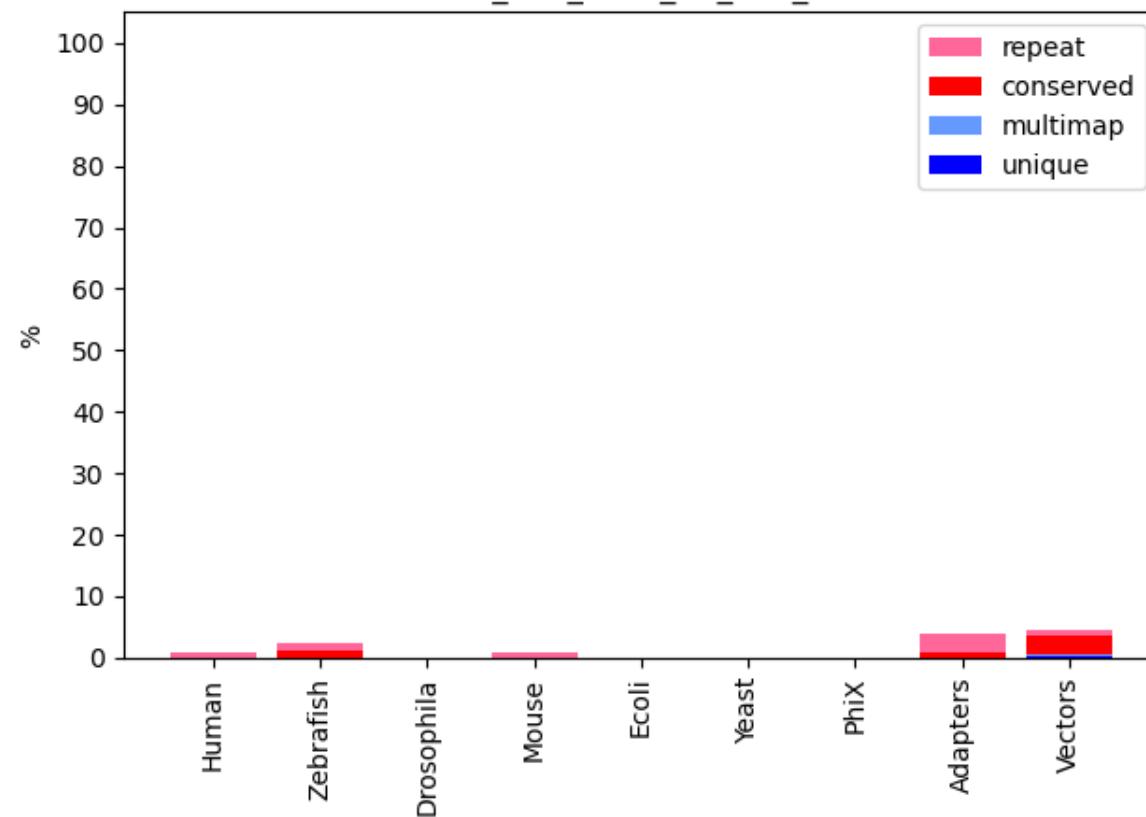
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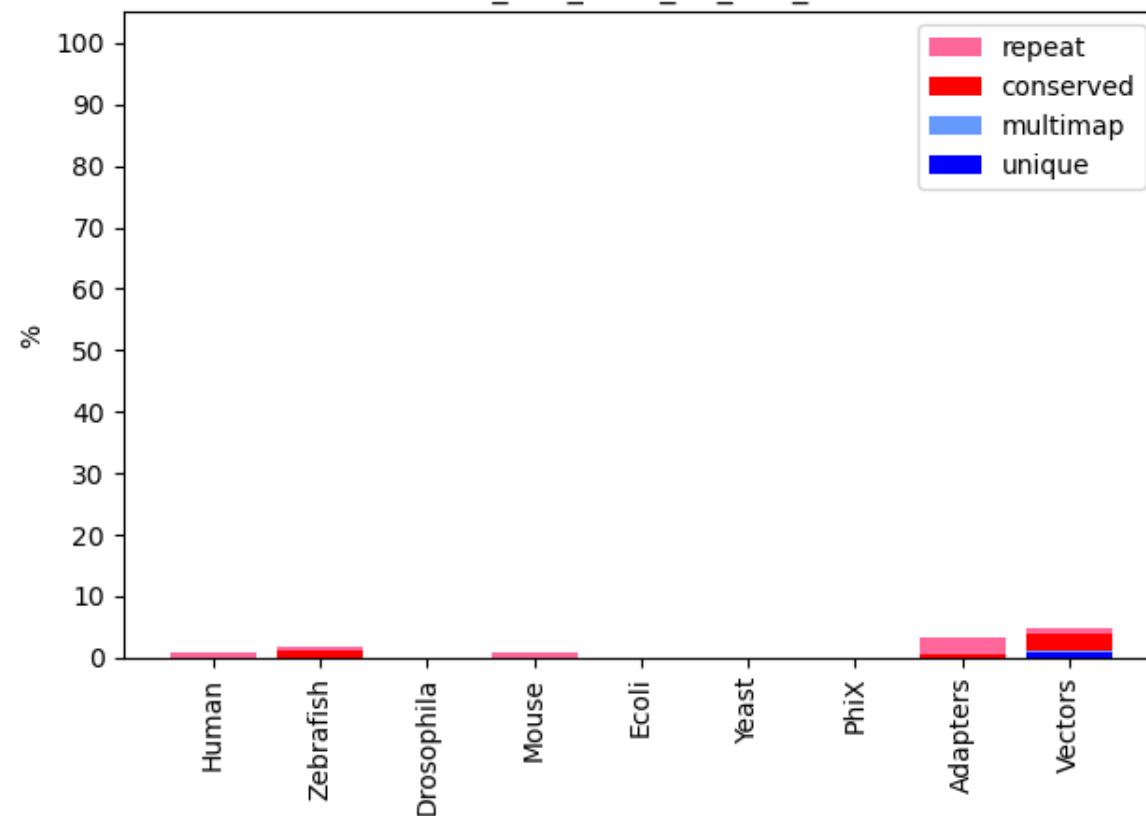
22L005062_S64_L001_R2_001_screen.txt



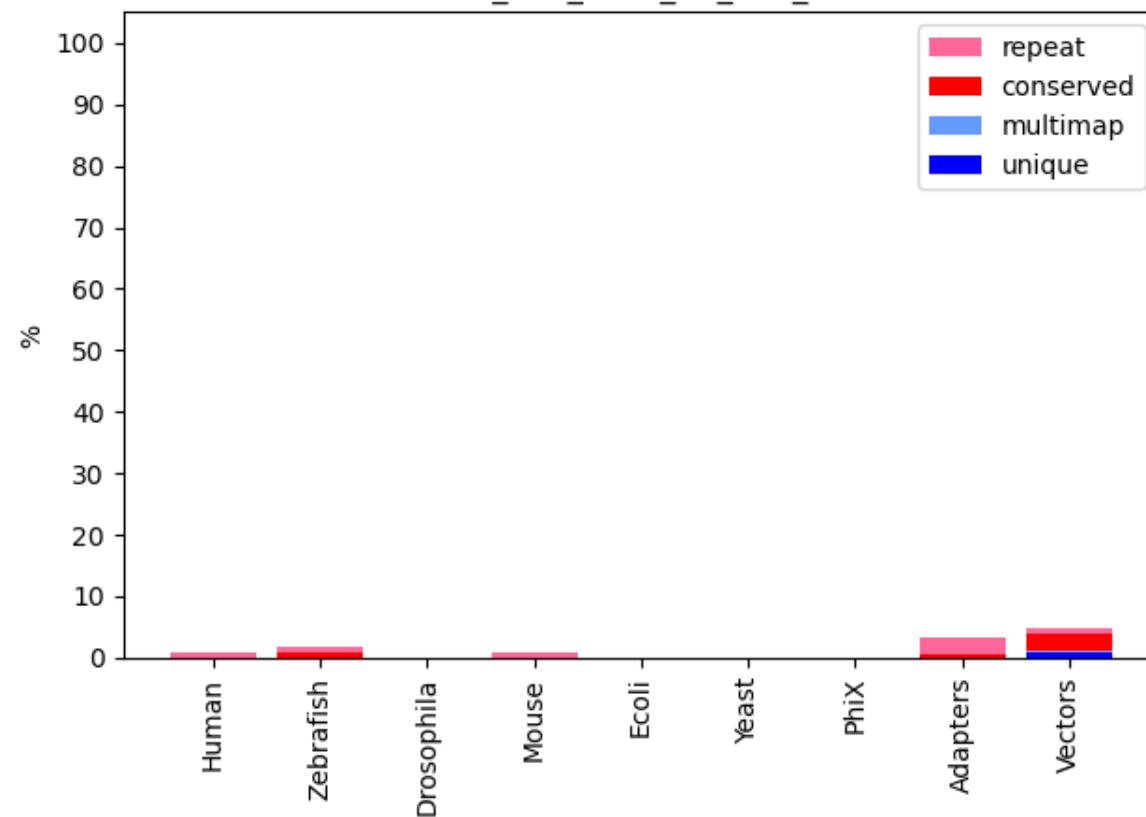
22L005062_S64_L002_R2_001_screen.txt



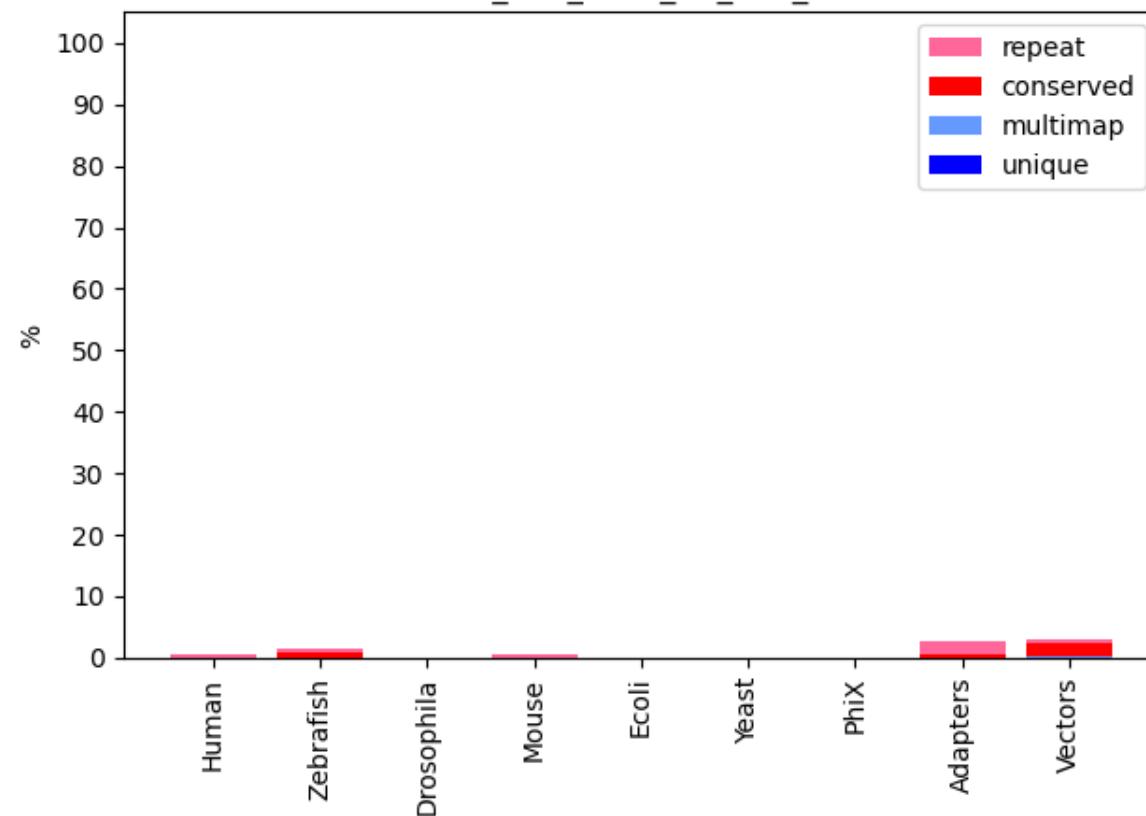
22L005063_S65_L001_R2_001_screen.txt



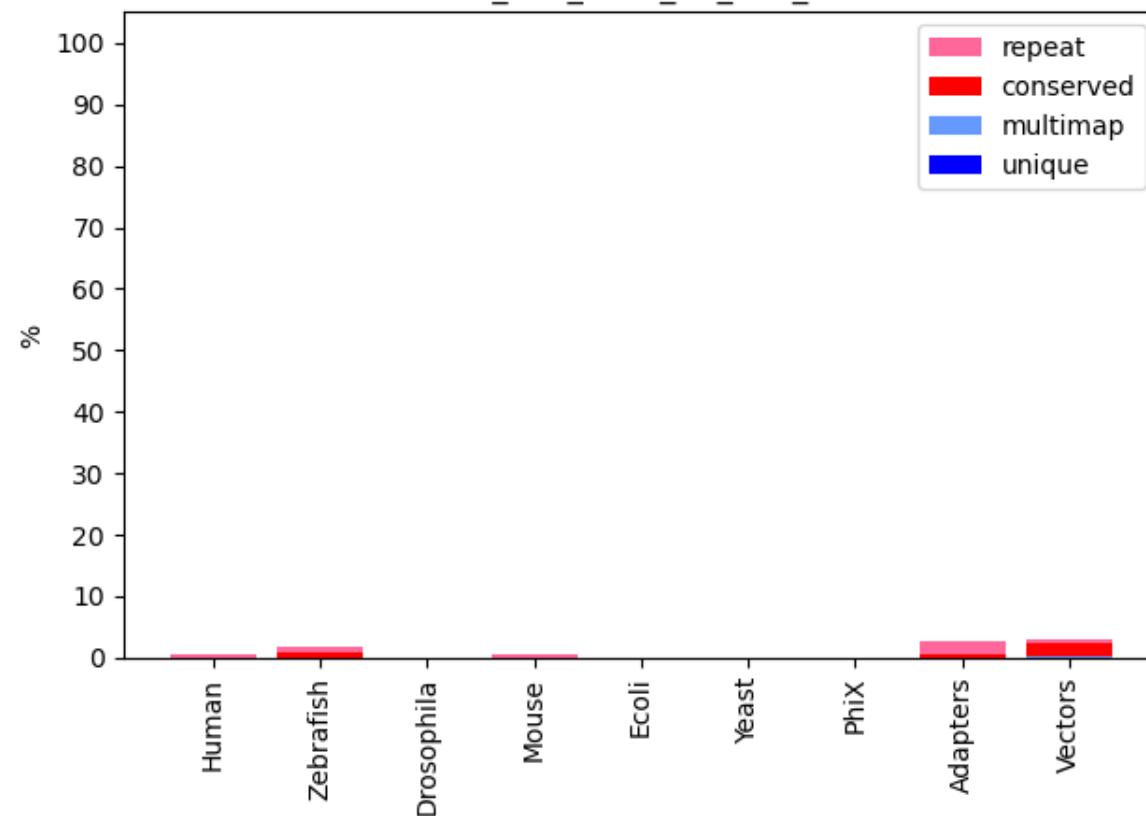
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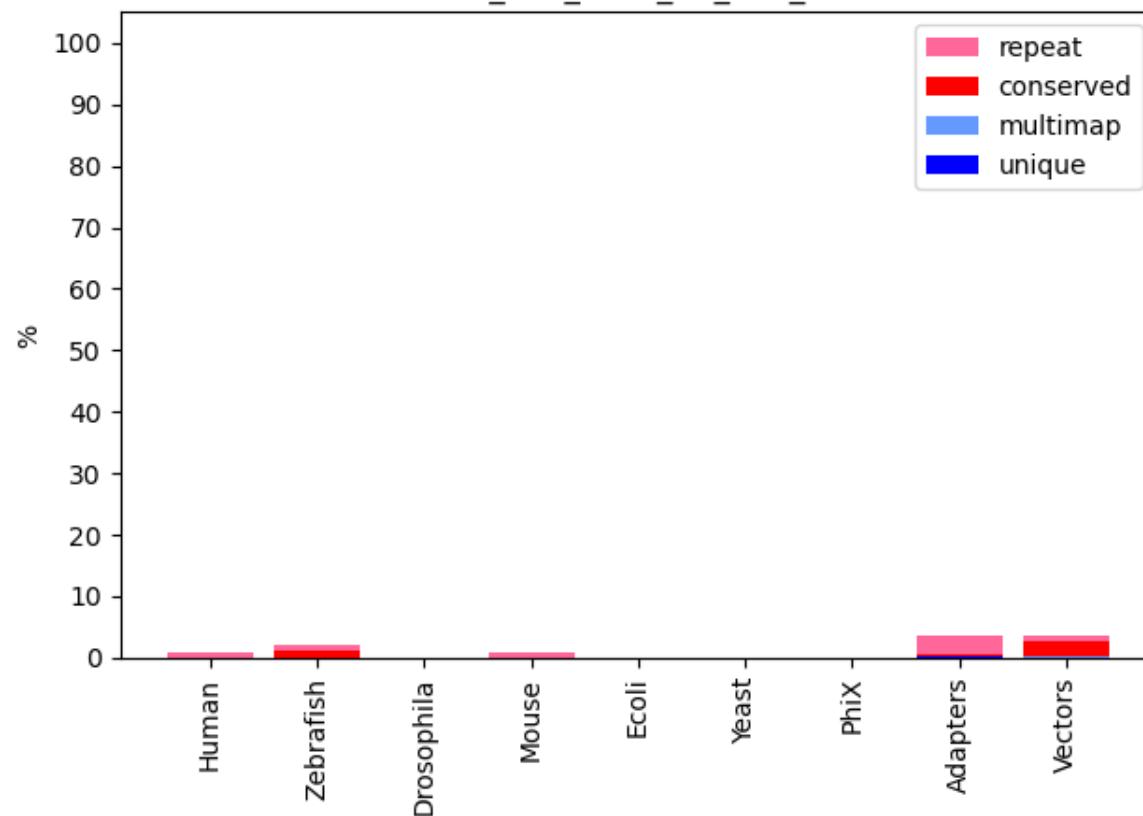
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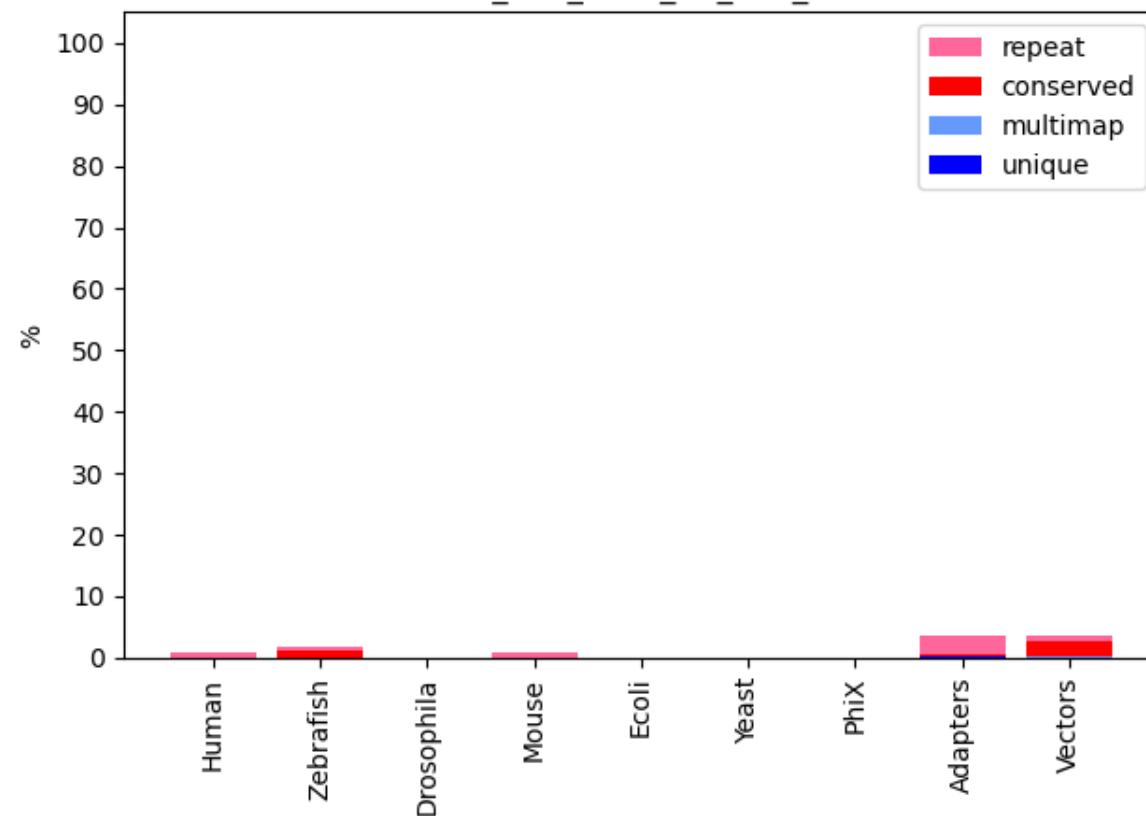
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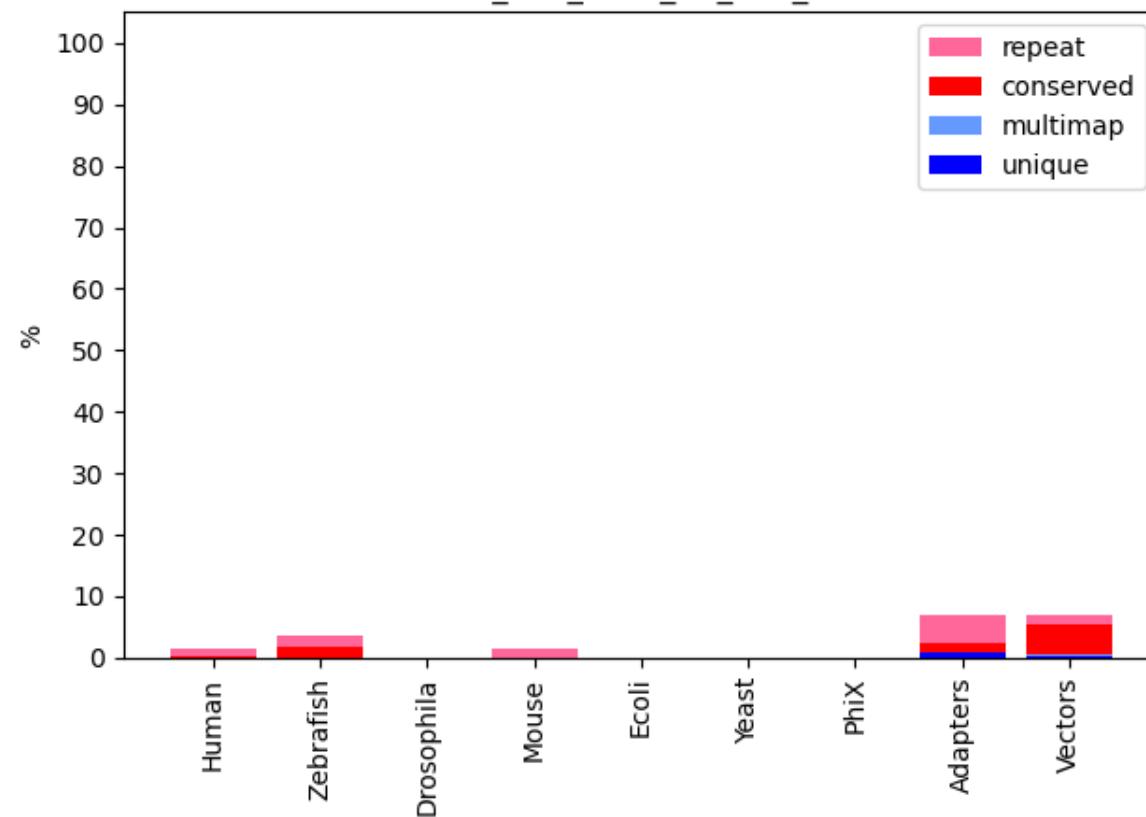
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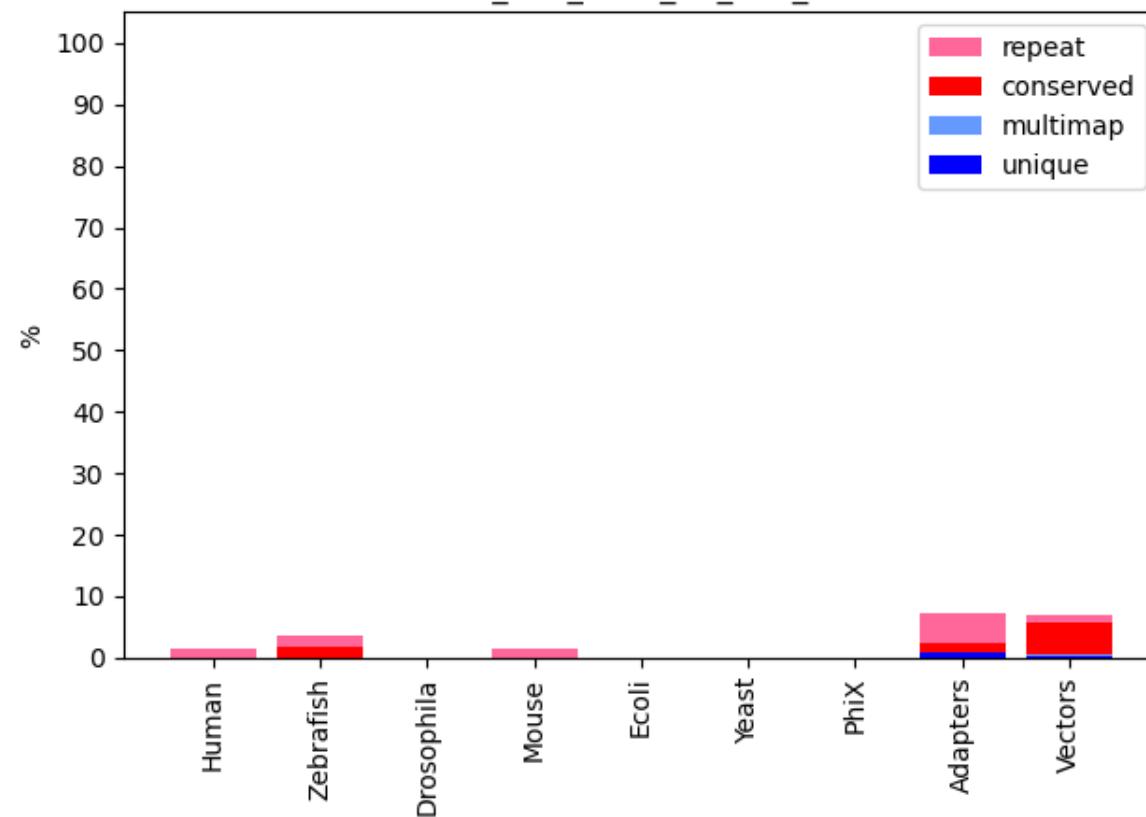
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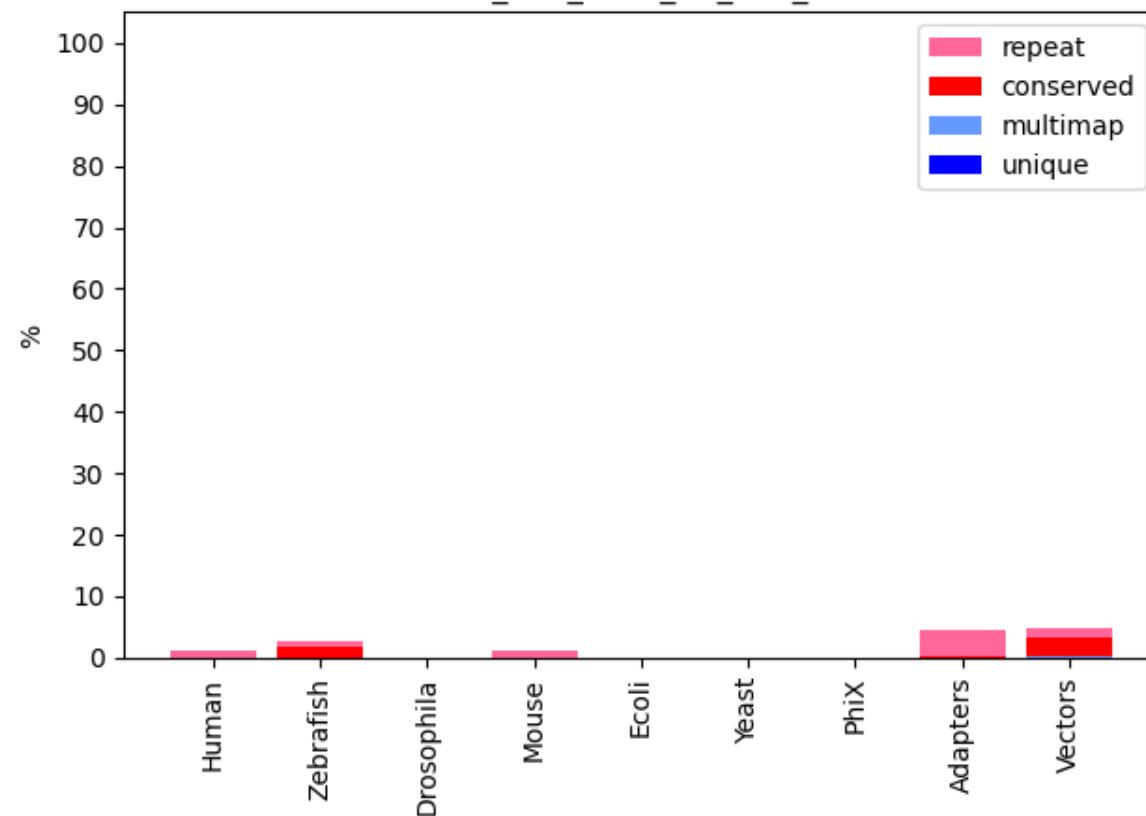
22L005066_S68_L001_R2_001_screen.txt



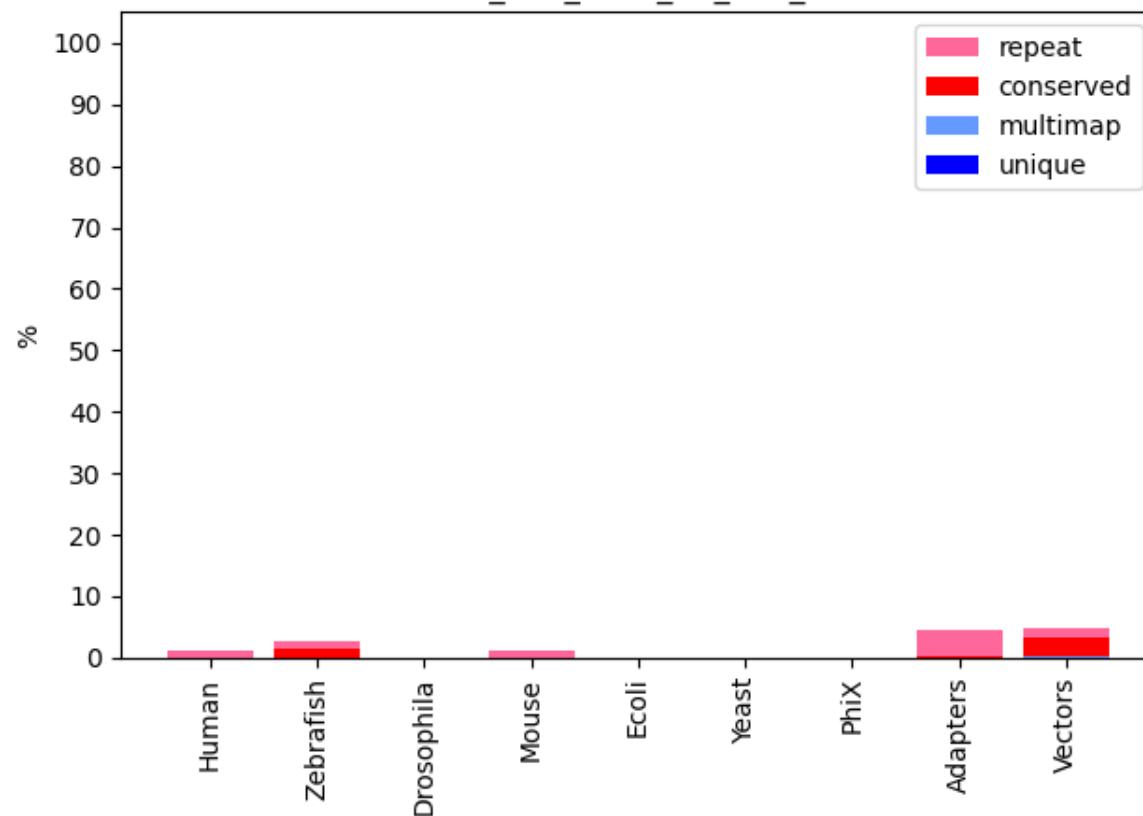
22L005066_S68_L002_R2_001_screen.txt



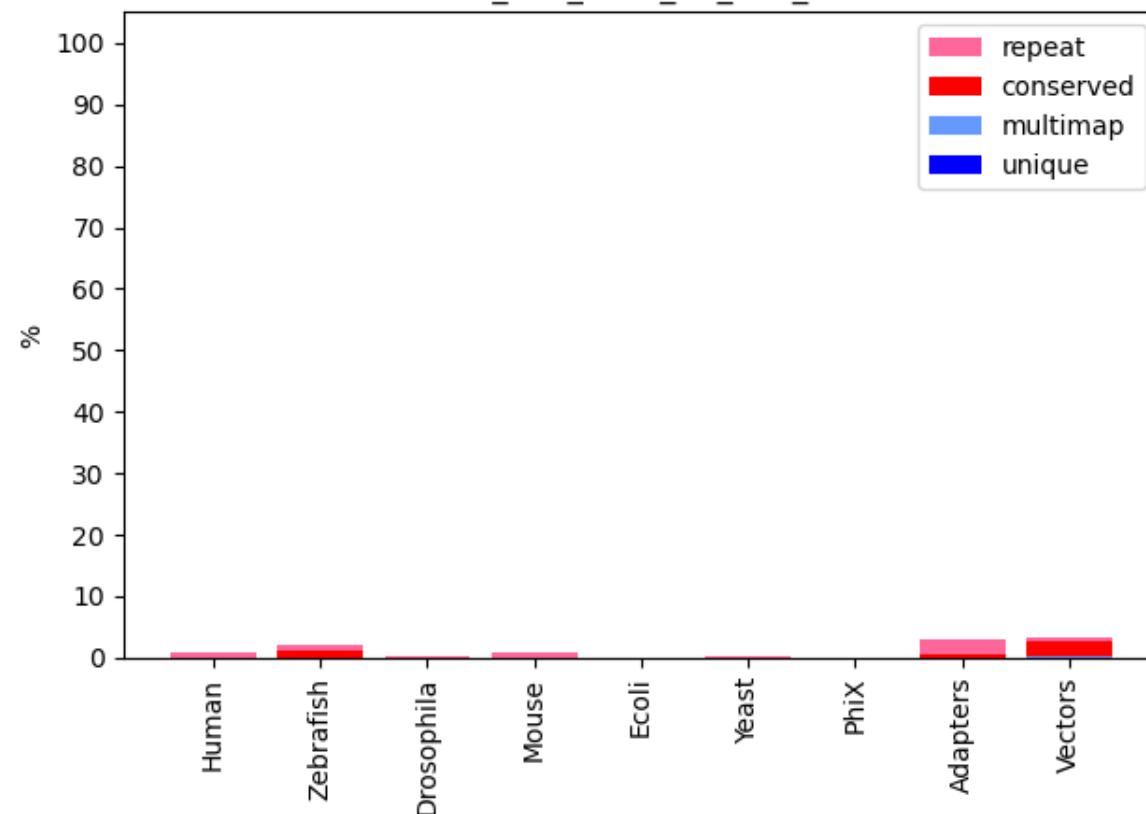
22L005067_S69_L001_R2_001_screen.txt



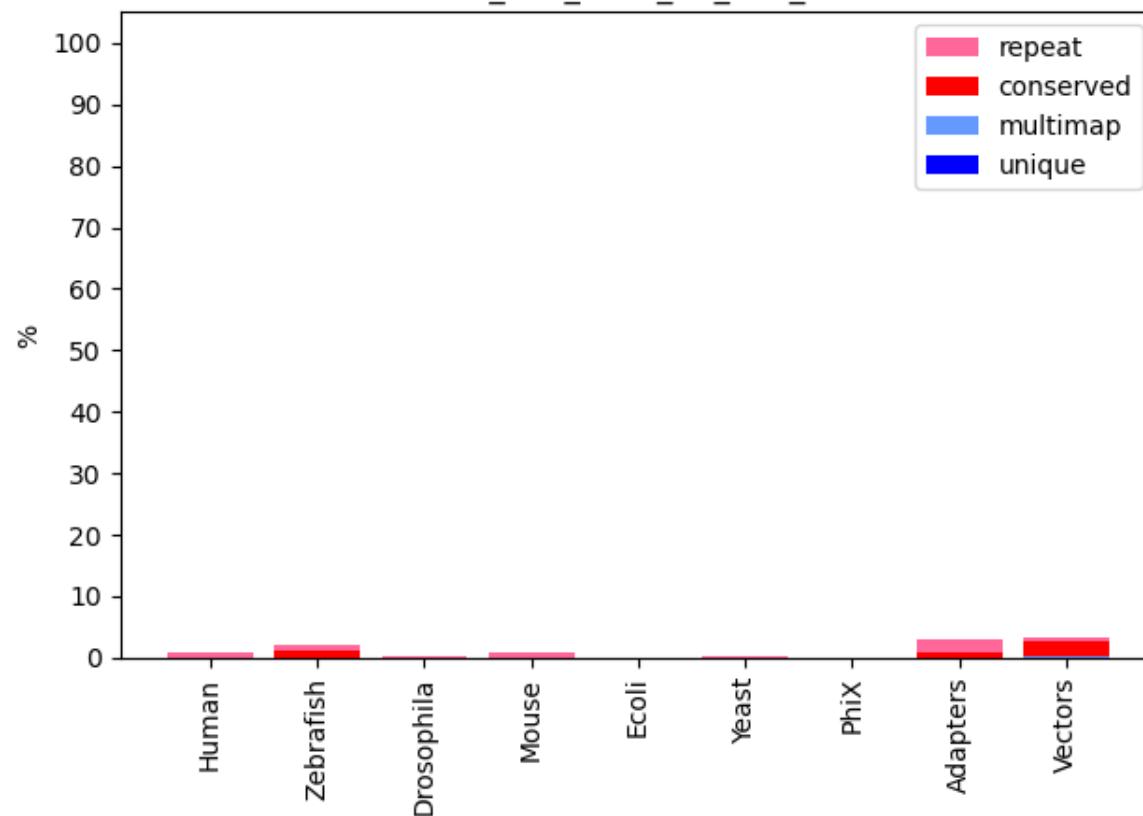
22L005067_S69_L002_R2_001_screen.txt



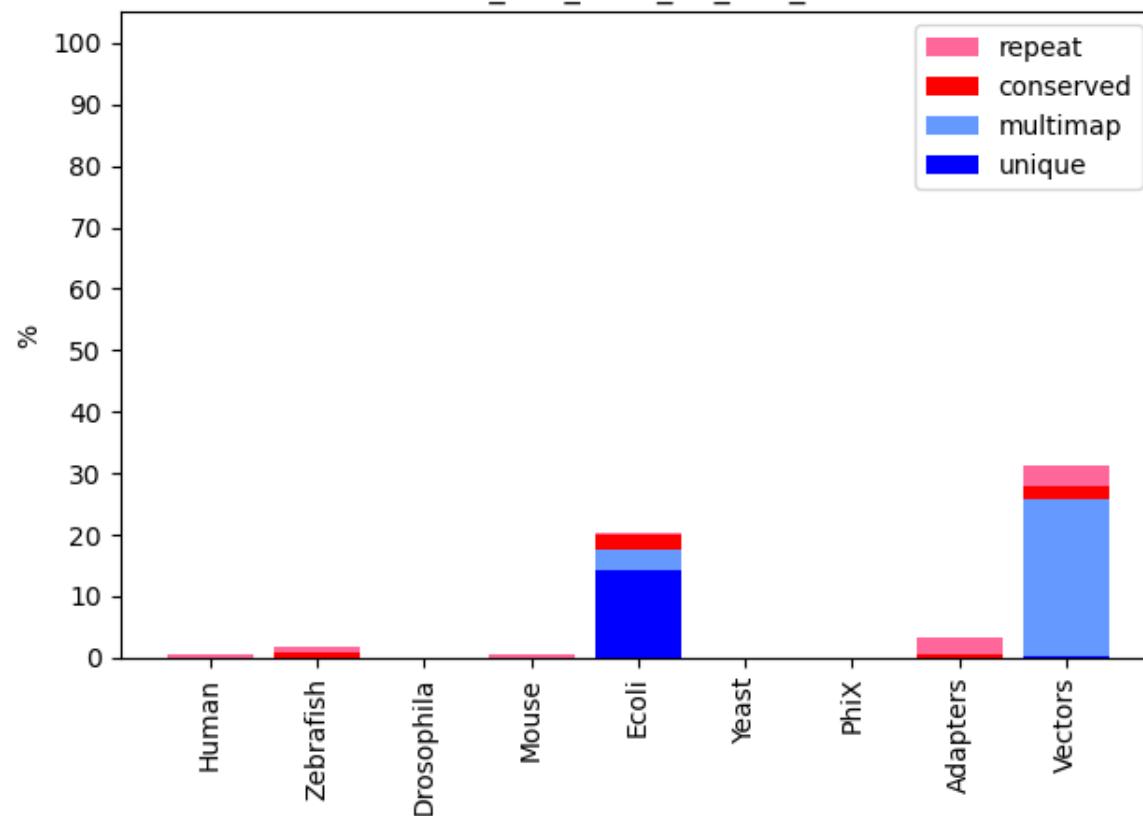
22L005068_S70_L001_R2_001_screen.txt



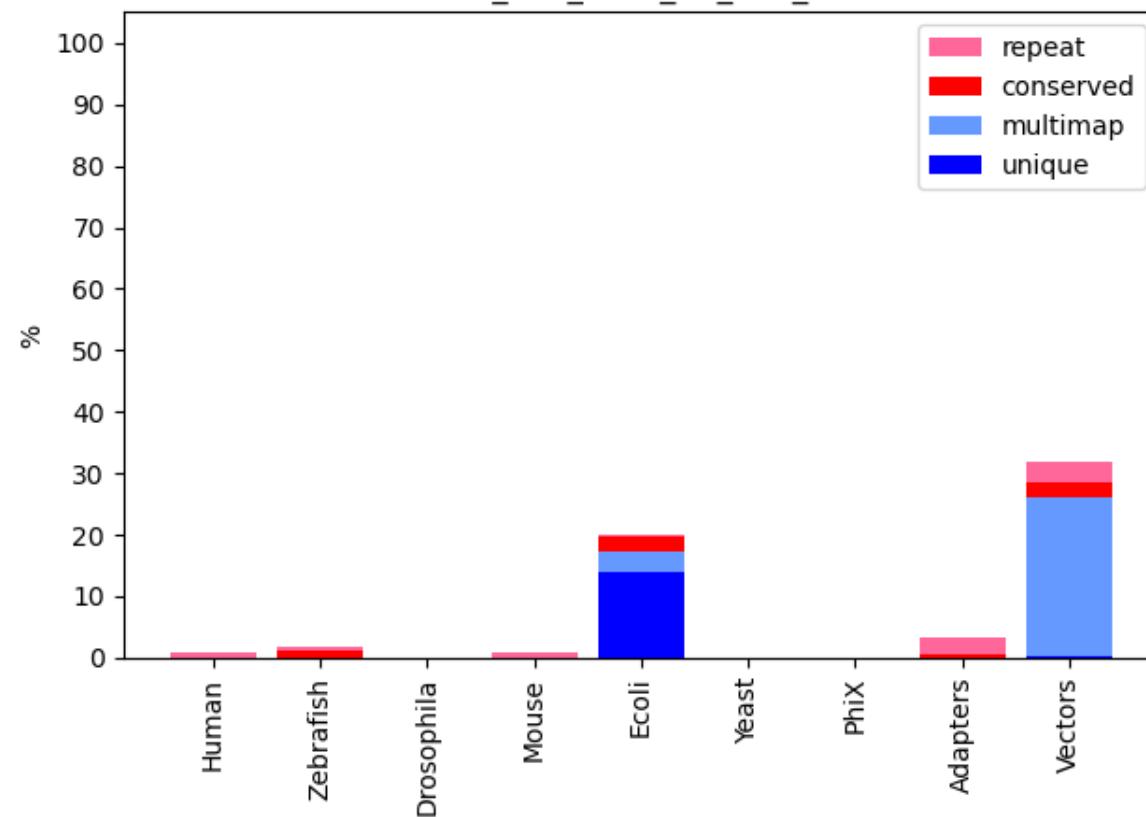
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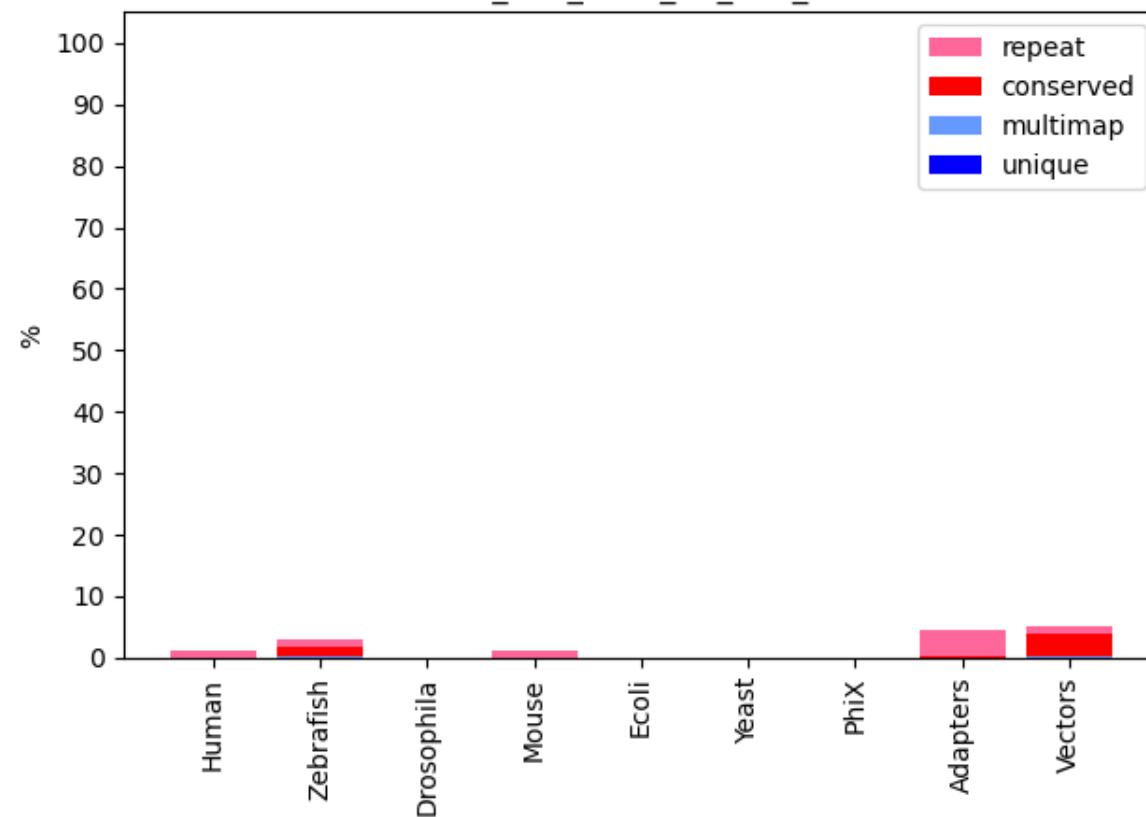
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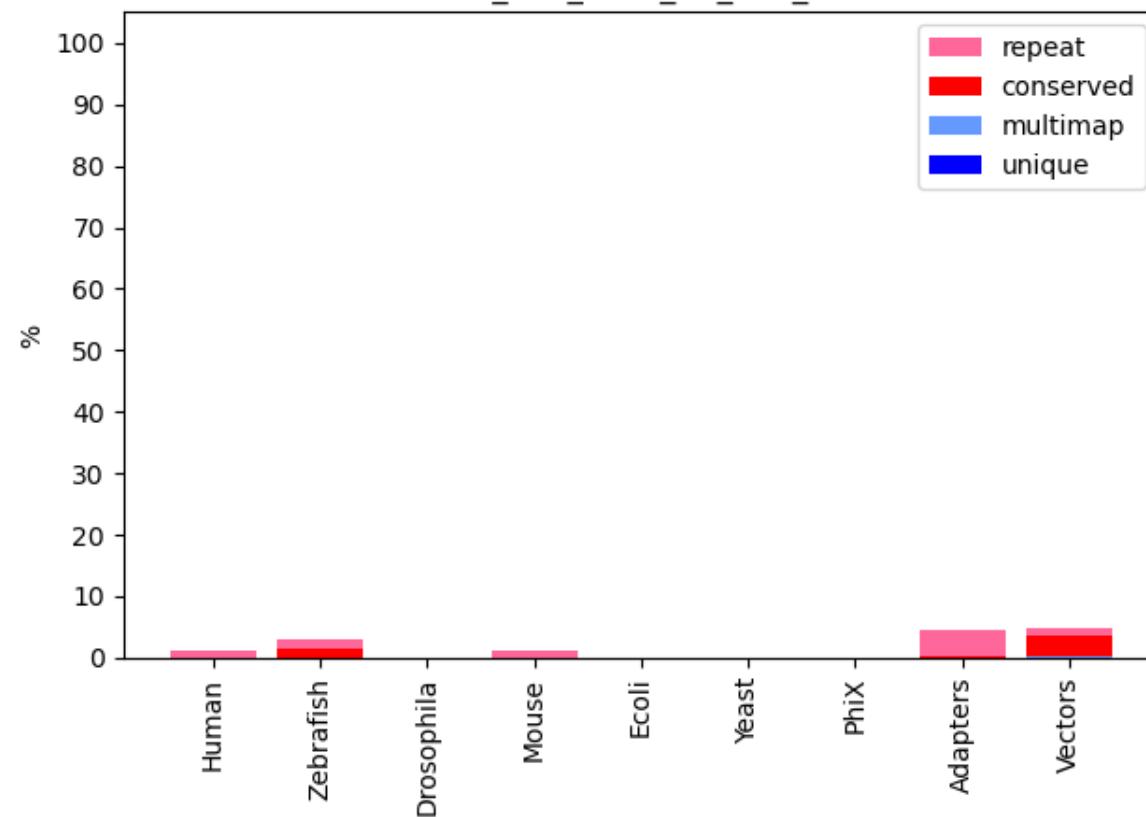
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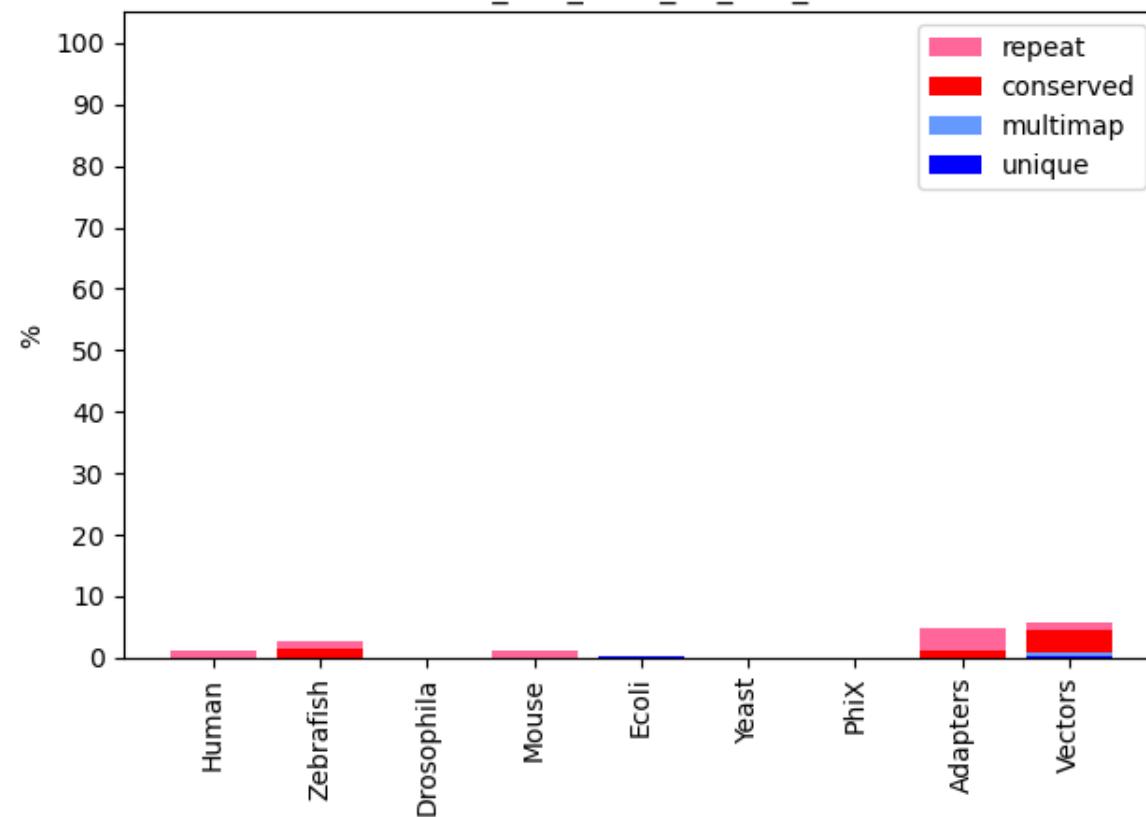
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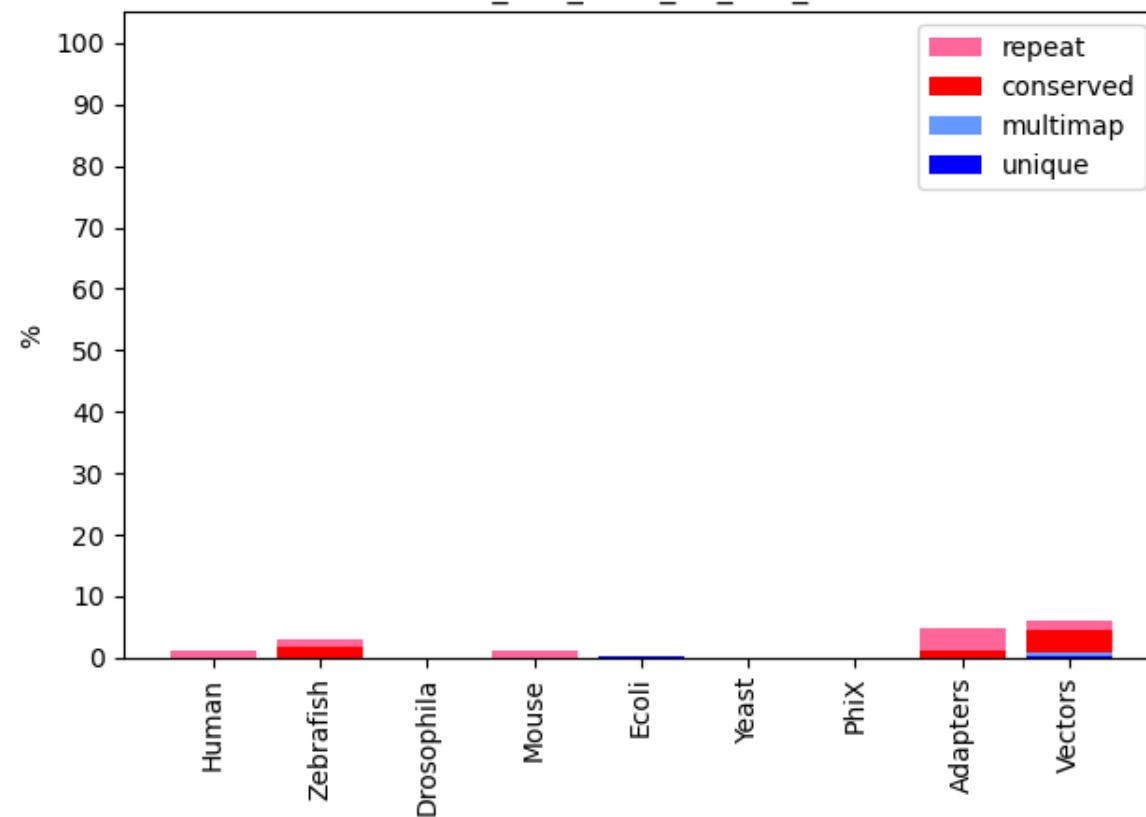
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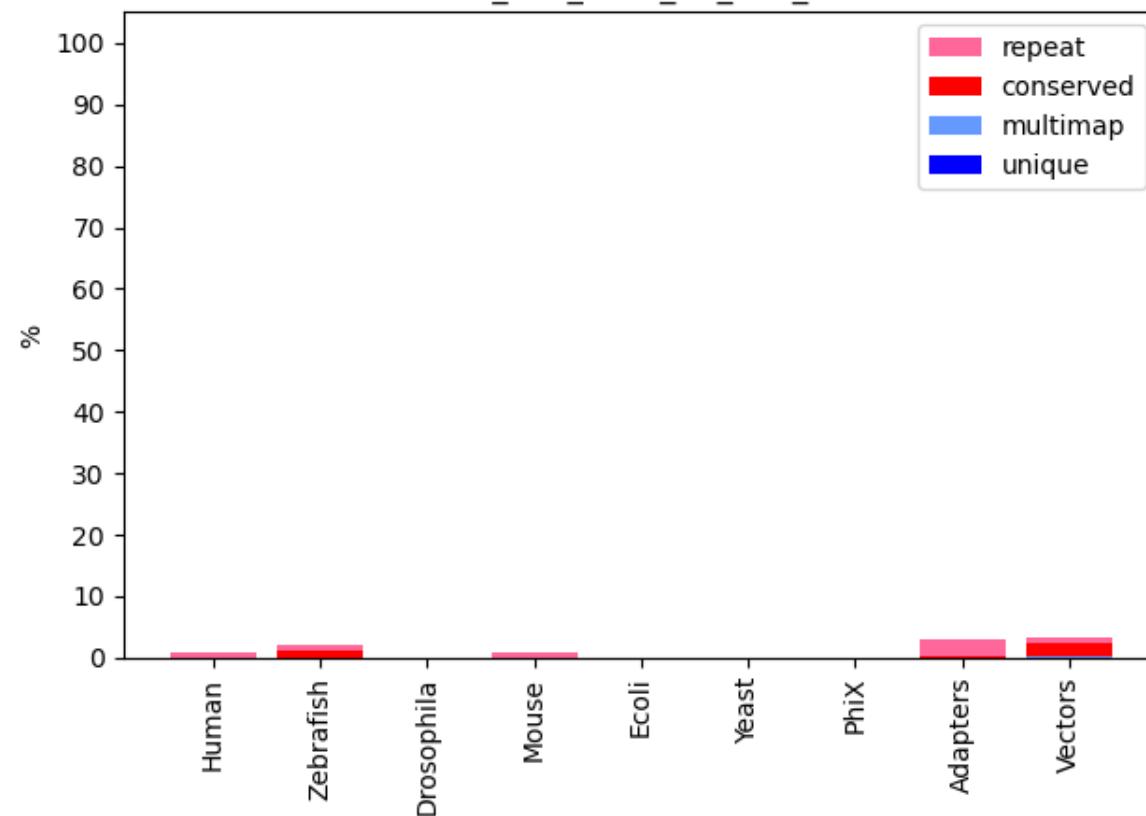
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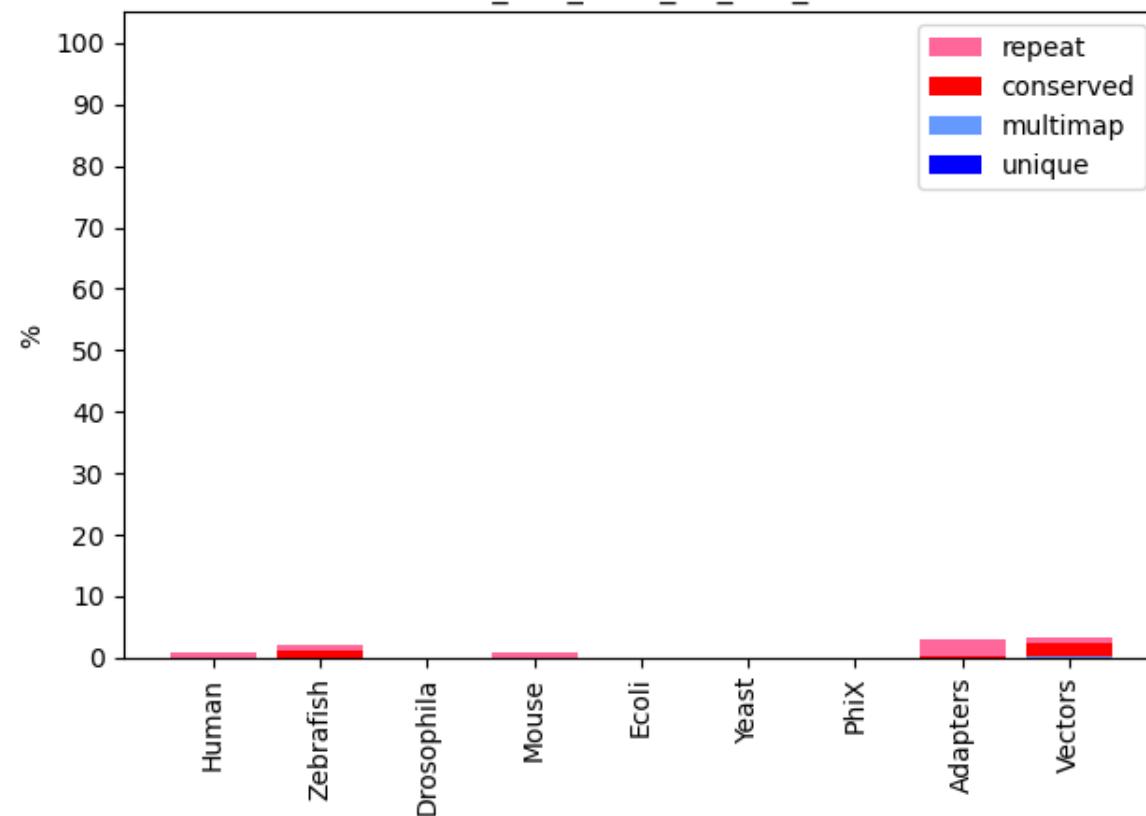
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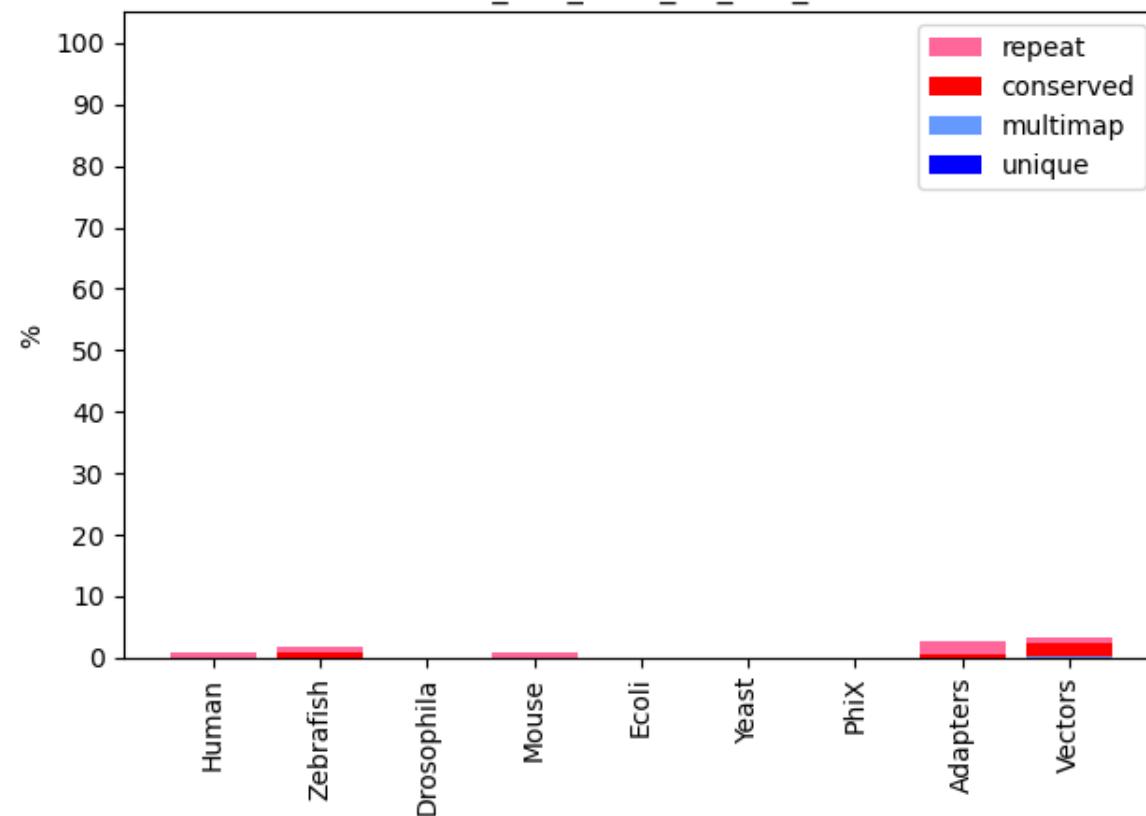
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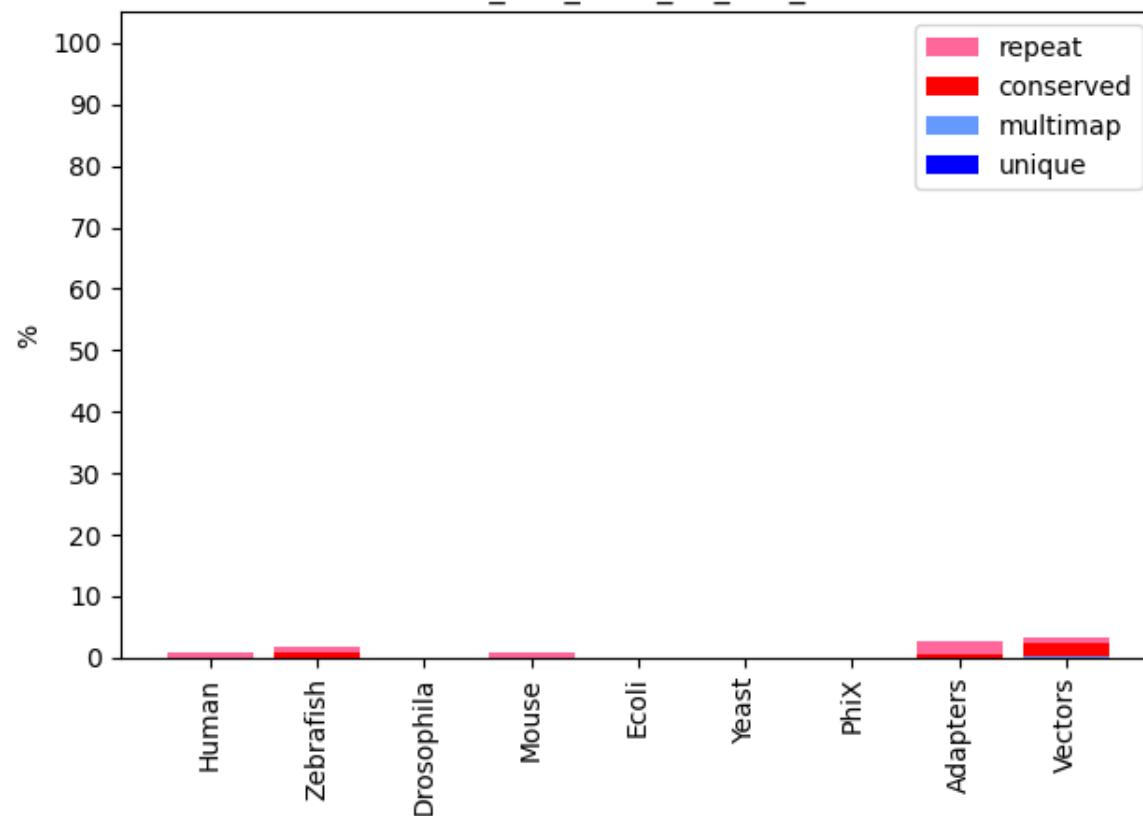
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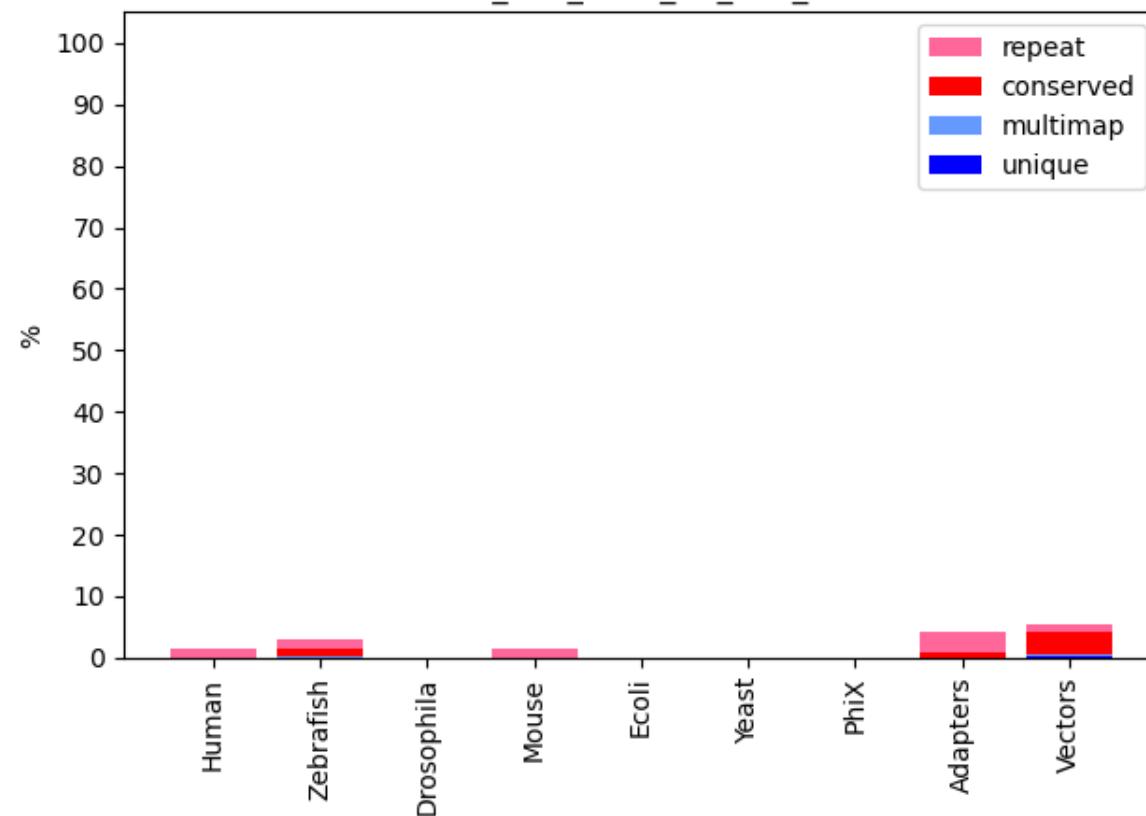
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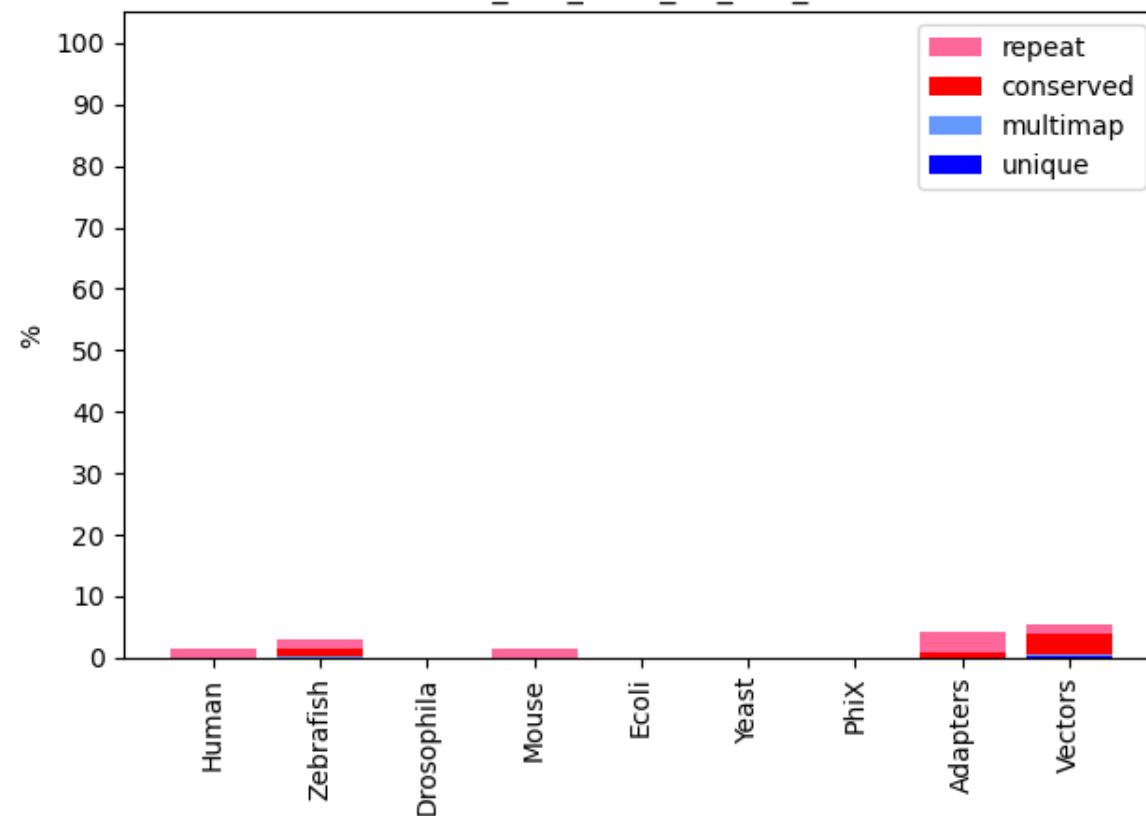
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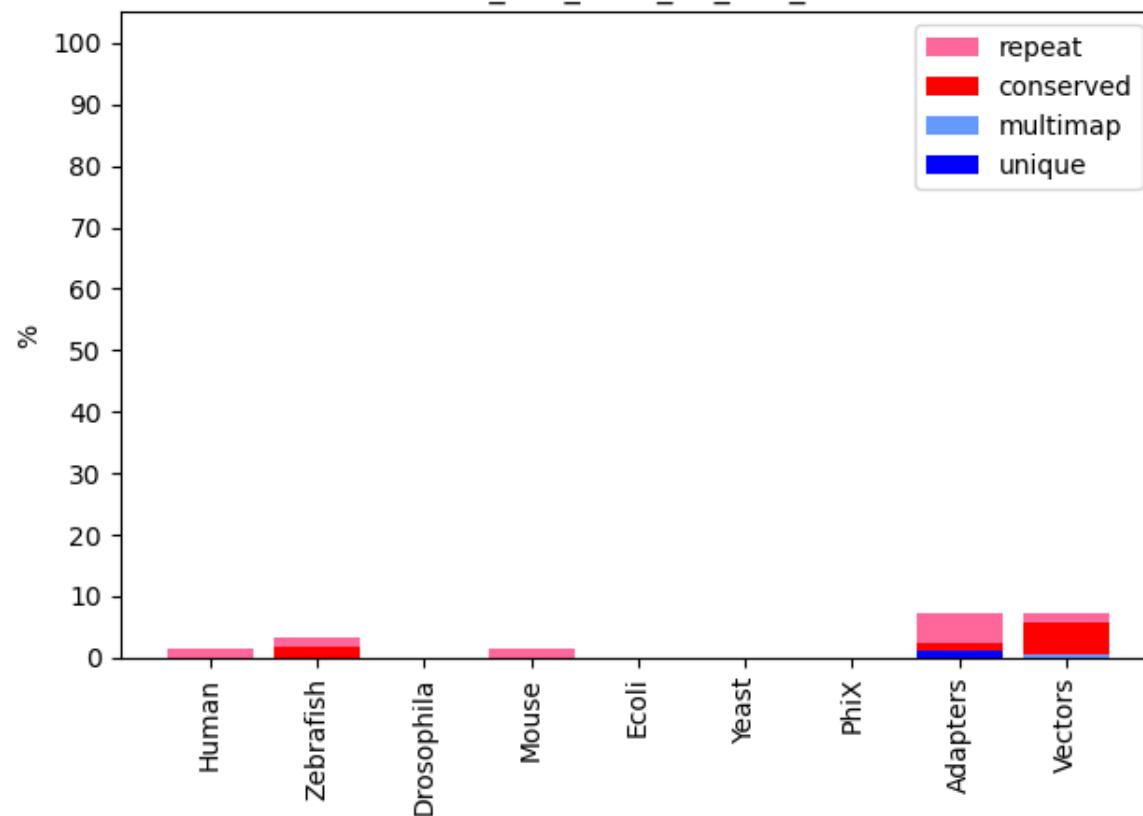
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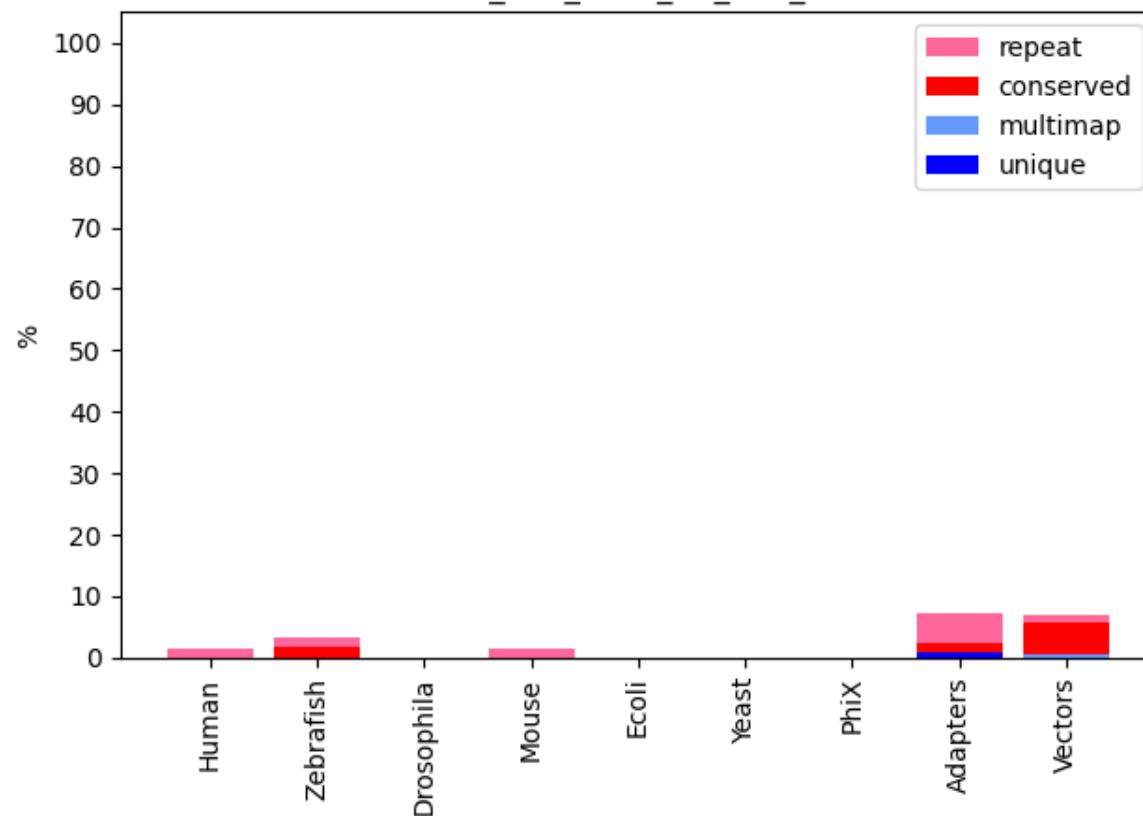
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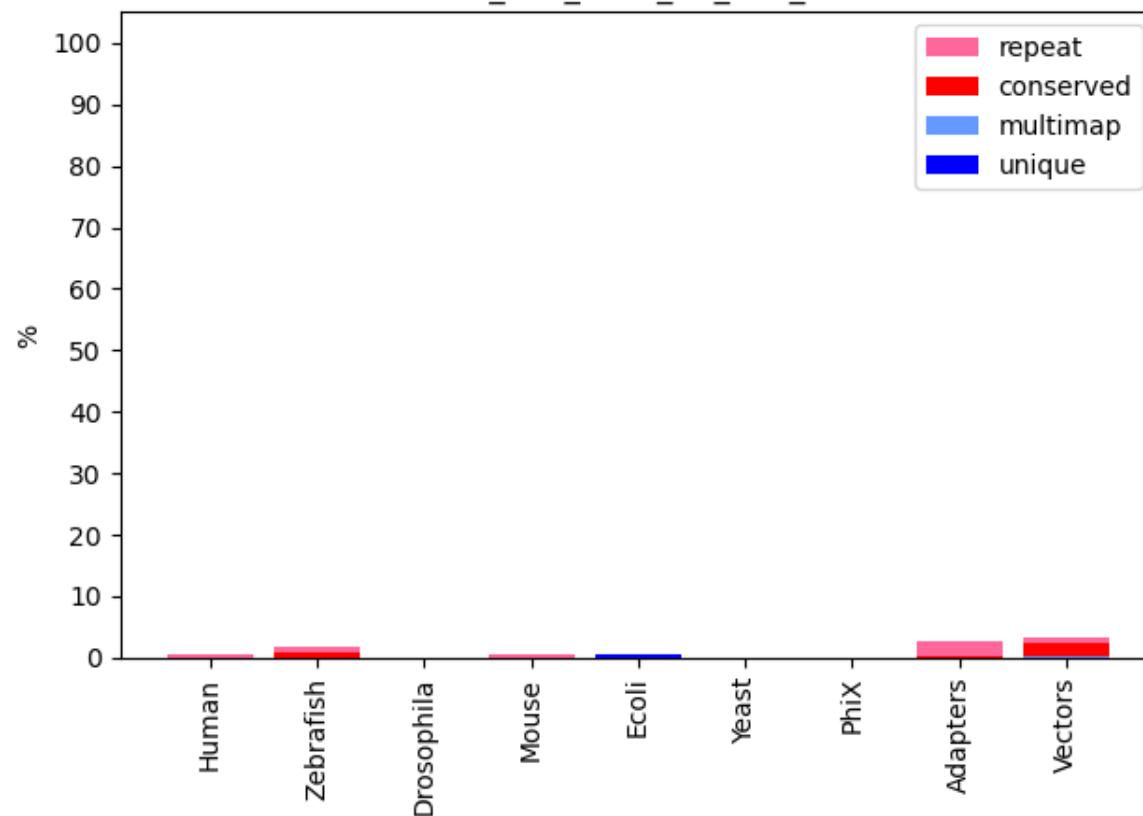
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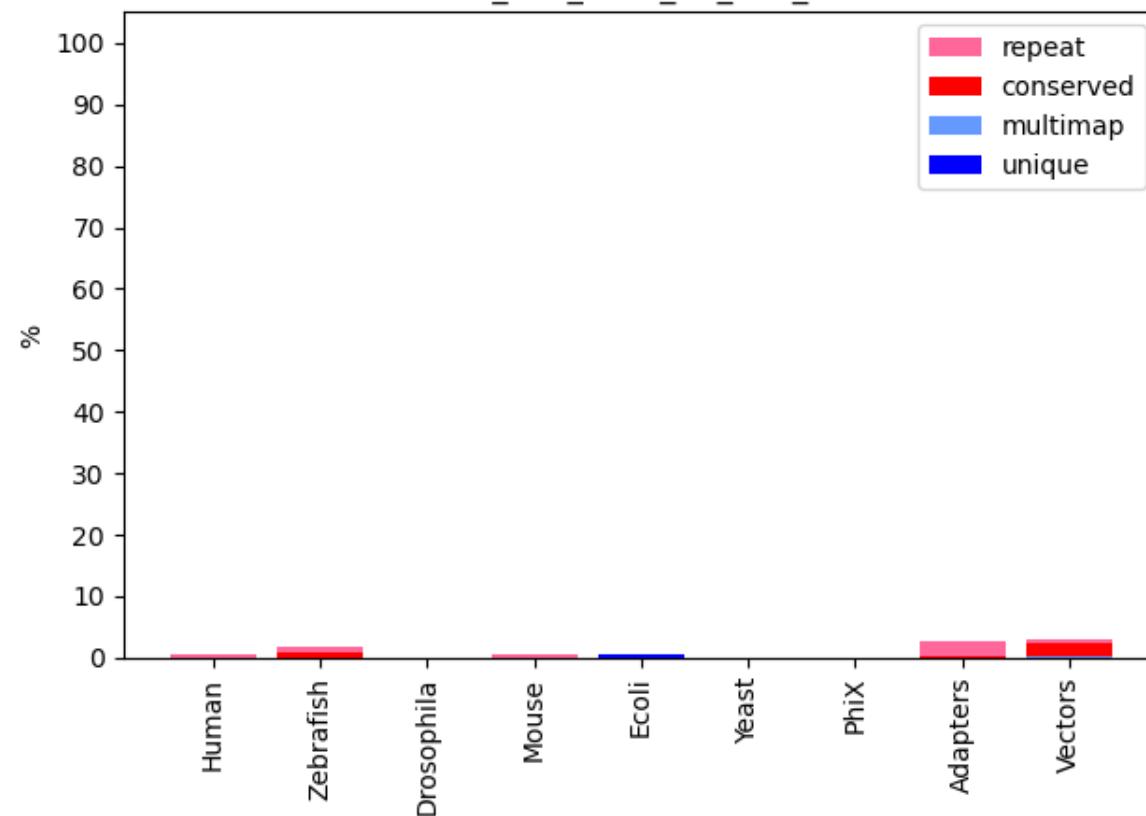
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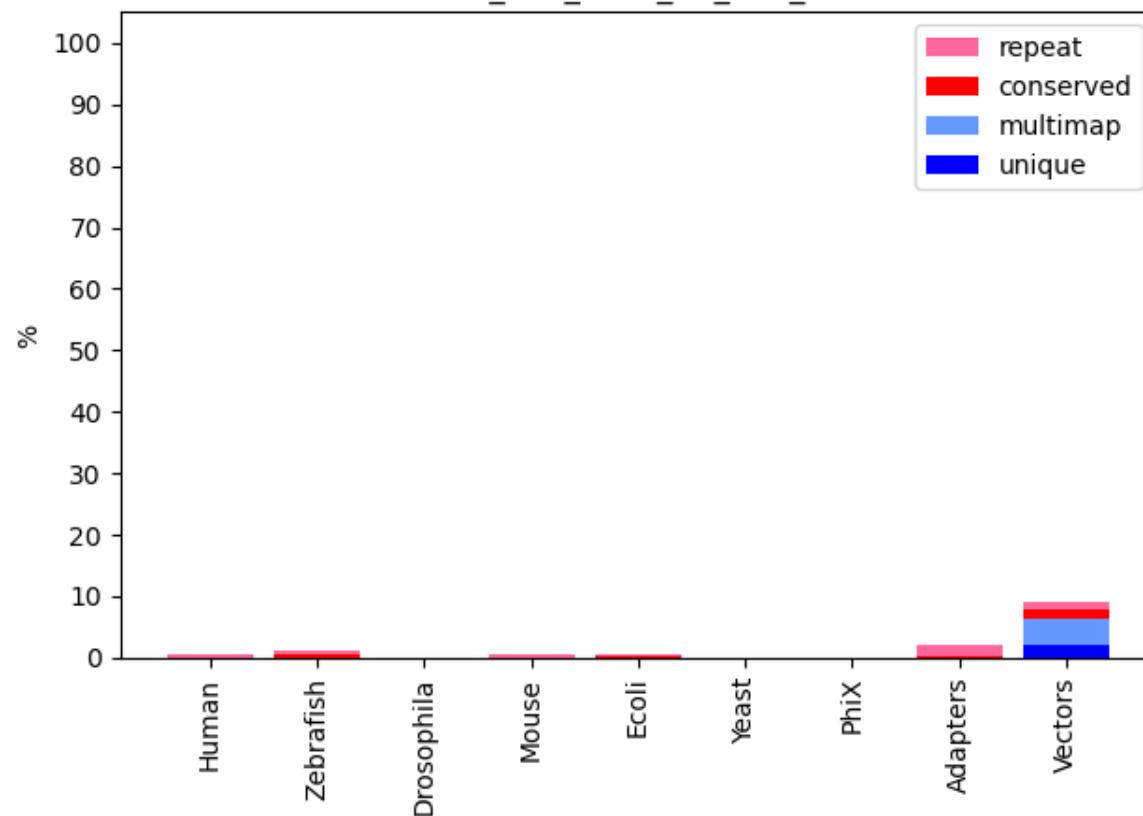
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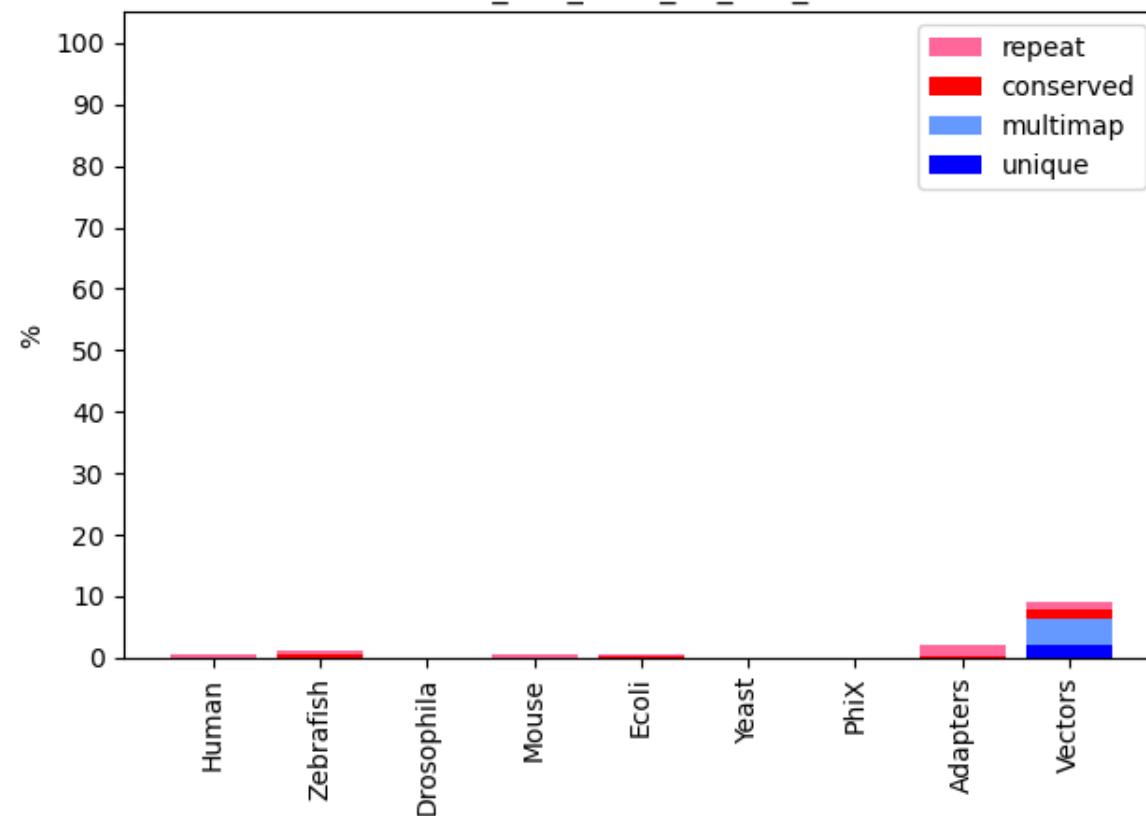
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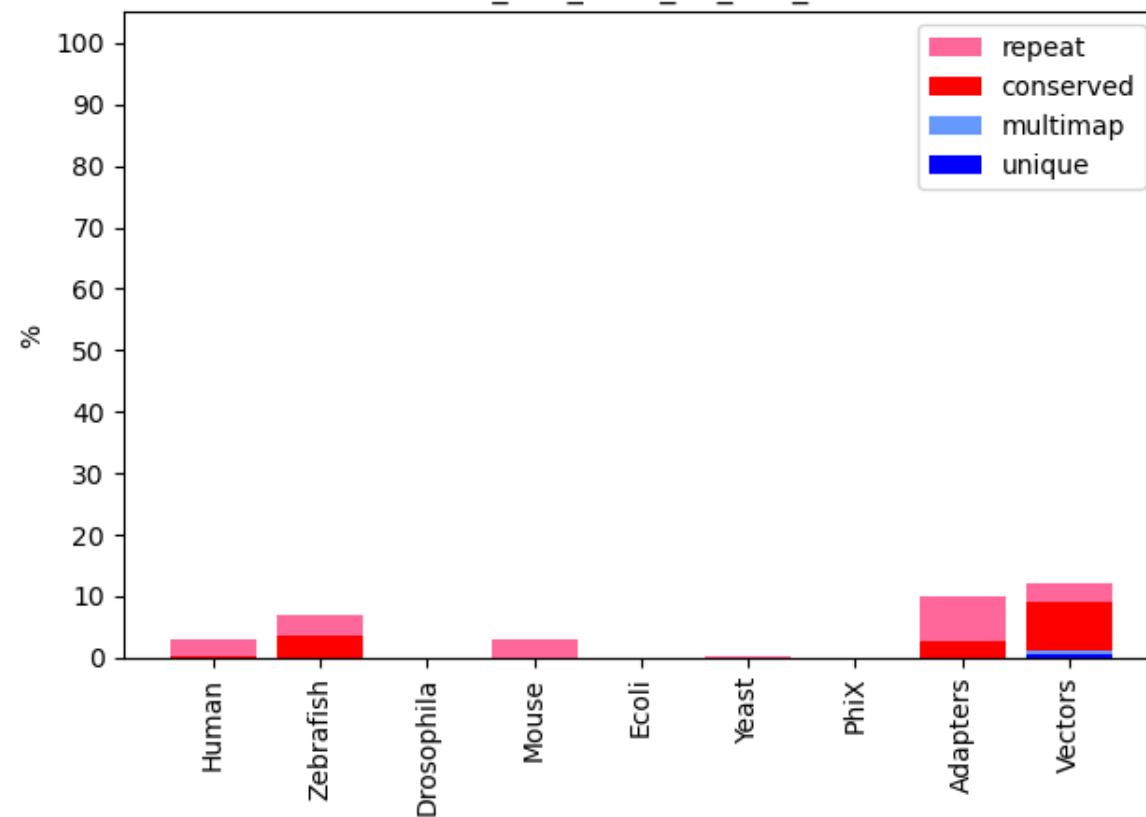
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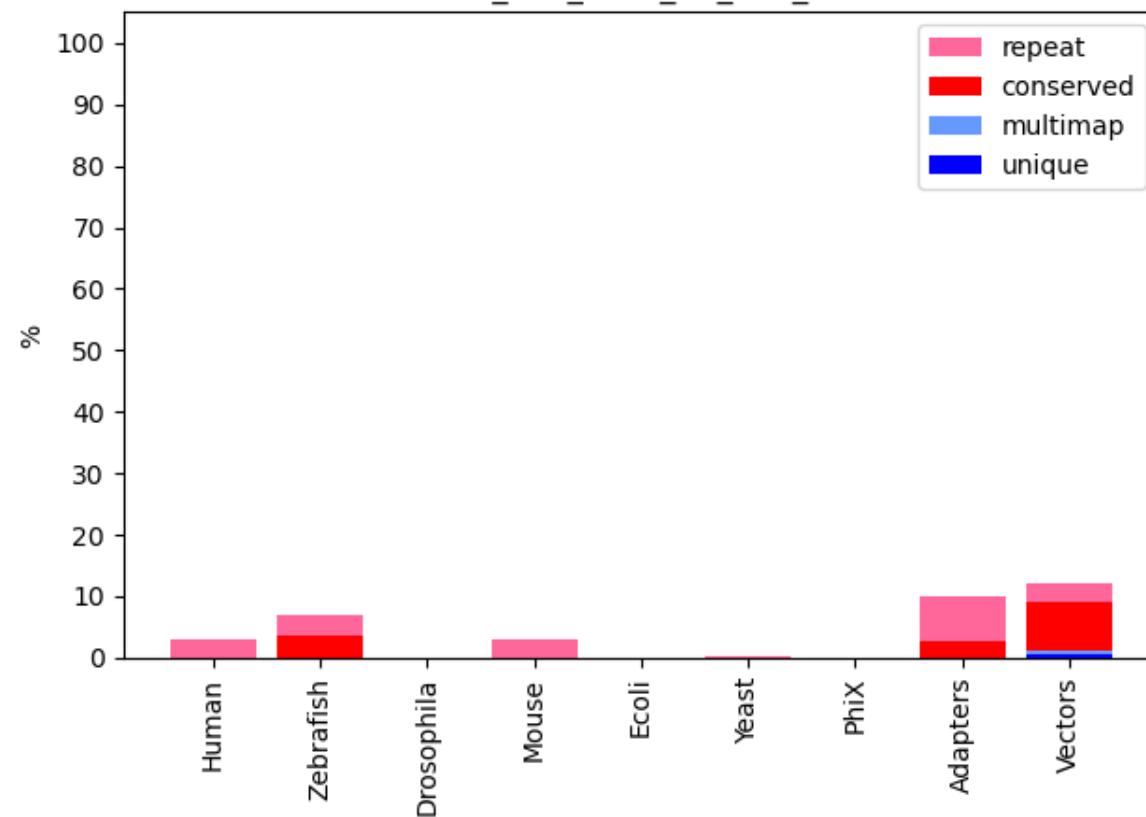
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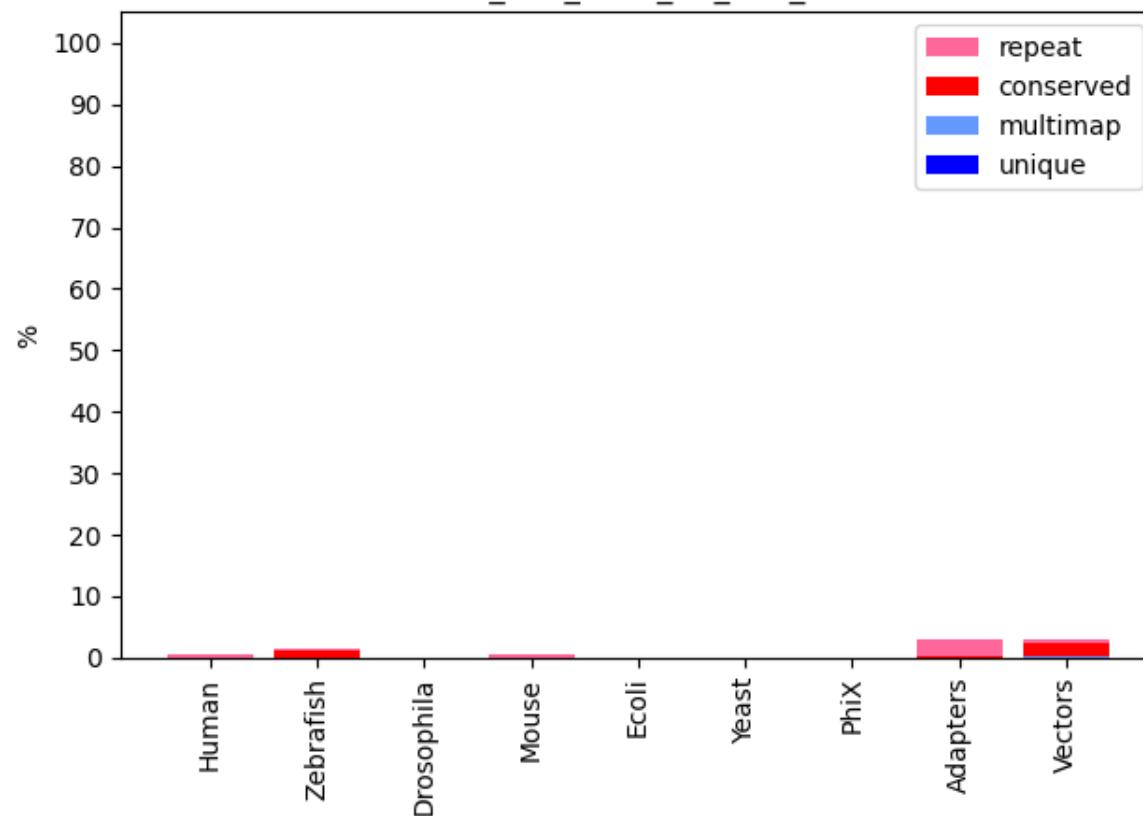
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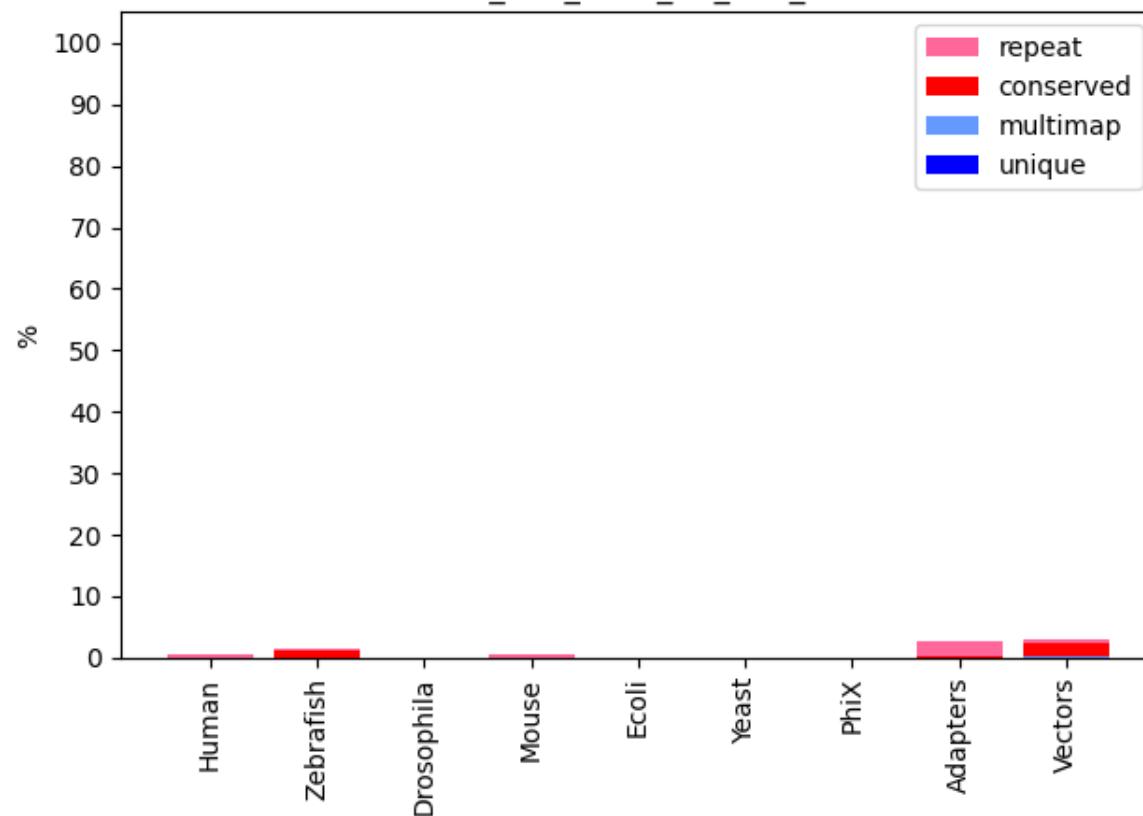
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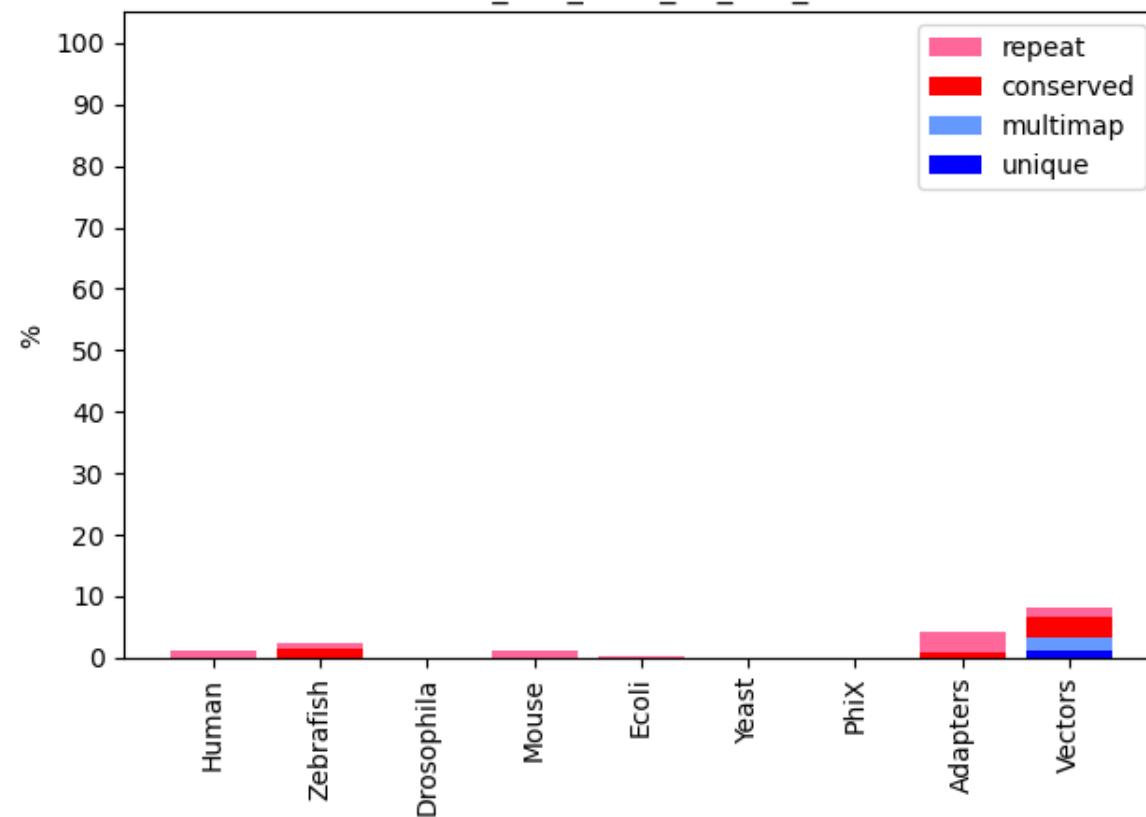
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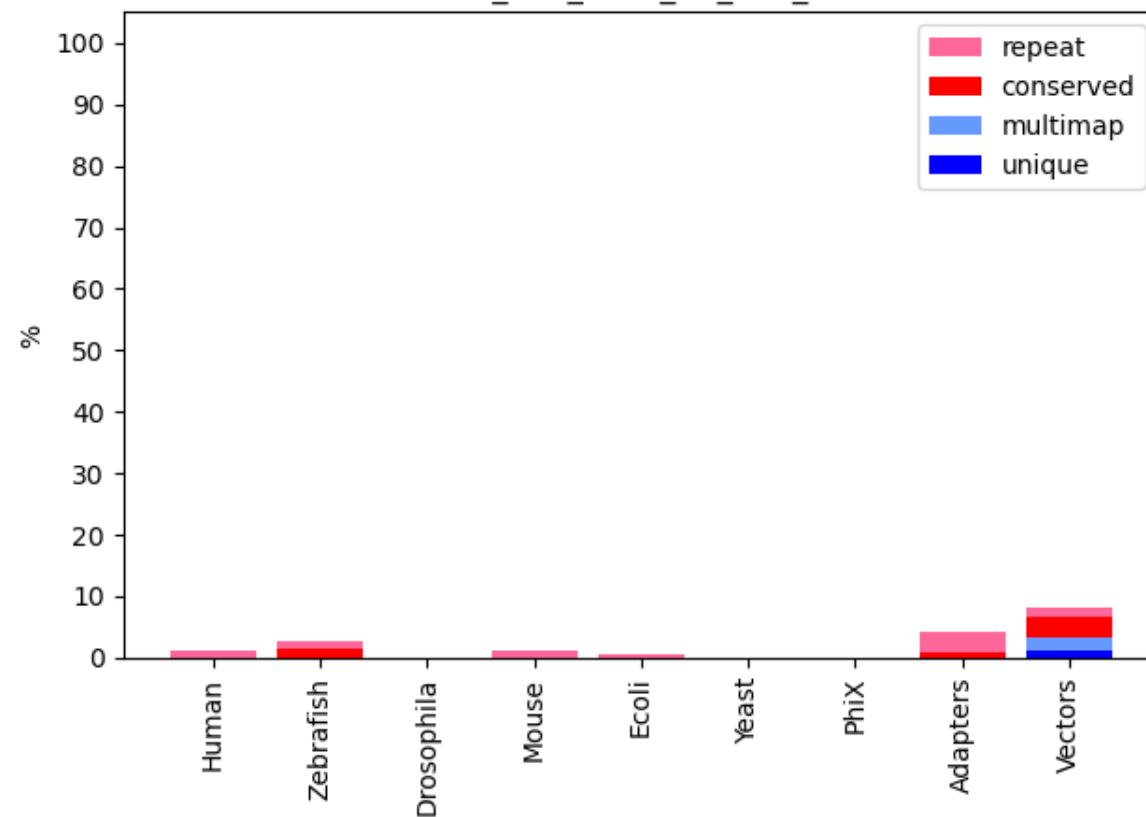
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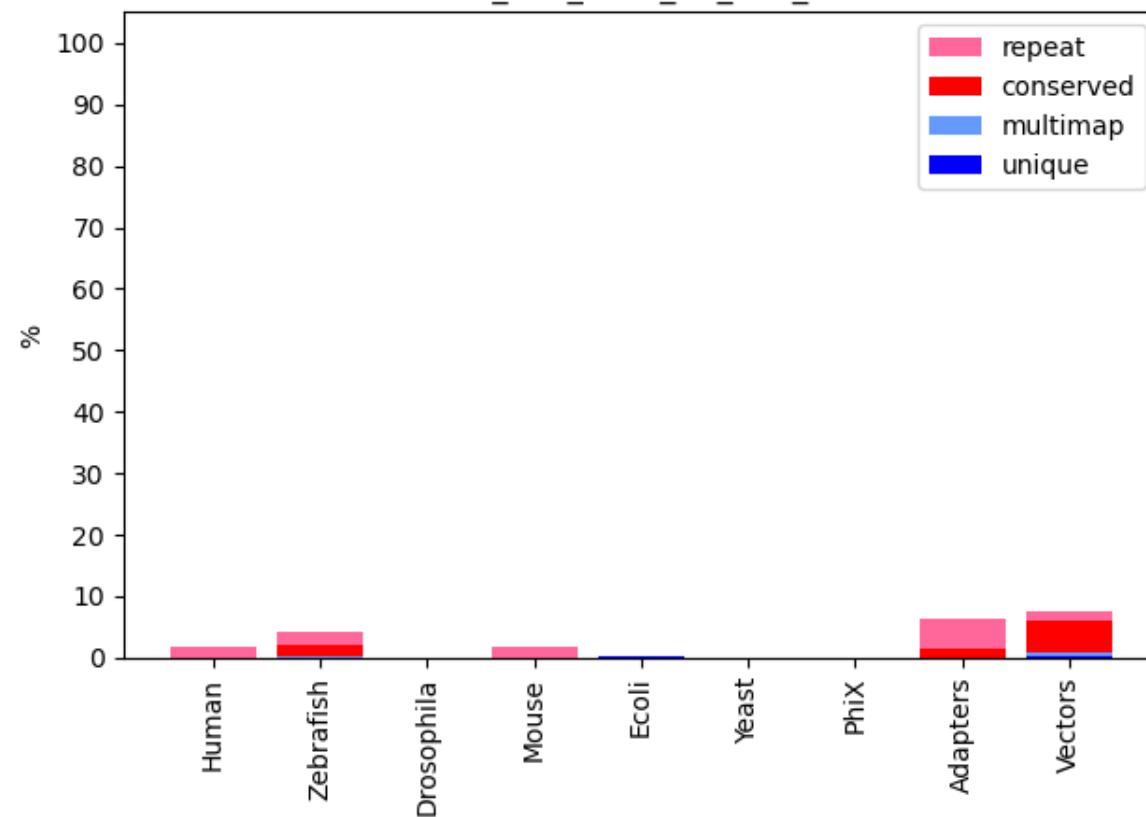
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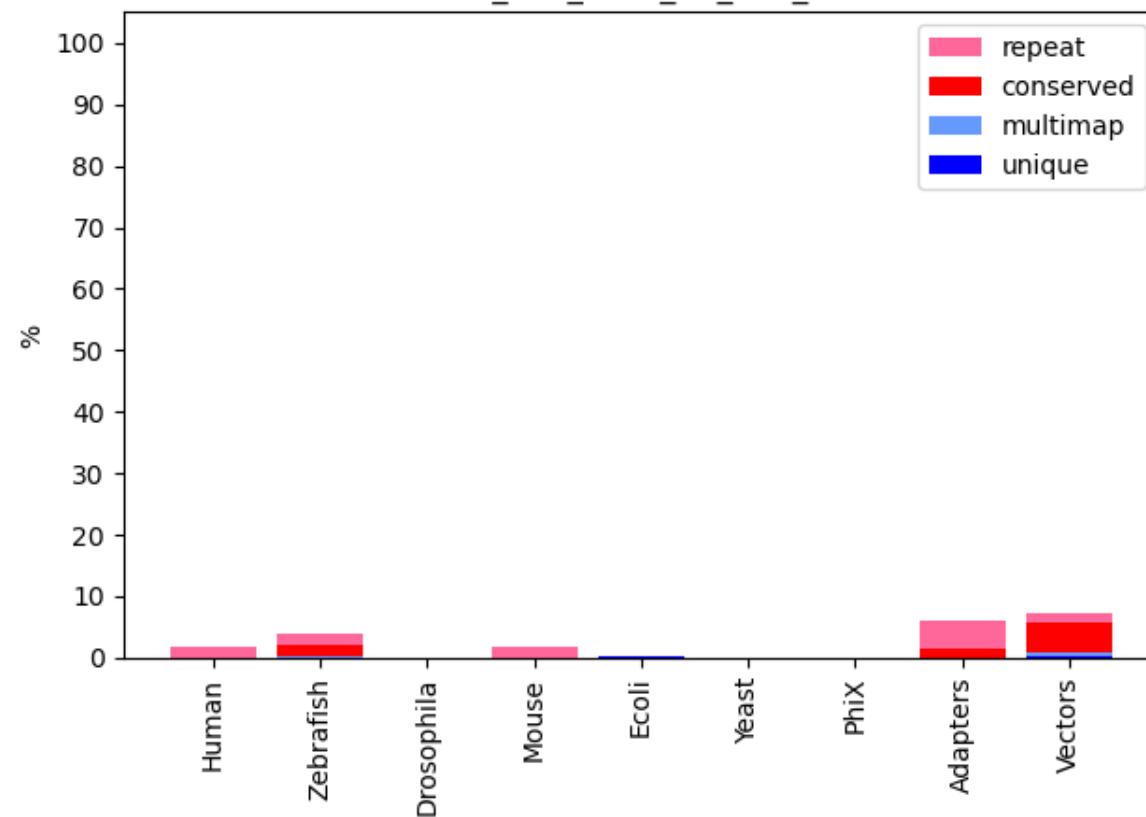
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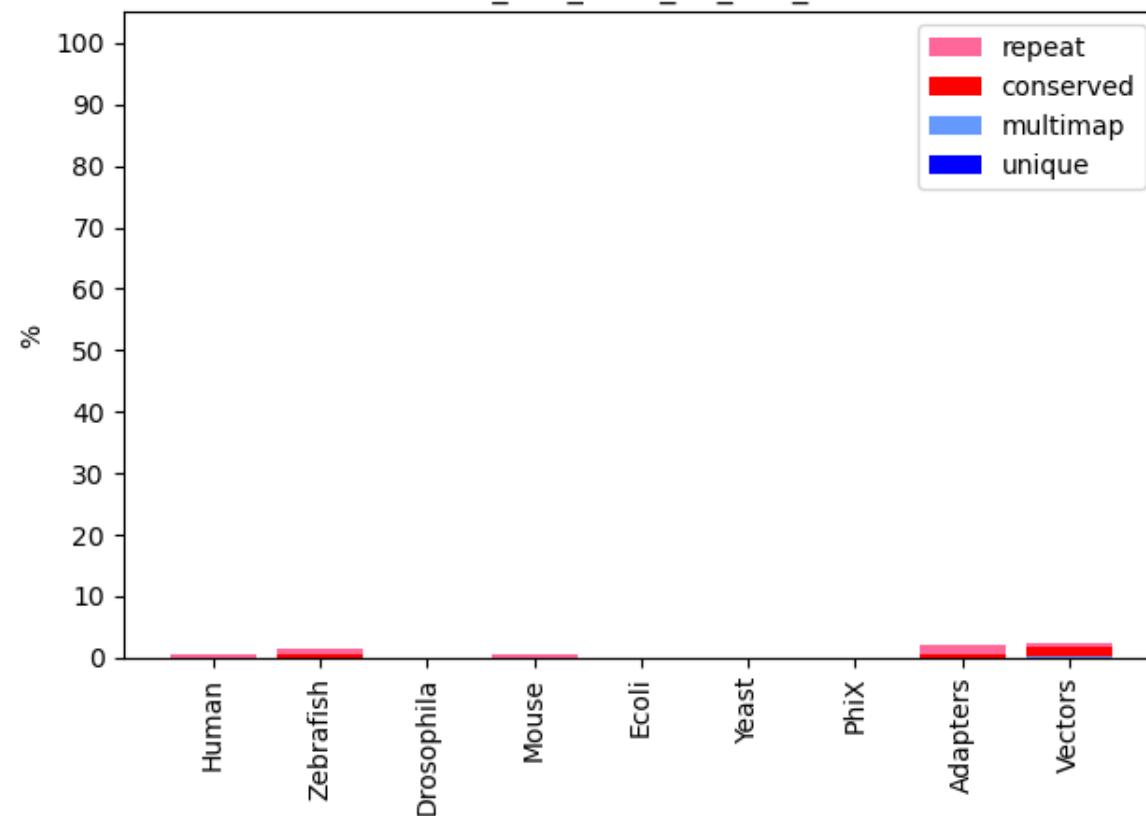
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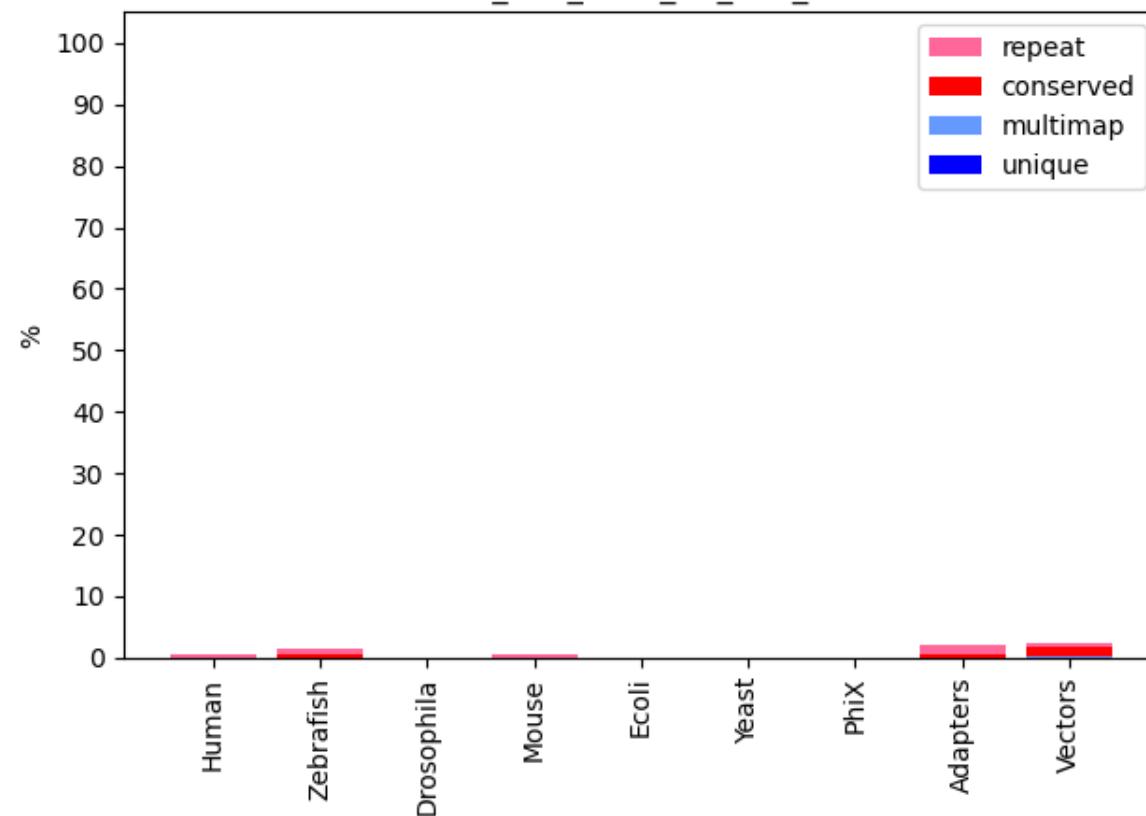
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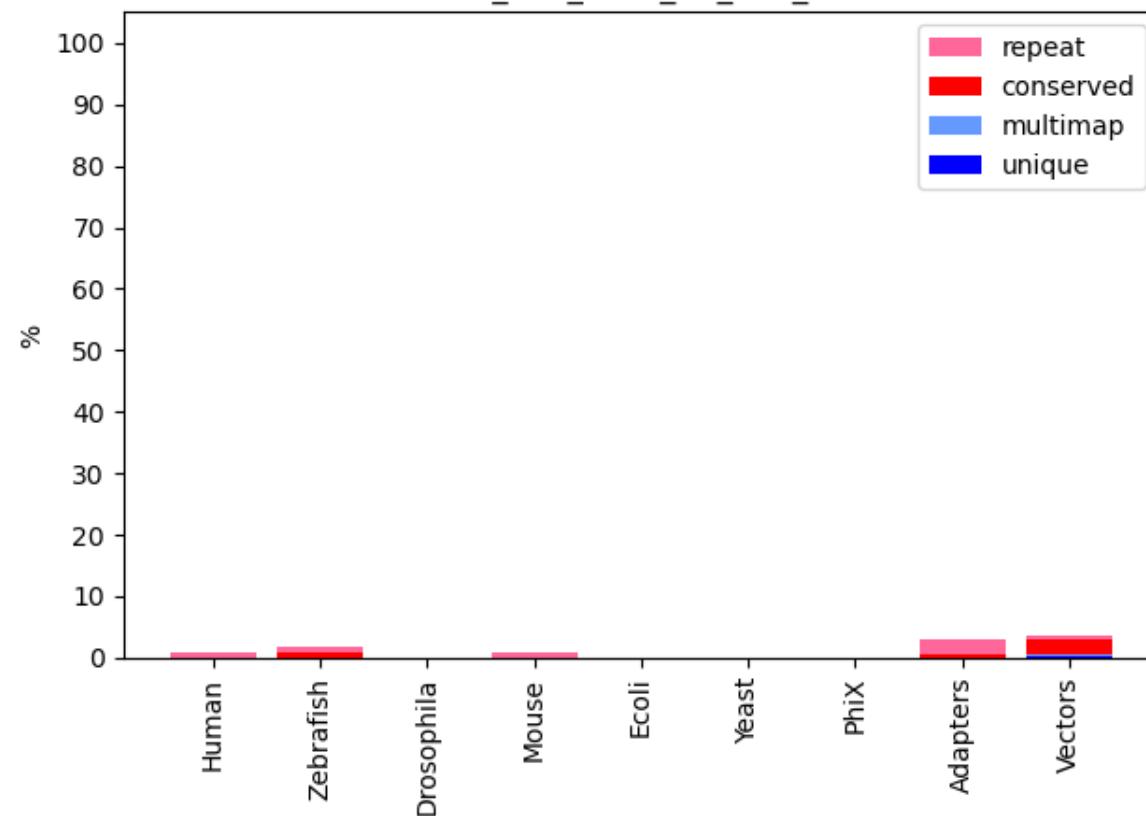
22L005082_S84_L001_R2_001_screen.txt



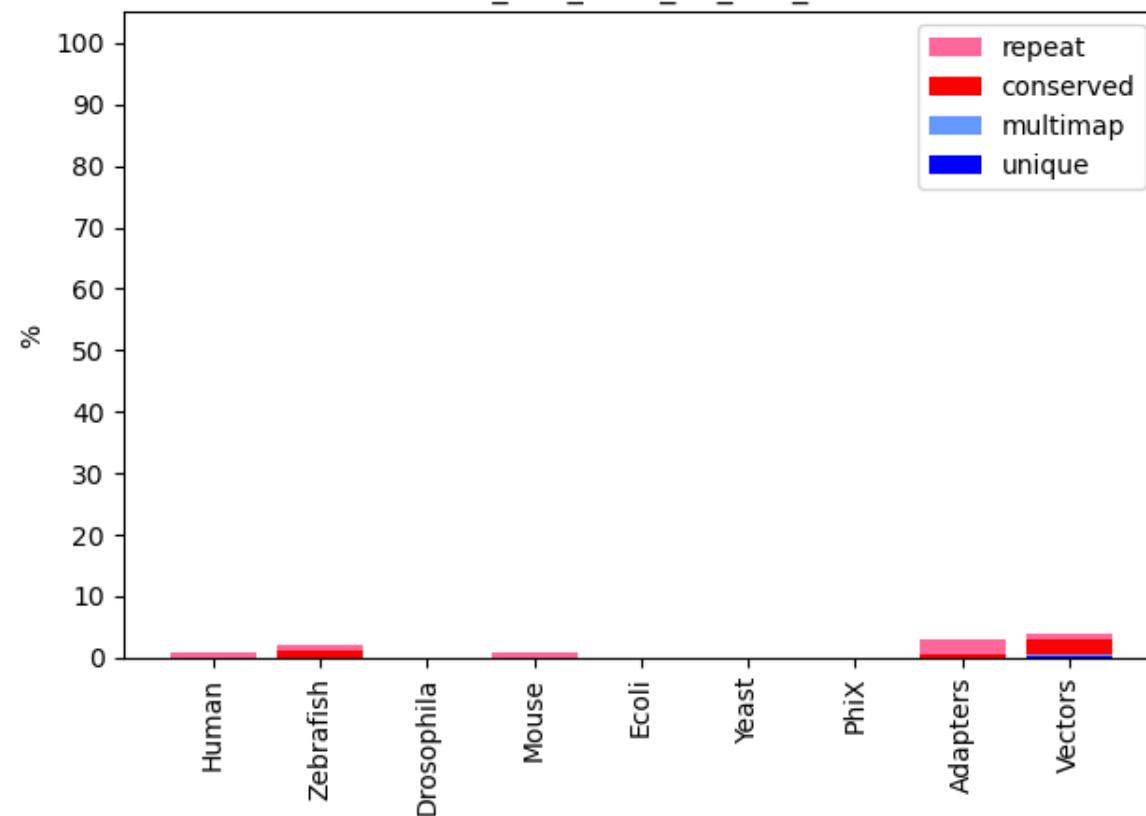
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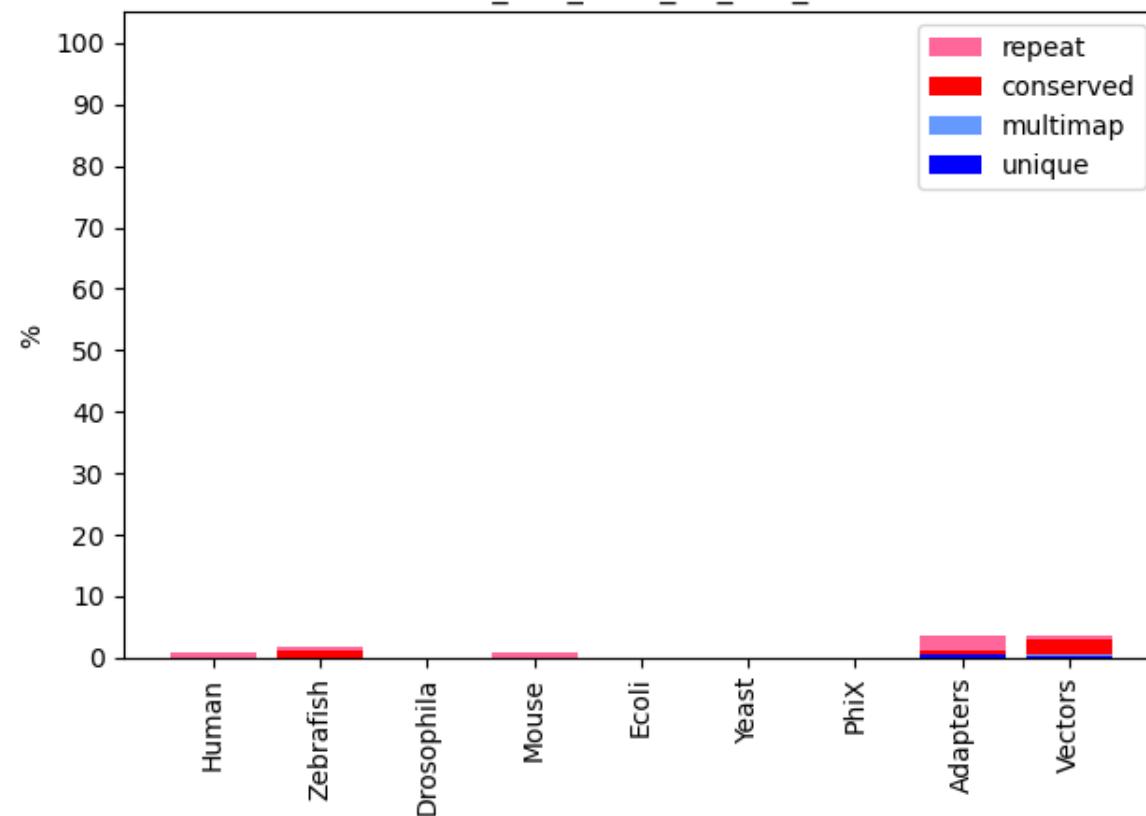
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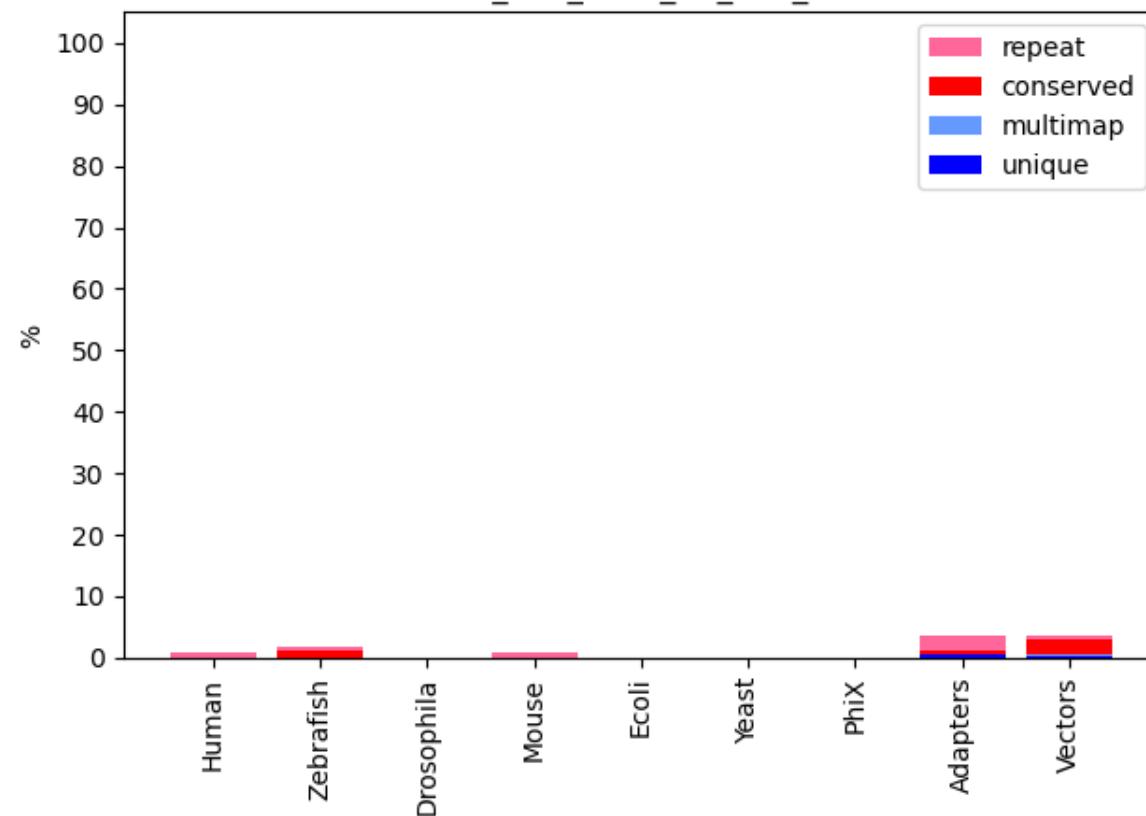
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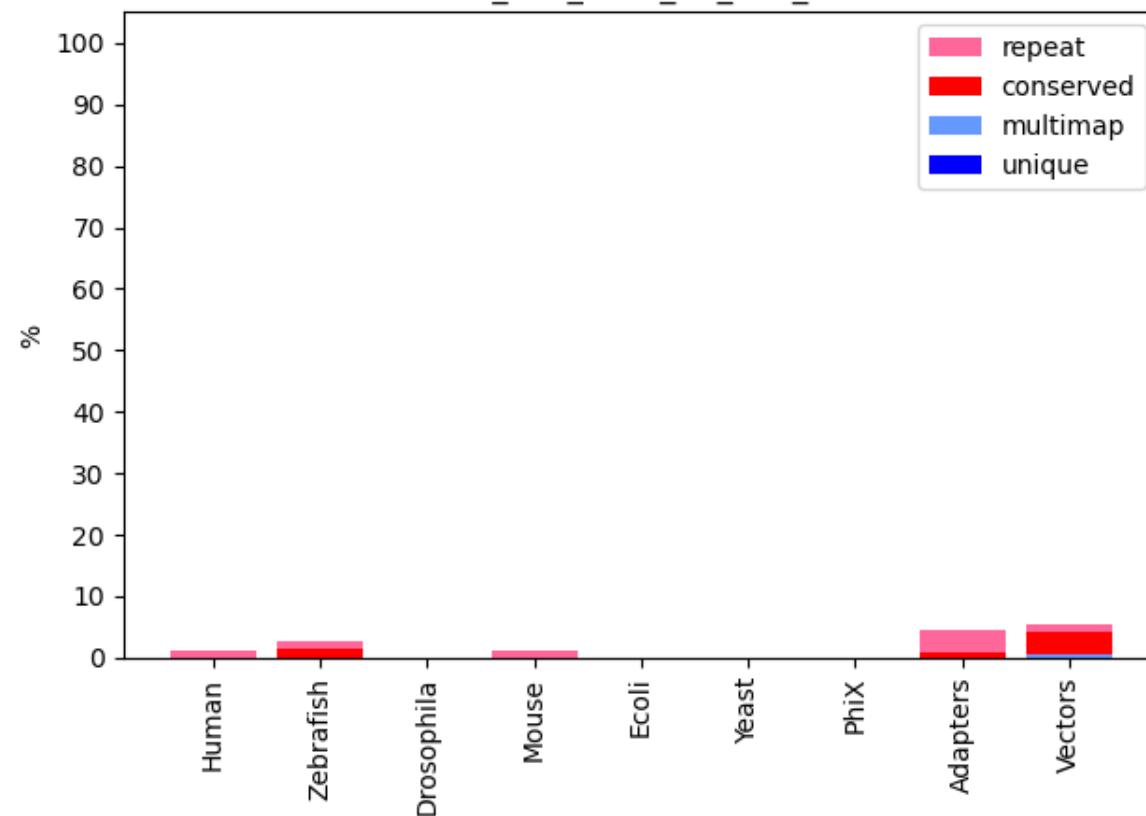
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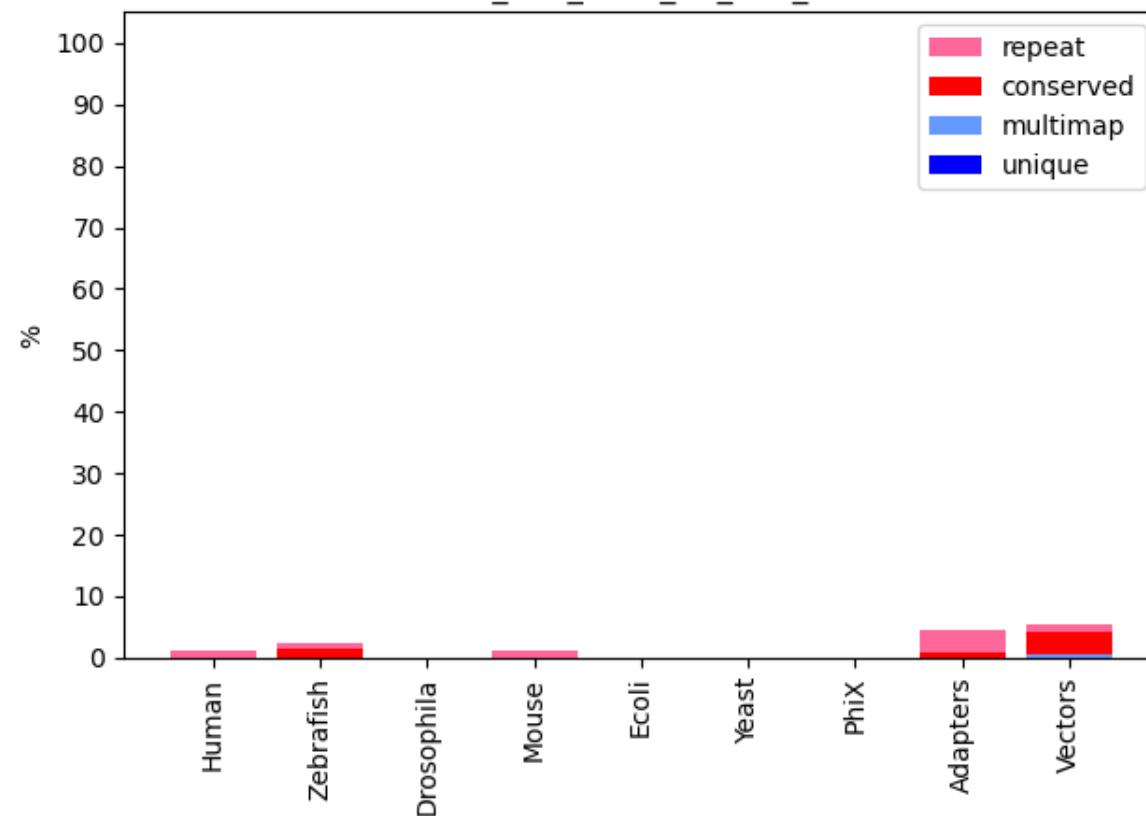
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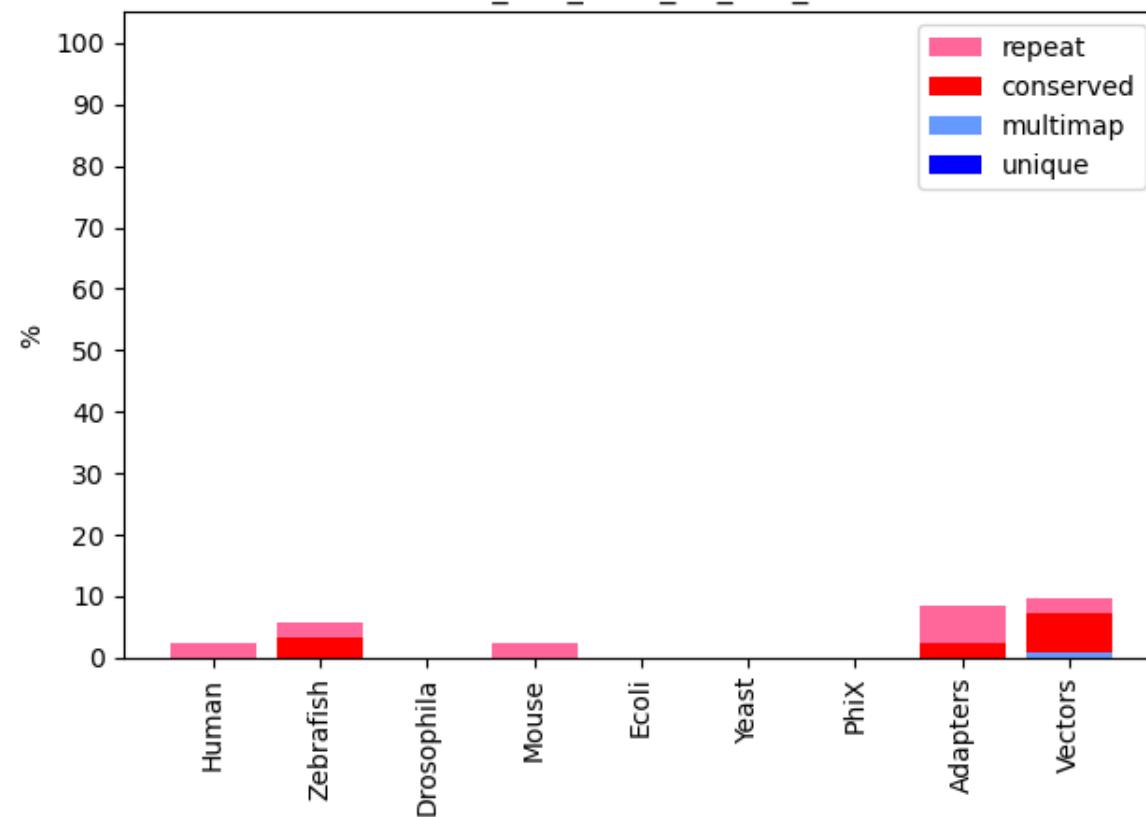
22L005085_S87_L001_R2_001_screen.txt



22L005085_S87_L002_R2_001_screen.txt



22L005086_S88_L001_R2_001_screen.txt



22L005086_S88_L002_R2_001_screen.txt

